

**Supplemental Table 2. List of 16,548 peptides of 1,174 identified nuclear proteins**

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GP:AB002330_1	H05	6580	2	1342.5	(+0.8)	3.100	0.284	0.964	1	K.L*YSIL*QGDSPTK#.W
GP:AB002330_1	H05	5556	2	1416.5	(-0.5)	2.543	0.328	0.899	1	R.TIQGHL*QSENFK#.Q
GP:AB002330_1	H08	6437	2	1322.5	(+0.2)	2.723	0.408	0.960	1	K.LYSILQGDSPTK.W
GP:AB007510_1	H03	8392	3	3181.5	(+0.6)	4.779	0.529	0.996	1	R.ASEM@AGPPQM@PNDFL*SFQDIATEAAHPIR.L
GP:AB007510_1	H03	10290	2	2084.4	(-0.5)	3.079	0.432	0.975	1	K.ATEPQMVLFNLYDDWLK.T
GP:AB007510_1	H03	6762	2	1417.5	(+0.1)	3.700	0.478	1.000	1	K.DGVWNL*QNEVTK#.E
GP:AB007510_1	H03	6738	2	1403.5	(+0.4)	3.394	0.384	0.990	1	K.DGVWNLQNEVTK.E
GP:AB007510_1	H03	7236	2	1604.9	(+0.7)	3.188	0.451	0.991	1	R.LIVDHNIADYMTAK.N
GP:AB007510_1	H03	4780	2	972.1	(+0.6)	2.848	0.222	0.951	1	K.NNVVINYK#.D
GP:AB007510_1	H03	9720	2	2751.0	(-1.0)	3.616	0.417	0.942	1	K.SQEPLPDDDEEFELPEFVEPFLK.D
GP:AB007510_1	H03	10926	2	2199.5	(-0.8)	2.768	0.358	0.791	1	R.TDMIQAL*GGVEGIL*EHTL*FK#.G
GP:AB007510_1	H04	10949	2	2173.5	(-0.1)	4.033	0.437	0.986	1	R.TDMIQALGGVEGILEHTLFGK.G
GP:AB007510_1	H04	10941	2	2199.5	(+0.3)	2.396	0.386	0.908	1	R.TDMIQAL*GGVEGIL*EHTL*FK#.G
GP:AB007510_1	H03	7700	2	1578.9	(+0.1)	2.367	0.278	0.784	1	K.VPGL*PTPIENM@IL*R.Y
GP:AB007510_1	H03	8714	2	1550.9	(+0.9)	2.203	0.301	0.860	1	K.VPGLPTPIENMILR.Y
GP:AB007510_1	H03	5912	3	2246.4	(+0.5)	4.611	0.368	0.997	1	R.YL*TEHPDPNNENIVGYNNK#.K
GP:AB007510_1	H05	5980	3	2246.4	(+0.1)	4.313	0.440	0.970	1	R.YL*TEHPDPNNENIVGYNNK#.K
GP:AB011126_1	H10	2229	2	1131.3	(+0.7)	3.081	0.373	0.988	5	K.LAEVSQNIK.L
GP:AB011126_1	H12	2050	2	1131.3	(+0.9)	3.616	0.412	0.994	5	K.LAEVSQNIK.L
GP:AB011126_1	H12	7440	2	2188.4	(-0.2)	2.494	0.330	0.882	5	K.SGFEPFGDIEFEDYTQPMK.R
GP:AB019494_1	H03	10892	2	1682.0	(+0.5)	4.102	0.491	1.000	1	R.AFLISLLNLFDDTAK.T
GP:AB019494_1	H03	10560	2	1533.8	(+0.0)	3.729	0.447	1.000	1	R.QLILEEIFTSLAR.L
GP:AB019494_1	H03	10566	2	1551.8	(+0.0)	3.242	0.330	0.957	1	R.QL*IL*EEIFTS*AR.L
GP:AB019494_1	H04	10545	2	1533.8	(+0.5)	2.788	0.396	0.982	1	R.QLILEEIFTSLAR.L
GP:AB023482_13	H03	8424	2	1393.7	(+0.8)	2.653	0.287	0.943	2	K.FSPIPFPLSYK.H
GP:AB023482_13	H03	8460	2	1407.7	(+0.4)	2.320	0.334	0.934	2	K.FSPIPFPL*SYK#.H
GP:AB023482_13	H03	8660	2	1421.6	(+1.0)	2.799	0.431	0.989	2	R.FTLWWSPTINR.A
GP:AB023482_13	H03	8624	2	1427.6	(+0.7)	2.785	0.454	0.990	2	R.FTL*WWSPTINR.A
GP:AB023482_13	H05	8612	2	1427.6	(+1.0)	2.435	0.409	0.978	2	R.FTL*WWSPTINR.A
GP:AB023482_13	H04	9197	2	1776.0	(+0.2)	3.438	0.450	0.977	2	K.GTYFPTWEGFL*FWEK#.A
GP:AB023482_13	H04	9193	2	1762.0	(+0.4)	3.230	0.397	0.985	2	K.GTYFPTWEGFL*FWEK#.A
GP:AB023482_13	H05	9314	2	1762.0	(+0.2)	2.822	0.289	0.896	2	K.GTYFPTWEGFL*FWEK#.A
GP:AB023482_13	H05	9310	2	1776.0	(-0.3)	2.711	0.323	0.879	2	K.GTYFPTWEGFL*FWEK#.A
GP:AB023482_13	H03	8236	2	1510.6	(-0.5)	2.562	0.306	0.893	2	R.L*TL*EDL*EDSWDR.G
GP:AB023482_13	H03	7990	2	1666.8	(+0.8)	2.220	0.311	0.906	2	R.RL*TL*EDL*EDSWDR.G
GP:AB023482_13	H03	7906	2	1354.6	(+0.6)	3.335	0.386	0.989	2	R.TILQHLSEAWR.C
GP:AB023482_13	H04	7781	2	1354.6	(+0.2)	2.672	0.371	0.953	2	R.TILQHLSEAWR.C
GP:AB023482_13	H05	8214	2	1510.6	(+0.3)	2.234	0.496	0.967	2	R.L*TL*EDL*EDSWDR.G
GP:AB032251_1	H01	5372	2	1166.2	(+0.6)	2.721	0.445	0.988	1	K.GNDFFIDDSK#.L
GP:AB032251_1	H02	5724	2	1561.8	(-0.2)	2.530	0.401	0.940	1	K.LSTPSTGGSVDIISVK.E
GP:AB032251_1	H02	4658	2	1385.5	(+0.4)	2.982	0.396	0.964	1	K.VGSPATVTFQQNK#.N
GP:AB032251_1	H02	5560	2	1166.2	(+0.8)	2.429	0.344	0.929	1	K.GNDFFIDDSK#.L
GP:AB032976_1	H09	5319	3	1731.9	(+0.8)	4.100	0.314	0.960	1	K.L*PSRPGAQGVPEQNL*R.T
GP:AB032976_1	H09	5561	2	2005.2	(-0.3)	3.612	0.506	1.000	1	R.L*QQQAAL*SPTTAPAVSSVSK#.Q
GP:AB043584_1	H05	8224	2	1710.9	(-0.0)	2.606	0.321	0.890	1	R.GGGFAPGTEPFPGL*FPR.K
GP:AB043584_1	H06	8142	2	1710.9	(+0.4)	3.553	0.497	0.999	1	R.GGGFAPGTEPFPGL*FPR.K
GP:AB043584_1	H06	8132	2	1704.9	(+0.5)	3.212	0.414	0.988	1	R.GGGFAPGTEPFPGL*FPR.K
GP:AB043584_1	H06	6378	2	1600.8	(+0.3)	3.392	0.479	0.986	1	R.IYL*EPGPASSL*TPR.L
GP:AB043584_1	H06	6738	2	1687.9	(-0.0)	2.973	0.431	0.972	1	R.L*NPM@AIDSPAMDFSR.R
GP:AB043584_1	H06	8344	2	2118.5	(+0.8)	3.939	0.499	0.999	1	K.VMENVGLGALPQYGELLADK.Q
GP:AB043584_1	H06	2060	2	1572.7	(+0.7)	2.241	0.336	0.917	1	R.EL*AGNSSTPPPSPGR.G
GP:AB058697_1	H05	7242	3	2383.5	(+0.9)	4.078	0.436	0.999	2	R.DL*SQDIHGHL*GDIDQDVEVEK#.T
GP:AB058697_1	H05	7174	2	1456.7	(+0.5)	2.646	0.389	0.979	2	K.IFSAVQQFYQPK.I
GP:AB058697_1	H05	8430	2	1825.0	(+0.0)	2.315	0.317	0.828	2	R.SLLNLLSSQEEDFNSK.E
GP:AB058721_1	H04	2073	2	1614.8	(+0.4)	3.087	0.385	0.980		K.AIQPQAAQGPAAVQK#.I
GP:AB058721_1	H02	5602	2	1463.7	(+0.6)	2.510	0.428	0.980	1	K.TQFLTTPISQAQK.L

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GP:AB058721_1	H04	6153	2	1477.7	(-0.1)	2.236	0.232	0.587	1	K.TQFL*TPISQAQK#.L
GP:AB065003_1	H05	7550	3	2581.6	(+0.4)	5.720	0.528	1.000	2	K.L*EFFGFEDHETGGDEGGSGSSNYK#.I
GP:AB065003_1	H05	7554	3	2567.6	(+0.3)	5.407	0.453	0.994	2	K.LEFFGFEDHETGGDEGGSGSSNYK.I
GP:AB065003_1	H05	8576	2	1763.9	(+0.9)	2.780	0.519	0.990	2	R.TGL*FEWDNDFDIR.S
GP:AB088099_1	H03	8562	3	2147.7	(+1.0)	3.759	0.426	0.991	2	K.HLAPPPLLSPLLPSIKPTVR.K
GP:AB088099_1	H03	4924	3	2249.4	(+0.5)	3.874	0.459	0.999	2	K.L*EPSTSTDQPVTPPEPTSQATR.G
GP:AB088099_1	H03	5680	2	1168.3	(+0.6)	2.729	0.448	0.988	2	K.TPETL*VPTAPK#.L
GP:AB088099_1	H03	5056	2	1105.2	(-0.3)	2.585	0.217	0.810	2	R.GPL*TVEETPR.V
GP:AC004893_1	H02	4094	2	1251.3	(+0.6)	3.155	0.470	0.993	2	R.DETLSPGSELTAK.L
GP:AC004893_1	H02	8586	2	1619.0	(+0.7)	3.242	0.411	0.989	2	R.KNFIQAILTSLIEK.S
GP:AC004893_1	H02	9167	2	1490.8	(+0.9)	4.667	0.484	0.999	2	K.NFIQAILTSLIEK.S
GP:AC004893_1	H03	11144	2	1510.8	(-0.0)	3.544	0.381	0.976	2	K.NFIQAIL*TSL*IEK#.S
GP:AC004893_1	H03	11136	2	1490.8	(+0.4)	3.475	0.411	0.989	2	K.NFIQAILTSLIEK.S
GP:AC004893_1	H04	11175	2	1510.8	(-0.1)	3.061	0.304	0.924	2	K.NFIQAIL*TSL*IEK#.S
GP:AC004893_1	H04	11177	2	1490.8	(-0.7)	2.937	0.340	0.841	2	K.NFIQAILTSLIEK.S
GP:AC004893_1	H04	8389	2	1250.5	(+0.5)	2.588	0.369	0.975	2	K.L*L*L*NL*ISQVGR.V
GP:AF057299_1	H04	6629	2	1265.4	(-0.1)	2.351	0.361	0.927	1	K.GYEEEEIIHFK.K
GP:AF057299_1	H05	6886	2	1273.4	(+0.4)	2.669	0.463	0.989	1	K.GYEEEEIIHFK#.K
GP:AF057299_1	H05	5096	2	1102.2	(+0.6)	2.548	0.212	0.894	1	K.L*EENIDNIK#.R
GP:AF057299_1	H05	6154	2	1205.4	(+0.6)	2.332	0.245	0.872	1	K.MEIVISL*QNEK#.A
GP:AF057299_1	H05	4852	2	1031.2	(+0.5)	3.025	0.134	0.864	1	K.SELLVEQGR.L
GP:AF057299_1	H05	4802	2	1043.2	(+0.6)	2.680	0.338	0.977	1	K.SEL*L*VEQGR.L
GP:AF057299_1	H04	8951	3	2085.3	(+0.8)	4.706	0.448	0.981	1	R.VFQTEAEL*QEVIDSL*QSK#.L
GP:AF057299_1	H05	9072	3	2085.3	(+0.7)	4.171	0.412	0.879	1	R.VFQTEAEL*QEVIDSL*QSK#.L
GP:AF057299_1	H05	7046	2	1177.3	(+0.2)	2.369	0.235	0.801	1	R.WL*QDNL*TL*R.K
GP:AF057299_1	H05	5966	2	1437.5	(-0.3)	3.095	0.407	0.976	1	K.YEL*QQL*EGSSDR.I
GP:AF057299_1	H05	5982	2	1214.4	(+0.8)	2.262	0.338	0.931	1	R.DVNGELIAVQR.S
GP:AF078849_1	H10	10303	2	1927.2	(+0.4)	4.124	0.451	1.000		K.AGATSEGVLANFFNSLLSK.K
GP:AF078849_1	H10	2475	2	1887.1	(-0.1)	3.830	0.542	0.956		R.KPVTVSPTTPTSPTTEGEAS.-
GP:AF078849_1	H10	2469	2	1895.1	(-0.3)	3.616	0.415	0.982		R.K#PVTVSPTTPTSPTTEGEAS.-
GP:AF078849_1	H10	5795	2	1595.8	(+0.3)	3.514	0.549	1.000		R.SVSSNVA SVSPIAGSK#.K
GP:AF078849_1	H10	10337	2	1927.2	(-1.0)	2.871	0.362	0.836		K.AGATSEGVLANFFNSLLSK.K
GP:AF113534_1	H08	7687	2	1602.8	(+0.8)	3.624	0.496	0.999		K.TIPSWATLSASQLAR.A
GP:AF113534_1	H08	4491	2	909.0	(+1.0)	2.555	0.344	0.955	1	K.GASGTFQLK.K
GP:AF177387_1	H04	4331	2	1080.1	(+1.0)	2.978	0.407	0.989	5	R.AEDNFNLEK.E
GP:AF177387_1	H04	4143	2	1456.5	(+0.0)	3.736	0.524	0.998	6	K.SEDSSGAAGL*SGL*HR.T
GP:AF177387_1	H04	3963	2	1444.5	(+0.8)	3.545	0.587	1.000	6	K.SEDSSGAAGLSGLHR.T
GP:AF177387_1	H04	4127	2	1444.5	(+1.0)	3.496	0.500	1.000	6	K.SEDSSGAAGLSGLHR.T
GP:AF177387_1	H04	4057	2	1456.5	(+0.1)	3.462	0.473	0.986	6	K.SEDSSGAAGL*SGL*HR.T
GP:AF177387_1	H04	3981	2	1456.5	(-0.5)	2.890	0.465	0.977	6	K.SEDSSGAAGL*SGL*HR.T
GP:AF177387_1	H04	3905	2	1456.5	(-0.2)	2.577	0.342	0.906	6	K.SEDSSGAAGL*SGL*HR.T
GP:AF177387_1	H04	4377	2	1094.1	(+0.3)	2.549	0.262	0.870	5	R.AEDNFNL*EK#.E
GP:AF231056_1	H03	4362	3	2556.6	(+0.9)	4.130	0.567	0.997		K.ELQDGAESNGGGGGGAGSGGGPGAEPDLK.N
GP:AF231056_1	H03	4776	3	3103.2	(+0.1)	5.317	0.523	1.000		R.GGTPGSGAAAAAGSK#PPSSSSASASSSSSSFAQQR.F
GP:AF231056_1	H03	4754	3	3095.2	(-0.1)	4.861	0.544	1.000		R.GGTPGSGAAAAAGSKPPSSSSASASSSSSSFAQQR.F
GP:AF231056_1	H03	4868	2	1997.0	(-0.8)	4.421	0.562	0.999	1	R.GYQGYPGDYSGGPQDGGAGK#.G
GP:AF231056_1	H03	4862	2	1989.0	(-0.8)	4.256	0.556	0.995	1	R.GYQGYPGDYSGGPQDGGAGK.G
GP:AF231056_1	H03	7852	3	3314.7	(+0.3)	3.915	0.413	0.995		R.FGAMGGGGPSAAGGGTPQPTATPTLNQLLTSPSSAR.G
GP:AF385437_1	H01	4742	2	1275.4	(+0.8)	2.370	0.417	0.976	1	K.ESGPSGIETELR.S
GP:AF385437_1	H01	7430	2	1613.0	(+0.8)	3.271	0.493	0.983	1	K.SAPFFIPTIPGLVPR.Y
GP:AF385437_1	H01	7434	2	1619.0	(+0.3)	3.096	0.364	0.957	1	K.SAPFFIPTIPGL*VPR.Y
GP:AF385437_1	H02	7634	2	1613.0	(+0.8)	3.528	0.470	0.990	1	K.SAPFFIPTIPGLVPR.Y
GP:AF385437_1	H02	7632	2	1619.0	(+0.3)	2.724	0.406	0.955	1	K.SAPFFIPTIPGL*VPR.Y
GP:AF385437_1	H02	5752	2	1061.3	(+0.2)	3.001	0.466	0.983	1	K.VVNL*GVL*AQK#.S
GP:AF385437_1	H02	4740	2	939.1	(+0.9)	2.665	0.247	0.946	1	K.SLGHGLINK.K
GP:AF418569_1	H04	8663	2	1401.7	(+0.8)	3.986	0.489	1.000	3	R.AELVQLVSPFLGK.F

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GP:AF418569_1	H05	8768	2	1401.7	(+1.0)	4.159	0.498	1.000	3	R.AELVQLVSPFLGK.F
GP:AF418569_1	H05	8762	2	1427.7	(-0.0)	3.094	0.365	0.959	3	R.AEL*VQL*VSPFL*GK#.F
GP:AF418569_1	H05	6694	2	1309.4	(-0.0)	3.677	0.440	1.000	3	K.HGGGTESTL*FFDK#.V
GP:AF418569_1	H05	6708	2	1295.4	(+0.5)	3.509	0.527	1.000	3	K.HGGGTESTLFFDK.V
GP:AF418569_1	H05	8078	2	1621.9	(+0.7)	4.618	0.509	1.000	3	R.LKVEDALSYLDQVK.L
GP:AF418569_1	H05	9094	2	2164.4	(-0.2)	3.866	0.494	1.000	3	K.L*QFGSQPQVYNDFL*DIMK#.E
GP:AF418569_1	H05	5660	2	1159.3	(+0.6)	2.550	0.160*	0.357	3	K.SLDHQGINFK.Q
GP:AF418569_1	H04	8933	2	1581.7	(+0.7)	3.987	0.456	1.000	3	K.SLLNEIESIYDER.Q
GP:AF418569_1	H04	8935	2	1593.7	(+0.1)	3.704	0.410	0.984	3	K.SL*L*NEIESIYDER.Q
GP:AF418569_1	H05	9040	2	1581.7	(+0.7)	3.900	0.392	0.993	3	K.SLLNEIESIYDER.Q
GP:AF418569_1	H05	5654	2	1173.3	(-0.1)	2.360	0.256*	0.122	3	K.SL*DHQGINFK#.Q
GP:AJ564104_1	H01	5576	2	1402.5	(+0.7)	2.654	0.294	0.949		K.LQDLEELQKSK.E
GP:AJ564104_1	H01	5118	2	1179.3	(+0.8)	3.025	0.367*	0.598		K.YQELQITAGR.H
GP:AJ564104_1	H11	2002	2	1061.1	(+0.0)	2.502	0.212*	0.216		R.QLLEGEESR.M
GP:AK022932_1	H04	8313	2	1573.9	(+1.0)	2.325	0.250	0.766		R.GATALEMGMPLLLQK.Q
GP:AK022932_1	H04	7765	3	1881.1	(+0.4)	4.138	0.441	0.999		K.HANTLITAVHDSFVAVGK.D
GP:AK022932_1	H03	10150	2	1911.2	(+0.5)	4.161	0.402	0.993		R.SGSFINSLLQLEELGFR.S
GP:AK022932_1	H06	10094	2	1911.2	(+0.2)	2.776	0.216	0.768		R.SGSFINSLLQLEELGFR.S
GP:AK075287_1	H18	7398	3	2870.0	(-0.6)	4.542	0.426	0.994		K.EQVHQGGVEL*QQL*EAGL*QEAGEEDTR.L
GP:AK075287_1	H18	6114	3	2263.5	(+0.9)	5.114	0.317	0.993		K.GIHHGPSVAQPIHL*DSTQL*SR.K
GP:AK075287_1	H18	7402	3	2852.0	(+0.4)	3.987	0.423	0.999		K.EQVHQGGVELQQLQLEAGLQEAGEEDTR.L
GP:AK091153_1	H02	5550	2	1676.8	(-0.2)	3.456	0.447	0.976	1	K.VDIEGPDVNIPEGPK#.L
GP:AK091153_1	H03	6390	2	1676.8	(-0.2)	4.359	0.524	0.995	1	K.VDIEGPDVNIPEGPK#.L
GP:AK091153_1	H03	6552	3	1927.1	(+0.8)	4.027	0.319	0.994		K.GPHVDVSGPDDIEGPEPK#.L
GP:AK092642_1	H19	8326	2	1497.7	(+1.0)	3.955	0.384	0.990	1	R.FDGLLGFPGGFVDR.R
GP:AK092642_1	H19	8310	2	1509.7	(+0.2)	2.801	0.367	0.946	1	R.FDGL*L*GFPGGFVDR.R
GP:AK092642_1	H19	7054	2	1249.4	(+1.0)	2.675	0.375	0.981	1	R.FWSL*EDGL*NR.V
GP:AK095745_1	H13	10026	2	2184.4	(-0.0)	2.731	0.487	0.974		K.NSEVYQEVQAMFDTL*GIPK#.S
GP:AK095745_1	H13	6988	2	1311.6	(-0.4)	2.494	0.230	0.759		K.TTITMAHL*L*AAR.E
GP:AK095745_1	H13	5340	2	1575.7	(-0.2)	2.397	0.212	0.662		K.MDL*NSEQAEQL*ER.I
GP:AL832200_1	H04	8159	3	2419.8	(+1.0)	5.032	0.554	0.999		R.AIPLPIQMYQQQPVSTSVVR.V
GP:AL832200_1	H04	5235	3	2550.8	(+0.7)	5.176	0.467	0.998		R.IPQNPSPTHQQQNAPVTVIQSK.A
GP:AL832200_1	H04	8871	3	2253.4	(+1.0)	4.622	0.491	1.000		K.SHEGTSGEWIWESLFHPPR.K
GP:AL834470_1	H06	6558	2	1541.8	(+0.7)	3.124	0.433	0.990		R.KVVVVVPNEEDWK.K
GP:AL834470_1	H06	7666	2	1620.9	(+0.2)	2.462	0.297	0.843		R.YNVL*GAETVL*NQMR.M
GP:AY278023_1	H09	5235	2	1318.5	(+0.2)	2.691	0.364	0.391	1	R.YPL*AAAAERPPR.L
GP:AY278023_1	H09	4963	2	1109.2	(+0.6)	2.449	0.235	0.908	1	K.L*EEPEL*NR.Q
GP:BC039843_1	H05	6972	3	2827.1	(+0.2)	4.165	0.314	0.856	1	K.ASHHIYPYSSSQDDEEWL*RPVM@R.K
GP:BC039843_1	H05	8098	2	2023.3	(+0.5)	3.274	0.589	1.000	1	K.DMEDPTVPNIEEVLPK.N
GP:BC039843_1	H05	6954	2	1416.6	(+0.8)	2.680	0.344	0.550	1	K.EKPVDLQNFGLR.T
GP:BC039843_1	H05	5086	2	977.1	(+0.2)	2.617	0.321	0.948	1	R.FDLQNPSR.M
GP:BC039843_1	H05	1580	2	1244.4	(+0.6)	2.765	0.368	0.980	1	K.KYVHADAPTNK.T
GP:BC039843_1	H05	1576	2	1260.4	(-0.2)	2.454	0.411	0.949	1	K.K#YVHADAPTNK#.T
GP:BC039843_1	H05	5562	2	1295.5	(+0.3)	2.590	0.159	0.658	1	R.NVEM@FM@NIEK#.T
GP:BC039843_1	H05	5260	2	1133.3	(+1.0)	3.159	0.289	0.982	1	R.RFDLQNPSR.M
GP:BC039843_1	H06	4716	2	1133.3	(+0.9)	2.595	0.262	0.937	1	R.RFDLQNPSR.M
GP:BC039843_1	H05	1620	2	1579.6	(+0.8)	3.436	0.405	0.808	1	R.SQKEEDEQEDLTK.D
GP:BC039843_1	H05	1624	2	1601.6	(-0.3)	3.236	0.305	0.381	1	R.SQK#EEDEQEDL*TK#.D
GP:BC039843_1	H05	11330	3	2078.4	(+0.8)	5.362	0.534	0.999	1	K.TLAGLVVQLLQFQEDAFGK.H
GP:BC039843_1	H05	11328	3	2110.4	(+0.2)	3.889	0.399	0.977	1	K.TL*AGL*VVQL*L*QFQEDAFGK#.H
GP:BC039843_1	H05	11336	2	2110.4	(-0.4)	3.683	0.510	1.000	1	K.TL*AGL*VVQL*L*QFQEDAFGK#.H
GP:BC039843_1	H05	11334	2	2078.4	(-0.5)	2.866	0.399	0.960	1	K.TLAGLVVQLLQFQEDAFGK.H
GP:BC039843_1	H06	11314	3	2110.4	(+0.6)	4.336	0.501	1.000	1	K.TL*AGL*VVQL*L*QFQEDAFGK#.H
GP:BC039843_1	H06	11320	2	2078.4	(+0.2)	4.262	0.518	1.000	1	K.TLAGLVVQLLQFQEDAFGK.H
GP:BC039843_1	H06	11324	2	2110.4	(+0.8)	3.118	0.339	0.973	1	K.TL*AGL*VVQL*L*QFQEDAFGK#.H
GP:BC039843_1	H09	11443	3	2110.4	(+0.5)	4.338	0.534	1.000	1	K.TL*AGL*VVQL*L*QFQEDAFGK#.H

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GP:BC039843_1	H09	11453	2	2078.4	(+0.3)	3.935	0.578	1.000	1	K.TLAGLVVQLLQFQEDAFGK.H
GP:BC039843_1	H09	11451	2	2110.4	(-0.8)	2.511	0.286	0.553	1	K.TL*AGL*VVQL*L*QFQEDAFGK#.H
GP:BC039843_1	H13	11486	2	2078.4	(+0.0)	2.388	0.394	0.922	1	K.TLAGLVVQLLQFQEDAFGK.H
GP:BC039843_1	H14	11177	3	2110.4	(+0.1)	3.947	0.446	0.998	1	K.TL*AGL*VVQL*L*QFQEDAFGK#.H
GP:BC039843_1	H16	10532	3	2110.4	(+0.0)	4.243	0.460	0.996	1	K.TL*AGL*VVQL*L*QFQEDAFGK#.H
GP:BC039843_1	H16	10536	3	2078.4	(+0.6)	4.242	0.550	0.999	1	K.TLAGLVVQLLQFQEDAFGK.H
GP:BC039843_1	H17	10454	3	2078.4	(+0.5)	4.853	0.562	0.996	1	K.TLAGLVVQLLQFQEDAFGK.H
GP:BC039843_1	H17	10456	3	2110.4	(-0.1)	4.531	0.494	0.998	1	K.TL*AGL*VVQL*L*QFQEDAFGK#.H
GP:BC039843_1	H17	10482	2	2078.4	(+0.5)	3.667	0.530	0.999	1	K.TLAGLVVQLLQFQEDAFGK.H
GP:BC039843_1	H17	10460	2	2110.4	(+0.1)	3.097	0.441	0.972	1	K.TL*AGL*VVQL*L*QFQEDAFGK#.H
GP:BC039843_1	H05	7422	2	1748.0	(+0.7)	3.958	0.525	1.000	1	R.VREEVPLELVEAHVK.K
GP:BC039843_1	H18	10952	3	2110.4	(+0.7)	4.032	0.524	0.999	1	K.TL*AGL*VVQL*L*QFQEDAFGK#.H
GP:BX537360_1	H18	6042	3	1911.1	(+0.5)	4.215	0.473	0.998		K.LPGGELDPGEDEVEGLKR.L
GP:BX537360_1	H18	6196	2	1754.9	(+0.2)	3.635	0.288	0.951		K.LPGGELDPGEDEVEGLK.R
GP:D86978_1	H04	2279	2	1108.3	(+0.2)	2.630	0.271	0.892		K.K#ADNVVNIAR.Y
GP:D86978_1	H04	9155	2	2164.4	(+0.1)	2.872	0.434	0.970		R.TSQDFLFSQLQYLPFSNK.E
GP:D86978_1	H04	4989	2	1251.3	(+1.0)	2.496	0.301	0.927		K.DLPSADSVQYR.H
GP:D87716_1	H08	9097	3	3169.5	(-0.1)	3.760	0.374	0.922	1	K.GKEDLQTNSEFPVLLTQGLSENDFEMLNK.V
GP:D87716_1	H08	7273	2	1028.2	(+0.8)	3.265	0.319	0.989	1	R.LLNVWQVR.S
GP:D87716_1	H08	9495	2	1748.2	(+0.6)	3.098	0.204	0.891	1	R.MPLHTIIPLLQELTK.R
GPN:AK009582_1	H04	5185	2	1278.4	(+0.5)	2.403	0.276	0.876	8	K.TYNEPGSQVFK#.D
GPN:AK009582_1	H04	5299	2	1169.3	(+0.4)	2.391	0.240	0.871	8	R.YNVPSAIYK.R
GPN:AK009582_1	H04	5597	2	1218.4	(+0.7)	2.375	0.153	0.771	8	K.YPDYYQIQK.M
GPN:AK026107_1	H05	5432	3	2620.6	(+0.8)	4.154	0.447	0.995	2	K.ASNGNARPETVTNDDEEAL*DEETK#.R
GPN:AK026107_1	H06	4968	3	2620.6	(+0.8)	4.797	0.431	0.997	2	K.ASNGNARPETVTNDDEEAL*DEETK#.R
GPN:AK026107_1	H06	8932	2	1570.0	(+0.4)	4.067	0.343	0.990	2	R.FPVAPLIPYPLITK.E
GPN:AK026107_1	H06	8910	2	1590.0	(+0.1)	2.926	0.278	0.885	2	R.FPVAPL*IPYPL*ITK#.E
GPN:AK026107_1	H05	8694	2	1746.2	(-0.2)	2.990	0.371	0.949	2	R.RFPVAPL*IPYPL*ITK#.E
GPN:AK026107_1	H06	8578	2	1746.2	(+0.7)	3.210	0.355	0.871	2	R.RFPVAPL*IPYPL*ITK#.E
GPN:AK026107_1	H06	2054	2	2040.1	(+0.3)	2.520	0.365	0.917	2	R.EYSSSEL*NAPSQESDSDSHPR.K
GPN:AK039567_1	H03	5188	2	1201.3	(-0.3)	2.402	0.405	0.940	1	K.ANSNLVLQADR.S
GPN:AK039567_1	H03	5202	2	1213.3	(+0.2)	2.264	0.271	0.787	1	K.ANSNL*VL*QADR.S
GPN:AK039567_1	H03	7260	2	1364.5	(+0.6)	3.103	0.525	0.981	1	R.DEPTGEVL*SL*VGK#.L
GPN:AK039567_1	H03	7178	2	1489.6	(-0.3)	2.779	0.330	0.930	2	R.EIDLLLGQTDDTR.Y
GPN:AK039567_1	H03	5742	2	1194.3	(+0.4)	3.395	0.379	0.990	2	R.FYDDAIVSQK#.K
GPN:AK039567_1	H04	5419	2	1186.3	(+0.5)	2.531	0.323	0.963	2	R.FYDDAIVSQK.K
GPN:AK039567_1	H03	7110	2	1186.4	(+0.5)	3.232	0.429	0.992	2	K.K#ADEVL*EIL*K#.T
GPN:AK039567_1	H04	5407	2	1194.3	(+0.0)	2.418	0.248	0.756	2	R.FYDDAIVSQK#.K
GPN:AK041594_1	H09	6749	2	1602.8	(-0.3)	2.932	0.281	0.888	1	K.DL*ANL*EVPHEL*PTK#.Q
GPN:AK041594_1	H09	6271	3	2528.8	(-0.2)	5.166	0.473	1.000	2	K.TPVVQNAASIVQPSPAHVGQQGL*SK#.L
GPN:AK041594_1	H09	5355	2	1398.6	(+0.8)	3.571	0.435	0.993	2	R.VIAPNPAQL*QGQR.G
GPN:AK041594_1	H09	5369	2	1392.6	(+0.4)	3.357	0.526	0.999	2	R.VIAPNPAQLQGQR.G
GPN:AK041594_1	H09	2071	2	1017.2	(+0.8)	2.362	0.345	0.964	2	R.TL*QGHSVIR.S
GPN:AK074420_1	H16	5404	2	2238.3	(-1.0)	3.513	0.452	0.950		R.AVYDEQGTVEDSDSPVLTQDR.D
GPN:AK074420_1	H16	7358	3	3245.4	(+0.2)	3.877	0.412	0.966		R.AVYDEQGTVEDSDSPVLTQDRDWEAYWR.L
GPN:AK074420_1	H16	6872	2	1441.6	(+0.5)	2.537	0.228	0.867	1	K.EMDNFL*AQMEAK#.Y
GPN:AK074420_1	H16	4530	2	1105.2	(+0.1)	2.835	0.281	0.917		K.GSEEL*ADIK#.Q
GPN:AK074420_1	H16	6852	2	1307.5	(+0.3)	3.330	0.372	0.974		K.ISL*EDIQAFEK#.T
GPN:AK074420_1	H16	6626	2	1421.6	(+0.6)	4.554	0.336	0.993		K.KISLEDIQAFEK.T
GPN:AK074420_1	H16	7850	2	2186.4	(+0.9)	3.948	0.540	1.000	1	R.NIIQQAIDAGEVPSYNAFVK#.E
GPN:AK074420_1	H16	7846	2	2178.4	(+0.9)	3.369	0.477	0.888	1	R.NIIQQAIDAGEVPSYNAFVK.E
GPN:AK074420_1	H16	4704	2	945.1	(+0.5)	2.447	0.337	0.967		K.VYSVL*SDR.E
GPN:AK098547_1	H10	9309	2	2051.3	(-0.1)	3.370	0.332	0.957	3	K.RFPEL*ESL*VPNAL*DYIR.T
GPN:AK098547_1	H10	9653	2	1877.1	(+0.8)	2.343	0.386	0.958	3	R.FPELESVLPNALDYIR.T
GPN:AY358264_1	H16	7542	2	2082.4	(+0.7)	3.766	0.577	0.999		R.VVALSMSPVDDTFISGSLDK.T
GPN:AY358264_1	H16	1480	2	1563.7	(+0.9)	2.839	0.492	0.988		R.YTHAANTVVYSSNK#.I

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GPN:AY358264_1	H16	5438	2	1248.4	(+0.2)	2.412	0.301	0.857	1	K.IHVWNGESGIK#.V
GPN:AY359102_1	H19	8836	2	1856.1	(+0.2)	2.483	0.235	0.718	1	R.ALVDELEWEIAQVDPK.K
GPN:AY359102_1	H19	5678	2	1430.5	(+0.8)	2.267	0.235	0.813		R.NGESSEL*DL*QGIR.I
GPN:AY363225_1	H14	1899	2	1621.7	(+0.9)	2.472	0.327	0.388		R.GEEGHDPKEPEQLR.K
GPN:AY363225_1	H14	7275	2	1714.8	(-0.3)	5.174	0.491	1.000		R.GFAFVTFDDHDTVDK.I
GPN:AY363225_1	H14	7297	2	1722.8	(-0.8)	3.317	0.304	0.811		R.GFAFVTFDDHDTVDK#.I
GPN:AY363225_1	H15	7270	2	1714.8	(+0.5)	3.906	0.475	1.000		R.GFAFVTFDDHDTVDK.I
GPN:AY363225_1	H14	6623	2	1898.1	(-0.3)	3.253	0.401	0.579		K.IFVGGIK#EDTEEYNL*R.D
GPN:AY363225_1	H16	6814	2	1722.8	(+0.4)	4.860	0.544	0.999		R.GFAFVTFDDHDTVDK#.I
GPN:AY422990_1	H12	6954	2	1408.7	(-0.2)	3.093	0.380	0.963	8	R.L*VHPGVAEVVFVK#.K
GPN:AY422990_1	H12	6100	2	1399.6	(+0.1)	2.235	0.393	0.915	7	R.VGIQQGL*L*SQSTR.T
GPN:BC000001_1	H14	7887	3	2478.7	(+0.8)	4.991	0.504	1.000	4	R.HFAGDVL*GYVTPWNSHGYDVTK#.V
GPN:BC000001_1	H14	6787	2	1640.7	(+0.5)	3.165	0.536	1.000	6	R.NVL*DSEDEIEEL*SK#.T
GPN:BC000001_1	H14	8617	2	1632.8	(+0.1)	3.068	0.375	0.967	7	R.L*L*FEDWTYDDFR.N
GPN:BC000017_1	H09	5601	2	1465.6	(-0.8)	3.031	0.399	0.895	5	K.L*L*EEEEIQAPTSSEK#.R
GPN:BC000017_1	H08	8457	2	1613.9	(+0.1)	2.432	0.436	0.947	4	R.VTPVEVMPVFPDFK#.M
GPN:BC000017_1	H09	8447	2	1613.9	(+0.0)	2.909	0.367	0.946	4	R.VTPVEVMPVFPDFK#.M
GPN:BC000488_1	H09	5475	2	1568.8	(+0.5)	2.951	0.386	0.679	2	R.AIEAL*HGHEL*RPGR.A
GPN:BC000488_1	H09	4961	2	1212.3	(+0.8)	2.879	0.392	0.984	1	R.AQPSASL*GVGYR.T
GPN:BC000488_1	H09	4969	2	1206.3	(+0.8)	2.870	0.368	0.981	1	R.AQPSASLGVGYR.T
GPN:BC000488_1	H09	5041	2	1212.3	(+0.7)	2.348	0.267	0.873	1	R.AQPSASL*GVGYR.T
GPN:BC000488_1	H09	5425	2	1220.4	(+0.9)	3.091	0.469	0.993	1	R.AQPSVSLGAAYR.A
GPN:BC000488_1	H09	5419	2	1226.4	(+0.3)	2.777	0.532	0.986	1	R.AQPSVSL*GAAYR.A
GPN:BC000488_1	H09	5521	2	1226.4	(+0.8)	2.456	0.502	0.974	1	R.AQPSVSL*GAAYR.A
GPN:BC000488_1	H09	5501	2	1252.4	(+0.9)	2.358	0.430	0.978	1	R.AQPSVSL*GAPYR.G
GPN:BC000488_1	H09	6019	2	1609.8	(+0.5)	2.621	0.386	0.971	1	R.ASYVAPLTAQPATYR.A
GPN:BC000488_1	H09	6005	2	1615.8	(+0.4)	2.572	0.415	0.977	1	R.ASYVAPL*TAQPATYR.A
GPN:BC000488_1	H09	4813	2	1164.3	(+0.7)	2.693	0.388	0.969	2	K.DYAFVHM@EK#.E
GPN:BC000488_1	H09	5129	2	979.1	(+0.9)	2.244	0.305	0.945	1	R.L*AEL*SDYR.R
GPN:BC000488_1	H09	5815	2	1079.2	(+0.0)	2.455	0.334	0.929	1	R.L*SESQL*SFR.R
GPN:BC000488_1	H09	5477	2	1238.3	(+0.9)	3.264	0.432	0.993	1	R.YSGSYNDYLR.A
GPN:BC000488_1	H09	5551	2	1246.4	(+1.0)	2.220	0.310	0.912	1	R.AQPSVSLGAPYR.G
GPN:BC000994_1	H18	6078	2	1332.5	(+0.8)	3.938	0.468	1.000	1	K.HETEFAELEVK.T
GPN:BC000994_1	H18	6074	2	1346.5	(+0.8)	3.659	0.340	0.989	1	K.HETEFANEL*EVK#.T
GPN:BC000994_1	H18	6442	2	1052.2	(+0.8)	2.292	0.306	0.934	1	K.TSFEIAEL*K#.E
GPN:BC000994_1	H18	5954	2	1345.5	(+0.1)	2.239	0.247	0.675	1	K.L*FQSDTNAML*GK#.K
GPN:BC001013_1	H19	9248	2	1763.1	(+0.9)	2.907	0.473	0.990		K.LYPAAVDTIVAIMAEGK.Q
GPN:BC001013_1	H19	9484	2	2396.8	(+0.1)	4.411	0.546	1.000		K.NQLIEQFPPIEPWLNQIMPK.K
GPN:BC001013_1	H19	6396	2	1499.7	(+0.1)	3.218	0.188	0.845		K.YPFIL*PHQQVDK#.G
GPN:BC001013_1	H19	9266	2	1763.1	(-0.3)	2.531	0.482	0.970		K.LYPAAVDTIVAIMAEGK.Q
GPN:BC001107_1	H19	8644	2	1918.2	(+0.6)	2.863	0.451	0.986	2	R.YGPIVDVYVPLDFYTR.R
GPN:BC001107_1	H18	6724	2	1475.7	(+0.1)	2.441	0.292	0.184	2	R.YL*RPPNTSL*FVR.N
GPN:BC001107_1	H19	6564	2	1475.7	(+0.6)	2.669	0.264	0.349	2	R.YL*RPPNTSL*FVR.N
GPN:BC001364_1	H18	4672	2	991.1	(+0.2)	2.951	0.532	1.000		R.GEALSALDSK.A
GPN:BC001364_1	H18	4648	2	1011.1	(+0.4)	2.342	0.328	0.945		R.GEAL*SAL*DSK#.A
GPN:BC001364_1	H18	7730	2	1421.7	(+0.7)	4.332	0.425	1.000		R.IMVANIEEVL*QR.G
GPN:BC001364_1	H18	7338	2	1437.7	(+0.7)	3.815	0.403	0.992		R.IM@VANIEEVL*QR.G
GPN:BC001364_1	H18	6268	2	1599.7	(-0.1)	4.177	0.439	0.897		R.NL*GSINTEL*QDVQR.I
GPN:BC001364_1	H19	6080	2	1599.7	(+0.7)	3.558	0.479	0.979		R.NL*GSINTEL*QDVQR.I
GPN:BC001384_1	H10	8073	3	2465.7	(+0.5)	4.082	0.448	0.990	5	K.NTTYDL*IANIVHDGK#PSEGSYR.I
GPN:BC001384_1	H10	8111	2	1714.0	(-0.5)	3.205	0.481	0.984	5	K.NPTIVNFPITNVDLR.E
GPN:BC001403_1	H18	6914	2	1246.5	(+0.3)	3.665	0.265	0.966	1	K.KLFLVQLQEK.A
GPN:BC001403_1	H18	7128	2	1118.4	(-0.3)	3.087	0.229	0.926	1	K.LFLVQLQEK.A
GPN:BC001403_1	H18	6062	2	1910.1	(+0.7)	4.562	0.505*	0.163		K.LPGGELNPGEDEVEGLKR.L

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta M$	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GPN:BC001403_1	H18	6040	3	1936.1	(+0.0)	4.271	0.351*	0.008		K.L*PGGEL*NPGEDEVEGL*K#R.L
GPN:BC001403_1	H18	6056	3	1910.1	(-0.5)	3.888	0.392	0.968		K.LPGGELNPGEDEVEGLKR.L
GPN:BC001403_1	H18	6054	2	1936.1	(-0.5)	3.310	0.254	0.279		K.L*PGGEL*NPGEDEVEGL*K#R.L
GPN:BC001403_1	H18	9338	2	1728.1	(-0.2)	5.029	0.443	1.000	1	R.LPHVLLQLGTTFFK.L
GPN:BC001403_1	H18	5806	3	1545.8	(+0.2)	3.827	0.343	0.991	1	R.RTVEGVLIVHEHR.L
GPN:BC001403_1	H18	7906	3	1767.0	(+1.0)	3.741	0.420	0.999	1	R.TINL*YPL*TNYFTGK#E
GPN:BC001403_1	H18	5876	2	1389.6	(-0.4)	3.303	0.576	1.000	1	R.TVEGVLIVHEHR.L
GPN:BC001403_1	H18	5866	2	1395.6	(-0.6)	3.007	0.411	0.975	1	R.TVEGVL*IVHEHR.L
GPN:BC001403_1	H18	5538	2	1490.7	(+0.1)	2.612	0.295	0.237	1	K.YIQQTKPLTLER.T
GPN:BC001403_1	H18	5536	2	1510.7	(-0.3)	2.416	0.222	0.089	1	K.YIQQTK#PL*TL*ER.T
GPN:BC003090_1	H19	6694	2	1561.7	(+0.7)	3.289	0.366	0.984		K.SANSELGGIWSVGQR.I
GPN:BC003090_1	H19	5850	2	1368.6	(+0.0)	3.273	0.479	0.985		R.K#PVAGAL*DVSFNK#F
GPN:BC003413_1	H18	6530	2	1077.2	(-0.2)	3.030	0.185	0.883		K.VDEIFGQLR.D
GPN:BC003413_1	H18	7054	2	1568.8	(-0.1)	2.682	0.270	0.845		K.VPYFNAPVYL*ENK#E
GPN:BC004169_1	H18	7796	2	1463.6	(+0.8)	3.887	0.462	0.999		K.DQWYNVL*EFSR.T
GPN:BC004169_1	H18	6772	2	1274.4	(+0.2)	3.145	0.411	0.976		K.L*EAESMGFFTK#E
GPN:BC004169_1	H18	4278	2	1248.4	(-0.8)	2.495	0.285	0.633		R.L*ISGEEHFSSK#K
GPN:BC004169_1	H18	4218	2	1248.4	(+0.6)	2.291	0.306	0.917		R.L*ISGEEHFSSK#K
GPN:BC004169_1	H18	8574	2	974.2	(+0.8)	3.289	0.363	0.991		K.SMLALLLGR.T
GPN:BC004169_1	H18	9664	3	3204.4	(-0.8)	4.345	0.307	0.868		R.TVHADL*SNYDEDGAWPVL*L*DEFVEWQK#V
GPN:BC004169_1	H18	5930	2	1290.4	(-0.0)	2.228	0.382	0.907		K.L*EAESM@GFFTK#E
GPN:BC004951_1	H14	4719	2	1059.2	(+0.9)	2.900	0.343	0.984	2	R.MHVQLSTSR.L
GPN:BC004951_1	H14	5999	2	1230.3	(+0.9)	2.517	0.481	0.989	3	K.NYGFVHIEDK#T
GPN:BC004951_1	H14	5997	2	1222.3	(+0.7)	2.361	0.395	0.889	3	K.NYGFVHIEDK.T
GPN:BC005097_1	H05	9160	2	1241.5	(+1.0)	3.748	0.331	0.990	1	K.NVIQSVLQAIR.K
GPN:BC005097_1	H05	7402	2	1358.5	(+0.6)	2.351	0.397	0.972	4	R.TVL*PFSQEFQR.D
GPN:BC005102_1	H19	6510	2	1225.5	(+0.8)	3.907	0.541	0.999		K.GKPLALVEEIR.N
GPN:BC005102_1	H19	8148	2	1837.2	(+0.6)	3.507	0.371	0.987		R.QLSTPGTILGTIPVPK.G
GPN:BC005152_1	H19	6050	2	1301.4	(+0.7)	3.198	0.462	0.994	1	R.AYGTNYIETLR.V
GPN:BC005152_1	H19	6254	2	1461.6	(+0.7)	3.231	0.370	0.985	1	R.L*YSEDEL*PAEFK#L
GPN:BC005152_1	H19	9132	2	2096.3	(+0.5)	3.017	0.379	0.981		R.LDDGWNQIQFNLLDFTR.R
GPN:BC006224_1	H18	5452	2	1954.1	(+0.6)	4.655	0.665	1.000		K.ASAEPLLGPAAAPSGEGAGSK.G
GPN:BC006224_1	H18	5476	2	1954.1	(-0.6)	4.086	0.593	0.998		K.ASAEPLLGPAAAPSGEGAGSK.G
GPN:BC006224_1	H18	4938	2	1523.6	(+0.3)	2.325	0.451	0.952		R.EL*DEEGSDPPL*PGR.A
GPN:BC006282_1	H19	2328	2	1166.3	(+0.6)	2.897	0.406	0.989		R.ALQALQQEHK.A
GPN:BC006282_1	H19	2240	2	1166.3	(+0.7)	2.798	0.346	0.979		R.ALQALQQEHK.A
GPN:BC006282_1	H19	2502	2	1166.3	(+0.6)	2.584	0.392	0.981		R.ALQALQQEHK.A
GPN:BC006282_1	H19	2396	2	1166.3	(+0.8)	2.561	0.281	0.947		R.ALQALQQEHK.A
GPN:BC006282_1	H19	2364	2	1186.3	(+0.7)	2.553	0.416	0.982		R.AL*QAL*QQEHK#A
GPN:BC006282_1	H19	2428	2	1186.3	(-0.5)	2.442	0.332	0.907		R.AL*QAL*QQEHK#A
GPN:BC006282_1	H19	2298	2	1186.3	(+0.4)	2.425	0.349	0.960		R.AL*QAL*QQEHK#A
GPN:BC006282_1	H19	2232	2	1186.3	(-0.5)	2.297	0.183	0.580		R.AL*QAL*QQEHK#A
GPN:BC006282_1	H19	2490	2	1186.3	(+0.6)	2.235	0.382	0.960		R.AL*QAL*QQEHK#A
GPN:BC006282_1	H19	8074	2	1685.9	(+0.6)	3.966	0.454	0.999		R.FPPFFTL*QPNVDTR.Q
GPN:BC006282_1	H19	8288	2	1679.9	(+0.1)	3.966	0.503	1.000		R.FPPFFTLQPNVDTR.Q
GPN:BC006282_1	H19	8210	2	1679.9	(+0.3)	3.259	0.418	0.977		R.FPPFFTLQPNVDTR.Q
GPN:BC006282_1	H19	8156	2	1685.9	(+0.5)	3.052	0.374	0.982		R.FPPFFTL*QPNVDTR.Q
GPN:BC006282_1	H19	8132	2	1679.9	(-1.0)	2.525	0.287	0.614		R.FPPFFTLQPNVDTR.Q
GPN:BC006282_1	H19	8540	3	3846.0	(+1.0)	4.856	0.429	0.999		R.SGQNNVFTLYELTNGEDTEDEEFHGLDEATLLR.A
GPN:BC006282_1	H19	5846	2	1131.3	(+0.3)	2.212	0.163	0.506		K.K#GNL*EWL*DK#S
GPN:BC006504_1	H17	5630	2	1427.6	(-0.0)	3.650	0.354	0.627	3	R.TK#EEVNEWFTK#Y
GPN:BC006504_1	H17	6266	2	1118.3	(+0.9)	3.071	0.280	0.974	3	R.GEVGL*L*FTNR.T
GPN:BC006512_1	H16	6438	2	1449.6	(+0.4)	3.615	0.339	0.986		K.ANDLTHSLSSYLK.G
GPN:BC006512_1	H16	6440	2	1475.6	(+0.6)	2.427	0.357	0.908		K.ANDL*THSL*SSYL*K#G
GPN:BC006512_1	H16	4838	2	1098.3	(+0.6)	2.380	0.350	0.949		R.VVHL*GVGTPGR.I

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GPN:BC009597_1	H13	8154	3	1985.1	(+1.0)	3.850	0.521	1.000	2	R.DTL*VQGL*NEAGDDL*EAVAK#.F
GPN:BC009597_1	H13	5240	2	1286.5	(-0.4)	2.435	0.236	0.753	1	K.K#EEL*VAEQAL*K#.H
GPN:BC009734_1	H10	8827	2	2388.6	(-0.1)	2.520	0.320	0.875	5	K.AQSSQDAVSSMNLFDLGGQYLR.V
GPN:BC009734_1	H10	5465	2	1191.4	(+0.9)	2.841	0.240	0.949	5	R.KQESTVMVLR.N
GPN:BC009734_1	H10	5461	2	1205.4	(+0.3)	2.391	0.304	0.884	5	R.K#QESTVMVL*R.N
GPN:BC009734_1	H10	2337	2	1344.5	(+0.1)	2.470	0.321	0.903	5	R.K#VVAEVDQER.F
GPN:BC009734_1	H10	7267	2	1408.6	(+0.4)	2.343	0.380	0.959	5	K.SIDMSWDSVTMK#.H
GPN:BC009734_1	H21	4292	2	1344.5	(-0.1)	2.397	0.368	0.929	5	R.K#VVAEVDQER.F
GPN:BC010077_1	H16	4650	2	2008.2	(-0.7)	3.693	0.513	1.000	1	K.AL*SGTSPDDVQPGPSVGPPSK#.D
GPN:BC010077_1	H16	4652	2	1994.2	(-0.7)	3.345	0.542	1.000	1	K.ALSGTSPDDVQPGPSVGPPSK.D
GPN:BC010077_1	H16	7732	2	1357.6	(+0.9)	4.104	0.363	0.994	3	R.EAILEYLHQQ.K
GPN:BC010077_1	H16	7724	2	1377.6	(+0.4)	3.155	0.386	0.987	3	R.EAIL*EYIL*HQQ#.K
GPN:BC010077_1	H16	8278	2	1706.0	(-0.2)	2.733	0.343	0.913		K.VL*PSFWIPSL*TPEAK#.A
GPN:BC010077_1	H16	5974	2	1354.6	(+0.5)	2.431	0.169	0.116	1	K.L*TDRDIIVL*QR.G
GPN:BC011017_1	H12	6640	2	1696.9	(+0.5)	4.123	0.455	1.000	2	K.AYHNSPAYLAYINAK.S
GPN:BC011017_1	H12	6642	2	1710.9	(-0.5)	3.086	0.286	0.904	2	K.AYHNSPAYL*AYINAK#.S
GPN:BC011017_1	H12	6058	3	2275.3	(+0.5)	3.989	0.382	0.987	2	R.DL*TDEEK#QEYL*NEYEAEK#.I
GPN:BC011017_1	H12	6492	2	1564.7	(-0.4)	3.451	0.341	0.964	2	K.FL*ESTDSFNEL*K#.R
GPN:BC011017_1	H12	6984	2	1497.7	(+0.2)	3.069	0.377	0.968	2	R.K#L*EAEL*L*QIEER.H
GPN:BC011017_1	H12	6364	2	1720.8	(-0.1)	2.700	0.315	0.265	2	K.FL*ESTDSFNEL*K#.R.L
GPN:BC011355_1	H10	5057	2	1078.2	(+0.0)	2.815	0.322	0.937	6	K.RPAL*FSSSAK#.A
GPN:BC011355_1	H10	5577	2	1184.3	(+0.8)	2.607	0.431	0.986	6	K.HGYAPSDLPVK.A
GPN:BC011709_1	H20	10576	3	2367.6	(+0.4)	4.192	0.351	0.997		R.L*QWENVSAMIEEVFEATDIK#.I
GPN:BC011709_1	H20	10582	3	2353.6	(+0.5)	4.024	0.450	0.987		R.LQWENVSAMIEEVFEATDIK.I
GPN:BC011709_1	H20	9574	2	2383.6	(+0.4)	2.984	0.475	0.989		R.L*QWENVSAM@IEEVFEATDIK#.I
GPN:BC011709_1	H20	6686	2	1077.3	(+1.0)	2.371	0.431	0.986		R.YIYYLITK.K
GPN:BC011981_1	H16	6022	2	1474.6	(+0.1)	2.400	0.216	0.644	1	K.ANPETDPEAL*FQK#.E
GPN:BC011981_1	H16	4154	2	1312.3	(+0.8)	2.261	0.304	0.921	1	K.YEVDDIDEEGK.E
GPN:BC012559_1	H11	6326	2	1650.8	(+0.2)	4.074	0.565	1.000	2	K.VL*GGNQL*TVNVEGTK#.T
GPN:BC012559_1	H11	5750	2	1425.6	(+0.7)	3.537	0.460	1.000	3	R.SQQQLVESLHK.V
GPN:BC013916_1	H18	6304	2	1165.3	(+0.8)	2.706	0.540	0.989	2	K.FGFAIGSQTTK#.K
GPN:BC013916_1	H18	4016	2	1587.7	(+0.2)	3.506	0.451	0.705	2	R.SAEAAAADLPTKPTK.I
GPN:BC013916_1	H18	4094	2	1587.7	(-0.3)	3.416	0.371	0.555	2	R.SAEAAAADLPTKPTK.I
GPN:BC013916_1	H18	6286	2	1157.3	(+0.4)	2.570	0.514	0.992	2	K.FGFAIGSQTTK.K
GPN:BC013949_1	H17	6492	2	1451.6	(+0.9)	3.556	0.304	0.982		R.AAFTAFEEAQLPR.L
GPN:BC013949_1	H17	1524	2	1095.2	(+0.4)	2.750	0.353	0.979		R.VL*EEGSVEAR.T
GPN:BC014046_1	H01	5284	2	1167.3	(+0.7)	2.707	0.360	0.977	1	K.AASITSEVFNK.F
GPN:BC014046_1	H02	4408	2	1216.3	(+0.4)	2.695	0.408	0.985	1	K.ELAAQLNEEAK.R
GPN:BC014046_1	H01	5648	3	2408.4	(+0.8)	4.685	0.462	0.993	1	K.NEDEEEEEEEKDEAEDLLGR.G
GPN:BC014046_1	H02	5754	3	2408.4	(+0.8)	4.567	0.445	0.638	1	K.NEDEEEEEEEKDEAEDLLGR.G
GPN:BC014046_1	H05	7446	2	1677.9	(+0.6)	3.760	0.454	0.994	1	R.NEGNIFPNPEATFVK.E
GPN:BC014046_1	H05	4610	2	1216.3	(+0.7)	2.415	0.393	0.974	1	K.ELAAQLNEEAK.R
GPN:BC014184_1	H09	9447	3	2559.8	(+0.9)	4.706	0.568	1.000	3	K.NL*SPVVSNEL*L*EQAFSQFGPVEK#.A
GPN:BC014184_1	H10	9557	2	2533.8	(+0.1)	4.918	0.441	1.000	3	K.NLSPVVSNELLEQAFSQFGPVEK.A
GPN:BC014184_1	H10	8159	2	1859.1	(-0.3)	2.733	0.416	0.954	4	R.L*FVGNL*PTDITEEDFK#.R
GPN:BC015474_1	H09	7863	2	1443.7	(+0.5)	2.623	0.400	0.980	4	K.TQGIWL*SPL*YPR.I
GPN:BC015474_1	H09	4367	2	1003.1	(+0.6)	2.484	0.320	0.964	3	K.YNSGALHIK.D
GPN:BC015584_1	H09	6253	2	1637.7	(+0.2)	3.242	0.362	0.502	2	K.EK#EPEEEL*YDL*SK#.V
GPN:BC015584_1	H09	9297	2	2145.3	(-0.4)	3.043	0.337	0.943	3	R.GEEL*DEDL*FL*QL*TGGEAF.-
GPN:BC015584_1	H09	5671	2	1243.4	(+0.9)	3.365	0.326	0.986	3	R.KDEILGIANNR.L
GPN:BC015584_1	H09	5657	2	1257.4	(-0.1)	2.976	0.417	0.977	3	R.K#DEIL*GIANNR.L
GPN:BC015584_1	H09	8883	2	2100.4	(-0.4)	4.025	0.465	1.000	2	K.LEGSAPTDVLDLSTIPELK.D

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GPN:BC015584_1	H09	8241	2	1705.0	(+0.6)	2.417	0.508	0.987	2	K.LLVSPSEGMSEIYLR.C
GPN:BC015584_1	H01	7200	3	3027.3	(+1.0)	4.060	0.487	0.963	2	K.LSQSGEVGEPAGTDPGLDDLDVALSNLEVK.L
GPN:BC015584_1	H09	4445	2	1122.3	(+0.5)	2.660	0.255	0.950	2	R.LTQLYEQAR.W
GPN:BC015584_1	H15	4788	2	1122.3	(+0.6)	2.872	0.416	0.990	2	R.LTQLYEQAR.W
GPN:BC015584_1	H01	5816	3	2784.0	(+0.3)	5.855	0.603	1.000	3	R.TGSGGPGNHPHPGDASAEGLNPNYGLVAPR.F
GPN:BC015584_1	H02	5918	3	2784.0	(+0.5)	6.837	0.601	1.000	3	R.TGSGGPGNHPHPGDASAEGLNPNYGLVAPR.F
GPN:BC015584_1	H09	6683	3	2784.0	(+0.6)	5.745	0.647	0.974	3	R.TGSGGPGNHPHPGDASAEGLNPNYGLVAPR.F
GPN:BC015584_1	H09	6679	3	2796.0	(+0.5)	5.640	0.578	0.999	3	R.TGSGGPGNHPHPGDASAEGLNPNYGL*VAPR.F
GPN:BC015584_1	H09	6107	2	1330.5	(+0.5)	3.066	0.420	0.987	2	R.VTGESHIGGV*L*K#.I
GPN:BC015584_1	H09	7615	2	1282.6	(+0.4)	3.381	0.465	0.994	2	K.VVL*AGGVAPAL*FR.G
GPN:BC015584_1	H01	6686	2	1309.4	(+0.8)	2.650	0.462	0.989	2	K.YYSFFDL*DPK#.T
GPN:BC015584_1	H01	6678	2	1295.4	(+0.6)	2.490	0.318	0.959	2	K.YYSFFDLDPK.T
GPN:BC015584_1	H16	7476	2	1295.4	(+0.7)	2.281	0.301	0.883	2	K.YYSFFDLDPK.T
GPN:BC016353_1	H18	6236	2	1373.6	(+0.4)	2.578	0.310	0.945	2	K.ENPGL*TQDIIMK#.I
GPN:BC016353_1	H18	7286	2	1595.9	(-0.3)	3.103	0.447	0.978	2	R.L*IHQTNL*IL*QTFK#.T
GPN:BC016353_1	H18	7190	3	2930.2	(+0.4)	4.759	0.589*	0.027	1	R.M@AADDVEEYMIERPEPEFQDL*NEK#.A
GPN:BC016353_1	H18	7472	2	1394.6	(+0.7)	2.633	0.437	0.985	2	K.SVEVNFTESSLR.M
GPN:BC016353_1	H18	5302	2	1085.2	(+0.8)	3.060	0.395	0.990	2	R.VNL*SAAQTL*R.A
GPN:BC016353_1	H18	7464	2	1406.6	(-0.4)	2.310	0.285	0.810	2	K.SVEVNFTESL*L*R.M
GPN:BC016707_1	H11	7400	2	1640.9	(+0.9)	4.891	0.464	1.000	3	R.GLGHQVATDALVAMEK.A
GPN:BC016707_1	H11	2436	2	1359.4	(-0.6)	2.701	0.311	0.905	3	R.TNL*DESDVQPVK#.E
GPN:BC016707_1	H11	7256	2	1406.5	(-0.2)	2.496	0.112	0.431	3	R.SYNDEL*QFL*EK#.I
GPN:BC017393_1	H05	6004	2	1330.4	(+0.0)	3.026	0.372	0.960	3	R.L*L*EL*EQDASSAK#.L
GPN:BC017393_1	H05	7006	3	2325.6	(+0.1)	3.899	0.447	0.995	3	R.VL*ESVTVHNPENQSYL*IAYK#.D
GPN:BC017393_1	H05	6006	2	1304.4	(+0.7)	2.975	0.340	0.978	3	R.LLELEQDASSAK.L
GPN:BC017693_1	H18	6714	2	1410.6	(+0.6)	2.933	0.194	0.888		R.TEFIPSTDPPFQK.A
GPN:BC017693_1	H18	6722	2	1418.6	(+0.3)	2.911	0.373	0.956		R.TEFIPSTDPPFQK#.A
GPN:BC017693_1	H18	6332	2	1266.4	(+0.4)	2.504	0.400	0.977		R.TSLDPSLEIYK.K
GPN:BC017709_1	H11	6788	2	1142.4	(+0.9)	2.651	0.335	0.972	3	K.ITNNINVLK.D
GPN:BC017709_1	H11	6880	2	1758.9	(-0.3)	3.692	0.542	1.000	2	R.NYGIL*ADATEQVGVQHK#.D
GPN:BC017709_1	H11	6248	2	1464.5	(+0.8)	3.247	0.412	0.991	1	K.YSSNLGNFNYSR.S
GPN:BC017709_1	H11	6864	2	1472.6	(+0.7)	2.485	0.283	0.919	3	K.ELPQFATGENLPR.V
GPN:BC017724_1	H09	8101	2	1654.9	(+0.7)	4.497	0.519	1.000	3	R.LPGAIDVIGQTITISR.V
GPN:BC017724_1	H09	8095	2	1660.9	(+0.2)	4.087	0.559	1.000	3	R.L*PGAIDVIGQTITISR.V
GPN:BC017724_1	H09	5201	2	1480.6	(+0.5)	3.433	0.329	0.984	2	R.ANENSNIQVL*SER.S
GPN:BC017732_1	H08	6013	2	1358.4	(+0.4)	3.459	0.537	1.000	2	K.HVSDWL*DETNIK#.G
GPN:BC017732_1	H08	5447	2	1330.6	(+0.5)	3.645	0.385	0.838	5	R.LNQIRPGLQYK.L
GPN:BC017732_1	H08	5443	2	1350.6	(+0.1)	2.675	0.170	0.078	5	R.L*NQIRPGL*QYK#.L
GPN:BC017732_1	H08	6133	2	1387.6	(-0.0)	2.291	0.151	0.026	2	K.DK#PTETL*L*NTVK#.D
GPN:BC018698_1	H11	9390	2	2033.3	(+0.0)	2.931	0.446	0.974		K.ALQDEWDAVMLHSFTLR.Q
GPN:BC018698_1	H11	6794	2	1341.5	(+0.5)	3.100	0.389	0.987		K.TL*QL*DNNFEVK#.S
GPN:BC018698_1	H11	8450	3	3617.9	(-0.1)	5.258	0.482	1.000		R.TNVANFPGHSGPITSIAFSENGYYL*ATAADDSSVK#.L
GPN:BC018698_1	H11	8368	3	3603.9	(+0.9)	4.264	0.546	1.000		R.TNVANFPGHSGPITSIAFSENGYYLATAADDSSVK.L
GPN:BC018698_1	H11	6538	2	1598.8	(+0.7)	3.352	0.493	0.868		K.TVPEELVKPEELSK.Y
GPN:BC018698_1	H11	6552	2	1598.8	(-0.5)	3.211	0.493	0.732		K.TVPEELVKPEELSK.Y
GPN:BC018698_1	H11	7822	2	2716.0	(-0.7)	3.505	0.453	0.950		K.YIAENGTDPINNQLPSEEQLIDIK.V
GPN:BC018698_1	H11	6582	2	1110.3	(+0.5)	2.335	0.302	0.928		K.SSEQIL*ATL*K#.G
GPN:BC020166_1	H11	4922	2	1105.2	(+0.8)	3.025	0.338	0.980	1	R.NPALYASNVR.R
GPN:BC020166_1	H11	10024	2	1606.9	(+0.7)	4.513	0.551	0.958	3	K.TALGVAELTVTDLFR.A
GPN:BC020166_1	H11	4910	2	1111.2	(+0.2)	2.583	0.410	0.966	1	R.NPAL*YASNVR.R
GPN:BC020599_1	H19	8868	3	2692.0	(-0.0)	4.103	0.324	0.984	2	R.K#QFHV*L*STIHEL*QQT*ENDEK#.L
GPN:BC020599_1	H19	2206	2	1222.3	(+0.7)	2.383	0.381	0.543	3	K.NRQEYDAL*AK#.V
GPN:BC022352_1	H17	6916	3	2683.0	(+0.5)	5.699	0.585	0.988	1	K.IYITLTGVHQVPTENVQVHFTER.S
GPN:BC022352_1	H17	6368	2	2529.9	(+0.1)	5.313	0.545	1.000	1	K.KAELLDNEKPAAVVAPITTYTVK.I
GPN:BC022352_1	H17	6354	3	2565.9	(-0.5)	4.920	0.493	0.989	1	K.K#AEL*L*DNEK#PAAVVAPITTYTVK#.I



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GPN:BC022352_1	H17	7662	2	2167.5	(+0.1)	4.171	0.538	0.999	1	K.SYSMIVNLLKPISEVGSSK.K
GPN:BC022352_1	H17	5774	2	1196.3	(+0.6)	2.831	0.369	0.978	1	R.WDYL*TQVEK#.E
GPN:BC022352_1	H18	6820	3	2565.9	(-0.6)	4.583	0.415	0.987	1	K.K#AEL*L*DNEK#PAAVVAPITTYTVK#.I
GPN:BC022797_1	H21	6172	2	1235.5	(+0.8)	2.627	0.350	0.964		K.M@AEM@L*VEL*VR.R
GPN:BC022797_1	H21	5816	3	2524.6	(+1.0)	4.260	0.437	0.999		K.TQVEASEESALNHLQNPGDAAEGR.A
GPN:BC022797_1	H21	5826	2	2524.6	(-0.2)	4.089	0.425	0.987		K.TQVEASEESALNHLQNPGDAAEGR.A
GPN:BC022797_1	H21	6756	2	1586.9	(+0.3)	2.292	0.180	0.489	3	K.L*WEM@DNM@L*IQIK#.T
GPN:BC023588_1	H19	1944	2	1626.6	(+0.2)	3.265	0.397	0.974	1	R.DSGTDDQEEEL*ER.D
GPN:BC023588_1	H19	1952	2	1620.6	(+0.7)	2.933	0.141	0.808	1	R.DSGTDDQEEELER.D
GPN:BC023588_1	H19	8358	2	1960.2	(+0.1)	2.489	0.271	0.796	1	R.GAL*TWPSL*AAAIHAQVPED.-
GPN:BC026222_1	H04	6771	3	3315.4	(+0.4)	6.063	0.679	0.997	3	K.ADPAFGL*ESSGIAGTTSDEPERIEESGNDEAR.V
GPN:BC026222_1	H05	8350	2	1886.1	(-0.0)	3.785	0.586	1.000	4	R.DIGEGNLSTAAAAALAAAVK.A
GPN:BC026222_1	H05	8346	2	1906.1	(+0.5)	3.599	0.557	1.000	4	R.DIGEGNL*STAAAAAL*AAAVK#.A
GPN:BC026222_1	H05	6338	2	1442.6	(+0.6)	3.017	0.414	0.989	4	R.HFEEL*ETIM@DR.E
GPN:BC026222_1	H05	7290	2	1426.6	(+0.6)	2.614	0.378	0.978	4	R.HFEEL*ETIMDR.E
GPN:BC026222_1	H04	6435	3	1710.0	(+0.6)	4.713	0.467	1.000	3	K.MKEEVPTALVEAHVR.K
GPN:BC026222_1	H04	11573	3	2184.5	(+0.3)	4.377	0.483	1.000	3	K.SL*SSL*VVQL*L*QFQEEVFGK#.H
GPN:BC026222_1	H04	11585	2	2152.5	(+0.9)	3.760	0.551	1.000	3	K.SLSSLVQLLQFQEEVFGK.H
GPN:BC026222_1	H05	11552	3	2184.5	(+0.4)	4.330	0.492	1.000	3	K.SL*SSL*VVQL*L*QFQEEVFGK#.H
GPN:BC026222_1	H05	1788	2	925.0	(+0.5)	2.244	0.220	0.870	3	K.HLAAVEER.K
GPN:BC026303_1	H13	5854	2	1099.3	(+0.3)	2.343	0.336	0.906	1	R.L*M@EL*FPANK#.Q
GPN:BC026303_1	H13	5252	2	1258.5	(+0.5)	2.314	0.182*	0.208		K.KEELVAEQAIK.H
GPN:BC029482_1	H21	5958	2	1668.8	(+0.8)	3.447	0.610	1.000	1	K.GPVEGYEENEEFLR.T
GPN:BC029482_1	H21	5960	2	1674.8	(+0.8)	3.211	0.431	0.990	1	K.GPVEGYEENEEFL*R.T
GPN:BC029482_1	H21	6004	2	1414.6	(-0.3)	2.996	0.461	0.981	3	K.L*L*THNL*L*SSHVR.G
GPN:BC032638_1	H17	8794	3	3722.1	(+0.2)	5.100	0.571	1.000	1	K.GLQGVGPGSNDETLLSAVASALHTSSAPITGQVSAAVEK.N
GPN:BC032638_1	H13	7130	2	1622.8	(-0.4)	2.689	0.427	0.956	1	R.L*QGL*SASDVTEQIIK#.T
GPN:BC032638_1	H17	6496	2	1602.8	(+0.2)	3.642	0.520	1.000	1	R.LQGLSASDVTEQIIK.T
GPN:BC032643_1	H09	9271	2	1594.8	(+0.0)	3.187	0.331	0.944	6	R.DLFEDELVPLFEK.A
GPN:BC032643_1	H09	9275	2	1620.8	(-0.6)	2.742	0.182	0.691	6	R.DL*FEDEL*VPL*FEK#.A
GPN:BC032643_1	H09	8555	2	1709.9	(+0.4)	3.507	0.556	1.000	5	K.EFNEDGALAVLQQFK.D
GPN:BC032643_1	H09	7787	2	1494.7	(+0.2)	3.696	0.377	0.978	6	R.NL*ANTVTEEIL*EK#.A
GPN:BC032643_1	H10	7231	2	1944.1	(+0.5)	2.441	0.372	0.959	5	K.VTEGLTDVILYHQPPDK.K
GPN:BC032643_1	H11	9546	2	1594.8	(+0.8)	2.360	0.290	0.908	6	R.DLFEDELVPLFEK.A
GPN:BC033822_1	H11	11036	2	2237.6	(-0.1)	2.891	0.429	0.969	4	K.QFEAPTLAEGFSAILEIPFR.L
GPN:BC033822_1	H11	8874	2	1580.8	(+0.6)	3.161	0.449	0.991	5	K.WPAAGFEL*PAFDPR.T
GPN:BC033822_1	H11	5884	2	1358.5	(+0.0)	2.749	0.341	0.940	3	R.TQVELVADPETR.T
GPN:BC034346_1	H07	8766	3	3416.7	(+0.6)	5.106	0.565	1.000		R.ILHTLLASGEDALDFTQESEPSYISDVGPPGR.S
GPN:BC034346_1	H07	5512	2	1126.3	(+1.0)	2.777	0.411	0.987		R.GLDISHISQR.L
GPN:BC036187_1	H05	5778	2	1865.9	(+0.7)	3.434	0.342	0.983		K.KETESAEADNLLDLEK.H
GPN:BC036187_1	H05	7750	2	1440.8	(+0.6)	3.595	0.385	0.819	2	K.VNLEVIKPWITK.R
GPN:BC036187_1	H04	4909	2	1247.5	(+0.1)	2.420	0.403	0.386	1	K.VPK#PEPIPEPK#.E
GPN:BC036187_1	H05	7758	2	1462.8	(+0.7)	3.007	0.319	0.565	2	K.VNL*EVIK#PWITK#.R
GPN:BC036744_1	H15	2212	2	1094.3	(-0.4)	2.698	0.363	0.951	2	K.K#VNQTVAAL*K#.T
GPN:BC036744_1	H15	5700	2	1434.6	(+0.8)	2.892	0.413	0.985	2	K.LPEPSASLPNPPSK.K
GPN:BC036744_1	H15	1864	2	1126.3	(+0.7)	2.648	0.424	0.987	2	K.L*L*HHVTEEK#.G
GPN:BC037428_1	H08	9405	3	3309.6	(-0.2)	4.380	0.406	0.997	2	K.GFAVLEYETAEMAEAAQQQADGLSLGGSHLR.V
GPN:BC037428_1	H08	9401	3	3333.6	(-0.8)	3.926	0.423	0.988	2	K.GFAVL*EYETAEMAEAAQQQADGL*SL*GGSHL*R.V
GPN:BC037428_1	H08	9107	2	1633.9	(+0.5)	3.230	0.451	0.991	2	R.SML*AAL*IAAQATAL*NR.G
GPN:BC039256_1	H04	5321	2	1452.6	(+0.7)	2.686	0.327	0.961	3	R.IYAPEAPYTSPDK.L
GPN:BC039256_1	H04	8163	3	1810.1	(+0.8)	3.863	0.490	0.999	2	K.KDILLVNDHLLNFVR.E
GPN:BC039256_1	H04	8165	3	1842.1	(+0.9)	3.738	0.325	0.993	2	K.K#DIL*L*VNDHL*L*NFVR.E
GPN:BC039256_1	H04	9175	2	1337.7	(-0.9)	2.334	0.139	0.179	5	R.LLVACCLADIFR.I

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GPN:BC039256_1	H04	10897	3	2435.8	(+0.1)	3.774	0.371	0.991	3	R.TAQAIPEYITNFFNQVL*M@L*GK#.T
GPN:BC039256_1	H05	8708	2	1682.0	(+0.7)	3.682	0.477	1.000	2	K.DILLVNDHLLNFVR.E
GPN:BC040943_1	H09	9667	2	2187.4	(-0.2)	3.383	0.439	0.981		K.YAEDIFGEL*FTQANTFASR.V
GPN:BC040943_1	H09	7423	2	1359.5	(+0.3)	2.223	0.296	0.788	3	R.DVVGNDVATILSR.R
GPN:BC041361_1	H05	8838	2	1573.8	(+0.6)	4.815	0.463	1.000	1	R.DLALVNDQLLGFVR.E
GPN:BC041361_1	H05	8832	2	1597.8	(-0.2)	3.291	0.338	0.958	1	R.DL*AL*VNDQL*L*GFVR.E
GPN:BC041361_1	H05	6820	2	1374.5	(+0.7)	3.292	0.323	0.982	1	R.TLFSVINNSHNK.K
GPN:BC041361_1	H05	6808	2	1388.5	(+0.0)	2.654	0.287	0.874	1	R.TL*FSVINNSHNK#.K
GPN:BC041361_1	H06	8758	2	1597.8	(-0.7)	2.244	0.154	0.155	1	R.DL*AL*VNDQL*L*GFVR.E
GPN:BC043619_1	H16	8688	2	1619.9	(+1.0)	3.538	0.542	1.000	1	K.LSGLNAFDIAEELVK.T
GPN:BC043619_1	H16	6756	2	1637.8	(+0.1)	3.439	0.408	0.977	1	R.YL*GGSM@DL*STDFDR.T
GPN:BC043619_1	H16	7472	2	1609.8	(-0.2)	3.106	0.477	0.983	1	R.YLGGSMDLSTDFDR.T
GPN:BC043619_1	H16	8710	2	1645.9	(+0.2)	2.910	0.449	0.971	1	K.L*SGL*NAFDIAEEL*VK#.T
GPN:BC048134_1	H06	7016	3	2212.3	(+1.0)	5.694	0.571	1.000	6	K.HWDQDDDFEFTGSHL*TVR.N
GPN:BC048134_1	H06	8080	2	1608.9	(+0.3)	2.329	0.361	0.894	6	R.IADQFL*GAMYTL*PR.Q
GPN:BC048134_1	H06	9302	2	2550.0	(-0.0)	2.498	0.307	0.827	5	R.KGNYVADLGAMVVTGLGGNPMVAVSK.Q
GPN:BC048134_1	H06	6904	2	1569.8	(-0.5)	3.311	0.499	0.944	5	R.NYPATVHGALLSGLR.E
GPN:BC048134_1	H06	6896	2	1587.8	(-0.3)	2.660	0.299	0.874	5	R.NYPATVHGAL*L*SGL*RE
GPN:BC048134_1	H06	2326	2	1465.6	(+0.3)	2.311	0.216	0.067	6	K.HVK#DEQIEHWK#.K
GPN:BC050546_1	H05	8562	3	2326.5	(+0.8)	4.089	0.383	0.998	2	R.AM@FL*QPDL*DSL*VDFSTNNQK#.K
GPN:BC050546_1	H05	11154	2	2105.4	(+0.7)	2.598	0.304	0.936	2	R.EAVSSAFFSLLQTLSTQFK.Q
GPN:BC050546_1	H05	9260	2	1719.0	(+0.8)	4.027	0.521	0.999	2	R.FLSPPALQGYVAWL.R.A
GPN:BC050546_1	H05	7726	2	1330.6	(+0.1)	3.421	0.448	0.984	2	R.K#AL*VDIL*SEVSK#.A
GPN:BC050546_1	H05	7728	2	1302.6	(-0.1)	3.106	0.490	0.986	2	R.KALVDILSEVSK.A
GPN:BC050546_1	H05	8372	2	1223.5	(+0.9)	2.900	0.506	0.994	2	R.KLPAIALDLLR.L
GPN:BC050546_1	H05	8804	2	1228.5	(+0.8)	3.527	0.553	1.000	3	R.VLDLVEVLVTK.Q
GPN:BC050546_1	H05	8800	2	1254.5	(+0.4)	3.204	0.505	1.000	3	R.VL*DL*VEVL*VTK#.Q
GPN:BC050546_1	H06	9216	2	1719.0	(+0.7)	2.384	0.233	0.781	2	R.FLSPPALQGYVAWL.R.A
GPN:BC050674_1	H15	8674	2	2038.4	(+1.0)	3.793	0.624	1.000		R.AVPLAVPLGQTEVFQALQR.L
GPN:BC050674_1	H15	4790	2	1373.5	(+0.8)	3.832	0.443	0.994	1	R.SPEVLSSGGEDGAVR.L
GPN:BC050674_1	H15	4792	2	1379.5	(+0.9)	3.720	0.460	0.997	1	R.SPEVL*SSGGEDGAVR.L
GPN:BC053908_1	H10	4963	2	1488.7	(+0.0)	4.031	0.421	0.984	1	K.AGGAAVVITEPEHTK#.E
GPN:BC053908_1	H10	4981	2	1480.7	(+0.1)	3.778	0.448	0.985	1	K.AGGAAVVITEPEHTK.E
GPN:BC053908_1	H11	5392	2	1488.7	(+0.9)	4.510	0.424	1.000	1	K.AGGAAVVITEPEHTK#.E
GPN:BC053908_1	H11	5310	2	1488.7	(+0.2)	2.892	0.247	0.829	1	K.AGGAAVVITEPEHTK#.E
GPN:BC053908_1	H13	4650	2	1480.7	(-0.1)	3.525	0.391	0.977	1	K.AGGAAVVITEPEHTK.E
GPN:BC053908_1	H16	4490	2	1488.7	(+0.4)	3.070	0.321	0.966	1	K.AGGAAVVITEPEHTK#.E
GPN:BC053908_1	H18	4816	2	1480.7	(+0.4)	3.857	0.490	0.999	1	K.AGGAAVVITEPEHTK.E
GPN:BC053908_1	H10	6437	2	1304.4	(+0.6)	2.297	0.218	0.817	1	R.NL*GQNL*WGPHR.Y
GPN:BC053908_1	H11	6620	2	1304.4	(+0.3)	2.829	0.302	0.784	1	R.NL*GQNL*WGPHR.Y
GPN:BC053908_1	H12	6350	2	1292.4	(+0.9)	2.587	0.469	0.989	1	R.NL*GQNL*WGPHR.Y
GPN:BC053908_1	H16	5888	2	1304.4	(+0.4)	2.498	0.202	0.853	1	R.NL*GQNL*WGPHR.Y
GPN:BC053908_1	H22	4870	2	1480.7	(+0.7)	4.153	0.505	1.000	1	K.AGGAAVVITEPEHTK.E
GPN:BC054004_1	H08	9585	2	2011.3	(-1.0)	4.692	0.612	1.000	6	K.APVDFGYVGIDSILEQMR.R
GPN:BC054004_1	H08	9569	2	2011.3	(+0.3)	4.317	0.636	1.000	6	K.APVDFGYVGIDSILEQMR.R
GPN:BC054004_1	H08	8535	2	2033.3	(-0.2)	3.041	0.348	0.949	6	K.APVDFGYVGIDSIL*EQM@R.R
GPN:BC054004_1	H09	9597	2	2011.3	(-0.1)	4.327	0.511	1.000	6	K.APVDFGYVGIDSILEQMR.R
GPN:BC054004_1	H09	9599	2	2017.3	(-0.6)	3.546	0.584	1.000	6	K.APVDFGYVGIDSIL*EQMR.R
GPN:BC054004_1	H14	9399	2	2011.3	(+0.6)	5.738	0.680	1.000	6	K.APVDFGYVGIDSILEQMR.R
GPN:BC054004_1	H14	9397	2	2017.3	(+1.0)	5.421	0.611	1.000	6	K.APVDFGYVGIDSIL*EQMR.R
GPN:BC054004_1	H08	1971	2	1072.2	(+0.9)	2.563	0.349	0.976	6	K.SITHDIEEK.G
GPN:BC054004_1	H08	1979	2	1080.2	(+0.9)	2.345	0.163	0.755	6	K.SITHDIEEK#.G
GPN:BC054004_1	H08	5097	2	1472.7	(+0.1)	3.523	0.457	0.983	4	K.VPEVPTAPATDAAPK#.R
GPN:BC054004_1	H08	5101	2	1464.7	(+0.4)	3.214	0.400	0.987	4	K.VPEVPTAPATDAAPK.R
GPN:BC054004_1	H09	5175	2	1464.7	(+0.1)	3.281	0.379	0.968	4	K.VPEVPTAPATDAAPK.R
GPN:BC054004_1	H09	5181	2	1472.7	(-0.0)	2.638	0.320	0.879	4	K.VPEVPTAPATDAAPK#.R
GPN:BC054004_1	H14	2121	2	1080.2	(+0.7)	2.461	0.251	0.917	6	K.SITHDIEEK#.G

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
PIR1:S64732	H05	6556	3	2864.0	(+0.1)	4.567	0.349	0.942	4	K.SEPVK#EESSEL*EQPFAQDTSSVGPDR.K
PIR1:S64732	H05	6560	3	2850.0	(+0.5)	4.501	0.381	0.986	4	K.SEPVKEESSELEQPFAQDTSSVGPDR.K
PIR1:S64732	H05	7218	2	1361.5	(+0.3)	2.471	0.406	0.950	2	R.NFWVWGL*STTR.A
PIR1:UQHUB	H21	6122	2	1068.3	(+0.9)	2.241	0.233	0.867	65	K.ESTLHLVLR.L
PIR1:UQHUB	H19	6480	2	1789.0	(+0.4)	2.219	0.354*	0.116	58	K.TITLEVEPSDTIENVK.A
PIR1:UQHUB	H22	6470	2	1789.0	(+0.8)	3.684	0.536*	0.653	58	K.TITLEVEPSDTIENVK.A
PIR1:UQHUB	H22	6468	2	1803.0	(+0.3)	3.431	0.492	0.986	58	K.TITL*EVEPSDTIENVK#.A
PIR1:UQHUB	H19	4422	2	1096.2	(+0.4)	2.245	0.389	0.967	67	R.TL*SDYNIQK#.E
PIR1:UQHUB	H22	4596	2	1096.2	(+0.4)	2.602	0.374	0.979	67	R.TL*SDYNIQK#.E
PIR2:A38219	H10	9759	2	2247.5	(+0.9)	5.388	0.570	0.996	2	K.DSLDPSFTHAMQLLTAEIEK.I
PIR2:A38219	H10	7355	2	1781.9	(+0.3)	3.134	0.542	1.000	3	K.K#DDEENYL*DL*FSHK#.N
PIR2:A38219	H10	7547	2	1645.7	(+0.4)	3.052	0.354	0.978	3	K.DDEENYL*DL*FSHK#.N
PIR2:A42184	H03	4786	2	1017.1	(+0.8)	2.735	0.287	0.967	2	R.AEELGQELK.A
PIR2:A42184	H03	8368	2	1514.8	(+0.8)	4.771	0.476	1.000		K.GEVLGDVLQLETLK.Q
PIR2:A42184	H04	5467	2	1233.4	(+0.5)	2.793	0.322	0.970	1	K.LADDLSTLQEK.M
PIR2:A42184	H03	6228	2	1188.4	(+0.9)	3.258	0.477	1.000	3	K.VLEGSELELAK.M
PIR2:A42184	H03	5686	2	1049.2	(+0.6)	2.367	0.188	0.805	2	K.YVQELAAVR.A
PIR2:A42184	H04	4419	2	1256.4	(+0.7)	2.228	0.363	0.953		R.HQVEQLSSSLK.Q
PIR2:A54857	H13	7782	2	1790.1	(-0.1)	2.679	0.117	0.419		K.GTMTTGHNVADL*VVIL*K#.I
PIR2:A54857	H13	8074	2	1436.7	(-0.2)	2.722	0.185	0.658		K.IL*PTL*EAVAAL*GNK#.V
PIR2:A54857	H13	2266	2	887.0	(+0.4)	2.347	0.291	0.948	1	R.ILSHGGFR.K
PIR2:A54857	H13	7930	2	2100.3	(+0.6)	4.759	0.632	1.000		R.NQDLAPNSAEQASILSLVTK.I
PIR2:A54857	H13	7942	3	2100.3	(-0.0)	4.690	0.607	1.000		R.NQDLAPNSAEQASILSLVTK.I
PIR2:A54857	H13	7672	2	2256.5	(+0.2)	2.900	0.443	0.973		K.RNQDLAPNSAEQASILSLVTK.I
PIR2:A54857	H13	6412	2	1054.3	(+0.7)	3.289	0.369	0.990	1	K.VL*QSAL*AAIR.H
PIR2:A54857	H13	5314	2	1434.5	(+0.4)	3.575	0.516	0.999	1	R.WFEENASQSTVK#.V
PIR2:A54857	H19	6500	2	1761.0	(-0.6)	2.318	0.429	0.338		R.VK#PAPDETSFSEAL*L*K#.R
PIR2:G02919	H09	8069	2	1574.8	(+0.6)	2.873	0.418	0.986	6	R.AYIVQL*QIEDL*TR.K
PIR2:G02919	H08	1709	2	1482.6	(+0.1)	2.394	0.366	0.264	6	K.FQRPGDPQSAQDK#.A
PIR2:G02919	H07	8408	3	2937.4	(+0.4)	3.873	0.451	0.993	6	R.HNLITEMVALNPDPFKPPADYKPPATR.V
PIR2:G02919	H09	8209	3	2965.4	(-0.3)	5.027	0.454	0.994	6	R.HNL*ITEMVAL*NPDPFK#PPADYK#PPATR.V
PIR2:G02919	H08	5679	2	1379.6	(+0.5)	3.167	0.243	0.499	6	R.IL*RPWQSSETR.S
PIR2:G02919	H09	5719	2	1379.6	(-0.3)	2.937	0.271	0.306	6	R.IL*RPWQSSETR.S
PIR2:G02919	H09	5709	2	1373.6	(+0.5)	2.745	0.368	0.649	6	R.ILRPWQSSETR.S
PIR2:G02919	H09	1789	2	1482.6	(+0.8)	2.256	0.468	0.622	6	K.FQRPGDPQSAQDK#.A
PIR2:I38414	H03	6728	2	1023.2	(+0.9)	2.426	0.431	0.985	1	K.ALVGDFMNR.R
PIR2:I38414	H03	7782	2	1212.4	(+0.8)	2.387	0.384	0.970	3	R.L*IESL*FTIQK#.M
PIR2:I38414	H03	6168	2	1049.2	(+0.3)	2.563	0.220	0.833	3	R.NL*SEEGL*L*R.L
PIR2:I38414	H03	6174	2	1031.2	(+0.8)	2.549	0.342	0.973	3	R.NLSEEGLLR.L
PIR2:I38414	H03	8518	3	2253.6	(+0.8)	5.581	0.392	0.981	2	R.RDPVALEDVYPIHMILENK.D
PIR2:I38414	H03	8002	3	2289.6	(-0.7)	4.035	0.373	0.986	2	R.RDPVAL*EDVYPIHM@IL*ENK#.D
PIR2:I38414	H04	8401	3	2253.6	(+0.9)	4.274	0.351	0.964	2	R.RDPVALEDVYPIHMILENK.D
PIR2:I38414	H03	7926	2	1374.6	(+0.6)	2.540	0.379	0.976	1	R.YIFSVVENL*QR.L
PIR2:I38414	H04	8265	2	1256.5	(+0.6)	2.429	0.327	0.937	3	R.NLIIEAVTNLR.L
PIR2:I38968	H06	8264	2	1973.1	(+0.8)	2.716	0.409	0.979	2	K.DTNGENIAESL*VAEGL*ATR.R
PIR2:I38968	H06	8450	2	2307.6	(+0.2)	4.944	0.523	1.000	3	R.NLPGLVQEGEPFSEEATLFTK.E
PIR2:I38968	H06	6126	2	1162.3	(-0.1)	2.263	0.169	0.518	2	R.L*GTL*SPAFSTR.V
PIR2:JC7168	H08	7233	2	1647.8	(+0.1)	3.400	0.301	0.943	5	K.GFNEGL*WEIDNPNK#.V
PIR2:JC7168	H08	7235	2	1633.8	(+0.1)	3.178	0.283	0.927	5	K.GFNEGLWEIDNPNK.V
PIR2:JC7168	H08	9051	2	1943.3	(+0.7)	4.225	0.646	1.000	5	K.L*PIFFFGTHETAFL*GPK#.D
PIR2:JC7168	H08	9041	2	1923.3	(-0.1)	3.740	0.617	0.999	5	K.LPIFFFGTHETAFLGPK.D
PIR2:JC7168	H08	9035	2	1985.3	(+0.9)	4.624	0.509	1.000	3	K.NMFL*VGEEDSVITQVL*NK#.S
PIR2:JC7168	H08	9047	2	1965.3	(+0.2)	4.157	0.572	0.991	3	K.NMFLVGEEDSVITQVLNK.S
PIR2:JC7168	H09	9039	2	1965.3	(+0.1)	4.846	0.527	0.780	3	K.NMFLVGEEDSVITQVLNK.S
PIR2:JC7168	H09	8427	2	2001.3	(-0.3)	3.536	0.478	0.985	3	K.NM@FL*VGEEDSVITQVL*NK#.S
PIR2:JC7168	H08	2381	2	1566.8	(+0.7)	2.651	0.335	0.361	6	R.VDEVPDGAVKPPTNK.L
PIR2:JC7168	H10	9155	2	1965.3	(+0.5)	4.056	0.526	1.000	3	K.NMFLVGEEDSVITQVLNK.S

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PIR2:JC7363	H05	6868	3	2573.7	(+0.3)	4.652	0.475	0.939	4	K.K#EEL*VPSEEDFQGITPGAQGPSSR.G
PIR2:JC7363	H05	6520	2	1443.6	(+0.2)	2.529	0.284	0.861	4	R.RLQDLATQLQE.K
PIR2:JC7363	H05	2258	2	1569.6	(+0.3)	2.511	0.442	0.957	3	R.GDSEPLSEAAQAHR.E
PIR2:JE0291	H06	9740	3	3302.7	(+0.6)	5.117	0.514	1.000	1	K.GPQGPGGGGINVQEILTSIMGSPNSHPSEELLK.Q
PIR2:JE0291	H06	9738	3	3328.7	(-0.3)	4.343	0.429	0.998	1	K.GPQGPGGGGINVQEIL*TSIMGSPNSHPSEEL*L*K#.Q
PIR2:JE0291	H06	8808	3	3344.7	(-0.1)	4.260	0.344	0.990	1	K.GPQGPGGGGINVQEIL*TSIM@GSPNSHPSEEL*L*K#.Q
PIR2:JE0291	H06	9110	2	1582.9	(-0.3)	2.495	0.249	0.728	1	K.L*PPVL*ANL*MGSMGAGK#.G
PIR2:S43974	H10	8553	2	2287.6	(-0.2)	3.102	0.429	0.971	1	K.DSL*DPSFTHAMQL*L*SVEIEK#.K
PIR2:S43974	H10	7269	2	1780.9	(+0.4)	4.563	0.560*	0.836		K.K#DDEENYL*NL*FSHK#.E
PIR2:S43974	H10	8473	2	2287.6	(-0.0)	2.936	0.229	0.666	1	K.DSL*DPSFTHAMQL*L*SVEIEK#.K
PIR2:S47271	H03	7102	2	1704.9	(-0.2)	3.040	0.445*	0.222	1	K.VDIDVPDVNIEGPKDAK#.L
PIR2:S47271	H03	5708	2	1179.4	(+0.1)	2.738	0.350*	0.011	8	K.VK#GDVDVSL*PK#.V
PIR2:S47271	H03	7480	2	1279.5	(+0.6)	2.253	0.358*	0.164	3	K.ISMPEVDL*NL*K#.G
PIR2:S49326	H16	7216	2	1550.9	(+0.5)	3.758	0.418	0.854	1	K.NILFVITKPDVYK.S
PIR2:S49326	H17	6062	2	1485.6	(+0.8)	4.716	0.560	1.000		K.SPASDTYIVFGEAK.I
PIR2:S50852	H08	9613	3	1765.0	(+0.9)	4.576	0.469	1.000	2	R.FL*AFESNIGDL*ASIL*K#.V
PIR2:S50852	H08	9607	2	1765.0	(-0.3)	2.494	0.357	0.896	2	R.FL*AFESNIGDL*ASIL*K#.V
PIR2:S50852	H08	8925	2	1913.4	(+0.9)	3.042	0.432	0.988	2	K.LAAIIPDPVVAPSIVPK.D
PIR2:S50852	H08	9327	2	1966.2	(-0.2)	2.945	0.306	0.916	2	K.L*EENPYDL*DAWSIL*IR.E
PIR2:S50852	H08	6463	2	1428.5	(-0.2)	3.272	0.436	0.983	1	K.LFSDEAANIYER.A
PIR2:S50852	H08	6451	2	1434.5	(-0.2)	2.926	0.319	0.941	1	K.L*FSDEAANIYER.A
PIR2:S50852	H08	9649	2	2139.6	(+0.8)	2.865	0.396	0.981	1	R.LLAIEDIDPTLVYIQYMK.F
PIR2:S50852	H08	5109	2	1068.2	(+0.7)	2.468	0.314	0.955	2	R.L*VAQFPSSGR.F
PIR2:S50852	H08	1945	2	1049.2	(+0.7)	2.595	0.216	0.917	1	R.TEDQLITK.R
PIR2:S50852	H08	6099	2	1303.4	(+0.6)	2.206	0.271	0.862	1	K.M@AQAYDFAL*DK#.I
PIR2:S57447	H10	11219	2	2453.7	(-0.5)	4.626	0.586	0.998	4	R.AVSDASAGDYGSAIETLVTAISLIK.Q
PIR2:S57447	H10	11215	2	2473.7	(+0.7)	4.575	0.560	0.999	4	R.AVSDASAGDYGSAIETL*VTAISL*IK#.Q
PIR2:S57447	H11	11306	3	2473.7	(+0.6)	4.211	0.455	0.998	4	R.AVSDASAGDYGSAIETL*VTAISL*IK#.Q
PIR2:S57447	H09	5619	2	1341.5	(+0.6)	2.592	0.573	0.994	4	K.GAAPNVVYTYTGK.R
PIR2:S57447	H10	5845	2	1341.5	(+0.9)	2.748	0.529	0.993	4	K.GAAPNVVYTYTGK.R
PIR2:S57447	H09	7637	2	1672.8	(+0.3)	4.086	0.425	1.000	4	R.TPL*SEAEFEEIMNR.N
PIR2:S57447	H12	7584	2	1672.8	(-0.8)	2.360	0.300	0.578	4	R.TPL*SEAEFEEIMNR.N
PIR2:T00034	H06	5018	2	1257.4	(+0.8)	3.816	0.451	1.000	1	R.LQAQSLSTVGR.L
PIR2:T00034	H06	8690	2	2104.2	(+0.4)	3.956	0.487	1.000	1	K.TLGEDDPWLDTTAAWIER.S
PIR2:T00034	H06	8708	2	2116.2	(-0.1)	3.537	0.337	0.965	1	K.TL*GEDDPWL*DDTAAWIER.S
PIR2:T00034	H06	5006	2	1269.4	(+0.4)	3.267	0.523	1.000	1	R.L*QAQSL*STVGR.L
PIR2:T00059	H04	4911	2	1305.4	(+0.4)	2.634	0.455	0.986		K.SNAVQEADSEL*K#.Q
PIR2:T00059	H04	4209	2	1291.4	(+0.4)	2.298	0.424	0.973		R.L*AAQSQHVGFAR.S
PIR2:T00372	H04	8425	2	1284.5	(+0.7)	2.857	0.543	1.000	2	R.ANL*GVFSVFAPR.G
PIR2:T00372	H04	6077	2	1569.8	(+0.3)	2.474	0.194	0.032	2	K.EKDQLSQSIVMYK.S
PIR2:T00372	H04	6243	2	1623.7	(+0.5)	4.373	0.519	1.000	2	K.GSNEEDTDTPLFIGK.V
PIR2:T00372	H04	6237	2	1637.7	(-0.3)	3.427	0.434	0.979	2	K.GSNEEDTDTPL*FIGK#.V
PIR2:T00372	H04	5411	2	1281.4	(+0.7)	3.251	0.387	0.987	2	K.IAHLAQIEDDR.A
PIR2:T00372	H04	7819	3	2301.7	(-0.3)	4.672	0.387	0.992	2	K.IHNIDIPTTQQVPHIEAL*L*K#.R
PIR2:T00372	H04	7837	3	2281.7	(+0.9)	4.439	0.443	1.000	2	K.IHNIDIPTTQQVPHIEALLK.R
PIR2:T00372	H04	7589	2	1523.8	(+0.5)	2.636	0.332	0.435	3	K.LYFKPIGDPVFAR.D
PIR2:T00372	H04	5169	2	1024.2	(+0.4)	2.670	0.366	0.977	1	R.VQL*ISGPPAK#.L
PIR2:T00372	H04	5173	2	1010.2	(+1.0)	2.595	0.330	0.969	1	R.VQLISGPPAK.L
PIR2:T00372	H04	8869	2	1272.5	(-0.1)	2.344	0.202	0.660	1	K.L*L*IDWPEL*K#.E
PIR2:T00374	H05	2078	2	1556.7	(+0.7)	3.572	0.545	1.000	2	R.AAVGQESPGGLEAGNAK.A
PIR2:T00374	H05	2076	2	1570.7	(-0.4)	2.642	0.152	0.517	2	R.AAVGQESPGGL*EAGNAK#.A
PIR2:T00374	H05	8530	2	1530.8	(+0.0)	3.773	0.313	0.964	1	K.EVQLAQIFELSR.S
PIR2:T00374	H05	8504	2	1542.8	(+0.7)	2.660	0.247	0.912	1	K.EVQL*AQIFEL*SR.S
PIR2:T00374	H05	2808	2	1165.2	(+0.7)	3.101	0.403	0.990	2	K.FNQVLGDDEK.L
PIR2:T00374	H05	2928	2	1165.2	(+0.5)	2.905	0.346	0.982	2	K.FNQVLGDDEK.L
PIR2:T00374	H05	2574	2	1179.2	(+0.8)	2.399	0.264	0.907	2	K.FNQVL*GDDEK#.L

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
PIR2:T00374	H05	2648	2	1179.2	(+0.7)	2.368	0.210	0.831	2	K.FNQVL*GDDEK#.L
PIR2:T00374	H05	2796	2	1179.2	(+0.1)	2.238	0.254	0.739	2	K.FNQVL*GDDEK#.L
PIR2:T00374	H05	2940	2	1179.2	(+0.4)	2.221	0.304	0.913	2	K.FNQVL*GDDEK#.L
PIR2:T00374	H05	7754	2	1678.0	(-0.0)	3.229	0.430	0.974	1	R.IAPVHIDSEAISAL*VK#.L
PIR2:T00374	H05	7294	2	1699.9	(+0.8)	3.815	0.521	1.000	1	K.LWSPDEEVSPVELAK.V
PIR2:T00374	H05	8056	2	1642.0	(+0.0)	2.490	0.206	0.644	2	K.LYTVCDVALCVINSK.S
PIR2:T00374	H05	5686	3	2356.4	(+0.9)	5.192	0.477	0.993	2	R.STGTETGSNINVNSEL*NPSTGNR.S
PIR2:T00374	H05	5694	3	2350.4	(+0.4)	3.947	0.398	0.998	2	R.STGTETGSNINVNSELNPSTGNR.S
PIR2:T00374	H05	1864	2	1339.5	(-0.6)	2.604	0.256	0.806	2	R.TVTAAGAENIQK#.T
PIR2:T00374	H05	1650	2	1345.5	(-0.7)	2.244	0.242	0.023	2	K.VDESGPPAPSK#PR.R
PIR2:T00374	H05	2724	2	1179.2	(+0.2)	2.214	0.386	0.916	2	K.FNQVL*GDDEK#.L
PIR2:T02632	H03	7534	2	1657.8	(+0.5)	4.077	0.476	1.000	2	R.FVDFNDPNFGDELK.A
PIR2:T02632	H03	7546	2	1671.8	(+0.2)	3.649	0.434	0.983	2	R.FVDFNDPNFGDEL*K#.A
PIR2:T02632	H04	7373	2	1671.8	(+0.3)	3.358	0.445	0.981	2	R.FVDFNDPNFGDEL*K#.A
PIR2:T02632	H03	6802	2	1348.5	(+0.7)	3.447	0.413	0.992	2	R.LGFTPSVTIEQR.R
PIR2:T02632	H03	6788	2	1354.5	(+0.4)	2.506	0.409	0.974	2	R.L*GFTPSVTIEQR.R
PIR2:T02632	H04	4797	2	994.2	(+0.4)	2.232	0.134	0.607	2	R.IYQELVTK.Y
PIR2:T08599	H05	5740	2	1171.3	(-0.3)	2.308	0.339	0.903		R.K#QVFDQYVK#.T
PIR2:T08599	H05	6756	2	1315.5	(+1.0)	4.181	0.379	1.000		K.LFNEHIEALTK.K
PIR2:T08599	H05	6748	2	1335.5	(+0.5)	3.237	0.428	0.991		K.L*FNEHIEAL*TK#.K
PIR2:T08599	H05	7388	2	1304.5	(+0.4)	2.562	0.398	0.975		K.L*IVAYVDDL*DR.R
PIR2:T08599	H04	7055	2	1460.7	(+0.7)	2.203	0.321	0.302		K.L*IVAYVDDL*DRR.G
PIR2:T08599	H05	6372	2	1589.8	(+0.6)	3.701	0.483	0.980		R.TLESTWEKPELQK.E
PIR2:T08599	H05	6364	2	1617.8	(-0.5)	2.656	0.201	0.085		R.TL*ESTWEK#PQEL*K#.E
PIR2:T08599	H05	1934	2	1231.4	(+0.9)	2.234	0.172	0.696		K.L*IQESDQHL*K#.D
PIR2:T08661	H19	5858	2	1851.0	(+0.3)	4.210	0.567	1.000	2	R.VGYVNNYEYETELR.E
PIR2:T08661	H19	6026	2	1441.5	(+0.7)	3.487	0.142	0.924	2	R.FHINWEDNTEK#.L
PIR2:T08745	H06	8948	2	1625.9	(-0.1)	3.179	0.393	0.973	5	K.EL*L*DL*AMQNAWFR.K
PIR2:T08745	H06	5072	2	1343.5	(-0.1)	3.704	0.458	0.994	2	K.K#ANAEEL*ANNL*K#.Q
PIR2:T08745	H06	1450	2	1211.3	(+0.6)	2.283	0.360	0.950	5	R.NL*EGANQHVSQ#.E
PIR2:T08745	H06	4682	2	1303.4	(+0.3)	2.820	0.410	0.965	5	K.SHFVAASL*SNQK#.A
PIR2:T08745	H06	4694	2	1289.4	(+0.5)	2.224	0.167	0.467	5	K.SHFVAASLSNQK.A
PIR2:T12456	H12	8556	2	1965.1	(-0.2)	2.615	0.269	0.804	6	R.FDQL*FDESDFEVL*K#.A
PIR2:T12456	H12	1536	2	1270.4	(+0.9)	2.842	0.440	0.988	6	R.RPDQQL*QGEGK#.I
PIR2:T12456	H12	1334	2	1469.5	(+0.8)	4.092	0.573	1.000	4	K.SAAQAAAQNTNSNAAGK#.Q
PIR2:T12456	H12	1408	2	1461.5	(+0.4)	3.877	0.535	1.000	4	K.SAAQAAAQNTNSNAAGK#.Q
PIR2:T12456	H12	1424	2	1469.5	(+0.4)	3.803	0.608	0.997	4	K.SAAQAAAQNTNSNAAGK#.Q
PIR2:T12456	H12	1330	2	1461.5	(+0.4)	3.617	0.561	1.000	4	K.SAAQAAAQNTNSNAAGK#.Q
PIR2:T12456	H12	1256	2	1469.5	(+0.4)	2.622	0.521	0.989	4	K.SAAQAAAQNTNSNAAGK#.Q
PIR2:T12456	H12	5282	3	2121.2	(+0.8)	4.095	0.528	0.999	7	K.SK#SEEAHAEDSVMDHHR.K
PIR2:T12456	H12	1248	2	1461.5	(+0.1)	2.282	0.329	0.838	4	K.SAAQAAAQNTNSNAAGK#.Q
PIR2:T12471	H16	4246	2	1076.2	(+0.7)	2.689	0.466	0.792	3	R.SLGPSLATDKS.-
PIR2:T12471	H16	3798	2	1264.4	(+0.5)	2.803	0.449	0.989	3	K.VDVTEQPGL*SGR.F
PIR2:T12471	H16	3880	2	1264.4	(+1.0)	2.545	0.455	0.981	3	K.VDVTEQPGL*SGR.F
PIR2:T12471	H16	3792	2	1258.4	(+0.8)	2.519	0.384	0.974	3	K.VDVTEQPGLSGR.F
PIR2:T12518	H03	8064	2	1490.7	(+0.7)	2.826	0.322	0.947	2	R.GL*EEIPVFDISEK#.T
PIR2:T12518	H03	8072	2	1476.7	(+0.7)	2.806	0.363	0.976	2	R.GLEEIPVFDISEK.T
PIR2:T12518	H03	8944	2	1849.2	(-0.5)	3.049	0.405	0.964	2	R.L*VSDIIDPVAL*EIPL*SK#.N
PIR2:T12518	H04	8815	2	1823.2	(+0.7)	3.940	0.436	0.994	2	R.LVSDIIDPVALEIPLSK.N
PIR2:T12518	H04	8805	2	1849.2	(+0.2)	3.249	0.497	0.984	2	R.L*VSDIIDPVAL*EIPL*SK#.N
PIR2:T12518	H03	7160	2	1449.6	(+0.9)	3.970	0.454	0.998	3	K.TIGDLSTLTASEIK.T
PIR2:T12518	H03	7156	2	1469.6	(+0.1)	3.022	0.373	0.955	3	K.TIGDL*STL*TASEIK#.T
PIR2:T12518	H03	7878	2	1973.1	(-0.6)	3.196	0.391	0.891	2	R.VSFADPIYQAGL*ADDIDR.R
PIR2:T12518	H04	7759	2	1973.1	(-0.5)	2.643	0.253	0.804	2	R.VSFADPIYQAGL*ADDIDR.R
PIR2:T12518	H05	8928	2	1823.2	(+0.1)	2.918	0.375	0.953	2	R.LVSDIIDPVALEIPLSK.N
PIR2:T12519	H08	4291	2	1060.1	(+0.4)	2.491	0.270	0.941	6	K.ADTL*TL*EER.V
PIR2:T12519	H08	4371	2	1060.1	(+0.3)	2.360	0.288	0.775	6	K.ADTL*TL*EER.V
PIR2:T12519	H09	4651	2	1060.1	(+0.7)	2.394	0.185*	0.260	6	K.ADTL*TL*EER.V

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
PIR2:T12519	H14	4915	2	1048.1	(-0.6)	2.566	0.249*	0.160	6	K.ADTLTLEER.V
PIR2:T12519	H14	2329	2	1065.1	(+0.9)	2.422	0.132	0.754	7	K.FINDQYEK#.Y
PIR2:T12519	H14	7611	3	2871.0	(+0.9)	4.666	0.491	0.998	6	R.ITADLLSNGIDVYPQKEFDESEDRL
PIR2:T12519	H14	5349	2	1278.4	(+0.9)	3.954	0.406	1.000	7	K.YLQEEVNINR.K
PIR2:T12519	H14	5347	2	1284.4	(-0.1)	2.805	0.281	0.923	7	K.YL*QEEVNINR.K
PIR2:T12519	H17	4288	2	1048.1	(+0.2)	2.342	0.221	0.763	6	K.ADTLTLEER.V
PIR2:T14790	H03	6130	3	1605.7	(+1.0)	3.841	0.414	0.997	3	K.K#HEAFETDFTVHK#.D
PIR2:T14790	H04	2367	2	1724.9	(+0.5)	2.819	0.467	0.988	4	R.LIQSHPESAEDLQEK.C
PIR2:T14790	H05	2346	2	1724.9	(+0.4)	3.039	0.535	0.994	4	R.LIQSHPESAEDLQEK.C
PIR2:T17282	H05	4640	2	1230.4	(+1.0)	2.619	0.403	0.679	4	R.DKSDSPAQLR.L
PIR2:T17282	H05	4560	2	1230.4	(+0.4)	2.591	0.429	0.717	4	R.DKSDSPAQLR.L
PIR2:T17282	H05	9290	3	2546.9	(+0.7)	4.479	0.417	0.994	4	R.LKEPMDVDVEDYYPFLDMVR.S
PIR2:T17282	H05	7106	2	1931.0	(-0.5)	3.466	0.322	0.957	4	R.SL*L*DGNIDSSQYEDSL*R.E
PIR2:T17282	H05	4652	2	1244.4	(+0.1)	2.300	0.295	0.166	4	R.DK#SDSPAQLR.L
PIR2:T42659	H02	4908	2	1590.6	(-0.4)	3.248	0.377	0.969	3	K.DASSTYSQVENL*NR.E
PIR2:T42659	H02	4910	2	1584.6	(-0.3)	3.016	0.329	0.942	3	K.DASSTYSQVENLNR.E
PIR2:T42659	H01	4638	2	1482.6	(-0.2)	2.339	0.327	0.851	3	K.FM@ATL*GPEEEAEK#.A
PIR2:T42659	H02	5408	2	1452.6	(+0.3)	2.980	0.430	0.976	3	K.FMATLGPEEEAEK.A
PIR2:T42659	H02	5048	2	1482.6	(+0.0)	2.825	0.311	0.911	3	K.FM@ATL*GPEEEAEK#.A
PIR2:T42659	H02	7098	2	2146.4	(-0.0)	4.865	0.542	1.000	3	K.LEELSLEGNPFLTVDNLK.V
PIR2:T42659	H01	6732	3	3085.4	(+0.6)	6.433	0.560	1.000	2	R.LTQLQELDLSNNHLETLPDNLGLSHLR.V
PIR2:T42659	H02	6890	3	3085.4	(+0.5)	7.111	0.576	0.998	2	R.LTQLQELDLSNNHLETLPDNLGLSHLR.V
PIR2:T42659	H01	5166	2	1411.6	(+0.7)	3.078	0.451	0.991	3	K.RPDDVPLSLSPSK.R
PIR2:T42659	H02	5392	2	1431.6	(-0.4)	2.856	0.145	0.635	3	K.RPDDVPL*SL*SPSK#.R
PIR2:T42659	H02	6596	2	1600.7	(+0.7)	3.020	0.400	0.986	3	R.YGPESLSEFTQWR.V
PIR2:T42659	H02	6602	2	1606.7	(+0.2)	2.627	0.383	0.947	3	R.YGPESL*SEFTQWR.V
PIR2:T46248	H05	5964	2	1431.6	(-0.1)	2.723	0.391	0.956	7	R.AVGPSSTQL*YM@VR.T
PIR2:T46248	H05	6026	2	1258.4	(+0.1)	2.226	0.249	0.698	6	K.TVEVL*EPEVTK#.L
PIR2:T46248	H06	5770	2	1258.4	(+0.8)	2.204	0.201	0.729	6	K.TVEVL*EPEVTK#.L
PIR2:T46248	H07	5598	2	1431.6	(+0.6)	2.201	0.218	0.740	7	R.AVGPSSTQL*YM@VR.T
PIR2:T46334	H11	7924	2	1523.7	(+0.3)	3.108	0.401	0.969	2	R.L*DIISEDISEL*QK#.N
PIR2:T46334	H11	7408	2	1923.1	(+0.1)	2.536	0.283	0.808	4	R.VQL*DTIQGEL*NAPTQFK#.V
PIR2:T46344	H11	5822	2	1310.5	(+0.4)	2.627	0.510	0.991	4	K.L*VMEEAPESYK#.N
PIR2:T46344	H11	7508	2	1207.3	(-0.3)	2.867	0.433	0.980	4	R.NLDFQDVLDK.L
PIR2:T46344	H11	7494	2	1227.3	(+0.5)	2.755	0.298	0.962	4	R.NL*DFQDVL*DK#.L
PIR2:T46344	H11	1624	2	1019.1	(+1.0)	2.496	0.408	0.982	4	K.VEQHVVDGK#.E
PIR2:T46344	H11	5628	2	982.2	(+1.0)	2.275	0.315	0.945	4	K.L*ADM@GIAIR.V
PIR2:T46440	H19	8474	2	1367.6	(+0.4)	2.409	0.236	0.837	1	R.SLLEPFVYLASK.M
PIR2:T46440	H19	5998	2	1081.2	(+0.9)	2.248	0.264	0.903	2	K.L*WEVSVADR.R
PIR2:T47145	H05	8110	3	2060.3	(+0.1)	4.465	0.307	0.990	10	R.HEYGSPGIL*EFFHHQL*K#.D
PIR2:T47145	H05	10910	2	1809.2	(+0.4)	2.629	0.513	0.989	10	R.L*L*GYQGIIVMEEL*L*K#.I
PIR2:T47145	H05	8400	2	1389.6	(+0.0)	2.500	0.368	0.925	11	K.SL*L*QGTL*QYVK#.T
PIR2:T50630	H11	7540	2	1412.7	(+0.7)	2.980	0.236	0.924	3	K.DGQIL*PVPNVVVR.D
PIR2:T50630	H11	7842	3	2057.2	(+0.9)	4.186	0.441	0.999	3	R.NHTL*AL*TETGSVFAGENK#.M
PIR2:T50630	H11	8380	3	3248.6	(+0.7)	3.792	0.427	0.988	3	K.SSIIVAADESTISWGSPPTFGELGYGDHKPK.S
PIR2:T50630	H12	8030	3	3248.6	(-0.2)	4.672	0.509	0.999	3	K.SSIIVAADESTISWGSPPTFGELGYGDHKPK.S
PIR2:T50630	H11	7282	2	1635.9	(+0.9)	3.886	0.541	1.000	3	K.TKDGQILPVPNVVVR.D
PIR2:T50630	H11	7274	2	1649.9	(+0.1)	3.814	0.552	1.000	3	K.TK#DGQIL*PVPNVVVR.D
PIR2:T50630	H18	7064	2	1412.7	(+0.7)	2.856	0.220	0.894	3	K.DGQIL*PVPNVVVR.D
SW:143E_HUMAN	H17	3634	2	1238.4	(+0.9)	2.693	0.394	0.981	1	K.HLIPAANTGESK.V
SW:143E_HUMAN	H17	5096	2	1257.3	(+0.3)	2.500	0.305	0.888	2	R.YLAEFATGNDR.K
SW:143E_HUMAN	H17	3582	2	1252.4	(+0.6)	2.382	0.321	0.932	1	K.HL*IPAANTGESK#.V
SW:143G_HUMAN	H17	4868	2	1644.7	(-0.5)	3.984	0.500	1.000	1	K.NVTELNEPLSNEER.N
SW:143G_HUMAN	H17	4872	2	1656.7	(-0.1)	2.827	0.204	0.771	1	K.NVTEL*NEPL*SNEER.N
SW:143G_HUMAN	H17	8034	2	2132.2	(+0.7)	3.183	0.479	0.992	1	K.TAFDDAIAELDTLNEDSYK.D

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:143G_HUMAN	H17	4106	2	1095.2	(+0.7)	3.480	0.350	0.989	1	R.YL*AEVATGEK#R
SW:143G_HUMAN	H18	4462	2	1081.2	(+0.9)	3.069	0.323	0.982	1	R.YLAEVATGEK.R
SW:143T_HUMAN	H17	1586	2	1533.6	(+0.6)	3.818	0.470	1.000		K.AVTEQGAELSNEER.N
SW:143T_HUMAN	H18	8618	2	2146.3	(+0.3)	3.664	0.523	1.000	1	K.TAFDEAIAELDTLNEDSYK.D
SW:143T_HUMAN	H18	5120	2	1335.5	(+0.3)	2.800	0.172	0.711	1	K.YL*IANATNPESK#.V
SW:143T_HUMAN	H18	5102	2	1321.5	(-0.4)	2.218	0.305	0.817	1	K.YLIANATNPESK.V
SW:143Z_HUMAN	H17	6602	2	2042.2	(+0.8)	4.993	0.639	1.000	2	K.GIVDQSQQAYQEAFEISK.K
SW:143Z_HUMAN	H17	1664	2	1549.6	(+0.6)	3.475	0.440	0.993	3	K.SVTEQGAELSNEER.N
SW:143Z_HUMAN	H17	3588	2	1302.4	(-0.1)	2.695	0.335	0.314	2	R.YL*AEVAAGDDK#K#.G
SW:143Z_HUMAN	H17	3510	2	1302.4	(-0.2)	2.562	0.351	0.305	2	R.YL*AEVAAGDDK#K#.G
SW:143Z_HUMAN	H18	2072	2	1549.6	(+0.5)	3.743	0.465	1.000	3	K.SVTEQGAELSNEER.N
SW:3MG_HUMAN	H16	6608	2	1015.2	(+1.0)	2.321	0.373	0.971	8	R.AFL*GQVL*VR.R
SW:3MG_HUMAN	H16	6892	2	1457.6	(+0.7)	3.964	0.487	0.999	9	R.DL*AQDEAVWL*ER.G
SW:3MG_HUMAN	H15	5946	2	1470.7	(+0.5)	2.648	0.177	0.787	9	R.GPL*EPSEPAVVAAR.V
SW:3MG_HUMAN	H15	8558	2	1692.0	(+0.2)	2.492	0.445	0.955	8	R.L*GL*EFFDQPAVPL*AR.A
SW:3MG_HUMAN	H16	7924	2	1674.0	(+0.9)	3.968	0.484	0.996	8	R.LGLEFFDQPAVPLAR.A
SW:3MG_HUMAN	H16	6234	2	1393.6	(-0.2)	2.216	0.344	0.847	8	R.AL*EPL*EGL*ETM@R.H
SW:6PGD_HUMAN	H13	6764	2	1592.7	(+0.6)	4.538	0.570	1.000	3	K.GILFVGSVSGGEEGAR.Y
SW:6PGD_HUMAN	H13	6748	2	1598.7	(+0.1)	3.130	0.413	0.972	3	K.GIL*FVGSVSGGEEGAR.Y
SW:6PGD_HUMAN	H13	9550	2	1706.9	(+0.5)	2.701	0.561	0.994	4	R.NPELQNLLLDDFFK.S
SW:A1B1_HUMAN	H06	8464	2	1569.8	(+0.8)	3.013	0.412	0.986	4	R.LASQANIAQVLAELK.E
SW:A1B1_HUMAN	H06	5040	2	1012.2	(+0.2)	2.298	0.109	0.472	4	K.YNDPIYVK.L
SW:A2B1_HUMAN	H06	9622	2	2017.3	(+0.3)	3.848	0.370	0.920	3	R.APEVSQYIYQVYDSILK.N
SW:A2B1_HUMAN	H06	9698	2	2266.7	(-0.3)	2.969	0.496	0.983	2	K.LAPPLVTLISGEPEVQYVALR.N
SW:A32B_HUMAN	H17	6312	2	1230.4	(+0.6)	2.665	0.144	0.775		R.IFGGL*DM@L*AEK#.L
SW:A32B_HUMAN	H17	7010	2	1194.4	(+0.9)	2.576	0.346	0.969		R.IFGGLDMLAEK.L
SW:A32B_HUMAN	H16	6326	2	1453.6	(-0.2)	2.892	0.333	0.933		K.L*PNL*THL*NL*SGNK#.L
SW:A32B_HUMAN	H17	6214	2	1453.6	(+0.7)	2.917	0.377	0.978		K.L*PNL*THL*NL*SGNK#.L
SW:A32B_HUMAN	H17	6242	2	1421.6	(-0.0)	2.365	0.330	0.847		K.LPNLTHLNLSGNK.L
SW:ABE1_HUMAN	H10	5313	2	1317.4	(+0.6)	3.418	0.322	0.984	1	R.NVEDLSSGELQR.F
SW:ABE1_HUMAN	H10	9773	2	1965.1	(-0.7)	2.792	0.320	0.755	1	K.YDDPPDWQEIL*TYFR.G
SW:ACIN_HUMAN	H04	5857	2	1326.5	(+0.4)	2.942	0.419	0.987	4	K.K#PSISITTESL*K#.S
SW:ACIN_HUMAN	H04	5029	2	1215.4	(+0.6)	2.687	0.346	0.583	4	R.GLLVDRPSETK.T
SW:ACLY_HUMAN	H06	8048	2	1568.8	(-0.5)	3.507	0.482	1.000	3	K.AFDSGIIPMEFVNK.M
SW:ACLY_HUMAN	H06	9750	2	1647.9	(+0.9)	4.475	0.477	1.000	2	K.DLVSSLTSGLLTIGDR.F
SW:ACLY_HUMAN	H06	9754	2	1671.9	(-0.7)	2.510	0.157	0.233	2	K.DL*VSSL*TSGL*L*TIGDR.F
SW:ACLY_HUMAN	H06	2438	2	921.0	(+0.5)	2.785	0.430	0.989	3	R.FGGALDAAK.M
SW:ACLY_HUMAN	H06	8060	2	1398.7	(+0.9)	2.424	0.555*	0.191	1	K.LGLVGVNLTLDGVK.S
SW:ACLY_HUMAN	H06	8484	3	2599.1	(+1.0)	5.298	0.423	0.997	2	R.LLQDHPWLLSQNLVVKPDQLIK.R
SW:ACLY_HUMAN	H06	6810	2	1492.6	(+0.9)	3.821	0.249	0.975	3	R.SGGMSNELNIIISR.T
SW:ACLY_HUMAN	H06	6088	2	1514.6	(+0.8)	2.376	0.177	0.708	3	R.SGGM@SNEL*NNIIISR.T
SW:ACLY_HUMAN	H06	8258	2	1568.9	(+0.9)	4.772	0.476	0.999	3	R.TIAIIAEGIPEALTR.K
SW:ACLY_HUMAN	H06	1978	2	1091.2	(-0.1)	2.285	0.120	0.349	2	R.GGPNYQEGLR.V
SW:ACTA_HUMAN	H14	4563	2	1172.4	(-0.1)	2.689	0.356	0.948	13	R.HQGMVGMGQK.D
SW:ACTA_HUMAN	H13	7112	2	1970.2	(+1.0)	3.170	0.433	0.983	6	K.YPIEHGIITNWDDMEK#.I
SW:ACTA_HUMAN	H14	7057	2	1970.2	(-0.5)	3.262	0.428	0.975	6	K.YPIEHGIITNWDDMEK#.I
SW:ACTA_HUMAN	H14	7053	2	1962.2	(+0.4)	2.422	0.352	0.948	6	K.YPIEHGIITNWDDMEK.I
SW:ACTA_HUMAN	H14	6557	2	1986.2	(-0.5)	2.209	0.186	0.412	6	K.YPIEHGIITNWDDM@EK#.I
SW:ACTB_HUMAN	H14	7011	2	2244.5	(+0.8)	4.225	0.583	1.000	11	K.DL*YANTVL*SGGTTM@YPIADR.M
SW:ACTB_HUMAN	H14	7515	2	2216.5	(+0.1)	3.241	0.461	0.982	11	K.DLYANTVLSGGTTMYPPIADR.M
SW:ACTB_HUMAN	H13	6500	2	1516.7	(+0.9)	3.412	0.499	1.000	10	K.IWHHTFYNELR.V
SW:ACTB_HUMAN	H13	6504	2	1522.7	(+0.7)	3.023	0.379	0.987	10	K.IWHHTFYNEL*R.V
SW:ACTB_HUMAN	H14	6481	3	1516.7	(-0.4)	4.000	0.423	0.999	10	K.IWHHTFYNELR.V
SW:ACTB_HUMAN	H13	8118	3	3197.6	(+0.7)	6.370	0.535	0.999	7	R.TTGIVMDSGDGVTHTVPIYEGYAL*PHAIL*R.L

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ACTB_HUMAN	H13	8114	3	3185.6	(+0.4)	4.791	0.535	1.000	7	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L
SW:ACTB_HUMAN	H13	7886	3	3213.6	(+0.2)	4.701	0.508	0.991	7	R.TTGIVM@DSGDGVTHTVPIYEGYAL*PHAIL*R.L
SW:ACTB_HUMAN	H14	8099	3	3185.6	(+0.7)	6.144	0.572	0.999	7	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L
SW:ACTB_HUMAN	H14	8077	3	3197.6	(-0.8)	4.802	0.490	0.998	7	R.TTGIVMDSGDGVTHTVPIYEGYAL*PHAIL*R.L
SW:ACTB_HUMAN	H14	7851	3	3213.6	(-0.3)	4.541	0.492	0.999	7	R.TTGIVM@DSGDGVTHTVPIYEGYAL*PHAIL*R.L
SW:ACTB_HUMAN	H13	6704	2	1955.3	(+1.0)	4.902	0.604*	0.875	5	R.VAPEEHPVLLTEAPLNPK.A
SW:ACTB_HUMAN	H14	6695	2	1955.3	(+0.9)	3.644	0.572	1.000	5	R.VAPEEHPVLLTEAPLNPK.A
SW:ACTB_HUMAN	H14	6471	2	1522.7	(+0.6)	2.325	0.395	0.970	10	K.IWHHTFYNEL*R.V
SW:ACTZ_HUMAN	H13	7744	3	2559.8	(+0.4)	5.166	0.506	0.990		K.DQL*QTFSEEHPVL*L*TEAPL*NPR.K
SW:ACTZ_HUMAN	H13	7748	3	2535.8	(+0.5)	3.926	0.515	1.000		K.DQLQTFSEEHPVLLTEAPLNPR.K
SW:ACTZ_HUMAN	H14	7705	3	2559.8	(+0.7)	5.013	0.436	0.994		K.DQL*QTFSEEHPVL*L*TEAPL*NPR.K
SW:ACTZ_HUMAN	H14	9113	2	1711.0	(-0.2)	3.070	0.317	0.924		R.TL*FSNIVL*SGGSTL*FK#.G
SW:ACYO_HUMAN	H21	4548	2	1327.5	(+0.5)	2.506	0.387	0.967	1	R.GTVQGQL*QGPISK#.V
SW:ACYO_HUMAN	H22	6678	2	1228.4	(+0.9)	2.405	0.352	0.965	1	K.LDYSDFQIVK.-
SW:ACYO_HUMAN	H22	6940	2	1370.5	(+0.6)	2.811	0.561	1.000	1	K.L*GL*VGWVQNTDR.G
SW:ACYO_HUMAN	H22	6680	2	1242.4	(+0.9)	2.309	0.363	0.963	1	K.L*DYSDQIVK#.-
SW:ADA_HUMAN	H14	9589	3	3347.7	(+0.5)	4.643	0.571	1.000	2	K.VEPIPWNAEGDLTPDEVVALVGQGLQEGER.D
SW:ADA_HUMAN	H14	4945	2	1303.4	(+1.0)	2.536	0.195	0.852	3	K.STLDDTDYQMTK.R
SW:AHNK_HUMAN	H02	5344	2	1282.4	(-0.1)	3.135	0.433	0.976	5	K.AEGPEVDVNL*PK#.A
SW:AHNK_HUMAN	H04	5819	2	1282.4	(+0.3)	3.049	0.479	0.983	5	K.AEGPEVDVNL*PK#.A
SW:AHNK_HUMAN	H03	7082	2	1515.7	(+0.3)	3.173	0.371	0.954	1	K.APDVEGQGLDWSLK.I
SW:AHNK_HUMAN	H01	5062	2	1240.4	(+0.7)	3.033	0.433	0.990	3	K.GEGPDVDVNLPK.A
SW:AHNK_HUMAN	H03	5992	2	1240.4	(+0.8)	3.171	0.448	0.991	3	K.GEGPDVDVNLPK.A
SW:AHNK_HUMAN	H04	5707	2	1254.4	(+0.2)	2.758	0.467	0.975	3	K.GEGPDVDVNL*PK#.A
SW:AHNK_HUMAN	H05	6060	2	1240.4	(+0.7)	2.470	0.343	0.955	3	K.GEGPDVDVNLPK.A
SW:AHNK_HUMAN	H02	5366	2	1213.3	(+0.7)	2.302	0.269	0.885	2	K.GEGPDVDVSLPK.A
SW:AHNK_HUMAN	H03	6094	2	1254.4	(-0.1)	2.283	0.225	0.667	4	K.GEGPEVDVNLPK.A
SW:AHNK_HUMAN	H03	6066	2	1268.4	(+0.1)	2.228	0.246	0.667	4	K.GEGPEVDVNL*PK#.A
SW:AHNK_HUMAN	H02	5778	3	2419.7	(+0.5)	3.717	0.490	0.999	2	K.GGQIGLQAPGLSVSGPQGHLESGSGK.V
SW:AHNK_HUMAN	H03	7772	2	1259.5	(+0.8)	2.550	0.372*	0.318	2	K.ISMPDIDLNLK.G
SW:AHNK_HUMAN	H02	4804	2	1006.1	(+0.3)	2.397	0.431	0.962	2	R.L*DFEGPDAK#.L
SW:AHNK_HUMAN	H02	5044	2	958.1	(+1.0)	2.527	0.329	0.931	2	K.LEGPDVSLK.G
SW:AHNK_HUMAN	H02	5240	2	1240.4	(+0.7)	3.518	0.314	0.984	2	K.LPTGQISGPEIK.G
SW:AHNK_HUMAN	H03	5930	2	1254.4	(+0.8)	3.194	0.399	0.988	2	K.L*PTGQISGPEIK#.G
SW:AHNK_HUMAN	H04	5627	2	1254.4	(-0.1)	2.773	0.366	0.946	2	K.L*PTGQISGPEIK#.G
SW:AHNK_HUMAN	H03	6730	2	1669.8	(-0.1)	2.614	0.159	0.525	1	K.VDIEAPDVSL*EGPEGK#.L
SW:AHNK_HUMAN	H02	5788	2	1690.8	(-0.2)	2.923	0.393	0.955	2	K.VDVEDVDPVNIIEGPDVSL*EGPEGK#.L
SW:AHNK_HUMAN	H02	5938	2	1683.8	(-0.2)	3.060	0.346	0.942	3	K.VDVEVPDVSL*EGPEGK#.L
SW:AHNK_HUMAN	H03	6972	2	1683.8	(-1.0)	2.594	0.371	0.773	3	K.VDVEVPDVSL*EGPEGK#.L
SW:AHNK_HUMAN	H02	5902	3	2508.7	(-0.2)	4.242	0.427	0.935	2	K.VEAPSL*DVHM@DSPDINIEGPDVK#.I
SW:AHNK_HUMAN	H03	6960	3	2508.7	(+0.7)	5.270	0.522	0.994	2	K.VEAPSL*DVHM@DSPDINIEGPDVK#.I
SW:AHNK_HUMAN	H04	6733	3	2508.7	(+0.4)	4.831	0.335	0.996	2	K.VEAPSL*DVHM@DSPDINIEGPDVK#.I
SW:AHNK_HUMAN	H02	5870	2	1638.8	(-0.2)	3.418	0.410	0.978	1	K.VGVEVPDVNIIEGPEGK.L
SW:AHNK_HUMAN	H02	4070	2	1143.3	(+0.8)	2.474	0.196	0.162	2	K.VKGDVDVSVPK.V
SW:AHNK_HUMAN	H02	5926	2	1631.8	(-0.1)	2.839	0.219	0.767	1	K.VNVEAPDVNL*EGL*GGK#.L
SW:AHNK_HUMAN	H02	5922	2	1611.8	(-0.1)	2.636	0.473	0.970	1	K.VNVEAPDVNL*EGL*GGK#.L
SW:AHNK_HUMAN	H03	6756	2	1171.3	(+0.1)	2.425	0.480	0.973	2	K.VSGPDLDLNLK.G
SW:AHNK_HUMAN	H05	7496	2	1511.8	(+0.9)	2.421	0.263	0.847	2	K.GPGVDLPSVNLSPK.V
SW:ALFA_HUMAN	H14	1563	1	731.8	(-0.1)	1.901	0.212	0.000	10	K.DGADFAK#.W
SW:ALFA_HUMAN	H14	7163	2	1676.9	(+0.9)	5.116	0.594	1.000	5	K.FSHEEIAMATVTALR.R
SW:ALFA_HUMAN	H14	7159	2	1682.9	(+0.4)	5.071	0.533	0.977	5	K.FSHEEIAMATVTAL*R.R
SW:ALFA_HUMAN	H14	7225	2	1676.9	(-0.5)	4.149	0.445	1.000	5	K.FSHEEIAMATVTALR.R
SW:ALFA_HUMAN	H14	7259	2	1682.9	(+0.5)	3.975	0.484	0.999	5	K.FSHEEIAMATVTAL*R.R
SW:ALFA_HUMAN	H14	5513	2	1347.5	(+0.4)	3.530	0.575	1.000	3	K.GIL*AADESTGSIK#.R
SW:ALFA_HUMAN	H14	5595	2	1347.5	(+0.3)	3.121	0.574	1.000	3	K.GIL*AADESTGSIK#.R
SW:ALFA_HUMAN	H14	5433	2	1347.5	(-0.2)	2.712	0.326	0.902	3	K.GIL*AADESTGSIK#.R
SW:ALFA_HUMAN	H18	5422	2	1333.5	(+0.1)	3.433	0.506	1.000	3	K.GILAADESTGSIK.R
SW:ALFA_HUMAN	H21	5170	2	1347.5	(+0.3)	3.419	0.555	1.000	3	K.GIL*AADESTGSIK#.R
SW:ALFA_HUMAN	H14	6667	2	2273.5	(+0.6)	5.034	0.612*	0.887	4	K.GVVPLAGTNGETTTQGLDGLSER.C
SW:ALFA_HUMAN	H14	6391	2	2273.5	(+0.4)	3.677	0.539*	0.651	4	K.GVVPLAGTNGETTTQGLDGLSER.C
SW:ALFA_HUMAN	H14	6431	2	2291.5	(-1.0)	3.651	0.532	0.999	4	K.GVVPL*AGTNGETTTQGL*DGL*SER.C



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta M$	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ALFA_HUMAN	H14	6753	2	2291.5	(-0.9)	3.257	0.428	0.929	4	K.GVVPL*AGTNGETTTQGL*DGL*SER.C
SW:ALFA_HUMAN	H14	8015	2	2120.4	(+1.0)	4.543	0.510	1.000	5	K.IGEHTPSAL*AIMENANVL*AR.Y
SW:ALFA_HUMAN	H14	2127	2	1069.2	(+1.0)	2.394	0.336	0.962	3	K.KELSDIAHR.I
SW:ALFA_HUMAN	H14	2063	2	1653.7	(+0.9)	2.403	0.126	0.020	3	R.L*QSIGTENTEENRR.F
SW:ALFA_HUMAN	H14	5711	2	1449.6	(+0.5)	3.489	0.463	1.000		-.PYQYPAL*TPEQK#.K
SW:ALFA_HUMAN	H14	5615	2	1449.6	(-0.1)	3.416	0.366	0.972		-.PYQYPAL*TPEQK#.K
SW:ALFA_HUMAN	H14	5703	2	1435.6	(+0.9)	3.319	0.371	0.988		-.PYQYPALTPEQK.K
SW:ALFA_HUMAN	H14	5623	2	1435.6	(-0.5)	3.293	0.377	0.975		-.PYQYPALTPEQK.K
SW:ALFA_HUMAN	H14	4689	1	778.0	(-0.3)	2.036	0.227	0.000	16	K.VL*AAVYK#.A
SW:ALFA_HUMAN	H14	4603	1	764.0	(-0.2)	1.953	0.279	0.000	16	K.VLAAVYK.A
SW:ALFA_HUMAN	H14	6811	2	2235.4	(+0.4)	5.175	0.547	1.000	5	K.YTPSGQAGAAAASESL*FVSNHAY.-
SW:ALFA_HUMAN	H14	6855	2	2229.4	(+0.7)	4.894	0.581	0.969	5	K.YTPSGQAGAAAASESLFVSNHAY.-
SW:ALFA_HUMAN	H14	6847	2	2235.4	(-0.9)	4.095	0.423	0.957	5	K.YTPSGQAGAAAASESL*FVSNHAY.-
SW:ALFA_HUMAN	H14	6731	2	2229.4	(+0.2)	3.548	0.481	0.987	5	K.YTPSGQAGAAAASESLFVSNHAY.-
SW:ALFA_HUMAN	H14	6729	2	2235.4	(+0.2)	3.458	0.479	0.986	5	K.YTPSGQAGAAAASESL*FVSNHAY.-
SW:ALFA_HUMAN	H14	12823	2	2235.4	(+0.7)	3.303	0.575	1.000	5	K.YTPSGQAGAAAASESL*FVSNHAY.-
SW:ALFA_HUMAN	H14	13005	2	2235.4	(+0.2)	2.635	0.372	0.933	5	K.YTPSGQAGAAAASESL*FVSNHAY.-
SW:ALFA_HUMAN	H21	5356	2	1449.6	(+0.1)	2.319	0.280	0.742		-.PYQYPAL*TPEQK#.K
SW:ALFC_HUMAN	H14	5507	2	1274.4	(+0.6)	2.404	0.361	0.954	4	R.DNAGAATEEFIK#.R
SW:ALFC_HUMAN	H14	6749	2	2274.4	(+0.2)	4.834	0.592	1.000	4	K.GVVPLAGTDGETTTQGLDGLSER.C
SW:ALFC_HUMAN	H14	6571	3	2292.4	(+0.6)	4.033	0.389	0.579	4	K.GVVPL*AGTDGETTTQGL*DGL*SER.C
SW:ALFC_HUMAN	H14	8641	2	1653.9	(+0.8)	4.564	0.450	1.000	4	R.TPSALAILLENANVLAR.Y
SW:ALFC_HUMAN	H14	6515	3	2251.3	(+0.8)	4.061	0.463	0.999	3	K.YEGSGEDGAAAQSL*YIANHAY.-
SW:ALFC_HUMAN	H14	8951	2	1672.9	(+0.9)	4.326	0.488	1.000	4	K.YTPEEIAMATVTAL*R.R
SW:ALFC_HUMAN	H14	8955	2	1666.9	(+1.0)	4.221	0.398	0.994	4	K.YTPEEIAMATVTALR.R
SW:ALFC_HUMAN	H14	8299	2	1688.9	(+0.2)	2.409	0.361	0.900	4	K.YTPEEIAM@ATVTAL*R.R
SW:ALFC_HUMAN	H14	4521	2	1495.6	(-0.1)	2.227	0.243	0.668	4	R.L*SQIGVENTEENR.R
SW:ANM1_HUMAN	H14	5797	2	1378.6	(+0.3)	3.534	0.395	0.503	7	K.GK#VEEVEL*PVEK#.V
SW:ANM1_HUMAN	H14	6379	2	1252.4	(+0.9)	2.420	0.420	0.980	5	R.ATLYVTAIEDR.Q
SW:ANX2_HUMAN	H15	5732	2	1846.0	(+0.6)	3.524	0.521	1.000	6	K.LSLEGDHSTPPSAYGSVK.A
SW:ANX2_HUMAN	H15	5724	2	1866.0	(+0.1)	3.148	0.497	0.982	6	K.L*SL*EGDHSTPPSAYGSVK#.A
SW:ANX2_HUMAN	H15	6298	2	1102.2	(+0.4)	2.338	0.207	0.816	6	R.DAL*NIETAIK#.T
SW:APE1_HUMAN	H14	5113	2	1787.9	(+0.6)	2.943	0.358	0.975	6	K.EAAGEGPALYEDPPDQK.T
SW:APE1_HUMAN	H15	5056	2	1801.9	(+0.2)	2.403	0.242	0.676	6	K.EAAGEGPAL*YEDPPDQK#.T
SW:APE1_HUMAN	H15	6120	2	1138.3	(-0.5)	2.546	0.288	0.860	7	K.EGYSGVGLLSR.Q
SW:APE1_HUMAN	H16	5744	2	1150.3	(+0.9)	2.274	0.353	0.952	7	K.EGYSGVGL*L*SR.Q
SW:APE1_HUMAN	H15	2386	2	1787.9	(+0.7)	2.689	0.414	0.649	7	K.GAVAEDGDELRTPEAK.K
SW:APE1_HUMAN	H15	2380	2	1801.9	(-0.5)	2.674	0.366	0.318	7	K.GAVAEDGDEL*RTPEAK#.K
SW:APE1_HUMAN	H15	7916	3	2499.7	(-0.0)	5.871	0.518	0.996	7	K.L*PAEL*QEL*PGL*SHQYWSAPSDK#.E
SW:APE1_HUMAN	H15	7936	2	2467.7	(-0.0)	4.324	0.542	0.913	7	K.LPAELQELPGLSHQYWSAPSDK.E
SW:APE1_HUMAN	H14	9065	2	1867.1	(+0.4)	2.497	0.376	0.963	5	R.QGFGEL*L*QAVPL*ADSFR.H
SW:APE1_HUMAN	H15	9440	2	1867.1	(+0.8)	2.732	0.469	0.988	5	R.QGFGEL*L*QAVPL*ADSFR.H
SW:APE1_HUMAN	H22	8522	2	1849.1	(+0.2)	2.441	0.404	0.935	5	R.QGFGELLQAVPLADSFR.H
SW:APE1_HUMAN	H22	8512	2	1867.1	(+0.6)	2.221	0.363	0.936	5	R.QGFGEL*L*QAVPL*ADSFR.H
SW:AR1B_HUMAN	H15	4840	2	1629.7	(+0.7)	5.271	0.577	1.000		K.ASSEGGAAGAGLDSLHK.N
SW:AR1B_HUMAN	H16	5402	2	1290.4	(+0.3)	2.971	0.427	0.971		K.NSVSQISVL*SGGK#.A
SW:AR1B_HUMAN	H22	4754	2	1629.7	(+0.8)	3.952	0.534	1.000		K.ASSEGGAAGAGLDSLHK.N
SW:AR20_HUMAN	H19	6778	2	1269.5	(-0.1)	2.725	0.294	0.898	5	K.ELLQPVTISR.N
SW:AR20_HUMAN	H19	1786	2	1116.2	(+0.8)	2.338	0.185	0.109	5	R.HNK#PEVEVR.S
SW:AR20_HUMAN	H19	8270	3	2684.0	(+0.3)	5.381	0.452	0.998	4	R.K#PVEGYDISFL*ITNFHTEQMYK#.H
SW:AR20_HUMAN	H19	8044	3	2700.0	(+0.6)	4.136	0.502	0.998	4	R.K#PVEGYDISFL*ITNFHTEQM@YK#.H
SW:AR20_HUMAN	H19	5628	2	1193.4	(+0.8)	2.982	0.259	0.958	5	K.VL*IEGSINSVR.V
SW:AR20_HUMAN	H20	6814	2	1287.5	(+1.0)	2.401	0.343	0.943	5	K.EL*L*L*QPVTISR.N
SW:AR34_HUMAN	H16	5294	2	1324.5	(+0.7)	2.549	0.421	0.982	3	K.ELQAHADELK.R
SW:AR34_HUMAN	H16	8628	3	3638.9	(-0.2)	6.506	0.568	0.982	1	K.FENAAAAGNKPEAVEVTFADFDGVLVYHISNPNGDK.T
SW:AR34_HUMAN	H16	8548	3	3660.9	(+0.9)	5.162	0.569	0.999	1	K.FENAAAAGNK#PEAVEVTFADFDGVL*YHISNPNGDK#.T
SW:AR34_HUMAN	H16	5312	2	1176.3	(+0.9)	3.275	0.488	1.000	4	K.YFQFQEEGK.E
SW:AR34_HUMAN	H16	5316	2	1184.3	(+0.9)	2.874	0.382	0.986	4	K.YFQFQEEGK#.E
SW:AR34_HUMAN	H16	6204	2	1114.3	(+0.3)	2.281	0.271	0.833	1	-.MIL*L*EVNRR.I

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ARF1_HUMAN	H19	7302	3	2154.3	(+1.0)	4.182	0.347	0.994	6	R.HYFQNTQGLIFVVDNSDR.E
SW:ARF1_HUMAN	H19	7380	2	1566.7	(+0.6)	4.358	0.591	1.000	2	K.NISFTVWDVGGQDK.I
SW:ARF1_HUMAN	H19	7390	2	1574.7	(-0.1)	3.620	0.523	1.000	2	K.NISFTVWDVGGQDK#.I
SW:ARF1_HUMAN	H20	7336	2	1566.7	(+0.1)	3.200	0.552	1.000	2	K.NISFTVWDVGGQDK.I
SW:ARME_HUMAN	H19	7824	2	1963.2	(+0.5)	4.430	0.395	0.850	3	K.DRDVTFSPATIENEL*IK#.F
SW:ARME_HUMAN	H20	7726	2	1963.2	(-0.4)	3.704	0.516	0.999	3	K.DRDVTFSPATIENEL*IK#.F
SW:ARME_HUMAN	H19	8114	2	1691.9	(+0.6)	3.005	0.395	0.969	3	R.DVTFSPATIENEL*IK#.F
SW:ARME_HUMAN	H20	8056	2	1691.9	(-0.3)	2.278	0.320	0.803	3	R.DVTFSPATIENEL*IK#.F
SW:ARP2_HUMAN	H14	6123	2	1221.4	(+0.6)	2.445	0.386	0.640	2	K.DK#DNFWMTR.Q
SW:ARP2_HUMAN	H14	6259	2	1801.1	(+0.4)	4.316	0.492	1.000	2	K.HIVL*SGGSTM@YPGL*PSR.L
SW:ARP2_HUMAN	H14	7161	2	1407.5	(+1.0)	3.108	0.470	0.993	3	K.HL*WDYTFGPEK#.L
SW:ARP2_HUMAN	H14	6339	2	1354.6	(+0.9)	2.648	0.415	0.980	3	K.ILLTEPPMNPTK.N
SW:ARP2_HUMAN	H14	6125	2	1347.5	(-0.6)	2.352	0.172	0.547	2	K.DL*MVGDEASEL*R.S
SW:ARP3_HUMAN	H13	10442	2	1410.7	(-0.8)	2.497	0.324	0.745	5	R.DITYFIQQLLR.D
SW:ARP3_HUMAN	H13	7372	2	1500.7	(+0.6)	3.507	0.484	1.000		R.HGIVEDWDLMER.F
SW:ARP3_HUMAN	H13	10422	2	1422.7	(+0.9)	2.449	0.354	0.965	5	R.DITYFIQQL*L*R.D
SW:ARS2_HUMAN	H06	8402	2	1530.7	(+0.8)	3.730	0.474	1.000	7	K.EVAFFNNFL*TDAK#.R
SW:ARS2_HUMAN	H06	2156	2	2128.3	(-0.3)	4.082	0.360	0.657	3	R.ILEQEEEEEQAGKPGEPSK.K
SW:ARS2_HUMAN	H06	8386	2	1516.7	(+1.0)	2.771	0.545	0.994	7	K.EVAFFNNFLTDK.R
SW:B53A_HUMAN	H13	5310	2	1603.7	(-0.5)	2.891	0.391	0.431	2	R.DDGSTL*MEIDGDK#GK#.Q
SW:B53A_HUMAN	H13	1978	2	1137.3	(+1.0)	3.004	0.265	0.968	2	K.L*IANNTTVER.R
SW:B53A_HUMAN	H13	9372	2	2284.5	(+0.9)	3.845	0.519	0.985	1	K.NGMVEDWDSFQAIL*DHTYK#.M
SW:B53A_HUMAN	H13	7574	3	3119.5	(-0.1)	5.570	0.557	1.000	2	R.STGL*IL*DSGATHTTAIPVHDGYVL*QQGIVK#.S
SW:B53A_HUMAN	H13	7402	2	2026.3	(+0.2)	2.874	0.474	0.978	2	K.SEASLHPVLMSEAPWNTR.A
SW:BA1A_HUMAN	H04	8845	2	1404.6	(+0.3)	3.398	0.379	0.980	2	R.DFIEDYVDIL*R.Q
SW:BA1A_HUMAN	H04	2091	2	1376.5	(+0.2)	2.786	0.319	0.921	3	R.IHISQEDNVANK#.Q
SW:BA1A_HUMAN	H05	5830	3	2038.2	(+0.8)	4.145	0.518	1.000	3	K.FHFSKPKQPDSPKPTYSR.G
SW:BP28_HUMAN	H04	7625	2	1386.5	(+0.6)	2.481	0.252	0.909		K.GDIWWNPEQLK.E
SW:BP28_HUMAN	H04	8315	2	1288.4	(+0.7)	3.065	0.114	0.847		R.GWEEALENVK.S
SW:BP28_HUMAN	H04	11225	3	1999.3	(+0.8)	3.923	0.414	0.992	2	R.L*L*ETVL*GYISAVAQSMER.N
SW:BP28_HUMAN	H04	10351	2	2237.6	(-0.1)	2.586	0.315	0.877	2	K.NTSELVSSSEVYLLSALAALQK.V
SW:BP28_HUMAN	H04	8627	2	1684.0	(+0.5)	2.851	0.357	0.972	2	K.VNALLPTETFIPVIR.G
SW:BP28_HUMAN	H04	8881	2	1542.9	(+0.3)	3.227	0.385	0.972		K.VSLLNEQFLPLIR.L
SW:BP28_HUMAN	H04	8889	2	1566.9	(+0.3)	3.051	0.392	0.970		K.VSL*L*NEQFL*PL*IR.L
SW:BP28_HUMAN	H04	10739	3	2863.4	(+0.8)	4.095	0.490	1.000	2	K.VVETLPHFISPYLEGILSQVIHLEK.I
SW:BP28_HUMAN	H04	8525	2	1237.5	(+0.9)	2.403	0.450	0.984	2	K.LVPDLLAIVQR.K
SW:BRD3_HUMAN	H04	6683	2	1180.4	(+0.8)	2.414	0.501	0.991	6	R.K#L*QDVFEMR.F
SW:BRD3_HUMAN	H06	5388	2	1072.2	(+0.6)	2.443	0.177	0.840	6	R.LAELQEQLK.A
SW:BRD3_HUMAN	H06	5394	2	1098.2	(+0.1)	2.228	0.164	0.520	6	R.L*AEL*QEQL*K#.A
SW:BRD4_HUMAN	H04	6293	2	1435.8	(+0.9)	3.962	0.393	0.992		R.AASVQPQPLVVVK.E
SW:BRD4_HUMAN	H04	6285	2	1449.8	(-0.0)	2.866	0.318	0.914		R.AASVQPQPL*VVVK#.E
SW:BRD4_HUMAN	H04	6437	3	2605.9	(+0.1)	5.116	0.495	1.000	4	R.K#ADTTTPTTIDPIHEPPSL*PPEPK#.T
SW:BRD4_HUMAN	H04	6923	2	1221.4	(+1.0)	2.617	0.435	0.981	1	K.NMGSWASLVQK.H
SW:BRD4_HUMAN	H04	1923	2	1425.4	(+0.9)	3.972	0.405	0.870	1	R.SREDEDAL*EQAR.R
SW:BRD4_HUMAN	H04	1921	2	1419.4	(+0.5)	3.598	0.343	0.765	1	R.SREDEDALEQAR.R
SW:BRD4_HUMAN	H04	6919	2	1235.4	(+0.6)	2.469	0.313	0.941	1	K.NMGSWASL*VQK#.H
SW:BUB3_HUMAN	H14	4817	2	1398.5	(+0.1)	2.505	0.387	0.931		K.L*NQPPEDGISSVK#.F
SW:BUB3_HUMAN	H14	4927	2	1398.5	(-0.0)	2.311	0.234	0.440		K.L*NQPPEDGISSVK#.F
SW:BUB3_HUMAN	H15	4784	2	1398.5	(+0.2)	2.840	0.357	0.942		K.L*NQPPEDGISSVK#.F
SW:BUB3_HUMAN	H14	5953	3	2289.5	(+0.4)	6.171	0.597	1.000		K.MHDL*NTDQENL*VGTHDAPIR.C
SW:BUB3_HUMAN	H15	5762	3	2305.5	(+0.8)	6.442	0.520	1.000		K.M@HDL*NTDQENL*VGTHDAPIR.C
SW:BUB3_HUMAN	H15	5976	3	2289.5	(+0.2)	5.948	0.517	0.999		K.MHDL*NTDQENL*VGTHDAPIR.C
SW:BUB3_HUMAN	H18	5696	3	2305.5	(+0.1)	4.845	0.453	0.999		K.M@HDL*NTDQENL*VGTHDAPIR.C
SW:BUB3_HUMAN	H14	6041	2	1574.8	(-0.3)	3.602	0.432	0.966		R.VAVEYLDPSPEVQK.K
SW:BUB3_HUMAN	H14	6033	2	1588.8	(+0.0)	3.381	0.322	0.952		R.VAVEYL*DPSPPEVQK#.K

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:BUB3_HUMAN	H15	6070	2	1574.8	(+0.6)	3.623	0.526	1.000		R.VAVEYLDPSPEVQK.K
SW:BUB3_HUMAN	H15	6066	2	1588.8	(-0.1)	3.386	0.449	0.982		R.VAVEYL*DPSPEVQK#.K
SW:BUB3_HUMAN	H14	5311	2	1097.2	(+0.8)	2.405	0.410	0.979		K.VYTLVSVSGDR.L
SW:BUB3_HUMAN	H18	5150	2	1103.2	(+0.9)	2.400	0.424	0.982		K.VYTL*SVSGDR.L
SW:C1TC_HUMAN	H06	8046	2	1652.9	(+0.7)	3.353	0.553	1.000	4	R.AAQAPSSFQLLYDLK.L
SW:C1TC_HUMAN	H06	5568	2	1181.3	(+1.0)	2.660	0.211	0.909	3	R.DDSNLYINVK.L
SW:C1TC_HUMAN	H06	5274	2	1224.3	(+0.9)	3.194	0.419	0.991	3	K.DVDGL*TSINAGR.L
SW:C1TC_HUMAN	H06	6142	2	1110.3	(+0.8)	2.580	0.312	0.957	4	K.GAL*AL*AQAVQR.A
SW:C1TC_HUMAN	H06	4996	2	1232.4	(+0.3)	2.732	0.166	0.757	3	R.IFHELTQTDK.A
SW:C1TC_HUMAN	H06	7300	2	1487.7	(+0.7)	3.880	0.369	0.991	3	R.LDIDPETITWQR.V
SW:C1TC_HUMAN	H06	5134	2	1505.6	(+0.5)	3.307	0.331	0.982	3	K.TDPTTLTDEEINR.F
SW:C1TC_HUMAN	H06	5150	2	1511.6	(+0.7)	3.081	0.293	0.960	3	K.TDPTTL*TDEEINR.F
SW:C1TC_HUMAN	H06	6336	2	1379.5	(+0.7)	3.137	0.424	0.991	3	K.TDTESELDLISR.L
SW:C1TC_HUMAN	H06	6858	2	1631.9	(+0.4)	4.470	0.560	1.000	3	K.YVVVTGITPTPLGEGK.S
SW:C1TC_HUMAN	H06	6860	2	1645.9	(+0.0)	3.226	0.370	0.960	3	K.YVVVTGITPTPL*GEGK#.S
SW:C1TC_HUMAN	H06	9238	2	1500.9	(+0.5)	2.409	0.424	0.971	4	R.MFGIPVVAVNAFK#.T
SW:CAFB_HUMAN	H09	8443	2	1245.5	(+0.9)	2.698	0.456	0.989		K.AIVEFL*SNL*AR.H
SW:CAFB_HUMAN	H09	2051	2	1109.2	(+0.3)	2.566	0.400	0.958		R.L*ASAGVDTNVR.I
SW:CAFB_HUMAN	H10	5171	2	1197.3	(+0.3)	3.108	0.529	0.995		K.ML*SGIGAEGEAR.S
SW:CALM_HUMAN	H20	6116	2	1769.9	(-0.2)	3.888	0.371	0.645	5	R.VFDK#DGNGYISAAEL*R.H
SW:CALM_HUMAN	H20	6664	2	1846.0	(+0.8)	2.339	0.354	0.386	4	K.EAFSLFDKDGDTITTK.E
SW:CALX_HUMAN	H08	6453	3	2125.3	(+0.7)	4.575	0.459	0.998	3	K.IPDPEAVK#PDDWDEDAPAK#.I
SW:CALX_HUMAN	H08	7493	2	1503.6	(+0.5)	3.030	0.379	0.981	2	R.IVDDWANDGWGL*K#.K
SW:CALX_HUMAN	H08	6501	2	1457.6	(+0.6)	4.281	0.431	1.000	1	K.TPELNLDQFHDK.T
SW:CALX_HUMAN	H08	6499	2	1477.6	(+0.2)	3.607	0.407	0.982	1	K.TPEL*NL*DQFHDK#.T
SW:CALX_HUMAN	H08	9013	2	1742.9	(-0.1)	2.538	0.333	0.899	2	K.IPNPDFFEDL*EPFR.M
SW:CAPB_HUMAN	H16	5134	2	1338.5	(+0.6)	3.058	0.410	0.987	1	K.SGSGTMNLGGSLTR.Q
SW:CAPB_HUMAN	H16	5132	2	1350.5	(+0.4)	2.665	0.293	0.940	1	K.SGSGTMNL*GGSL*TR.Q
SW:CAPB_HUMAN	H16	6054	2	1186.3	(+0.4)	2.263	0.365	0.956	1	R.STL*NEIFYGK#.T
SW:CBFB_HUMAN	H14	5175	3	2724.9	(+1.0)	4.519	0.451	0.984	2	K.EK#DSPHM@QDPNQADEEAM@TQIIR.V
SW:CBFB_HUMAN	H14	8301	2	2114.5	(+0.2)	4.455	0.601	0.999	2	R.IPLPGAEMLEEEPLYVNAK.Q
SW:CBX3_HUMAN	H19	5174	2	1196.3	(+0.1)	3.364	0.383	0.854	3	K.DSDEADL*VL*AK#.E
SW:CBX3_HUMAN	H19	5176	2	1176.3	(+0.9)	2.940	0.389	0.986	3	K.DSDEADLVLAK.E
SW:CBX3_HUMAN	H19	5580	2	1678.8	(+0.2)	5.690	0.551	1.000	2	K.K#VEEAPEEFVVEK#.V
SW:CBX3_HUMAN	H19	5562	2	1662.8	(-0.3)	2.393	0.257	0.752	2	K.KVEEAPEEFVVEK.V
SW:CBX3_HUMAN	H19	5648	2	1542.7	(+0.9)	4.453	0.487	0.999	2	K.VEEAPEEFVVEK#.V
SW:CBX3_HUMAN	H19	5906	2	1518.7	(-0.2)	3.478	0.379	0.590	3	K.WK#DSDEADL*VL*AK#.E
SW:CBX3_HUMAN	H19	5200	2	1176.3	(-0.7)	2.362	0.264	0.552	3	K.DSDEADLVLAK.E
SW:CBX5_HUMAN	H18	5484	2	1190.3	(+0.2)	2.852	0.276	0.915	1	K.DTDEADLVLAK.E
SW:CBX5_HUMAN	H19	7962	2	1716.1	(-0.6)	2.381	0.109	0.294	1	K.IIGATDSCGDLMLMK.W
SW:CD3E_HUMAN	H19	6884	2	1693.9	(-0.2)	3.411	0.475	0.738	1	R.GSK#PEDANFYL*YL*R.A
SW:CD3E_HUMAN	H19	5414	2	2272.3	(+0.2)	4.709	0.515	1.000		K.NIGGEDDKNIGSDEDHLSLK.E
SW:CD3E_HUMAN	H19	4914	2	1078.2	(+0.2)	2.381	0.380	0.938		R.DL*YSGL*NQR.R
SW:CDC2_HUMAN	H16	7264	3	2310.5	(+0.7)	4.477	0.411	0.999	2	R.AL*GTPNNEVWPEVESL*QDYK#.N
SW:CDC2_HUMAN	H16	7218	2	2310.5	(+0.6)	2.815	0.418	0.979	2	R.AL*GTPNNEVWPEVESL*QDYK#.N
SW:CDC2_HUMAN	H16	7210	2	2290.5	(-0.4)	2.689	0.384	0.944	2	R.ALGTPNNEVWPEVESLQDYK.N
SW:CDC2_HUMAN	H16	7246	2	1853.1	(+0.5)	3.415	0.578	1.000	2	R.HPNIVSLQDVLMLQDSR.L
SW:CDC2_HUMAN	H16	7244	2	1865.1	(-0.3)	2.565	0.306	0.866	2	R.HPNIVSL*QDVL*MQDSR.L
SW:CDC2_HUMAN	H16	6882	2	1881.1	(+0.1)	2.446	0.282	0.804	2	R.HPNIVSL*QDVL*M@QDSR.L
SW:CDC2_HUMAN	H16	5048	2	1194.4	(+0.9)	3.040	0.361	0.983	5	K.IGEGTYGVVYK#.G
SW:CDC2_HUMAN	H16	5046	2	1186.4	(+0.7)	2.457	0.311	0.947	5	K.IGEGTYGVVYK.G
SW:CDC2_HUMAN	H16	7060	2	1823.0	(-0.2)	3.360	0.368	0.968	2	K.K#PL*FHGDSEIDQL*FR.I
SW:CDC2_HUMAN	H16	4618	2	1517.6	(+0.1)	2.708	0.348	0.929	2	R.LESEEEGVPSTAIR.E
SW:CDC2_HUMAN	H16	6148	3	1970.2	(+0.4)	4.342	0.507	0.971	2	K.M@AL*NHPYFNDL*DNQIK#.K
SW:CDC2_HUMAN	H16	6456	3	1954.2	(+0.9)	4.238	0.419	0.999	2	K.MAL*NHPYFNDL*DNQIK#.K
SW:CDC2_HUMAN	H16	6376	2	1363.5	(+0.5)	3.033	0.265	0.954	2	K.NL*DENGL*DL*L*SK#.M

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:CDC2_HUMAN	H16	10386	2	2213.5	(-0.8)	2.809	0.524	0.945	2	R.YSTPVDIWSIGTIFAELATK.K
SW:CDC2_HUMAN	H16	10354	2	2213.5	(+0.5)	2.758	0.460	0.987	2	R.YSTPVDIWSIGTIFAELATK.K
SW:CDC2_HUMAN	H16	6086	2	1446.6	(-0.1)	2.368	0.202	0.057	1	R.DL*K#PQNL*L*IDDK#.G
SW:CDK2_HUMAN	H15	8778	2	1608.8	(+1.0)	2.606	0.527	0.987	3	R.ALFPDSEIDQLFR.I
SW:CDK2_HUMAN	H16	8058	2	1730.1	(+0.0)	3.650	0.421	0.979	2	K.FM@DASAL*TGIPL*PL*IK#.S
SW:CDK2_HUMAN	H16	8532	2	1714.1	(-0.3)	2.562	0.351	0.900	2	K.FMDASAL*TGIPL*PL*IK#.S
SW:CDK2_HUMAN	H16	5436	2	1202.4	(+0.2)	2.813	0.502	0.984	2	K.L*L*DVIHTENK#.L
SW:CDK2_HUMAN	H16	6796	2	1802.1	(-0.9)	2.224	0.120	0.003	2	R.DL*K#PQNL*L*INTEGAIK#.L
SW:CEB1_HUMAN	H08	1953	2	1216.3	(+0.4)	3.873	0.414	0.994		R.AQEAEEGAALR.T
SW:CEB1_HUMAN	H08	5315	2	1385.5	(+0.6)	2.303	0.247	0.839		R.DFSL*M@ASDDPEK#.L
SW:CEB1_HUMAN	H08	7389	2	1649.9	(+0.8)	3.558	0.373	0.987		K.ELGAQLHQLVLSAR.E
SW:CEB1_HUMAN	H08	4933	2	1313.4	(+0.7)	2.944	0.339	0.973		K.ELGGEEPEPSLR.E
SW:CEB1_HUMAN	H08	4919	2	1325.4	(+0.7)	2.434	0.272	0.911		K.EL*GGEEPEPSL*R.E
SW:CEB1_HUMAN	H08	7035	2	1777.9	(-0.1)	3.570	0.372	0.972		R.GAESL*EAAL*THNAEVPR.R
SW:CEB1_HUMAN	H08	5421	3	2093.3	(+0.5)	5.467	0.530	0.999		R.L*VEAQATHFQQGHEEL*SR.L
SW:CEB1_HUMAN	H08	7603	2	1669.9	(+0.2)	2.585	0.338	0.905		R.WFTIQSNQL*VYQK#.K
SW:CEB1_HUMAN	H08	6313	2	1369.5	(-0.2)	2.272	0.312	0.824		R.DFSL*MASDDPEK#.L
SW:CGB1_HUMAN	H11	5840	2	1453.6	(+0.1)	3.096	0.362	0.958	5	K.IGEVDVEQHTL*AK#.Y
SW:CGB1_HUMAN	H12	5220	2	1453.6	(+0.0)	2.973	0.314	0.927	5	K.IGEVDVEQHTL*AK#.Y
SW:CGB1_HUMAN	H12	5056	2	1217.4	(+0.7)	2.403	0.283	0.914		K.NVVMVNLQGL*TK#.H
SW:CH10_HUMAN	H22	7270	2	1530.8	(+1.0)	3.621	0.499	0.996	3	K.VVLDDKDYFLFR.D
SW:CH10_HUMAN	H22	5282	2	1316.5	(+1.0)	3.174	0.530	0.999	3	K.VLQATVAVGSGSK.G
SW:CH60_HUMAN	H10	10097	3	2162.6	(-0.0)	4.059	0.520	1.000	1	R.AL*ML*QGVDL*L*ADAVAVTM@GPK#.G
SW:CH60_HUMAN	H10	8185	2	1920.2	(-0.2)	3.591	0.526	1.000	1	K.ISSIQSIVPALEIANAHR.K
SW:CH60_HUMAN	H10	6011	3	2561.7	(+1.0)	3.876	0.408	0.998	1	K.LVQDVANNTNEEAGDGTTTATVLAR.S
SW:CH60_HUMAN	H10	12173	3	2483.9	(+0.4)	4.530	0.529	1.000	2	R.TALLDAAGVASLLTAEVTVTEIPK.E
SW:CH60_HUMAN	H10	8157	2	1505.7	(+0.8)	2.843	0.456	0.989	2	K.TLNDELEIIEGMK.F
SW:CH60_HUMAN	H10	8155	2	1525.7	(-0.7)	2.503	0.323	0.681	2	K.TL*NDEL*EIIIEGMK#.F
SW:CH60_HUMAN	H10	6403	2	1345.5	(+0.9)	3.337	0.398	0.990		R.TVIIEQSWGSPK.V
SW:CH60_HUMAN	H10	7003	2	1390.6	(+0.8)	2.374	0.379	0.965	1	R.GYISPYFINTSK.G
SW:CHD3_HUMAN	H01	7902	3	1894.1	(+0.3)	3.727	0.451	0.999	4	R.FNNL*EGFL*EEFADISK#.E
SW:CHD3_HUMAN	H02	8210	3	1894.1	(+1.0)	3.986	0.519	1.000	4	R.FNNL*EGFL*EEFADISK#.E
SW:CHD3_HUMAN	H03	10118	2	1874.1	(+0.1)	2.831	0.440	0.968	4	R.FNNLEGFLEEFADISK.E
SW:CHD3_HUMAN	H04	9547	2	1901.2	(+0.8)	4.409	0.534	1.000	3	K.GPFLVSAPLSTIINWER.E
SW:CHD3_HUMAN	H04	9533	2	1913.2	(+0.4)	3.215	0.449	0.988	3	K.GPFL*VSAPL*STIINWER.E
SW:CHD3_HUMAN	H03	1846	2	1560.6	(+0.8)	3.165	0.444	0.992	7	R.HHYEQQEDL*AR.N
SW:CHD3_HUMAN	H04	1779	2	1554.6	(+1.0)	2.884	0.386	0.984	7	R.HHYEQQEDLAR.N
SW:CHD3_HUMAN	H03	7170	2	1382.6	(+0.9)	2.947	0.357	0.979	1	R.VGGNIEVL*GFNTR.Q
SW:CHD3_HUMAN	H04	5513	2	973.1	(+0.6)	2.296	0.193	0.797	1	R.IDGGITGALR.Q
SW:CHD4_HUMAN	H03	6610	3	2053.1	(+0.4)	4.429	0.470	0.998	1	K.FGTEEL*FK#DEATDGGGDNK#.E
SW:CHD4_HUMAN	H03	9234	3	1670.9	(+0.2)	4.082	0.405	0.971	1	R.GGGNQVSL*L*NVVMDL*K#.K
SW:CHD4_HUMAN	H03	8626	3	1686.9	(+1.0)	3.984	0.282	0.988	1	R.GGGNQVSL*L*NVVM@DL*K#.K
SW:CHD4_HUMAN	H03	8618	2	1686.9	(-0.1)	2.444	0.270	0.757	1	R.GGGNQVSL*L*NVVM@DL*K#.K
SW:CHD4_HUMAN	H03	9286	2	1901.1	(-0.9)	3.192	0.339	0.838	1	K.M@L*DL*L*EDFL*EHGYK#.Y
SW:CHD4_HUMAN	H03	8142	3	2499.6	(+0.2)	4.755	0.523	1.000	1	R.NQDETEDTEL*QGMNEYL*SSFK#.V
SW:CHD4_HUMAN	H03	8344	2	1533.8	(+0.1)	3.333	0.570	1.000	1	K.TVQTAVFLYSLYK.E
SW:CHD4_HUMAN	H03	8340	2	1553.8	(+0.2)	3.044	0.454	0.978	1	K.TVQTAVFL*YSL*YK#.E
SW:CHD4_HUMAN	H03	7158	2	1352.5	(+1.0)	3.833	0.478	0.999	5	R.VGGNIEVL*GFNAR.Q
SW:CHD4_HUMAN	H03	7164	2	1346.5	(+1.0)	3.626	0.486	0.999	5	R.VGGNIEVLGFNAR.Q
SW:CHD4_HUMAN	H03	9244	2	1644.9	(+0.6)	2.301	0.411	0.965	1	R.GGGNQVSL*NVVMDL*K#.K
SW:CIRP_HUMAN	H19	7776	2	1560.7	(+0.5)	3.669	0.488	1.000	2	R.GFGFVTFENIDDAK.D
SW:CIRP_HUMAN	H20	5926	2	1229.4	(+0.7)	2.491	0.350	0.961	2	K.YGQISEVVVK#.D
SW:CKS1_HUMAN	H22	6068	2	2164.2	(+0.4)	3.204	0.400	0.708	1	K.QIYYSKYDDEEFYR.H
SW:CKS1_HUMAN	H22	4626	2	1298.4	(+0.6)	2.336	0.377	0.969	2	K.THL*M@SESEWR.N
SW:CLH1_HUMAN	H04	10415	2	1948.3	(+0.5)	2.205	0.295	0.869	7	K.AFMTADLPNELIELLEK.I
SW:CLH1_HUMAN	H04	7159	2	1485.6	(-0.2)	2.214	0.140	0.283	3	R.AL*EHFTDL*YDIK#.R

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:CLH1_HUMAN	H04	10779	2	2122.3	(+0.2)	3.079	0.315	0.934	3	K.DTELAEEELLQWFLQEEK.R
SW:CLH1_HUMAN	H04	7065	2	1552.7	(+0.7)	3.965	0.493	1.000	8	R.GQFSTDELVAEVEK.R
SW:CLH1_HUMAN	H04	7473	3	2465.7	(+0.6)	4.638	0.473	1.000	2	R.LAELEEFINGPNNNAHIQVVGDR.C
SW:CLH1_HUMAN	H04	8771	2	1354.7	(+0.9)	4.272	0.415	0.981	7	R.NLQNLLILTAIK.A
SW:CLH1_HUMAN	H04	8775	2	1386.7	(-0.3)	2.551	0.213	0.721	7	R.NL*QNL*L*IL*TAIK#.A
SW:CLH1_HUMAN	H04	6907	2	1317.4	(+0.5)	2.570	0.369	0.972	2	R.NNL*AGAEEL*FAR.K
SW:CLH1_HUMAN	H04	9329	2	1480.7	(+0.7)	3.508	0.421	0.993	7	K.VGYTPDWIFLLR.N
SW:CLH1_HUMAN	H07	9530	3	2369.7	(+1.0)	5.428	0.564	1.000	2	R.KFDVNTSAVQVLIHIGNLDR.A
SW:CNG6_HUMAN	H18	7942	2	1532.8	(-0.0)	2.939	0.228	0.841		K.AGVM@AL*ANL*L*QIQR.H
SW:CNG6_HUMAN	H18	6566	2	1134.3	(+0.9)	3.187	0.406	0.993		R.HDDYLVMLK.A
SW:CNG6_HUMAN	H18	5942	2	1170.3	(+0.8)	2.736	0.322	0.968		R.HDDYL*VM@L*K#.A
SW:CNG6_HUMAN	H18	6564	2	1154.3	(-0.4)	2.734	0.385	0.965		R.HDDYL*VML*K#.A
SW:CNG6_HUMAN	H18	9222	2	2154.4	(-0.6)	5.516	0.569	0.990		K.HILGFDTGDAVLNEAAQILR.L
SW:CNG6_HUMAN	H18	7184	2	1834.0	(-0.6)	3.372	0.369	0.962		K.NAEPL*INL*DVNNPDFK#.A
SW:CNG6_HUMAN	H18	8158	2	1306.5	(+0.6)	2.932	0.336	0.979		R.NFIVWL*EDQK#.I
SW:CNG6_HUMAN	H18	7198	2	1814.0	(-0.9)	2.684	0.389	0.838		K.NAEPLINLDVNNPDFK.A
SW:CO1A_HUMAN	H12	2474	2	1286.5	(+1.0)	3.749	0.455	0.917	1	R.KLQATVQELQK.R
SW:CO1A_HUMAN	H12	2936	2	1286.5	(+0.7)	3.546	0.351	0.990	1	R.KLQATVQELQK.R
SW:CO1A_HUMAN	H12	2686	2	1286.5	(+0.9)	3.121	0.229	0.951	1	R.KLQATVQELQK.R
SW:CO1A_HUMAN	H12	2858	2	1286.5	(+0.7)	2.960	0.363	0.984	1	R.KLQATVQELQK.R
SW:CO1A_HUMAN	H12	4052	2	1286.5	(+0.9)	2.939	0.356	0.982	1	R.KLQATVQELQK.R
SW:CO1A_HUMAN	H12	2786	2	1286.5	(+0.4)	2.832	0.327	0.973	1	R.KLQATVQELQK.R
SW:CO1A_HUMAN	H12	2470	2	1314.5	(+0.0)	2.682	0.283	0.886	1	R.K#L*QATVQEL*QK#.R
SW:CO1A_HUMAN	H12	2884	2	1314.5	(+0.4)	2.576	0.210	0.865	1	R.K#L*QATVQEL*QK#.R
SW:CO1A_HUMAN	H12	3106	2	1314.5	(+0.3)	2.553	0.373	0.938	1	R.K#L*QATVQEL*QK#.R
SW:CO1A_HUMAN	H12	2708	2	1314.5	(-0.1)	2.532	0.257	0.822	1	R.K#L*QATVQEL*QK#.R
SW:CO1A_HUMAN	H12	2960	2	1314.5	(+0.6)	2.470	0.132	0.628	1	R.K#L*QATVQEL*QK#.R
SW:CO1A_HUMAN	H12	4094	2	1286.5	(-0.9)	2.293	0.254	0.428	1	R.KLQATVQELQK.R
SW:CO1A_HUMAN	H12	8958	3	3175.5	(+0.8)	4.331	0.517	0.999	1	R.KSDFQEDLYPPTAGPDPALTAEEWLGGRR.D
SW:CO1A_HUMAN	H12	2328	2	1158.3	(+0.9)	2.790	0.304	0.970	1	K.LQATVQELQK.R
SW:CO1A_HUMAN	H12	1748	2	884.0	(+0.5)	2.293	0.324	0.912	1	R.HVFGQPAK.A
SW:COF1_HUMAN	H19	7614	2	2167.4	(+0.8)	5.866	0.656	1.000	1	K.EILVGDVGQTVDDPYATFVK.M
SW:COF1_HUMAN	H20	8762	2	1991.3	(+0.4)	4.771	0.489	0.997	2	K.KEDLVFIFWAPESAPLK.S
SW:COF1_HUMAN	H19	5466	2	1352.5	(+0.6)	3.651	0.447	0.999	2	R.YAL*YDATYETK#.E
SW:COF1_HUMAN	H19	5452	2	1338.5	(+1.0)	3.196	0.440	0.993	2	R.YALYDATYETK.E
SW:COF1_HUMAN	H20	7556	2	2167.4	(+0.5)	4.275	0.606	1.000	1	K.EILVGDVGQTVDDPYATFVK.M
SW:CPSA_HUMAN	H01	7418	2	1901.1	(+0.1)	2.802	0.397	0.932	2	K.IGTTPDIILDDLLETDR.V
SW:CPSA_HUMAN	H02	7622	2	1901.1	(+0.5)	3.540	0.482	0.994	2	K.IGTTPDIILDDLLETDR.V
SW:CPSA_HUMAN	H01	7206	2	2029.3	(+0.6)	3.260	0.465	0.992	2	K.KIGTTPDIILDDLLETDR.V
SW:CPSA_HUMAN	H02	7378	2	2029.3	(+0.8)	2.486	0.442	0.979	2	K.KIGTTPDIILDDLLETDR.V
SW:CPSA_HUMAN	H01	5380	2	858.1	(+0.4)	2.468	0.181	0.876	1	R.LGNSLLK.Y
SW:CPSA_HUMAN	H02	5168	2	950.1	(+0.9)	2.364	0.316	0.947	1	K.NGAL*SVL*QK#.S
SW:CPSA_HUMAN	H01	6752	2	1403.6	(+0.6)	2.989	0.445	0.990	1	R.SSFL*PSYIIDVR.A
SW:CPSA_HUMAN	H01	5068	2	1792.9	(+0.6)	4.262	0.543	1.000	1	R.VLVDSSFGQPTTQGEAR.R
SW:CPSA_HUMAN	H01	6150	2	1251.5	(+0.7)	2.721	0.322	0.968	1	R.YIVQVSPL*GIR.L
SW:CPSA_HUMAN	H02	6248	2	1251.5	(+0.7)	2.272	0.200	0.780	1	R.YIVQVSPL*GIR.L
SW:CPSA_HUMAN	H04	9219	2	1901.1	(+0.2)	3.209	0.450	0.980	2	K.IGTTPDIILDDLLETDR.V
SW:CRTC_HUMAN	H11	6780	2	1417.5	(+0.6)	2.701	0.501	0.992		K.EQFL*DGDGWTSR.W
SW:CRTC_HUMAN	H12	6514	2	1411.5	(+0.7)	2.265	0.426	0.973		K.EQFLDGDGWTSR.W
SW:CRTC_HUMAN	H11	8214	2	1608.8	(+0.7)	5.279	0.537	1.000		R.FYALSASFEPFSNK.G
SW:CRTC_HUMAN	H11	8208	2	1622.8	(+0.5)	3.872	0.519	0.999		R.FYAL*SASFEPFSNK#.G
SW:CRTC_HUMAN	H12	7870	2	1622.8	(+0.4)	3.432	0.462	0.987		R.FYAL*SASFEPFSNK#.G
SW:CRTC_HUMAN	H11	5472	2	1801.9	(-0.3)	3.005	0.508	0.707		K.IKDPDASKPEDWDER.A
SW:CRTC_HUMAN	H12	2362	2	1817.9	(+0.1)	3.404	0.478	0.729		K.IK#DPDASK#PEDWDER.A
SW:CRTC_HUMAN	H12	2350	2	1801.9	(+0.5)	2.901	0.396	0.669		K.IKDPDASKPEDWDER.A
SW:CRTC_HUMAN	H11	7938	3	2962.2	(+0.5)	3.766	0.405	0.998		K.KPEDWDEEMDGEWEPPIQNPEYK.G
SW:CRTC_HUMAN	H12	6204	2	1164.4	(+0.6)	2.600	0.468	0.985		K.K#VHVIFNYK#.G
SW:CRTC_HUMAN	H12	1906	1	700.9	(+0.1)	2.020	0.152*	0.000		K.NVLINK.D
SW:CSL4_HUMAN	H19	6934	2	1357.7	(+0.9)	4.158	0.508	1.000		K.VHILYVGSMPK.N
SW:CSL4_HUMAN	H19	6268	2	1393.7	(+0.3)	3.267	0.525	1.000		K.VHIL*YVGSMPK#.N

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:CSL4_HUMAN	H19	6926	2	1377.7	(+0.1)	3.258	0.300	0.944		K.VHIL*YVGSMPK*#K.N
SW:CSL4_HUMAN	H19	6138	2	1217.4	(+1.0)	2.699	0.195	0.206	1	K.SFRPGDIVL*AK#.V
SW:CST1_HUMAN	H13	7738	3	2322.6	(+0.8)	4.035	0.509	0.955	1	R.SISFHPSGDFIL*VGTQHPHL*R.L
SW:CST1_HUMAN	H13	5750	2	1159.3	(+0.9)	2.256	0.170	0.758	1	K.YIQEAEML*R.S
SW:CST2_HUMAN	H09	5213	2	1137.2	(+0.4)	2.283	0.351	0.952	7	R.GL*L*GDAPNDPR.G
SW:CST2_HUMAN	H10	6785	2	1415.6	(+0.2)	2.201	0.474	0.953	5	R.GGTLLSVTGEVEPR.G
SW:CT20_HUMAN	H16	8050	2	1586.8	(+0.1)	2.630	0.199	0.674		R.NFVLPPEIIQEV.R
SW:CT20_HUMAN	H17	1346	2	1458.6	(+0.5)	3.042	0.536	0.991		K.VL*TANSPSSPSAAK#.R
SW:CT43_HUMAN	H15	2192	2	1902.0	(-0.2)	2.408	0.324	0.170	4	K.AAESVSK#PDVSEEAPGPK#.V
SW:CT43_HUMAN	H15	4564	2	1079.2	(+0.9)	2.335	0.341	0.955	5	K.SLFTTHSSAK.R
SW:CT43_HUMAN	H15	4582	2	1093.2	(-0.2)	2.295	0.309	0.855	5	K.SL*FTTHSSAK#.R
SW:CTOG_HUMAN	H03	7540	2	1458.6	(+0.1)	3.586	0.361	0.970	1	K.EGL*DEVAGIINDAK#.F
SW:CTOG_HUMAN	H04	7375	2	1444.6	(+0.7)	3.037	0.353	0.979	1	K.EGLDEVAGIINDAK.F
SW:CTOG_HUMAN	H04	7041	2	1659.9	(+0.7)	4.455	0.471	1.000	1	K.FGQYAGHVPTILEK.F
SW:CTOG_HUMAN	H07	7106	2	1659.9	(+0.8)	4.415	0.510	0.998	1	K.FGQYAGHVPTILEK.F
SW:CTOG_HUMAN	H03	6310	2	1335.5	(+0.0)	2.822	0.155	0.672	2	K.FVTDNSNAVVL*#K#.G
SW:CTOG_HUMAN	H04	5545	2	1136.3	(+0.6)	2.242	0.204	0.776	2	K.GEAVQEEL*L*#K#.G
SW:CTOG_HUMAN	H03	7452	2	1051.4	(+0.3)	2.210	0.177	0.051	2	K.IILLKPIIK.V
SW:CTOG_HUMAN	H03	8474	2	1645.9	(-0.9)	3.178	0.312	0.813	2	K.L*DDIFEPVL*IPEPK#.I
SW:CTOG_HUMAN	H03	8466	2	1625.9	(-0.6)	2.630	0.414	0.956	2	K.LDDIFEPVLIPEPK.I
SW:CTOG_HUMAN	H04	8351	2	1625.9	(+0.1)	2.275	0.323	0.837	2	K.LDDIFEPVLIPEPK.I
SW:CTOG_HUMAN	H05	8444	2	1645.9	(+0.6)	3.097	0.399	0.984	2	K.L*DDIFEPVL*IPEPK#.I
SW:CTOG_HUMAN	H05	8446	2	1625.9	(-0.6)	2.595	0.358	0.925	2	K.LDDIFEPVLIPEPK.I
SW:CTOG_HUMAN	H06	8368	2	1645.9	(+1.0)	3.305	0.488	0.993	2	K.L*DDIFEPVL*IPEPK#.I
SW:CTOG_HUMAN	H03	6470	2	1214.3	(-0.2)	2.435	0.250	0.781	1	K.L*EAGDYADL*VK#.A
SW:CTOG_HUMAN	H03	8670	3	2432.7	(+0.1)	5.035	0.514*	0.020	1	R.M@FFEDEK#PAL*L*SQIDAEFEK#.M
SW:CTOG_HUMAN	H04	8545	3	2432.7	(+0.4)	4.508	0.454*	0.028	1	R.M@FFEDEK#PAL*L*SQIDAEFEK#.M
SW:CTOG_HUMAN	H04	8829	3	2416.7	(+0.1)	4.413	0.354*	0.010	1	R.MFFEDEK#PAL*L*SQIDAEFEK#.M
SW:CTOG_HUMAN	H03	8770	2	1460.7	(-0.8)	2.945	0.356	0.827	1	K.NL*GIPIITVL*GDSK#.N
SW:CTOG_HUMAN	H05	8734	2	1460.7	(+0.4)	2.420	0.184	0.713	1	K.NL*GIPIITVL*GDSK#.N
SW:CTOG_HUMAN	H03	8056	2	1638.8	(-0.6)	2.405	0.297	0.810	2	K.NQSETL*NWL*SNAIK#.E
SW:CTOG_HUMAN	H04	7913	2	1618.8	(+0.9)	3.768	0.422	0.973	2	K.NQSETLNWLSNAIK.E
SW:CTOG_HUMAN	H07	8046	2	1618.8	(+0.9)	3.212	0.396	0.987	2	K.NQSETLNWLSNAIK.E
SW:CTOG_HUMAN	H03	2384	2	1085.2	(+0.2)	2.817	0.401	0.969	1	K.TALAATNPAVR.T
SW:CTOG_HUMAN	H03	4600	2	1171.3	(+0.9)	2.938	0.457	0.990	2	K.TTGEVVSQVSK#.V
SW:CTOG_HUMAN	H03	4522	2	1171.3	(-0.4)	2.828	0.360	0.947	2	K.TTGEVVSQVSK#.V
SW:CTOG_HUMAN	H03	4506	2	1163.3	(+0.8)	2.817	0.339	0.974	2	K.TTGEVVSQVSK#.V
SW:CTOG_HUMAN	H03	4622	2	1171.3	(-0.5)	2.532	0.396	0.942	2	K.TTGEVVSQVSK#.V
SW:CTOG_HUMAN	H04	8861	2	1210.4	(+0.8)	3.119	0.440	0.992	2	K.VNDL*AEIFK#.K
SW:CTOG_HUMAN	H05	8994	2	1210.4	(+0.8)	3.589	0.425	1.000	2	K.VNDL*AEIFK#.K
SW:CTOG_HUMAN	H03	7124	2	1298.4	(+0.9)	3.575	0.409	0.993	2	K.YSDADIEPFLK.N
SW:CTOG_HUMAN	H03	7132	2	1312.4	(+0.4)	3.277	0.451	0.993	2	K.YSDADIEPFL*#K#.N
SW:CTOG_HUMAN	H05	7134	2	1312.4	(+0.1)	2.225	0.204	0.572	2	K.YSDADIEPFL*#K#.N
SW:CTOG_HUMAN	H09	6653	2	1442.7	(+0.5)	3.005	0.464	0.991	2	K.ALAVMVDHLESEK.E
SW:CUL1_HUMAN	H07	8480	2	1709.9	(+0.5)	2.658	0.556	0.993	3	K.HQQLLGEVLTQLSSR.F
SW:CUL1_HUMAN	H07	11662	2	1546.9	(-0.7)	2.633	0.170	0.322	3	K.M@DIL*AQVL*QIL*L*#K#.S
SW:CV19_HUMAN	H08	1795	2	1676.8	(+0.3)	2.968	0.316	0.926	1	K.AEVTM@GDPHQQL*AR.L
SW:CV19_HUMAN	H08	2473	2	1654.8	(+0.4)	2.929	0.419	0.980	1	K.AEVTMGDPHQQLAR.L
SW:CV19_HUMAN	H08	8193	2	1751.9	(+0.3)	2.506	0.309	0.867	1	K.HEEIDLVSLEEFYK.E
SW:CV19_HUMAN	H08	4831	2	1431.5	(-0.0)	3.626	0.482	0.997	2	K.TPNPANQYQFDK#.V
SW:CV19_HUMAN	H08	4817	2	1423.5	(+0.2)	3.160	0.393	0.975	2	K.TPNPANQYQFDK.V
SW:CV19_HUMAN	H08	8189	2	1771.9	(-0.2)	2.492	0.216	0.661	1	K.HEEIDL*VSL*EEFYK#.E
SW:CYC_HUMAN	H21	8830	2	2009.3	(+0.5)	4.723	0.457	0.999	3	K.GIIWGEDTLMEYLENPK.K
SW:CYC_HUMAN	H21	8822	2	2029.3	(-0.3)	3.531	0.479	0.985	3	K.GIIWGEDTL*MEYL*ENPK#.K
SW:CYC_HUMAN	H21	8544	2	2137.5	(-0.6)	4.871	0.587	1.000	3	K.GIIWGEDTLMEYLENPKK.Y
SW:CYC_HUMAN	H21	1996	2	1573.7	(+0.0)	4.749	0.558	1.000	3	R.K#TGQAPGYSYTAANK#.N
SW:CYC_HUMAN	H21	2046	2	1437.5	(+0.3)	3.101	0.453	0.977	3	K.TGQAPGYSYTAANK#.N
SW:CYC_HUMAN	H21	2042	2	1429.5	(+0.7)	2.980	0.457	0.990	3	K.TGQAPGYSYTAANK.N

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:CYC_HUMAN	H21	8538	2	2165.5	(-0.9)	2.709	0.325	0.088	3	K.GIIWGEDTL*MEYL*ENPK#K#.Y
SW:DB83_HUMAN	H18	7752	2	1238.5	(-0.3)	2.515	0.169	0.619	1	R.AL*L*ANAL*TSAL*R.L
SW:DB83_HUMAN	H19	7686	2	1238.5	(-0.0)	2.921	0.239	0.877	1	R.AL*L*ANAL*TSAL*R.L
SW:DB83_HUMAN	H18	4772	2	1129.3	(+0.5)	2.852	0.378	0.985	1	K.LSANQQNILK.F
SW:DB83_HUMAN	H18	4736	2	1149.3	(+0.0)	2.328	0.190	0.618	1	K.L*SANQQNIL*K#.F
SW:DB83_HUMAN	H19	4694	2	1149.3	(+0.1)	2.464	0.411	0.942	1	K.L*SANQQNIL*K#.F
SW:DD17_HUMAN	H08	6515	2	1233.4	(+0.8)	2.574	0.495	0.990	5	K.APIL*IATDVASR.G
SW:DD17_HUMAN	H10	6563	2	1227.4	(-0.5)	3.193	0.480	0.987	5	K.APILATDVASR.G
SW:DD17_HUMAN	H10	6527	2	1298.5	(-0.7)	2.478	0.188	0.337	2	R.CTYLVLDEADR.M
SW:DD17_HUMAN	H08	6725	2	1706.8	(-0.0)	4.292	0.547	0.902	1	R.EL*AQQVQQVADDYGK#.C
SW:DD17_HUMAN	H09	6573	2	1706.8	(-0.9)	3.361	0.450	0.915	1	R.EL*AQQVQQVADDYGK#.C
SW:DD17_HUMAN	H10	6737	2	1692.8	(+0.7)	4.629	0.516	1.000	1	R.ELAQVQQVADDYGK.C
SW:DD17_HUMAN	H10	6735	2	1706.8	(-0.7)	2.749	0.401	0.846	1	R.EL*AQQVQQVADDYGK#.C
SW:DD17_HUMAN	H11	6890	2	1692.8	(+0.1)	3.341	0.413	0.976	1	R.ELAQVQQVADDYGK.C
SW:DD17_HUMAN	H10	4709	2	875.0	(+1.0)	2.453	0.303	0.962	4	R.GLDVEDVK.F
SW:DD17_HUMAN	H10	4599	1	889.0	(-0.4)	1.950	0.295	0.000	4	R.GL*DVEDVK#.F
SW:DD17_HUMAN	H08	7393	2	1417.6	(+0.9)	2.662	0.426	0.983	1	K.GTAYTFFTPGNLK.Q
SW:DD17_HUMAN	H08	7391	2	1431.6	(+0.3)	2.326	0.327	0.847	1	K.GTAYTFFTPGNL*K#.Q
SW:DD17_HUMAN	H09	7277	2	1417.6	(+0.7)	3.527	0.502	1.000	1	K.GTAYTFFTPGNLK.Q
SW:DD17_HUMAN	H08	7179	2	1042.2	(+0.7)	2.236	0.307	0.927	1	R.L*IDFL*ESGK#.T
SW:DD17_HUMAN	H08	8783	2	1448.8	(+0.8)	2.555	0.433	0.983	1	K.LIQLMEEIMAEK.E
SW:DD17_HUMAN	H09	8755	2	1468.8	(+0.3)	2.839	0.371	0.953	1	K.L*IQL*MEEIMAEK#.E
SW:DD17_HUMAN	H08	6103	2	1375.6	(+0.1)	2.613	0.275	0.880	10	R.M@L*DM@GFEPQIR.K
SW:DD17_HUMAN	H09	7229	2	1343.6	(+1.0)	3.632	0.529	1.000	10	R.ML*DMGFEPQIR.K
SW:DD17_HUMAN	H09	6015	2	1375.6	(+0.8)	2.608	0.296	0.952	10	R.M@L*DM@GFEPQIR.K
SW:DD17_HUMAN	H10	6199	2	1375.6	(+0.6)	2.645	0.299	0.956	10	R.M@L*DM@GFEPQIR.K
SW:DD17_HUMAN	H08	4103	2	1340.5	(-0.1)	2.909	0.424	0.971	1	K.VL*EEANQAINPK#.L
SW:DD17_HUMAN	H08	4209	2	1340.5	(-0.6)	2.783	0.355	0.942	1	K.VL*EEANQAINPK#.L
SW:DD17_HUMAN	H08	4331	2	1340.5	(-0.4)	2.668	0.192	0.713	1	K.VL*EEANQAINPK#.L
SW:DD17_HUMAN	H08	4155	2	1326.5	(+0.2)	2.512	0.148	0.555	1	K.VLEEANQAINPK.L
SW:DD17_HUMAN	H08	4233	2	1326.5	(+0.2)	2.297	0.109	0.319	1	K.VLEEANQAINPK.L
SW:DD17_HUMAN	H09	4509	2	1340.5	(-0.5)	3.289	0.387	0.974	1	K.VL*EEANQAINPK#.L
SW:DD17_HUMAN	H09	4487	2	1340.5	(+0.8)	2.791	0.460	0.988	1	K.VL*EEANQAINPK#.L
SW:DD17_HUMAN	H09	4609	2	1340.5	(+0.9)	2.707	0.454	0.987	1	K.VL*EEANQAINPK#.L
SW:DD17_HUMAN	H11	5168	2	1326.5	(-0.2)	2.484	0.110	0.418	1	K.VLEEANQAINPK.L
SW:DD17_HUMAN	H14	4867	2	1340.5	(-0.2)	2.401	0.288	0.821	1	K.VL*EEANQAINPK#.L
SW:DD18_HUMAN	H08	8037	2	1442.6	(+0.3)	3.752	0.467	1.000	4	K.VPLSEFDVSWSK.I
SW:DD18_HUMAN	H08	9359	3	2272.7	(+0.1)	5.411	0.414	0.998	6	K.YHYELLYIDLPVLAHKG.Q
SW:DD18_HUMAN	H08	5065	2	1161.3	(+0.1)	2.473	0.137	0.569	3	K.ISDIQSLEK.L
SW:DD21_HUMAN	H07	5520	2	1393.5	(+0.7)	3.638	0.399	0.716	3	K.EEYQLVQVEQK.A
SW:DD21_HUMAN	H07	6318	2	1390.7	(+1.0)	2.651	0.479	0.775	3	R.GRAPQVL*VL*APTR.E
SW:DD21_HUMAN	H01	6746	2	1221.5	(+0.5)	3.016	0.527	1.000	3	R.GVTFLFPIQAK.T
SW:DD21_HUMAN	H07	2136	2	1728.8	(+0.3)	3.268	0.328	0.396	3	K.NEEPSEEEIDAPK#PK#.K
SW:DD21_HUMAN	H07	5836	2	1267.4	(+0.6)	2.689	0.362	0.971	3	K.STYEQVDL*IGK#.K
SW:DD21_HUMAN	H07	2542	1	833.9	(-0.3)	1.942	0.375*	0.000	3	K.DFSDITK#.K
SW:DD48_HUMAN	H13	6382	2	1829.1	(-0.3)	3.588	0.522	1.000	7	R.GIYAYGFEEKPSAIQQR.A
SW:DD48_HUMAN	H13	4982	2	1598.8	(+0.8)	5.181	0.570	0.998	2	R.KLDYGGHVAGTPGR.V
SW:DD48_HUMAN	H13	7924	2	1547.8	(-0.1)	3.790	0.388	0.980	2	K.ML*VL*DEADEML*NK#.G
SW:DD48_HUMAN	H13	6046	2	1194.3	(+0.8)	2.625	0.372	0.976	2	K.RDEL*TL*EGIK#.Q
SW:DD48_HUMAN	H13	5706	2	1788.0	(-0.0)	2.542	0.379	0.920	2	R.EANFTVSSMHGDMPPQK#.E
SW:DDB2_HUMAN	H13	4712	2	1077.3	(+0.7)	2.306	0.254	0.268	2	K.TSEIVL*RPR.N
SW:DDB2_HUMAN	H14	5967	3	1962.2	(+0.7)	3.826	0.486	1.000	2	R.ATSL*AWHPTHSTVAVGSK#.G
SW:DDX1_HUMAN	H07	10096	3	2397.6	(+0.3)	5.684	0.542	0.998	2	R.FL*VL*DEADGL*L*SQGYSDFINR.M
SW:DDX1_HUMAN	H07	4092	2	1014.1	(+1.0)	2.507	0.265	0.682	2	K.VPVDEFDVGK#.V
SW:DDX1_HUMAN	H07	3916	2	1014.1	(-0.2)	2.476	0.194	0.732	2	K.VPVDEFDVGK#.V
SW:DDX1_HUMAN	H07	4078	2	1006.1	(+0.7)	2.269	0.220	0.855	2	K.VPVDEFDVGK.V
SW:DDX1_HUMAN	H10	10131	3	2397.6	(+0.7)	4.185	0.463	0.999	2	R.FL*VL*DEADGL*L*SQGYSDFINR.M
SW:DDX3_HUMAN	H09	4391	2	1307.4	(+0.5)	2.869	0.331	0.638	4	R.DREEAL*HQFR.S

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:DDX3_HUMAN	H09	4361	2	1301.4	(+0.1)	2.558	0.316	0.307	4	R.DREEALHQFR.S
SW:DDX3_HUMAN	H09	4309	2	1307.4	(+0.2)	2.279	0.248	0.113	4	R.DREEAL*HQFR.S
SW:DDX3_HUMAN	H09	8349	2	2084.3	(+0.6)	4.142	0.540	1.000	4	K.HVINFDLPSDIEEYVHR.I
SW:DDX3_HUMAN	H08	9291	2	1324.5	(+0.1)	2.695	0.416	0.961	2	R.SFL*L*DL*L*NATGK#.D
SW:DDX3_HUMAN	H09	9303	2	1324.5	(+0.1)	2.736	0.485	0.978	2	R.SFL*L*DL*L*NATGK#.D
SW:DDX3_HUMAN	H09	10477	2	2333.7	(-1.0)	3.087	0.433*	0.095	2	K.TAAFLLPILSQIYSDGPGEALR.A
SW:DDX3_HUMAN	H09	7949	2	1525.7	(+0.8)	4.395	0.551	1.000	2	R.VGNLGLATSSFFNER.N
SW:DDX3_HUMAN	H09	7921	2	1537.7	(+0.3)	2.960	0.421	0.971	2	R.VGNL*GL*ATSSFFNER.N
SW:DDX3_HUMAN	H09	9043	2	1161.3	(+0.2)	2.228	0.213	0.631	4	K.DL*L*DL*L*VEAK#.Q
SW:DDX5_HUMAN	H10	5693	2	1390.5	(+0.8)	4.040	0.315	0.991	3	K.NFYQEHPDLAR.R
SW:DDX5_HUMAN	H10	5729	2	1396.5	(+0.3)	3.432	0.361	0.978	3	K.NFYQEHPDL*AR.R
SW:DDX5_HUMAN	H10	7241	2	1583.8	(+0.1)	3.841	0.450	1.000	2	K.TGTAYTFFTPNNIK#.Q
SW:DDX5_HUMAN	H10	7245	2	1575.8	(-0.3)	3.224	0.369	0.961	2	K.TGTAYTFFTPNNIK.Q
SW:DDX5_HUMAN	H10	8841	2	2362.8	(+0.2)	4.269	0.496	1.000	3	K.TLSYLLPAIVHINHQPFLER.G
SW:DDX5_HUMAN	H10	6519	2	1308.4	(+0.1)	2.925	0.442	0.980	2	R.TTYL*VL*DEADR.M
SW:DDX5_HUMAN	H10	6409	2	1004.2	(+0.3)	2.455	0.338	0.942	1	K.L*L*QL*VEDR.G
SW:DEK_HUMAN	H12	2466	2	1528.7	(+0.1)	4.041	0.453	0.979		K.KPPTDEELKETIK.K
SW:DEK_HUMAN	H12	6118	2	1806.0	(-0.8)	3.289	0.437	0.938	1	K.K#VYENPTYDL*TER.K
SW:DEK_HUMAN	H12	6760	2	1445.7	(-0.8)	2.885	0.468	0.926		K.L*L*ASANL*EEVLMK#.Q
SW:DEK_HUMAN	H12	6798	2	1419.7	(-0.1)	2.645	0.142	0.570		K.LLASANLEEVMTK.Q
SW:DEK_HUMAN	H12	6358	2	1461.7	(-0.6)	2.581	0.444	0.961		K.L*L*ASANL*EEVTM@K#.Q
SW:DEK_HUMAN	H12	5896	2	1474.7	(-0.1)	3.475	0.393	0.614	2	K.L*L*YNRPGTVSSL*K#.K
SW:DEK_HUMAN	H12	7276	2	1365.5	(-0.5)	3.241	0.125	0.737	2	K.NVGQFSGFPFEK#.G
SW:DEK_HUMAN	H12	6184	2	1663.8	(-0.4)	3.676	0.474	1.000	1	K.VYENPTYDLTER.K
SW:DEK_HUMAN	H12	5736	2	1175.4	(+0.0)	2.282	0.346	0.902	1	R.L*TMQVSSL*QR.E
SW:DENR_HUMAN	H16	4956	2	975.1	(+0.6)	2.478	0.239	0.932	1	K.L*DADYPL*R.V
SW:DENR_HUMAN	H17	4792	2	975.1	(+0.8)	2.843	0.327	0.983	1	K.L*DADYPL*R.V
SW:DENR_HUMAN	H16	6888	2	1860.9	(-0.2)	4.273	0.430	1.000	2	K.WPEVDDSDIEDL*GEVK#.K
SW:DENR_HUMAN	H17	6790	2	1860.9	(+0.1)	4.818	0.462	0.996	2	K.WPEVDDSDIEDL*GEVK#.K
SW:DENR_HUMAN	H18	5294	2	963.1	(+0.6)	2.755	0.262	0.952	1	K.LDADYPLR.V
SW:DESM_HUMAN	H11	5896	2	1608.7	(+0.1)	3.204	0.336	0.472	21	R.TNEK#VEL*QEL*NDR.F
SW:DESM_HUMAN	H17	4598	2	1116.2	(+0.3)	2.587	0.393	0.965	21	K.VELQELNDR.F
SW:DHX9_HUMAN	H05	2048	2	1484.6	(+0.8)	2.562	0.306	0.948	2	K.HL*EM@NPHFGSHR.Y
SW:DHX9_HUMAN	H05	6544	2	1302.6	(-0.2)	2.910	0.322	0.928	2	R.K#VFDPVPVGVTK#.V
SW:DHX9_HUMAN	H05	8888	2	2057.3	(+0.9)	3.615	0.455	0.986	3	K.TTQVPQFIL*DDFIQNDR.A
SW:DHX9_HUMAN	H05	6682	2	1158.4	(+0.9)	2.568	0.298	0.950	2	K.VFDPVPVGVTK.V
SW:DHX9_HUMAN	H05	8154	2	1715.9	(+0.5)	4.221	0.602	0.999	3	K.VQSDGQIVLVDWIK.L
SW:DHX9_HUMAN	H05	8160	2	1729.9	(+0.2)	3.562	0.455	0.983	3	K.VQSDGQIVL*VDDWIK#.L
SW:DHX9_HUMAN	H05	8362	2	1326.5	(+0.8)	2.872	0.415	0.986	1	K.YPSPFFVFGEK#.I
SW:DHX9_HUMAN	H05	7060	2	1477.7	(+1.0)	2.599	0.368	0.973	3	R.YQIL*PL*HSQIPR.E
SW:DHX9_HUMAN	H05	7062	2	1465.7	(+0.1)	2.561	0.356	0.932	3	R.YQILPLHSQIPR.E
SW:DIA2_HUMAN	H05	5576	2	1151.2	(+0.7)	2.447	0.316	0.949	1	K.K#FDEEFTAR.Q
SW:DIA2_HUMAN	H05	6656	2	1784.0	(+0.5)	3.264	0.351	0.981	2	K.SNL*ASM@EQQIVHL*ER.D
SW:DIA2_HUMAN	H05	9608	2	1795.0	(-0.2)	2.239	0.436	0.935	2	K.TVSIEEFFGDL*NNFR.T
SW:DIL2_HUMAN	H06	5464	2	1355.5	(+0.3)	2.797	0.270	0.882	5	K.SSDQPLTVPVSPK.F
SW:DIL2_HUMAN	H06	5456	2	1349.4	(+0.4)	2.980	0.256	0.953	4	K.STAELEAELEK.L
SW:DIL2_HUMAN	H06	5444	2	1369.4	(+0.1)	2.618	0.150	0.578	4	K.STAEL*EAEEL*EK#.L
SW:DJA1_HUMAN	H13	5814	2	1393.7	(+1.0)	3.802	0.529	1.000	4	R.TIVITSHPGQIVK.H
SW:DJA1_HUMAN	H13	5816	2	1401.7	(+0.7)	3.613	0.519	1.000	4	R.TIVITSHPGQIVK#.H
SW:DJA1_HUMAN	H13	6928	2	1464.6	(+0.8)	2.464	0.387	0.970	3	K.VNFPENGFLSPDK.L
SW:DJA2_HUMAN	H13	9694	3	3786.1	(+0.9)	6.350	0.542	0.956	2	K.LSELEDLLPSRPEVPNIIGETEEVELQEFDSTR.G
SW:DJA2_HUMAN	H13	7888	2	1864.0	(+0.7)	2.384	0.335	0.922	2	K.FDVQFPENNWINPDK.L
SW:DJB1_HUMAN	H14	8423	2	1961.2	(+0.9)	3.294	0.451	0.992	2	K.EGDQTSNNIPADIVFLK.D
SW:DJB1_HUMAN	H14	6505	2	1478.6	(+0.7)	3.342	0.451	0.993	2	K.EIAEAYDVLSDPR.K
SW:DJB1_HUMAN	H14	6503	2	1484.6	(+0.3)	2.299	0.187	0.540	2	K.EIAEAYDVL*SDPR.K



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:DJC8_HUMAN	H16	6010	3	2005.2	(+0.1)	4.223	0.440	0.992	3	K.K#EGK#PTIVEEDDPEL*FK#.Q
SW:DJC8_HUMAN	H16	8946	3	3352.7	(+0.8)	5.894	0.571	0.999	1	R.LTRPGSSYFNLPFVQLDPEVTDEEIK.K
SW:DJC8_HUMAN	H16	6012	3	1975.2	(+0.5)	4.050	0.482	0.996	3	K.KEGKPTIVEEDDPEL*FK#.Q
SW:DKC1_HUMAN	H11	9100	2	2110.5	(+0.1)	3.821	0.582	0.999	3	R.ALETLTGALFQRPLIAAVK.R
SW:DKC1_HUMAN	H11	5128	2	1396.5	(+0.3)	3.714	0.393	0.983	3	R.LHNAIEGGTQLSR.A
SW:DKC1_HUMAN	H11	5126	2	1408.5	(+0.7)	3.267	0.310	0.978	3	R.L*HNAIEGGTQL*SR.A
SW:DKC1_HUMAN	H11	2028	2	984.1	(+0.4)	2.315	0.367	0.965	3	K.APQVVAEAAK.T
SW:DNL3_HUMAN	H06	4786	2	1368.4	(+0.2)	2.826	0.336	0.943	1	R.DL*EQGDVSETIR.V
SW:DNL3_HUMAN	H06	4814	2	1362.4	(+0.3)	2.511	0.373	0.937	1	R.DLEQGDVSETIR.V
SW:DNL3_HUMAN	H06	5898	2	1631.7	(+0.1)	3.071	0.387	0.966	1	K.EDEQQQALQDIASR.C
SW:DNL3_HUMAN	H06	7542	2	1703.9	(+0.4)	3.631	0.528	1.000	1	K.HVLDALDPNAYEAFK.A
SW:DNL3_HUMAN	H06	7540	2	1723.9	(-0.6)	2.680	0.294	0.856	1	K.HVL*DAL*DPNAYEAFK#.A
SW:DNL3_HUMAN	H06	7676	2	1475.7	(+0.6)	2.481	0.411	0.975	2	K.IYYPDFIVPDPK#.K
SW:DNL3_HUMAN	H06	4728	2	979.1	(+0.9)	2.244	0.266	0.899	1	R.NL*QDVVER.V
SW:DNL3_HUMAN	H06	1792	2	1748.9	(+0.1)	2.496	0.430	0.432	1	R.VL*HNAQVEK#EPGQR.R
SW:DNL3_HUMAN	H06	8372	2	1145.4	(+0.7)	2.966	0.374	0.987		K.VL*L*DIFTGVR.L
SW:DNL3_HUMAN	H07	7620	2	1703.9	(+0.4)	2.251	0.491	0.982	1	K.HVLDALDPNAYEAFK.A
SW:DNM1_HUMAN	H04	5709	2	1068.3	(+0.6)	2.418	0.252	0.884	2	R.AIIL*AAAPGEK#.L
SW:DNM1_HUMAN	H04	7329	3	2572.7	(+1.0)	4.111	0.509*	0.086	3	K.APSENWAMEGGM@DPESL*L*EGDDGK#.T
SW:DNM1_HUMAN	H04	5093	2	1472.5	(+0.8)	3.124	0.509	0.993		K.DL*SL*ENGAHAYNR.E
SW:DNM1_HUMAN	H04	3937	2	1185.3	(+0.8)	2.555	0.343	0.970	2	R.DTM@SDL*PEVR.N
SW:DNM1_HUMAN	H04	3791	2	1185.3	(+0.9)	2.265	0.420	0.976	2	R.DTM@SDL*PEVR.N
SW:DNM1_HUMAN	H04	4089	2	1185.3	(+0.3)	2.261	0.386	0.932	2	R.DTM@SDL*PEVR.N
SW:DNM1_HUMAN	H04	2905	2	1185.3	(+0.7)	2.248	0.349	0.953	2	R.DTM@SDL*PEVR.N
SW:DNM1_HUMAN	H04	3863	2	1185.3	(+0.7)	2.226	0.333	0.943	2	R.DTM@SDL*PEVR.N
SW:DNM1_HUMAN	H04	5275	2	1052.2	(+0.9)	2.226	0.310	0.935	2	R.GAQYQPIL*R.D
SW:DNM1_HUMAN	H04	5163	2	1424.5	(-0.2)	2.639	0.267	0.846		R.K#EEL*SEEGYL*AK#.V
SW:DNM1_HUMAN	H04	5741	2	1804.9	(-0.1)	3.604	0.423	0.984	3	R.K#EPVDEDL*YPEHYR.K
SW:DNM1_HUMAN	H04	8639	2	1630.9	(-0.3)	4.071	0.438	1.000		K.L*NL*L*HEFL*QTEIK#.N
SW:DNM1_HUMAN	H05	8756	2	1630.9	(-0.4)	3.374	0.278	0.935		K.L*NL*L*HEFL*QTEIK#.N
SW:DNM1_HUMAN	H06	8660	2	1598.9	(+0.7)	3.842	0.470	1.000		K.LNLLHEFLQTEIK.N
SW:DNM1_HUMAN	H06	8662	2	1630.9	(-0.9)	2.927	0.255	0.665		K.L*NL*L*HEFL*QTEIK#.N
SW:DNM1_HUMAN	H07	8900	2	1630.9	(+0.4)	2.872	0.335	0.968		K.L*NL*L*HEFL*QTEIK#.N
SW:DNM1_HUMAN	H04	8599	2	1634.0	(+0.5)	3.744	0.435	0.994	2	K.LPLFPEPLHVFAPR.A
SW:DNM1_HUMAN	H04	8597	2	1652.0	(+0.2)	2.992	0.517	0.986	2	K.L*PL*FPEPL*HVFAPR.A
SW:DNM1_HUMAN	H04	8901	2	2034.2	(+1.0)	4.773	0.607	1.000	3	K.NLGPINEWWITGFDGGEK.A
SW:DNM1_HUMAN	H04	8849	2	2048.2	(-0.4)	3.373	0.431	0.978	3	K.NL*GPINEWWITGFDGGEK#.A
SW:DNM1_HUMAN	H05	9030	2	2034.2	(-0.5)	2.950	0.507	0.984	3	K.NLGPINEWWITGFDGGEK.A
SW:DNM1_HUMAN	H05	9026	2	2048.2	(-0.7)	2.880	0.462	0.913	3	K.NL*GPINEWWITGFDGGEK#.A
SW:DNM1_HUMAN	H04	2163	2	1370.5	(+0.7)	2.745	0.213	0.219	2	R.VARPL*PAEPPER.A
SW:DNM1_HUMAN	H04	2161	2	1364.5	(+0.6)	2.507	0.320	0.426	2	R.VARPLPAEPPER.A
SW:DNM1_HUMAN	H04	6395	2	1335.4	(+0.3)	2.571	0.352	0.924	3	R.VL*EQL*EDL*DSR.V
SW:DNM1_HUMAN	H05	6700	2	1317.4	(+0.6)	3.497	0.422	0.993	3	R.VLEQLEDLDSR.V
SW:DNM1_HUMAN	H06	6474	2	1335.4	(+0.1)	2.410	0.301	0.872	3	R.VL*EQL*EDL*DSR.V
SW:DNM1_HUMAN	H04	8027	2	1676.0	(-0.8)	3.433	0.430	0.939		R.VPTL*AVPAISL*PDDVR.R
SW:DNM1_HUMAN	H05	8114	2	1676.0	(+0.5)	3.610	0.504	1.000		R.VPTL*AVPAISL*PDDVR.R
SW:DNM1_HUMAN	H06	8028	2	1676.0	(+0.4)	2.941	0.382	0.980		R.VPTL*AVPAISL*PDDVR.R
SW:DNM1_HUMAN	H04	5293	3	2200.4	(+0.7)	5.276	0.318	0.997	3	K.YGQHPPDAVDEPQM@L*TNEK#.L
SW:DNM1_HUMAN	H05	5672	3	2200.4	(-0.6)	4.272	0.355	0.994	3	K.YGQHPPDAVDEPQM@L*TNEK#.L
SW:DNM1_HUMAN	H06	5350	3	2200.4	(+0.1)	4.048	0.254	0.945	3	K.YGQHPPDAVDEPQM@L*TNEK#.L
SW:DNM1_HUMAN	H09	8045	2	1676.0	(+0.2)	3.272	0.428	0.975		R.VPTL*AVPAISL*PDDVR.R
SW:DRG1_HUMAN	H14	4739	2	1262.3	(+0.4)	3.271	0.474	0.992	2	K.GGGGGPGEGFDVAK.T
SW:DRG1_HUMAN	H14	8253	2	1692.9	(+0.4)	3.390	0.451	0.992	3	K.IDQISIEELDIYK.V
SW:DRG1_HUMAN	H14	7393	2	1396.6	(-0.2)	3.213	0.374	0.972	2	K.IIENEL*EGFGIR.L
SW:DRG1_HUMAN	H14	8867	2	1480.8	(+1.0)	3.943	0.397	0.992	2	K.IQLLDLPGIIEGAK.D
SW:DRG1_HUMAN	H14	7479	2	1690.8	(+0.9)	4.655	0.480	1.000	3	R.SDATADDLIDVVEGNR.V
SW:DRG1_HUMAN	H14	7487	2	1696.8	(+0.7)	4.083	0.476	1.000	3	R.SDATADDL*IDVVEGNR.V
SW:DRG1_HUMAN	H14	8869	2	1506.8	(-0.2)	2.611	0.245	0.772	2	K.IQL*L*DL*PGIIEGAK#.D
SW:DRI1_HUMAN	H09	8479	2	1680.9	(-0.5)	2.996	0.367	0.954	5	K.GL*NL*PTSITSAAFTL*R.T
SW:DRI1_HUMAN	H09	2943	2	1167.3	(+0.6)	2.732	0.449	0.990	3	K.MAL*VADEQQR.L

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:DSRA_HUMAN	H06	6900	2	1572.8	(+0.6)	2.983	0.363	0.971	3	R.MGFTEVTPVTGASL*R.R
SW:DSRA_HUMAN	H06	7824	2	1679.9	(+0.4)	3.680	0.483	1.000	5	K.SVTLGYLFSQGHLTR.A
SW:DSRA_HUMAN	H06	7822	2	1697.9	(-0.2)	2.952	0.410	0.966	5	K.SVTL*GYL*FSQGH*TR.A
SW:DSRA_HUMAN	H06	7992	2	1680.9	(+0.7)	4.734	0.534	0.999	5	R.YLNTNPVGGLLLEYAR.S
SW:DSRA_HUMAN	H06	7994	2	1698.9	(-0.3)	2.743	0.154	0.599	5	R.YL*NTNPVGG*LY*EYAR.S
SW:DYHC_HUMAN	H02	5068	2	1048.2	(+0.8)	2.467	0.334	0.963		R.AATSPALFNR.C
SW:DYHC_HUMAN	H02	7084	2	1580.9	(+0.4)	2.382	0.453	0.980	1	K.ASVVTLPVYLNFR.A
SW:DYHC_HUMAN	H04	8421	2	1592.9	(+0.5)	2.495	0.299	0.927	1	K.ASVVTL*PVYL*NFTR.A
SW:DYHC_HUMAN	H03	7466	2	1479.6	(+1.0)	3.449	0.398	0.988		R.AWTQVL*L*GQAEDK#.A
SW:DYHC_HUMAN	H02	7468	2	1691.9	(+1.0)	4.265	0.485	0.999		K.DFPLNDLLSATLQDK.I
SW:DYHC_HUMAN	H03	9178	2	1723.9	(-0.8)	2.700	0.333	0.730		K.DFPL*NDL*L*SATEL*DK#.I
SW:DYHC_HUMAN	H04	9009	2	1691.9	(+0.6)	3.803	0.481	1.000		K.DFPLNDLLSATLQDK.I
SW:DYHC_HUMAN	H06	9060	2	1691.9	(+0.6)	3.619	0.480	1.000		K.DFPLNDLLSATLQDK.I
SW:DYHC_HUMAN	H03	5664	2	1402.5	(+0.7)	3.379	0.369	0.988		K.DHLYGTLDPNTR.E
SW:DYHC_HUMAN	H03	5662	2	1414.5	(+0.0)	3.085	0.166	0.805		K.DHL*YGT*DPNTR.E
SW:DYHC_HUMAN	H04	5309	2	1414.5	(-0.1)	2.706	0.129	0.587		K.DHL*YGT*DPNTR.E
SW:DYHC_HUMAN	H04	7535	2	1383.6	(+0.9)	2.223	0.245	0.756		R.DLPPVSGSIIWAK.Q
SW:DYHC_HUMAN	H03	10460	2	1954.2	(+0.8)	3.448	0.403	0.986	1	K.DVL*L*VAQGEM@AL*EEFL*K#.Q
SW:DYHC_HUMAN	H04	9115	3	2599.9	(+0.8)	4.914	0.521	0.997		R.FGNPLLVDVESYDPVLPVLR.E
SW:DYHC_HUMAN	H04	9147	3	2623.9	(+0.0)	3.743	0.367	0.988		R.FGNPL*L*VQDVESYDPVL*NPVL*NR.E
SW:DYHC_HUMAN	H03	7572	2	1580.7	(+0.7)	4.384	0.502	1.000	1	K.FNYGFEYLVQVQDL.P
SW:DYHC_HUMAN	H04	9011	2	1535.8	(+0.6)	2.275	0.107	0.425	1	R.FQSISTEFL*AL*MK#.K
SW:DYHC_HUMAN	H02	7786	2	1960.2	(+0.1)	3.334	0.414	0.977	1	R.FYFVGDEDLLEIIGNSK.N
SW:DYHC_HUMAN	H03	9814	2	2124.5	(+0.8)	3.277	0.352	0.673		R.GIFEALRPLETLPVEGLIR.I
SW:DYHC_HUMAN	H03	5656	2	1307.4	(+0.6)	2.557	0.407	0.978	1	R.GNEIVL*SAGSTPR.I
SW:DYHC_HUMAN	H03	9308	2	1718.0	(+0.7)	5.472	0.512	0.991		R.ILDDDTIITTLLENL.K.R
SW:DYHC_HUMAN	H03	9314	2	1744.0	(-0.1)	2.532	0.259	0.762		R.IL*DDDTIITTL*ENL*K#.R
SW:DYHC_HUMAN	H04	9169	2	1718.0	(-0.1)	3.966	0.520	1.000		R.ILDDDTIITTLLENL.K.R
SW:DYHC_HUMAN	H03	7944	2	1245.5	(+0.9)	3.176	0.442	0.993	1	K.INEWLTLVEK.E
SW:DYHC_HUMAN	H04	7803	2	1265.5	(+0.3)	2.231	0.245	0.716	1	K.INEWL*TL*VEK#.E
SW:DYHC_HUMAN	H03	7506	2	1616.9	(+0.4)	3.152	0.359	0.665	1	R.KLEHLITLVDHQR.D
SW:DYHC_HUMAN	H04	5629	2	1488.6	(+0.8)	2.831	0.342	0.974		R.KYTGEDFDLRLR.T
SW:DYHC_HUMAN	H04	9837	3	2556.8	(+0.6)	4.087	0.327	0.950		K.L*DRDPASGTAL*QEISFWL*NL*ER.A
SW:DYHC_HUMAN	H03	5592	2	1160.3	(+0.3)	2.944	0.445	0.974	3	R.L*GGSPFGPAGTGK#.T
SW:DYHC_HUMAN	H03	5604	2	1146.3	(+0.8)	2.667	0.419	0.983	3	R.LGGSPFGPAGTGK.T
SW:DYHC_HUMAN	H02	6744	2	1508.6	(-0.0)	2.375	0.152	0.496		K.LNTQEIFDDWAR.K
SW:DYHC_HUMAN	H02	6750	2	1514.6	(+0.6)	2.336	0.555	0.991		K.L*NTQEIFDDWAR.K
SW:DYHC_HUMAN	H03	8094	2	1514.6	(+0.8)	3.616	0.502	1.000		K.L*NTQEIFDDWAR.K
SW:DYHC_HUMAN	H04	7955	2	1514.6	(+0.7)	3.318	0.564	1.000		K.L*NTQEIFDDWAR.K
SW:DYHC_HUMAN	H05	8038	2	1508.6	(+0.9)	3.305	0.478	0.994		K.LNTQEIFDDWAR.K
SW:DYHC_HUMAN	H05	8034	2	1514.6	(+0.4)	2.615	0.524	0.992		K.L*NTQEIFDDWAR.K
SW:DYHC_HUMAN	H06	7952	2	1514.6	(+1.0)	2.984	0.503	0.993		K.L*NTQEIFDDWAR.K
SW:DYHC_HUMAN	H03	8158	2	1155.4	(+0.2)	2.220	0.374	0.899		R.NTISL*L*VAGL*K#.K
SW:DYHC_HUMAN	H03	7560	3	2521.8	(+0.8)	5.583	0.509	0.999		R.NVAQYNANHPDFPMQIEQL*ER.Y
SW:DYHC_HUMAN	H03	7758	2	1184.4	(+1.0)	3.398	0.308	0.988	1	K.SFEWLSQMR.F
SW:DYHC_HUMAN	H02	4484	2	1459.5	(+0.4)	2.268	0.439	0.975		R.SIPLDEGEDEAQR.R
SW:DYHC_HUMAN	H04	7413	2	1141.3	(+0.7)	2.555	0.445	0.986		K.SL*L*QAL*NEVK#.G
SW:DYHC_HUMAN	H05	7562	2	1141.3	(+0.7)	2.482	0.411	0.979		K.SL*L*QAL*NEVK#.G
SW:DYHC_HUMAN	H02	6918	2	1670.0	(+0.7)	3.673	0.455	0.994	1	K.SPLVMDVLNIQGVQR.S
SW:DYHC_HUMAN	H03	4964	2	974.1	(+0.3)	2.567	0.218	0.807		K.SVLVSAGNVK.R
SW:DYHC_HUMAN	H03	6180	2	1197.4	(-0.2)	2.301	0.333	0.886	1	K.TLMAQSIYGGRR.V
SW:DYHC_HUMAN	H03	6870	2	1413.7	(+0.5)	4.321	0.496	1.000		R.TPNGVVL*APVQL*GK#.W
SW:DYHC_HUMAN	H03	2196	2	1117.3	(-0.2)	2.597	0.340	0.931	1	K.TPVSITEHPK#.I
SW:DYHC_HUMAN	H04	2069	2	1109.3	(+0.6)	2.791	0.449	0.988	1	K.TPVSITEHPK.I
SW:DYHC_HUMAN	H05	2054	2	1117.3	(+0.8)	3.054	0.460	0.992	1	K.TPVSITEHPK#.I
SW:DYHC_HUMAN	H02	6212	2	1072.2	(+0.9)	2.260	0.322	0.947		R.TSFLDDAFR.K
SW:DYHC_HUMAN	H04	6419	2	1346.5	(+0.3)	2.744	0.374	0.470	1	R.TVENIK#DPL*FR.F
SW:DYHC_HUMAN	H03	7172	2	1207.4	(+0.8)	2.427	0.295	0.934		K.VDDL*L*IIIEK#.I
SW:DYHC_HUMAN	H04	6715	2	1482.6	(+0.4)	3.356	0.494	1.000	1	K.VFEEDAL*SWEDK#.L
SW:DYHC_HUMAN	H04	6727	2	1468.6	(+0.0)	2.727	0.352	0.943	1	K.VFEEDALSWEDK.L
SW:DYHC_HUMAN	H03	2218	2	1321.4	(+0.7)	2.589	0.421	0.674		R.VK#DDIESL*HDK#.F
SW:DYHC_HUMAN	H04	2087	2	1299.4	(+0.3)	2.773	0.363	0.455		R.VKDDIESLHDK.F
SW:DYHC_HUMAN	H04	2093	2	1321.4	(+0.6)	2.653	0.372	0.596		R.VK#DDIESL*HDK#.F
SW:DYHC_HUMAN	H03	8758	2	1394.7	(+0.1)	2.812	0.277	0.888		K.VNFL*PEIITL*SK#.E
SW:DYHC_HUMAN	H04	8619	2	1394.7	(+0.4)	2.968	0.452	0.990		K.VNFL*PEIITL*SK#.E

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:DYHC_HUMAN	H05	8752	2	1394.7	(+0.6)	3.382	0.419	0.991		K.VNFL*PEIITL*SK#.E
SW:DYHC_HUMAN	H03	7484	2	1411.6	(-0.2)	2.662	0.143	0.577	1	R.VQVAL*EEL*QDL*K#.G
SW:DYHC_HUMAN	H03	7706	3	2580.8	(+0.8)	5.394	0.463	0.999		K.VTDFGDKVEDPTFLNQLQSGVNR.W
SW:DYHC_HUMAN	H03	7704	3	2600.8	(-0.3)	4.566	0.475	0.993		K.VTDFGDK#VEDPTFL*NQL*QSGVNR.W
SW:DYHC_HUMAN	H04	5929	2	1185.4	(+0.6)	2.320	0.133	0.668	1	K.VWEQIDQMK#.E
SW:DYHC_HUMAN	H02	5710	2	1405.5	(+0.8)	2.467	0.267	0.911		R.WTDENIDTVALK.H
SW:DYHC_HUMAN	H03	6606	2	1419.5	(-0.5)	2.203	0.208	0.544		R.WTDENIDTVAL*K#.H
SW:DYHC_HUMAN	H02	5284	2	1360.4	(+0.4)	2.867	0.388	0.985		K.YTGEDFDEDLR.T
SW:DYHC_HUMAN	H06	8648	2	1374.7	(+0.7)	2.602	0.319	0.957		K.VNFLPEIITLSK.E
SW:DYLX_HUMAN	H21	5020	2	1683.8	(-0.2)	3.140	0.370	0.954		K.EAIESAIGGNAYQHSK#.V
SW:DYLX_HUMAN	H21	8770	2	2110.3	(-0.7)	3.845	0.426	0.944		K.VNQWTTNVEQTL*SQL*TK#.L
SW:DYLX_HUMAN	H21	8874	2	2110.3	(+0.5)	2.400	0.269	0.862		K.VNQWTTNVEQTL*SQL*TK#.L
SW:DYLX_HUMAN	H22	8652	2	2090.3	(+0.5)	3.547	0.515	1.000		K.VNQWTTNVEQTLSQLTK.L
SW:DYLX_HUMAN	H22	8656	2	2110.3	(-0.6)	3.197	0.365	0.940		K.VNQWTTNVEQTL*SQL*TK#.L
SW:DYN2_HUMAN	H07	9416	2	1328.7	(+0.9)	2.855	0.380	0.984	3	R.RPLILQLIFSK.T
SW:DYN2_HUMAN	H07	9414	2	1354.7	(-0.2)	2.604	0.125	0.527	3	R.RPL*IL*QL*IFSK#.T
SW:DYN2_HUMAN	H06	9070	2	1622.9	(+0.9)	3.099	0.450	0.989	3	R.TGLFTPDLAFAEIVK.K
SW:DYN2_HUMAN	H06	9066	2	1642.9	(+0.5)	2.932	0.417*	0.342	3	R.TGL*FTPDL*AFEIVK#.K
SW:DYN2_HUMAN	H07	9144	3	2126.5	(+0.5)	3.924	0.346	0.991	7	R.VYSPHVL*NL*TL*IDL*PGITK#.V
SW:DYN2_HUMAN	H07	5454	2	1350.5	(+0.2)	2.228	0.217	0.644	3	K.TL*NQQL*TNHIR.E
SW:E2BA_HUMAN	H16	7228	2	1643.8	(-0.5)	2.541	0.437	0.954		R.FISL*ASL*EYSDYSK#.C
SW:E2BA_HUMAN	H16	1694	2	1131.2	(+0.9)	2.277	0.349	0.405		R.DK#GETIQGL*R.A
SW:E2BB_HUMAN	H14	8563	2	2034.3	(+1.0)	3.415	0.409	0.989	1	K.FVAPEEVLPTFTEGDILEK.V
SW:E2BB_HUMAN	H14	6959	2	1569.8	(+0.6)	2.792	0.502	0.975	1	R.LMSELYHPDDHVL.-
SW:EF11_HUMAN	H13	7032	1	1341.6	(-0.8)	2.008	0.155	0.000	8	R.EHAL*L*AYTL*GVK#.Q
SW:EF11_HUMAN	H13	9226	3	3736.2	(+0.8)	5.311	0.433*	0.237	8	K.K#IGYNPDTVAFVPISGWNGDNM@L*EPSANMPWFK#.G
SW:EF11_HUMAN	H13	8800	3	3752.2	(+0.3)	4.217	0.394	0.996	8	K.K#IGYNPDTVAFVPISGWNGDNM@L*EPSANM@PWFK#.G
SW:EF11_HUMAN	H01	5228	2	976.2	(+0.4)	2.293	0.238	0.902	11	R.LPLQDVYK.I
SW:EF11_HUMAN	H02	5446	2	976.2	(-0.4)	3.062	0.275	0.958	11	R.LPLQDVYK.I
SW:EF11_HUMAN	H03	6194	2	996.2	(+0.3)	2.314	0.322	0.859	11	R.L*PL*QDVYK#.I
SW:EF11_HUMAN	H10	6137	2	976.2	(+0.9)	2.459	0.178	0.853	11	R.LPLQDVYK.I
SW:EF11_HUMAN	H12	6068	2	996.2	(+0.4)	2.309	0.254	0.909	11	R.L*PL*QDVYK#.I
SW:EF11_HUMAN	H13	5858	2	976.2	(-0.3)	3.118	0.264	0.957	11	R.LPLQDVYK.I
SW:EF11_HUMAN	H14	5935	2	976.2	(-0.5)	2.685	0.269	0.925	11	R.LPLQDVYK.I
SW:EF11_HUMAN	H15	5982	2	996.2	(+0.3)	2.207	0.254	0.746	11	R.L*PL*QDVYK#.I
SW:EF11_HUMAN	H18	5856	2	996.2	(+0.5)	2.379	0.327	0.928	11	R.L*PL*QDVYK#.I
SW:EF11_HUMAN	H13	4698	1	885.1	(-0.4)	2.024	0.168	0.000	9	K.QL*IVGVNK#.M
SW:EF11_HUMAN	H13	4792	1	885.1	(+0.6)	1.942	0.324	0.000	9	K.QL*IVGVNK#.M
SW:EF11_HUMAN	H01	2002	2	1121.3	(+0.3)	2.204	0.441	0.954	4	K.STTTGHLIYK.C
SW:EF11_HUMAN	H03	4656	2	1121.3	(-0.2)	2.810	0.429	0.978	4	K.STTTGHLIYK.C
SW:EF11_HUMAN	H04	2359	2	1121.3	(+0.7)	2.661	0.397	0.984	4	K.STTTGHLIYK.C
SW:EF11_HUMAN	H05	2352	2	1121.3	(+0.8)	2.746	0.418	0.988	4	K.STTTGHLIYK.C
SW:EF11_HUMAN	H06	2240	2	1121.3	(-0.1)	2.653	0.358	0.952	4	K.STTTGHLIYK.C
SW:EF11_HUMAN	H10	2375	2	1121.3	(+0.5)	2.514	0.338	0.961	4	K.STTTGHLIYK.C
SW:EF11_HUMAN	H11	2952	2	1121.3	(-0.6)	3.062	0.413	0.978	4	K.STTTGHLIYK.C
SW:EF11_HUMAN	H11	2758	2	1121.3	(+0.1)	3.023	0.446	0.983	4	K.STTTGHLIYK.C
SW:EF11_HUMAN	H11	2864	2	1135.3	(+0.5)	2.846	0.344	0.978	4	K.STTTGHL*IYK#.C
SW:EF11_HUMAN	H11	2696	2	1135.3	(+0.7)	2.471	0.365	0.967	4	K.STTTGHL*IYK#.C
SW:EF11_HUMAN	H11	2786	2	1135.3	(+0.7)	2.423	0.308	0.942	4	K.STTTGHL*IYK#.C
SW:EF11_HUMAN	H11	3028	2	1135.3	(+0.2)	2.358	0.341	0.902	4	K.STTTGHL*IYK#.C
SW:EF11_HUMAN	H11	3106	2	1135.3	(+0.2)	2.245	0.337	0.877	4	K.STTTGHL*IYK#.C
SW:EF11_HUMAN	H12	2158	2	1121.3	(-0.6)	2.730	0.420	0.974	4	K.STTTGHLIYK.C
SW:EF11_HUMAN	H12	2242	2	1121.3	(+0.7)	2.723	0.465	0.991	4	K.STTTGHLIYK.C
SW:EF11_HUMAN	H12	2194	2	1135.3	(-0.4)	2.492	0.263	0.804	4	K.STTTGHL*IYK#.C
SW:EF11_HUMAN	H12	5042	2	1135.3	(+0.1)	2.414	0.290	0.857	4	K.STTTGHL*IYK#.C
SW:EF11_HUMAN	H13	2370	2	1135.3	(+1.0)	2.946	0.273	0.962	4	K.STTTGHL*IYK#.C
SW:EF11_HUMAN	H13	4346	2	1135.3	(+0.6)	2.852	0.256	0.951	4	K.STTTGHL*IYK#.C
SW:EF11_HUMAN	H13	2288	2	1121.3	(+1.0)	2.802	0.469	0.990	4	K.STTTGHLIYK.C
SW:EF11_HUMAN	H13	4142	2	1135.3	(-0.1)	2.786	0.321	0.937	4	K.STTTGHL*IYK#.C
SW:EF11_HUMAN	H13	2302	2	1121.3	(-0.8)	2.769	0.422	0.921	4	K.STTTGHLIYK.C
SW:EF11_HUMAN	H13	2410	2	1121.3	(+0.3)	2.691	0.404	0.969	4	K.STTTGHLIYK.C

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:EF11_HUMAN	H13	2290	2	1135.3	(+0.7)	2.571	0.311	0.955	4	K.STTTGHL*YK#.C
SW:EF11_HUMAN	H13	4510	2	1135.3	(+1.0)	2.469	0.258	0.912	4	K.STTTGHL*YK#.C
SW:EF11_HUMAN	H13	2448	2	1135.3	(+0.5)	2.469	0.364	0.968	4	K.STTTGHL*YK#.C
SW:EF11_HUMAN	H13	4426	2	1135.3	(+0.7)	2.467	0.258	0.912	4	K.STTTGHL*YK#.C
SW:EF11_HUMAN	H13	4828	2	1135.3	(+1.0)	2.427	0.373	0.969	4	K.STTTGHL*YK#.C
SW:EF11_HUMAN	H13	4146	2	1121.3	(+0.8)	2.336	0.300	0.812	4	K.STTTGHLYK.C
SW:EF11_HUMAN	H13	4220	2	1135.3	(+0.5)	2.305	0.277	0.903	4	K.STTTGHL*YK#.C
SW:EF11_HUMAN	H13	4266	2	1135.3	(-0.8)	2.283	0.205	0.342	4	K.STTTGHL*YK#.C
SW:EF11_HUMAN	H13	4914	2	1135.3	(-0.0)	2.277	0.269	0.785	4	K.STTTGHL*YK#.C
SW:EF11_HUMAN	H13	4172	2	1121.3	(-0.7)	2.252	0.354	0.745	4	K.STTTGHLYK.C
SW:EF11_HUMAN	H14	4523	2	1135.3	(+0.1)	2.701	0.331	0.936	4	K.STTTGHL*YK#.C
SW:EF11_HUMAN	H15	2930	2	1121.3	(-0.6)	3.134	0.474	0.987	4	K.STTTGHLYK.C
SW:EF11_HUMAN	H15	3026	2	1121.3	(-0.9)	2.797	0.566	1.000	4	K.STTTGHLYK.C
SW:EF11_HUMAN	H15	2964	2	1135.3	(+0.1)	2.577	0.359	0.940	4	K.STTTGHL*YK#.C
SW:EF11_HUMAN	H15	3098	2	1135.3	(+0.5)	2.245	0.250	0.858	4	K.STTTGHL*YK#.C
SW:EF11_HUMAN	H16	3932	2	1121.3	(-0.7)	2.370	0.363	0.798	4	K.STTTGHLYK.C
SW:EF11_HUMAN	H16	3882	2	1135.3	(+0.5)	2.313	0.252	0.876	4	K.STTTGHL*YK#.C
SW:EF11_HUMAN	H17	3964	2	1121.3	(+0.8)	3.062	0.505	1.000	4	K.STTTGHLYK.C
SW:EF11_HUMAN	H17	3958	2	1135.3	(+0.4)	2.402	0.314	0.929	4	K.STTTGHL*YK#.C
SW:EF11_HUMAN	H19	4480	2	1135.3	(+0.5)	2.486	0.299	0.943	4	K.STTTGHL*YK#.C
SW:EF11_HUMAN	H19	4376	2	1121.3	(+0.4)	2.470	0.385	0.973	4	K.STTTGHLYK.C
SW:EF11_HUMAN	H19	4378	2	1135.3	(+0.4)	2.461	0.316	0.949	4	K.STTTGHL*YK#.C
SW:EF11_HUMAN	H20	4564	2	1121.3	(-0.6)	2.504	0.407	0.961	4	K.STTTGHLYK.C
SW:EF11_HUMAN	H20	4670	2	1121.3	(-0.2)	2.278	0.290	0.565	4	K.STTTGHLYK.C
SW:EF11_HUMAN	H21	4358	2	1121.3	(-0.2)	2.544	0.407	0.963	4	K.STTTGHLYK.C
SW:EF11_HUMAN	H21	4348	2	1135.3	(+1.0)	2.237	0.200	0.765	4	K.STTTGHL*YK#.C
SW:EF11_HUMAN	H22	4508	2	1135.3	(+0.1)	2.747	0.383	0.956	4	K.STTTGHL*YK#.C
SW:EF11_HUMAN	H12	10786	2	1589.8	(+0.7)	4.711	0.582	1.000	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H12	13042	2	1589.8	(+0.1)	4.670	0.596	0.997	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H12	13192	3	1597.8	(-0.8)	4.616	0.468	0.999	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	11162	2	1589.8	(+0.2)	4.560	0.543	0.999	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H12	11276	2	1589.8	(+0.7)	4.503	0.502	1.000	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H12	10906	2	1589.8	(+0.4)	4.427	0.569	0.999	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H12	12226	2	1589.8	(-0.0)	4.324	0.524	1.000	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H12	6630	2	1589.8	(+0.8)	4.318	0.568	1.000	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H12	11368	2	1589.8	(+0.2)	4.210	0.635	0.998	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H12	12146	2	1589.8	(+0.5)	4.149	0.538	0.999	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H12	10600	2	1597.8	(+0.6)	4.080	0.528	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	12174	2	1597.8	(+0.4)	4.031	0.604	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	11378	2	1597.8	(+0.7)	4.027	0.523	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	12778	2	1597.8	(-0.2)	4.015	0.518	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	11914	2	1589.8	(+0.1)	3.929	0.508	1.000	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H12	11544	2	1597.8	(+0.1)	3.913	0.434	0.985	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	12726	2	1589.8	(-0.1)	3.867	0.559	1.000	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H12	10780	2	1597.8	(+0.9)	3.862	0.573	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	12314	2	1589.8	(+0.1)	3.855	0.490	1.000	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H12	11802	2	1597.8	(+0.7)	3.836	0.501	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	11880	2	1597.8	(+0.3)	3.822	0.483	0.993	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	6806	2	1589.8	(+0.5)	3.817	0.578	0.998	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H12	10482	2	1597.8	(+0.5)	3.812	0.555	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	12512	2	1589.8	(+0.5)	3.773	0.478	1.000	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H12	11820	2	1589.8	(+0.4)	3.726	0.505	1.000	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H12	13418	2	1589.8	(+0.4)	3.704	0.554	0.997	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H12	12396	2	1589.8	(+0.6)	3.688	0.493	1.000	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H12	11952	2	1597.8	(+0.8)	3.668	0.510	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	12016	2	1589.8	(+0.5)	3.658	0.504	0.999	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H12	12096	2	1597.8	(+0.2)	3.657	0.591	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	12630	2	1597.8	(+0.9)	3.653	0.521	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	11222	2	1597.8	(+0.1)	3.625	0.535	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	13010	2	1597.8	(+0.7)	3.601	0.511	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	11148	2	1597.8	(-0.1)	3.598	0.530	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	12836	2	1589.8	(+0.7)	3.597	0.538	1.000	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H12	11460	2	1597.8	(+0.7)	3.563	0.524	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	9736	2	1589.8	(+0.9)	3.546	0.491	0.996	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H12	12936	2	1589.8	(+0.3)	3.529	0.438	0.983	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H12	12400	2	1597.8	(+0.9)	3.524	0.421	0.990	4	K.THINIVVIGHVDSGK#.S

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:EF11_HUMAN	H12	10970	2	1597.8	(+0.4)	3.522	0.555	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	11050	2	1597.8	(+0.6)	3.488	0.526	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	12324	2	1597.8	(+0.4)	3.488	0.520	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	8444	2	1597.8	(+0.4)	3.485	0.521	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	12704	2	1597.8	(+0.3)	3.481	0.554	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	12590	2	1589.8	(+0.6)	3.471	0.472	0.994	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H12	12252	2	1597.8	(+0.2)	3.431	0.581	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	13342	2	1597.8	(+0.5)	3.405	0.450	0.991	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	10362	2	1597.8	(+0.3)	3.382	0.501	0.986	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	11704	2	1597.8	(+0.4)	3.368	0.501	0.993	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	12938	2	1597.8	(+0.6)	3.357	0.478	0.992	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	12554	2	1597.8	(+0.4)	3.336	0.530	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	8990	2	1597.8	(+0.5)	3.284	0.523	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	8910	2	1597.8	(+0.8)	3.267	0.528	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	11492	2	1589.8	(-0.5)	3.213	0.421	0.976	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H12	12024	2	1597.8	(+0.2)	3.076	0.501	0.982	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	13640	2	1597.8	(+0.7)	2.925	0.478	0.943	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	13572	2	1597.8	(+0.5)	2.908	0.535	0.993	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	12484	2	1597.8	(+0.7)	2.733	0.369	0.967	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	7192	2	1589.8	(-0.2)	2.650	0.341	0.912	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H12	8168	2	1589.8	(-0.2)	2.608	0.462	0.966	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H12	10132	2	1597.8	(+0.8)	2.386	0.377	0.951	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	10160	2	1589.8	(+0.5)	5.544	0.621	0.997	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	11386	2	1589.8	(+0.9)	5.324	0.576	1.000	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	11610	2	1589.8	(+1.0)	5.239	0.607	1.000	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	11992	2	1597.8	(+0.7)	5.231	0.540	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	11818	2	1597.8	(+0.9)	5.128	0.541	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	12674	2	1597.8	(+0.8)	5.048	0.543	0.996	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	11910	2	1597.8	(+0.8)	5.041	0.464	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	10638	2	1597.8	(+0.6)	5.038	0.510	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	12368	2	1597.8	(+0.7)	4.940	0.554	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	12524	2	1597.8	(+0.8)	4.903	0.534	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	11474	2	1597.8	(+0.6)	4.891	0.548	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	10458	2	1597.8	(+0.3)	4.890	0.475	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	11912	2	1589.8	(+0.9)	4.842	0.574	0.999	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	12442	2	1597.8	(+1.0)	4.830	0.592	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	11762	2	1589.8	(+0.6)	4.796	0.573	0.999	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	13464	2	1597.8	(+0.7)	4.791	0.499	0.999	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	11234	2	1589.8	(+0.9)	4.788	0.576	1.000	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	10048	2	1589.8	(+0.9)	4.767	0.611	1.000	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	11400	2	1597.8	(+0.8)	4.742	0.549	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	12218	2	1597.8	(+0.9)	4.714	0.561	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	12120	2	1589.8	(-0.1)	4.704	0.580	0.999	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	12292	2	1597.8	(+0.0)	4.701	0.584	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	11686	2	1589.8	(+0.8)	4.699	0.586	0.965	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	12912	2	1597.8	(+0.8)	4.685	0.510	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	12984	2	1597.8	(+0.3)	4.670	0.558	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	12982	2	1589.8	(+0.2)	4.638	0.584	1.000	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	12888	2	1589.8	(+0.4)	4.635	0.593	0.997	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	13176	2	1589.8	(+0.8)	4.619	0.622	1.000	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	11248	2	1597.8	(+0.1)	4.614	0.490	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	13530	2	1589.8	(+0.9)	4.611	0.602	0.998	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	11072	2	1597.8	(+0.7)	4.584	0.554	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	12346	2	1589.8	(+0.8)	4.565	0.589	0.998	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	13296	2	1597.8	(+0.4)	4.555	0.538	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	11156	2	1589.8	(+0.8)	4.545	0.613	1.000	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	13454	2	1589.8	(+0.8)	4.527	0.576	1.000	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	13538	2	1597.8	(+0.6)	4.522	0.582	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	11738	2	1597.8	(+0.3)	4.485	0.565	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	6554	2	1597.8	(+0.2)	4.440	0.511	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	12762	2	1597.8	(+0.7)	4.430	0.530	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	13102	2	1589.8	(-0.2)	4.374	0.519	0.999	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	13338	2	1589.8	(+0.6)	4.361	0.591	1.000	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	12472	2	1589.8	(-0.5)	4.354	0.563	1.000	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	12070	2	1597.8	(+0.2)	4.332	0.524	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	13378	2	1597.8	(+0.7)	4.325	0.532	1.000	4	K.THINIVVIGHVDSGK#.S

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:EF11_HUMAN	H13	12586	2	1597.8	(-0.5)	4.277	0.495	0.999	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	10392	2	1589.8	(+0.9)	4.275	0.563	0.995	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	13700	2	1597.8	(+0.8)	4.264	0.501	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	13140	2	1597.8	(+0.3)	4.236	0.545	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	11080	2	1589.8	(+0.9)	4.203	0.565	1.000	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	13614	2	1597.8	(+0.9)	4.167	0.478	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	7330	2	1589.8	(+0.0)	4.139	0.540	0.999	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	12144	2	1597.8	(-0.7)	4.137	0.510	0.999	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	13064	2	1597.8	(+0.8)	4.124	0.517	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	13826	2	1589.8	(+0.8)	4.118	0.585	0.999	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	12836	2	1597.8	(+0.6)	4.109	0.563	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	11002	2	1589.8	(+0.6)	4.055	0.633	1.000	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	9432	2	1589.8	(+0.3)	4.040	0.588	0.999	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	7470	3	1589.8	(-0.6)	3.872	0.480	0.999	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	9350	2	1589.8	(+0.7)	3.814	0.528	1.000	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	14050	2	1597.8	(+0.5)	3.758	0.446	0.993	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	13866	2	1597.8	(+0.6)	3.752	0.472	0.999	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	13756	2	1589.8	(+0.9)	3.735	0.550	1.000	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	9426	2	1597.8	(+0.2)	3.714	0.547	1.000	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	13982	2	1589.8	(+0.7)	3.557	0.456	0.993	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	10656	2	1589.8	(+0.8)	3.399	0.426	0.991	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	10478	2	1589.8	(+1.0)	3.350	0.507	0.994	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	6998	2	1589.8	(-0.3)	3.349	0.417	0.978	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	10916	2	1597.8	(-0.2)	3.211	0.434	0.975	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	10536	2	1597.8	(+0.4)	3.204	0.373	0.981	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	13972	2	1597.8	(+0.9)	2.992	0.410	0.983	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	10808	2	1597.8	(+0.4)	2.853	0.380	0.974	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	8694	2	1589.8	(+0.8)	2.782	0.507	0.991	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	10554	2	1589.8	(+0.8)	2.673	0.502	0.990	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	10738	2	1589.8	(+0.4)	2.579	0.519	0.990	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H13	7860	2	1597.8	(+0.3)	2.474	0.221	0.649	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H13	10846	2	1589.8	(-0.2)	2.391	0.241	0.698	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H21	6198	2	1589.8	(+0.5)	3.788	0.495	0.999	4	K.THINIVVIGHVDSGK.S
SW:EF11_HUMAN	H22	6302	2	1597.8	(-0.1)	3.524	0.440	0.980	4	K.THINIVVIGHVDSGK#.S
SW:EF11_HUMAN	H12	7930	2	2539.0	(+0.3)	5.560	0.551	1.000	9	R.VETGVL*K#PGMVVTFAPVNVTTTEVK#.S
SW:EF11_HUMAN	H12	7928	2	2517.0	(+0.2)	4.676	0.593	1.000	9	R.VETGVLKPGMVVTFAPVNVTTTEVK.S
SW:EF11_HUMAN	H12	7482	3	2555.0	(+0.2)	4.515	0.396	0.980	9	R.VETGVL*K#PGM@VVFAPVNVTTTEVK#.S
SW:EF11_HUMAN	H12	8004	3	2539.0	(+0.5)	4.157	0.358	0.840	9	R.VETGVL*K#PGMVVTFAPVNVTTTEVK#.S
SW:EF11_HUMAN	H12	11888	3	2517.0	(+0.9)	3.901	0.314	0.914	9	R.VETGVLKPGMVVTFAPVNVTTTEVK.S
SW:EF11_HUMAN	H12	12456	3	2517.0	(+0.5)	3.758	0.307	0.888	9	R.VETGVLKPGMVVTFAPVNVTTTEVK.S
SW:EF11_HUMAN	H13	7962	2	2517.0	(+0.1)	5.191	0.564	0.999	9	R.VETGVLKPGMVVTFAPVNVTTTEVK.S
SW:EF11_HUMAN	H13	8054	3	2539.0	(+0.1)	4.243	0.348	0.850	9	R.VETGVL*K#PGMVVTFAPVNVTTTEVK#.S
SW:EF11_HUMAN	H22	4592	2	1135.3	(-0.2)	2.375	0.372	0.899	4	K.STTTGHL*YK#.C
SW:EF1B_HUMAN	H15	1742	1	726.9	(-0.0)	2.271	0.284	0.000	8	K.KPALVAK.S
SW:EF1B_HUMAN	H16	6056	2	1348.5	(+0.9)	4.421	0.508	1.000	2	R.SIQADGLVWGSSK.L
SW:EF1B_HUMAN	H16	5860	2	1362.5	(-0.6)	2.271	0.166	0.424	2	R.SIQADGL*VWGSSK#.L
SW:EF1B_HUMAN	H17	5918	2	1348.5	(+1.0)	4.856	0.599	1.000	2	R.SIQADGLVWGSSK.L
SW:EF1B_HUMAN	H17	5998	2	1348.5	(+0.8)	4.322	0.585	1.000	2	R.SIQADGLVWGSSK.L
SW:EF1B_HUMAN	H17	5596	2	1348.5	(+0.7)	4.274	0.580	1.000	2	R.SIQADGLVWGSSK.L
SW:EF1B_HUMAN	H17	5974	2	1362.5	(+0.3)	3.794	0.382	0.980	2	R.SIQADGL*VWGSSK#.L
SW:EF1B_HUMAN	H17	11949	2	1348.5	(+0.9)	3.688	0.544	0.999	2	R.SIQADGLVWGSSK.L
SW:EF1B_HUMAN	H17	6076	2	1348.5	(+0.7)	3.554	0.459	0.993	2	R.SIQADGLVWGSSK.L
SW:EF1B_HUMAN	H17	5592	2	1362.5	(-0.0)	3.432	0.384	0.973	2	R.SIQADGL*VWGSSK#.L
SW:EF1B_HUMAN	H17	10688	2	1348.5	(+0.9)	3.000	0.481	0.992	2	R.SIQADGLVWGSSK.L
SW:EF1B_HUMAN	H17	10554	2	1348.5	(+0.6)	2.981	0.467	0.991	2	R.SIQADGLVWGSSK.L
SW:EF1B_HUMAN	H17	12161	2	1348.5	(+0.6)	2.961	0.539	1.000	2	R.SIQADGLVWGSSK.L
SW:EF1B_HUMAN	H17	10796	2	1348.5	(+0.6)	2.855	0.414	0.985	2	R.SIQADGLVWGSSK.L
SW:EF1B_HUMAN	H17	5894	2	1362.5	(+0.3)	2.709	0.416	0.959	2	R.SIQADGL*VWGSSK#.L
SW:EF1B_HUMAN	H17	10476	2	1348.5	(+0.1)	2.665	0.438	0.968	2	R.SIQADGLVWGSSK.L
SW:EF1B_HUMAN	H17	10710	2	1348.5	(-0.6)	2.632	0.452	0.970	2	R.SIQADGLVWGSSK.L
SW:EF1B_HUMAN	H17	11188	2	1362.5	(+0.1)	2.603	0.331	0.901	2	R.SIQADGL*VWGSSK#.L
SW:EF1B_HUMAN	H17	12269	2	1348.5	(+1.0)	2.553	0.407	0.978	2	R.SIQADGLVWGSSK.L
SW:EF1B_HUMAN	H17	9756	2	1348.5	(+0.5)	2.551	0.484	0.988	2	R.SIQADGLVWGSSK.L
SW:EF1B_HUMAN	H17	10380	2	1348.5	(-0.0)	2.533	0.513	0.974	2	R.SIQADGLVWGSSK.L
SW:EF1B_HUMAN	H17	11989	2	1362.5	(+0.4)	2.509	0.402	0.971	2	R.SIQADGL*VWGSSK#.L

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:EF1B_HUMAN	H17	12319	2	1362.5	(-0.0)	2.484	0.339	0.892	2	R.SIQADGL*VWGSSK#.L
SW:EF1B_HUMAN	H17	12079	2	1348.5	(-0.1)	2.480	0.483	0.972	2	R.SIQADGLVWGSSK.L
SW:EF1B_HUMAN	H17	11238	2	1348.5	(+0.4)	2.363	0.349	0.949	2	R.SIQADGLVWGSSK.L
SW:EF1B_HUMAN	H17	11254	2	1362.5	(+0.9)	2.277	0.287	0.877	2	R.SIQADGL*VWGSSK#.L
SW:EF1B_HUMAN	H17	10920	2	1348.5	(+0.5)	2.276	0.353	0.932	2	R.SIQADGLVWGSSK.L
SW:EF1B_HUMAN	H17	11378	2	1348.5	(-0.7)	2.226	0.381	0.735	2	R.SIQADGLVWGSSK.L
SW:EF1B_HUMAN	H18	6348	2	1362.5	(-0.4)	3.221	0.396	0.971	2	R.SIQADGL*VWGSSK#.L
SW:EF1B_HUMAN	H20	6264	2	1348.5	(+0.7)	3.697	0.520	1.000	2	R.SIQADGLVWGSSK.L
SW:EF1B_HUMAN	H16	7324	2	1630.8	(-0.0)	3.346	0.434	0.977	2	K.SPAGL*QVL*NDYL*ADK#.S
SW:EF1B_HUMAN	H17	6980	2	1604.8	(+0.6)	5.360	0.572	1.000	2	K.SPAGLQVLNDYLADK.S
SW:EF1B_HUMAN	H17	7244	2	1604.8	(+0.9)	5.291	0.621	1.000	2	K.SPAGLQVLNDYLADK.S
SW:EF1B_HUMAN	H17	7160	2	1604.8	(+0.8)	5.122	0.629	1.000	2	K.SPAGLQVLNDYLADK.S
SW:EF1B_HUMAN	H17	7156	2	1630.8	(-0.1)	4.586	0.465	0.992	2	K.SPAGL*QVL*NDYL*ADK#.S
SW:EF1B_HUMAN	H17	6358	2	1630.8	(+0.3)	4.557	0.500	1.000	2	K.SPAGL*QVL*NDYL*ADK#.S
SW:EF1B_HUMAN	H17	7438	2	1630.8	(+0.5)	4.056	0.462	0.999	2	K.SPAGL*QVL*NDYL*ADK#.S
SW:EF1B_HUMAN	H17	7234	2	1630.8	(-0.7)	3.925	0.328	0.901	2	K.SPAGL*QVL*NDYL*ADK#.S
SW:EF1B_HUMAN	H17	6970	2	1630.8	(-0.5)	3.480	0.502	1.000	2	K.SPAGL*QVL*NDYL*ADK#.S
SW:EF1B_HUMAN	H18	7720	2	1604.8	(-0.6)	4.602	0.550	1.000	2	K.SPAGLQVLNDYLADK.S
SW:EF1B_HUMAN	H18	7684	2	1604.8	(+0.7)	3.076	0.370	0.977	2	K.SPAGLQVLNDYLADK.S
SW:EF1B_HUMAN	H17	6988	2	2064.3	(-0.1)	4.974	0.534	1.000	2	K.SILLDVKPWDDETDMAK.L
SW:EF1B_HUMAN	H17	9684	2	3083.4	(-0.4)	3.728	0.543	1.000	2	K.VGTDML*EEQITAFEDYVQSM DVAAFNK#.I
SW:EF1B_HUMAN	H17	3690	2	1771.8	(+0.5)	4.134	0.496	1.000	2	K.YGPADVEDTTGSGATDSK.D
SW:EF1B_HUMAN	H17	3806	2	1779.8	(+0.0)	3.512	0.360	0.966	2	K.YGPADVEDTTGSGATDSK#.D
SW:EF1B_HUMAN	H17	3648	2	1779.8	(+0.2)	3.400	0.436	0.979	2	K.YGPADVEDTTGSGATDSK#.D
SW:EF1B_HUMAN	H17	3612	2	1771.8	(+0.2)	2.588	0.402	0.946	2	K.YGPADVEDTTGSGATDSK.D
SW:EF1B_HUMAN	H17	6224	3	4026.9	(+0.1)	6.993	0.572	1.000	2	K.YGPADVEDTTGSGATDSKDDDDIDLFGSDDEESEEAK.R
SW:EF1B_HUMAN	H22	7414	2	1630.8	(-0.2)	3.681	0.467	0.986	2	K.SPAGL*QVL*NDYL*ADK#.S
SW:EF1D_HUMAN	H15	6576	2	1734.9	(+0.5)	4.273	0.553	0.995	4	K.FEEHVQSV D IA AFNK.I
SW:EF1D_HUMAN	H15	6570	2	1742.9	(-0.2)	3.503	0.376	0.970	4	K.FEEHVQSV D IA AFNK#.I
SW:EF1D_HUMAN	H16	6154	2	1734.9	(-0.9)	4.872	0.517	1.000	4	K.FEEHVQSV D IA AFNK.I
SW:EF1D_HUMAN	H15	2030	2	1044.1	(+0.9)	2.301	0.104	0.019	5	K.FKYDDAER.R
SW:EF1D_HUMAN	H15	7730	2	1314.5	(+0.5)	3.534	0.331	0.985	5	R.GVVQEL*QQAISK#.L
SW:EF1D_HUMAN	H15	7706	2	1300.5	(-0.5)	2.681	0.242	0.836	5	R.GVVQELQQAISK.L
SW:EF1D_HUMAN	H16	7132	2	1314.5	(+0.7)	3.595	0.329	0.962	5	R.GVVQEL*QQAISK#.L
SW:EF1D_HUMAN	H17	7030	2	1314.5	(+0.7)	3.074	0.363	0.982	5	R.GVVQEL*QQAISK#.L
SW:EF1D_HUMAN	H18	7520	2	1300.5	(+0.4)	3.141	0.342	0.982	5	R.GVVQELQQAISK.L
SW:EF1D_HUMAN	H18	7516	2	1314.5	(+0.0)	2.691	0.227	0.794	5	R.GVVQEL*QQAISK#.L
SW:EF1D_HUMAN	H20	7398	2	1314.5	(+0.7)	3.214	0.271	0.965	5	R.GVVQEL*QQAISK#.L
SW:EF1D_HUMAN	H21	7290	2	1314.5	(+0.9)	2.651	0.317	0.954	5	R.GVVQEL*QQAISK#.L
SW:EF1D_HUMAN	H15	5800	2	1371.5	(+0.2)	3.234	0.269	0.936	5	R.IASL*EVENQSL*R.G
SW:EF1D_HUMAN	H15	5812	2	1359.5	(-0.6)	3.054	0.289	0.934	5	R.IASLEVENQSLR.G
SW:EF1D_HUMAN	H16	5364	2	1359.5	(+0.9)	2.853	0.355	0.978	5	R.IASLEVENQSLR.G
SW:EF1D_HUMAN	H16	5366	2	1371.5	(+0.3)	2.377	0.272	0.807	5	R.IASL*EVENQSL*R.G
SW:EF1D_HUMAN	H17	5148	2	1359.5	(+0.9)	3.594	0.383	0.991	5	R.IASLEVENQSLR.G
SW:EF1D_HUMAN	H17	5146	2	1371.5	(+0.5)	2.289	0.329	0.936	5	R.IASL*EVENQSL*R.G
SW:EF1D_HUMAN	H15	6772	3	3579.6	(-0.7)	4.891	0.500	0.999	5	K.KPATPAEDEDDDDIDLFGSDNEEEDKEAAQLR.E
SW:EF1D_HUMAN	H15	7760	2	1374.6	(+0.0)	4.037	0.471	1.000	5	R.SIQLDGLVWGASK.L
SW:EF1D_HUMAN	H16	7236	2	1394.6	(+0.8)	3.872	0.394	0.992	5	R.SIQL*DGL*VWGASK#.L
SW:EF1D_HUMAN	H16	6908	2	1394.6	(-0.2)	3.161	0.204	0.843	5	R.SIQL*DGL*VWGASK#.L
SW:EF1D_HUMAN	H16	4918	2	2198.3	(+0.8)	4.316	0.554	0.999	4	K.SL*AGSSGPGASSGTSGDHGEL*VVR.I
SW:EF1D_HUMAN	H16	4916	2	2186.3	(-0.8)	3.710	0.548	1.000	4	K.SLAGSSGPGASSGTSGDHGELVVR.I
SW:EF1D_HUMAN	H16	6284	2	1367.5	(+0.4)	3.258	0.372	0.986	4	K.VGTDL*L*EEEITK#.F
SW:EF1D_HUMAN	H15	10064	3	3091.4	(-0.5)	7.326	0.523	1.000	4	K.VGTDL*L*EEEITK#FEEHVQSV D IA AFNK#.I
SW:EF1D_HUMAN	H16	9238	3	3091.4	(-0.4)	6.031	0.565	1.000	4	K.VGTDL*L*EEEITK#FEEHVQSV D IA AFNK#.I
SW:EF1D_HUMAN	H20	9472	3	3091.4	(+0.3)	4.825	0.401	0.985	4	K.VGTDL*L*EEEITK#FEEHVQSV D IA AFNK#.I
SW:EF1D_HUMAN	H22	5588	2	1359.5	(+0.4)	2.628	0.178	0.831	5	R.IASLEVENQSLR.G
SW:EF1G_HUMAN	H13	5676	2	1124.3	(-0.6)	2.698	0.343	0.373	4	K.AKDPFAHLPK.S
SW:EF1G_HUMAN	H12	5734	2	1348.5	(-0.2)	4.124	0.443	1.000	2	K.ALIAAQYSGAQVR.V
SW:EF1G_HUMAN	H12	5862	2	1354.5	(+0.3)	4.098	0.479	0.999	2	K.AL*IAAQYSGAQVR.V
SW:EF1G_HUMAN	H12	5726	2	1354.5	(+0.5)	3.582	0.498	1.000	2	K.AL*IAAQYSGAQVR.V
SW:EF1G_HUMAN	H13	5576	2	1354.5	(+0.8)	4.840	0.534	1.000	2	K.AL*IAAQYSGAQVR.V
SW:EF1G_HUMAN	H13	5768	2	1354.5	(+0.9)	3.640	0.479	1.000	2	K.AL*IAAQYSGAQVR.V
SW:EF1G_HUMAN	H13	5694	2	1348.5	(-0.4)	3.295	0.459	0.985	2	K.ALIAAQYSGAQVR.V
SW:EF1G_HUMAN	H13	5656	2	1354.5	(+0.9)	3.190	0.535	1.000	2	K.AL*IAAQYSGAQVR.V

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:EF1G_HUMAN	H13	5668	2	1348.5	(+0.8)	2.963	0.516	0.992	2	K.ALIAAQYSGAQVR.V
SW:EF1G_HUMAN	H13	5588	1	1348.5	(-0.8)	2.226	0.216	0.000	2	K.ALIAAQYSGAQVR.V
SW:EF1G_HUMAN	H17	5050	2	1354.5	(+0.3)	4.215	0.536	1.000	2	K.AL*IAAQYSGAQVR.V
SW:EF1G_HUMAN	H19	5386	2	1348.5	(+0.3)	4.326	0.552	1.000	2	K.ALIAAQYSGAQVR.V
SW:EF1G_HUMAN	H19	5378	2	1354.5	(-0.0)	3.803	0.425	0.987	2	K.AL*IAAQYSGAQVR.V
SW:EF1G_HUMAN	H21	5342	2	1354.5	(+0.9)	2.569	0.362	0.962	2	K.AL*IAAQYSGAQVR.V
SW:EF1G_HUMAN	H22	5478	2	1348.5	(+0.9)	3.843	0.546	1.000	2	K.ALIAAQYSGAQVR.V
SW:EF1G_HUMAN	H22	5472	2	1354.5	(+0.6)	3.790	0.551	1.000	2	K.AL*IAAQYSGAQVR.V
SW:EF1G_HUMAN	H13	7850	2	1462.6	(-0.9)	3.037	0.481	0.955	4	K.DGWSLWYSEYR.F
SW:EF1G_HUMAN	H12	7616	2	1693.8	(+0.6)	2.634	0.462	0.984	4	R.EYFSWEGAFQHVKG#.A
SW:EF1G_HUMAN	H13	7630	2	1693.8	(+0.7)	3.607	0.490	0.999	4	R.EYFSWEGAFQHVKG#.A
SW:EF1G_HUMAN	H13	7628	2	1685.8	(+0.4)	3.345	0.431	0.991	4	R.EYFSWEGAFQHVKG#.A
SW:EF1G_HUMAN	H13	7904	2	1693.8	(+0.3)	3.309	0.407	0.974	4	R.EYFSWEGAFQHVKG#.A
SW:EF1G_HUMAN	H13	9088	2	2688.9	(+0.2)	3.785	0.491	0.994	4	R.GQELAFPLSPDWQVDYESYTW.R.K
SW:EF1G_HUMAN	H13	9168	2	2700.9	(-0.8)	3.012	0.416	0.905	4	R.GQEL*AFPL*SPDWQVDYESYTW.R.K
SW:EF1G_HUMAN	H13	8636	2	1151.4	(+0.1)	2.438	0.398	0.943	4	R.IL*GL*L*DAYL*K#.T
SW:EF1G_HUMAN	H13	8550	2	1151.4	(+0.5)	2.336	0.409	0.974	4	R.IL*GL*L*DAYL*K#.T
SW:EF1G_HUMAN	H14	8549	2	1151.4	(-0.2)	2.340	0.179	0.592	4	R.IL*GL*L*DAYL*K#.T
SW:EF1G_HUMAN	H17	7888	2	1151.4	(+0.2)	2.491	0.342	0.921	4	R.IL*GL*L*DAYL*K#.T
SW:EF1G_HUMAN	H19	8314	2	1151.4	(+0.4)	2.215	0.361	0.950	4	R.IL*GL*L*DAYL*K#.T
SW:EF1G_HUMAN	H12	5074	2	1573.7	(-0.2)	3.291	0.492	0.987	4	R.KLDPGSEETQTLV.R.E
SW:EF1G_HUMAN	H12	5072	2	1593.7	(-0.7)	2.771	0.232	0.509	4	R.K#L*DPGSEETQTL*V.R.E
SW:EF1G_HUMAN	H13	5258	2	1573.7	(-0.3)	3.948	0.476	0.992	4	R.KLDPGSEETQTLV.R.E
SW:EF1G_HUMAN	H13	5166	2	1593.7	(+0.0)	3.940	0.443	1.000	4	R.K#L*DPGSEETQTL*V.R.E
SW:EF1G_HUMAN	H13	5248	2	1593.7	(-0.3)	2.937	0.361	0.860	4	R.K#L*DPGSEETQTL*V.R.E
SW:EF1G_HUMAN	H19	5064	2	1573.7	(+0.6)	2.289	0.198	0.675	4	R.KLDPGSEETQTLV.R.E
SW:EF1G_HUMAN	H19	5058	2	1593.7	(-0.2)	2.223	0.225	0.502	4	R.K#L*DPGSEETQTL*V.R.E
SW:EF1G_HUMAN	H20	5182	2	1573.7	(-0.7)	2.528	0.270	0.569	4	R.KLDPGSEETQTLV.R.E
SW:EF1G_HUMAN	H13	8916	2	2590.9	(-0.1)	4.260	0.480	1.000	4	R.KYSNEDTLSVALPYFWEHFDK.D
SW:EF1G_HUMAN	H13	8390	2	1307.6	(+0.1)	2.711	0.372	0.950	4	R.RIL*GL*L*DAYL*K#.T
SW:EF1G_HUMAN	H19	6532	2	1242.4	(+0.4)	2.528	0.296	0.430	4	K.STFVLDEFKR.K
SW:EF1G_HUMAN	H12	6546	2	1708.9	(+0.4)	2.957	0.527	0.700	2	R.VLSAPPHFHFGQTNR.T
SW:EF1G_HUMAN	H13	6410	2	1708.9	(+0.1)	3.697	0.604	1.000	2	R.VLSAPPHFHFGQTNR.T
SW:EF1G_HUMAN	H13	6406	2	1714.9	(+0.7)	3.665	0.550	1.000	2	R.VL*SAPPHFHFGQTNR.T
SW:EF1G_HUMAN	H13	6422	2	1714.9	(-0.7)	2.845	0.471	0.925	2	R.VL*SAPPHFHFGQTNR.T
SW:EF1G_HUMAN	H13	9242	2	2462.7	(+0.3)	3.890	0.396	0.979	4	K.YSNEDTLSVALPYFWEHFDK.D
SW:EF1G_HUMAN	H13	9244	2	2482.7	(+0.8)	3.889	0.498	0.998	4	K.YSNEDTL*SVAL*PYFWEHFDK#.D
SW:EF1G_HUMAN	H13	9322	2	2462.7	(-0.9)	3.130	0.361	0.871	4	K.YSNEDTLSVALPYFWEHFDK.D
SW:EF1G_HUMAN	H22	5146	2	1593.7	(+0.0)	3.237	0.357	0.957	4	R.K#L*DPGSEETQTL*V.R.E
SW:EF2_HUMAN	H07	9738	2	1445.7	(+0.5)	2.787	0.352	0.581	3	K.EGIPALDNFLDKL.-
SW:EF2_HUMAN	H07	9358	2	2221.5	(-0.1)	2.528	0.272	0.808	2	R.ALLELQLEPEELYQTFQR.I
SW:ELM1_HUMAN	H08	5859	2	1436.6	(+0.3)	2.819	0.379	0.457	2	R.ALTTKPSSLDQFK.S
SW:ELM1_HUMAN	H08	2175	2	1706.8	(-0.6)	3.178	0.353	0.957	1	R.L*TTSPAQNAQQL*HER.I
SW:ELM1_HUMAN	H08	6357	3	2619.8	(+0.1)	5.116	0.507	1.000	2	K.VL*HYGDL*EESPQGEVPHDSL*QDK#.L
SW:ELM1_HUMAN	H08	5715	2	1316.5	(+0.7)	2.767	0.283	0.951	1	R.RQEMANIL*AQK#.Q
SW:ELV1_HUMAN	H15	7154	2	1587.8	(+0.0)	2.303	0.334	0.859		K.NVAL*L*SQL*YHSPAR.R
SW:ELV1_HUMAN	H16	6702	2	1569.8	(-0.2)	4.626	0.539	0.998		K.NVALLSQLYHSPAR.R
SW:ELV1_HUMAN	H16	6690	2	1587.8	(-0.2)	3.036	0.351	0.953		K.NVAL*L*SQL*YHSPAR.R
SW:ELV1_HUMAN	H16	6016	3	2629.8	(+0.2)	4.520	0.505	0.997		R.SEAEAAITSFNGHK#PPGSSEPIVTK#.F
SW:ELV1_HUMAN	H16	6720	2	1368.5	(+0.7)	3.500	0.418	0.991		R.SL*FSSIGEVESAK#.L
SW:ELV1_HUMAN	H16	6718	2	1354.5	(+0.8)	2.948	0.479	0.992		R.SLFSSIGEVESAK.L
SW:ELV1_HUMAN	H15	7930	2	2163.5	(+0.7)	2.670	0.397*	0.266		R.TNLIVNYLPQNMTQDEL.R.S
SW:ELV1_HUMAN	H18	6448	2	1219.4	(+0.4)	2.778	0.473	0.991		K.DANLYISGLPR.T
SW:ENOA_HUMAN	H13	8850	2	2511.7	(+0.6)	3.584	0.443	0.993	8	K.DYPVVSIEDPFDQDDWGAWQK.F
SW:ENOA_HUMAN	H13	5808	2	1281.5	(+0.9)	2.450	0.404	0.978	4	K.LMIEMDGTENK.S
SW:ENOA_HUMAN	H13	5010	2	1158.3	(-0.2)	2.315	0.188	0.605	9	R.IGAEVYHNL*K#.N
SW:ENPL_HUMAN	H07	6746	2	2261.4	(-0.3)	2.926	0.402	0.963	2	R.FQSSHPTDITSLDQYVER.M
SW:ENPL_HUMAN	H07	6458	2	1486.6	(+0.9)	4.043	0.485	1.000	2	K.GVVDSDDLPLNVS.R.E
SW:ENPL_HUMAN	H07	6456	2	1498.6	(+0.1)	2.839	0.166	0.691	2	K.GVVDSDDL*PL*NVS.R.E
SW:ENPL_HUMAN	H07	6274	2	1532.7	(-0.2)	2.927	0.274	0.258	2	K.IADDK#YNDTFWK#.E
SW:ENPL_HUMAN	H07	9286	2	1880.2	(+0.6)	2.773	0.378	0.974	3	K.YSQFINFPIYVWSSK.T



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ENPL_HUMAN	H07	5634	2	1276.4	(-1.0)	2.404	0.415	0.848	8	R.ELISNASDALDK.I
SW:EZRI_HUMAN	H08	7813	2	1684.9	(+0.5)	3.540	0.362	0.985	4	R.EVWYFGL*HYVDNK#.G
SW:EZRI_HUMAN	H08	5857	2	960.2	(+0.1)	2.324	0.217	0.080	17	K.FVIKPIDK.K
SW:EZRI_HUMAN	H08	10417	2	2039.2	(-0.3)	2.726	0.276	0.857	4	K.FYPEDVAEELIQDITQK.L
SW:EZRI_HUMAN	H09	10471	2	2039.2	(+0.3)	2.677	0.365	0.933	4	K.FYPEDVAEELIQDITQK.L
SW:EZRI_HUMAN	H18	10020	3	2039.2	(+0.0)	3.867	0.414	0.997	4	K.FYPEDVAEELIQDITQK.L
SW:EZRI_HUMAN	H08	8143	2	1978.2	(-0.5)	2.276	0.157	0.356	4	K.IAQL*EM@YGINYFEIK#.N
SW:EZRI_HUMAN	H08	7039	2	1319.5	(+0.8)	3.666	0.511	1.000	16	K.K#APDFVYFAPR.L
SW:EZRI_HUMAN	H08	2375	2	1333.5	(-0.4)	2.245	0.165	0.401	15	R.K#PDTIEVQQMK#.A
SW:EZRI_HUMAN	H08	2307	2	1473.7	(+0.1)	2.422	0.331	0.247	15	R.RKPDTIEVQQMK#.A
SW:EZRI_HUMAN	H09	2445	2	1473.7	(+0.8)	2.963	0.420	0.768	15	R.RKPDTIEVQQMK#.A
SW:EZRI_HUMAN	H08	7213	2	1672.8	(-0.2)	3.946	0.474	1.000	4	K.SQEQL*AAEL*AEYAK#.I
SW:EZRI_HUMAN	H08	7323	2	1672.8	(+0.8)	2.605	0.275	0.904	4	K.SQEQL*AAEL*AEYAK#.I
SW:EZRI_HUMAN	H21	9746	3	2039.2	(+0.9)	3.762	0.421	0.999	4	K.FYPEDVAEELIQDITQK.L
SW:FALZ_HUMAN	H02	4722	2	1347.5	(+0.0)	2.737	0.349	0.941	2	R.HM@DITEDL*TNK#.A
SW:FALZ_HUMAN	H04	8717	2	1675.9	(+0.9)	2.509	0.147	0.399	2	K.SFL*AAANEEL*ESIR.A
SW:FBRL_HUMAN	H15	5912	3	2445.7	(+0.1)	3.765	0.398	0.965	5	K.M@QQENM@K#PQEQL*TL*EPYER.D
SW:FBRL_HUMAN	H15	5450	2	1519.6	(+0.7)	2.785	0.384	0.642	5	R.VSISEGDDK#IEYR.A
SW:FBRL_HUMAN	H15	7194	2	1901.2	(+0.3)	2.630	0.331	0.237	6	K.L*AAAIL*GGVDQIHIK#PGAK#.V
SW:FEN1_HUMAN	H13	8176	3	2355.6	(+0.8)	4.595	0.384	0.999		K.EAHQL*FL*EPEVL*DPEVEL*K#.W
SW:FEN1_HUMAN	H13	8184	2	2323.6	(+0.5)	3.529	0.506	0.961		K.EAHQLFLEPEVLDPESVELK.W
SW:FEN1_HUMAN	H13	8186	2	2355.6	(-0.2)	3.404	0.387	0.969		K.EAHQL*FL*EPEVL*DPEVEL*K#.W
SW:FEN1_HUMAN	H13	7316	3	2322.8	(+0.3)	4.145	0.403	0.978		R.MMENGIK#PVYVFDGK#PPQL*K#.S
SW:FEN1_HUMAN	H13	6200	2	1374.5	(+0.1)	2.566	0.270	0.865		K.WSEPNEEELIK.F
SW:FEN1_HUMAN	H22	5888	2	1132.3	(+0.9)	2.243	0.275	0.889		K.L*IADVAPSAIR.E
SW:FKB3_HUMAN	H17	5510	2	1745.9	(+0.2)	4.717	0.482	0.971	2	K.FLQEHGSDSFLAEHK.L
SW:FKB3_HUMAN	H17	6284	2	1335.5	(+0.8)	2.804	0.196	0.817	2	R.LEIEPEWAYGK.K
SW:FKB3_HUMAN	H17	6316	2	1349.5	(-0.3)	2.577	0.206	0.738	2	R.L*EIEPEWAYGK#.K
SW:FLNA_HUMAN	H03	6506	2	1227.4	(+1.0)	2.976	0.526	0.994	2	R.AWGPGLEGGVVGK.S
SW:FLNA_HUMAN	H03	2412	2	1100.2	(+0.7)	2.338	0.230	0.870	3	K.GTVEPQLEAR.G
SW:FLNA_HUMAN	H03	6922	2	1434.6	(-0.1)	2.796	0.277	0.883	4	R.IANL*QTDL*SDGL*R.L
SW:FLNA_HUMAN	H03	7616	2	1286.5	(+0.8)	2.239	0.201	0.765	4	K.LPQLPITNFSR.D
SW:FLNA_HUMAN	H03	6250	2	1262.4	(+0.3)	2.561	0.483	0.976	3	R.LTVSSLQESGLK.V
SW:FLNA_HUMAN	H03	6406	2	1084.2	(+1.0)	2.964	0.417	0.988	4	K.SPFEVYVDK.S
SW:FLNA_HUMAN	H03	7492	2	1534.7	(+0.6)	4.078	0.531*	0.753	2	K.SPFSVAVSPSLDLSK.I
SW:FLNA_HUMAN	H04	7327	2	1534.7	(+0.8)	4.091	0.471	1.000	2	K.SPFSVAVSPSLDLSK.I
SW:FLNA_HUMAN	H03	5836	2	1764.9	(-0.4)	3.917	0.538	1.000	3	R.VANPSGNLTETYVQDR.G
SW:FLNA_HUMAN	H03	1784	2	1635.8	(+0.2)	2.982	0.456	0.620	4	R.VHGPGIQSGTTNKPNK.F
SW:FLNA_HUMAN	H03	1850	2	1168.3	(+0.8)	2.226	0.237	0.800	4	K.VPVHDTVTDASK.V
SW:FLNA_HUMAN	H03	7764	3	2441.7	(+1.0)	4.301	0.405	0.999	4	R.VSGQGLHEGHTFEPAEIIDTR.D
SW:FLNA_HUMAN	H03	5252	2	1653.8	(-1.0)	2.653	0.482	0.917	3	K.VTAQGPGLEPSGNIANK.T
SW:FLNA_HUMAN	H04	1819	2	1109.3	(+0.5)	2.370	0.268	0.905	4	R.ALTQTGGPHVK.A
SW:FUS_HUMAN	H09	5101	2	1429.5	(+0.8)	3.863	0.409	0.992	9	K.GEATVSFDDPPSAK#.A
SW:FUS_HUMAN	H10	5303	2	1429.5	(-0.5)	3.381	0.432	0.973	9	K.GEATVSFDDPPSAK#.A
SW:FUS_HUMAN	H10	5311	2	1421.5	(-0.4)	2.607	0.407	0.952	9	K.GEATVSFDDPPSAK#.A
SW:FUS_HUMAN	H12	4804	2	1421.5	(-0.7)	2.492	0.395	0.819	9	K.GEATVSFDDPPSAK#.A
SW:FUS_HUMAN	H10	9429	3	3601.7	(-0.2)	6.174	0.537	1.000	5	R.HDSEQDNSDNTIFVQGL*GENVTIESVADYFK#.Q
SW:FUS_HUMAN	H10	9451	3	3587.7	(+0.6)	5.795	0.485	1.000	5	R.HDSEQDNSDNTIFVQGLGENVTIESVADYFK.Q
SW:FUS_HUMAN	H10	9373	3	3587.7	(-0.0)	5.295	0.400	0.998	5	R.HDSEQDNSDNTIFVQGLGENVTIESVADYFK.Q
SW:FUS_HUMAN	H10	9651	3	3587.7	(+0.3)	3.795	0.423	0.991	5	R.HDSEQDNSDNTIFVQGLGENVTIESVADYFK.Q
SW:FUS_HUMAN	H10	5767	2	1684.8	(-0.7)	3.791	0.489	1.000	6	K.L*K#GEATVSFDDPPSAK#.A
SW:FUS_HUMAN	H10	6489	2	1409.6	(+0.8)	3.055	0.276	0.965	6	K.TGQPMINLYTDR.E
SW:FUS_HUMAN	H10	6485	2	1415.6	(+0.5)	2.690	0.312	0.948	6	K.TGQPMINL*YTDR.E
SW:FUS_HUMAN	H10	5903	2	1431.6	(+0.5)	2.379	0.221	0.836	6	K.TGQPM@INL*YTDR.E
SW:FUS_HUMAN	H12	4724	2	1421.5	(-0.7)	2.279	0.399	0.772	9	K.GEATVSFDDPPSAK#.A
SW:G10_HUMAN	H19	7532	2	1576.8	(+0.1)	2.697	0.262	0.063	1	R.DTNFGTNCICRVPK#.S
SW:G10_HUMAN	H20	8130	2	2295.6	(+0.5)	4.141	0.437	1.000		R.KAPPDGWELIEPTLDELQDK.M
SW:G10_HUMAN	H20	7778	2	1289.5	(+0.2)	3.029	0.391	0.977	1	R.K#VESL*WPIFR.I

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:G19P_HUMAN	H08	5807	2	1463.6	(+0.1)	4.124	0.477	0.999	2	K.AQQEQEL*AADAFK#.E
SW:G19P_HUMAN	H08	5813	2	1449.6	(-0.5)	3.101	0.557	1.000	2	K.AQQEQELAADAFK.E
SW:G19P_HUMAN	H08	6057	2	1292.4	(+0.1)	2.230	0.273	0.779	1	R.ESLQQMAEVTR.E
SW:G19P_HUMAN	H08	6209	2	1159.3	(+1.0)	2.352	0.392	0.974	2	K.LWEEQLAAAK.A
SW:G19P_HUMAN	H09	6125	2	1159.3	(+0.9)	2.333	0.412	0.977	2	K.LWEEQLAAAK.A
SW:G19P_HUMAN	H09	6123	2	1179.3	(+0.8)	2.205	0.470	0.981	2	K.L*WEEQL*AAAK#.A
SW:G3BP_HUMAN	H10	5579	3	2387.5	(+0.9)	3.971	0.291	0.904	1	K.NSSVYHGGGL*DSNGK#PADAVYGGK#.E
SW:G3BP_HUMAN	H10	8775	2	1939.2	(+0.8)	3.251	0.396	0.987	1	K.LPNFGFVVDSEPVQK.V
SW:G3P1_HUMAN	H15	1892	2	910.1	(+0.4)	2.270	0.215*	0.008	1	K.AGAHLKGGAK.R
SW:G3P1_HUMAN	H15	6212	2	1216.5	(-0.1)	3.896	0.502	1.000	5	R.VVDL*MAHMASK#.E
SW:G3P1_HUMAN	H15	5062	2	1232.5	(+0.0)	3.244	0.391*	0.417	5	R.VVDL*M@AHMASK#.E
SW:G3P1_HUMAN	H15	6188	2	1202.5	(-0.7)	2.388	0.462	0.898	5	R.VVDLMAHMASK.E
SW:G3P1_HUMAN	H16	5868	2	1202.5	(+0.5)	3.484	0.486	1.000	5	R.VVDLMAHMASK.E
SW:G3P1_HUMAN	H16	5866	2	1216.5	(+1.0)	3.401	0.428	0.990	5	R.VVDL*MAHMASK#.E
SW:G3P1_HUMAN	H19	2096	2	1248.5	(+0.4)	2.271	0.205	0.766	5	R.VVDL*M@AHM@ASK#.E
SW:G3P1_HUMAN	H15	6290	2	1345.6	(+0.1)	3.988	0.570	1.000	4	R.VVDL*MAHMASK#.E.-
SW:G3P1_HUMAN	H15	2092	2	1377.6	(+0.6)	2.366	0.108	0.044	4	R.VVDL*M@AHM@ASK#.E.-
SW:G3P1_HUMAN	H20	2040	2	1248.5	(+0.8)	2.364	0.156	0.687	5	R.VVDL*M@AHM@ASK#.E
SW:G3P2_HUMAN	H15	1264	2	910.0	(+0.8)	2.680	0.217*	0.427	3	K.AGAHLQGGAK.R
SW:G3P2_HUMAN	H15	1386	2	924.0	(+0.6)	2.519	0.277*	0.311	3	K.AGAHL*QGGAK#.R
SW:G3P2_HUMAN	H15	1396	2	910.0	(-0.6)	2.423	0.271*	0.157	3	K.AGAHLQGGAK.R
SW:G3P2_HUMAN	H15	1308	2	924.0	(-0.1)	2.359	0.137*	0.095	3	K.AGAHL*QGGAK#.R
SW:G3P2_HUMAN	H15	1420	1	910.0	(-0.4)	2.039	0.341*	0.000	3	K.AGAHLQGGAK.R
SW:G3P2_HUMAN	H01	5624	2	1412.6	(+0.7)	3.068	0.252	0.942	3	R.GALQNIIPASTGAAK.A
SW:G3P2_HUMAN	H15	6428	2	1426.6	(+0.5)	3.441	0.411	0.988	3	R.GAL*QNIIPASTGAAK#.A
SW:G3P2_HUMAN	H15	6350	2	1412.6	(-0.3)	2.968	0.319	0.928	3	R.GALQNIIPASTGAAK.A
SW:G3P2_HUMAN	H16	5972	2	1426.6	(-0.2)	2.598	0.322	0.837	3	R.GAL*QNIIPASTGAAK#.A
SW:G3P2_HUMAN	H17	5822	2	1426.6	(+0.5)	3.371	0.355	0.981	3	R.GAL*QNIIPASTGAAK#.A
SW:G3P2_HUMAN	H17	5786	2	1412.6	(+0.8)	3.199	0.171	0.849	3	R.GALQNIIPASTGAAK.A
SW:G3P2_HUMAN	H18	6280	2	1412.6	(+1.0)	3.228	0.238	0.926	3	R.GALQNIIPASTGAAK.A
SW:G3P2_HUMAN	H18	6278	2	1426.6	(+0.4)	3.201	0.415	0.986	3	R.GAL*QNIIPASTGAAK#.A
SW:G3P2_HUMAN	H19	6092	2	1426.6	(-0.4)	2.899	0.274	0.867	3	R.GAL*QNIIPASTGAAK#.A
SW:G3P2_HUMAN	H21	6094	2	1426.6	(+0.1)	2.711	0.268	0.824	3	R.GAL*QNIIPASTGAAK#.A
SW:G3P2_HUMAN	H15	10404	3	4039.3	(+0.0)	8.363	0.640	1.000	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	10710	3	4039.3	(-0.1)	8.353	0.595	1.000	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	10786	3	4039.3	(+0.1)	8.335	0.601	1.000	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	10244	3	4039.3	(-0.0)	8.227	0.591	1.000	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	11250	3	4039.3	(+0.1)	8.084	0.626	1.000	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	11326	3	4039.3	(+0.0)	8.012	0.591	1.000	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	11402	3	4039.3	(-0.0)	7.954	0.553	1.000	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	11806	3	4039.3	(-0.2)	7.953	0.628	0.999	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	10088	3	4039.3	(-0.5)	7.907	0.539	0.994	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	11174	3	4039.3	(+0.1)	7.902	0.634	0.997	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	12476	3	4039.3	(+0.1)	7.892	0.615	0.996	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	12178	3	4039.3	(+0.0)	7.874	0.633	1.000	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	9638	3	4039.3	(-0.0)	7.844	0.628	1.000	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	9378	3	4039.3	(+0.3)	7.825	0.608	0.999	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	10328	3	4039.3	(-0.1)	7.816	0.612	1.000	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	13218	3	4039.3	(+0.1)	7.784	0.592	1.000	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	11042	3	4059.3	(+0.9)	7.781	0.583	0.998	3	K.GIL*GYTEHQVVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	10864	3	4039.3	(+0.1)	7.766	0.642	1.000	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	10482	3	4039.3	(-0.0)	7.754	0.629	1.000	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	13446	3	4039.3	(-0.1)	7.734	0.618	1.000	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	11018	3	4039.3	(+0.0)	7.733	0.626	1.000	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	12700	3	4039.3	(+0.3)	7.728	0.637	0.998	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	11556	3	4039.3	(-0.1)	7.725	0.579	1.000	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	10168	3	4039.3	(-0.1)	7.630	0.615	1.000	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	10634	3	4039.3	(-0.2)	7.620	0.583	1.000	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	9458	3	4039.3	(+0.2)	7.599	0.603	1.000	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	12626	3	4039.3	(-0.0)	7.538	0.631	1.000	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	11478	3	4039.3	(-0.1)	7.491	0.605	0.995	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	10558	3	4039.3	(-0.0)	7.479	0.616	1.000	3	K.GILGYTEHQVVSSDFNSDTHSSTFDAGAGIALNDHFVK.L

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:G3P2_HUMAN	H15	10940	3	4039.3	(+0.0)	7.434	0.550	0.998	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	12550	3	4039.3	(-0.2)	7.349	0.611	1.000	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	9218	3	4039.3	(-0.0)	7.344	0.583	1.000	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	13370	3	4039.3	(+0.1)	7.315	0.605	1.000	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	11902	3	4059.3	(+0.6)	7.281	0.599	1.000	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	11884	3	4039.3	(-0.2)	7.274	0.523	1.000	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	11960	3	4039.3	(-0.1)	7.271	0.578	1.000	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	12252	3	4039.3	(-0.1)	7.259	0.579	1.000	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	11098	3	4039.3	(-0.0)	7.245	0.617	1.000	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	12686	3	4059.3	(+0.6)	7.237	0.569	0.996	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	11500	3	4059.3	(-0.6)	7.209	0.576	1.000	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	10934	3	4059.3	(-0.8)	7.159	0.546	1.000	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	9538	3	4039.3	(-0.1)	7.061	0.605	0.998	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	10626	3	4059.3	(-0.6)	7.058	0.582	1.000	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	11732	3	4039.3	(+0.1)	7.057	0.631	1.000	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	13066	3	4039.3	(-0.1)	7.052	0.607	0.999	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	11198	3	4059.3	(-0.8)	7.016	0.561	1.000	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	13674	3	4039.3	(+0.2)	7.001	0.595	1.000	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	12000	3	4059.3	(-0.3)	6.948	0.562	1.000	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	12236	3	4059.3	(-0.4)	6.922	0.605	0.996	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	10486	3	4059.3	(-0.7)	6.920	0.541	1.000	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	12324	3	4039.3	(-0.1)	6.904	0.597	1.000	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	13140	3	4039.3	(+0.1)	6.896	0.613	1.000	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	9540	3	4059.3	(-0.2)	6.878	0.534	1.000	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	13306	3	4059.3	(+0.9)	6.840	0.641	1.000	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	9296	3	4039.3	(-0.4)	6.836	0.595	0.981	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	12920	3	4039.3	(+0.2)	6.782	0.609	1.000	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	10072	3	4059.3	(-0.9)	6.761	0.552	1.000	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	8122	3	4039.3	(-0.8)	6.758	0.597	1.000	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	12398	3	4039.3	(+0.1)	6.751	0.570	1.000	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	8606	3	4059.3	(-0.8)	6.744	0.601	0.998	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	12994	3	4039.3	(+0.0)	6.740	0.638	1.000	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	8076	3	4059.3	(+0.2)	6.719	0.559	0.995	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	10410	3	4059.3	(-0.8)	6.677	0.518	1.000	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	11754	3	4059.3	(-0.8)	6.647	0.569	1.000	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	12310	3	4059.3	(-0.6)	6.621	0.595	1.000	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	11574	3	4059.3	(-0.8)	6.597	0.528	1.000	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	9212	3	4059.3	(-1.0)	6.582	0.574	1.000	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	13524	3	4039.3	(+0.1)	6.581	0.578	1.000	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	10776	3	4059.3	(-0.5)	6.575	0.557	1.000	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	13398	3	4059.3	(-0.7)	6.555	0.526	1.000	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	12162	3	4059.3	(-0.6)	6.531	0.580	1.000	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	9380	3	4059.3	(-0.9)	6.525	0.565	0.999	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	12460	3	4059.3	(-0.8)	6.493	0.532	1.000	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	11650	3	4039.3	(+0.4)	6.472	0.587	1.000	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	8336	3	4059.3	(-0.7)	6.454	0.551	1.000	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	13600	3	4039.3	(-0.1)	6.381	0.578	1.000	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	9720	3	4039.3	(-0.0)	6.338	0.519	1.000	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	13016	3	4059.3	(-0.6)	6.252	0.591	1.000	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	9888	3	4039.3	(-0.7)	6.237	0.541	1.000	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	9302	3	4059.3	(-0.9)	6.129	0.534	1.000	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	12848	3	4039.3	(+0.1)	6.108	0.584	1.000	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	10150	3	4059.3	(-1.0)	6.030	0.559	1.000	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	9698	3	4059.3	(-0.8)	5.997	0.411	0.998	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	12774	3	4039.3	(-0.0)	5.988	0.613	1.000	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	12386	3	4059.3	(-0.7)	5.940	0.518	1.000	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	13748	3	4039.3	(-0.0)	5.916	0.527	1.000	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	12772	3	4059.3	(-0.4)	5.907	0.529	0.999	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	12864	3	4059.3	(-0.6)	5.741	0.526	1.000	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	13792	3	4059.3	(-0.5)	5.625	0.508	1.000	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	13564	3	4059.3	(-0.7)	5.243	0.505	1.000	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	13820	3	4039.3	(-0.1)	5.110	0.537	1.000	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H15	13642	3	4059.3	(-1.0)	4.908	0.477	0.999	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	13872	3	4059.3	(-0.6)	4.696	0.432	0.998	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	13956	3	4059.3	(-0.8)	4.512	0.398	0.923	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H15	13904	3	4039.3	(-0.0)	4.225	0.518	1.000	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:G3P2_HUMAN	H16	12120	3	4059.3	(-0.8)	4.670	0.428	0.995	3	K.GIL*GYTEHQVSSDFNSDTHSSTFDAGAGIAL*NDHFVK#.L
SW:G3P2_HUMAN	H16	12106	3	4039.3	(-0.0)	4.656	0.506	1.000	3	K.GILGYTEHQVSSDFNSDTHSSTFDAGAGIALNDHFVK.L
SW:G3P2_HUMAN	H14	7451	2	1764.9	(+0.7)	3.024	0.572	1.000	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	7496	2	1770.9	(+0.7)	4.544	0.549	1.000	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	7510	2	1764.9	(+1.0)	4.199	0.563	0.998	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	10280	2	1770.9	(+0.3)	3.439	0.531	1.000	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	13056	2	1770.9	(+0.2)	3.251	0.426	0.978	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	13768	2	1770.9	(+0.3)	3.221	0.529	1.000	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	10108	2	1770.9	(-0.0)	3.204	0.467	0.983	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	10218	2	1764.9	(+0.5)	3.181	0.538	1.000	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	10204	2	1770.9	(-0.0)	3.086	0.523	0.985	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	12902	2	1770.9	(+0.5)	3.035	0.519	0.994	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	10490	2	1764.9	(-0.2)	2.995	0.560	1.000	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	12526	2	1764.9	(+0.3)	2.948	0.541	0.987	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	10658	2	1764.9	(+0.8)	2.932	0.501	0.992	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	10364	2	1770.9	(+0.2)	2.924	0.519	0.985	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	10442	2	1770.9	(+0.6)	2.915	0.444	0.987	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	12746	2	1770.9	(+0.6)	2.903	0.534	0.994	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	12300	2	1770.9	(+0.9)	2.876	0.564	1.000	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	13658	2	1764.9	(+0.6)	2.860	0.508	0.992	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	10294	2	1764.9	(+0.5)	2.844	0.525	0.993	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	13232	2	1770.9	(+0.0)	2.833	0.535	0.986	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	13840	2	1770.9	(+0.2)	2.816	0.535	0.985	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	10136	2	1764.9	(-0.1)	2.810	0.452	0.974	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	12984	2	1770.9	(+0.5)	2.763	0.423	0.984	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	13312	2	1770.9	(+0.7)	2.762	0.470	0.989	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	10518	2	1770.9	(+0.0)	2.762	0.519	0.983	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	12674	2	1764.9	(+0.4)	2.733	0.511	0.991	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	9484	2	1764.9	(+0.6)	2.733	0.516	0.991	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	13744	2	1764.9	(+0.4)	2.715	0.398	0.979	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	12490	2	1770.9	(+0.4)	2.711	0.557	0.994	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	10366	2	1764.9	(-0.8)	2.698	0.592	1.000	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	13258	2	1764.9	(+0.7)	2.697	0.430	0.983	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	10820	2	1770.9	(+0.5)	2.647	0.489	0.989	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	11978	2	1764.9	(+0.5)	2.646	0.497	0.990	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	12672	2	1770.9	(-0.3)	2.628	0.539	0.980	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	12146	2	1770.9	(+0.2)	2.614	0.487	0.975	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	12846	2	1764.9	(+0.7)	2.595	0.522	0.991	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	13082	2	1764.9	(+0.7)	2.589	0.556	0.993	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	13960	2	1764.9	(+0.6)	2.589	0.490	0.988	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	12598	2	1770.9	(+0.3)	2.585	0.466	0.970	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	12600	2	1764.9	(+0.4)	2.569	0.549	0.992	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	10814	2	1764.9	(+0.7)	2.558	0.554	0.991	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	13008	2	1764.9	(+0.6)	2.553	0.543	0.992	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	10662	2	1770.9	(+0.5)	2.534	0.462	0.983	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	13128	2	1770.9	(+0.1)	2.531	0.495	0.974	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	12368	2	1764.9	(+0.6)	2.515	0.513	0.989	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	7336	2	1764.9	(+0.6)	2.515	0.479	0.986	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	12448	2	1764.9	(+0.4)	2.515	0.490	0.987	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	10970	2	1764.9	(+0.8)	2.485	0.416	0.976	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	10738	2	1764.9	(+0.5)	2.484	0.456	0.983	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	12134	2	1764.9	(+0.6)	2.474	0.474	0.985	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	12224	2	1770.9	(+0.5)	2.473	0.498	0.988	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	7852	2	1770.9	(-0.2)	2.464	0.366	0.917	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	10580	2	1764.9	(+0.3)	2.451	0.390	0.932	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	9476	2	1770.9	(+0.4)	2.388	0.522	0.988	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	12210	2	1764.9	(+0.5)	2.382	0.490	0.985	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	9014	2	1764.9	(+0.4)	2.356	0.491	0.985	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	13946	2	1770.9	(+0.8)	2.347	0.440	0.976	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	11832	2	1770.9	(+0.1)	2.338	0.435	0.945	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	13470	2	1770.9	(+0.2)	2.328	0.458	0.955	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	12754	2	1764.9	(+0.5)	2.326	0.492	0.984	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	13334	2	1764.9	(+0.2)	2.302	0.431	0.941	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	12930	2	1764.9	(+0.7)	2.292	0.462	0.979	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	13816	2	1764.9	(+0.5)	2.256	0.503	0.984	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	9838	2	1764.9	(+0.7)	2.249	0.424	0.968	3	K.LISWYDNEFGYSNR.V

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta M$	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:G3P2_HUMAN	H15	9656	2	1770.9	(+0.2)	2.247	0.289	0.768	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	12072	2	1770.9	(+0.5)	2.218	0.500	0.983	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	11992	2	1770.9	(+0.1)	2.216	0.463	0.950	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	11908	2	1770.9	(+0.2)	2.210	0.415	0.922	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	11748	2	1770.9	(+0.6)	2.203	0.469	0.883	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H16	6928	2	1770.9	(+0.3)	3.513	0.592	1.000	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H18	7300	2	1770.9	(-0.2)	4.037	0.540	0.999	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H19	7172	2	1770.9	(+0.6)	2.801	0.459	0.987	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H19	7290	2	1770.9	(+0.7)	2.341	0.275	0.881	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H20	7192	2	1770.9	(+0.7)	3.861	0.564	0.997	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H20	7190	2	1764.9	(+0.6)	2.244	0.436	0.971	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H21	7074	2	1770.9	(+0.0)	2.425	0.407	0.939	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H22	7060	2	1770.9	(+0.5)	3.462	0.584	1.000	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H22	7062	2	1764.9	(+0.5)	3.348	0.578	1.000	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	H15	8262	2	1620.9	(-0.3)	3.512	0.531	1.000	3	K.L*VINGNPITIFQER.D
SW:G3P2_HUMAN	H15	8250	2	1614.9	(+0.2)	3.486	0.573	1.000	3	K.LVINGNPITIFQER.D
SW:G3P2_HUMAN	H15	8084	2	1620.9	(-0.4)	3.387	0.506	1.000	3	K.L*VINGNPITIFQER.D
SW:G3P2_HUMAN	H15	8020	1	1620.9	(-0.2)	2.716	0.410	0.065	3	K.L*VINGNPITIFQER.D
SW:G3P2_HUMAN	H15	8028	1	1614.9	(-0.2)	2.147	0.192	0.000	3	K.LVINGNPITIFQER.D
SW:G3P2_HUMAN	H15	8104	1	1620.9	(+0.7)	2.095	0.433	0.000	3	K.L*VINGNPITIFQER.D
SW:G3P2_HUMAN	H16	7558	2	1614.9	(-0.2)	3.918	0.538	1.000	3	K.LVINGNPITIFQER.D
SW:G3P2_HUMAN	H16	7504	2	1620.9	(+0.9)	3.795	0.520	1.000	3	K.L*VINGNPITIFQER.D
SW:G3P2_HUMAN	H17	7414	2	1614.9	(+0.3)	3.428	0.607	1.000	3	K.LVINGNPITIFQER.D
SW:G3P2_HUMAN	H18	7904	2	1620.9	(+0.3)	3.008	0.482	0.981	3	K.L*VINGNPITIFQER.D
SW:G3P2_HUMAN	H18	7900	2	1614.9	(+0.6)	2.562	0.441	0.982	3	K.LVINGNPITIFQER.D
SW:G3P2_HUMAN	H19	7838	2	1620.9	(+0.9)	3.951	0.471	0.997	3	K.L*VINGNPITIFQER.D
SW:G3P2_HUMAN	H21	7640	2	1614.9	(-0.1)	2.511	0.504	0.975	3	K.LVINGNPITIFQER.D
SW:G3P2_HUMAN	H22	7576	2	1620.9	(-0.3)	3.345	0.518	1.000	3	K.L*VINGNPITIFQER.D
SW:G3P2_HUMAN	H15	7820	2	2056.3	(-0.5)	2.255	0.257	0.067	3	K.L*VINGNPITIFQERDPSK#.I
SW:G3P2_HUMAN	H15	6972	2	2394.8	(-0.3)	3.836	0.473*	0.477	4	K.RVIISAPSADAPM@FVMGVNHEK#.Y
SW:G3P2_HUMAN	H15	9774	3	2611.0	(+0.9)	7.258	0.580	0.987	3	K.VIHDNFGIVEGL*MTTVHAITATQK#.T
SW:G3P2_HUMAN	H15	9924	3	2611.0	(+0.9)	6.988	0.611	0.998	3	K.VIHDNFGIVEGL*MTTVHAITATQK#.T
SW:G3P2_HUMAN	H15	9088	3	2627.0	(+0.9)	6.156	0.649*	0.409	3	K.VIHDNFGIVEGL*M@TTVHAITATQK#.T
SW:G3P2_HUMAN	H15	9952	2	2611.0	(+0.6)	5.878	0.585	0.999	3	K.VIHDNFGIVEGL*MTTVHAITATQK#.T
SW:G3P2_HUMAN	H15	9786	2	2611.0	(+0.2)	5.776	0.538	1.000	3	K.VIHDNFGIVEGL*MTTVHAITATQK#.T
SW:G3P2_HUMAN	H15	8940	2	2627.0	(+0.2)	5.613	0.582	1.000	3	K.VIHDNFGIVEGL*M@TTVHAITATQK#.T
SW:G3P2_HUMAN	H15	9784	2	2597.0	(-0.0)	5.570	0.569	1.000	3	K.VIHDNFGIVEGLMTTVHAITATQK.T
SW:G3P2_HUMAN	H15	10406	3	2597.0	(+0.5)	5.476	0.463	1.000	3	K.VIHDNFGIVEGLMTTVHAITATQK.T
SW:G3P2_HUMAN	H15	9866	2	2611.0	(+0.2)	5.297	0.543	1.000	3	K.VIHDNFGIVEGL*MTTVHAITATQK#.T
SW:G3P2_HUMAN	H15	9026	2	2627.0	(-0.4)	5.271	0.542	1.000	3	K.VIHDNFGIVEGL*M@TTVHAITATQK#.T
SW:G3P2_HUMAN	H15	10206	3	2611.0	(-0.5)	5.074	0.579	0.999	3	K.VIHDNFGIVEGL*MTTVHAITATQK#.T
SW:G3P2_HUMAN	H15	12040	3	2597.0	(+0.9)	4.319	0.537	1.000	3	K.VIHDNFGIVEGLMTTVHAITATQK.T
SW:G3P2_HUMAN	H15	12504	3	2597.0	(+0.9)	4.156	0.508	1.000	3	K.VIHDNFGIVEGLMTTVHAITATQK.T
SW:G3P2_HUMAN	H15	13738	3	2597.0	(+0.8)	4.119	0.507	0.961	3	K.VIHDNFGIVEGLMTTVHAITATQK.T
SW:G3P2_HUMAN	H15	12346	3	2597.0	(+1.0)	3.995	0.529	1.000	3	K.VIHDNFGIVEGLMTTVHAITATQK.T
SW:G3P2_HUMAN	H15	12966	3	2597.0	(+1.0)	3.743	0.514	0.946	3	K.VIHDNFGIVEGLMTTVHAITATQK.T
SW:G3P2_HUMAN	H15	9030	2	2611.0	(+1.0)	2.831	0.237	0.897	3	K.VIHDNFGIVEGL*MTTVHAITATQK#.T
SW:G3P2_HUMAN	H17	8240	3	2627.0	(+0.0)	3.785	0.506	0.990	3	K.VIHDNFGIVEGL*M@TTVHAITATQK#.T
SW:G3P2_HUMAN	H19	8570	3	2627.0	(+0.5)	3.823	0.454*	0.062	3	K.VIHDNFGIVEGL*M@TTVHAITATQK#.T
SW:G3P2_HUMAN	H15	7550	2	2222.6	(+0.8)	4.245	0.470	1.000	4	R.VIISAPSADAPMFVMGVNHEK#.Y
SW:G3P2_HUMAN	H15	7748	2	2214.6	(+0.7)	3.585	0.542	1.000	4	R.VIISAPSADAPMFVMGVNHEK#.Y
SW:G3P2_HUMAN	H15	7640	2	2222.6	(+0.8)	3.564	0.560	1.000	4	R.VIISAPSADAPMFVMGVNHEK#.Y
SW:G3P2_HUMAN	H15	6600	2	2254.6	(+0.2)	3.514	0.553	0.944	4	R.VIISAPSADAPM@FVM@GVNHEK#.Y
SW:G3P2_HUMAN	H15	7554	2	2214.6	(+0.7)	3.284	0.497	0.727	4	R.VIISAPSADAPMFVMGVNHEK#.Y
SW:G3P2_HUMAN	H15	7644	2	2214.6	(-0.8)	2.752	0.425	0.886	4	R.VIISAPSADAPMFVMGVNHEK#.Y
SW:G3P2_HUMAN	H15	10832	2	2286.5	(+0.7)	5.357	0.597	1.000	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	8380	2	2278.5	(+0.8)	5.323	0.632	0.999	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	10912	2	2286.5	(+0.7)	5.198	0.650	0.998	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	11378	2	2286.5	(+0.7)	5.056	0.620	0.999	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	13246	2	2286.5	(+0.9)	5.013	0.590	0.987	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	13594	2	2278.5	(+0.5)	5.009	0.622	1.000	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	10826	2	2278.5	(-0.4)	4.978	0.644	1.000	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	11128	2	2278.5	(+0.7)	4.894	0.509	0.999	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	13422	2	2286.5	(+0.6)	4.848	0.611	1.000	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	10932	2	2278.5	(+0.6)	4.833	0.613	0.999	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	11888	2	2286.5	(-0.4)	4.827	0.492	1.000	3	K.WGDAGAEYVVESTGVFTTMEK#.A

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta M$	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:G3P2_HUMAN	H15	12164	2	2278.5	(-0.1)	4.810	0.645	1.000	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	13256	2	2278.5	(+0.1)	4.807	0.611	1.000	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	12018	2	2286.5	(+0.8)	4.781	0.561	0.946	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	13332	2	2278.5	(+0.3)	4.752	0.609	1.000	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	13156	2	2286.5	(-0.4)	4.715	0.554	0.999	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	11272	2	2286.5	(+0.6)	4.699	0.619	1.000	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	12508	2	2286.5	(+0.6)	4.697	0.593	1.000	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	10562	2	2278.5	(+0.7)	4.685	0.594	0.999	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	8376	2	2286.5	(+0.1)	4.636	0.465	1.000	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	11570	2	2278.5	(+0.4)	4.633	0.586	1.000	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	11614	2	2286.5	(-0.4)	4.598	0.463	0.971	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	11354	2	2278.5	(-0.4)	4.597	0.596	1.000	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	7798	2	2302.5	(+0.4)	4.581	0.648	1.000	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	10652	2	2278.5	(-0.1)	4.548	0.651	1.000	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	12380	2	2286.5	(+0.6)	4.434	0.561	0.992	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	12714	2	2278.5	(-0.2)	4.410	0.566	0.999	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	11706	2	2286.5	(+0.7)	4.404	0.588	0.996	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	11254	2	2278.5	(+0.9)	4.379	0.577	0.998	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	10254	2	2278.5	(+0.6)	4.344	0.529	1.000	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	11944	2	2278.5	(-0.0)	4.298	0.598	1.000	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	13520	2	2278.5	(+0.3)	4.279	0.585	0.999	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	11430	2	2278.5	(+0.9)	4.278	0.560	1.000	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	12038	2	2278.5	(-0.4)	4.249	0.560	1.000	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	12896	2	2278.5	(-0.3)	4.238	0.606	1.000	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	12298	2	2278.5	(+0.8)	4.231	0.570	1.000	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	11746	2	2278.5	(+0.7)	4.216	0.582	0.999	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	8548	2	2286.5	(-0.3)	4.198	0.509	1.000	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	13092	2	2278.5	(+0.0)	4.190	0.631	1.000	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	11278	2	2302.5	(-0.4)	4.163	0.583	1.000	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	10162	2	2278.5	(+0.8)	4.156	0.618	1.000	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	13688	2	2286.5	(-0.4)	4.129	0.508	1.000	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	13562	2	2302.5	(-0.0)	4.126	0.512	1.000	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	12420	2	2278.5	(-0.0)	4.083	0.560	0.999	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	13180	2	2278.5	(-0.8)	4.081	0.595	1.000	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	11812	2	2286.5	(-0.7)	4.060	0.430	0.953	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	13052	2	2286.5	(-0.1)	4.056	0.492	1.000	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	10642	2	2286.5	(-0.6)	4.003	0.487	1.000	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	12522	2	2278.5	(-0.0)	3.978	0.576	1.000	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	11008	2	2286.5	(-0.9)	3.939	0.408	0.943	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	12676	2	2286.5	(+0.4)	3.905	0.450	0.976	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	13010	2	2278.5	(-0.4)	3.879	0.598	1.000	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	13466	2	2302.5	(-0.6)	3.873	0.486	1.000	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	10996	2	2278.5	(-0.8)	3.856	0.556	1.000	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	8464	2	2286.5	(-0.8)	3.828	0.408	0.938	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	12552	2	2286.5	(-0.7)	3.809	0.419	0.942	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	13588	2	2286.5	(-0.8)	3.744	0.448	0.948	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	13694	2	2278.5	(+0.0)	3.740	0.573	1.000	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	12464	2	2302.5	(-0.8)	3.716	0.517	1.000	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	11490	2	2278.5	(-0.8)	3.659	0.528	1.000	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	12944	2	2286.5	(-0.3)	3.626	0.505	0.999	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	13974	2	2278.5	(+0.2)	3.613	0.571	1.000	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	12630	2	2278.5	(-0.0)	3.556	0.539	1.000	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	13942	2	2286.5	(+0.4)	3.521	0.494	0.999	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	8774	2	2286.5	(-0.6)	3.479	0.429	0.979	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	12854	2	2286.5	(-0.5)	3.426	0.503	1.000	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	13882	2	2278.5	(-0.2)	3.388	0.525	1.000	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	10338	2	2278.5	(-0.1)	3.348	0.589	1.000	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	10446	2	2286.5	(-0.8)	3.331	0.458	0.938	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	13786	2	2286.5	(-0.4)	3.311	0.403	0.971	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	13692	2	2302.5	(-0.4)	3.298	0.473	0.982	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	10438	2	2278.5	(-0.4)	3.294	0.544	1.000	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	10540	2	2286.5	(-0.7)	3.134	0.441	0.919	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	10210	2	2286.5	(-0.8)	2.864	0.473	0.918	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	12996	2	2302.5	(-0.4)	2.809	0.379	0.941	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	14044	2	2286.5	(-0.3)	2.774	0.318	0.897	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	10990	2	2302.5	(-0.8)	2.720	0.297	0.658	3	K.WGDAGAEYVVESTGVFTTMEK#.A

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:G3P2_HUMAN	H15	14062	2	2278.5	(-0.1)	2.698	0.472	0.973	3	K.WGDAGAEYVVESTGVFTTMEK.A
SW:G3P2_HUMAN	H15	13864	2	2286.5	(-0.2)	2.657	0.419	0.943	3	K.WGDAGAEYVVESTGVFTTMEK#.A
SW:G3P2_HUMAN	H15	13892	2	2302.5	(-0.3)	2.542	0.441	0.953	3	K.WGDAGAEYVVESTGVFTTM@EK#.A
SW:G3P2_HUMAN	H15	10756	2	2302.5	(-0.9)	2.434	0.335	0.650	3	K.WGDAGAEYVVESTGVFTTM@EK#.A
SW:G3P2_HUMAN	H16	10780	3	2302.5	(+1.0)	3.760	0.419	0.999	3	K.WGDAGAEYVVESTGVFTTM@EK#.A
SW:G3P2_HUMAN	H22	7624	2	1614.9	(-0.1)	2.268	0.427	0.936	3	K.LVINGNPITIFQER.D
SW:GBLP_HUMAN	H16	6500	2	1497.6	(-0.8)	3.312	0.232	0.719	1	K.DGQAML*WDL*NEGK#.H
SW:GBLP_HUMAN	H16	5962	2	1513.6	(-1.0)	2.968	0.368	0.860	1	K.DGQAM@L*WDL*NEGK#.H
SW:GBLP_HUMAN	H16	6258	2	1310.4	(+1.0)	3.934	0.533	1.000	1	K.DVLSVAFSSDNR.Q
SW:GBLP_HUMAN	H16	6250	2	1316.4	(+0.8)	3.056	0.357	0.848	1	K.DVL*SVAFSSDNR.Q
SW:GBLP_HUMAN	H16	7930	3	2629.0	(+0.6)	4.341	0.252	0.968	1	K.GHNGWVTQIATTPQFPDMILSASR.D
SW:GBLP_HUMAN	H16	7486	3	2651.0	(+1.0)	3.868	0.404	0.998	1	K.GHNGWVTQIATTPQFPDM@IL*SASR.D
SW:GBLP_HUMAN	H16	6576	2	1790.1	(+0.9)	5.148	0.508	1.000	1	K.IIVDELKQEVISTSSK.A
SW:GBLP_HUMAN	H16	6570	2	1812.1	(-0.9)	4.119	0.463	1.000	1	K.IIVDEL*K#QEVISTSSK#.A
SW:GBLP_HUMAN	H16	6062	2	1277.4	(+0.8)	2.756	0.341	0.974	1	R.L*WDL*TTGTTTR.R
SW:GDIS_HUMAN	H18	5788	2	1693.9	(-0.4)	3.759	0.334	0.571		K.ELQEMDKDESILK.Y
SW:GDIS_HUMAN	H17	5430	2	1312.5	(+0.9)	2.831	0.408	0.984		K.TLLGDGPVVTDPK.A
SW:GDIS_HUMAN	H18	5992	2	1332.5	(-0.7)	2.736	0.478	0.920		K.TL*L*GDGPVVTDPK#.A
SW:GDIS_HUMAN	H19	4752	1	731.9	(-0.2)	1.954	0.196	0.000		R.DIVSGLK.Y
SW:GR75_HUMAN	H09	8087	2	2075.2	(+0.8)	3.142	0.445	0.990	3	K.STNGDTFL*GGEDFDQAL*L*R.H
SW:GR75_HUMAN	H09	7105	2	1646.9	(+0.7)	3.830	0.144	0.925	3	R.VINEPTAAALAYGLDK.S
SW:GR75_HUMAN	H09	6519	2	1291.4	(+0.9)	3.446	0.448	0.992	3	K.VQQTVDLDFGR.A
SW:GR75_HUMAN	H09	8225	2	1368.6	(+0.8)	2.619	0.383	0.977	3	R.AQFEGIVTDL*IR.R
SW:GR78_HUMAN	H09	7769	2	1513.8	(+0.8)	3.399	0.520	0.998	2	R.AKFEELNMDLFR.S
SW:GR78_HUMAN	H09	7027	2	1398.6	(+0.9)	3.341	0.344	0.986	2	K.ELEEIVQPIISK.L
SW:GR78_HUMAN	H09	7205	2	1674.9	(-0.2)	4.560	0.404	1.000	13	R.IINEPTAAAIAYGL*DK#.R
SW:GR78_HUMAN	H09	7181	2	1660.9	(+0.7)	4.041	0.611	1.000	13	R.IINEPTAAAIAYGLDK.R
SW:GR78_HUMAN	H09	5741	2	2197.3	(-0.8)	3.372	0.478	0.438	1	K.L*YGSAGPPPTGEEDTAEK#DEL*.-
SW:GR78_HUMAN	H09	5731	2	2177.3	(-0.9)	3.130	0.493	0.418	1	K.LYGSAGPPPTGEEDTAEKDEL.-
SW:GR78_HUMAN	H09	5949	2	1678.8	(-0.1)	4.303	0.347	0.981	2	K.NQLTSNPENTVFDK.R
SW:GR78_HUMAN	H09	5945	2	1692.8	(-0.0)	4.274	0.517	0.993	2	K.NQL*TSNPENTVFDK#.R
SW:GR78_HUMAN	H09	6217	2	1838.0	(+0.8)	4.505	0.583	1.000	1	K.SQIFSTASDNQPTVTIK.V
SW:GR78_HUMAN	H09	6215	2	1846.0	(+0.1)	3.148	0.462	0.978	1	K.SQIFSTASDNQPTVTIK#.V
SW:GR78_HUMAN	H09	6243	2	1838.0	(-0.4)	2.405	0.343	0.881	1	K.SQIFSTASDNQPTVTIK.V
SW:GR78_HUMAN	H09	5971	2	1621.8	(-0.4)	3.343	0.518	1.000	2	K.TK#PYIQVDIGGGQTK#.T
SW:GR78_HUMAN	H09	5459	2	1439.5	(+1.0)	3.918	0.496	1.000	2	R.TWNDPSVQQDIK#.F
SW:GR78_HUMAN	H09	8107	2	1551.8	(-0.0)	2.347	0.364	0.887	2	K.TFAPEEISAMVL*TK#.M
SW:GSN2_HUMAN	H01	5490	2	1231.4	(+0.2)	3.012	0.373	0.968	3	K.HYEVEIL*DAK#.T
SW:GSN2_HUMAN	H02	5630	2	1231.4	(-0.2)	3.678	0.448	1.000	3	K.HYEVEIL*DAK#.T
SW:GSN2_HUMAN	H02	5624	2	1217.4	(+0.8)	3.663	0.338	0.991	3	K.HYEVEILDAK.T
SW:GSN2_HUMAN	H03	6452	2	1231.4	(+0.0)	2.910	0.384	0.967	3	K.HYEVEIL*DAK#.T
SW:GSN2_HUMAN	H02	4536	2	1175.3	(+0.7)	2.784	0.284	0.503	3	K.SLKDEDVLQK.L
SW:GSN2_HUMAN	H03	5132	2	1175.3	(-0.6)	2.243	0.321	0.209	3	K.SLKDEDVLQK.L
SW:H11_HUMAN	H16	4314	2	1108.2	(-0.4)	3.909	0.504	1.000	12	K.ALAAAGYDVEK.N
SW:H11_HUMAN	H16	4474	2	1108.2	(+0.7)	3.449	0.469	1.000	12	K.ALAAAGYDVEK.N
SW:H11_HUMAN	H16	4592	2	1122.2	(+0.4)	3.446	0.442	0.993	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	H16	4348	2	1122.2	(+0.2)	3.355	0.462	1.000	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	H16	4428	2	1122.2	(+0.1)	3.283	0.460	0.985	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	H16	4512	2	1122.2	(+0.0)	3.141	0.429	0.979	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	H16	4252	2	1122.2	(-0.3)	2.762	0.401	0.950	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	H20	4696	2	1108.2	(+1.0)	3.625	0.420	0.993	12	K.ALAAAGYDVEK.N
SW:H11_HUMAN	H16	4130	2	1258.4	(+0.2)	2.335	0.292	0.809	12	K.K#AL*AAAGYDVEK#.N
SW:H11_HUMAN	H16	4166	2	1236.4	(+0.2)	2.296	0.412	0.939	12	K.KALAAAGYDVEK.N
SW:H11_HUMAN	H21	4528	2	1122.2	(+0.2)	2.952	0.347	0.954	12	K.AL*AAAGYDVEK#.N
SW:H12_HUMAN	H16	5648	2	1199.4	(+0.9)	2.975	0.365	0.983	5	K.ASGPPVSELITK.A
SW:H12_HUMAN	H16	5512	2	1349.6	(-0.1)	3.437	0.433	0.981	5	R.K#ASGPPVSEL*ITK#.A
SW:H12_HUMAN	H16	5504	2	1327.6	(+0.9)	3.025	0.467	0.991	5	R.KASGPPVSELITK.A
SW:H12_HUMAN	H16	5164	2	1002.2	(+0.3)	2.276	0.326	0.206	5	R.SGVSL*AAL*K#K#.A

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:H15_HUMAN	H15	4470	2	1108.2	(+0.5)	3.116	0.454	0.992	1	K.AL*AAGGYDVEK#.N
SW:H15_HUMAN	H15	4554	2	1094.2	(+0.3)	2.679	0.307	0.919	1	K.ALAAGGYDVEK.N
SW:H15_HUMAN	H16	4022	2	1108.2	(+0.2)	3.282	0.472	1.000	1	K.AL*AAGGYDVEK#.N
SW:H15_HUMAN	H16	4102	2	1108.2	(+0.6)	3.203	0.403	0.980	1	K.AL*AAGGYDVEK#.N
SW:H15_HUMAN	H16	4158	2	1094.2	(+0.8)	3.136	0.459	0.993	1	K.ALAAGGYDVEK.N
SW:H15_HUMAN	H20	4520	2	1094.2	(-0.3)	2.904	0.336	0.953	1	K.ALAAGGYDVEK.N
SW:H15_HUMAN	H20	4492	2	1108.2	(+0.8)	2.689	0.328	0.947	1	K.AL*AAGGYDVEK#.N
SW:H15_HUMAN	H16	3554	2	1244.4	(+0.4)	2.350	0.390	0.963	1	K.K#AL*AAGGYDVEK#.N
SW:H15_HUMAN	H16	3652	2	1244.4	(-0.1)	2.301	0.193	0.552	1	K.K#AL*AAGGYDVEK#.N
SW:H15_HUMAN	H16	5580	2	1363.6	(-0.0)	2.759	0.229	0.798	1	R.K#ATGPPVSEL*ITK#.A
SW:H15_HUMAN	H16	5610	2	1341.6	(-0.9)	2.679	0.401	0.869	1	R.KATGPPVSELITK.A
SW:H15_HUMAN	H21	4298	2	1094.2	(+1.0)	2.447	0.210	0.784	1	K.ALAAGGYDVEK.N
SW:H1X_HUMAN	H17	1232	2	1332.5	(-0.3)	3.264	0.499	0.986		R.GAPAAATAPAPTAHK.A
SW:H1X_HUMAN	H18	6176	2	1208.4	(+0.6)	3.163	0.354	0.987		K.YSQLVETIR.R
SW:H1X_HUMAN	H18	1648	2	1332.5	(+0.7)	2.749	0.491	0.990		R.GAPAAATAPAPTAHK.A
SW:H2AA_HUMAN	H21	5936	2	945.1	(-0.5)	2.719	0.355	0.960	24	R.AGLQFPVGR.V
SW:H2AA_HUMAN	H21	5864	2	945.1	(+0.8)	2.687	0.311	0.971	24	R.AGLQFPVGR.V
SW:H2AA_HUMAN	H19	8536	2	1932.4	(+0.3)	2.729	0.282	0.865	14	R.VTIAQGGVLPNIQAVLLPK.K
SW:H2AA_HUMAN	H21	8356	2	1932.4	(+0.4)	5.435	0.414	0.998	14	R.VTIAQGGVLPNIQAVLLPK.K
SW:H2AA_HUMAN	H21	5530	2	851.0	(-0.6)	2.350	0.238	0.855	20	R.HLQLAIR.N
SW:H2AZ_HUMAN	H21	5662	2	1371.6	(-0.2)	3.079	0.404	0.971	1	K.ATIAGGGVIPHIHK.S
SW:H2AZ_HUMAN	H21	6102	2	1119.2	(-0.6)	3.813	0.288	0.968	1	R.GDEELDSLIA.A
SW:H2AZ_HUMAN	H21	6090	2	1139.2	(+0.1)	2.574	0.285	0.884	1	R.GDEEL*DSL*IK#.A
SW:H2BA_HUMAN	H20	5334	2	1282.4	(+0.3)	2.907	0.474	0.938	15	R.K#ESYSVYVYK#.V
SW:H2BA_HUMAN	H20	5350	2	1266.4	(-0.8)	2.618	0.480	0.938	15	R.KESYSVYVYK.V
SW:H2BA_HUMAN	H20	664	2	828.9	(-0.3)	2.437	0.374	0.956	28	K.HAVSEGTK.A
SW:H4_HUMAN	H20	5186	2	1326.5	(+0.9)	2.313	0.286	0.267	2	R.DNIQGITKPAIR.R
SW:H4_HUMAN	H21	4978	2	1334.5	(-0.1)	2.894	0.260	0.248	2	R.DNIQGITK#PAIR.R
SW:H4_HUMAN	H21	4984	2	1326.5	(+0.6)	2.836	0.283	0.457	2	R.DNIQGITKPAIR.R
SW:H4_HUMAN	H01	5384	2	1181.3	(+0.4)	2.616	0.453	0.989	2	R.ISGLIYEETR.G
SW:H4_HUMAN	H21	5846	2	1343.5	(+0.8)	2.916	0.241	0.947	2	K.RISGL*IYEETR.G
SW:H4_HUMAN	H01	6572	2	1311.6	(+0.9)	3.177	0.529	0.999	2	K.TVTAMDVVYALK.R
SW:H4_HUMAN	H21	6536	2	1341.6	(+0.2)	2.618	0.388	0.944	2	K.TVTAM@DVVYAL*K#.R
SW:H4_HUMAN	H21	6604	2	990.2	(-0.5)	2.840	0.353	0.926	2	K.VFLENVIR.D
SW:H4_HUMAN	H21	5066	2	1326.5	(+0.9)	2.217	0.188	0.084	2	R.DNIQGITKPAIR.R
SW:HCC1_HUMAN	H16	5080	2	944.1	(-0.6)	2.224	0.259	0.770	1	R.FGISSVPTK#.G
SW:HCC1_HUMAN	H16	5150	2	1873.0	(+0.8)	4.021	0.614	0.994	1	R.FGIVTSSAGTGTTEDTEAK.K
SW:HCC1_HUMAN	H16	5068	2	1881.0	(-0.4)	3.802	0.615	1.000	1	R.FGIVTSSAGTGTTEDTEAK#.K
SW:HCC1_HUMAN	H16	6044	2	1080.2	(-0.1)	3.600	0.387	0.985	1	R.FGLNVSSISR.K
SW:HCC1_HUMAN	H16	5026	2	1518.7	(-0.6)	2.417	0.306	0.174	1	K.GLSSDNKPMVNLDK.L
SW:HCC1_HUMAN	H17	5808	2	1134.3	(+0.4)	2.549	0.228	0.860	2	R.FNVPVSL*ESK#.K
SW:HCDH_HUMAN	H16	7024	3	2763.1	(+0.8)	4.531	0.394	0.986	3	K.FIVDGWHEMDAENPLHQPSPLNK.L
SW:HCDH_HUMAN	H16	9474	2	2358.7	(-0.7)	2.900	0.376	0.854	3	K.LGAGYPMGPFELLDYVGLDTTK.F
SW:HCDH_HUMAN	H16	6704	2	1187.3	(+0.3)	2.797	0.353	0.953	3	K.TFESL*VDFSK#.A
SW:HDA1_HUMAN	H10	7889	2	2061.3	(-0.2)	2.692	0.236	0.109	3	R.DGIDDESIEAIFK#PVMSK#.V
SW:HDA1_HUMAN	H10	7389	2	2077.3	(-1.0)	2.410	0.318	0.054	3	R.DGIDDESIEAIFK#PVM@SK#.V
SW:HDA1_HUMAN	H10	6353	3	2254.4	(+0.7)	5.859	0.476	1.000	3	K.L*HISPSNMTNQNTNEYL*EK#.I
SW:HDA1_HUMAN	H10	6359	2	2234.4	(+0.8)	5.567	0.584*	0.920	3	K.LHISPSNMTNQNTNEYLEK.I
SW:HDA1_HUMAN	H10	5827	3	2270.4	(+0.8)	4.776	0.358	0.995	3	K.L*HISPSNM@TNQNTNEYL*EK#.I
SW:HDA1_HUMAN	H10	7433	2	1648.9	(+1.0)	2.803	0.360	0.975	5	R.M@THNL*L*NYGL*YR.K
SW:HDA1_HUMAN	H10	9525	2	1828.2	(+0.1)	2.512	0.510	0.975	3	K.SFNLPMLMLGGGGYTIR.N
SW:HDA1_HUMAN	H10	2397	2	1435.6	(+0.6)	2.431	0.241	0.193	5	R.SIRPDNMSEYSK#.Q
SW:HDA1_HUMAN	H10	6587	2	1381.5	(+0.6)	3.991	0.500	1.000	5	K.YGEYFPGTGDL*R.D
SW:HDA1_HUMAN	H10	6297	2	1165.3	(+0.9)	2.309	0.283	0.929	3	K.YYAVNYPL*R.D
SW:HDA1_HUMAN	H12	6284	3	2254.4	(+0.1)	4.896	0.381	0.997	3	K.L*HISPSNMTNQNTNEYL*EK#.I
SW:HDA2_HUMAN	H10	5743	3	2265.5	(+0.4)	4.619	0.443	1.000	1	K.L*HISPSNM@TNQNTPEYMEK#.I
SW:HDA2_HUMAN	H10	6271	3	2249.5	(+0.8)	4.146	0.443	0.987	1	K.L*HISPSNMTNQNTPEYMEK#.I



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:HDA2_HUMAN	H10	9789	2	1824.2	(+0.7)	3.415	0.593	1.000	1	K.TFNLPLLLMLGGGGYTIR.N
SW:HDA2_HUMAN	H10	9279	2	1864.2	(+0.6)	2.512	0.442	0.980	1	K.TFNL*PL*L*M@L*GGGGYTIR.N
SW:HE47_HUMAN	H13	6816	2	1494.6	(+0.4)	5.260	0.516	0.994	6	K.GL*AITFVSDENDAK#.I
SW:HE47_HUMAN	H13	6734	2	1494.6	(+0.0)	4.688	0.477	1.000	6	K.GL*AITFVSDENDAK#.I
SW:HE47_HUMAN	H13	6820	2	1489.7	(-0.3)	2.891	0.339	0.941	7	K.L*TL*HGL*QQYYVK#.L
SW:HE47_HUMAN	H13	7306	2	2307.5	(+0.4)	4.690	0.500	0.996	3	R.VNIAFNVDMPEDSDTYL*HR.V
SW:HE47_HUMAN	H13	7308	2	2301.5	(+0.0)	4.451	0.532	0.987	3	R.VNIAFNVDMPEDSDTYLHR.V
SW:HE47_HUMAN	H19	6492	2	1494.6	(+0.5)	4.996	0.549	1.000	6	K.GL*AITFVSDENDAK#.I
SW:HFC1_HUMAN	H04	4671	2	1067.2	(+0.6)	2.208	0.223	0.505	4	K.GAPGQPGTILR.T
SW:HFC1_HUMAN	H06	4290	2	1067.2	(+0.8)	2.280	0.278	0.767	4	K.GAPGQPGTILR.T
SW:HFC1_HUMAN	H05	5876	2	1636.9	(+0.8)	3.862	0.489	0.999	3	K.IATGHGQQGVTVQVVLK.G
SW:HFC1_HUMAN	H05	5862	2	1650.9	(-0.6)	3.181	0.422	0.972	3	K.IATGHGQQGVTVQVVL*K#.G
SW:HFC1_HUMAN	H06	5560	2	1650.9	(-0.3)	3.148	0.452	0.977	3	K.IATGHGQQGVTVQVVL*K#.G
SW:HFC1_HUMAN	H06	9544	3	2980.4	(+0.9)	5.179	0.482	1.000	1	R.LGDLWTLIDITLTWNKPSLSGVAPLPR.S
SW:HFC1_HUMAN	H05	9442	2	1887.2	(-0.3)	3.416	0.408	0.971	4	K.M@YVFGGWVPL*VMDDVK#.V
SW:HFC1_HUMAN	H06	9378	2	1887.2	(-0.1)	3.010	0.423	0.964	4	K.M@YVFGGWVPL*VMDDVK#.V
SW:HFC1_HUMAN	H05	1818	2	1143.3	(+0.8)	2.421	0.476	0.985	3	R.SL*HSATTIGNK#.M
SW:HFC1_HUMAN	H05	7200	2	1345.6	(+0.3)	2.232	0.237	0.627	1	R.SPAFVQLAPLSSK.V
SW:HFC1_HUMAN	H03	7612	2	1617.9	(-0.4)	3.032	0.343	0.937	3	K.SPISVPGGSAL*ISNL*GK#.V
SW:HFC1_HUMAN	H04	7457	2	1597.9	(+0.1)	2.992	0.525	0.985	3	K.SPISVPGGSALISNLGK.V
SW:HFC1_HUMAN	H04	7451	2	1617.9	(-0.5)	2.893	0.392	0.952	3	K.SPISVPGGSAL*ISNL*GK#.V
SW:HFC1_HUMAN	H05	7568	2	1597.9	(+0.6)	3.101	0.572	1.000	3	K.SPISVPGGSALISNLGK.V
SW:HFC1_HUMAN	H06	7470	2	1597.9	(-0.1)	2.311	0.445	0.946	3	K.SPISVPGGSALISNLGK.V
SW:HFC1_HUMAN	H05	6224	2	1459.6	(+0.7)	5.032	0.440	1.000	4	K.YSNDLYELQASR.W
SW:HFC1_HUMAN	H05	6216	2	1471.6	(+0.1)	3.068	0.263	0.918	4	K.YSNDL*YEL*QASR.W
SW:HFC1_HUMAN	H06	5974	2	1471.6	(+0.0)	2.759	0.138	0.637	4	K.YSNDL*YEL*QASR.W
SW:HFC1_HUMAN	H08	7165	2	1365.6	(+0.4)	2.624	0.311	0.943	1	R.SPAFVQL*APL*SSK#.V
SW:HM1X_HUMAN	H16	5356	2	1280.4	(+0.9)	3.567	0.429	0.993	6	K.GEHPGLSIGDVAK.K
SW:HM1X_HUMAN	H17	5084	2	1294.4	(+0.5)	3.663	0.320	0.982	6	K.GEHPGL*SIGDVAK#.K
SW:HM1X_HUMAN	H17	5098	2	1280.4	(+0.7)	3.414	0.553	1.000	6	K.GEHPGLSIGDVAK.K
SW:HM1X_HUMAN	H17	5112	1	1280.4	(-1.0)	1.999	0.412	0.000	6	K.GEHPGLSIGDVAK.K
SW:HM1X_HUMAN	H18	5682	2	1294.4	(+0.1)	2.512	0.291	0.839	6	K.GEHPGL*SIGDVAK#.K
SW:HM1X_HUMAN	H16	5500	2	1543.8	(+0.1)	3.267	0.506	0.717	6	K.IK#GEHPGL*SIGDVAK#.K
SW:HM1X_HUMAN	H17	5220	2	1543.8	(-0.1)	4.066	0.523	1.000	6	K.IK#GEHPGL*SIGDVAK#.K
SW:HM1X_HUMAN	H20	5692	2	1543.8	(-0.2)	3.445	0.469	0.695	6	K.IK#GEHPGL*SIGDVAK#.K
SW:HM1X_HUMAN	H17	5126	2	1615.8	(-0.3)	5.255	0.472	1.000	6	K.K#L*GEMWNNTAADDK#.Q
SW:HM1X_HUMAN	H17	4986	2	1479.6	(-0.0)	4.106	0.402	0.986	6	K.L*GEMWNNTAADDK#.Q
SW:HM1X_HUMAN	H17	4076	2	1495.6	(+0.4)	2.960	0.308	0.963	6	K.L*GEM@WNNTAADDK#.Q
SW:HM1X_HUMAN	H17	4994	2	1465.6	(-0.5)	2.847	0.327	0.934	6	K.LGEMWNNTAADDK.Q
SW:HM1X_HUMAN	H16	5562	3	2133.3	(+0.3)	4.067	0.459	0.994	5	K.L*GEMWNNTAADDK#QPYEK#.K
SW:HM1X_HUMAN	H17	5256	2	2111.3	(-0.7)	3.930	0.475	1.000	5	K.LGEMWNNTAADDKQPYEK.K
SW:HM1X_HUMAN	H17	5172	3	2133.3	(+0.6)	3.801	0.379	0.985	5	K.L*GEMWNNTAADDK#QPYEK#.K
SW:HM1X_HUMAN	H17	5400	2	2133.3	(-0.7)	3.609	0.337	0.225	5	K.L*GEMWNNTAADDK#QPYEK#.K
SW:HM1X_HUMAN	H17	4680	2	2149.3	(-0.7)	2.825	0.268	0.059	5	K.L*GEM@WNNTAADDK#QPYEK#.K
SW:HM1X_HUMAN	H18	5200	3	2149.3	(-0.1)	3.721	0.351	0.928	5	K.L*GEM@WNNTAADDK#QPYEK#.K
SW:HM1X_HUMAN	H20	5700	2	1521.8	(-0.5)	3.121	0.488	0.699	6	K.IKGEHPGLSIGDVAK.K
SW:HM4L_HUMAN	H18	6300	2	1678.9	(-0.2)	5.096	0.490	1.000	2	K.KLGEMWNNLNDSEK.Q
SW:HM4L_HUMAN	H18	6292	2	1706.9	(-0.4)	3.012	0.257	0.874	2	K.K#L*GEMWNNL*NDSEK#.Q
SW:HM4L_HUMAN	H17	6278	3	1622.8	(-0.1)	3.859	0.377	0.996	3	K.K#NPEVPVNFVFAEFSK#.K
SW:HM4L_HUMAN	H17	6280	2	1606.8	(+0.8)	2.423	0.230	0.834	3	K.KNPEVPVNFVFAEFSK.K
SW:HM4L_HUMAN	H18	6734	3	1606.8	(+0.1)	5.472	0.354	0.998	3	K.KNPEVPVNFVFAEFSK.K
SW:HM4L_HUMAN	H17	6520	2	1486.6	(+0.3)	2.336	0.316	0.834	3	K.NPEVPVNFVFAEFSK#.K
SW:HM4L_HUMAN	H17	5082	2	1267.4	(+0.6)	3.703	0.365	0.989	2	K.STNPGISIGDVAK#.K
SW:HM4L_HUMAN	H17	5080	2	1259.4	(+0.2)	2.393	0.327	0.877	2	K.STNPGISIGDVAK.K
SW:HM4L_HUMAN	H18	5628	2	1259.4	(+0.9)	2.758	0.585	1.000	2	K.STNPGISIGDVAK.K
SW:HM4L_HUMAN	H18	5646	1	1267.4	(-1.0)	1.963	0.375	0.000	2	K.STNPGISIGDVAK#.K
SW:HMG1_HUMAN	H16	5768	2	1465.6	(+0.4)	3.080	0.482*	0.496	6	K.HPDASVNFSEFSK.K
SW:HMG1_HUMAN	H17	5652	2	1465.6	(-0.0)	3.042	0.360	0.960	6	K.HPDASVNFSEFSK.K
SW:HMG1_HUMAN	H17	5628	2	1473.6	(+0.5)	2.952	0.410*	0.408	6	K.HPDASVNFSEFSK#.K
SW:HMG1_HUMAN	H17	5518	2	1465.6	(+1.0)	2.851	0.414*	0.395	6	K.HPDASVNFSEFSK.K
SW:HMG1_HUMAN	H17	5532	2	1465.6	(-0.3)	2.710	0.421*	0.184	6	K.HPDASVNFSEFSK.K

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:HMG1_HUMAN	H17	3818	3	3880.4	(-0.7)	4.566	0.372	0.988	1	K.KEEEEDEEEDDEEEEEDEEEDDDDE.-
SW:HMG1_HUMAN	H17	3898	3	3880.4	(-0.9)	3.722	0.219	0.583	1	K.KEEEEDEEEDDEEEEEDEEEDDDDE.-
SW:HMG1_HUMAN	H17	5424	2	1609.7	(-0.6)	3.162	0.353*	0.283	6	K.K#HPDASVNFSEFSK#.K
SW:HMG1_HUMAN	H17	5558	2	1593.7	(+0.8)	2.927	0.365	0.978	6	K.KHPDASVNFSEFSK.K
SW:HMG1_HUMAN	H17	5540	2	1473.6	(+0.6)	2.235	0.201	0.700	6	K.HPDASVNFSEFSK#.K
SW:HMG2_HUMAN	H17	5458	2	1473.6	(+0.2)	2.439	0.316*	0.098	3	K.HPDSSVNFAEFSK#.K
SW:HMG2_HUMAN	H17	4666	2	1553.8	(-0.5)	3.950	0.526	1.000	3	K.IKSEHPGLSIGDTAK.K
SW:HMG2_HUMAN	H17	4676	3	1553.8	(-0.9)	3.804	0.405	0.955	3	K.IKSEHPGLSIGDTAK.K
SW:HMG2_HUMAN	H17	4662	2	1575.8	(+0.2)	3.224	0.460	0.644	3	K.IK#SEHPGL*SIGDTAK#.K
SW:HMG2_HUMAN	H17	5316	3	1609.7	(+0.7)	3.915	0.330	0.996	3	K.K#HPDSSVNFAEFSK#.K
SW:HMG2_HUMAN	H17	5322	2	1609.7	(+0.3)	3.001	0.396*	0.231	3	K.K#HPDSSVNFAEFSK#.K
SW:HMG2_HUMAN	H18	5952	2	1593.7	(-0.2)	2.680	0.416*	0.158	3	K.KHPDSSVNFAEFSK.K
SW:HMG2_HUMAN	H18	5950	2	1609.7	(-0.2)	2.663	0.356*	0.137	3	K.K#HPDSSVNFAEFSK#.K
SW:HMG2_HUMAN	H17	5100	2	1394.6	(-0.5)	4.104	0.503	1.000	3	K.KLGEMWSEQSAK.D
SW:HMG2_HUMAN	H17	5068	2	1416.6	(-0.2)	3.111	0.344	0.955	3	K.K#L*GEMWSEQSAK#.D
SW:HMG2_HUMAN	H17	5018	2	1280.4	(+0.5)	3.508	0.611	1.000	3	K.L*GEMWSEQSAK#.D
SW:HMG2_HUMAN	H17	4926	2	1280.4	(+0.3)	3.110	0.574	1.000	3	K.L*GEMWSEQSAK#.D
SW:HMG2_HUMAN	H17	4078	2	1296.4	(-0.1)	2.572	0.375	0.941	3	K.L*GEM@WSEQSAK#.D
SW:HMG2_HUMAN	H17	3978	2	1296.4	(-0.3)	2.300	0.191	0.566	3	K.L*GEM@WSEQSAK#.D
SW:HMG2_HUMAN	H18	4320	2	1296.4	(-0.7)	2.766	0.347	0.829	3	K.L*GEM@WSEQSAK#.D
SW:HMG2_HUMAN	H18	5478	2	1266.4	(+0.2)	2.261	0.108	0.324	3	K.LGEMWSEQSAK.D
SW:HMG2_HUMAN	H17	4402	2	1326.4	(+0.5)	2.901	0.372	0.977	3	K.SEHPGL*SIGDTAK#.K
SW:HMG2_HUMAN	H17	4410	1	1312.4	(-0.0)	2.717	0.416	0.063	3	K.SEHPGLSIGDTAK.K
SW:HMG2_HUMAN	H17	4480	2	1312.4	(-0.2)	2.545	0.294	0.867	3	K.SEHPGLSIGDTAK.K
SW:HMG2_HUMAN	H17	4328	1	1312.4	(-1.0)	2.124	0.335	0.000	3	K.SEHPGLSIGDTAK.K
SW:HMG2_HUMAN	H21	4682	2	1312.4	(+0.9)	2.864	0.461	0.990	3	K.SEHPGLSIGDTAK.K
SW:HMG2_HUMAN	H22	5860	2	1609.7	(+0.3)	2.871	0.311*	0.192	3	K.K#HPDSSVNFAEFSK#.K
SW:HS72_HUMAN	H09	7303	2	1481.7	(+0.2)	3.603	0.422	0.728	5	R.ARFEELNADLFR.G
SW:HS72_HUMAN	H09	7293	2	1493.7	(+1.0)	2.307	0.331	0.371	5	R.ARFEEL*NADL*FR.G
SW:HS72_HUMAN	H09	7309	2	1266.4	(+0.5)	2.840	0.252	0.954	5	R.FEEL*NADL*FR.G
SW:HS72_HUMAN	H09	7199	2	1082.2	(-0.2)	2.679	0.402	0.970	7	K.LLQDFFNK.E
SW:HS72_HUMAN	H09	4523	2	1692.7	(-0.6)	4.306	0.472	1.000	5	K.STAGDTHLGGEDFDNR.M
SW:HS72_HUMAN	H09	4603	2	1692.7	(+0.9)	4.173	0.452	1.000	5	K.STAGDTHLGGEDFDNR.M
SW:HS72_HUMAN	H09	4439	2	1692.7	(+0.9)	3.938	0.442	0.993	5	K.STAGDTHLGGEDFDNR.M
SW:HS72_HUMAN	H09	4457	2	1698.7	(+0.9)	3.571	0.364	0.987	5	K.STAGDTHL*GGEDFDNR.M
SW:HS72_HUMAN	H09	4599	2	1698.7	(-1.0)	3.093	0.455	0.933	5	K.STAGDTHL*GGEDFDNR.M
SW:HS72_HUMAN	H09	4519	2	1698.7	(-0.9)	3.078	0.421	0.914	5	K.STAGDTHL*GGEDFDNR.M
SW:HS72_HUMAN	H09	1953	1	793.9	(-0.1)	2.029	0.152	0.000	7	K.DNNL*L*GK#.F
SW:HS7C_HUMAN	H09	6903	2	1200.4	(-0.3)	2.587	0.279	0.868	2	K.DAGTIAGLNVL.R
SW:HS7C_HUMAN	H09	5289	2	1263.4	(+0.4)	3.539	0.514	1.000	2	R.FDDAVVQSDMK#.H
SW:HS7C_HUMAN	H09	11823	3	2515.8	(+1.0)	4.854	0.510	1.000	3	R.GVPQIEVTFDIDANGILNNSAVDK.S
SW:HS7C_HUMAN	H09	12661	3	2515.8	(+0.5)	4.835	0.391	0.999	3	R.GVPQIEVTFDIDANGILNNSAVDK.S
SW:HS7C_HUMAN	H09	12559	3	2515.8	(+0.7)	4.442	0.449	0.999	3	R.GVPQIEVTFDIDANGILNNSAVDK.S
SW:HS7C_HUMAN	H09	12523	3	2529.8	(+0.8)	4.423	0.439	0.996	3	R.GVPQIEVTFDIDANGIL*NNSAVDK#.S
SW:HS7C_HUMAN	H09	13361	3	2515.8	(+0.4)	4.361	0.469	0.999	3	R.GVPQIEVTFDIDANGILNNSAVDK.S
SW:HS7C_HUMAN	H09	13457	3	2515.8	(+0.0)	4.347	0.451	0.998	3	R.GVPQIEVTFDIDANGILNNSAVDK.S
SW:HS7C_HUMAN	H09	12451	3	2529.8	(+0.3)	4.320	0.541	0.999	3	R.GVPQIEVTFDIDANGIL*NNSAVDK#.S
SW:HS7C_HUMAN	H09	11327	3	2529.8	(+0.9)	4.216	0.430	0.996	3	R.GVPQIEVTFDIDANGIL*NNSAVDK#.S
SW:HS7C_HUMAN	H09	13287	3	2515.8	(-0.1)	4.175	0.460	0.999	3	R.GVPQIEVTFDIDANGILNNSAVDK.S
SW:HS7C_HUMAN	H09	13339	3	2529.8	(+1.0)	4.118	0.525	0.995	3	R.GVPQIEVTFDIDANGIL*NNSAVDK#.S
SW:HS7C_HUMAN	H09	11287	3	2515.8	(+0.9)	4.091	0.425	0.999	3	R.GVPQIEVTFDIDANGILNNSAVDK.S
SW:HS7C_HUMAN	H09	12281	3	2529.8	(+0.7)	4.083	0.362	0.997	3	R.GVPQIEVTFDIDANGIL*NNSAVDK#.S
SW:HS7C_HUMAN	H09	12911	3	2515.8	(+0.3)	3.994	0.403	0.995	3	R.GVPQIEVTFDIDANGILNNSAVDK.S
SW:HS7C_HUMAN	H09	13553	3	2529.8	(-0.1)	3.992	0.421	0.997	3	R.GVPQIEVTFDIDANGIL*NNSAVDK#.S
SW:HS7C_HUMAN	H09	12259	3	2515.8	(+0.2)	3.985	0.275	0.936	3	R.GVPQIEVTFDIDANGILNNSAVDK.S
SW:HS7C_HUMAN	H09	11407	3	2529.8	(-0.2)	3.957	0.352	0.984	3	R.GVPQIEVTFDIDANGIL*NNSAVDK#.S
SW:HS7C_HUMAN	H09	11755	3	2529.8	(+1.0)	3.928	0.430	0.999	3	R.GVPQIEVTFDIDANGIL*NNSAVDK#.S
SW:HS7C_HUMAN	H09	11471	3	2515.8	(-0.4)	3.812	0.435	0.997	3	R.GVPQIEVTFDIDANGILNNSAVDK.S
SW:HS7C_HUMAN	H09	11753	3	2515.8	(-0.4)	3.756	0.452	0.998	3	R.GVPQIEVTFDIDANGILNNSAVDK.S
SW:HS7C_HUMAN	H09	12861	3	2529.8	(-0.8)	3.748	0.341	0.960	3	R.GVPQIEVTFDIDANGIL*NNSAVDK#.S
SW:HS7C_HUMAN	H09	13413	3	2529.8	(-0.1)	3.717	0.373	0.990	3	R.GVPQIEVTFDIDANGIL*NNSAVDK#.S
SW:HS7C_HUMAN	H09	7173	2	1654.9	(+0.1)	2.984	0.441	0.609	2	K.HWPFMVNDAGRPK.V
SW:HS7C_HUMAN	H09	6803	2	1244.5	(+0.7)	2.980	0.385	0.986	2	R.MVNHFIAEFK#.R

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:HS7C_HUMAN	H09	6485	2	1260.5	(+0.6)	2.907	0.322	0.975	2	R.M@VNHFIAEFK#R
SW:HS7C_HUMAN	H09	1693	2	1746.8	(+0.8)	3.256	0.546	1.000	5	K.NQTAEKEEFEHQK.E
SW:HS7C_HUMAN	H09	1697	2	1762.8	(-1.0)	2.335	0.391	0.103	5	K.NQTAEK#EEFEHQK#.E
SW:HS7C_HUMAN	H09	6131	2	1650.8	(+0.7)	3.741	0.589	0.999	1	K.NQVAMNPTNTVFDK.R
SW:HS7C_HUMAN	H09	6133	2	1658.8	(+0.6)	3.329	0.450	0.991	1	K.NQVAMNPTNTVFDK#.R
SW:HS7C_HUMAN	H09	6727	2	1318.5	(+0.3)	2.827	0.505	0.984	5	K.NSL*ESYAFNMK#.A
SW:HS7C_HUMAN	H09	5913	2	1334.5	(+0.3)	2.474	0.317	0.887	5	K.NSL*ESYAFNM@K#.A
SW:HS7C_HUMAN	H09	7645	2	2776.0	(-0.9)	2.530	0.396	0.819	3	K.QTQTFTTYSNQPGLVLIQVYEGE.R
SW:HS7C_HUMAN	H09	5445	2	1419.6	(-0.6)	3.703	0.449	0.918	2	R.RFDDAVVQSDMK#.H
SW:HS7C_HUMAN	H09	5421	2	1419.6	(+0.7)	3.486	0.456	0.993	2	R.RFDDAVVQSDMK#.H
SW:HS7C_HUMAN	H09	5449	2	1411.6	(-0.2)	3.283	0.391	0.935	2	R.RFDDAVVQSDMK.H
SW:HS7C_HUMAN	H09	6865	2	1647.9	(-0.1)	4.304	0.470	0.999	2	K.SFYPEEVSSM@VL*TK#.M
SW:HS7C_HUMAN	H09	7583	2	1617.9	(+0.5)	3.131	0.469	0.992	2	K.SFYPEEVSSMVLTK.M
SW:HS7C_HUMAN	H09	7587	2	1631.9	(+0.2)	2.522	0.294	0.834	2	K.SFYPEEVSSMVL*TK#.M
SW:HS7C_HUMAN	H09	8841	2	2275.5	(+0.6)	5.230	0.602	0.999	2	K.SINPDEAVAYGAAVQAAIL*SGDK#.S
SW:HS7C_HUMAN	H09	8835	2	2261.5	(-0.4)	4.217	0.458	1.000	2	K.SINPDEAVAYGAAVQAAILSGDK.S
SW:HS7C_HUMAN	H09	12533	3	2261.5	(+0.5)	4.061	0.491	0.999	2	K.SINPDEAVAYGAAVQAAILSGDK.S
SW:HS7C_HUMAN	H09	12749	3	2261.5	(+0.6)	3.827	0.459	0.998	2	K.SINPDEAVAYGAAVQAAILSGDK.S
SW:HS7C_HUMAN	H09	12923	3	2261.5	(+0.7)	3.822	0.451	0.999	2	K.SINPDEAVAYGAAVQAAILSGDK.S
SW:HS7C_HUMAN	H09	12455	3	2261.5	(-0.3)	3.821	0.457	0.998	2	K.SINPDEAVAYGAAVQAAILSGDK.S
SW:HS7C_HUMAN	H09	11309	3	2261.5	(+0.7)	3.799	0.446	0.999	2	K.SINPDEAVAYGAAVQAAILSGDK.S
SW:HS7C_HUMAN	H09	9069	3	2261.5	(+1.0)	3.773	0.448	0.999	2	K.SINPDEAVAYGAAVQAAILSGDK.S
SW:HS7C_HUMAN	H09	13357	3	2261.5	(+0.7)	3.735	0.548	1.000	2	K.SINPDEAVAYGAAVQAAILSGDK.S
SW:HS7C_HUMAN	H09	6199	2	1488.7	(+0.8)	4.480	0.495	1.000	2	K.SQIHDIIVL*VGGSTR.I
SW:HS7C_HUMAN	H09	6197	2	1482.7	(+0.7)	3.963	0.471	1.000	2	K.SQIHDIIVLVGGSTR.I
SW:HS7C_HUMAN	H19	6600	2	1200.4	(+0.4)	2.826	0.289	0.958	2	K.DAGTIAGLNLVLR.I
SW:HS9A_HUMAN	H07	5556	2	1417.5	(+1.0)	2.661	0.176	0.836	14	K.EGLELPEDEEEK.K
SW:HS9A_HUMAN	H07	4862	2	1292.4	(+0.7)	3.021	0.316	0.974	6	R.ELISNSSDALDK.I
SW:HS9A_HUMAN	H07	6852	2	1526.7	(+0.4)	2.293	0.217	0.772	13	R.GVVDSEDL*PL*NISR.E
SW:HS9A_HUMAN	H08	6967	2	1514.7	(+0.9)	3.897	0.439*	0.738	13	R.GVVDSEDLPLNISR.E
SW:HS9A_HUMAN	H08	6977	2	1526.7	(+0.0)	2.967	0.226	0.843	13	R.GVVDSEDL*PL*NISR.E
SW:HS9A_HUMAN	H07	5364	2	1233.4	(+0.6)	2.252	0.318	0.929	7	K.HIYYITGETK#.D
SW:HS9A_HUMAN	H08	5351	2	1225.4	(+0.4)	2.464	0.410	0.981	7	K.HIYYITGETK.D
SW:HS9A_HUMAN	H07	8716	2	1780.1	(+0.4)	2.753	0.397	0.978	6	K.HSQFIGYPITLFEVEK.E
SW:HS9A_HUMAN	H07	6778	2	1528.7	(+0.9)	4.337	0.467	0.999	13	K.SLTNDWEDHLAVK.H
SW:HS9A_HUMAN	H08	7009	2	1243.4	(+0.6)	2.391	0.428	0.978	15	K.ADLINNLGTIAK.S
SW:IF16_HUMAN	H07	1880	2	921.0	(+0.8)	2.827	0.192	0.330	5	K.FRGDAGLGK.L
SW:IF16_HUMAN	H06	6182	2	1673.8	(-0.2)	4.183	0.527	1.000	4	R.GEFTYYEIQDNTGK#.M
SW:IF16_HUMAN	H07	6118	2	1665.8	(+0.7)	3.527	0.523	1.000	4	R.GEFTYYEIQDNTGK.M
SW:IF16_HUMAN	H07	6116	2	1673.8	(+0.6)	3.469	0.490	0.999	4	R.GEFTYYEIQDNTGK#.M
SW:IF16_HUMAN	H06	6806	2	1363.5	(+0.6)	2.558	0.354	0.969	6	K.GLEVINDYHFR.M
SW:IF16_HUMAN	H06	6790	2	1369.5	(+0.1)	2.539	0.372	0.944	6	K.GL*EVINDYHFR.M
SW:IF16_HUMAN	H07	6846	2	1363.5	(-0.4)	2.471	0.380	0.941	6	K.GLEVINDYHFR.M
SW:IF16_HUMAN	H02	7968	2	1848.1	(+0.9)	2.713	0.434	0.983	5	K.IFEDIPTLEDLAETLK.K
SW:IF16_HUMAN	H06	9296	2	1976.3	(+0.2)	3.929	0.298	0.504	5	K.IFEDIPTLEDLAETLKK.E
SW:IF16_HUMAN	H07	9438	2	1976.3	(+0.4)	2.612	0.433	0.660	5	K.IFEDIPTLEDLAETLKK.E
SW:IF16_HUMAN	H07	7046	2	1204.4	(+0.8)	2.487	0.314	0.950	6	K.IQIADL*MEEK#.F
SW:IF16_HUMAN	H07	7406	2	1460.7	(+0.3)	2.404	0.340	0.889	4	K.L*ISEMHSFIQK#.K
SW:IF16_HUMAN	H07	6606	2	1476.7	(+0.4)	2.324	0.211	0.780	4	K.L*ISEM@HSFIQK#.K
SW:IF16_HUMAN	H01	5352	3	2119.3	(+1.0)	5.205	0.271	0.957	4	R.LKTEPEEVSIEDSAQSCLK.E
SW:IF16_HUMAN	H01	5364	3	2147.3	(-0.7)	5.196	0.381	0.977	4	R.L*K#TEPEEVSIEDSAQSCLK#.E
SW:IF16_HUMAN	H06	6112	3	2147.3	(+0.1)	5.020	0.256	0.872	4	R.L*K#TEPEEVSIEDSAQSCLK#.E
SW:IF16_HUMAN	H07	6048	2	2147.3	(-0.6)	4.934	0.445	1.000	4	R.L*K#TEPEEVSIEDSAQSCLK#.E
SW:IF16_HUMAN	H07	6044	2	2119.3	(-0.5)	4.540	0.579	1.000	4	R.LKTEPEEVSIEDSAQSCLK.E
SW:IF16_HUMAN	H07	9760	2	2141.4	(-0.3)	2.974	0.436	0.973	5	R.NGFLEVYPFTLVADVADR.N
SW:IF16_HUMAN	H07	9988	2	2153.4	(-0.8)	2.669	0.428	0.878	5	R.NGFL*EVYPFTLVADVADR.N
SW:IF16_HUMAN	H07	1276	2	1168.2	(+0.5)	2.375	0.274	0.891	5	K.TEGAEATPGAQK#.R
SW:IF16_HUMAN	H07	1354	2	1168.2	(+0.6)	2.271	0.402	0.962	5	K.TEGAEATPGAQK#.R
SW:IF16_HUMAN	H07	6228	3	2158.5	(+0.7)	3.862	0.288	0.899	5	K.VLSTTKPFYETPEMEKK.I
SW:IF16_HUMAN	H08	6187	3	2147.3	(+0.6)	4.389	0.298	0.957	4	R.L*K#TEPEEVSIEDSAQSCLK#.E
SW:IF2A_HUMAN	H16	6476	2	1277.4	(+1.0)	2.787	0.310	0.971	2	K.DEQL*ESL*FQR.T
SW:IF2A_HUMAN	H16	4988	2	1085.2	(+0.6)	2.560	0.187	0.879	2	R.EVLINNINR.R
SW:IF2A_HUMAN	H16	5000	2	1091.2	(+0.7)	2.281	0.154	0.732	2	R.EVL*INNINR.R

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:IF2A_HUMAN	H15	8416	3	3192.5	(+0.7)	3.995	0.499	0.998	2	K.HAVSDPSILDSLNLNEDEREVLINNINR.R
SW:IF2A_HUMAN	H15	5664	2	1203.4	(+0.5)	2.463	0.512	0.990	2	R.HVAEVL*EYTK#.D
SW:IF2A_HUMAN	H15	7922	3	2461.7	(+0.2)	4.918	0.551	0.999	2	R.HVAEVL*EYTK#DEQL*ESL*FQR.T
SW:IF2A_HUMAN	H16	7364	3	2461.7	(+0.9)	5.091	0.545	1.000	2	R.HVAEVL*EYTK#DEQL*ESL*FQR.T
SW:IF2A_HUMAN	H15	5684	2	1245.4	(+0.0)	2.883	0.353	0.958	2	K.RPGYGAYDAFK.H
SW:IF2A_HUMAN	H16	5234	2	1245.4	(+0.8)	3.065	0.349	0.984	2	K.RPGYGAYDAFK.H
SW:IF2A_HUMAN	H15	8820	2	1547.9	(+0.7)	3.106	0.478	0.989	2	R.TEGLSVLSQAMAVIK.E
SW:IF2A_HUMAN	H15	8814	2	1567.9	(+0.1)	2.368	0.105	0.251	2	R.TEGL*SVL*SQAMAVIK#.E
SW:IF2A_HUMAN	H16	8160	2	1547.9	(-0.3)	3.070	0.407	0.968	2	R.TEGLSVLSQAMAVIK.E
SW:IF2A_HUMAN	H16	2274	2	1349.4	(-0.1)	2.293	0.435	0.944	2	K.VVTDTDDELAR.Q
SW:IF2A_HUMAN	H15	5544	2	1215.4	(+0.6)	2.486	0.418	0.983	2	R.YVMTTTTLLER.T
SW:IF2A_HUMAN	H15	5546	2	1221.4	(+0.2)	2.227	0.349	0.899	2	R.YVMTTTTL*ER.T
SW:IF2A_HUMAN	H21	4034	2	1355.4	(+0.6)	2.865	0.486	0.992	2	K.VVTDTDDEL*AR.Q
SW:IF2B_HUMAN	H12	2392	2	2347.4	(+0.5)	3.109	0.532	0.870	2	K.EVEPEPTEDKDLEADEEDTR.K
SW:IF2B_HUMAN	H12	6650	2	1373.5	(+0.7)	3.733	0.477	1.000	2	K.IFDIDEAEEGVK#.D
SW:IF2B_HUMAN	H12	6636	2	1365.5	(+0.7)	2.988	0.381	0.985	2	K.IFDIDEAEEGVK.D
SW:IF2B_HUMAN	H13	6550	2	1365.5	(+0.7)	3.691	0.359	0.991	2	K.IFDIDEAEEGVK.D
SW:IF2B_HUMAN	H13	6556	2	1373.5	(+0.9)	3.481	0.463	1.000	2	K.IFDIDEAEEGVK#.D
SW:IF2B_HUMAN	H12	6568	2	1509.7	(+0.4)	3.994	0.482	1.000	2	K.K#IFDIDEAEEGVK#.D
SW:IF2B_HUMAN	H13	4778	2	2347.4	(-0.9)	2.635	0.361	0.125	2	K.EVEPEPTEDKDLEADEEDTR.K
SW:IF2G_HUMAN	H11	5034	2	859.0	(+0.7)	2.248	0.304	0.912	1	K.GGVAGGSILK.G
SW:IF2G_HUMAN	H11	6118	2	1519.8	(+0.5)	3.872	0.364	0.779	1	K.VGQEIEVRPGIVSK#.D
SW:IF2G_HUMAN	H11	6112	2	1511.8	(+0.8)	3.559	0.439	0.845	1	K.VGQEIEVRPGIVSK.D
SW:IF2G_HUMAN	H12	5740	2	1511.8	(+0.6)	4.292	0.431	0.997	1	K.VGQEIEVRPGIVSK.D
SW:IF2G_HUMAN	H21	5100	2	1134.3	(+0.6)	2.468	0.311	0.945	1	R.QDLTTLDVDK.L
SW:IF2P_HUMAN	H04	5373	2	1269.5	(+0.7)	2.762	0.332	0.970	5	K.LLQAQGVVPSK.D
SW:IF2P_HUMAN	H04	5433	2	1445.6	(+0.9)	3.000	0.472	0.991	5	K.VTVDTGVIPASEEK.A
SW:IF2P_HUMAN	H08	6687	2	1260.4	(+0.7)	2.200	0.469	0.981	8	R.HFEATDILVSK.I
SW:IF41_HUMAN	H13	5076	2	1395.5	(+1.0)	4.911	0.608	1.000	4	K.GYDVIAQAQSGTGK.T
SW:IF41_HUMAN	H13	5078	2	1403.5	(+0.2)	4.041	0.575	1.000	4	K.GYDVIAQAQSGTGK#.T
SW:IF41_HUMAN	H13	8380	2	1556.8	(+0.9)	4.563	0.509	1.000	5	K.MFVLDEADEMLSR.G
SW:IF41_HUMAN	H13	7746	2	1502.7	(+0.8)	3.903	0.388	0.851	1	R.GFKDQIYDIFQK.L
SW:IF5A_HUMAN	H20	8820	2	2581.8	(+0.0)	5.325	0.564	1.000	2	R.NDFQLIGIQDGYLSLLQDSGEVR.E
SW:IF5A_HUMAN	H20	8966	2	2581.8	(-0.0)	4.745	0.483	0.998	2	R.NDFQLIGIQDGYLSLLQDSGEVR.E
SW:IF5A_HUMAN	H20	8970	2	2605.8	(+0.3)	4.049	0.547	0.979	2	R.NDFQL*IGIQDGYL*SL*L*QDSGEVR.E
SW:IF5A_HUMAN	H20	8728	2	2762.0	(-0.4)	2.593	0.191	0.513	2	K.RNDFQL*IGIQDGYL*SL*L*QDSGEVR.E
SW:IF5A_HUMAN	H20	7534	2	1313.6	(+0.2)	3.152	0.512	1.000	4	K.VHL*VGIDIFTGK#.K
SW:IF5A_HUMAN	H20	5566	2	927.1	(+0.4)	2.218	0.330	0.943	4	R.K#NGFVVL*K#.G
SW:IKAR_HUMAN	H08	5311	2	1310.4	(+0.2)	3.088	0.394	0.969	2	R.DQGSSAL*SGVGGIR.L
SW:IKAR_HUMAN	H09	5361	2	1310.4	(-0.3)	3.027	0.295	0.923	2	R.DQGSSAL*SGVGGIR.L
SW:IKAR_HUMAN	H09	4931	2	1634.7	(+0.0)	3.420	0.440	0.978	2	K.GL*SDTPYDSSASYEK#.E
SW:IKAR_HUMAN	H10	5137	2	1634.7	(-0.9)	3.748	0.460	0.953	2	K.GL*SDTPYDSSASYEK#.E
SW:IKAR_HUMAN	H12	2478	2	1634.7	(-0.6)	2.738	0.406	0.950	2	K.GL*SDTPYDSSASYEK#.E
SW:IKAR_HUMAN	H10	7057	2	1675.9	(+0.3)	4.174	0.410	0.986	1	R.SGL*YI*TNHIAPHAR.N
SW:IKAR_HUMAN	H09	7647	2	1927.1	(+0.1)	3.724	0.559	1.000	1	R.SNNSAQDSAVENLLLLSK.A
SW:IKAR_HUMAN	H10	7785	2	1959.1	(-0.4)	3.571	0.448	0.983	1	R.SNNSAQDSAVENL*L*L*SK#.A
SW:IKAR_HUMAN	H14	7615	2	1927.1	(+0.4)	2.867	0.483	0.955	1	R.SNNSAQDSAVENLLLLSK.A
SW:ILF3_HUMAN	H06	6038	2	1320.4	(+0.9)	3.031	0.407	0.989	6	K.AVSDWIDEQEK.G
SW:ILF3_HUMAN	H06	3754	2	1204.3	(+1.0)	2.366	0.336	0.952	13	K.EATDAIGHL*DR.Q
SW:ILF3_HUMAN	H06	3990	2	1204.3	(+0.6)	2.312	0.254	0.855	13	K.EATDAIGHL*DR.Q
SW:ILF3_HUMAN	H06	4010	2	1198.3	(+0.9)	2.277	0.150	0.656	13	K.EATDAIGHLDR.Q
SW:ILF3_HUMAN	H06	3636	2	1198.3	(+0.9)	2.273	0.369	0.959	13	K.EATDAIGHLDR.Q
SW:ILF3_HUMAN	H08	4125	2	1198.3	(+1.0)	2.426	0.292	0.933	13	K.EATDAIGHLDR.Q
SW:ILF3_HUMAN	H06	5226	2	1369.5	(+0.8)	3.568	0.310	0.983	14	R.EDITQSAQHALR.L
SW:ILF3_HUMAN	H06	5222	2	1375.5	(+1.0)	3.432	0.457	0.994	14	R.EDITQSAQHAL*R.L
SW:ILF3_HUMAN	H07	5214	2	1369.5	(-0.1)	3.079	0.301	0.942	14	R.EDITQSAQHALR.L
SW:ILF3_HUMAN	H07	5210	2	1375.5	(+0.6)	2.940	0.466	0.992	14	R.EDITQSAQHAL*R.L
SW:ILF3_HUMAN	H08	5201	2	1375.5	(+0.4)	2.788	0.423	0.987	14	R.EDITQSAQHAL*R.L
SW:ILF3_HUMAN	H06	5138	3	3263.2	(+0.1)	6.141	0.546	1.000	1	K.GYNHGQGSYSYSNSYNSPGGGGSDYNYESK#.F

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ILF3_HUMAN	H07	5378	2	1302.6	(+1.0)	2.950	0.171	0.255	13	R.LNLQKPLQYK.L
SW:ILF3_HUMAN	H06	4732	2	1088.2	(+0.8)	2.318	0.255	0.896	23	K.NPVMEL*NEK#.R
SW:ILF3_HUMAN	H07	5188	2	1601.8	(+0.7)	3.518	0.290	0.600	12	K.SIGTANRPMGAGEALR.R
SW:ILF3_HUMAN	H07	5182	2	1607.8	(+0.6)	3.264	0.371	0.704	12	K.SIGTANRPMGAGEAL*R.R
SW:ILF3_HUMAN	H06	4912	2	1093.3	(+0.1)	2.460	0.388	0.933	14	K.VL*GM@DPL*PSK#.M
SW:ILF3_HUMAN	H07	4988	2	1093.3	(+0.3)	2.201	0.373	0.875	14	K.VL*GM@DPL*PSK#.M
SW:ILF3_HUMAN	H06	6138	2	1456.6	(+0.0)	3.828	0.417	0.985	17	K.VL*QDMGL*PTGAEGR.D
SW:ILF3_HUMAN	H07	4876	2	1472.6	(-0.0)	3.172	0.297	0.930	17	K.VL*QDM@GL*PTGAEGR.D
SW:ILF3_HUMAN	H07	6094	2	1444.6	(-1.0)	2.453	0.330	0.691	17	K.VLQDMGLPTGAEGR.D
SW:ILF3_HUMAN	H08	6199	2	1456.6	(-0.2)	3.506	0.254	0.926	17	K.VL*QDMGL*PTGAEGR.D
SW:ILF3_HUMAN	H06	4652	2	1606.7	(+0.5)	2.289	0.342	0.352	23	K.YEL*ISETGGSMDK#R.F
SW:ILF3_HUMAN	H07	4716	2	1592.7	(-0.0)	3.794	0.484	1.000	23	K.YELISETGGSHDKR.F
SW:ILF3_HUMAN	H07	4702	2	1606.7	(-0.2)	3.104	0.364	0.485	23	K.YEL*ISETGGSMDK#R.F
SW:ILF3_HUMAN	H07	4782	2	1606.7	(-0.5)	2.711	0.370	0.384	23	K.YEL*ISETGGSMDK#R.F
SW:ILF3_HUMAN	H08	4043	2	1198.3	(+1.0)	2.201	0.174	0.570	13	K.EATDAIGHLDR.Q
SW:IMA2_HUMAN	H11	7316	2	1689.8	(+0.7)	4.334	0.544	1.000	3	R.NNQGTVNWSVDDIVK.G
SW:IMA2_HUMAN	H11	7314	2	1697.8	(-0.0)	3.542	0.408	0.977	3	R.NNQGTVNWSVDDIVK#.G
SW:IMA2_HUMAN	H11	8318	2	1550.9	(+0.8)	2.508	0.395	0.970	3	K.LLGASELPIVTPALR.A
SW:IMB1_HUMAN	H07	8430	2	1606.9	(+0.8)	3.638	0.431	0.993	1	K.LAATNALLNSLEFTK.A
SW:IMB1_HUMAN	H07	2384	2	1898.0	(+0.6)	2.376	0.265	0.200	1	K.L*L*ETDRPDGHQNNL*R.S
SW:IMB1_HUMAN	H07	9132	2	1452.7	(+0.9)	2.698	0.315	0.957	1	K.SNEIL*TAIQGMR.K
SW:IMB1_HUMAN	H07	5652	2	1577.7	(+0.2)	3.017	0.158	0.082	1	K.TVSPDRL*EL*EAAQK#.F
SW:IMB1_HUMAN	H07	8750	2	1615.0	(+0.8)	3.780	0.506	1.000	1	K.YMEAFKPFGLGILK.N
SW:IMB1_HUMAN	H07	8740	2	1643.0	(+0.6)	3.364	0.369	0.708	1	K.YMEAFK#PFL*GIGL*K#.N
SW:IMB1_HUMAN	H07	2412	2	1880.0	(-0.0)	2.363	0.247	0.083	1	K.LLETTDRPDGHQNNLR.S
SW:K052_HUMAN	H06	9182	3	2580.9	(+0.3)	4.405	0.354	0.993	6	K.RFPDGIPL*L*DPIDDMGIQDQGL*K#.K
SW:K052_HUMAN	H06	10396	2	2342.7	(-0.6)	3.177	0.358	0.472	6	K.SNVKPNSELDPLVVEVLLR.C
SW:K117_HUMAN	H12	5224	3	2316.4	(+0.6)	4.057	0.494	0.998	3	R.NEEEEESTSQIERPL*SQEPAK#.K
SW:K117_HUMAN	H12	4910	2	1497.6	(-0.0)	2.873	0.468	0.980	3	K.IL*DDTETDVVSQR.K
SW:K6PP_HUMAN	H08	6277	2	1433.5	(+0.6)	2.783	0.434	0.986	4	R.DL*QSNVEHL*TEK#.M
SW:K6PP_HUMAN	H08	8105	2	2120.3	(-0.0)	2.893	0.446	0.973	3	K.EIGWTDVGGWTGQGSILGTK.R
SW:K6PP_HUMAN	H08	5241	2	1059.2	(+0.7)	2.286	0.236	0.865	1	K.FLEHLSGAGK.A
SW:KF22_HUMAN	H09	6275	2	1501.7	(+0.6)	3.108	0.338	0.979	5	R.KLESLDALEPEEK.A
SW:KF22_HUMAN	H09	8473	2	1596.9	(+0.9)	4.361	0.409	0.994	3	K.VLDLLDPASGDLVIR.E
SW:KF22_HUMAN	H09	8465	2	1620.9	(-0.2)	2.692	0.163	0.605	3	K.VL*DL*L*DPASGDL*VIR.E
SW:KF2C_HUMAN	H07	5970	2	1512.7	(+0.6)	3.368	0.458	0.993	4	K.DNLPLQENVTIQK.Q
SW:KF2C_HUMAN	H07	5964	2	1532.7	(-0.3)	2.461	0.169	0.533	4	K.DNL*PL*QENVTIQK#.Q
SW:KF2C_HUMAN	H08	6087	2	1512.7	(+0.7)	3.804	0.469	1.000	4	K.DNLPLQENVTIQK.Q
SW:KF2C_HUMAN	H08	6249	2	1245.5	(+0.2)	2.270	0.309	0.833	5	K.K#EIDVISIPSK#.C
SW:KF2C_HUMAN	H08	6255	2	1229.5	(+0.6)	2.202	0.411	0.968	5	K.KEIDVISIPSK.C
SW:KF4A_HUMAN	H05	4060	2	1159.3	(+0.4)	2.509	0.385	0.978	5	R.IILTEQANEK.M
SW:KF4A_HUMAN	H05	3972	2	1159.3	(+0.4)	2.397	0.344	0.962	5	R.IILTEQANEK.M
SW:KF4A_HUMAN	H05	4996	2	1334.4	(+0.8)	2.677	0.333	0.966	7	R.SSDAFTTQHALR.Q
SW:KF4A_HUMAN	H05	5014	2	1340.4	(+0.6)	2.544	0.493	0.989	7	R.SSDAFTTQHAL*R.Q
SW:KF4A_HUMAN	H05	2158	2	1116.2	(+0.2)	2.325	0.226	0.712	5	R.SAQIADL*QQK#.L
SW:KFC1_HUMAN	H08	3949	2	1402.5	(+0.7)	2.648	0.441	0.984	3	R.AGPGSEELTVTNAR.Y
SW:KFC1_HUMAN	H09	4511	2	1402.5	(+0.0)	2.699	0.393	0.952	3	R.AGPGSEELTVTNAR.Y
SW:KFC1_HUMAN	H08	4477	2	1113.3	(+0.3)	2.932	0.362	0.947	3	K.APSQLPLSGSR.L
SW:KFC1_HUMAN	H08	4459	2	1125.3	(+0.4)	2.603	0.327	0.957	3	K.APSQL*PL*SGSR.L
SW:KFC1_HUMAN	H08	4397	2	1113.3	(-0.3)	2.472	0.439	0.965	3	K.APSQLPLSGSR.L
SW:KFC1_HUMAN	H08	4379	2	1125.3	(+0.5)	2.317	0.273	0.857	3	K.APSQL*PL*SGSR.L
SW:KFC1_HUMAN	H08	6081	2	1195.4	(+1.0)	2.592	0.405	0.980	3	R.LDPGLALGPPER.E
SW:KFC1_HUMAN	H08	8355	3	3103.6	(+0.5)	4.054	0.416	0.987	3	R.VRPVLPGEPTPPGGLLLFPSGPGGSPDPTR.L
SW:KFC1_HUMAN	H09	8353	3	3103.6	(+0.7)	3.808	0.341	0.942	3	R.VRPVLPGEPTPPGGLLLFPSGPGGSPDPTR.L
SW:KFC1_HUMAN	H09	4695	2	1113.3	(+0.4)	2.245	0.265	0.879	3	K.APSQLPLSGSR.L
SW:KG09_HUMAN	H06	8844	2	1580.8	(+0.5)	3.755	0.496	1.000	4	R.EEELFLPYDLK.R

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:KG09_HUMAN	H06	8850	2	1612.8	(-0.8)	2.379	0.310	0.602	4	R.EEL*EAL*FL*PYDL*K#.R
SW:KG09_HUMAN	H06	9686	2	1750.9	(+0.4)	3.623	0.478	0.994	3	K.QDDPFELFIAATNIR.Y
SW:KG09_HUMAN	H06	9134	3	2154.3	(+0.6)	4.158	0.490	1.000	4	K.TLTDEDEADQGGWLAAFWK.D
SW:KG09_HUMAN	H06	5242	2	1114.3	(+0.7)	2.237	0.257	0.878	4	R.ILIENGVAER.Q
SW:KPY1_HUMAN	H10	7323	2	1643.8	(+0.8)	4.681	0.596	1.000	15	K.DPVQEAWAEDVDLR.V
SW:KPY1_HUMAN	H10	7325	2	1649.8	(+0.5)	3.960	0.498	0.999	15	K.DPVQEAWAEDVDL*R.V
SW:KPY1_HUMAN	H01	5542	2	1142.3	(+0.9)	2.255	0.272	0.889	21	R.GDLGIEIPA EK.V
SW:KPY1_HUMAN	H10	7205	2	1657.9	(+0.2)	4.443	0.530	0.998	14	K.GVNL*PGA AVDL*PAVSEK#.D
SW:KPY1_HUMAN	H11	7340	2	1657.9	(+0.1)	3.136	0.293	0.914	14	K.GVNL*PGA AVDL*PAVSEK#.D
SW:KPY1_HUMAN	H10	7801	2	1483.7	(-0.3)	2.374	0.176	0.509	12	K.IYVDDGL*ISL*QVK#.Q
SW:KPY1_HUMAN	H10	8099	2	2176.4	(+0.1)	2.700	0.430	0.962	16	R.LAPITSDPTEATAVGA VEASFK.C
SW:KPY1_HUMAN	H11	8232	2	2176.4	(+0.1)	2.741	0.457	0.971	16	R.LAPITSDPTEATAVGA VEASFK.C
SW:KPY1_HUMAN	H01	5280	2	1198.4	(+0.6)	2.766	0.425	0.988	12	R.LDIDSPPITAR.N
SW:KPY1_HUMAN	H10	6187	2	1204.4	(+0.6)	3.074	0.398	0.989	12	R.L*DIDSPPITAR.N
SW:KPY1_HUMAN	H10	8341	2	2466.8	(+0.2)	3.779	0.471	1.000	11	R.TATESFASDPILYRPAVALDTK.G
SW:KPY1_HUMAN	H11	2450	1	705.9	(+0.0)	2.041	0.225	0.000	21	K.VFLAQK.M
SW:KU70_HUMAN	H09	7163	2	1395.5	(+0.7)	3.263	0.390	0.989	1	R.DIIIAEDEDL*R.V
SW:KU70_HUMAN	H09	8867	2	1429.7	(+0.1)	2.925	0.310	0.928	1	R.DTGIFL*DL*MHL*K#.K
SW:KU70_HUMAN	H09	5983	2	1535.7	(+0.2)	2.643	0.349	0.920	1	K.EL*VYPPDYNPEGK#.V
SW:KU70_HUMAN	H09	5889	2	1535.7	(+0.6)	2.458	0.311	0.928	1	K.EL*VYPPDYNPEGK#.V
SW:KU70_HUMAN	H09	6075	2	1535.7	(-0.0)	2.418	0.361	0.884	1	K.EL*VYPPDYNPEGK#.V
SW:KU70_HUMAN	H09	2239	2	1074.3	(-0.2)	2.274	0.213	0.679	1	K.IMATPEQV GK.M
SW:KU70_HUMAN	H09	5873	2	1934.1	(-0.5)	4.337	0.474	0.999	1	R.IM@L*FTNEDNPHGND SAK#.A
SW:KU70_HUMAN	H09	9941	2	2153.5	(+0.9)	4.048	0.458	1.000	1	K.IQVTPPGFQL*VFL*PFADDK#.R
SW:KU70_HUMAN	H09	9947	3	2133.5	(-0.9)	3.783	0.329	0.954	1	K.IQVTPPGFQLVFLPFADDK.R
SW:KU70_HUMAN	H09	9549	2	2289.7	(+0.1)	4.204	0.549	1.000	1	K.IQVTPPGFQLVFLPFADDKR.K
SW:KU70_HUMAN	H09	7809	2	1400.6	(+0.4)	3.117	0.491	0.994	1	K.KPGGFDISLFYR.D
SW:KU70_HUMAN	H09	7811	2	1414.6	(+0.3)	2.835	0.432	0.970	1	K.K#PGGFDISL*FYR.D
SW:KU70_HUMAN	H09	6559	2	1173.4	(-0.5)	2.670	0.221	0.839	1	K.KQELLEALTK.H
SW:KU70_HUMAN	H09	8535	2	2345.6	(-1.0)	2.584	0.306	0.664	1	R.NIPPYFVALVPQEEELDDQK.I
SW:KU70_HUMAN	H09	8491	2	2345.6	(+0.3)	2.567	0.307	0.868	1	R.NIPPYFVALVPQEEELDDQK.I
SW:KU70_HUMAN	H09	7351	2	1594.8	(+0.6)	3.617	0.384	0.989	1	K.NIYVL*QEL*DNPGAK#.R
SW:KU70_HUMAN	H09	6615	2	1704.8	(-0.6)	3.437	0.458	0.985	2	R.SDSFENPVLQQHFR.N
SW:KU70_HUMAN	H09	5095	3	2502.4	(+0.5)	4.379	0.587	1.000	1	K.TEGDEEAE EEEQEENLEASGDYK.Y
SW:KU70_HUMAN	H09	13217	3	2502.4	(+0.4)	3.842	0.449	0.999	1	K.TEGDEEAE EEEQEENLEASGDYK.Y
SW:KU70_HUMAN	H09	12971	3	2502.4	(+0.7)	3.779	0.497	0.999	1	K.TEGDEEAE EEEQEENLEASGDYK.Y
SW:KU70_HUMAN	H09	6613	2	1835.0	(-0.6)	2.544	0.286	0.162	1	R.TFNTSTGGL*L*L*PSDTK#.R.S
SW:KU70_HUMAN	H10	10041	3	2153.5	(+0.9)	3.936	0.219	0.947	1	K.IQVTPPGFQL*VFL*PFADDK#.R
SW:KU86_HUMAN	H07	6504	2	1386.6	(+0.2)	2.326	0.295	0.796	1	R.ANPQVGVA FPHIK#.H
SW:KU86_HUMAN	H07	9554	2	1916.2	(+0.6)	2.857	0.392	0.980	1	R.HLMLPDFDLLEDIESK.I
SW:KU86_HUMAN	H08	9195	2	1964.2	(-0.1)	3.314	0.298	0.932	1	R.HL*M@L*PDFDL*L*EDIESK#.I
SW:KU86_HUMAN	H08	7769	2	1287.5	(+0.1)	3.181	0.308	0.950	1	K.SQL*DIIHSL*K#.K
SW:KU86_HUMAN	H07	9850	2	2322.6	(+0.1)	5.206	0.542	1.000	1	K.YAPTEAQLNAVDALIDSMSLAK.K
SW:KU86_HUMAN	H08	9739	3	2348.6	(-0.1)	4.581	0.486	0.999	1	K.YAPTEAQL*NAVDAL*IDSMSL*AK#.K
SW:KU86_HUMAN	H08	9745	2	2322.6	(+0.7)	3.441	0.461	0.993	1	K.YAPTEAQLNAVDALIDSMSLAK.K
SW:KU86_HUMAN	H08	6417	2	1130.4	(+0.6)	2.255	0.369	0.966	1	K.K#VITMFVQR.Q
SW:LAM1_HUMAN	H09	7507	2	2151.3	(-0.6)	2.541	0.191	0.592	2	R.DQM@QQQL*NDYEQL*L*DVK#.L
SW:LAM1_HUMAN	H09	6567	2	1447.6	(+0.8)	3.916	0.466	1.000	2	R.IESLSSQLSNLQK.E
SW:LAM1_HUMAN	H09	6557	2	1473.6	(-0.4)	2.867	0.256	0.862	2	R.IESL*SSQL*SNL*QK#.E
SW:LAM1_HUMAN	H09	4185	2	1081.3	(-0.5)	2.290	0.227	0.755	2	K.L*AQAL*HEMR.E
SW:LAM1_HUMAN	H09	4777	2	1314.5	(+0.4)	2.403	0.150	0.078	2	K.L*REYEAAL*NSK#.D
SW:LAM1_HUMAN	H09	10841	2	2529.8	(+0.2)	5.294	0.486	0.992	2	K.SLEGDLEDLKDQIAQLEASLAAAK.K
SW:LAM1_HUMAN	H18	10286	3	2529.8	(+0.8)	4.726	0.565	1.000	2	K.SLEGDLEDLKDQIAQLEASLAAAK.K
SW:LAM1_HUMAN	H18	5322	2	1046.2	(+0.5)	2.941	0.332	0.978	2	K.DAALATALGDK.K
SW:LSM2_HUMAN	H22	5014	2	1218.3	(+0.7)	2.693	0.420	0.986		K.LTDISVTDPEK.Y
SW:LSM2_HUMAN	H22	5012	2	1232.3	(+0.5)	2.330	0.439	0.977		K.L*TDISVTDPEK#.Y
SW:LSM2_HUMAN	H22	7656	2	1113.3	(+0.9)	2.568	0.259	0.946		-M@L*FYSFFK#.S
SW:LSM2_HUMAN	H22	7162	2	2146.4	(+0.7)	6.141	0.552	1.000		R.YVQLPADEVDTQLLQDAAR.K
SW:LSM2_HUMAN	H22	5030	1	816.0	(-0.3)	1.958	0.250	0.000		K.DVVVEL*K#.N
SW:LSM4_HUMAN	H21	6938	2	1173.4	(+0.6)	3.841	0.429	0.998		R.IPDEIIDMVK.E

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:LSM4_HUMAN	H21	5790	2	1401.6	(-0.1)	3.253	0.431	0.971		K.TAQNHPLM*VEL*K#.N
SW:LSM6_HUMAN	H22	5420	2	1237.4	(+0.8)	2.469	0.377	0.971		R.GNNVLYISTQK.R
SW:LSM6_HUMAN	H22	5182	2	1064.2	(+0.8)	2.556	0.305	0.963		R.KQTPSDFLK.Q
SW:LSM6_HUMAN	H22	5180	2	1086.2	(+0.8)	2.212	0.196	0.773		R.K#QTPSDFL*K#.Q
SW:LSM6_HUMAN	H22	5370	2	1109.4	(+0.8)	2.543	0.291	0.350		K.QIIGRPVVVK.L
SW:LSM6_HUMAN	H22	5378	2	1251.4	(-0.0)	2.210	0.129	0.329		R.GNNVL*YISTQK#.R
SW:LSM8_HUMAN	H21	11947	3	2516.7	(+0.2)	3.706	0.358	0.972	1	R.GDNVAVIGEIDEETDSALDLGNIR.A
SW:LSM8_HUMAN	H21	7888	2	1888.0	(+0.9)	3.450	0.511	1.000	2	K.GFDQNTINLILDESHER.V
SW:MAE1_HUMAN	H16	4874	2	1085.1	(+0.4)	2.515	0.465	0.988	5	K.FFDANYDGK#.D
SW:MAE1_HUMAN	H17	8296	2	1643.8	(+0.3)	3.480	0.556	1.000	2	K.FQDNFEFVQWFK#.K
SW:MAE1_HUMAN	H16	5328	2	1321.5	(+0.3)	3.567	0.390	0.984	1	K.LEHEYIQNFK.I
SW:MAE1_HUMAN	H17	8290	2	1635.8	(+0.7)	3.033	0.496	0.992	2	K.FQDNFEFVQWFK.K
SW:MAP4_HUMAN	H04	6403	2	1413.6	(+0.5)	2.948	0.436	0.988	2	K.DGVLTLANNVTPAK.D
SW:MAP4_HUMAN	H04	5311	2	1544.7	(-0.1)	2.954	0.429	0.967	4	K.DM@AQL*PETEIAPAK#.D
SW:MAP4_HUMAN	H04	7203	2	1509.7	(+0.3)	2.659	0.346	0.865	4	K.DMSPLSETEMALGK.D
SW:MAP4_HUMAN	H04	2171	2	1131.3	(+0.5)	2.608	0.387	0.979	8	R.LATNTSAPDLK.N
SW:MAP4_HUMAN	H04	8799	3	3398.6	(-0.5)	3.977	0.352	0.988	3	K.M@YHDDDL*ADL*VFPSSATADTSIFAGQNDPL*K#.D
SW:MAP4_HUMAN	H04	5897	2	1468.7	(-0.4)	2.905	0.407	0.966	4	K.NVVLPTEDEVAPAK.D
SW:MAP4_HUMAN	H04	5881	2	1482.7	(-0.1)	2.532	0.412	0.942	4	K.NVVL*PTETEDEVAPAK#.D
SW:MAP4_HUMAN	H05	6234	2	1468.7	(-0.3)	2.360	0.225	0.398	4	K.NVVLPTETEDEVAPAK.D
SW:MAP4_HUMAN	H04	7703	2	1421.6	(+0.0)	3.122	0.248	0.912	4	K.TDYIPLLDVDEK.T
SW:MAP4_HUMAN	H04	5337	2	1586.8	(+0.6)	2.987	0.457	0.990	7	K.TTTL*SGTAPAAGVVPSR.V
SW:MAP4_HUMAN	H04	5341	2	1592.8	(-0.1)	2.912	0.448	0.971	7	K.TTTL*SGTAPAAGVVPSR.V
SW:MAP4_HUMAN	H04	5909	2	1591.8	(+0.3)	5.083	0.506	1.000	7	K.VGSLDNVGHLPAGGAVK.T
SW:MAP4_HUMAN	H04	5913	2	1611.8	(-0.3)	4.402	0.479	1.000	7	K.VGSL*DNVGHLPAGGAVK#.T
SW:MAP4_HUMAN	H04	4967	2	1229.3	(+0.1)	2.832	0.335	0.940	4	R.WPTETDVSSAK#.N
SW:MAP4_HUMAN	H04	4959	2	1221.3	(-0.1)	2.562	0.332	0.923	4	R.WPTETDVSSAK#.N
SW:MAP4_HUMAN	H05	6688	2	1413.6	(+0.7)	2.306	0.322	0.878	2	K.DGVLTLANNVTPAK.D
SW:MAT3_HUMAN	H06	6792	3	2375.5	(+0.9)	4.324	0.319	0.942	1	R.DSFDDRGPSSL*NPVL*DYDHGSR.S
SW:MAT3_HUMAN	H06	6798	3	2363.5	(+0.5)	4.260	0.411	0.868	1	R.DSFDDRGPSSLNPVLDYDHGSR.S
SW:MAT3_HUMAN	H06	8430	2	1793.9	(+0.8)	3.890	0.572	1.000	1	R.GDADQASNILASFGLSAR.D
SW:MAT3_HUMAN	H06	8422	2	1805.9	(+0.0)	2.220	0.332	0.827	1	R.GDADQASNIL*ASFGL*SAR.D
SW:MAT3_HUMAN	H06	2356	2	1092.2	(+0.8)	2.560	0.333	0.962	1	R.GPLPLSSQHR.G
SW:MAT3_HUMAN	H06	7924	2	1970.3	(-0.3)	2.872	0.485	0.979	3	R.IGPYQPNVPGIDYVIPK.T
SW:MAT3_HUMAN	H06	9120	2	1621.0	(+0.8)	2.649	0.129	0.690	1	K.ITPENLPQILLQLK.R
SW:MAT3_HUMAN	H08	9187	2	1621.0	(+0.8)	3.031	0.339	0.968	1	K.ITPENLPQILLQLK.R
SW:MAT3_HUMAN	H06	2292	2	1372.5	(-0.4)	2.331	0.192	0.598	1	R.RTEEGPTL*SYGR.D
SW:MAT3_HUMAN	H06	6714	2	2064.3	(-0.7)	3.947	0.347	0.915	3	R.VIHL*SNL*PHSGYSDSAVL*K#.L
SW:MAT3_HUMAN	H08	6855	3	2038.3	(+0.5)	4.177	0.452	0.999	3	R.VIHL*SNL*PHSGYSDSAVLK.L
SW:MAT3_HUMAN	H06	9932	2	2439.9	(-0.1)	4.229	0.405	0.987	1	R.YQLLQLVEPFGVISNHLILNK.I
SW:MAT3_HUMAN	H09	9199	2	1621.0	(+0.5)	3.017	0.365	0.980	1	K.ITPENLPQILLQLK.R
SW:MCM2_HUMAN	H06	9278	2	1364.6	(+0.6)	2.498	0.138	0.698	9	R.DNNEL*L*L*FIL*K#.Q
SW:MCM2_HUMAN	H06	6906	2	1491.6	(+0.3)	2.854	0.368	0.954	9	R.ESL*VVNYEDL*AAR.E
SW:MCM2_HUMAN	H06	5112	2	1341.5	(+0.3)	2.459	0.366	0.903	10	K.QL*VAEQVYQR.N
SW:MCM2_HUMAN	H06	5470	2	1275.4	(+1.0)	3.934	0.512	1.000	9	K.VAVGELTDEDVK.M
SW:MCM2_HUMAN	H06	5460	2	1289.4	(-0.5)	2.381	0.252	0.746	9	K.VAVGEL*TDEDVK#.M
SW:MCM3_HUMAN	H07	5586	2	1379.5	(+0.9)	2.795	0.408	0.983	3	K.DAQPSFSAEDIAK.I
SW:MCM3_HUMAN	H07	5402	2	1438.6	(-0.3)	2.696	0.219	0.761	3	K.SL*APSIHGHDYVK#.K
SW:MCM3_HUMAN	H07	5382	2	1424.6	(+0.9)	2.392	0.328	0.941	3	K.SLAPSIHGHDYVK.K
SW:MCM3_HUMAN	H07	2420	2	1138.2	(+0.7)	2.333	0.187	0.823	3	R.ELISDNQYR.L
SW:MCM4_HUMAN	H06	9690	3	2154.5	(+0.9)	4.247	0.389	0.993	2	R.NL*NPEDIDQL*ITISGMVIR.T
SW:MCM4_HUMAN	H06	9232	2	1611.9	(+0.1)	2.442	0.355	0.911	2	K.SQL*L*QYVYNL*VPR.G
SW:MCM7_HUMAN	H08	8897	2	2034.4	(-0.1)	4.194	0.553	1.000	3	R.IAQPGDHVSVTGIFLPILR.T
SW:MCM7_HUMAN	H08	8489	2	1635.9	(+0.4)	2.974	0.269	0.939	2	K.LFADAVQELLPQYK.E
SW:MCM7_HUMAN	H08	2481	2	1456.6	(+0.6)	2.586	0.347	0.965	2	R.SPQNQYPAEL*M@R.R
SW:MDHM_HUMAN	H05	5952	2	1105.3	(+0.5)	2.479	0.307	0.910		K.EGVVECSFVK#.S

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:MDHM_HUMAN	H15	8190	3	2392.7	(+0.3)	6.967	0.574	1.000		R.L*TL*YDIAHTPGVAADL*SHIETK#.A
SW:MDHM_HUMAN	H16	7578	3	2392.7	(+0.0)	5.369	0.514	1.000		R.L*TL*YDIAHTPGVAADL*SHIETK#.A
SW:MDHM_HUMAN	H16	6752	2	1561.7	(+0.7)	3.628	0.441	0.981		K.VDFPQDQLTALTGR.I
SW:MDHM_HUMAN	H16	5278	2	1148.4	(+1.0)	3.197	0.510	0.999		R.VNVPVIGGHAGK.T
SW:MDHM_HUMAN	H16	7560	2	1328.6	(+0.4)	2.943	0.402	0.987		R.FVFSLV DAMNGK.E
SW:MEM1_HUMAN	H06	10714	2	2041.3	(+0.9)	4.264	0.524	0.999	3	K.AYIGFIQSL*AQFL*GADASR.V
SW:MEM1_HUMAN	H06	7584	2	1713.9	(+0.1)	2.403	0.346	0.870	2	K.EL*ETVL*ADEPGL*L*GPK#.A
SW:MEM1_HUMAN	H06	1736	2	1252.4	(+1.0)	2.311	0.432	0.978		R.NSTQHL*GPVHR.E
SW:MG15_HUMAN	H14	6351	2	1458.7	(+0.3)	2.326	0.332	0.854	6	R.IGAM@L*AYTPL*DEK#.S
SW:MG15_HUMAN	H14	9237	2	2239.6	(+0.3)	5.080	0.552*	0.125	6	K.IPEELKPWLVDWDLITR.Q
SW:MG15_HUMAN	H14	9219	3	2265.6	(+0.1)	3.755	0.407*	0.004	6	K.IPEEL*K#PWL*VDDWDL*ITR.Q
SW:MG15_HUMAN	H14	9243	2	2265.6	(+0.9)	2.944	0.307	0.483	6	K.IPEEL*K#PWL*VDDWDL*ITR.Q
SW:MG15_HUMAN	H15	9444	3	2265.6	(+0.9)	4.319	0.478*	0.022	6	K.IPEEL*K#PWL*VDDWDL*ITR.Q
SW:MG15_HUMAN	H14	10697	2	1661.0	(-0.7)	4.398	0.497	1.000	6	K.SLALLLNLYLHDFLK.Y
SW:MG15_HUMAN	H14	6581	2	1315.5	(+0.8)	2.712	0.365	0.969	4	K.YFIHYSGWNK.N
SW:MG15_HUMAN	H16	5954	2	1458.7	(-0.0)	2.756	0.253	0.836	6	R.IGAM@L*AYTPL*DEK#.S
SW:MGMT_HUMAN	H18	7952	2	1927.2	(-0.6)	4.305	0.470	0.998	2	K.FGEVISYQQL*AAL*AGNPK#.A
SW:MGMT_HUMAN	H19	7004	2	1710.0	(-0.9)	2.955	0.218	0.042	2	R.L*GK#PGL*GGSSGL*AGAWL*K#.G
SW:MGMT_HUMAN	H19	5834	2	1248.4	(+0.8)	2.658	0.398	0.984	2	K.EWLLAHEGHR.L
SW:MGN_HUMAN	H20	7494	2	1870.0	(+0.5)	3.104	0.552	1.000	1	K.FGHEFL*EFEFRPDGK#.L
SW:MGN_HUMAN	H20	7456	2	1308.5	(+0.9)	3.440	0.292	0.982	2	R.VFYFL*VQDL*K#.C
SW:MGN_HUMAN	H20	6922	2	2326.5	(-0.7)	2.412	0.221	0.021	1	R.IIDDSEITKEDDALWPPDR.V
SW:MLEN_HUMAN	H18	5066	2	1355.5	(+0.0)	2.511	0.328	0.862	7	R.ALGNPTNAEVLK.V
SW:MLEN_HUMAN	H20	5068	2	1355.5	(+0.6)	3.659	0.527*	0.705	7	R.ALGNPTNAEVLK.V
SW:MLEN_HUMAN	H21	4860	2	1355.5	(+0.8)	3.079	0.468*	0.496	7	R.ALGNPTNAEVLK.V
SW:MLEN_HUMAN	H21	4882	2	1355.5	(-0.8)	2.963	0.346	0.853	7	R.ALGNPTNAEVLK.V
SW:MLEN_HUMAN	H21	6086	2	1545.6	(+0.5)	3.836	0.504	0.999	8	K.DQGTIEDYVEGLR.V
SW:MLEN_HUMAN	H21	6064	2	1551.6	(+0.3)	3.115	0.434	0.979	8	K.DQGTIEDYVEGLR.V
SW:MLEN_HUMAN	H21	5942	2	1801.9	(-0.6)	4.137	0.461	1.000	8	K.NK#DQGTIEDYVEGLR.V
SW:MLEN_HUMAN	H21	8980	2	1889.3	(-0.7)	3.930	0.446	0.960	7	K.VLDFEHFLPMLQTVAK.N
SW:MLEN_HUMAN	H21	8964	2	1889.3	(+0.6)	3.321	0.420	0.990	7	K.VLDFEHFLPMLQTVAK.N
SW:MLEN_HUMAN	H21	8976	2	1915.3	(-0.1)	2.423	0.400	0.922	7	K.VL*DFEHFL*PML*QTVAK#.N
SW:MLRM_HUMAN	H19	5938	2	1416.5	(+0.9)	4.463	0.463	1.000	2	R.FTDEEVDLYR.E
SW:MLRM_HUMAN	H19	8196	2	2092.3	(-0.2)	4.453	0.462	0.996	7	R.ATSNVAMFDQSQIQEFK.E
SW:MOES_HUMAN	H08	4963	2	1046.2	(+0.5)	2.488	0.241	0.911	1	K.ALTSELANAR.D
SW:MOES_HUMAN	H08	4969	2	1058.2	(-0.6)	2.207	0.195	0.598	1	K.AL*TSEL*ANAR.D
SW:MOES_HUMAN	H09	5077	2	1046.2	(+0.8)	2.802	0.401	0.987	1	K.ALTSELANAR.D
SW:MOES_HUMAN	H09	5079	2	1058.2	(-0.2)	2.554	0.327	0.927	1	K.AL*TSEL*ANAR.D
SW:MOES_HUMAN	H09	2391	2	1205.3	(-0.2)	2.502	0.261	0.839	1	K.AQMVQEDL*EK#.T
SW:MOES_HUMAN	H09	9317	2	2083.3	(+0.2)	4.399	0.472	1.000	3	K.FYPEDVSEELIQDITQR.L
SW:MOES_HUMAN	H09	9261	3	2363.6	(+0.7)	3.920	0.538	0.997	3	K.GSELWLGVDALGLNIYEQNDR.L
SW:MOES_HUMAN	H09	4325	2	948.1	(+0.8)	2.793	0.262	0.968	2	R.ISQLEMAR.Q
SW:MOES_HUMAN	H09	4349	2	954.1	(+0.7)	2.735	0.299	0.974	2	R.ISQL*EMAR.Q
SW:MOES_HUMAN	H09	7399	2	1833.1	(+0.7)	3.913	0.547	0.999	2	K.KTQEQLALEMAELTAR.I
SW:MOES_HUMAN	H09	5531	3	3314.4	(+0.8)	5.859	0.582	1.000	1	K.TAMSTPHVAEPAENEQDEQDENGAEASADLR.A
SW:MOES_HUMAN	H09	4461	2	948.1	(+0.1)	2.378	0.355	0.943	2	R.ISQLEMAR.Q
SW:MTA1_HUMAN	H08	6367	2	1282.5	(+1.0)	3.297	0.401	0.990	2	R.LPEASQSPLVLK.Q
SW:MTA1_HUMAN	H08	8765	2	1653.8	(+0.7)	2.702	0.494	0.991	1	K.DFTDIQQDFLPWK.S
SW:MTA2_HUMAN	H08	6591	2	1550.6	(+0.7)	4.036	0.557	1.000	2	R.DISSSLNLSLADSNAR.E
SW:MTA2_HUMAN	H08	6583	2	1562.6	(-0.2)	2.823	0.366	0.944	2	R.DISSSL*NSL*ADSNAR.E
SW:MTA2_HUMAN	H09	6445	2	1562.6	(-0.0)	3.867	0.461	1.000	2	R.DISSSL*NSL*ADSNAR.E
SW:MTA2_HUMAN	H08	5303	2	1180.4	(+0.6)	2.594	0.383	0.626	2	K.DLVAQAPLKP.T
SW:MTA2_HUMAN	H09	5339	2	1180.4	(-0.6)	2.456	0.422	0.475	2	K.DLVAQAPLKP.T
SW:MTA2_HUMAN	H08	5531	3	2185.3	(+0.8)	4.385	0.397	0.991	2	R.GHL*SRPEAQL*SPYTTSANR.A
SW:MTA2_HUMAN	H09	5539	3	2185.3	(+0.7)	4.071	0.421	0.993	2	R.GHL*SRPEAQL*SPYTTSANR.A
SW:MTA2_HUMAN	H08	7301	2	1667.9	(+0.4)	2.621	0.361	0.959	1	K.L*NPADAPNPVVFVATK#.D
SW:MTA2_HUMAN	H09	5559	2	1336.6	(+0.2)	3.559	0.431	0.984	2	R.RPYAPINANAIAK#.A



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:MTA2_HUMAN	H09	7957	3	3256.8	(+0.2)	4.116	0.444	0.983	1	K.VKPTLIIVRPPVPLPAPSHPASTNEPIVLED.-
SW:MTA2_HUMAN	H09	7955	3	3282.8	(-0.6)	4.027	0.501	0.967	1	K.VK#PTL*IAVRPPVPL*PAPSHPASTNEPIVL*ED.-
SW:MTA2_HUMAN	H09	5337	2	1208.4	(+0.1)	2.257	0.344	0.212	2	K.DL*VAQAPL*K#PK#.T
SW:MYH9_HUMAN	H04	6167	2	1224.4	(+0.3)	2.919	0.364	0.964	6	R.AGVLAHLEEEER.D
SW:MYH9_HUMAN	H05	6482	2	1224.4	(+0.4)	2.660	0.399	0.983	6	R.AGVLAHLEEEER.D
SW:MYH9_HUMAN	H03	5622	2	1205.4	(+0.5)	3.170	0.298	0.979	4	R.ALEQQVEEMK.T
SW:MYH9_HUMAN	H03	7424	2	1871.1	(-0.3)	4.909	0.554	1.000	2	K.ANLQIDQINTDLNLER.S
SW:MYH9_HUMAN	H03	5280	2	904.1	(+1.0)	2.353	0.356*	0.293	4	K.ASITALEAK.I
SW:MYH9_HUMAN	H03	5670	2	1349.4	(+0.7)	4.477	0.575	0.998	4	R.DELADEIANSSGK.G
SW:MYH9_HUMAN	H07	5368	2	1349.4	(+0.6)	3.670	0.517	1.000	4	R.DELADEIANSSGK.G
SW:MYH9_HUMAN	H03	8740	2	2494.6	(-0.3)	4.036	0.479	1.000	4	K.DFSALESQLQDQTQELLQEENR.Q
SW:MYH9_HUMAN	H07	8918	2	2494.6	(-0.2)	3.689	0.480	1.000	4	K.DFSALESQLQDQTQELLQEENR.Q
SW:MYH9_HUMAN	H03	2358	2	1213.3	(+0.9)	2.615	0.386	0.979	4	K.DLEAHIDSANK.N
SW:MYH9_HUMAN	H03	5182	2	1566.6	(-0.9)	2.205	0.247	0.355	3	R.ELEDATETADAMNR.E
SW:MYH9_HUMAN	H06	4476	2	1566.6	(-0.1)	3.147	0.490	0.985	3	R.ELEDATETADAMNR.E
SW:MYH9_HUMAN	H07	4680	2	1566.6	(-0.6)	3.286	0.452	0.983	3	R.ELEDATETADAMNR.E
SW:MYH9_HUMAN	H07	4660	2	1566.6	(+0.6)	3.177	0.547	0.999	3	R.ELEDATETADAMNR.E
SW:MYH9_HUMAN	H03	2374	2	1379.5	(+0.6)	3.260	0.404	0.812	4	R.EMAELEDERK.Q
SW:MYH9_HUMAN	H03	6188	2	1344.5	(+0.2)	3.470	0.501	0.990	5	K.HEAMITDLER.L
SW:MYH9_HUMAN	H03	7392	2	1841.0	(+0.3)	5.756	0.630	1.000	4	K.HSQAVEELAEQLEQTK.R
SW:MYH9_HUMAN	H07	7266	2	1841.0	(+0.6)	4.841	0.657	1.000	4	K.HSQAVEELAEQLEQTK.R
SW:MYH9_HUMAN	H03	6038	2	1531.7	(+0.6)	3.958	0.496	1.000	4	K.IAQLEEQLDNETK.E
SW:MYH9_HUMAN	H07	5774	2	1531.7	(-0.4)	4.595	0.527	1.000	4	K.IAQLEEQLDNETK.E
SW:MYH9_HUMAN	H03	8642	2	2019.4	(+0.7)	4.205	0.446	1.000	5	R.IIGLDQVAGMSETALPGAFK.T
SW:MYH9_HUMAN	H03	5736	2	1258.4	(+0.8)	3.598	0.336	0.989	11	K.KEEELQAALAR.V
SW:MYH9_HUMAN	H04	5371	2	1258.4	(+0.8)	3.255	0.323	0.983	11	K.KEEELQAALAR.V
SW:MYH9_HUMAN	H04	5921	2	1221.4	(+0.9)	2.873	0.253	0.957	13	K.KFDQLLAEEK.T
SW:MYH9_HUMAN	H03	6376	2	1072.3	(+0.5)	2.404	0.233	0.902	4	K.KLVWVPSDK.S
SW:MYH9_HUMAN	H04	6111	2	1072.3	(+0.9)	2.215	0.249	0.872	4	K.KLVWVPSDK.S
SW:MYH9_HUMAN	H05	6444	2	1072.3	(+1.0)	2.243	0.362	0.961	4	K.KLVWVPSDK.S
SW:MYH9_HUMAN	H03	9454	2	2488.7	(-0.5)	5.495	0.570	1.000	5	K.LEGDSTDLSDQIAELQAQIAELK.M
SW:MYH9_HUMAN	H03	8036	2	1947.1	(+0.3)	5.588	0.589	1.000	4	K.LQVLEDNVTGLLSQSDSK.S
SW:MYH9_HUMAN	H03	7654	3	2334.5	(+0.9)	5.076	0.474	0.997	6	K.MQQNIQELEEQLLEEEESAR.Q
SW:MYH9_HUMAN	H04	7519	3	2334.5	(+0.8)	4.242	0.471	0.993	6	K.MQQNIQELEEQLLEEEESAR.Q
SW:MYH9_HUMAN	H03	7798	2	1673.9	(+0.0)	5.769	0.515	0.999	4	K.NFINNPLAQADWAAK.K
SW:MYH9_HUMAN	H03	8712	2	1754.0	(+0.0)	2.779	0.316	0.895	10	R.QL*L*QANPIL*EAFGNK#.T
SW:MYH9_HUMAN	H04	6717	2	1156.4	(+0.8)	2.827	0.436	0.990	3	R.RGDLPFVVR.R
SW:MYH9_HUMAN	H06	6764	2	1156.4	(+0.8)	2.448	0.435	0.984	3	R.RGDLPFVVR.R
SW:MYH9_HUMAN	H07	9074	2	2050.3	(+0.6)	2.212	0.474	0.977	4	K.SMEAEMIQLQEELAAAER.A
SW:MYH9_HUMAN	H03	7890	2	1963.1	(-0.4)	3.515	0.396	0.977	10	K.TQLEEELEDELQATEDAK.L
SW:MYH9_HUMAN	H04	7787	2	1963.1	(-0.2)	3.728	0.489	1.000	10	K.TQLEEELEDELQATEDAK.L
SW:MYH9_HUMAN	H07	7910	2	1963.1	(-0.1)	2.956	0.439	0.973	10	K.TQLEEELEDELQATEDAK.L
SW:MYH9_HUMAN	H03	7828	2	1572.8	(-0.5)	4.113	0.487	1.000	5	K.VSHLLGINVDFTR.G
SW:MYH9_HUMAN	H08	5247	2	1205.4	(+0.5)	2.701	0.367	0.980	4	R.ALEQQVEEMK.T
SW:MYHA_HUMAN	H03	4160	2	1520.5	(+0.4)	3.741	0.560	0.999	2	R.ELDDATEANEGLSR.E
SW:MYHA_HUMAN	H03	4240	2	1520.5	(-0.1)	3.646	0.470	1.000	2	R.ELDDATEANEGLSR.E
SW:MYHA_HUMAN	H03	4860	2	960.1	(+0.9)	2.758	0.435	0.991	1	R.HGFEAASIK.E
SW:MYHA_HUMAN	H03	4782	2	960.1	(+0.5)	2.677	0.420	0.988	1	R.HGFEAASIK.E
SW:MYHA_HUMAN	H03	8210	3	2533.7	(+0.7)	4.798	0.572	0.992	1	R.IAQLEEEEEEQSNMELLNDR.F
SW:MYHA_HUMAN	H03	9284	3	2716.0	(+0.9)	4.709	0.524	0.997	1	R.KLDGETTDLQDQIAELQAQIDELK.L
SW:MYHA_HUMAN	H03	8258	2	1756.0	(+0.2)	3.255	0.512	1.000	1	K.NLPIYSENIIMYR.G
SW:MYHA_HUMAN	H03	8220	2	1525.8	(+0.6)	3.571	0.459	0.994	1	K.VVSSVLQFGNISFK.K
SW:MYHA_HUMAN	H04	9135	3	2716.0	(+0.9)	3.734	0.446	0.999	1	R.KLDGETTDLQDQIAELQAQIDELK.L
SW:NC5R_HUMAN	H16	5476	2	1139.3	(-0.1)	2.882	0.276	0.898	10	R.GPSGL*L*VYQKG#.G
SW:NC5R_HUMAN	H16	6992	2	1520.7	(-0.1)	2.272	0.185	0.044	11	K.DIL*L*RPEL*EEL*R.N
SW:NCO5_HUMAN	H10	4895	2	1198.3	(+0.2)	3.118	0.378	0.976	4	K.M@ADEAIL*QER.E
SW:NCO5_HUMAN	H10	5241	2	1223.3	(+0.5)	2.577	0.341	0.964	3	R.SSTDSL*PGPISR.Q
SW:NCO5_HUMAN	H10	9361	2	1905.1	(-0.4)	2.372	0.142	0.390	4	R.GGHPAIQSL*INL*L*ADNR.Y
SW:NDKA_HUMAN	H20	4340	2	1486.6	(+0.7)	3.661	0.511	1.000	3	R.NIIHGSDSVESAIEK.E
SW:NDKA_HUMAN	H20	4380	2	1494.6	(+0.6)	2.859	0.441	0.986	3	R.NIIHGSDSVESAIEK#.E
SW:NDKA_HUMAN	H20	5862	2	1353.6	(+0.6)	2.253	0.252	0.180	6	R.TFIAIK#PDGVQR.G

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:NDKA_HUMAN	H21	4174	2	1486.6	(+0.6)	3.333	0.488	0.994	3	R.NIIHGSDSVESAEK.E
SW:NEP1_HUMAN	H18	6792	2	1371.6	(+0.2)	4.097	0.493	1.000	2	R.AGLLQVYIHTQK.N
SW:NEP1_HUMAN	H18	6786	2	1391.6	(-0.4)	3.361	0.449	0.984	2	R.AGL*L*QVYIHTQK#.N
SW:NEP1_HUMAN	H18	5860	2	1283.5	(-0.2)	3.199	0.312	0.955	2	K.NVLIEVNPQTR.I
SW:NO56_HUMAN	H09	9129	2	1858.2	(-0.4)	3.929	0.558	0.997	4	K.MSQVAPSL SALIGEAVGAR.L
SW:NO56_HUMAN	H09	6193	2	1391.6	(+0.4)	3.345	0.381	0.987	5	K.YPASTVQIL*GAEK#.A
SW:NO56_HUMAN	H09	6081	2	1335.6	(-0.1)	2.311	0.119	0.302	4	R.L*IAHAGSL*TNL*AK#.Y
SW:NOL1_HUMAN	H06	5280	2	1391.5	(+0.7)	3.428	0.434	0.991	2	K.GADSELSTVPSVTK.T
SW:NOL1_HUMAN	H06	6568	2	1552.7	(+0.9)	2.488	0.361	0.955	2	R.L*GVTNTIISHYDGR.Q
SW:NOL1_HUMAN	H06	7402	2	1637.8	(+0.9)	3.599	0.584	1.000	2	R.LVPTGLDFGQEGFTR.F
SW:NOL1_HUMAN	H06	4644	2	1464.6	(+0.6)	3.059	0.328	0.974	2	K.NTGVL*ANDANAER.L
SW:NOL1_HUMAN	H06	5262	2	1405.5	(-0.1)	2.371	0.416	0.931	2	K.GADSEL*STVPSVTK#.T
SW:NP14_HUMAN	H06	1830	2	1132.2	(+0.4)	2.533	0.208	0.870	3	R.DNQL*SEVANK#.F
SW:NP14_HUMAN	H07	10390	2	1689.1	(+0.4)	2.209	0.391	0.884	3	R.VVPSDLYPLVLGFLR.D
SW:NPM_HUMAN	H15	7718	2	2160.4	(+0.6)	5.197	0.547	1.000	12	K.DEL*HIVEAEAMNYEGSPIK#.V
SW:NPM_HUMAN	H15	7714	2	2146.4	(-0.7)	3.884	0.382	0.938	12	K.DELHIVEAEAMNYEGSPIK.V
SW:NPM_HUMAN	H15	5020	3	3725.3	(+0.1)	4.114	0.451	0.998	9	K.LAADEDDDDDEEDDDDDDDDFDDEEAEEK.A
SW:NPM_HUMAN	H15	1760	1	815.0	(-0.3)	1.926	0.135	0.000	12	K.MQASIEK#.G
SW:NPM_HUMAN	H15	8802	2	2256.7	(+0.7)	5.016	0.596	0.993	13	K.M@SVQPTVSL*GGFEITPPVVL*R.L
SW:NPM_HUMAN	H15	8974	2	2228.7	(+0.5)	4.798	0.535	1.000	13	K.MSVQPTVSLGGFEITPPVVL.R.L
SW:NPM_HUMAN	H15	8978	2	2240.7	(+0.6)	4.401	0.558	0.999	13	K.MSVQPTVSL*GGFEITPPVVL*R.L
SW:NPM_HUMAN	H19	8438	2	2256.7	(+0.1)	4.018	0.563	1.000	13	K.M@SVQPTVSL*GGFEITPPVVL*R.L
SW:NPM_HUMAN	H19	8614	2	2228.7	(+0.4)	2.682	0.462	0.984	13	K.MSVQPTVSLGGFEITPPVVL.R.L
SW:NPM_HUMAN	H15	8206	2	1843.0	(+0.7)	3.298	0.393	0.988	9	R.M@TDQEAIDL*WQWR.K
SW:NPM_HUMAN	H20	7892	2	1843.0	(+0.3)	3.609	0.404	0.981	9	R.M@TDQEAIDL*WQWR.K
SW:NPM_HUMAN	H21	7768	2	1843.0	(+0.4)	3.411	0.331	0.978	9	R.M@TDQEAIDL*WQWR.K
SW:NPM_HUMAN	H15	4024	2	1569.6	(+0.9)	3.807	0.389	0.990	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	H15	3942	2	1569.6	(+0.9)	3.746	0.402	0.988	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	H15	4204	2	1569.6	(+0.8)	3.727	0.394	0.987	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	H15	4304	2	1569.6	(+0.9)	3.717	0.383	0.986	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	H15	3562	2	1569.6	(+1.0)	3.480	0.358	0.988	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	H15	4120	2	1569.6	(+0.9)	3.437	0.440	0.993	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	H15	3268	2	1569.6	(-0.4)	3.430	0.316	0.961	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	H15	3364	2	1581.6	(+0.5)	3.305	0.475	0.994	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	H15	4042	2	1569.6	(-0.9)	3.258	0.249	0.766	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	H15	3876	2	1581.6	(+0.2)	3.221	0.363	0.967	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	H15	4372	2	1569.6	(-0.4)	3.214	0.397	0.969	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	H15	3344	2	1569.6	(-0.3)	3.186	0.266	0.923	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	H15	4112	2	1581.6	(+0.6)	3.124	0.459	0.990	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	H15	4748	2	1581.6	(+0.3)	3.063	0.436	0.840	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	H15	3212	2	1581.6	(-0.6)	2.984	0.339	0.949	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	H15	4654	2	1569.6	(+0.3)	2.960	0.357	0.955	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	H15	4764	2	1581.6	(-1.0)	2.937	0.325	0.822	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	H15	4030	2	1581.6	(+1.0)	2.934	0.447	0.989	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	H15	3436	2	1581.6	(+0.3)	2.874	0.416	0.970	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	H15	4208	2	1581.6	(+0.6)	2.864	0.424	0.987	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	H15	3288	2	1581.6	(-0.6)	2.778	0.283	0.892	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	H15	4290	2	1581.6	(+0.5)	2.767	0.427	0.985	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	H15	4464	2	1581.6	(+0.7)	2.716	0.445	0.986	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	H15	3136	2	1581.6	(-0.3)	2.551	0.154	0.563	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	H15	4584	2	1581.6	(+0.6)	2.291	0.291	0.898	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	H16	4000	2	1569.6	(+0.8)	3.405	0.396	0.990	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	H16	3990	2	1581.6	(+0.2)	2.427	0.331	0.888	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	H17	4032	2	1569.6	(+0.8)	3.413	0.342	0.984	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	H19	4360	2	1581.6	(+1.0)	2.861	0.463	0.990	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	H20	4544	2	1569.6	(-0.5)	3.179	0.241	0.902	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	H20	4554	2	1581.6	(+0.4)	3.047	0.492	0.993	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	H21	4338	2	1581.6	(+0.3)	2.472	0.252	0.783	12	K.VDNDENEHQL*SL*R.T
SW:NR54_HUMAN	H11	2294	2	1229.4	(-0.6)	2.449	0.384	0.367	6	R.AAPGAEFAPNKR.R
SW:NR54_HUMAN	H11	3200	2	901.1	(+0.0)	2.442	0.283	0.884	4	K.AGEVFIHK.D

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:NR54_HUMAN	H11	6030	2	1337.5	(+1.0)	2.579	0.365	0.588	5	R.EKLEMMEAAR.H
SW:NR54_HUMAN	H11	6070	2	1351.5	(-0.8)	2.550	0.227	0.043	5	R.EK#L*EMEMEAAR.H
SW:NR54_HUMAN	H11	5506	2	1367.5	(+0.3)	2.419	0.327*	0.003	5	R.EK#L*EMEM@EAAR.H
SW:NR54_HUMAN	H11	5918	2	1240.4	(+0.6)	2.682	0.299	0.441	5	K.GIVEFSGK#PAAR.K
SW:NR54_HUMAN	H11	5558	2	1181.4	(+0.9)	2.834	0.358	0.979	6	R.HEHQVMLMR.Q
SW:NR54_HUMAN	H11	5550	2	1187.4	(+0.9)	2.653	0.437	0.990	6	R.HEHQVML*MR.Q
SW:NR54_HUMAN	H11	5732	2	1086.3	(+1.0)	2.538	0.257	0.940	5	K.L*EMEMEAAR.H
SW:NR54_HUMAN	H11	7980	2	1861.1	(+0.7)	2.913	0.354	0.974	4	R.LFVGNLPPDITEEMR.K
SW:NR54_HUMAN	H11	1936	2	1399.5	(+0.1)	2.788	0.210	0.807	6	R.MEEL*HNQEVQK#.R
SW:NR54_HUMAN	H11	1712	2	1415.5	(+0.7)	2.443	0.317	0.942	6	R.M@EEL*HNQEVQK#.R
SW:NR54_HUMAN	H11	11308	2	2670.0	(+0.2)	4.627	0.592	0.999	5	R.NLPQYVSNELLEAFSVFGQVER.A
SW:NR54_HUMAN	H11	11380	3	2688.0	(+0.6)	4.305	0.504	0.999	5	R.NL*PQYVSNEL*L*EEAFSVFGQVER.A
SW:NR54_HUMAN	H11	11294	2	2688.0	(-0.2)	4.291	0.440	1.000	5	R.NL*PQYVSNEL*L*EEAFSVFGQVER.A
SW:NR54_HUMAN	H10	1901	2	1555.7	(-0.6)	2.279	0.267	0.741	6	R.RMEEL*HNQEVQK#.R
SW:NR54_HUMAN	H11	1970	2	1555.7	(+0.1)	2.916	0.406	0.967	6	R.RMEEL*HNQEVQK#.R
SW:NR54_HUMAN	H11	1968	2	1541.7	(+0.5)	2.826	0.304	0.964	6	R.RMEELHNQEVQK.R
SW:NR54_HUMAN	H11	1704	2	1571.7	(-0.7)	2.503	0.281	0.598	6	R.RM@EEL*HNQEVQK#.R
SW:NR54_HUMAN	H10	2263	1	759.9	(-0.1)	2.021	0.181	0.000	8	R.TL*AEIAK#.V
SW:NR54_HUMAN	H11	6496	2	1087.3	(-0.5)	3.002	0.403	0.980	4	K.VELDNMPLR.G
SW:NR54_HUMAN	H11	1938	2	1385.5	(+0.9)	2.255	0.134	0.595	6	R.MEELHNQEVQK.R
SW:NU62_HUMAN	H10	9937	2	1627.9	(-0.2)	3.329	0.279	0.935	2	K.ELEDLLSPLEELVK.E
SW:NU62_HUMAN	H10	6775	2	1720.9	(+0.6)	4.184	0.497	1.000	2	R.HFL*QQATQVNAWDR.T
SW:NU62_HUMAN	H10	5563	2	1135.3	(+0.1)	2.364	0.320	0.882	2	K.L*AENIDAQL*K#.R
SW:NU98_HUMAN	H07	4104	2	1057.1	(+0.2)	2.714	0.369	0.964	6	R.L*ADINYEGR.L
SW:NU98_HUMAN	H06	9562	2	1512.7	(+0.5)	2.216	0.333	0.918	6	K.NSPVEAVFSYLTGK.R
SW:NU98_HUMAN	H07	4272	2	1057.1	(+0.9)	2.631	0.393	0.984	6	R.L*ADINYEGR.L
SW:NUCL_HUMAN	H06	7394	2	1649.8	(-0.2)	2.879	0.332	0.934	3	K.FGYVDFESAEDLEK.A
SW:NUCL_HUMAN	H06	7276	2	1570.6	(+0.6)	4.642	0.568	1.000	5	K.GFGVDFNSEEDAK#.E
SW:NUCL_HUMAN	H07	7298	2	1570.6	(+0.5)	2.847	0.466	0.981	5	K.GFGVDFNSEEDAK#.E
SW:NUCL_HUMAN	H09	7259	2	1570.6	(+0.9)	3.513	0.538	1.000	5	K.GFGVDFNSEEDAK#.E
SW:NUCL_HUMAN	H11	7572	2	1562.6	(+0.8)	2.402	0.402	0.969	5	K.GFGVDFNSEEDAK#.E
SW:NUCL_HUMAN	H17	6632	2	1562.6	(+0.7)	4.055	0.372	0.992	5	K.GFGVDFNSEEDAK#.E
SW:NUCL_HUMAN	H09	4125	2	1323.4	(+0.4)	2.936	0.397	0.985	4	K.GLSEDTEETLK.E
SW:NUCL_HUMAN	H09	4097	2	1343.4	(+0.1)	2.682	0.355	0.934	4	K.GL*SEDTEETL*K#.E
SW:NUCL_HUMAN	H09	4193	2	1343.4	(+0.3)	2.493	0.466	0.966	4	K.GL*SEDTEETL*K#.E
SW:NUCL_HUMAN	H06	11578	2	1595.7	(+0.7)	2.241	0.133	0.503	4	K.GYAFIEFASFEDAK.E
SW:NUCL_HUMAN	H06	7138	2	1799.9	(+0.9)	3.127	0.291	0.958	3	R.K#FGYVDFESAEDL*EK#.A
SW:NUCL_HUMAN	H06	5626	2	1001.1	(+0.8)	2.595	0.402	0.985	3	K.NDLAVVDVR.I
SW:NUCL_HUMAN	H06	9460	3	2534.8	(-0.4)	4.800	0.585	0.999	4	K.TL*VL*SNL*SYSATEETL*QEVFEK#.A
SW:NUCL_HUMAN	H07	9636	2	2502.8	(-0.5)	2.749	0.383	0.947	4	K.TLVLSNLSYSATEETLQEVFEK.A
SW:NUCL_HUMAN	H06	1510	1	764.9	(-0.1)	2.108	0.350	0.000	3	K.VAVATPAK#.K
SW:NUCL_HUMAN	H06	1506	1	756.9	(-0.2)	1.902	0.398	0.000	3	K.VAVATPAK.K
SW:NUCL_HUMAN	H07	1648	1	764.9	(-0.2)	2.069	0.255	0.000	3	K.VAVATPAK#.K
SW:NUCL_HUMAN	H06	9118	3	2333.6	(+0.7)	5.047	0.465	0.840	3	K.VEGTEPTTAFNL*FVGNL*NFNK#.S
SW:NUCL_HUMAN	H06	9074	2	2313.6	(-0.7)	3.790	0.504	1.000	3	K.VEGTEPTTAFNLFVGNLNFNK.S
SW:NUCL_HUMAN	H07	9292	2	2313.6	(+1.0)	5.005	0.548	1.000	3	K.VEGTEPTTAFNLFVGNLNFNK.S
SW:NUCL_HUMAN	H07	9276	3	2333.6	(+0.7)	4.165	0.391	0.999	3	K.VEGTEPTTAFNL*FVGNL*NFNK#.S
SW:NUCL_HUMAN	H09	9123	3	2333.6	(+0.3)	4.960	0.426	0.995	3	K.VEGTEPTTAFNL*FVGNL*NFNK#.S
SW:NUCL_HUMAN	H10	9257	3	2333.6	(+1.0)	4.218	0.470	0.999	3	K.VEGTEPTTAFNL*FVGNL*NFNK#.S
SW:NUCL_HUMAN	H18	7086	2	1562.6	(-0.5)	2.873	0.379	0.948	5	K.GFGVDFNSEEDAK.E
SW:ORC2_HUMAN	H09	8451	3	2272.5	(+0.9)	5.396	0.481	0.996	1	K.M@L*EVHFGDDDDVL*NHIL*DR.E
SW:ORC2_HUMAN	H09	9179	2	1464.7	(+0.8)	3.350	0.391	0.982	1	R.SIL*DQL*DWIVNK#.F
SW:ORC2_HUMAN	H09	5065	2	1014.1	(+0.8)	2.452	0.341	0.969	1	K.SEFL*STAPR.S
SW:ORC3_HUMAN	H08	8391	2	1646.0	(+0.2)	2.980	0.484	0.666	2	R.AVSELELLGFIKPTK.Q
SW:ORC3_HUMAN	H08	7505	2	1795.1	(+0.9)	3.053	0.524	0.994	3	R.IALHTALNNPYYLK.N
SW:ORC3_HUMAN	H08	11111	2	2178.5	(+0.7)	4.353	0.614	1.000	3	R.LINLVDWSEAFATVVTAAEK.M
SW:ORC3_HUMAN	H08	1563	2	1437.5	(+0.2)	2.567	0.408	0.461	4	K.SK#EEESVHVTQR.K
SW:ORC3_HUMAN	H09	10707	2	1520.7	(+0.5)	2.580	0.304	0.941	3	K.NL*FDNL*IEFL*QK#.S
SW:ORC4_HUMAN	H13	5996	2	1559.6	(+0.7)	3.332	0.473	0.994	2	K.WNENVQYL*SEDR.S
SW:ORC4_HUMAN	H13	7946	2	1647.9	(-0.2)	2.625	0.197	0.664	2	K.L*L*L*DNTQIMNAL*QK#.Y

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ORC6_HUMAN	H17	5654	2	1585.6	(+0.1)	4.348	0.449	1.000		K.DEDL*TQDYEEWK#.R
SW:ORC6_HUMAN	H17	5666	2	1571.6	(+0.3)	2.717	0.272	0.882		K.DEDLTQDYEEWK.R
SW:ORC6_HUMAN	H17	6110	2	1133.3	(-0.3)	2.389	0.180	0.652	1	R.L*GL*AEPDML*R.K
SW:OXRP_HUMAN	H05	6168	2	1296.6	(+0.9)	3.581	0.350	0.776		K.LPATEKPVLLSK.D
SW:OXRP_HUMAN	H05	6746	2	1348.5	(+0.6)	2.827	0.354	0.977		R.SLAEDFAEQPIK.D
SW:P2G4_HUMAN	H13	1968	2	945.1	(+0.9)	2.594	0.409	0.986	3	K.AL*L*QSSASR.K
SW:P2G4_HUMAN	H13	4572	2	1190.3	(+0.3)	3.498	0.467	1.000	2	K.GDAMIMEETGK#.I
SW:P2G4_HUMAN	H13	7802	2	1656.9	(+0.4)	2.455	0.177	0.732	3	K.HEL*L*QPFNVL*YEK#.E
SW:P2G4_HUMAN	H13	10872	3	3243.6	(+0.8)	3.933	0.383	0.997	3	K.IDL*GVHVDGFIANVAHTFVVDVAQGTQVTGR.K
SW:P2G4_HUMAN	H13	10796	3	3243.6	(+0.3)	3.839	0.522	0.999	3	K.IDL*GVHVDGFIANVAHTFVVDVAQGTQVTGR.K
SW:P2G4_HUMAN	H13	6468	2	1367.5	(+0.3)	2.952	0.394	0.529	3	R.ITSGPFEPDLYK.S
SW:P2G4_HUMAN	H13	4812	2	1279.4	(+0.8)	3.968	0.383	0.994	3	K.SEMEVQDAELK.A
SW:P2G4_HUMAN	H13	4804	2	1293.4	(+0.7)	3.418	0.338	0.986	3	K.SEMEVQDAEL*K#.A
SW:P2G4_HUMAN	H13	4724	2	1293.4	(-0.2)	2.344	0.122	0.381	3	K.SEMEVQDAEL*K#.A
SW:PAB1_HUMAN	H09	6675	2	1429.6	(-0.1)	3.919	0.437	1.000	2	R.K#EFSPFGTITSAK#.V
SW:PAB1_HUMAN	H09	6331	3	1716.9	(+0.8)	4.782	0.572*	0.056	5	R.SK#VDEAVAVL*QAHQAK#.E
SW:PAB1_HUMAN	H09	7237	2	1267.5	(+0.8)	2.947	0.396	0.987	4	R.ALDTMNFVLIK.G
SW:PCB1_HUMAN	H14	9551	3	3380.9	(-0.2)	4.438	0.494	0.995		K.AFAMIIDKLEEDINSSMTNSTAASRPPVTLR.L
SW:PCB1_HUMAN	H14	5213	2	2113.3	(+0.9)	4.154	0.546	1.000	4	R.ESTGAQVQVAGDM@L*PNSTER.A
SW:PCB1_HUMAN	H14	5987	2	2097.3	(-0.7)	3.655	0.515	1.000	4	R.ESTGAQVQVAGDML*PNSTER.A
SW:PCB1_HUMAN	H14	5985	2	2091.3	(-0.7)	3.325	0.481	0.953	4	R.ESTGAQVQVAGDMLPNSTER.A
SW:PCB1_HUMAN	H15	5270	2	2113.3	(+0.3)	2.405	0.361	0.899	4	R.ESTGAQVQVAGDM@L*PNSTER.A
SW:PCB1_HUMAN	H14	5699	3	2518.7	(+0.5)	3.942	0.436	0.992		K.L*EEDINSSM@TNSTAASRPPVTL*R.L
SW:PCB1_HUMAN	H15	6000	2	2097.3	(-0.5)	2.225	0.208	0.525	4	R.ESTGAQVQVAGDML*PNSTER.A
SW:PCB2_HUMAN	H14	9819	3	3353.8	(+0.5)	3.972	0.479	0.991		K.AFAMIIDKLEEDISSMTNSTAASRPPVTLR.L
SW:PCB2_HUMAN	H14	9817	3	3373.8	(-0.2)	3.740	0.372	0.916		K.AFAMIIDK#L*EEDISSMTNSTAASRPPVTL*R.L
SW:PCB2_HUMAN	H15	10054	3	3373.8	(-0.6)	4.467	0.392	0.969		K.AFAMIIDK#L*EEDISSMTNSTAASRPPVTL*R.L
SW:PCB2_HUMAN	H15	10068	3	3353.8	(+0.4)	4.456	0.491	0.998		K.AFAMIIDKLEEDISSMTNSTAASRPPVTLR.L
SW:PCB2_HUMAN	H14	7627	2	1359.7	(-0.9)	3.274	0.454	0.948		R.IITLAGPTNAIFK.A
SW:PCB2_HUMAN	H16	7112	2	1359.7	(+0.7)	3.095	0.357	0.980		R.IITLAGPTNAIFK.A
SW:PCB2_HUMAN	H16	7110	2	1373.7	(+0.6)	2.339	0.347	0.939		R.IITL*AGPTNAIFK#.A
SW:PCB2_HUMAN	H15	6902	3	3384.8	(+0.7)	6.903	0.607	0.985		K.LHQLAMQQSHFPMTHGNTGFSGIESSSPEVK.G
SW:PCB2_HUMAN	H15	6898	3	3404.8	(-0.8)	4.957	0.502	1.000		K.L*HQL*AMQQSHFPMTHGNTGFSGIESSSPEVK#.G
SW:PCB2_HUMAN	H18	7474	2	1373.7	(+0.5)	2.279	0.448	0.973		R.IITL*AGPTNAIFK#.A
SW:PCNA_HUMAN	H16	5002	2	1308.4	(+1.0)	2.984	0.379	0.981		K.FSASGEL*GNGNIK#.L
SW:PCNA_HUMAN	H16	5778	2	1402.6	(-0.3)	3.347	0.432*	0.378		R.NL*AM@GVNL*TSMSK#.I
SW:PCNA_HUMAN	H16	4862	2	1418.6	(+0.1)	3.171	0.378	0.964		R.NL*AM@GVNL*TSM@SK#.I
SW:PCNA_HUMAN	H16	6300	2	1386.6	(-0.0)	3.101	0.342	0.951		R.NL*AMGVNL*TSMSK#.I
SW:PCNA_HUMAN	H16	4852	2	1294.4	(+0.4)	2.526	0.398	0.975		K.FSASGELGNGNIK.L
SW:PDA3_HUMAN	H11	8506	2	1383.5	(+0.9)	2.829	0.409	0.985	7	R.EL*SDFISYL*QR.E
SW:PDA3_HUMAN	H11	2402	2	1192.3	(+1.0)	2.935	0.421	0.989	7	R.LAPEYEAATR.L
SW:PDA3_HUMAN	H11	7622	2	1360.5	(+0.2)	2.585	0.335	0.928	5	R.FLQDYFDGNLK.R
SW:PDA4_HUMAN	H08	6457	2	1141.3	(+0.9)	2.236	0.262	0.865		R.FDVSGYPTL*K#.I
SW:PDA4_HUMAN	H08	5525	2	1318.5	(+0.6)	2.628	0.241	0.920		K.FHHTFSTEIAK.F
SW:PDA4_HUMAN	H08	5199	2	1191.3	(+1.0)	3.265	0.412	0.991		K.IDATSASVLASR.F
SW:PDA4_HUMAN	H09	7693	2	1636.8	(+0.4)	3.356	0.511	0.999		K.VEGFPTIYFAPSGDK#.K
SW:PDA4_HUMAN	H09	5247	2	1197.3	(+0.3)	2.723	0.397	0.961		K.IDATSASVL*ASR.F
SW:PDX1_HUMAN	H19	5050	2	1173.3	(+0.9)	2.574	0.189	0.746	1	K.ATAVMPDGGQFK#.D
SW:PDX1_HUMAN	H19	5154	1	941.0	(+0.6)	2.230	0.112	0.000	1	K.DISLSDYK.G
SW:PDX1_HUMAN	H18	6862	2	935.1	(+0.6)	2.340	0.206	0.833	3	R.GL*FIIDDK#.G
SW:PDX1_HUMAN	H19	6732	2	935.1	(+0.8)	2.696	0.191	0.898	3	R.GL*FIIDDK#.G
SW:PDX1_HUMAN	H19	6648	2	921.1	(+0.6)	2.679	0.256	0.941	3	R.GLFIIDDK.G
SW:PDX1_HUMAN	H19	6714	2	921.1	(-0.7)	2.579	0.163	0.495	3	R.GLFIIDDK.G
SW:PDX1_HUMAN	H19	6664	1	935.1	(-0.4)	2.399	0.218	0.000	3	R.GL*FIIDDK#.G
SW:PDX1_HUMAN	H19	4322	2	981.1	(+0.3)	2.592	0.340*	0.255	1	K.IGHPAPNFK.A
SW:PDX1_HUMAN	H19	6204	2	1796.1	(-0.5)	3.152	0.348	0.948	2	K.K#QGGL*GPM@NIPL*VSDPK#.R

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:PDX1_HUMAN	H19	6908	2	1780.1	(-0.3)	2.722	0.251	0.798	2	K.K#QGGL*GPMNIPL*VSDPK#.R
SW:PDX1_HUMAN	H18	6406	2	1211.4	(+0.8)	3.270	0.424	0.992	2	R.L*VQAFQFTDK#.H
SW:PDX1_HUMAN	H18	6402	2	1197.4	(+1.0)	3.264	0.499	0.999	2	R.LVQAFQFTDK.H
SW:PDX1_HUMAN	H19	6196	2	1211.4	(+0.4)	3.071	0.366	0.985	2	R.L*VQAFQFTDK#.H
SW:PDX1_HUMAN	H19	6082	2	1211.4	(+0.6)	3.022	0.346	0.981	2	R.L*VQAFQFTDK#.H
SW:PDX1_HUMAN	H19	6206	1	1211.4	(-0.8)	2.399	0.156	0.000	2	R.L*VQAFQFTDK#.H
SW:PDX1_HUMAN	H21	6210	2	1197.4	(+0.8)	3.339	0.438	0.993	2	R.LVQAFQFTDK.H
SW:PDX1_HUMAN	H19	7194	2	1643.9	(-0.6)	2.877	0.372	0.942	2	K.QGGL*GPMNIPL*VSDPK#.R
SW:PDX1_HUMAN	H19	6570	2	1643.9	(-0.5)	2.434	0.246	0.698	2	K.QGGL*GPMNIPL*VSDPK#.R
SW:PDX1_HUMAN	H19	5566	2	1122.3	(-0.4)	3.047	0.349	0.964	2	R.TIAQDYGVL*K#.A
SW:PDX1_HUMAN	H19	5574	2	1108.3	(-0.3)	2.517	0.380	0.952	2	R.TIAQDYGVLK.A
SW:PDX1_HUMAN	H21	6206	2	1211.4	(+0.9)	2.745	0.291	0.957	2	R.L*VQAFQFTDK#.H
SW:PDX2_HUMAN	H19	8908	2	1736.0	(+0.8)	3.549	0.543	0.998	1	K.EGGLGPLNIPLLDVTR.R
SW:PDX2_HUMAN	H19	5220	2	1024.2	(-0.4)	2.649	0.349	0.954	2	R.LSEYGVLK.T
SW:PDX2_HUMAN	H19	5210	2	1044.2	(+0.3)	2.203	0.296	0.829	2	R.L*SEYGVLK#.T
SW:PERI_HUMAN	H11	7122	2	1318.5	(+0.8)	2.691	0.108	0.728	9	K.M@AL*DIEIATYR.K
SW:PERI_HUMAN	H11	6556	2	1324.4	(+0.1)	3.030	0.337	0.959	9	K.NL*QEAEWYK#.S
SW:PERI_HUMAN	H11	6580	2	1310.4	(+0.0)	2.994	0.292	0.946	9	K.NLQEAEWYK.S
SW:PERI_HUMAN	H12	6286	2	1324.4	(+0.3)	2.860	0.390	0.968	9	K.NL*QEAEWYK#.S
SW:PERI_HUMAN	H18	6090	2	1310.4	(+0.6)	3.451	0.453	1.000	9	K.NLQEAEWYK.S
SW:PGK1_HUMAN	H13	5372	2	1368.6	(+0.8)	4.289	0.467	1.000	1	R.AHSSMVGVNLPQK.A
SW:PGK1_HUMAN	H13	2528	2	1398.6	(+0.7)	3.702	0.571*	0.689	1	R.AHSSM@VGNL*PQK#.A
SW:PGK1_HUMAN	H13	2744	2	1398.6	(+0.3)	3.240	0.481*	0.339	1	R.AHSSM@VGNL*PQK#.A
SW:PGK1_HUMAN	H13	5374	2	1382.6	(+0.5)	3.204	0.467*	0.469	1	R.AHSSMVGVNLPQK#.A
SW:PGK1_HUMAN	H13	2818	2	1398.6	(+0.6)	2.996	0.527*	0.427	1	R.AHSSM@VGNL*PQK#.A
SW:PGK1_HUMAN	H13	2672	2	1398.6	(+0.4)	2.936	0.483*	0.401	1	R.AHSSM@VGNL*PQK#.A
SW:PGK1_HUMAN	H13	3030	2	1398.6	(-0.3)	2.886	0.479	0.978	1	R.AHSSM@VGNL*PQK#.A
SW:PGK1_HUMAN	H13	2600	2	1398.6	(+0.4)	2.821	0.505*	0.350	1	R.AHSSM@VGNL*PQK#.A
SW:PGK1_HUMAN	H13	2450	2	1398.6	(-0.5)	2.694	0.365	0.935	1	R.AHSSM@VGNL*PQK#.A
SW:PGK1_HUMAN	H13	8252	2	1796.1	(-0.7)	3.077	0.244	0.064	1	K.AL*ESPERPFL*AIL*GGAK#.V
SW:PGK1_HUMAN	H13	6370	2	1641.8	(+0.5)	4.026	0.549	1.000	8	K.L*GDVYVNDAFGTAHR.A
SW:PGK1_HUMAN	H13	3120	2	1398.6	(+0.5)	2.599	0.589*	0.255	1	R.AHSSM@VGNL*PQK#.A
SW:PIN1_HUMAN	H20	7186	2	1750.0	(+0.9)	4.102	0.504	0.995		R.TKEEALELINGYIQK.I
SW:PIN1_HUMAN	H20	7180	2	1778.0	(-0.1)	4.020	0.434	0.725		R.TK#EEAL*EL*INGYIQK#.I
SW:PIN1_HUMAN	H20	7360	2	2053.3	(+0.1)	3.319	0.497	0.987		R.TGEM@SGPVFTDSGIHIL*.R.T
SW:PLSL_HUMAN	H10	10919	2	2700.1	(-0.9)	3.379	0.427	0.935	2	K.ISTSLPVLDLIDAIQPGSINYDLLK.T
SW:PLSL_HUMAN	H10	10903	2	2700.1	(+0.4)	2.986	0.360	0.977	2	K.ISTSLPVLDLIDAIQPGSINYDLLK.T
SW:PLSL_HUMAN	H09	7013	3	2540.8	(+0.2)	4.230	0.370	0.906	2	R.YPALHKPENQDIDWGALEGETR.E
SW:PLSL_HUMAN	H10	7171	3	2540.8	(+0.4)	3.754	0.415	0.987	2	R.YPALHKPENQDIDWGALEGETR.E
SW:PLSL_HUMAN	H10	7303	2	1676.8	(+0.3)	2.508	0.345	0.899	2	K.FSLVGIGGQDLNEG.NR.T
SW:PP1A_HUMAN	H15	6770	2	1648.8	(+0.7)	4.047	0.406	0.993	8	R.AHQVVEDGYEFFAK#.R
SW:PP1A_HUMAN	H15	9808	2	1954.4	(+0.8)	4.238	0.625	1.000	8	R.EIFLSQPILLELEAPL.K.I
SW:PP1A_HUMAN	H15	7966	2	1460.7	(-0.1)	2.301	0.246	0.103	8	K.IK#YPENFFL*L*.R.G
SW:PP1A_HUMAN	H15	2398	2	1204.4	(-0.9)	2.249	0.321*	0.001		R.L*L*EVQGSRPGK#.N
SW:PPIA_HUMAN	H20	8674	2	1953.2	(+0.5)	4.051	0.542	1.000		-.VNPTVFFDIAVDGEPL*GR.V
SW:PPIA_HUMAN	H20	8432	2	1947.2	(+0.4)	2.699	0.443	0.984		-.VNPTVFFDIAVDGEPLGR.V
SW:PPIA_HUMAN	H20	8682	2	1947.2	(-0.9)	2.413	0.480	0.890		-.VNPTVFFDIAVDGEPLGR.V
SW:PPIA_HUMAN	H21	8594	2	1947.2	(+0.1)	3.668	0.555	1.000		-.VNPTVFFDIAVDGEPLGR.V
SW:PPIA_HUMAN	H20	7058	2	1070.2	(+0.6)	2.676	0.479	0.991	4	R.VSFEL*FADK#.V
SW:PPIA_HUMAN	H21	8546	2	1953.2	(+0.2)	3.603	0.548	1.000		-.VNPTVFFDIAVDGEPL*GR.V
SW:PPIB_HUMAN	H19	6546	2	1466.6	(+0.5)	3.986	0.420	0.994	2	K.DTNGSQFFITTVK#.T
SW:PPIB_HUMAN	H19	6460	2	1458.6	(+0.0)	3.847	0.549	0.999	2	K.DTNGSQFFITTVK.T
SW:PPIB_HUMAN	H19	6434	2	1466.6	(+0.2)	3.608	0.403	0.980	2	K.DTNGSQFFITTVK#.T
SW:PPIB_HUMAN	H19	5888	2	1475.7	(+1.0)	4.618	0.549	1.000	2	K.HYGPWVSMANAGK.D
SW:PPIB_HUMAN	H19	5882	2	1483.7	(+0.4)	4.191	0.476	1.000	2	K.HYGPWVSMANAGK#.D
SW:PPIB_HUMAN	H19	5940	2	1261.5	(+0.4)	2.863	0.210	0.287	2	K.IEVEK#PFAIAK#.E
SW:PPIB_HUMAN	H19	6848	2	1365.5	(+0.5)	3.702	0.470	0.999	2	K.TVDNFVALATGEK.G
SW:PPIB_HUMAN	H19	4054	2	1054.2	(-0.8)	2.301	0.336	0.741	2	K.VL*EGM@EVVR.K

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:PPIE_HUMAN	H16	6422	2	1507.7	(+0.3)	4.969	0.569	1.000	2	R.VLYVGGLAEEVDDK.V
SW:PPIE_HUMAN	H16	7356	2	1682.9	(-1.0)	2.841	0.302	0.733	3	K.HVVFGEVTEGL*DVL*R.Q
SW:PPOL_HUMAN	H06	6072	2	1369.5	(-0.5)	2.623	0.265	0.855	5	K.AM@VEYEIDL*QK#.M
SW:PPOL_HUMAN	H06	7058	2	1229.4	(-0.6)	3.122	0.336	0.963	4	K.AQNDL*IWNK#.D
SW:PPOL_HUMAN	H06	7670	2	1728.9	(-0.5)	2.502	0.141	0.029	4	K.AQNDL*IWNK#DEL*K#.K
SW:PPOL_HUMAN	H06	6002	2	2010.1	(+0.3)	4.107	0.527	0.978	5	K.GGAAVDPDSSL*EHSAPV*EK#.G
SW:PPOL_HUMAN	H07	5918	2	1990.1	(-0.5)	3.954	0.509	1.000	5	K.GGAAVDPDSSGLEHSAHVLEK.G
SW:PPOL_HUMAN	H06	4622	2	1842.9	(-1.0)	3.434	0.201	0.063	5	R.GGSDSSK#DPIDVNYEK#.L
SW:PPOL_HUMAN	H07	4804	2	1826.9	(+0.9)	5.204	0.497	0.999	5	R.GGSDSSK#DPIDVNYEK.L
SW:PPOL_HUMAN	H07	4740	2	1842.9	(-0.6)	3.496	0.267	0.320	5	R.GGSDSSK#DPIDVNYEK#.L
SW:PPOL_HUMAN	H06	6522	2	1506.6	(+0.9)	2.829	0.366	0.977	5	R.HPDVEVDGFSEL*R.W
SW:PPOL_HUMAN	H07	7220	2	2045.3	(-0.5)	3.226	0.400	0.972	5	K.KFYPLEIDYGQDEEAVK.K
SW:PPOL_HUMAN	H07	2056	2	1377.4	(-1.0)	3.578	0.371	0.919	5	R.K#GDEVDGVDEVAK#.K
SW:PPOL_HUMAN	H06	5292	3	1523.7	(+0.8)	3.879	0.326	0.994	5	K.K#PPL*L*NNADSVQAK#.V
SW:PPOL_HUMAN	H06	5270	2	1523.7	(+0.1)	3.556	0.448	0.983	5	K.K#PPL*L*NNADSVQAK#.V
SW:PPOL_HUMAN	H06	4886	2	1523.7	(-0.7)	3.017	0.375	0.864	5	K.K#PPL*L*NNADSVQAK#.V
SW:PPOL_HUMAN	H06	4992	2	1523.7	(+0.6)	2.703	0.394	0.975	5	K.K#PPL*L*NNADSVQAK#.V
SW:PPOL_HUMAN	H07	4960	2	1523.7	(-0.7)	3.295	0.442	0.933	5	K.K#PPL*L*NNADSVQAK#.V
SW:PPOL_HUMAN	H06	6040	3	1972.2	(+0.4)	4.606	0.353*	0.035	4	K.L*EQMPK#EDAIEHFM@K#.L
SW:PPOL_HUMAN	H06	5474	3	1988.2	(+0.7)	4.162	0.389*	0.027	4	K.L*EQM@PSK#EDAIEHFM@K#.L
SW:PPOL_HUMAN	H06	5468	2	1399.5	(+0.0)	2.659	0.244	0.180	5	K.L*QL*L*EDDK#ENR.Y
SW:PPOL_HUMAN	H07	5430	2	1373.5	(+0.5)	3.216	0.324	0.689	5	K.LQLEDDKENR.Y
SW:PPOL_HUMAN	H06	6276	2	1495.8	(+0.5)	3.244	0.370*	0.531	6	R.M@AIMVQSPM@FDGK#.V
SW:PPOL_HUMAN	H06	6610	2	1479.8	(+0.3)	3.011	0.504*	0.257	6	R.MAIMVQSPM@FDGK#.V
SW:PPOL_HUMAN	H06	7280	2	1463.8	(+0.7)	2.957	0.499	0.986	6	R.MAIMVQSPMFDGK#.V
SW:PPOL_HUMAN	H06	5196	2	1276.5	(+0.3)	2.637	0.178	0.092	5	K.M@IFDVESM@K#K#.A
SW:PPOL_HUMAN	H06	6306	2	1643.9	(+0.0)	2.794	0.279	0.222	5	K.MVDPEK#PQL*GMIDR.W
SW:PPOL_HUMAN	H06	6300	2	2045.2	(-0.2)	2.712	0.317	0.232	5	K.NREEL*GFRPEYSASQL*K#.G
SW:PPOL_HUMAN	H06	8112	2	2217.4	(+0.9)	4.906	0.552	1.000	5	K.NTHATTHNAYDL*EVIDIFK#.I
SW:PPOL_HUMAN	H07	8284	2	2203.4	(+0.9)	4.525	0.534	1.000	5	K.NTHATTHNAYDLEVIDIFK.I
SW:PPOL_HUMAN	H17	7456	3	2217.4	(+0.1)	3.937	0.489	0.998	5	K.NTHATTHNAYDL*EVIDIFK#.I
SW:PPOL_HUMAN	H18	7956	3	2217.4	(+0.5)	4.421	0.478	1.000	5	K.NTHATTHNAYDL*EVIDIFK#.I
SW:PPOL_HUMAN	H06	5372	2	1406.5	(+0.7)	2.284	0.171	0.670	4	K.QQVPSGESAIL*DR.V
SW:PPOL_HUMAN	H07	5356	2	1400.5	(+0.8)	2.533	0.401	0.974	4	K.QQVPSGESAILDR.V
SW:PPOL_HUMAN	H06	9522	3	3511.8	(-0.4)	3.770	0.240	0.835	5	K.RQQAAYSIL*SEVQQAVSQGSSDSQIL*DL*SNR.F
SW:PPOL_HUMAN	H07	10086	2	2139.5	(-0.3)	5.410	0.558	1.000	5	K.SLQELFLAHILSPWGAEVK.A
SW:PPOL_HUMAN	H07	10056	2	2171.5	(+0.0)	4.612	0.536	0.999	5	K.SL*QEL*FL*AHIL*SPWGAEVK#.A
SW:PPOL_HUMAN	H08	9993	2	2139.5	(+0.1)	4.389	0.458	1.000	5	K.SLQELFLAHILSPWGAEVK.A
SW:PPOL_HUMAN	H09	10009	2	2139.5	(+0.4)	2.684	0.379	0.972	5	K.SLQELFLAHILSPWGAEVK.A
SW:PPOL_HUMAN	H10	10111	2	2139.5	(-0.5)	2.958	0.393	0.962	5	K.SLQELFLAHILSPWGAEVK.A
SW:PPOL_HUMAN	H06	6408	2	1200.3	(+0.4)	2.910	0.549	1.000	5	K.TL*GDFAAEYAK#.S
SW:PPOL_HUMAN	H07	6408	2	1200.3	(+0.7)	2.802	0.585	1.000	5	K.TL*GDFAAEYAK#.S
SW:PPOL_HUMAN	H18	6244	2	1200.3	(+0.7)	3.079	0.599	0.999	5	K.TL*GDFAAEYAK#.S
SW:PPOL_HUMAN	H06	7750	2	1390.6	(+0.6)	2.352	0.374	0.959	5	R.TTNFAGIL*SQGL*R.I
SW:PPOL_HUMAN	H07	7866	2	1378.6	(-0.8)	3.438	0.404	0.937	5	R.TTNFAGILSQGLR.I
SW:PPOL_HUMAN	H17	7094	2	1390.6	(+0.5)	3.378	0.407	0.991	5	R.TTNFAGIL*SQGL*R.I
SW:PPOL_HUMAN	H18	7572	2	1390.6	(+0.2)	2.380	0.404	0.938	5	R.TTNFAGIL*SQGL*R.I
SW:PPOL_HUMAN	H19	7508	2	1390.6	(+0.5)	3.334	0.478	0.994	5	R.TTNFAGIL*SQGL*R.I
SW:PPOL_HUMAN	H07	7146	2	1625.8	(-0.2)	3.158	0.474	0.983	5	R.VVSEDFLQDVSASTK.S
SW:PPOL_HUMAN	H19	6064	2	1200.3	(-0.0)	2.676	0.492	0.979	5	K.TL*GDFAAEYAK#.S
SW:PPR8_HUMAN	H13	6522	3	2423.7	(+0.5)	4.581	0.516	1.000		R.L*EPHK#PQQIPIDSTVSFGASTR.A
SW:PPR8_HUMAN	H13	5330	2	1474.6	(+0.5)	3.010	0.541	0.994	2	R.VEGPGSLGLEESGSR.R
SW:PR4B_HUMAN	H05	5784	2	849.0	(+0.4)	2.343	0.385	0.975	4	R.APEIIGK#.S
SW:PR4B_HUMAN	H05	7786	2	1741.0	(+0.2)	2.215	0.404	0.910	4	R.ISINQALQHAFIQEK.I
SW:PRKD_HUMAN	H04	8491	2	1176.4	(-0.2)	2.358	0.241	0.734	3	K.AAL*SAL*ESFL*K#.Q
SW:PRKD_HUMAN	H05	8596	2	1150.4	(+0.6)	2.512	0.426	0.983	3	K.AALSALSF.LK.Q
SW:PRKD_HUMAN	H02	7458	3	3144.6	(+0.5)	5.338	0.557	1.000	3	R.AGLLHNILPSQSTDLHHSVGTTELLSLVYK.G
SW:PRKD_HUMAN	H03	9148	3	3144.6	(+0.2)	4.176	0.505	0.999	3	R.AGLLHNILPSQSTDLHHSVGTTELLSLVYK.G
SW:PRKD_HUMAN	H05	9130	3	3144.6	(+0.6)	4.562	0.427	0.999	3	R.AGLLHNILPSQSTDLHHSVGTTELLSLVYK.G
SW:PRKD_HUMAN	H04	2311	2	1646.7	(+0.5)	2.792	0.320	0.952	4	R.AQEPESGL*SEETQVK#.C
SW:PRKD_HUMAN	H04	6611	2	1447.6	(-0.2)	2.490	0.252	0.783	2	K.DL*L*L*NTMSQEEK#.A

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:PRKD_HUMAN	H04	5515	2	1463.6	(-0.4)	2.409	0.247	0.746	2	K.DL*L*L*NTM@SQEEK#.A
SW:PRKD_HUMAN	H02	5662	2	1294.5	(-0.1)	2.321	0.301	0.824	4	R.DQNILLGTTYR.I
SW:PRKD_HUMAN	H03	6490	2	1294.5	(+0.8)	3.179	0.280	0.974	4	R.DQNILLGTTYR.I
SW:PRKD_HUMAN	H03	6482	2	1306.5	(-0.0)	2.337	0.199	0.645	4	R.DQNIL*L*GTTYR.I
SW:PRKD_HUMAN	H04	6227	2	1294.5	(+1.0)	3.393	0.286	0.981	4	R.DQNILLGTTYR.I
SW:PRKD_HUMAN	H03	10512	2	1588.9	(+0.5)	3.119	0.335	0.974	3	K.EVYAAAAEVLGLILR.Y
SW:PRKD_HUMAN	H03	10530	2	1606.9	(+0.4)	2.540	0.248	0.877	3	K.EVYAAAAEVL*GL*IL*R.Y
SW:PRKD_HUMAN	H02	7320	2	1363.7	(+0.3)	2.240	0.369	0.898	2	R.FM@NAVFFL*L*PK#.F
SW:PRKD_HUMAN	H03	8870	2	1363.7	(-0.4)	2.735	0.341	0.937	2	R.FM@NAVFFL*L*PK#.F
SW:PRKD_HUMAN	H03	9584	2	1347.7	(+0.1)	2.460	0.358	0.920	2	R.FMNAVFFL*L*PK#.F
SW:PRKD_HUMAN	H04	8745	2	1363.7	(-0.1)	2.689	0.237	0.829	2	R.FM@NAVFFL*L*PK#.F
SW:PRKD_HUMAN	H04	9485	2	1347.7	(+0.2)	2.618	0.385	0.949	2	R.FMNAVFFL*L*PK#.F
SW:PRKD_HUMAN	H04	7285	2	1642.8	(-0.5)	2.817	0.209	0.117	3	K.FYQGFL*FSEK#PEK#.N
SW:PRKD_HUMAN	H06	7306	2	1642.8	(+0.3)	2.636	0.279	0.175	3	K.FYQGFL*FSEK#PEK#.N
SW:PRKD_HUMAN	H02	8328	2	2337.7	(-0.0)	3.177	0.425	0.976	2	K.GQAVTLLPFFTSLTGGSLLEELR.R
SW:PRKD_HUMAN	H04	10249	2	2337.7	(-0.5)	2.237	0.181	0.444	2	K.GQAVTLLPFFTSLTGGSLLEELR.R
SW:PRKD_HUMAN	H03	6386	2	1150.3	(+0.5)	3.152	0.498	0.967	2	R.HGDL*PDIQIK#.H
SW:PRKD_HUMAN	H04	6121	2	1150.3	(+0.5)	3.522	0.439	1.000	2	R.HGDL*PDIQIK#.H
SW:PRKD_HUMAN	H05	6430	2	1150.3	(+0.7)	2.830	0.385	0.980	2	R.HGDL*PDIQIK#.H
SW:PRKD_HUMAN	H02	5022	2	867.0	(+0.4)	2.408	0.193*	0.433	2	R.HNLEIK.T
SW:PRKD_HUMAN	H04	6933	2	1521.8	(+0.1)	3.766	0.425	0.985	2	K.HSSLITPLQAVAQR.D
SW:PRKD_HUMAN	H04	6929	2	1533.8	(+0.2)	3.212	0.384	0.970	2	K.HSSL*ITPL*QAVAQR.D
SW:PRKD_HUMAN	H02	4800	2	1481.6	(-0.2)	3.574	0.476	1.000	4	R.ILELSGSSSEDEK.V
SW:PRKD_HUMAN	H04	4945	2	1481.6	(+0.6)	3.890	0.437	0.994	4	R.ILELSGSSSEDEK.V
SW:PRKD_HUMAN	H04	4935	2	1501.6	(-0.7)	3.636	0.432	0.943	4	R.IL*EL*SGSSSEDEK#.V
SW:PRKD_HUMAN	H04	6819	2	1575.8	(+0.5)	3.809	0.431	0.993	3	K.K#GGSWIQEINVAEK#.N
SW:PRKD_HUMAN	H03	7054	2	1231.4	(+0.8)	2.365	0.479	0.984	3	K.L*ATTIL*QHWK#.K
SW:PRKD_HUMAN	H04	7045	2	1339.5	(+0.8)	2.207	0.429	0.972	3	R.LGASLAFNNIYR.E
SW:PRKD_HUMAN	H02	8528	2	1661.9	(+0.1)	3.702	0.384	0.977	3	R.L*GL*IEWL*ENTVTL*K#.D
SW:PRKD_HUMAN	H03	10606	2	1661.9	(-0.3)	3.220	0.292	0.927	3	R.L*GL*IEWL*ENTVTL*K#.D
SW:PRKD_HUMAN	H04	10579	2	1661.9	(+0.4)	3.706	0.412	0.991	3	R.L*GL*IEWL*ENTVTL*K#.D
SW:PRKD_HUMAN	H05	10666	2	1629.9	(+0.7)	4.212	0.468	1.000	3	R.LGLIEWLENTVTLK.D
SW:PRKD_HUMAN	H05	10664	2	1661.9	(-0.1)	3.305	0.318	0.946	3	R.L*GL*IEWL*ENTVTL*K#.D
SW:PRKD_HUMAN	H08	10657	2	1629.9	(+0.6)	2.321	0.411	0.968	3	R.LGLIEWLENTVTLK.D
SW:PRKD_HUMAN	H09	10683	2	1661.9	(+0.3)	3.278	0.314	0.943	3	R.L*GL*IEWL*ENTVTL*K#.D
SW:PRKD_HUMAN	H03	5620	2	1177.3	(+0.7)	2.898	0.396	0.985	2	R.L*GL*PGDEVDNK#.V
SW:PRKD_HUMAN	H03	5618	2	1157.3	(+0.0)	2.384	0.297	0.862	2	R.LGLPGDEVDNK.V
SW:PRKD_HUMAN	H04	5247	2	1157.3	(+0.6)	2.904	0.505	0.994	2	R.LGLPGDEVDNK.V
SW:PRKD_HUMAN	H04	5229	2	1177.3	(+1.0)	2.249	0.349	0.940	2	R.L*GL*PGDEVDNK#.V
SW:PRKD_HUMAN	H03	7370	2	1206.5	(+0.7)	2.421	0.311	0.944	3	K.LGNPIVPLNIR.L
SW:PRKD_HUMAN	H04	8909	2	1905.2	(-0.1)	3.539	0.406	0.979	2	K.LLLQGEADQSLLTFIDK.A
SW:PRKD_HUMAN	H06	8958	2	1905.2	(+0.5)	2.502	0.427	0.977	2	K.LLLQGEADQSLLTFIDK.A
SW:PRKD_HUMAN	H05	5968	2	1018.2	(+0.9)	2.454	0.285	0.955	2	R.LLNTWTNR.Y
SW:PRKD_HUMAN	H02	5228	2	1397.5	(+0.1)	2.321	0.372	0.916	3	K.LNESTFDTQITK.K
SW:PRKD_HUMAN	H03	5924	2	1411.5	(+0.4)	3.947	0.549	0.999	3	K.L*NESTFDTQITK#.K
SW:PRKD_HUMAN	H03	5926	2	1397.5	(-0.4)	3.706	0.445	0.998	3	K.LNESTFDTQITK.K
SW:PRKD_HUMAN	H04	5611	2	1411.5	(+0.4)	3.675	0.492	0.990	3	K.L*NESTFDTQITK#.K
SW:PRKD_HUMAN	H04	5607	2	1397.5	(+0.7)	2.935	0.238	0.928	3	K.LNESTFDTQITK.K
SW:PRKD_HUMAN	H05	5986	2	1397.5	(+0.7)	3.599	0.428	0.994	3	K.LNESTFDTQITK.K
SW:PRKD_HUMAN	H05	5984	2	1411.5	(-0.0)	3.507	0.289	0.947	3	K.L*NESTFDTQITK#.K
SW:PRKD_HUMAN	H02	9179	2	2182.5	(+0.7)	4.233	0.417	0.994	2	K.LQSVQALTEIQEFISFISK.Q
SW:PRKD_HUMAN	H02	9173	3	2202.5	(+0.7)	3.787	0.422	0.998	2	K.L*QSVQAL*TEIQEFISFISK#.Q
SW:PRKD_HUMAN	H03	11158	2	2182.5	(+0.3)	3.740	0.454	0.987	2	K.LQSVQALTEIQEFISFISK.Q
SW:PRKD_HUMAN	H03	11160	2	2202.5	(-0.8)	3.103	0.299	0.764	2	K.L*QSVQAL*TEIQEFISFISK#.Q
SW:PRKD_HUMAN	H04	11197	2	2182.5	(+0.1)	4.132	0.454	1.000	2	K.LQSVQALTEIQEFISFISK.Q
SW:PRKD_HUMAN	H04	11261	3	2202.5	(+0.5)	3.755	0.375	0.997	2	K.L*QSVQAL*TEIQEFISFISK#.Q
SW:PRKD_HUMAN	H05	11230	2	2182.5	(-0.5)	2.514	0.281	0.820	2	K.LQSVQALTEIQEFISFISK.Q
SW:PRKD_HUMAN	H06	11206	2	2182.5	(+0.2)	3.501	0.423	0.981	2	K.LQSVQALTEIQEFISFISK.Q
SW:PRKD_HUMAN	H04	9073	2	1637.9	(+0.6)	4.706	0.443	1.000	3	K.LSDFNDITNMLLLK.M
SW:PRKD_HUMAN	H04	9071	2	1669.9	(+0.6)	3.131	0.360	0.979	3	K.L*SDFNDITNML*L*L*K#.M
SW:PRKD_HUMAN	H05	9200	2	1637.9	(+0.1)	4.384	0.396	1.000	3	K.LSDFNDITNMLLLK.M
SW:PRKD_HUMAN	H06	9128	2	1637.9	(+0.4)	3.981	0.305	0.986	3	K.LSDFNDITNMLLLK.M
SW:PRKD_HUMAN	H07	9340	2	1637.9	(+0.5)	2.944	0.330	0.971	3	K.LSDFNDITNMLLLK.M
SW:PRKD_HUMAN	H11	9440	2	1637.9	(+0.8)	2.770	0.299	0.950	3	K.LSDFNDITNMLLLK.M
SW:PRKD_HUMAN	H04	6921	2	1400.6	(+0.5)	2.769	0.351	0.971	3	R.L*YSL*AL*HPNAFK#.R
SW:PRKD_HUMAN	H04	4991	2	1381.6	(+0.0)	3.202	0.392	0.631	2	K.M@K#QDAQVVL*YR.S

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:PRKD_HUMAN	H04	7287	2	1697.0	(+0.9)	2.953	0.327	0.963	3	K.M@VSAVL*NGML*DQSFR.E
SW:PRKD_HUMAN	H05	5044	2	966.1	(+0.9)	2.578	0.400	0.984	4	R.MYAALGDPK.A
SW:PRKD_HUMAN	H05	6152	2	1391.5	(+0.4)	2.598	0.218	0.882	4	R.NELEIPGQYDGR.G
SW:PRKD_HUMAN	H02	8002	2	1445.7	(+0.9)	4.187	0.386	0.994	3	K.NLLIFENLIDLK.R
SW:PRKD_HUMAN	H02	7998	2	1477.7	(-0.5)	2.353	0.116	0.338	3	K.NL*L*IFENL*IDL*K#.R
SW:PRKD_HUMAN	H04	9689	2	1445.7	(+0.5)	3.242	0.322	0.981	3	K.NLLIFENLIDLK.R
SW:PRKD_HUMAN	H04	9691	2	1477.7	(+0.6)	2.701	0.174	0.822	3	K.NL*L*IFENL*IDL*K#.R
SW:PRKD_HUMAN	H04	5537	2	1521.7	(-0.3)	2.868	0.459	0.975	3	K.NL*L*TVTSSDEM@M@K#.S
SW:PRKD_HUMAN	H03	6904	2	1575.7	(+0.3)	4.447	0.515	0.918	3	K.NLSSNEAISLEEIR.I
SW:PRKD_HUMAN	H03	6914	2	1587.7	(+0.2)	4.205	0.487	1.000	3	K.NL*SSNEAISL*EEIR.I
SW:PRKD_HUMAN	H03	6984	2	1575.7	(+0.7)	2.273	0.210	0.527	3	K.NLSSNEAISLEEIR.I
SW:PRKD_HUMAN	H04	6673	2	1587.7	(+0.1)	3.844	0.523	0.997	3	K.NL*SSNEAISL*EEIR.I
SW:PRKD_HUMAN	H04	6675	2	1575.7	(+0.7)	3.722	0.507	1.000	3	K.NLSSNEAISLEEIR.I
SW:PRKD_HUMAN	H04	6053	2	1182.3	(+1.0)	2.422	0.417	0.981	3	K.NNWEVSAL*SR.A
SW:PRKD_HUMAN	H03	6284	2	1301.5	(+0.3)	2.671	0.346	0.936	2	K.QITQSALLAEAR.S
SW:PRKD_HUMAN	H05	9428	2	1366.6	(+0.7)	2.255	0.380	0.953	2	K.QL*FSSL*FSGIL*K#.E
SW:PRKD_HUMAN	H03	8346	2	1657.9	(-0.0)	3.433	0.371	0.967	4	R.SDPGL*L*TNTMDVFK#.E
SW:PRKD_HUMAN	H04	8223	2	1657.9	(-0.0)	3.370	0.374	0.966	4	R.SDPGL*L*TNTMDVFK#.E
SW:PRKD_HUMAN	H05	8312	2	1657.9	(-0.5)	3.466	0.419	0.976	4	R.SDPGL*L*TNTMDVFK#.E
SW:PRKD_HUMAN	H06	8234	2	1657.9	(+0.7)	3.214	0.445	0.989	4	R.SDPGL*L*TNTMDVFK#.E
SW:PRKD_HUMAN	H08	8257	2	1657.9	(+0.4)	3.175	0.293	0.961	4	R.SDPGL*L*TNTMDVFK#.E
SW:PRKD_HUMAN	H03	6364	2	1058.2	(+1.0)	2.311	0.327	0.953	2	R.SIGEYDVL*R.G
SW:PRKD_HUMAN	H02	4662	2	1474.6	(+0.4)	3.322	0.495	0.994	3	R.SL*GPPQGEEDSVPR.D
SW:PRKD_HUMAN	H04	4693	2	1474.6	(+0.9)	2.262	0.381	0.953	3	R.SL*GPPQGEEDSVPR.D
SW:PRKD_HUMAN	H02	7068	3	3236.5	(+0.3)	5.671	0.555	1.000	2	R.SSFDWLTGSSTDPDLDHTSPSSDLSLFAHK.R
SW:PRKD_HUMAN	H02	7070	3	3268.5	(-0.9)	4.999	0.522	0.999	2	R.SSFDWL*TGSTDPD*VDHTSPSSDSL*L*FAHK#.R
SW:PRKD_HUMAN	H03	8566	3	3236.5	(+0.5)	4.698	0.438	0.999	2	R.SSFDWLTGSSTDPDLDHTSPSSDLSLFAHK.R
SW:PRKD_HUMAN	H03	8564	3	3268.5	(-0.9)	4.588	0.505	1.000	2	R.SSFDWL*TGSTDPD*VDHTSPSSDSL*L*FAHK#.R
SW:PRKD_HUMAN	H04	8451	3	3236.5	(+0.3)	5.339	0.537	1.000	2	R.SSFDWLTGSSTDPDLDHTSPSSDLSLFAHK.R
SW:PRKD_HUMAN	H04	8443	3	3268.5	(-0.8)	5.315	0.514	1.000	2	R.SSFDWL*TGSTDPD*VDHTSPSSDSL*L*FAHK#.R
SW:PRKD_HUMAN	H03	8298	2	1816.1	(+0.9)	4.483	0.628	1.000	3	R.TVGALQVLGTEAQSSLLK.A
SW:PRKD_HUMAN	H03	8292	3	1848.1	(+0.6)	3.953	0.493	1.000	3	R.TVGAL*QVL*GTEAQSSL*L*K#.A
SW:PRKD_HUMAN	H03	8300	2	1848.1	(-0.9)	2.923	0.340	0.795	3	R.TVGAL*QVL*GTEAQSSL*L*K#.A
SW:PRKD_HUMAN	H03	7520	2	1795.9	(-0.7)	2.468	0.264	0.474	3	K.TVSL*L*DENNVSYSL*SK#.N
SW:PRKD_HUMAN	H04	7341	2	1795.9	(-0.9)	2.367	0.111	0.097	3	K.TVSL*L*DENNVSYSL*SK#.N
SW:PRKD_HUMAN	H04	7227	2	1795.9	(+0.6)	2.344	0.451	0.974	3	K.TVSL*L*DENNVSYSL*SK#.N
SW:PRKD_HUMAN	H05	7484	2	1795.9	(-0.2)	2.210	0.242	0.588	3	K.TVSL*L*DENNVSYSL*SK#.N
SW:PRKD_HUMAN	H02	4924	2	920.1	(+0.9)	2.327	0.391	0.978	4	K.VIAGLYQR.A
SW:PRKD_HUMAN	H03	5802	2	1176.3	(+1.0)	2.632	0.227	0.908	3	R.VTELALTASDR.Q
SW:PRKD_HUMAN	H04	5527	2	1188.3	(+0.6)	2.738	0.351	0.976	3	R.VTEL*AL*TASDR.Q
SW:PRKD_HUMAN	H04	5385	2	1188.3	(+0.2)	2.511	0.417	0.961	3	R.VTEL*AL*TASDR.Q
SW:PRKD_HUMAN	H04	5489	2	1176.3	(+0.9)	2.282	0.226	0.832	3	R.VTELALTASDR.Q
SW:PRKD_HUMAN	H03	6768	2	1332.5	(+0.1)	2.243	0.333	0.859	4	R.YPEETL*SL*MTK#.E
SW:PRKD_HUMAN	H04	6523	2	1312.5	(+0.7)	2.595	0.436	0.986	4	R.YPEETLSLMTK.E
SW:PRKD_HUMAN	H14	10417	2	1661.9	(-0.1)	2.341	0.304	0.804	3	R.L*GL*IEWL*ENTVTL*K#.D
SW:PRO1_HUMAN	H21	7390	2	1626.8	(+0.8)	3.460	0.514	1.000	2	R.DSLLQDGEFSMDLR.T
SW:PRO1_HUMAN	H21	6488	2	1471.7	(+0.2)	3.587	0.575	1.000	2	R.SSFYVNGLTGGQK.C
SW:PRO1_HUMAN	H21	6472	2	1491.7	(+0.6)	3.003	0.395	0.982	2	R.SSFYVNGL*TL*GGQK#.C
SW:PRO1_HUMAN	H21	7802	3	1645.0	(+0.6)	5.013	0.504	1.000	2	K.TFVNITPAEVGVLVGK.D
SW:PRO1_HUMAN	H21	7766	2	1645.0	(-0.9)	2.784	0.445	0.904	2	K.TFVNITPAEVGVLVGK.D
SW:PSB5_HUMAN	H19	4794	2	1281.5	(+0.9)	2.682	0.455	0.987	5	R.ATAGAYIASQTVK.K
SW:PSB5_HUMAN	H19	5536	2	1279.5	(+0.7)	2.449	0.389	0.973	5	K.L*L*ANM@VYQYK#.G
SW:PTB_HUMAN	H11	6482	2	1440.6	(+0.8)	3.383	0.484	1.000	3	R.GQPIYIQFSNHK#.E
SW:PTB_HUMAN	H11	6564	2	1440.6	(+0.6)	2.707	0.494	0.990	3	R.GQPIYIQFSNHK#.E
SW:PTB_HUMAN	H12	6308	2	1440.6	(+0.8)	3.057	0.392	0.985	3	R.GQPIYIQFSNHK#.E
SW:PTB_HUMAN	H10	2157	2	998.1	(+0.8)	2.331	0.133	0.694	3	K.HQNVQL*PR.E
SW:PTB_HUMAN	H11	9056	2	2300.6	(+0.7)	4.886	0.552	1.000	3	R.IAIPGL*AGAGNSVL*L*VSNL*NPER.V
SW:PTB_HUMAN	H11	9054	2	2276.6	(+0.6)	4.785	0.600	0.999	3	R.IAIPGLAGAGNSVLLVSNLNPER.V
SW:PTB_HUMAN	H11	9130	3	2300.6	(+0.9)	3.999	0.463	0.997	3	R.IAIPGL*AGAGNSVL*L*VSNL*NPER.V
SW:PTB_HUMAN	H11	9072	2	2276.6	(-0.6)	3.995	0.546	1.000	3	R.IAIPGLAGAGNSVLLVSNLNPER.V
SW:PTB_HUMAN	H12	8736	2	2300.6	(-0.9)	2.596	0.231	0.467	3	R.IAIPGL*AGAGNSVL*L*VSNL*NPER.V
SW:PTB_HUMAN	H13	8748	2	2276.6	(+0.1)	2.314	0.318	0.829	3	R.IAIPGLAGAGNSVLLVSNLNPER.V
SW:PTB_HUMAN	H14	8665	2	2276.6	(+0.5)	5.842	0.593	1.000	3	R.IAIPGLAGAGNSVLLVSNLNPER.V



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:PTB_HUMAN	H14	8687	2	2276.6	(-0.7)	4.226	0.538	1.000	3	R.IAIPGLAGAGNSVLLVSNLNPER.V
SW:PTB_HUMAN	H11	11434	2	2490.0	(-0.7)	4.635	0.458	1.000	3	R.IIVENLFYPVTLDLVHLQIFSK.F
SW:PTB_HUMAN	H13	11412	2	2490.0	(-0.8)	3.772	0.474	1.000	3	R.IIVENLFYPVTLDLVHLQIFSK.F
SW:PTB_HUMAN	H14	11113	2	2490.0	(-0.0)	3.759	0.422	0.983	3	R.IIVENLFYPVTLDLVHLQIFSK.F
SW:PTB_HUMAN	H21	8488	2	2113.5	(-0.2)	4.304	0.491	1.000	3	R.KLPIDVTEGEVISLGLPFGK.V
SW:PTB_HUMAN	H11	9496	2	1985.3	(+0.8)	3.944	0.599	1.000	3	K.LPIDVTEGEVISLGLPFGK.V
SW:PTB_HUMAN	H11	9490	2	2011.3	(+0.2)	3.434	0.445	0.981	3	K.L*PIDVTEGEVISL*GL*PFGK#.V
SW:PTB_HUMAN	H11	9570	2	2011.3	(+0.5)	3.118	0.506	0.992	3	K.L*PIDVTEGEVISL*GL*PFGK#.V
SW:PTB_HUMAN	H11	8338	2	2244.5	(+0.8)	5.984	0.569	1.000	3	K.NNQFQALLQYADPVSAQHA.K
SW:PTB_HUMAN	H12	8040	3	2264.5	(-0.5)	4.628	0.548	1.000	3	K.NNQFQAL*L*QYADPVSAQHA#.L
SW:PTB_HUMAN	H14	8035	2	2244.5	(+0.3)	4.951	0.559	1.000	3	K.NNQFQALLQYADPVSAQHA.K
SW:PTB_HUMAN	H11	10206	3	2052.4	(+0.3)	3.790	0.491	0.984	3	R.VTPQSL*FIL*FGVYGDVQR.V
SW:PTB_HUMAN	H11	10146	2	2052.4	(-0.2)	3.534	0.361	0.971	3	R.VTPQSL*FIL*FGVYGDVQR.V
SW:PTB_HUMAN	H11	10232	2	2052.4	(+0.8)	2.929	0.426	0.986	3	R.VTPQSL*FIL*FGVYGDVQR.V
SW:PTB_HUMAN	H21	8682	2	1985.3	(-0.3)	3.335	0.437	0.979	3	K.LPIDVTEGEVISLGLPFGK.V
SW:PTN6_HUMAN	H10	8525	2	1471.6	(-0.1)	4.060	0.207	0.950	7	K.AGFWEFESLQK.Q
SW:PTN6_HUMAN	H10	8519	2	1485.6	(+0.9)	3.745	0.456	1.000	7	K.AGFWEFESL*QK#.Q
SW:PTN6_HUMAN	H10	9083	2	2047.3	(+0.5)	2.906	0.507	0.992	5	R.ESLSQPGDFVLSVLSQPK.A
SW:PTN6_HUMAN	H10	2177	2	1535.7	(-0.0)	2.674	0.103	0.025	6	K.HK#EDVYENL*HTK#.N
SW:PTN6_HUMAN	H10	6697	2	1706.8	(+0.7)	3.495	0.466	0.991	7	R.IQNSGDFYDLYGGEK.F
SW:PTN6_HUMAN	H10	6663	2	1720.8	(-0.2)	3.189	0.192	0.799	7	R.IQNSGDFYDL*YGGEK#.F
SW:PTN6_HUMAN	H10	3109	2	1073.3	(+0.7)	3.041	0.228	0.955	7	K.KLEVLQSQK.G
SW:PTN6_HUMAN	H10	3007	2	1073.3	(+0.6)	2.826	0.222	0.935	7	K.KLEVLQSQK.G
SW:PTN6_HUMAN	H10	2903	2	1073.3	(+0.5)	2.742	0.297	0.854	7	K.KLEVLQSQK.G
SW:PTN6_HUMAN	H10	7141	2	1559.7	(+0.7)	3.980	0.467	1.000	7	R.TL*QVSPL*DNGLD*IR.E
SW:PTN6_HUMAN	H10	7157	2	1559.7	(-0.7)	3.482	0.318	0.876	7	R.TL*QVSPL*DNGLD*IR.E
SW:PTN6_HUMAN	H10	7163	2	1541.7	(-0.3)	3.233	0.481	0.985	7	R.TLQVSPLDNGLDIR.E
SW:PTN6_HUMAN	H10	6265	3	2051.3	(+0.4)	3.731	0.490	0.994	7	R.WYHGHM@SGGQAETL*L*QAK#.G
SW:PTN6_HUMAN	H10	10015	2	2272.5	(-0.5)	3.847	0.572	1.000	7	R.YTVGGLETDFDSLTDLVEHFK.K
SW:PTN6_HUMAN	H10	10029	2	2298.5	(-0.9)	2.898	0.292	0.700	7	R.YTVGGL*ETFDL*TDL*VEHFK#.K
SW:PTN6_HUMAN	H10	2183	2	1513.7	(+0.4)	2.559	0.330	0.472	6	K.HKEDVYENLHTK.N
SW:PWP2_HUMAN	H01	6068	2	1170.4	(+0.8)	2.449	0.363	0.971	3	R.FSNLLGTVYR.R
SW:PWP2_HUMAN	H02	6164	2	1170.4	(+0.5)	3.356	0.457	0.999	3	R.FSNLLGTVYR.R
SW:PWP2_HUMAN	H01	5556	2	1225.4	(+0.7)	3.146	0.270	0.970	2	K.LVQEALEAVPR.G
SW:PWP2_HUMAN	H01	7098	2	1806.0	(-0.2)	2.912	0.437	0.972	2	R.VL*FDPFEL*DTSVTPGR.V
SW:PWP2_HUMAN	H02	7274	2	1794.0	(+0.6)	3.543	0.551	1.000	2	R.VLDFPFELDTSVTPGR.V
SW:PWP2_HUMAN	H02	7270	2	1806.0	(+0.1)	2.455	0.456	0.959	2	R.VL*FDPFEL*DTSVTPGR.V
SW:PWP2_HUMAN	H02	7548	2	1454.8	(+0.5)	2.445	0.298	0.917	2	R.AGTL*L*PVIQFL*QK#.S
SW:R10A_HUMAN	H18	7044	2	1513.7	(-0.3)	4.245	0.431	1.000	2	K.K#YDAFL*ASESL*IK#.Q
SW:R10A_HUMAN	H18	7066	2	1485.7	(-0.3)	3.061	0.434	0.978	2	K.KYDAFLASESLIK.Q
SW:R10A_HUMAN	H18	7312	2	1357.5	(+0.8)	3.156	0.494	0.994	2	K.YDAFLASESLIK.Q
SW:R10A_HUMAN	H18	6690	2	1621.9	(+0.0)	2.743	0.245	0.803	2	K.FPSL*L*THNENMVAK#.V
SW:R11A_HUMAN	H18	6698	2	1208.3	(+0.8)	2.791	0.437	0.991	3	R.DDEYDYLK.V
SW:R11A_HUMAN	H18	7728	2	1290.5	(+0.8)	3.564	0.387	0.990	3	R.GAVGALLVYDIAK.H
SW:R11A_HUMAN	H18	7734	2	1310.5	(-0.4)	2.615	0.332	0.904	3	R.GAVGAL*L*VYDIAK#.H
SW:R13A_HUMAN	H18	5204	2	1109.3	(+0.5)	2.751	0.182	0.280	3	K.IDKYTEVLK.T
SW:R13A_HUMAN	H18	5420	2	869.0	(+0.7)	2.429	0.216	0.915	4	R.K#FAYL*GR.L
SW:RA1L_HUMAN	H14	5869	2	1442.7	(+0.5)	3.467	0.336	0.982	2	R.VAIHYINPPNPAK#.D
SW:RA1L_HUMAN	H14	1959	2	1028.2	(+0.1)	2.357	0.315	0.262	2	R.NAAEELKPR.N
SW:RA21_HUMAN	H06	8914	3	2406.6	(+0.8)	4.753	0.474	0.998		K.GGEADNLDEFLEFENPEVPR.E
SW:RA21_HUMAN	H06	4826	2	1224.4	(-0.4)	2.340	0.286	0.852		R.TQQML*HGL*QR.A
SW:RAB7_HUMAN	H18	7816	2	1476.7	(+0.7)	2.881	0.531	0.994	2	R.DPENFPFVVLGNK.I
SW:RAB7_HUMAN	H19	7710	2	1476.7	(+0.9)	4.689	0.508	1.000	2	R.DPENFPFVVLGNK.I
SW:RAB7_HUMAN	H19	7706	2	1490.7	(+0.7)	3.766	0.462*	0.706	2	R.DPENFPFVVL*GNK#.I
SW:RAB7_HUMAN	H19	7018	2	1648.9	(+0.9)	3.941	0.434*	0.748	2	R.LVTMQIWDTAGQER.F
SW:RAB7_HUMAN	H19	5650	2	1072.3	(+0.1)	2.332	0.133	0.409	2	K.VIIL*GDSGVGK#.T
SW:RAB7_HUMAN	H19	5642	2	1058.3	(+0.7)	2.327	0.276	0.907	2	K.VIILGDSGVGK.T

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:RALY_HUMAN	H15	5840	3	2295.6	(-0.2)	3.835	0.484	0.926	3	R.VL*AGQTL* <u>DINM</u> @AGEPK#PDRPK#.G
SW:RALY_HUMAN	H15	1952	2	1044.2	(-0.5)	2.932	0.246	0.914	2	R.L*EQIAAEQK#.A
SW:RAN_HUMAN	H01	5494	2	1295.4	(+0.8)	3.182	0.349*	0.618	4	K.FNVWDTAGQEK.F
SW:RAN_HUMAN	H01	5500	2	1303.4	(+0.5)	2.209	0.376*	0.148	4	K.FNVWDTAGQEK#.F
SW:RAN_HUMAN	H17	5560	2	1303.4	(+0.6)	3.591	0.410*	0.727	4	K.FNVWDTAGQEK#.F
SW:RAN_HUMAN	H18	6126	2	1295.4	(-0.2)	2.261	0.268*	0.095	4	K.FNVWDTAGQEK.F
SW:RAN_HUMAN	H01	5080	2	1215.3	(+1.0)	2.511	0.263	0.931	5	K.NLQYYDISAK.S
SW:RAN_HUMAN	H17	5120	2	1215.3	(+0.1)	2.465	0.354	0.935	5	K.NLQYYDISAK.S
SW:RAN_HUMAN	H17	7768	2	1786.0	(-0.0)	4.087	0.331	0.627	5	K.SNYNFEKPFLLWLAR.K
SW:RAN_HUMAN	H17	7738	2	1806.0	(+0.1)	2.788	0.207	0.113	5	K.SNYNFEK#PFL*WL*AR.K
SW:RAN_HUMAN	H18	5670	2	1229.3	(+0.2)	2.253	0.363	0.904	5	K.NL*QYYDISAK#.S
SW:RAPA_HUMAN	H19	9054	2	1501.7	(+0.6)	4.137	0.525	0.997	2	K.INVNEIFYDL*VR.Q
SW:RAPA_HUMAN	H19	5394	2	1006.2	(+0.9)	2.448	0.316	0.942	3	K.L*VVL*GSGGVGK#.S
SW:RB18_HUMAN	H19	6104	2	1266.4	(+0.8)	3.076	0.316	0.942		K.L*AIWDTAGQER.F
SW:RB18_HUMAN	H19	6202	2	1247.4	(+0.4)	2.393	0.404	0.972		R.NDIVNM@L*VGNK#.I
SW:RB1B_HUMAN	H19	6808	3	2287.5	(+0.6)	3.939	0.461	0.999	2	R.GAHGIIVVYDVTQESYANVK#.Q
SW:RB1B_HUMAN	H19	3932	2	1442.6	(+0.8)	3.469	0.446	0.833		R.MGPGAASGGERPNI.K
SW:RB1B_HUMAN	H19	1924	2	1472.6	(+0.4)	3.078	0.466	0.786		R.M@GPGAASGGERPNI*K#.I
SW:RB1B_HUMAN	H19	3908	2	1456.6	(+0.1)	3.047	0.357	0.403		R.MGPGAASGGERPNI*K#.I
SW:RB2A_HUMAN	H19	6708	2	1551.7	(+1.0)	4.381	0.574	1.000	3	K.LQIWDTAGQESFR.S
SW:RB2A_HUMAN	H19	5988	2	1144.3	(+0.8)	2.424	0.240	0.872	3	K.YIIIGDTGVGK#.S
SW:RB2A_HUMAN	H19	7374	2	1332.5	(+0.9)	2.277	0.323	0.924	4	R.GAAGAL*L*VYDITR.R
SW:RB8A_HUMAN	H19	5992	2	1380.5	(+0.6)	3.519	0.522	0.997	1	K.GYTL*VEYETYK#.E
SW:RB8A_HUMAN	H19	4838	2	957.1	(+0.4)	2.514	0.269	0.952	1	K.FAEYGEIK.N
SW:RBB4_HUMAN	H12	5868	2	1137.2	(+0.8)	3.452	0.534	1.000	1	K.GEFGGFGSVSGK#.I
SW:RBB4_HUMAN	H12	5892	2	1137.2	(-0.9)	3.298	0.471	0.952	1	K.GEFGGFGSVSGK#.I
SW:RBB4_HUMAN	H12	5972	2	1137.2	(+0.9)	2.995	0.595	1.000	1	K.GEFGGFGSVSGK#.I
SW:RBB4_HUMAN	H12	7246	3	2875.1	(+0.8)	4.950	0.570	1.000	1	K.IGEEQSPEDAEDGPPELLFIHGGHTAK.I
SW:RBB4_HUMAN	H12	7240	3	2895.1	(+0.0)	4.034	0.374	0.993	1	K.IGEEQSPEDAEDGPPEL*L*FIHGGHTAK#.I
SW:RBB4_HUMAN	H12	9588	3	3440.8	(+0.6)	7.050	0.652	1.000	1	K.TIFTGHTAVVEDVSWHLLHESLFGSVADDQK.L
SW:RBB4_HUMAN	H12	9586	3	3466.8	(-0.7)	6.178	0.571	1.000	1	K.TIFTGHTAVVEDVSWHL*L*HESL*FGSVADDQK#.L
SW:RBB4_HUMAN	H13	9628	3	3466.8	(-0.2)	4.941	0.497	1.000	1	K.TIFTGHTAVVEDVSWHL*L*HESL*FGSVADDQK#.L
SW:RBB4_HUMAN	H12	6960	2	1486.6	(+0.5)	3.748	0.450	1.000	2	K.TPSSDVL*VFDYTK#.H
SW:RBB4_HUMAN	H12	7000	2	1472.6	(+0.4)	3.262	0.387	0.987	2	K.TPSSDVLVFDYTK.H
SW:RBB4_HUMAN	H13	6924	2	1486.6	(+0.7)	4.140	0.511	1.000	2	K.TPSSDVL*VFDYTK#.H
SW:RBB4_HUMAN	H16	6480	2	1472.6	(+0.3)	3.953	0.514	1.000	2	K.TPSSDVLVFDYTK.H
SW:RBB4_HUMAN	H16	6478	2	1486.6	(-0.3)	3.236	0.423	0.977	2	K.TPSSDVL*VFDYTK#.H
SW:RBB4_HUMAN	H19	6676	2	1486.6	(-0.1)	3.267	0.392	0.971	2	K.TPSSDVL*VFDYTK#.H
SW:RBB4_HUMAN	H19	6678	2	1472.6	(+0.0)	2.294	0.220	0.547	2	K.TPSSDVLVFDYTK.H
SW:RBMF_HUMAN	H06	8338	3	2477.6	(+1.0)	3.840	0.441	0.998	10	K.ISEL*GSQL*SDEAVEDGL*FHEFK#.R
SW:RBMF_HUMAN	H06	5074	2	1194.4	(+0.3)	2.361	0.220	0.098	10	R.VRPAYSL*EPR.V
SW:RBP2_HUMAN	H02	6856	2	1565.8	(+1.0)	3.225	0.436	0.991	1	R.ELLQSFDSALQSVK.S
SW:RBP2_HUMAN	H03	8250	2	1565.8	(+0.0)	2.948	0.224	0.837	1	R.ELLQSFDSALQSVK.S
SW:RBP2_HUMAN	H04	8133	2	1591.8	(+0.1)	2.770	0.388	0.947	1	R.EL*L*QSFDSAL*QSVK#.S
SW:RBP2_HUMAN	H02	6672	2	1598.9	(+0.5)	2.986	0.487	0.989	1	K.ELVGPPLAETVFTPK.T
SW:RBP2_HUMAN	H02	6678	2	1618.9	(+0.1)	2.498	0.506	0.971	1	K.EL*VGPPL*AETVFTPK#.T
SW:RBP2_HUMAN	H03	7984	2	1598.9	(+0.9)	4.116	0.424	0.994	1	K.ELVGPPLAETVFTPK.T
SW:RBP2_HUMAN	H02	4568	2	1214.3	(+0.2)	2.621	0.262	0.804	3	K.FGISEPGNQEK#.K
SW:RBP2_HUMAN	H04	7117	3	3427.6	(-0.3)	4.188	0.404	0.968	2	K.GSGTGAAGASDTTIK#PNPENTGPTL*EWDNYDL*R.E
SW:RBP2_HUMAN	H04	6363	2	1354.6	(+0.1)	2.509	0.418	0.961	3	R.L*L*VQHEINTL*R.A
SW:RBP2_HUMAN	H02	4356	3	2411.4	(-0.0)	4.492	0.409	0.992	3	K.LNQSGTSVGTDEESDVTQEEER.D
SW:RBP2_HUMAN	H03	9100	3	2580.9	(+0.6)	3.827	0.456	0.952	2	K.SKPFAGFNSSATGSLFGFSFNAPLK.S
SW:RBP2_HUMAN	H02	5442	2	1064.2	(+0.7)	3.043	0.279	0.977	4	K.TPELAEEFK.Q
SW:RBP2_HUMAN	H03	4098	2	1248.3	(+0.7)	2.925	0.455	0.980	1	K.VELVTGEEDEK.V
SW:RBP2_HUMAN	H03	4010	2	1248.3	(+0.6)	2.819	0.443	0.990	1	K.VELVTGEEDEK.V
SW:RBP2_HUMAN	H03	4044	2	1262.3	(+0.2)	2.744	0.336	0.935	1	K.VEL*VTGEEDEK#.V
SW:RBP2_HUMAN	H03	3972	2	1262.3	(+0.7)	2.554	0.378	0.972	1	K.VEL*VTGEEDEK#.V

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:RBP2_HUMAN	H04	7833	2	1618.9	(-0.4)	2.393	0.381	0.903	1	K.EL*VGPL*AEVFTPK#.T
SW:RB_HUMAN	H01	5546	2	1285.4	(+0.2)	2.309	0.406	0.593	2	K.DLPHAVQETFK.R
SW:RB_HUMAN	H02	4226	2	1378.4	(+0.7)	3.428	0.527	1.000	2	R.FDIEGSDEADGSK#.H
SW:RB_HUMAN	H02	4154	2	1378.4	(+0.8)	2.578	0.518	0.986	2	R.FDIEGSDEADGSK#.H
SW:RB_HUMAN	H03	10524	2	2127.5	(-0.3)	3.248	0.338	0.948	2	R.IM@ESL*AWL*SDSPL*FDL*IK#.Q
SW:RB_HUMAN	H06	10490	2	2127.5	(+1.0)	2.941	0.467	0.988	2	R.IM@ESL*AWL*SDSPL*FDL*IK#.Q
SW:RB_HUMAN	H01	5884	2	1272.5	(+0.2)	3.146	0.415	0.978	3	R.IPGGNIYISPLK.S
SW:RB_HUMAN	H02	6002	2	1286.5	(-0.0)	2.517	0.422	0.954	3	R.IPGGNIYISPL*K#.S
SW:RB_HUMAN	H02	5496	2	1641.7	(-0.3)	2.817	0.419	0.966	2	K.TLQTDSDSDFETQR.T
SW:RB_HUMAN	H01	6504	3	2473.9	(+0.4)	4.740	0.521	1.000	2	K.TNILQYASTRPPTLSPIPHIPR.S
SW:RB_HUMAN	H02	6634	3	2485.9	(+0.7)	4.060	0.372	0.979	2	K.TNIL*QYASTRPPTL*SPIPHIPR.S
SW:RB_HUMAN	H06	10874	2	2111.5	(-0.1)	2.342	0.206	0.544	2	R.IMESL*AWL*SDSPL*FDL*IK#.Q
SW:RCC1_HUMAN	H13	7718	2	1639.0	(+0.6)	3.694	0.465	0.994	1	K.SMVPVQVQLDVPVVK.V
SW:RCC1_HUMAN	H13	7186	2	1669.0	(-0.2)	3.512	0.340	0.913	1	K.SM@VPVQVQL*DVPVVK#.V
SW:RCC1_HUMAN	H13	4840	2	1906.0	(-0.5)	4.155	0.507	1.000	1	K.VVQVSAGDSHTAAL*TDDGR.V
SW:RCC1_HUMAN	H13	7712	2	1653.0	(-0.1)	2.600	0.422	0.949	1	K.SMVPVQVQL*DVPVVK#.V
SW:RCQ1_HUMAN	H09	7619	2	1819.2	(+0.6)	4.271	0.534	0.999	3	K.FRPLQLETINVTMAGK.E
SW:RCQ1_HUMAN	H09	7625	2	1839.2	(-0.9)	3.415	0.230	0.082	3	K.FRPL*QL*ETINVTMAGK#.E
SW:RCQ1_HUMAN	H09	8175	2	1507.8	(+0.4)	3.397	0.446	0.992	3	K.IIAHFL*IQQYL*K#.E
SW:RCQ1_HUMAN	H09	6169	2	1558.8	(+0.3)	3.980	0.512	1.000	3	R.ISSMVMENVGQQK#.L
SW:RCQ1_HUMAN	H09	6539	2	1508.7	(+0.4)	4.360	0.602	1.000	3	K.QLGISATMLNASSSK.E
SW:RCQ1_HUMAN	H09	6533	2	1528.7	(-0.3)	3.316	0.415	0.972	3	K.QL*GISATML*NASSSK#.E
SW:RCQ1_HUMAN	H09	5625	2	1544.7	(-0.6)	3.205	0.328	0.941	3	K.QL*GISATM@L*NASSSK#.E
SW:RCQ1_HUMAN	H09	7267	2	1226.5	(+0.0)	2.617	0.394	0.464	3	K.VK#DIL*QNVFK#.L
SW:REQU_HUMAN	H13	8250	2	1688.9	(+0.9)	4.861	0.574	0.973	1	K.EGLISQDGSLSLEALLR.T
SW:REQU_HUMAN	H13	8526	2	2642.7	(-0.0)	4.310	0.406	0.987	1	R.ILEPDDFLDLDDEDEYEDTPK.R
SW:REQU_HUMAN	H13	8524	2	2668.7	(+0.6)	3.976	0.431	0.993	1	R.IL*EPDDL*DDL*DDEDEYEDTPK#.R
SW:REQU_HUMAN	H13	6112	2	1651.7	(+0.8)	4.481	0.404	1.000	1	R.VDDDSLGEFPTNSR.A
SW:REQU_HUMAN	H13	6116	2	1657.7	(+0.4)	3.917	0.430	0.993	1	R.VDDDSL*GEFPTNSR.A
SW:REQU_HUMAN	H13	6042	2	1549.7	(+0.4)	3.135	0.494	0.993	1	R.GPGL*ASGQL*YSYPAR.R
SW:RFA3_HUMAN	H21	9846	3	2512.8	(+0.1)	4.165	0.500	0.996		K.NGTIEL*MEPL*DEEISGIVEVGR.V
SW:RFA3_HUMAN	H21	9038	3	2528.8	(+0.8)	3.704	0.417	0.873		K.NGTIEL*M@EPL*DEEISGIVEVGR.V
SW:RFA3_HUMAN	H21	7986	2	2040.3	(+0.4)	3.102	0.487	0.992		K.IIHDFPQFYPLGIVQHD.-
SW:RFC1_HUMAN	H05	8840	2	1161.4	(+0.7)	2.688	0.345	0.969	4	R.GGIQEL*IGL*IK#.H
SW:RFC1_HUMAN	H05	8220	2	1343.6	(+0.1)	2.265	0.321	0.865	4	R.TVNMDYL*SL*L*.R.D
SW:RFC2_HUMAN	H14	6919	2	1655.8	(+0.1)	3.979	0.419	0.984	3	K.APGSAGHYEL*PWVEK#.Y
SW:RFC2_HUMAN	H14	6551	2	1642.9	(+0.7)	3.745	0.431	0.992	3	R.EGNVPNIIIAGPPGTGK#.T
SW:RFC2_HUMAN	H14	6569	2	1634.9	(+0.4)	3.558	0.487	1.000	3	R.EGNVPNIIIAGPPGTGK.T
SW:RFC2_HUMAN	H14	9679	2	1757.1	(+0.8)	4.298	0.557	1.000	3	K.IAEGVNSLLQMAGLLAR.L
SW:RFC2_HUMAN	H14	7807	2	2061.3	(+0.6)	4.068	0.567	1.000	1	K.IIILDEADSMTDGAQQALR.R
SW:RFC2_HUMAN	H14	4997	2	1452.6	(+0.7)	4.706	0.339	0.992	2	K.L*NEIVGNEDTVSR.L
SW:RFC2_HUMAN	H14	5019	2	1446.6	(+0.2)	4.042	0.320	0.977	2	K.LNEIVGNEDTVSR.L
SW:RFC2_HUMAN	H14	9043	3	2583.8	(+0.3)	4.034	0.484	0.999	3	R.QAL*NNL*QSTFSGFGFINSENVFK#.V
SW:RFC2_HUMAN	H14	5477	2	1043.2	(+0.7)	2.604	0.399	0.985	3	K.L*TDAQIL*TR.L
SW:RFC3_HUMAN	H14	6289	2	1335.5	(+0.2)	2.466	0.336	0.906		K.EGLNLPSQLAHR.L
SW:RFC3_HUMAN	H14	1803	2	1596.7	(+0.7)	3.770	0.322	0.986		K.TVAQSQQLE*ETNSQR.D
SW:RFC3_HUMAN	H14	1805	2	1590.7	(+0.6)	3.718	0.481	1.000		K.TVAQSQQLE*ETNSQR.D
SW:RFC3_HUMAN	H15	1842	2	1596.7	(+0.5)	2.842	0.206	0.879		K.TVAQSQQLE*ETNSQR.D
SW:RFC4_HUMAN	H15	9136	3	3120.4	(-0.5)	6.702	0.522	0.999	2	K.DL*IDEGHAATQL*VNQL*HDVVVNNL*SDK#.Q
SW:RFC4_HUMAN	H15	5796	2	1180.3	(+0.7)	3.330	0.452	0.994	2	K.NFAQLTVSGSR.S
SW:RFC4_HUMAN	H15	5794	2	1186.3	(+0.8)	2.594	0.237	0.909	2	K.NFAQL*TVSGSR.S
SW:RFC4_HUMAN	H15	8636	2	2047.3	(+0.5)	2.763	0.508	0.988	2	K.SLEGADLPNLLFYGPPGTGK.T
SW:RFC4_HUMAN	H15	5018	2	1158.2	(+0.8)	2.541	0.279	0.944	3	R.VL*EL*NASDER.G
SW:RFC5_HUMAN	H15	9364	2	1559.8	(+0.2)	2.680	0.337	0.919		K.IQL*SSL*IAAFQVTR.D
SW:RFC5_HUMAN	H15	7978	3	2510.8	(+0.2)	6.037	0.506	0.973		K.YRPQTL*NDL*ISHQDIL*STIQK#.F
SW:RFC5_HUMAN	H15	7848	2	1369.7	(-0.1)	2.401	0.338	0.899		R.FGPL*TPEL*MVPR.L

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:RFX5_HUMAN	H09	5859	2	1143.3	(+0.5)	3.148	0.321	0.981		K.VEGIL*QDVQK#.F
SW:RFX5_HUMAN	H09	2195	2	1647.8	(+0.5)	2.253	0.342	0.916	1	R.TAEVPVSEASGQAPPAK#.A
SW:RGP1_HUMAN	H08	7249	2	1490.6	(+0.5)	2.948	0.393	0.983	1	R.L*ENDGATAL*AEAFR.V
SW:RGP1_HUMAN	H08	6207	2	1422.6	(-0.3)	2.248	0.273	0.742	1	R.VINL*NDNTFTEK#.G
SW:RGP1_HUMAN	H10	5649	2	1136.3	(+0.8)	2.222	0.378	0.959	1	K.TQVAGGQLSFK.G
SW:RIB1_HUMAN	H09	7853	3	2569.9	(+0.9)	4.751	0.466	0.998	1	R.APDELHYTYLDTFGRPVIVAYK.K
SW:RIB1_HUMAN	H09	7861	3	2589.9	(+0.4)	4.627	0.434	0.997	1	R.APDEL*HYTYL*DTFGRPVIVAYK#.K
SW:RIB1_HUMAN	H09	8811	2	1660.9	(+0.7)	3.765	0.381	0.990	2	R.ATSFLLALEPELEAR.L
SW:RIB1_HUMAN	H09	8701	3	2898.3	(+0.0)	4.822	0.438	0.999	1	K.ISVIVETVYTHVL*HPYPTQITQSEK#.Q
SW:RIB1_HUMAN	H09	8721	3	2884.3	(+0.2)	4.583	0.491	0.999	1	K.ISVIVETVYTHVLHPYPTQITQSEK.Q
SW:RIB1_HUMAN	H10	7161	2	1666.9	(+0.2)	2.295	0.178	0.465	1	K.VTAEVVL*AHL*GGGSTRS.A
SW:RIB2_HUMAN	H01	7618	2	1373.5	(+0.6)	4.197	0.503	1.000	4	R.SIVEEIEDLVAR.L
SW:RIB2_HUMAN	H10	9737	2	1373.5	(+0.3)	3.535	0.486	1.000	4	R.SIVEEIEDLVAR.L
SW:RIB2_HUMAN	H10	9733	2	1379.5	(+0.6)	3.020	0.306	0.972	4	R.SIVEEIEDL*VAR.L
SW:RIB2_HUMAN	H11	10032	2	1636.9	(+1.0)	3.648	0.478	0.799	4	K.EDQVIQLMNAIFSK.K
SW:RL13_HUMAN	H17	5898	2	1395.7	(+0.3)	2.530	0.426	0.958	3	K.L*ATQL*TGPVMPVR.N
SW:RL13_HUMAN	H18	1900	2	1233.3	(+0.7)	2.661	0.461	0.989	5	K.STESLQANVQR.L
SW:RL14_HUMAN	H18	5694	2	1241.4	(+0.9)	3.679	0.479	0.988	9	R.VAYVSFGPHAGK#.L
SW:RL14_HUMAN	H18	5718	2	1241.4	(-0.4)	3.298	0.538	0.999	9	R.VAYVSFGPHAGK#.L
SW:RL14_HUMAN	H18	7424	2	1355.6	(+0.8)	3.008	0.476	0.993	9	K.LVAIVDVIDQNR.A
SW:RL15_HUMAN	H18	2028	2	1706.9	(+0.7)	3.186	0.496	0.850	5	K.GATYGKPVHHGVNQLK.F
SW:RL15_HUMAN	H18	5620	2	1580.8	(+0.1)	2.877	0.425*	0.010	4	R.NPDTQWITK#PVHK#.H
SW:RL15_HUMAN	H18	2208	2	1025.1	(+0.9)	2.557	0.391	0.982	4	R.SL*QSVAEER.A
SW:RL15_HUMAN	H18	6386	2	1675.8	(-0.9)	3.468	0.379	0.902	5	R.VL*NSYWVGEDSTYK#.F
SW:RL15_HUMAN	H18	2030	2	1728.9	(+0.0)	2.530	0.303	0.166	5	K.GATYGK#PVHHGVNQL*K#.F
SW:RL18_HUMAN	H18	7554	2	1461.7	(+0.6)	3.858	0.502	0.927	2	K.ILTFDQLALDSPK.G
SW:RL18_HUMAN	H18	7580	2	1487.7	(+0.1)	3.168	0.447	0.979	2	K.IL*TFDQL*AL*DSPK#.G
SW:RL18_HUMAN	H19	7478	2	1461.7	(+0.8)	3.936	0.524	1.000	2	K.ILTFDQLALDSPK.G
SW:RL18_HUMAN	H19	7480	2	1487.7	(+0.4)	3.633	0.530	1.000	2	K.IL*TFDQL*AL*DSPK#.G
SW:RL18_HUMAN	H18	4986	2	1153.3	(+1.0)	2.246	0.336	0.405	1	R.TNRPPL*SL*SR.M
SW:RL18_HUMAN	H19	4910	2	1153.3	(-0.9)	2.395	0.145	0.014	1	R.TNRPPL*SL*SR.M
SW:RL18_HUMAN	H19	1850	2	1556.7	(+0.3)	2.311	0.402	0.322	2	K.APGTPHSHTK#PYVR.S
SW:RL21_HUMAN	H19	7930	2	2115.4	(+0.6)	3.788	0.474	1.000	3	R.TNGK#EPEL*L*EPIPYEFM@A.-
SW:RL21_HUMAN	H19	7948	2	2115.4	(-0.7)	3.183	0.408	0.288	3	R.TNGK#EPEL*L*EPIPYEFM@A.-
SW:RL21_HUMAN	H19	8498	2	2079.4	(+0.9)	3.005	0.318	0.529	3	R.TNGKEPELLEPIPYEFMA.-
SW:RL21_HUMAN	H19	5950	2	1641.9	(-0.7)	5.074	0.577	0.996	2	R.VYNVTQHAVGIVVVK.Q
SW:RL21_HUMAN	H19	5932	2	1649.9	(+0.6)	4.418	0.508	1.000	2	R.VYNVTQHAVGIVVVK#.Q
SW:RL21_HUMAN	H19	5936	2	1641.9	(+0.8)	4.172	0.547	1.000	2	R.VYNVTQHAVGIVVVK.Q
SW:RL21_HUMAN	H19	7852	2	2115.4	(-0.7)	2.826	0.309	0.100	3	R.TNGK#EPEL*L*EPIPYEFM@A.-
SW:RL27_HUMAN	H20	6048	2	2273.4	(+0.6)	2.308	0.243	0.145	1	K.NIDDGTSRDPYSHALVAGIDR.Y
SW:RL27_HUMAN	H20	6024	2	1064.2	(+0.7)	2.521	0.360	0.967	1	R.YSVDIPL*DK#.T
SW:RL27_HUMAN	H20	4860	2	1430.6	(+0.6)	2.288	0.274	0.898	1	K.VYNYNHL*M@PTR.Y
SW:RL2B_HUMAN	H19	7740	2	1633.9	(-0.7)	2.366	0.254	0.366	3	K.IEDNNTL*VFIVDK#.A
SW:RL2B_HUMAN	H19	5392	2	1087.3	(+0.6)	2.674	0.229	0.928	3	K.K#L*YDIDVAK#.V
SW:RL2B_HUMAN	H19	5774	2	1405.5	(+0.8)	3.261	0.507	1.000	4	R.LAPDYDALDVANK.I
SW:RL2B_HUMAN	H19	4474	2	1242.4	(+0.1)	3.551	0.441	1.000	3	K.VNTLIRPDGEK.K
SW:RL2B_HUMAN	H19	4518	2	1256.4	(+0.4)	2.320	0.320	0.239	3	K.VNTL*IRPDGEK#.K
SW:RL2B_HUMAN	H19	1460	2	838.0	(+0.8)	2.291	0.139	0.738	2	K.KEAPAPPK.A
SW:RL30_HUMAN	H21	6106	2	1484.7	(-0.3)	3.751	0.473	0.999		R.K#SEIEYYAM@L*AK#.T
SW:RL30_HUMAN	H21	6666	2	1332.5	(+0.6)	3.734	0.470	1.000		K.SEIEYYAML*AK#.T
SW:RL31_HUMAN	H20	7876	2	1666.0	(-0.4)	2.391	0.357	0.887	1	K.L*YTL*VTYVPVTTTFK#.N
SW:RL31_HUMAN	H20	3908	2	1146.2	(+1.0)	2.201	0.156	0.663	1	K.NLQTVNVN DEN.-

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:RL38_HUMAN	H22	6890	2	1249.5	(+0.7)	2.607	0.359	0.973	1	R.YL*YTL*VITDK#.E
SW:RL38_HUMAN	H22	6668	2	1514.7	(+0.1)	2.636	0.292	0.214	1	R.YL*YTL*VITDK#EK#.A
SW:RL38_HUMAN	H22	6582	2	1486.7	(+0.4)	2.305	0.396	0.531	1	R.YLYTLVITDKEK.A
SW:RL4_HUMAN	H13	1946	2	957.1	(+0.9)	4.101	0.485	0.960	1	K.AAAAAAALQAK.S
SW:RL4_HUMAN	H13	7682	2	1609.9	(-0.1)	3.343	0.450	0.983		R.IEEVPELPLVVEDK.V
SW:RL4_HUMAN	H13	6440	2	1153.3	(+0.9)	2.575	0.316	0.968	2	K.LDELYGTWR.K
SW:RL4_HUMAN	H13	4366	2	1104.3	(-0.0)	2.556	0.387	0.962	2	K.SNYNLPMHK.M
SW:RL4_HUMAN	H13	4434	2	1118.3	(+0.5)	2.294	0.246	0.868	2	K.SNYNL*PMHK#.M
SW:RL5_HUMAN	H01	4758	2	1339.5	(+0.4)	3.116	0.350	0.979	3	K.GAVDGGLSIPHSTK.R
SW:RL5_HUMAN	H15	5506	2	1353.5	(+0.2)	3.022	0.265	0.885	3	K.GAVDGGI*SIPHSTK#.R
SW:RL5_HUMAN	H16	3344	2	1194.3	(+0.5)	2.332	0.128	0.621	3	K.RFPGYDSESK#.E
SW:RL6_HUMAN	H15	9976	2	1526.9	(-0.1)	3.586	0.555	1.000	7	R.ASITPGTILILTGR.H
SW:RL6_HUMAN	H15	5022	2	1341.4	(+0.8)	3.371	0.412	0.991	6	R.HQEGEIFDTEK#.E
SW:RL6_HUMAN	H15	4860	2	1341.4	(+0.2)	3.326	0.403	0.979	6	R.HQEGEIFDTEK#.E
SW:RL6_HUMAN	H15	4942	2	1341.4	(+0.4)	2.945	0.419	0.988	6	R.HQEGEIFDTEK#.E
SW:RL6_HUMAN	H15	4964	2	1333.4	(+0.7)	2.888	0.350	0.980	6	R.HQEGEIFDTEK.E
SW:RL6_HUMAN	H15	4832	2	1590.7	(+0.6)	4.705	0.484	1.000	6	R.HQEGEIFDTEKEK.Y
SW:RL6_HUMAN	H15	4834	2	1606.7	(-0.2)	4.233	0.424	1.000	6	R.HQEGEIFDTEK#EK#.Y
SW:RL6_HUMAN	H15	3216	2	1285.5	(+0.6)	2.871	0.434	0.756	7	K.VLATVTKPVGGDK.N
SW:RL6_HUMAN	H15	3076	2	1285.5	(+0.5)	2.795	0.432	0.737	7	K.VLATVTKPVGGDK.N
SW:RL6_HUMAN	H15	3308	2	1307.5	(+0.5)	2.701	0.261	0.301	7	K.VL*ATVTK#PVGGDK#.N
SW:RL6_HUMAN	H15	3442	2	1285.5	(+0.8)	2.699	0.456	0.753	7	K.VLATVTKPVGGDK.N
SW:RL6_HUMAN	H15	2888	2	1285.5	(+0.4)	2.584	0.407	0.637	7	K.VLATVTKPVGGDK.N
SW:RL6_HUMAN	H15	3232	2	1307.5	(-0.2)	2.539	0.286	0.165	7	K.VL*ATVTK#PVGGDK#.N
SW:RL6_HUMAN	H15	2984	2	1285.5	(+0.9)	2.528	0.387	0.575	7	K.VLATVTKPVGGDK.N
SW:RL6_HUMAN	H15	3080	2	1307.5	(-0.1)	2.418	0.276	0.126	7	K.VL*ATVTK#PVGGDK#.N
SW:RL6_HUMAN	H15	3966	2	1307.5	(+0.6)	2.308	0.160	0.058	7	K.VL*ATVTK#PVGGDK#.N
SW:RL6_HUMAN	H15	3156	2	1307.5	(-0.1)	2.213	0.131	0.015	7	K.VL*ATVTK#PVGGDK#.N
SW:RL7A_HUMAN	H16	5724	2	1360.5	(+0.4)	3.809	0.457	1.000	2	R.AGVNTVTTL*VENK#.K
SW:RL7A_HUMAN	H16	5728	2	1346.5	(+0.8)	2.764	0.371	0.977	2	R.AGVNTVTTLVENK.K
SW:RL7A_HUMAN	H16	7556	3	1832.1	(-0.3)	4.539	0.392	0.986	1	R.L*K#VPPAINQFTQAL*DR.Q
SW:RL7A_HUMAN	H17	7422	3	1832.1	(-0.3)	3.811	0.358	0.943	1	R.L*K#VPPAINQFTQAL*DR.Q
SW:RL7A_HUMAN	H16	5526	2	1217.4	(+0.9)	3.460	0.299	0.984	1	K.NFGIGQDIQPK.R
SW:RL7A_HUMAN	H16	5528	2	1225.4	(+0.7)	2.973	0.339	0.977	1	K.NFGIGQDIQPK#.R
SW:RL7A_HUMAN	H16	1454	1	860.1	(-0.4)	1.980	0.342	0.000	2	K.VAPAPAVVK#.K
SW:RL7A_HUMAN	H16	1452	1	852.1	(-0.3)	1.939	0.460	0.000	2	K.VAPAPAVVK.K
SW:RL7A_HUMAN	H16	7010	2	1570.8	(+0.5)	4.028	0.424	0.994	1	K.VPPAINQFTQALDR.Q
SW:RL7A_HUMAN	H16	7020	2	1576.8	(+0.5)	3.763	0.416	0.993	1	K.VPPAINQFTQAL*DR.Q
SW:RL7A_HUMAN	H17	5294	2	1225.4	(+0.4)	2.229	0.322	0.921	1	K.NFGIGQDIQPK#.R
SW:RL7_HUMAN	H16	7462	2	1664.0	(+0.2)	3.511	0.517*	0.435	2	R.IVEPYIAWGYPNLK.S
SW:RL7_HUMAN	H16	7466	2	1678.0	(+0.0)	2.760	0.404	0.954	2	R.IVEPYIAWGYPNL*K#.S
SW:RL7_HUMAN	H17	7352	2	1664.0	(-0.4)	4.009	0.499*	0.595	2	R.IVEPYIAWGYPNLK.S
SW:RL7_HUMAN	H17	4934	2	1321.5	(-0.3)	2.675	0.358*	0.194	1	R.KAGNFYVPAEPK.L
SW:RL7_HUMAN	H17	5892	2	1183.4	(+0.9)	2.642	0.461	0.988	1	R.IAL*TDNAL*IAR.S
SW:RL9_HUMAN	H18	6500	2	1185.3	(+0.3)	2.784	0.452	0.977	2	K.FL*DGIYVSEK#.G
SW:RL9_HUMAN	H18	7468	2	2114.4	(+0.7)	4.160	0.475	0.995		K.TILSNQTVDIPENVITLK.G
SW:RL9_HUMAN	H18	7490	2	2114.4	(-0.7)	2.947	0.366	0.852		K.TILSNQTVDIPENVITLK.G
SW:RL9_HUMAN	H18	6368	2	1321.5	(-0.1)	2.643	0.164	0.660	2	R.K#FL*DGIYVSEK#.G
SW:RLA2_HUMAN	H21	5368	2	1418.5	(+0.7)	2.564	0.536	0.992		K.ILDSVGIEADDDR.L
SW:RLA2_HUMAN	H21	5764	2	1793.9	(-0.8)	3.764	0.414	0.369		K.IL*DSVGIEADDDR*L*NK#.V
SW:RLA2_HUMAN	H21	6886	2	1265.4	(+1.0)	3.828	0.550	1.000		K.NIEDVIAQGIGK#.L
SW:RLA2_HUMAN	H21	7998	2	1870.1	(+0.0)	2.533	0.381	0.930		R.YVASYLLAALGGNSSPSAK.D
SW:RLA2_HUMAN	H21	2084	1	860.0	(-0.1)	1.905	0.276	0.000	1	K.VISELNGK.N
SW:RNHL_HUMAN	H16	5104	2	1899.0	(+0.9)	5.408	0.538	0.999	2	K.LQDLDDTDYGSYGNPDPK.T
SW:RNHL_HUMAN	H16	6354	2	1460.7	(-0.0)	3.471	0.336	0.892	1	R.L*QQSFPGIEVTVK#.A
SW:RNHL_HUMAN	H16	5102	2	1919.0	(-0.6)	3.324	0.420	0.975	2	K.L*QDL*DTDYGSYGNPDPK#.T
SW:RNP2_HUMAN	H09	4507	2	997.1	(+1.0)	2.626	0.363	0.977	3	R.TGIDL*GTTGR.L

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:RNP2_HUMAN	H09	4589	2	997.1	(+0.5)	2.378	0.257	0.908	3	R.TGIDL*GTTGR.L
SW:RNP2_HUMAN	H10	4765	2	997.1	(+1.0)	3.111	0.363	0.988	3	R.TGIDL*GTTGR.L
SW:RNP2_HUMAN	H10	4685	2	997.1	(+0.8)	2.707	0.394	0.984	3	R.TGIDL*GTTGR.L
SW:RNP2_HUMAN	H09	7433	2	1566.9	(-0.1)	3.102	0.456	0.976	2	R.VL*GVPIIQASQAQK#.N
SW:RNP2_HUMAN	H10	7595	2	1566.9	(+0.0)	3.702	0.536	1.000	2	R.VL*GVPIIQASQAQK#.N
SW:RNP2_HUMAN	H10	6757	2	1830.9	(-0.0)	2.500	0.353	0.905	2	R.TDASSASSFLDSDELER.T
SW:RNT1_HUMAN	H05	7074	2	1365.6	(+0.9)	3.117	0.486	0.993	3	K.LLGHEVEDVIK.C
SW:RNT1_HUMAN	H05	8230	2	1949.2	(+0.1)	3.482	0.453	0.984	4	R.YEDAYQYQNIQFGLVK.L
SW:RNT1_HUMAN	H05	8944	2	1239.5	(+0.7)	2.925	0.480	0.992	4	R.NVFL*L*GFIPAK#.A
SW:ROA0_HUMAN	H15	7880	2	2179.3	(+0.9)	4.866	0.653	1.000	1	K.GDVAEGDLIEHFSQFGTVEK.A
SW:ROA0_HUMAN	H15	7878	2	2193.3	(-0.5)	4.080	0.438	0.998	1	K.GDVAEGDL*IEHFSQFGTVEK#.A
SW:ROA0_HUMAN	H16	7332	2	2193.3	(+0.9)	4.514	0.380	0.993	1	K.GDVAEGDL*IEHFSQFGTVEK#.A
SW:ROA0_HUMAN	H16	7326	3	2193.3	(+0.4)	4.511	0.600	1.000	1	K.GDVAEGDL*IEHFSQFGTVEK#.A
SW:ROA0_HUMAN	H16	7336	2	2179.3	(+0.2)	4.309	0.606	0.999	1	K.GDVAEGDLIEHFSQFGTVEK.A
SW:ROA0_HUMAN	H15	7170	2	1724.8	(+0.4)	4.687	0.525	0.999	1	R.GFGFVYFQNHDAADK#.A
SW:ROA0_HUMAN	H15	7172	2	1716.8	(+0.9)	4.027	0.505	1.000	1	R.GFGFVYFQNHDAADK.A
SW:ROA0_HUMAN	H16	6724	2	1724.8	(-0.1)	4.940	0.533	1.000	1	R.GFGFVYFQNHDAADK#.A
SW:ROA0_HUMAN	H16	6922	2	1709.9	(-0.1)	4.239	0.425	1.000	2	K.L*FIGGL*NVQTSSEGL*R.G
SW:ROA0_HUMAN	H17	7226	2	2193.3	(-0.1)	3.082	0.179	0.748	1	K.GDVAEGDL*IEHFSQFGTVEK#.A
SW:ROA1_HUMAN	H16	4772	2	1050.1	(+0.8)	2.533	0.469*	0.390	1	R.DYFEQYQK.I
SW:ROA1_HUMAN	H17	1540	2	1438.6	(+0.8)	2.263	0.127	0.024	2	R.EDSQRPGAHLTVK.K
SW:ROA1_HUMAN	H20	2072	2	1452.6	(+0.2)	2.312	0.271	0.023	2	R.EDSQRPGAHL*TVK#.K
SW:ROA1_HUMAN	H14	7253	2	1708.8	(+0.5)	3.959	0.529	1.000	3	R.GFAFVTFDDHDSVDK#.I
SW:ROA1_HUMAN	H15	7208	2	1708.8	(-0.1)	4.154	0.494	0.975	3	R.GFAFVTFDDHDSVDK#.I
SW:ROA1_HUMAN	H15	7206	2	1700.8	(+0.5)	4.137	0.442	0.999	3	R.GFAFVTFDDHDSVDK.I
SW:ROA1_HUMAN	H15	7120	2	1708.8	(+0.6)	3.799	0.510	1.000	3	R.GFAFVTFDDHDSVDK#.I
SW:ROA1_HUMAN	H16	6772	2	1708.8	(+0.7)	4.811	0.493	1.000	3	R.GFAFVTFDDHDSVDK#.I
SW:ROA1_HUMAN	H16	6768	2	1700.8	(+0.7)	4.791	0.534	0.999	3	R.GFAFVTFDDHDSVDK.I
SW:ROA1_HUMAN	H17	6672	2	1700.8	(+0.8)	4.999	0.514	0.999	3	R.GFAFVTFDDHDSVDK.I
SW:ROA1_HUMAN	H19	7026	2	1700.8	(+0.7)	4.319	0.460	1.000	3	R.GFAFVTFDDHDSVDK.I
SW:ROA1_HUMAN	H19	7042	2	1700.8	(-0.5)	2.938	0.217	0.810	3	R.GFAFVTFDDHDSVDK.I
SW:ROA1_HUMAN	H15	8364	2	1786.0	(+0.7)	4.705	0.417	1.000	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	H15	8342	2	1804.0	(-0.4)	3.702	0.379	0.977	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	H15	12278	2	1786.0	(+0.6)	3.430	0.382	0.988	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	H15	11520	2	1786.0	(+0.5)	3.087	0.416	0.987	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	H15	12350	2	1786.0	(+1.0)	3.085	0.548	1.000	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	H15	9996	2	1786.0	(+0.6)	3.080	0.316	0.969	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	H15	12886	2	1786.0	(+0.7)	3.080	0.307	0.966	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	H15	12444	2	1786.0	(+0.1)	3.047	0.462	0.979	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	H15	12856	2	1804.0	(+0.9)	2.999	0.436	0.988	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	H15	12200	2	1786.0	(+0.1)	2.972	0.399	0.963	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	H15	12710	2	1786.0	(+1.0)	2.970	0.353	0.973	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	H15	13770	2	1804.0	(+0.4)	2.845	0.334	0.966	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	H15	10336	2	1786.0	(+0.2)	2.792	0.256	0.842	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	H15	13088	2	1804.0	(+0.3)	2.791	0.413	0.961	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	H15	12432	2	1804.0	(+0.1)	2.777	0.373	0.944	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	H15	10266	2	1804.0	(+0.2)	2.776	0.346	0.929	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	H15	12968	2	1804.0	(+0.3)	2.761	0.449	0.970	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	H15	13990	2	1804.0	(+0.5)	2.576	0.401	0.974	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	H15	10356	2	1804.0	(+0.5)	2.546	0.387	0.969	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	H15	9450	2	1804.0	(-0.4)	2.535	0.263	0.794	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	H15	12044	2	1786.0	(-0.1)	2.416	0.319	0.854	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	H15	9598	2	1786.0	(+0.5)	2.334	0.306	0.906	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	H15	9456	2	1786.0	(+0.3)	2.327	0.336	0.858	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	H15	11938	2	1804.0	(+0.2)	2.282	0.355	0.873	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	H15	12012	2	1804.0	(+0.1)	2.276	0.467	0.953	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	H15	10618	2	1804.0	(-0.4)	2.255	0.291	0.763	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	H16	7720	2	1804.0	(-0.9)	3.445	0.328	0.872	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	H16	7818	2	1786.0	(-0.4)	2.574	0.315	0.877	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	H17	7540	2	1804.0	(-0.2)	4.728	0.445	0.998	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	H18	8042	2	1804.0	(+0.1)	3.173	0.393	0.969	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	H19	8012	2	1786.0	(+0.1)	3.887	0.389	0.973	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	H19	8000	2	1804.0	(+0.1)	2.499	0.352	0.904	1	K.L*FIGGL*SFETTDESL*R.S

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ROA1_HUMAN	H20	7902	2	1804.0	(-0.8)	3.465	0.442	0.944	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	H20	7904	2	1786.0	(-0.2)	3.241	0.371	0.965	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	H15	5342	2	1629.8	(+0.8)	4.204	0.537	0.999	3	R.SSGPYGGGGQYFAKPR.N
SW:ROA1_HUMAN	H15	5388	2	1629.8	(-0.6)	3.687	0.486	1.000	3	R.SSGPYGGGGQYFAKPR.N
SW:ROA1_HUMAN	H15	5334	2	1637.8	(+0.5)	3.502	0.502	0.999	3	R.SSGPYGGGGQYFAK#PR.N
SW:ROA1_HUMAN	H22	7720	2	1804.0	(-0.3)	2.792	0.422	0.964	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA2_HUMAN	H15	5468	2	1059.1	(+0.9)	2.561	0.215	0.916	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	H15	5292	2	1059.1	(+0.3)	2.256	0.176	0.619	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	H15	3106	2	1355.5	(+0.4)	2.275	0.253	0.156	2	R.EESGK#PGAHVTVK#.K
SW:ROA2_HUMAN	H14	7287	2	1696.8	(+0.1)	4.685	0.492	0.998	2	R.GFGFVTFDDHDPVDK.I
SW:ROA2_HUMAN	H14	7285	2	1704.8	(+0.1)	4.051	0.551	0.993	2	R.GFGFVTFDDHDPVDK#.I
SW:ROA2_HUMAN	H15	7288	2	1704.8	(+0.8)	4.680	0.553	0.995	2	R.GFGFVTFDDHDPVDK#.I
SW:ROA2_HUMAN	H15	7274	2	1696.8	(-0.2)	4.622	0.469	0.858	2	R.GFGFVTFDDHDPVDK.I
SW:ROA2_HUMAN	H16	6830	2	1696.8	(+0.4)	4.853	0.487	1.000	2	R.GFGFVTFDDHDPVDK.I
SW:ROA2_HUMAN	H17	6732	2	1696.8	(+0.1)	4.569	0.529	0.943	2	R.GFGFVTFDDHDPVDK.I
SW:ROA2_HUMAN	H15	8072	2	1954.2	(-0.6)	2.581	0.357	0.918	2	R.K#L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H14	8303	2	1818.0	(+0.0)	2.622	0.308	0.878	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H14	9215	2	1800.0	(+0.9)	2.382	0.295	0.903	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	H15	10156	2	1818.0	(+0.0)	3.760	0.395	0.981	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H15	10340	2	1818.0	(+0.3)	3.697	0.448	0.986	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H15	8418	2	1818.0	(-0.6)	3.656	0.427	0.984	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H15	8394	2	1800.0	(-0.1)	3.516	0.461	0.986	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	H15	10416	2	1818.0	(-0.2)	3.384	0.483	0.986	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H15	10262	2	1818.0	(-0.2)	3.319	0.477	0.971	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H15	9554	2	1818.0	(+0.3)	3.310	0.499	0.987	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H15	11996	2	1818.0	(+0.4)	3.237	0.467	0.992	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H15	9462	2	1818.0	(+0.4)	3.223	0.439	0.990	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H15	12468	2	1800.0	(+0.4)	3.089	0.424	0.988	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	H15	13690	2	1818.0	(-0.0)	2.982	0.426	0.971	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H15	13776	2	1818.0	(-0.1)	2.898	0.355	0.683	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H15	9204	2	1818.0	(+0.1)	2.846	0.336	0.929	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H15	12558	2	1818.0	(+0.3)	2.838	0.385	0.953	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H15	12238	2	1818.0	(+0.0)	2.833	0.490	0.979	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H15	12272	2	1800.0	(+0.1)	2.818	0.355	0.938	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	H15	8568	2	1818.0	(+0.0)	2.796	0.367	0.940	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H15	10734	2	1818.0	(-0.8)	2.791	0.475	0.924	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H15	12312	2	1818.0	(+0.1)	2.746	0.476	0.975	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H15	9600	2	1800.0	(+0.1)	2.695	0.474	0.973	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	H15	10568	2	1818.0	(-0.2)	2.691	0.488	0.976	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H15	12632	2	1818.0	(-0.5)	2.670	0.264	0.829	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H15	12078	2	1818.0	(-0.1)	2.610	0.366	0.927	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H15	12704	2	1800.0	(+0.2)	2.600	0.439	0.961	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	H15	9706	2	1818.0	(-0.5)	2.594	0.375	0.928	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H15	12894	2	1800.0	(+0.3)	2.537	0.414	0.948	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	H15	9520	2	1800.0	(+0.5)	2.510	0.409	0.973	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	H15	10650	2	1818.0	(-0.6)	2.502	0.373	0.921	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H15	12542	2	1800.0	(-0.4)	2.497	0.443	0.957	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	H15	14086	2	1818.0	(-0.1)	2.397	0.390	0.922	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H15	12706	2	1818.0	(-0.0)	2.392	0.354	0.891	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H15	12176	2	1800.0	(+0.2)	2.269	0.311	0.806	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	H15	13896	2	1818.0	(+0.3)	2.230	0.425	0.927	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H16	7768	2	1800.0	(+0.2)	4.134	0.375	0.975	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	H16	7766	2	1818.0	(-0.3)	3.583	0.452	0.985	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H17	7658	2	1800.0	(-0.3)	3.585	0.415	0.981	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	H17	7640	2	1818.0	(-0.8)	2.402	0.344	0.689	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	H14	6193	3	1901.1	(+0.5)	3.935	0.466	0.997	2	K.L*FVGGIK#EDTEEHLR*.D
SW:ROA2_HUMAN	H15	6054	2	1881.1	(+0.5)	4.585	0.541*	0.165	2	K.LFVGGIKEDTEEHLR.D
SW:ROA2_HUMAN	H15	6214	2	1901.1	(-0.3)	3.175	0.299	0.342	2	K.L*FVGGIK#EDTEEHLR*.D
SW:ROA2_HUMAN	H15	5618	2	1070.2	(+0.8)	2.234	0.266	0.903		K.TL*ETVPL*ER.K
SW:ROA2_HUMAN	H18	8146	2	1800.0	(+0.5)	3.309	0.463	0.992	2	K.LFIGGLSFETTEESLR.N
SW:ROA3_HUMAN	H14	4099	2	1381.6	(+1.0)	3.051	0.344	0.640	2	R.EDSVKPGAHLTVK.K
SW:ROA3_HUMAN	H14	4297	2	1381.6	(+0.9)	2.680	0.249	0.294	2	R.EDSVKPGAHLTVK.K
SW:ROA3_HUMAN	H14	4219	2	1381.6	(-0.2)	2.566	0.193	0.076	2	R.EDSVKPGAHLTVK.K
SW:ROA3_HUMAN	H14	4141	2	1381.6	(-0.4)	2.467	0.255	0.124	2	R.EDSVKPGAHLTVK.K

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ROA3_HUMAN	H14	4381	2	1381.6	(-0.2)	2.242	0.178	0.034	2	R.EDSVKPGAHLTVK.K
SW:ROA3_HUMAN	H14	7919	2	1900.1	(+0.4)	4.511	0.550	1.000	2	R.KLFIGGLSFETTTDDSLR.E
SW:ROA3_HUMAN	H14	7923	2	1926.1	(-0.1)	4.125	0.473	1.000	2	R.K#L*FIGGL*SFETTTDDSL*R.E
SW:ROA3_HUMAN	H14	8465	2	1790.0	(+0.9)	3.463	0.344	0.983	2	K.L*FIGGL*SFETTTDDSL*R.E
SW:ROA3_HUMAN	H14	8283	2	1790.0	(-0.0)	3.265	0.332	0.953	2	K.L*FIGGL*SFETTTDDSL*R.E
SW:ROA3_HUMAN	H14	8621	2	1790.0	(+0.6)	2.922	0.371	0.977	2	K.L*FIGGL*SFETTTDDSL*R.E
SW:ROA3_HUMAN	H14	11621	2	1790.0	(+0.1)	2.328	0.355	0.881	2	K.L*FIGGL*SFETTTDDSL*R.E
SW:ROA3_HUMAN	H15	8350	2	1790.0	(+0.8)	3.901	0.223	0.968	2	K.L*FIGGL*SFETTTDDSL*R.E
SW:ROA3_HUMAN	H16	7672	2	1772.0	(+0.6)	3.921	0.444	0.994	2	K.LFIGGLSFETTTDDSLR.E
SW:ROCL_HUMAN	H14	5977	2	1124.3	(+0.5)	2.487	0.225	0.895	8	K.KSDVEAIFSK.Y
SW:ROCL_HUMAN	H15	4858	2	1129.3	(+0.2)	2.542	0.304	0.251	9	K.L*K#GDDL*QAIK#.Q
SW:ROCL_HUMAN	H15	4928	2	1101.3	(-0.0)	2.432	0.343	0.319	9	K.LKGDDLQAIK.Q
SW:ROCL_HUMAN	H15	4940	2	1129.3	(+0.1)	2.212	0.325	0.179	9	K.L*K#GDDL*QAIK#.Q
SW:ROCL_HUMAN	H16	4458	2	1129.3	(-0.5)	2.327	0.271	0.137	9	K.L*K#GDDL*QAIK#.Q
SW:ROCL_HUMAN	H14	7613	2	1317.6	(-0.5)	3.106	0.349	0.963	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	H15	7576	2	1337.6	(+0.4)	2.599	0.386	0.973	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	H16	7088	2	1337.6	(+0.3)	2.918	0.401	0.966	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	H18	7452	2	1337.6	(+0.8)	2.715	0.340	0.965	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	H19	5730	2	1124.3	(+0.8)	2.251	0.159	0.486	8	K.KSDVEAIFSK.Y
SW:ROC_HUMAN	H14	7187	2	1720.0	(+0.1)	3.396	0.507	0.999	6	R.M@IAGQVL*DINL*AAEPK#.V
SW:ROC_HUMAN	H14	8185	3	3469.7	(-0.6)	5.175	0.530	0.998	2	R.SAAEM@YGSVTEHPSPSPL*L*SSSFDL*DYDFQR.D
SW:ROC_HUMAN	H15	7734	2	1684.0	(+0.0)	3.193	0.460	0.981	6	R.MIAGQVLDINLAAEPK.V
SW:ROD_HUMAN	H13	8374	2	2162.4	(-0.0)	2.611	0.277	0.805	10	R.EYFGGFGEVESIELPMDNK.T
SW:ROD_HUMAN	H14	7863	2	2192.4	(+1.0)	4.656	0.514	1.000	10	R.EYFGGFGEVESIEL*PM@DNK#.T
SW:ROD_HUMAN	H14	8319	2	2162.4	(+0.2)	3.706	0.440	0.984	10	R.EYFGGFGEVESIELPMDNK.T
SW:ROD_HUMAN	H13	6210	2	1503.7	(-0.3)	3.156	0.317	0.937	10	K.IFVGGL*SPDTPPEEK#.I
SW:ROD_HUMAN	H14	6209	2	1503.7	(-0.8)	2.887	0.297	0.724	10	K.IFVGGL*SPDTPPEEK#.I
SW:ROD_HUMAN	H15	6254	2	1503.7	(+0.3)	3.734	0.468	0.999	10	K.IFVGGL*SPDTPPEEK#.I
SW:ROD_HUMAN	H17	5646	2	1503.7	(-0.3)	3.744	0.453	0.979	10	K.IFVGGL*SPDTPPEEK#.I
SW:ROD_HUMAN	H14	1829	2	1068.2	(+0.5)	2.287	0.150	0.697	9	K.K#YHNVGL*SK#.C
SW:ROD_HUMAN	H14	7653	2	1356.6	(+0.8)	3.608	0.436	0.994	9	K.MFIGGLSWDTTK.K
SW:ROD_HUMAN	H14	7687	2	1356.6	(-0.6)	3.491	0.470	1.000	9	K.MFIGGLSWDTTK.K
SW:ROD_HUMAN	H14	7699	2	1370.6	(+0.1)	3.481	0.531	1.000	9	K.MFIGGL*SWDTTK#.K
SW:ROD_HUMAN	H17	7042	2	1356.6	(-0.4)	2.445	0.365	0.926	9	K.MFIGGLSWDTTK.K
SW:ROD_HUMAN	H14	6839	2	1522.8	(-0.1)	2.422	0.281	0.133	9	K.M@FIGGL*SWDTTK#K#.D
SW:ROD_HUMAN	H19	5952	2	1503.7	(-0.2)	3.403	0.418	0.966	10	K.IFVGGL*SPDTPPEEK#.I
SW:ROG_HUMAN	H13	7646	2	1487.7	(+0.8)	4.532	0.470	1.000	5	R.GFAFVTFESPADAK.D
SW:ROG_HUMAN	H13	7642	2	1495.7	(+0.7)	4.061	0.483	1.000	5	R.GFAFVTFESPADAK#.D
SW:ROG_HUMAN	H16	7118	2	1487.7	(+1.0)	4.032	0.520	1.000	5	R.GFAFVTFESPADAK.D
SW:ROG_HUMAN	H16	7124	2	1495.7	(+0.8)	3.866	0.492	1.000	5	R.GFAFVTFESPADAK#.D
SW:ROG_HUMAN	H13	6486	2	1436.6	(+1.0)	4.241	0.384	0.993	3	K.LFIGGLNTTETNEK.A
SW:ROG_HUMAN	H18	7502	2	1487.7	(+0.9)	3.164	0.349	0.980	5	R.GFAFVTFESPADAK.D
SW:ROH1_HUMAN	H12	7144	2	1349.5	(+0.8)	3.041	0.272	0.962		K.SNNVEMDWVL*K#.H
SW:ROH1_HUMAN	H12	7726	2	1843.0	(+0.6)	2.833	0.352	0.970	1	R.STGEAFVQFASQEIAEK.A
SW:ROH1_HUMAN	H13	7804	2	1851.0	(+0.0)	3.804	0.514	1.000	1	R.STGEAFVQFASQEIAEK#.A
SW:ROH1_HUMAN	H12	6600	3	2187.4	(+0.8)	3.727	0.468*	0.066		R.VTGEADVEFATHEDAVAAMSK#.D
SW:ROH1_HUMAN	H12	5112	1	792.9	(-0.3)	1.913	0.295	0.000	3	R.YVEVFK#.S
SW:ROH1_HUMAN	H14	7767	2	1843.0	(+0.9)	3.159	0.388	0.985	1	R.STGEAFVQFASQEIAEK.A
SW:ROK_HUMAN	H10	4925	2	998.1	(+0.6)	2.288	0.178	0.788	1	R.GGDLMAYDR.R
SW:ROK_HUMAN	H11	7652	2	1932.2	(-0.4)	3.271	0.475	0.982	1	R.GSYGDL*GGPIITTQVTIPK#.D
SW:ROK_HUMAN	H11	2400	2	1260.3	(+1.0)	2.969	0.409	0.989	1	K.IDEPL*EGSEDR.I
SW:ROK_HUMAN	H11	4580	2	1266.3	(+1.0)	2.503	0.358	0.969	1	K.IDEPL*EGSEDR.I
SW:ROK_HUMAN	H11	4240	2	1260.3	(+0.7)	2.430	0.392	0.974	1	K.IDEPL*EGSEDR.I
SW:ROK_HUMAN	H11	4112	2	1260.3	(+1.0)	2.292	0.385	0.966	1	K.IDEPL*EGSEDR.I
SW:ROK_HUMAN	H11	4686	2	1266.3	(+0.8)	2.275	0.262	0.882	1	K.IDEPL*EGSEDR.I
SW:ROK_HUMAN	H14	3865	2	1266.3	(+0.7)	2.702	0.399	0.983	1	K.IDEPL*EGSEDR.I
SW:ROK_HUMAN	H14	4093	2	1266.3	(+0.8)	2.691	0.411	0.985	1	K.IDEPL*EGSEDR.I
SW:ROK_HUMAN	H14	3701	2	1266.3	(+0.8)	2.682	0.409	0.984	1	K.IDEPL*EGSEDR.I
SW:ROK_HUMAN	H14	4019	2	1260.3	(+0.9)	2.642	0.477	0.990	1	K.IDEPL*EGSEDR.I
SW:ROK_HUMAN	H14	3793	2	1260.3	(+1.0)	2.391	0.402	0.975	1	K.IDEPL*EGSEDR.I



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ROK_HUMAN	H14	4095	2	1260.3	(+0.9)	2.331	0.338	0.950	1	K.IDEPL*EGSEDR.I
SW:ROK_HUMAN	H17	3382	2	1266.3	(+1.0)	2.628	0.401	0.982	1	K.IDEPL*EGSEDR.I
SW:ROK_HUMAN	H11	8620	2	1341.6	(-0.5)	4.203	0.390	0.999	1	K.IILDISESPIK.G
SW:ROK_HUMAN	H11	8604	2	1361.6	(+0.0)	2.731	0.269	0.863	1	K.IIL*DL*ISESPIK#.G
SW:ROK_HUMAN	H14	8263	2	1361.6	(+0.2)	2.643	0.382	0.945	1	K.IIL*DL*ISESPIK#.G
SW:ROK_HUMAN	H17	7616	2	1361.6	(+0.0)	2.670	0.334	0.919	1	K.IIL*DL*ISESPIK#.G
SW:ROK_HUMAN	H11	8612	2	2590.9	(-0.1)	3.730	0.531	1.000	1	R.IITITGTQDQIQNAQYLLQNSVK.Q
SW:ROK_HUMAN	H11	8618	2	2610.9	(+0.3)	3.688	0.405	0.964	1	R.IITITGTQDQIQNAQYL*L*QNSVK#.Q
SW:ROK_HUMAN	H16	7696	3	2590.9	(+1.0)	5.997	0.637	1.000	1	R.IITITGTQDQIQNAQYLLQNSVK.Q
SW:ROK_HUMAN	H17	7570	3	2590.9	(+0.9)	6.035	0.585	1.000	1	R.IITITGTQDQIQNAQYLLQNSVK.Q
SW:ROK_HUMAN	H18	8074	3	2590.9	(+0.4)	5.107	0.538	1.000	1	R.IITITGTQDQIQNAQYLLQNSVK.Q
SW:ROK_HUMAN	H11	10662	2	1716.0	(+0.5)	4.190	0.530	0.999	1	R.ILSISADIETIGEILK.K
SW:ROK_HUMAN	H11	10444	2	1736.0	(-0.3)	3.388	0.446	0.980	1	R.IL*SISADIETIGEIL*K#.K
SW:ROK_HUMAN	H11	10562	2	1716.0	(+0.7)	3.277	0.465	0.992	1	R.ILSISADIETIGEILK.K
SW:ROK_HUMAN	H11	10762	2	1716.0	(+0.5)	3.157	0.449	0.990	1	R.ILSISADIETIGEILK.K
SW:ROK_HUMAN	H11	10524	2	1736.0	(+0.2)	2.695	0.363	0.924	1	R.IL*SISADIETIGEIL*K#.K
SW:ROK_HUMAN	H13	10176	2	1716.0	(+0.6)	2.907	0.465	0.989	1	R.ILSISADIETIGEILK.K
SW:ROK_HUMAN	H13	10298	2	1716.0	(+0.4)	2.282	0.388	0.955	1	R.ILSISADIETIGEILK.K
SW:ROK_HUMAN	H19	9660	2	1716.0	(+0.9)	2.760	0.479	0.987	1	R.ILSISADIETIGEILK.K
SW:ROK_HUMAN	H11	10016	2	1872.2	(+0.6)	3.505	0.459	0.830	1	R.IL*SISADIETIGEIL*K#.K.I
SW:ROK_HUMAN	H11	10028	2	1844.2	(+0.6)	3.252	0.554	1.000	1	R.ILSISADIETIGEILK.K.I
SW:ROK_HUMAN	H11	5740	2	1442.6	(-0.6)	2.538	0.321	0.903	1	K.L*FQECPPHSTLR.V
SW:ROK_HUMAN	H11	7660	2	1545.9	(-0.5)	4.535	0.526	0.999	1	R.L*L*IHQSL*AGGIIVK#.G
SW:ROK_HUMAN	H11	7740	2	1545.9	(-0.6)	3.010	0.323	0.925	1	R.L*L*IHQSL*AGGIIVK#.G
SW:ROK_HUMAN	H13	7428	2	1519.9	(+0.8)	3.631	0.442	0.991	1	R.LLIHQSLAGGIIVK#.G
SW:ROK_HUMAN	H14	7375	2	1519.9	(-0.0)	3.145	0.426	0.974	1	R.LLIHQSLAGGIIVK#.G
SW:ROK_HUMAN	H11	1728	1	737.9	(-0.0)	2.189	0.124	0.000	1	K.NAGAVIGK#.G
SW:ROK_HUMAN	H11	1746	1	729.9	(-0.1)	2.145	0.319	0.000	1	K.NAGAVIGK.G
SW:ROK_HUMAN	H11	5652	2	1113.2	(-1.0)	2.331	0.312	0.717	1	R.NTDEMVEL*R.I
SW:ROK_HUMAN	H12	4936	2	1113.2	(+0.5)	2.461	0.225	0.905	1	R.NTDEMVEL*R.I
SW:ROK_HUMAN	H12	4928	2	1107.2	(+0.5)	2.252	0.121	0.625	1	R.NTDEMVELR.I
SW:ROK_HUMAN	H16	4830	2	1113.2	(+0.6)	2.364	0.144	0.698	1	R.NTDEMVEL*R.I
SW:ROK_HUMAN	H11	2134	2	1604.7	(+0.5)	2.905	0.321	0.964	1	K.RPAEDM@EEEEQAFK#.R
SW:ROK_HUMAN	H13	4654	2	1580.7	(+0.5)	3.682	0.498	1.000	1	K.RPAEDMEEEEQAFK.R
SW:ROK_HUMAN	H14	5095	2	1580.7	(+0.5)	3.402	0.529	1.000	1	K.RPAEDMEEEEQAFK.R
SW:ROK_HUMAN	H11	5344	2	1744.9	(-0.2)	4.169	0.370	0.699	1	K.RPAEDMEEEEQAFK#.R.S
SW:ROK_HUMAN	H11	5354	3	1736.9	(-0.6)	3.920	0.421	0.987	1	K.RPAEDMEEEEQAFK.R.S
SW:ROK_HUMAN	H11	2156	2	1760.9	(+0.2)	2.589	0.102	0.024	1	K.RPAEDM@EEEEQAFK#.R.S
SW:ROK_HUMAN	H11	5226	2	1054.3	(-0.7)	2.573	0.227	0.050	1	R.VVLIGGKPD.R.V
SW:ROK_HUMAN	H11	5206	2	1054.3	(+0.8)	2.529	0.317	0.483	1	R.VVLIGGKPD.R.V
SW:ROK_HUMAN	H11	5300	2	1068.3	(+0.7)	2.465	0.313	0.446	1	R.VVL*IGGK#PDR.V
SW:ROK_HUMAN	H21	3970	2	1266.3	(+0.3)	2.614	0.302	0.907	1	K.IDEPL*EGSEDR.I
SW:ROL_HUMAN	H10	6927	2	1649.9	(+0.8)	4.662	0.454	1.000	1	R.AITHL*NNNFMFGQK#.L
SW:ROL_HUMAN	H10	6921	2	1635.9	(-0.0)	3.692	0.401	0.981	1	R.AITHLNNNFMFGQK.L
SW:ROL_HUMAN	H10	6453	2	1665.9	(+0.1)	3.518	0.432	0.981	1	R.AITHL*NNNFM@FGQK#.L
SW:ROL_HUMAN	H10	1755	2	978.1	(+0.3)	2.570	0.229	0.146	1	K.IEYAKPTR.L
SW:ROL_HUMAN	H10	1731	3	3224.2	(+0.3)	3.958	0.433	0.977	1	R.LKTDNAGDQHGGGGGGGGGAGAAGGGGGGGENYDDPHK.T
SW:ROL_HUMAN	H10	6019	2	2749.8	(-0.3)	4.012	0.494	1.000	1	K.NDQDTWDYTNPNL*SGQGDPGSNPNK#.R
SW:ROL_HUMAN	H10	5943	3	2891.9	(+0.7)	4.744	0.616	1.000	1	K.NDQDTWDYTNPNLSGQGDPGSNPNK.R.Q
SW:ROL_HUMAN	H10	5941	3	2905.9	(+0.3)	4.024	0.432	0.980	1	K.NDQDTWDYTNPNL*SGQGDPGSNPNK#.R.Q
SW:ROL_HUMAN	H10	5955	2	2891.9	(-0.3)	2.835	0.336	0.331	1	K.NDQDTWDYTNPNLSGQGDPGSNPNK.R.Q
SW:ROL_HUMAN	H10	5965	2	2905.9	(-0.8)	2.795	0.388	0.185	1	K.NDQDTWDYTNPNL*SGQGDPGSNPNK#.R.Q
SW:ROL_HUMAN	H10	8179	2	1894.1	(-0.9)	2.954	0.236	0.582	1	K.SDAL*ETL*GFL*NHYQM#.N
SW:ROL_HUMAN	H10	7821	2	1910.1	(+0.3)	2.771	0.408	0.953	1	K.SDAL*ETL*GFL*NHYQM@K#.N
SW:ROL_HUMAN	H10	6807	2	1877.1	(-0.2)	3.075	0.580	1.000	1	K.SK#PGAAMVEMADGYAVDR.A
SW:ROL_HUMAN	H10	1617	3	2990.9	(+0.5)	4.775	0.466	0.999	1	K.TDNAGDQHGGGGGGGGGAGAAGGGGGGGENYDDPHK#.T
SW:ROL_HUMAN	H10	1609	3	2982.9	(+0.7)	3.951	0.392	0.997	1	K.TDNAGDQHGGGGGGGGGAGAAGGGGGGGENYDDPHK.T
SW:ROL_HUMAN	H10	7809	3	3787.2	(+0.2)	7.539	0.634	1.000	1	R.YGPQYGHPPPPPPPEYGPHADSPVLMVYGLDQSK.M
SW:ROL_HUMAN	H10	7805	3	3807.2	(-1.0)	6.392	0.558	1.000	1	R.YGPQYGHPPPPPPPEYGPHADSPVL*MVYGL*DQSK#.M
SW:ROL_HUMAN	H14	5751	3	2905.9	(+0.6)	4.474	0.486	0.998	1	K.NDQDTWDYTNPNL*SGQGDPGSNPNK#.R.Q
SW:ROM_HUMAN	H09	6579	2	1135.3	(+0.6)	2.582	0.146	0.780	9	R.INEIL*SNAL*K#.R
SW:ROM_HUMAN	H08	7191	2	1427.6	(+1.0)	3.586	0.504	1.000	7	R.LGSTVFNLDYK.V
SW:ROM_HUMAN	H09	7111	2	1427.6	(+0.7)	3.093	0.500	0.994	7	R.LGSTVFNLDYK.V
SW:ROM_HUMAN	H09	2305	2	1877.0	(+0.8)	2.923	0.434	0.985	2	K.MEEESGAPGVPSGNGAPGPK#.G

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ROM_HUMAN	H09	2409	2	1877.0	(+0.8)	2.272	0.303	0.879	2	K.MEEESGAPGVPSGNGAPGPK#.G
SW:ROM_HUMAN	H08	2145	2	1108.3	(+0.4)	3.065	0.322	0.978	9	R.MGAGL*GHGMDR.V
SW:ROM_HUMAN	H08	4983	2	1164.3	(+0.4)	2.713	0.278	0.950	9	R.M@GAGM@GFGL*ER.M
SW:ROM_HUMAN	H09	6497	2	1132.3	(+0.7)	2.591	0.228	0.899	9	R.MGAGMGFGL*ER.M
SW:ROM_HUMAN	H09	5687	2	1148.3	(+0.0)	2.236	0.269	0.773	9	R.MGAGM@GFGL*ER.M
SW:ROM_HUMAN	H08	5223	2	1406.6	(+0.5)	3.351	0.461*	0.537	6	R.MGL*AM@GGGGGASFDRA
SW:ROM_HUMAN	H09	5549	2	1406.6	(-0.2)	3.349	0.380*	0.349	6	R.M@GL*AMGGGGGASFDRA
SW:ROM_HUMAN	H09	5285	2	1406.6	(+0.1)	2.959	0.410*	0.221	6	R.MGL*AM@GGGGGASFDRA
SW:ROM_HUMAN	H08	5203	2	1466.7	(+1.0)	3.513	0.410	0.990	8	R.M@GPAM@GPAL*GAGIER.M
SW:ROM_HUMAN	H08	6565	2	1428.7	(+0.9)	2.815	0.305	0.952	8	R.MGPAMGPALGAGIER.M
SW:ROM_HUMAN	H08	5797	2	1450.7	(-0.3)	2.798	0.275*	0.175	8	R.MGPAM@GPAL*GAGIER.M
SW:ROM_HUMAN	H08	6557	2	1434.7	(-0.4)	2.465	0.192	0.594	8	R.MGPAMGPAL*GAGIER.M
SW:ROM_HUMAN	H09	6009	2	1450.7	(+0.9)	3.530	0.320*	0.604	8	R.M@GPAMGPAL*GAGIER.M
SW:ROM_HUMAN	H09	5753	2	1450.7	(-0.7)	2.764	0.413*	0.056	8	R.MGPAM@GPAL*GAGIER.M
SW:ROM_HUMAN	H09	6433	2	1434.7	(-0.3)	2.653	0.240	0.780	8	R.MGPAMGPAL*GAGIER.M
SW:ROM_HUMAN	H08	7193	2	1626.9	(+0.1)	3.544	0.457	0.984	9	R.MGPL*GL*DHMMASSIER.M
SW:ROM_HUMAN	H09	6669	2	1642.9	(-0.9)	3.558	0.403	0.933	9	R.M@GPL*GL*DHMMASSIER.M
SW:ROM_HUMAN	H09	7049	2	1626.9	(-0.0)	3.498	0.477	0.987	9	R.MGPL*GL*DHMMASSIER.M
SW:ROM_HUMAN	H09	6147	2	1642.9	(-0.3)	2.917	0.312	0.918	9	R.MGPL*GL*DHM@ASSIER.M
SW:ROM_HUMAN	H09	5659	2	1658.9	(+0.6)	2.451	0.324	0.935	9	R.M@GPL*GL*DHM@ASSIER.M
SW:ROM_HUMAN	H16	7294	2	1273.5	(+0.9)	2.866	0.509	0.993	6	R.AFITNIPFDVK#.W
SW:ROR_HUMAN	H08	8495	2	1610.8	(+0.9)	4.236	0.506	1.000	2	R.DLYEDELVPLFEK.A
SW:ROR_HUMAN	H09	8489	2	1610.8	(+0.7)	2.612	0.387	0.975	2	R.DLYEDELVPLFEK.A
SW:ROR_HUMAN	H10	8621	2	1610.8	(+0.8)	3.322	0.434	0.992	2	R.DLYEDELVPLFEK.A
SW:ROR_HUMAN	H10	8617	2	1636.8	(-0.1)	2.762	0.158	0.635	2	R.DL*YEDEL*VPL*FEK#.A
SW:ROR_HUMAN	H08	6461	2	1262.5	(+0.6)	2.504	0.442	0.985	2	R.LMMDPLSGQNR.G
SW:ROR_HUMAN	H08	8361	2	1481.7	(-0.4)	3.062	0.453	0.978	2	R.NL*ATTVTEEIL*EK#.S
SW:ROR_HUMAN	H09	8365	2	1481.7	(-0.3)	3.117	0.304	0.932	2	R.NL*ATTVTEEIL*EK#.S
SW:ROR_HUMAN	H10	8505	2	1481.7	(-0.7)	2.407	0.297	0.579	2	R.NL*ATTVTEEIL*EK#.S
SW:ROR_HUMAN	H08	5325	2	1318.4	(+0.7)	2.854	0.388	0.983	8	R.TGYTL*DVTTGQR.K
SW:ROR_HUMAN	H09	5381	2	1318.4	(+0.7)	3.030	0.352	0.982	8	R.TGYTL*DVTTGQR.K
SW:ROR_HUMAN	H10	5607	2	1318.4	(+0.1)	2.294	0.151	0.388	8	R.TGYTL*DVTTGQR.K
SW:ROR_HUMAN	H13	5296	2	1312.4	(+0.8)	2.936	0.447	0.990	8	R.TGYTLDVTTGQR.K
SW:ROR_HUMAN	H08	6935	2	1360.5	(-0.4)	3.667	0.394	0.691	2	K.TK#ENIL*EEFSK#.V
SW:ROR_HUMAN	H10	6953	2	1360.5	(+0.6)	2.474	0.361	0.505	2	K.TK#ENIL*EEFSK#.V
SW:ROR_HUMAN	H08	5791	2	1090.3	(+0.3)	2.492	0.370	0.938	1	K.TL*IEAGL*PQK#.V
SW:ROR_HUMAN	H08	7941	2	1942.2	(+0.7)	2.862	0.445	0.987		K.VTEGLVDVILYHQPDDK.K
SW:ROR_HUMAN	H10	8071	2	1942.2	(+0.6)	2.885	0.454	0.988		K.VTEGLVDVILYHQPDDK.K
SW:ROR_HUMAN	H14	8293	2	1481.7	(+0.7)	3.185	0.511	1.000	2	R.NL*ATTVTEEIL*EK#.S
SW:ROU_HUMAN	H06	8546	2	2740.1	(-0.5)	3.271	0.284	0.334	6	K.EK#PYFFPIPEEYTFIQNVPL*EDR.V
SW:ROU_HUMAN	H06	8564	2	2726.1	(+0.1)	2.747	0.326	0.285	6	K.EKPYFFPIPEEYTFIQNVPLEDR.V
SW:ROU_HUMAN	H01	5736	2	1292.4	(-0.2)	2.250	0.223	0.699	5	R.GYFEYIEENK.Y
SW:ROU_HUMAN	H06	6596	2	1300.4	(+0.7)	3.146	0.350	0.984	5	R.GYFEYIEENK#.Y
SW:ROU_HUMAN	H06	6598	2	1292.4	(+0.8)	2.558	0.299	0.955	5	R.GYFEYIEENK.Y
SW:ROU_HUMAN	H06	6110	3	3168.3	(+0.3)	5.532	0.587	0.998	3	R.L*QAAL*DDEEAGGRPAM@EPGNGSL*DL*GGDSAGR.S
SW:ROU_HUMAN	H06	6496	2	1648.8	(-0.0)	3.501	0.399	0.978	6	R.NFILDQTNVSAQAQR.R
SW:ROU_HUMAN	H06	6492	2	1654.8	(+0.8)	3.312	0.448	0.992	6	R.NFIL*DQTNVSAQAQR.R
SW:ROU_HUMAN	H06	7462	3	3668.9	(-0.2)	4.838	0.448	0.987	6	K.NQSQGYNQWQQGQFWGQK#PWSQHYHQGY.-
SW:ROU_HUMAN	H06	7468	3	3660.9	(-0.2)	4.721	0.535	1.000	6	K.NQSQGYNQWQQGQFWGQK#PWSQHYHQGY.-
SW:ROU_HUMAN	H06	7460	2	1715.9	(+0.8)	2.935	0.362	0.976	4	K.SSGPTSLFAVTVAPPGAR.Q
SW:ROU_HUMAN	H06	6234	2	1413.6	(-0.7)	2.852	0.360	0.846	6	K.YNIL*GTNTIM@DK#.M
SW:ROU_HUMAN	H06	6870	2	1397.6	(+0.9)	2.842	0.322	0.966	6	K.YNIL*GTNTIMDK#.M
SW:ROU_HUMAN	H07	6510	2	1654.8	(+0.4)	4.040	0.449	1.000	6	R.NFIL*DQTNVSAQAQR.R
SW:RPA1_HUMAN	H04	6783	3	2463.7	(+0.1)	4.257	0.454	0.990		K.L*PEEVATPTTDEEK#DSL*IAIDR.S
SW:RPA1_HUMAN	H04	6785	3	2443.7	(+0.0)	4.164	0.412	0.978		K.LPEEVATPTTDEEKDSLIAIDR.S
SW:RPA1_HUMAN	H04	6579	2	1631.8	(+0.5)	3.261	0.464	0.992		R.AAL*NL*PEAASYDEV.R.G
SW:RPB5_HUMAN	H18	5358	2	1473.7	(-0.1)	3.222	0.393	0.968	3	R.AL*IVVQQGM@TPSAK#.Q
SW:RPB5_HUMAN	H18	8004	3	3199.5	(-1.0)	4.121	0.371	0.985	3	R.RTDL*TVL*VAHNDPTDQDM@FVFFPEEPK#.V
SW:RPB5_HUMAN	H18	8366	2	2029.2	(-0.6)	3.156	0.381	0.965	3	R.GYLVTQDELDTLEEFK.A
SW:RPB8_HUMAN	H20	5616	2	1784.9	(+0.9)	4.070	0.487	1.000	1	R.L*QGDANNL*HGFEVDSR.V
SW:RPB8_HUMAN	H20	6272	2	1359.5	(-0.4)	3.150	0.444	0.982	1	R.ADQFEYVMYGK#.V

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:RRP4_HUMAN	H16	5058	2	1108.3	(+1.0)	2.835	0.307	0.969	1	K.L*IASVAGSVER.V
SW:RRP4_HUMAN	H16	4064	2	1028.1	(+0.8)	2.875	0.403	0.989	1	R.SAEDEL*AMR.G
SW:RRP4_HUMAN	H16	6598	2	1550.8	(-0.3)	2.802	0.174	0.648	1	K.L*GQGVV*VQVSPSL*VK#.R
SW:RS13_HUMAN	H20	5312	2	1092.2	(-0.4)	2.812	0.389	0.970	1	K.GLSQSALPYR.R
SW:RS13_HUMAN	H20	7060	2	1266.5	(+0.3)	2.793	0.353	0.948	2	K.GL*TPSQIGVIL*R.D
SW:RS16_HUMAN	H20	4958	2	956.1	(+0.7)	2.246	0.103	0.514	1	K.ALVAYYQK.Y
SW:RS16_HUMAN	H20	6492	2	1188.4	(-0.2)	3.663	0.358	0.967	1	K.GPLQSVQVFGR.K
SW:RS16_HUMAN	H20	6418	2	1194.4	(+0.9)	2.469	0.355	0.966	1	K.GPL*QSVQVFGR.K
SW:RS16_HUMAN	H20	7890	2	1095.4	(-0.5)	2.750	0.340	0.951	1	K.LLEPVLLLKG.E
SW:RS16_HUMAN	H20	5236	2	897.1	(+0.9)	2.454	0.336	0.972	1	R.TL*L*VADPR.R
SW:RS16_HUMAN	H21	6374	2	1188.4	(+0.6)	3.519	0.337	0.988	1	K.GPLQSVQVFGR.K
SW:RS18_HUMAN	H20	2150	2	1248.3	(+0.0)	2.554	0.381	0.950		R.AGELTEDEVER.V
SW:RS18_HUMAN	H20	6866	2	948.2	(+1.0)	2.597	0.248	0.940		K.IAFAITAIK.G
SW:RS18_HUMAN	H20	5232	2	1322.5	(+0.7)	3.694	0.420	0.994		K.YSQVLANGLDNK.L
SW:RS18_HUMAN	H20	5230	2	1342.5	(-0.3)	2.368	0.255	0.748		K.YSQVL*ANGL*DNK#.L
SW:RS19_HUMAN	H20	7274	2	1710.8	(+0.4)	4.003	0.569	0.998	2	K.EL*APYDENWIFYTR.A
SW:RS19_HUMAN	H20	7268	2	1704.8	(+0.1)	3.070	0.420	0.976	2	K.ELAPYDENWIFYTR.A
SW:RS19_HUMAN	H20	6396	2	1153.4	(-0.9)	2.255	0.170	0.241	2	R.RVL*QAL*EGL*K#.M
SW:RS19_HUMAN	H20	6254	2	997.2	(+0.4)	2.336	0.257	0.902	2	R.VL*QAL*EGL*K#.M
SW:RS19_HUMAN	H20	6010	2	1073.2	(-0.0)	2.556	0.269	0.872	2	K.VPEWVDTVK.L
SW:RS19_HUMAN	H20	6268	1	971.2	(-0.5)	1.930	0.425	0.000	2	R.VLQALEGLK.M
SW:RS21_HUMAN	H22	5428	2	1565.7	(-0.4)	4.244	0.454	1.000	3	K.DHASIQMNVAEVDK#.V
SW:RS21_HUMAN	H22	5402	2	1565.7	(+0.8)	3.473	0.489	1.000	3	K.DHASIQMNVAEVDK#.V
SW:RS21_HUMAN	H22	4894	2	1129.2	(-0.0)	2.915	0.374	0.969	2	R.MGESDDSil*R.L
SW:RS23_HUMAN	H20	4982	2	1214.4	(+0.7)	2.498	0.346	0.961	1	R.K#GHAVGDIPGVR.F
SW:RS23_HUMAN	H20	7162	2	1217.5	(+0.3)	2.202	0.438	0.941	1	K.VANVSL*L*AL*YK#.G
SW:RS25_HUMAN	H20	6416	2	973.2	(-0.4)	3.554	0.331	0.669		R.AALQELLSK.G
SW:RS25_HUMAN	H20	6736	2	1102.3	(+0.9)	2.809	0.298	0.970		K.L*NNL*VL*FDK#.A
SW:RS27_HUMAN	H21	4852	2	1294.4	(+0.9)	3.235	0.338	0.985	3	K.DLLHPSPEEEK.R
SW:RS27_HUMAN	H22	4984	2	1294.4	(-0.3)	2.738	0.344	0.946	3	K.DLLHPSPEEEK.R
SW:RS27_HUMAN	H22	4950	2	1314.4	(+0.6)	2.683	0.181	0.848	3	K.DL*L*HPSPEEEK#.R
SW:RS27_HUMAN	H22	4998	2	1314.4	(-0.6)	2.590	0.263	0.756	3	K.DL*L*HPSPEEEK#.R
SW:RS27_HUMAN	H21	5996	2	1558.8	(+0.0)	3.797	0.481	1.000	4	R.L*VQSPNSYFM@DVK#.C
SW:RS27_HUMAN	H22	6090	2	1558.8	(-0.1)	3.561	0.230	0.918	4	R.L*VQSPNSYFM@DVK#.C
SW:RS27_HUMAN	H22	4958	2	1470.6	(-0.0)	2.483	0.393	0.399	3	K.DL*L*HPSPEEEK#.R.K
SW:RS3_HUMAN	H16	6838	2	1587.7	(+0.1)	4.051	0.446	0.993	4	R.FGFPEGSVEL*YAEK#.V
SW:RS3_HUMAN	H16	6844	2	1573.7	(-0.6)	3.764	0.536	1.000	4	R.FGFPEGSVELYAEK.V
SW:RS3_HUMAN	H16	6820	2	1573.7	(+0.7)	3.257	0.507	0.994	4	R.FGFPEGSVELYAEK.V
SW:RS3_HUMAN	H17	6738	2	1587.7	(+0.4)	3.643	0.476	1.000	4	R.FGFPEGSVEL*YAEK#.V
SW:RS3_HUMAN	H16	7062	3	2491.8	(+0.8)	4.704	0.525	1.000	5	K.FVDGL*M@IHSGDPVNYVDTAVR.H
SW:RS3_HUMAN	H16	5324	2	1582.8	(-0.3)	3.341	0.332	0.373	4	K.GGK#PEPPAMPQPVPPTA.-
SW:RS3_HUMAN	H16	3906	2	1598.8	(-0.2)	2.658	0.350*	0.006	4	K.GGK#PEPPAM@PQPVPPTA.-
SW:RS3_HUMAN	H17	3956	2	1598.8	(+0.7)	2.960	0.478*	0.023	4	K.GGK#PEPPAM@PQPVPPTA.-
SW:RS3_HUMAN	H17	5166	2	1459.7	(+0.8)	2.955	0.405	0.984	5	K.KPLPDHVSIVEPK.D
SW:RS3_HUMAN	H16	5784	2	817.0	(+0.9)	2.416	0.363	0.977	4	K.L*L*GGL*AVR.R
SW:RS3_HUMAN	H17	5524	2	817.0	(+0.7)	2.475	0.381	0.982	4	K.L*L*GGL*AVR.R
SW:RS4_HUMAN	H17	5704	2	1460.6	(+0.4)	3.934	0.412	0.993	2	K.VNDTIQIDL*ETGK#.I
SW:RS4_HUMAN	H17	7034	2	1911.2	(-0.3)	2.392	0.320	0.801	2	R.TDITYPAGFM@DVISIDK#.T
SW:RS7_HUMAN	H19	8484	2	1338.7	(+0.9)	3.707	0.402	0.991	1	K.AIIIFVVPQLK.S
SW:RS7_HUMAN	H19	8512	2	1352.7	(-0.4)	2.602	0.392*	0.153	1	K.AIIIFVVPQL*K#.S
SW:RS7_HUMAN	H19	8864	3	3332.7	(+0.5)	4.381	0.440	0.970	1	K.IVKPNGEKPDFESGISQALLELEMNSDLK.A
SW:RS7_HUMAN	H19	9028	2	2368.7	(+0.3)	5.311	0.619	1.000	1	R.TLTAHVDAILEDLVFPSEIVGK.R
SW:RS7_HUMAN	H19	8938	2	1391.5	(+1.0)	2.461	0.372	0.971	1	K.DVNFEPFEFQL*.-

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:RS8_HUMAN	H18	6684	2	1719.9	(+0.5)	5.124	0.437	1.000		R.IIDVVYNASNNELVR.T
SW:RS8_HUMAN	H18	6430	2	1527.7	(-0.0)	3.516	0.313	0.958	1	K.ISSL*L*EEQFQQGK#.L
SW:RS8_HUMAN	H18	6682	2	1725.9	(+0.3)	3.472	0.397	0.977		R.IIDVVYNASNNEL*VR.T
SW:RS9_HUMAN	H19	7092	2	1400.7	(+0.8)	3.617	0.393	0.988	2	R.KQVVNIPSFIVR.L
SW:RS9_HUMAN	H19	6780	2	1244.5	(+0.3)	2.433	0.210	0.090	3	K.M@K#L*DYIL*GL*K#.I
SW:RS9_HUMAN	H19	4874	2	1034.2	(+0.6)	2.244	0.267	0.909	3	R.RL*QTQVFK#.L
SW:RSMB_HUMAN	H17	5686	2	1555.8	(+0.8)	4.278	0.555	0.998	8	R.GENLVSMTEGPPPK.D
SW:RSMB_HUMAN	H17	4852	2	1585.8	(+0.0)	3.021	0.294	0.903	8	R.GENL*VSM@TVEGPPPK#.D
SW:RSMB_HUMAN	H17	5702	2	1555.8	(-0.6)	2.886	0.381	0.954	8	R.GENLVSMTEGPPPK.D
SW:RSMB_HUMAN	H18	6186	2	1555.8	(+0.6)	4.178	0.525	1.000	8	R.GENLVSMTEGPPPK.D
SW:RSMB_HUMAN	H18	6190	2	1569.8	(+0.5)	4.011	0.479	1.000	8	R.GENL*VSMTEGPPPK#.D
SW:RSMB_HUMAN	H18	6204	2	1569.8	(-1.0)	3.630	0.426	0.938	8	R.GENL*VSMTEGPPPK#.D
SW:RSMB_HUMAN	H18	5386	2	1585.8	(-0.2)	3.514	0.468	0.983	8	R.GENL*VSM@TVEGPPPK#.D
SW:RSMB_HUMAN	H17	4494	2	1082.3	(+0.7)	2.578	0.368	0.966	8	K.ML*QHIDYR.M
SW:RSMB_HUMAN	H17	4742	2	1199.4	(+0.6)	3.582	0.406	0.989	4	R.VPL*AGAAGGPGIGR.A
SW:RSMB_HUMAN	H17	4408	2	1199.4	(+0.9)	2.288	0.363	0.946	4	R.VPL*AGAAGGPGIGR.A
SW:RSMB_HUMAN	H18	5196	2	1199.4	(+0.4)	2.732	0.458	0.987	4	R.VPL*AGAAGGPGIGR.A
SW:RSP4_HUMAN	H14	5145	2	1732.8	(-0.1)	4.041	0.394	0.672	5	R.DPEEIEK#EEQAAAEEK#.A
SW:RSP4_HUMAN	H14	6841	2	1286.5	(+0.6)	2.738	0.439	0.987	6	R.K#SDGIYIINL*K#.R
SW:RU17_HUMAN	H10	2911	2	1660.7	(-0.1)	4.425	0.500	1.000	11	R.GGGGGQDNGLEGLGNSR.D
SW:RU17_HUMAN	H10	3083	2	1660.7	(-0.1)	4.259	0.483	1.000	11	R.GGGGGQDNGLEGLGNSR.D
SW:RU17_HUMAN	H10	3251	2	1660.7	(-0.2)	4.190	0.491	1.000	11	R.GGGGGQDNGLEGLGNSR.D
SW:RU17_HUMAN	H10	3163	2	1660.7	(-0.2)	4.181	0.518	1.000	11	R.GGGGGQDNGLEGLGNSR.D
SW:RU17_HUMAN	H10	2713	2	1660.7	(+0.6)	4.051	0.483	1.000	11	R.GGGGGQDNGLEGLGNSR.D
SW:RU17_HUMAN	H10	2835	2	1660.7	(+0.6)	4.026	0.478	1.000	11	R.GGGGGQDNGLEGLGNSR.D
SW:RU17_HUMAN	H10	3003	2	1660.7	(-0.1)	3.933	0.510	1.000	11	R.GGGGGQDNGLEGLGNSR.D
SW:RU17_HUMAN	H10	4725	2	1672.7	(+0.5)	3.902	0.505	1.000	11	R.GGGGGQDNL*EGL*GNSR.D
SW:RU17_HUMAN	H10	2583	2	1660.7	(+0.7)	3.822	0.535	1.000	11	R.GGGGGQDNGLEGLGNSR.D
SW:RU17_HUMAN	H10	2619	2	1672.7	(+0.1)	3.701	0.460	0.987	11	R.GGGGGQDNL*EGL*GNSR.D
SW:RU17_HUMAN	H10	3063	2	1672.7	(-0.0)	3.659	0.463	0.982	11	R.GGGGGQDNL*EGL*GNSR.D
SW:RU17_HUMAN	H10	2543	2	1672.7	(-0.4)	3.658	0.410	0.977	11	R.GGGGGQDNL*EGL*GNSR.D
SW:RU17_HUMAN	H10	2703	2	1672.7	(+0.1)	3.632	0.398	0.979	11	R.GGGGGQDNL*EGL*GNSR.D
SW:RU17_HUMAN	H10	2985	2	1672.7	(-0.1)	3.528	0.469	0.986	11	R.GGGGGQDNL*EGL*GNSR.D
SW:RU17_HUMAN	H10	2901	2	1672.7	(+0.5)	3.438	0.454	0.992	11	R.GGGGGQDNL*EGL*GNSR.D
SW:RU17_HUMAN	H10	4091	2	1672.7	(-0.8)	3.393	0.456	0.944	11	R.GGGGGQDNL*EGL*GNSR.D
SW:RU17_HUMAN	H10	4345	2	1672.7	(+0.0)	3.367	0.471	0.985	11	R.GGGGGQDNL*EGL*GNSR.D
SW:RU17_HUMAN	H10	3221	2	1672.7	(-0.3)	3.145	0.306	0.933	11	R.GGGGGQDNL*EGL*GNSR.D
SW:RU17_HUMAN	H10	2825	2	1672.7	(-1.0)	3.091	0.399	0.899	11	R.GGGGGQDNL*EGL*GNSR.D
SW:RU17_HUMAN	H10	3317	2	1672.7	(+0.6)	3.077	0.463	0.991	11	R.GGGGGQDNL*EGL*GNSR.D
SW:RU17_HUMAN	H10	3143	2	1672.7	(-0.8)	3.016	0.382	0.877	11	R.GGGGGQDNL*EGL*GNSR.D
SW:RU17_HUMAN	H10	3853	2	1672.7	(+0.4)	2.994	0.425	0.987	11	R.GGGGGQDNL*EGL*GNSR.D
SW:RU17_HUMAN	H10	5469	2	1868.0	(-0.5)	3.801	0.417	0.981	4	K.M@WDPHNDPNAQGDAFK#.T
SW:RU17_HUMAN	H10	5931	2	1844.0	(+0.4)	2.743	0.502	0.990	4	K.MWDPHNDPNAQGDAFK.T
SW:RU17_HUMAN	H10	6337	2	1246.4	(+0.7)	3.159	0.492	1.000	4	R.REFEVYGPIK#.R
SW:RU17_HUMAN	H10	2499	2	1660.7	(+0.1)	2.742	0.250	0.820	11	R.GGGGGQDNGLEGLGNSR.D
SW:RU1A_HUMAN	H16	6362	3	2865.4	(+0.8)	3.923	0.439	0.998		K.K#AVQGGGATPVVGAVQGPVPGMPPMTQAPR.I
SW:RU1A_HUMAN	H16	1420	2	1054.1	(+0.4)	2.233	0.326	0.939		K.EVSSATNAL*R.S
SW:RU1C_HUMAN	H19	6230	2	1478.7	(+0.7)	3.682	0.455	1.000	1	K.WMEEQAQSLIDK.T
SW:RU1C_HUMAN	H19	5586	2	1508.7	(+0.6)	3.545	0.378	0.990	1	K.WM@EEQAQSL*IDK#.T
SW:RU1C_HUMAN	H19	6846	2	2192.4	(-0.1)	2.660	0.186	0.658		K.FYCDYCDTYL*THDSPSVR.K
SW:RU2A_HUMAN	H17	4198	2	1135.2	(+0.9)	2.908	0.354	0.976	1	K.GGPPSPGDVEAIK#.N
SW:RU2A_HUMAN	H17	5088	2	1138.3	(+0.4)	2.310	0.289	0.810	2	K.GL*L*QSGQIPGR.E
SW:RU2A_HUMAN	H17	4122	2	1271.4	(+0.6)	2.678	0.449	0.985		K.K#GGPPSPGDVEAIK#.N
SW:RU2A_HUMAN	H17	6670	2	1085.3	(+0.3)	2.227	0.295	0.852	2	R.K#L*DFPFL*L*R.R
SW:RU2A_HUMAN	H17	7256	2	1892.1	(+1.0)	4.352	0.449	1.000	4	K.LTAEIEQAAQYTNVAVR.D
SW:RU2A_HUMAN	H17	7264	2	1904.1	(-0.4)	2.447	0.257	0.755	4	K.L*TAEI*IEQAAQYTNVAVR.D
SW:RU2A_HUMAN	H17	4960	2	1232.4	(+0.8)	2.505	0.281	0.917	2	K.TFNPAGL*PTDK#.K
SW:RU2A_HUMAN	H17	1838	2	944.1	(+0.0)	2.293	0.116	0.491	1	K.TLLVNNNR.I
SW:RU2A_HUMAN	H18	4578	2	1135.2	(-0.3)	2.204	0.213	0.560	1	K.GGPPSPGDVEAIK#.N

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:RUN1_HUMAN	H11	6014	2	1700.8	(-0.4)	2.336	0.312	0.154	7	K.L*DDQTK#PGSL*SFSEER.L
SW:RUN1_HUMAN	H11	6964	2	1491.6	(+0.8)	2.847	0.397	0.978	3	R.LSTAPDLTAFSDPR.Q
SW:RUN1_HUMAN	H11	6952	2	1503.6	(+0.3)	2.830	0.405	0.963	3	R.L*STAPDL*TAFSDFPR.Q
SW:RUN1_HUMAN	H11	7462	2	1664.9	(-0.6)	3.647	0.435	0.984	13	R.SMVEVL*ADHPGEL*VR.T
SW:RUN1_HUMAN	H12	7138	2	1664.9	(+0.3)	4.518	0.540	1.000	13	R.SMVEVL*ADHPGEL*VR.T
SW:RUV1_HUMAN	H12	8422	2	1695.0	(+0.8)	5.017	0.518	0.999	1	R.AL*ESSIPIVIFASNR.G
SW:RUV1_HUMAN	H12	8410	2	1689.0	(+0.9)	3.938	0.602	1.000	1	R.ALESSIPIVIFASNR.G
SW:RUV1_HUMAN	H12	7674	2	2325.5	(+0.2)	3.981	0.592	1.000	1	R.AQTEGINISEEALNHLGEIGTK.T
SW:RUV1_HUMAN	H12	5466	2	1081.3	(+0.5)	3.106	0.571	1.000	1	R.AVLLAGPPGTGK.T
SW:RUV1_HUMAN	H12	5480	2	1081.3	(-0.7)	2.430	0.172	0.224	1	R.AVLLAGPPGTGK.T
SW:RUV1_HUMAN	H12	7706	2	1950.2	(+0.2)	3.011	0.514	0.985	1	R.GTEDITSPHGIPLDLLDR.V
SW:RUV1_HUMAN	H12	6270	2	1267.5	(+0.3)	2.815	0.406	0.974	1	K.KTEVLMENFR.R
SW:RUV1_HUMAN	H12	6256	2	1281.5	(+0.8)	2.797	0.440	0.990	1	K.K#TEVL*MENFR.R
SW:RUV1_HUMAN	H12	5076	2	1297.5	(+0.3)	2.460	0.327	0.916	1	K.K#TEVL*M@ENFR.R
SW:RUV1_HUMAN	H12	6500	2	1095.3	(+0.8)	2.869	0.345	0.978	1	K.TISHVIIGL*K#.T
SW:RUV1_HUMAN	H12	8206	2	1531.8	(-0.1)	2.827	0.405	0.963	1	R.YSVQLLTPANLLAK.I
SW:RUV1_HUMAN	H12	5856	2	1060.2	(+1.0)	2.252	0.200	0.533	1	K.GLGLDESGLAK.Q
SW:RUV2_HUMAN	H12	2310	2	1112.3	(+0.0)	2.596	0.387	0.951	2	R.AVLIAGQPPTGK.T
SW:RUV2_HUMAN	H12	5396	2	1418.6	(+0.1)	3.633	0.420	0.684	1	K.DK#VQAGDVITIDK#.A
SW:RUV2_HUMAN	H12	5688	2	1418.6	(+0.2)	3.503	0.426	0.672	1	K.DK#VQAGDVITIDK#.A
SW:RUV2_HUMAN	H12	7826	2	1537.7	(-0.8)	2.725	0.290	0.703		K.EYQDAFL*FNEL*K#.G
SW:RUV2_HUMAN	H12	6836	2	1516.7	(+0.4)	3.561	0.423	0.989	2	K.TTEMETIYDL*GTK#.M
SW:RUV2_HUMAN	H12	6012	2	1532.7	(-0.5)	2.916	0.239	0.848	2	K.TTEM@ETIYDL*GTK#.M
SW:RUV2_HUMAN	H12	5418	2	1167.3	(+0.7)	3.696	0.298	0.983	1	K.VQAGDVITIDK#.A
SW:RUV2_HUMAN	H12	6504	2	1371.6	(-0.0)	2.491	0.293	0.850	1	R.L*L*IVSTTPYSEK#.D
SW:RUXE_HUMAN	H22	7132	2	1601.9	(+0.4)	3.650	0.523	1.000	3	R.IQVWL*YEQVNM@R.I
SW:RUXE_HUMAN	H22	7600	2	1352.7	(+0.7)	2.964	0.360	0.983	2	K.VM@VQPINL*IFR.Y
SW:RUXE_HUMAN	H22	7680	2	1352.7	(+0.8)	2.413	0.376	0.970	2	K.VM@VQPINL*IFR.Y
SW:RUXE_HUMAN	H22	6260	2	1273.4	(+0.4)	2.260	0.491	0.985	2	K.GDNITL*L*QSVSN.-
SW:S3A1_HUMAN	H06	6866	2	1536.7	(+0.0)	2.825	0.349	0.939	3	R.RTDIFGVEETAIGK.K
SW:S3A1_HUMAN	H06	1934	2	1429.6	(+1.0)	2.698	0.207	0.231	3	K.IGEEEEIQKPEEK.V
SW:S3A3_HUMAN	H11	9846	3	3273.5	(+0.8)	5.657	0.522	0.996		K.ETSSALTHAGAHLDLSAFSSWEELASLGLDR.L
SW:S3A3_HUMAN	H11	7754	2	1311.5	(+0.1)	2.553	0.483	0.976		K.SLESLDTSLFAK.N
SW:S3A3_HUMAN	H11	6438	2	1516.7	(+0.9)	3.932	0.423	0.868		R.VKPLQDQNELFGK.I
SW:S3A3_HUMAN	H11	6446	2	1544.7	(-0.2)	3.090	0.369	0.479		R.VK#PL*QDQNEL*FGK#.I
SW:S3A3_HUMAN	H11	5264	2	1210.3	(+0.1)	2.296	0.130	0.024		R.DLYDDKDGRLR.K
SW:S3B1_HUMAN	H05	9670	2	1690.0	(+0.9)	3.694	0.465	0.993	1	K.AIGPHDVLATLLNLLK.V
SW:S3B1_HUMAN	H05	9636	2	1722.0	(-0.2)	3.104	0.131	0.634	1	K.AIGPHDVL*ATL*L*NNL*K#.V
SW:S3B1_HUMAN	H06	9596	2	1690.0	(+0.6)	4.532	0.519	1.000	1	K.AIGPHDVLATLLNLLK.V
SW:S3B1_HUMAN	H05	9268	3	2250.6	(+0.4)	3.729	0.514	0.995	1	K.AIGYL*IPL*MDAEYANYYTR.E
SW:S3B1_HUMAN	H05	5904	2	1106.3	(+0.7)	2.282	0.107	0.520		K.AIVNVIGM@HK#.M
SW:S3B1_HUMAN	H05	9372	2	2033.3	(-0.7)	2.373	0.256	0.439	2	K.DYIYAVTPL*L*EDAL*M@DR.D
SW:S3B1_HUMAN	H05	5990	2	1369.6	(+0.0)	2.762	0.440	0.966		K.IMGNL*GAADIDHK#.L
SW:S3B1_HUMAN	H05	6198	2	1375.6	(+0.3)	2.447	0.277	0.158	1	K.L*DDL*VRPYVHK#.I
SW:S3B1_HUMAN	H05	8728	2	1838.1	(-0.1)	3.595	0.381	0.976	1	R.SLVEIIEHGLVDEQQK.V
SW:S3B1_HUMAN	H05	6632	2	1310.5	(+0.1)	2.573	0.405	0.956	1	R.VPELNVQNGVLK.S
SW:S3B1_HUMAN	H05	1496	2	1234.4	(+0.6)	2.689	0.408	0.939	1	K.VVNGAAASQPPSK#.R
SW:S3B1_HUMAN	H06	8638	2	1838.1	(+0.6)	3.734	0.435	0.993	1	R.SLVEIIEHGLVDEQQK.V
SW:S3B2_HUMAN	H05	5246	2	1041.2	(+1.0)	2.230	0.210	0.795	4	R.AAVL*L*EQER.Q
SW:S3B2_HUMAN	H05	6518	3	2407.6	(+0.7)	5.162	0.501	0.997	8	R.EQQAQVEK#EDFSMDVAEHAAC#.Q
SW:S3B2_HUMAN	H05	8382	2	1630.9	(+0.6)	3.159	0.262	0.459	6	R.GIEKPPFELPDFIK.R
SW:S3B2_HUMAN	H06	8306	2	1630.9	(+1.0)	3.020	0.250	0.340	6	R.GIEKPPFELPDFIK.R
SW:S3B2_HUMAN	H05	5586	2	1351.6	(+0.0)	2.209	0.420	0.921	7	R.ISL*GM@PVGPNAAK#.V
SW:S3B2_HUMAN	H05	5760	2	1239.4	(+0.9)	3.197	0.312	0.978	4	K.LAEIGAPIQGNR.E
SW:S3B2_HUMAN	H05	5756	2	1245.4	(+0.3)	3.094	0.349	0.962	4	K.L*AEIGAPIQGNR.E
SW:S3B2_HUMAN	H05	5790	2	1239.4	(-0.3)	2.548	0.362	0.934	4	K.LAEIGAPIQGNR.E
SW:S3B2_HUMAN	H05	5290	2	1315.4	(-0.2)	2.996	0.428	0.976	5	R.VGEPVALSEEER.L
SW:S3B2_HUMAN	H05	5288	2	1321.4	(+0.1)	2.799	0.437	0.974	5	R.VGEPVAL*SEEER.L

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:S3B2_HUMAN	H06	4758	2	1029.2	(+0.9)	2.695	0.153	0.868	4	R.AAVLLEQER.Q
SW:S3B3_HUMAN	H03	10408	3	2534.9	(+0.3)	4.809	0.533	1.000	3	R.ELAAEMAAAFLENENLPESIFGAPK.A
SW:S3B3_HUMAN	H04	9469	3	2576.9	(+0.9)	3.723	0.467	0.999	3	R.EL*AAEM@AAAF*LENL*PESIFGAPK#.A
SW:S3B3_HUMAN	H01	6232	2	1316.5	(+0.7)	2.841	0.420	0.987	1	R.FL*AVGL*VDNTR.I
SW:S3B3_HUMAN	H02	6328	2	1316.5	(+0.3)	4.188	0.472	1.000	1	R.FL*AVGL*VDNTR.I
SW:S3B3_HUMAN	H01	5860	2	1466.7	(+1.0)	2.891	0.357	0.582	2	K.ILELLRPDPNTGK.V
SW:S3B3_HUMAN	H01	5610	2	1190.4	(+0.9)	2.614	0.347	0.974	2	R.IVILEYQPSK.N
SW:S3B3_HUMAN	H02	5748	2	1190.4	(+0.6)	3.057	0.420	0.991	2	R.IVILEYQPSK.N
SW:S3B3_HUMAN	H03	6654	2	1190.4	(+0.9)	2.912	0.473	0.993	2	R.IVILEYQPSK.N
SW:S3B3_HUMAN	H02	6996	2	1922.2	(+0.9)	4.975	0.588	1.000	1	K.LGAVFNQVAFPLQYTPR.K
SW:S3B3_HUMAN	H02	7000	2	1934.2	(-0.6)	2.952	0.428	0.971	1	K.L*GAVFNQVAFPL*QYTPR.K
SW:S3B3_HUMAN	H03	8448	2	1922.2	(+0.2)	4.985	0.570	0.998	1	K.LGAVFNQVAFPLQYTPR.K
SW:S3B3_HUMAN	H01	5358	2	1196.4	(+0.6)	2.383	0.296	0.931	2	R.LTISSPLEAHK.A
SW:S3B3_HUMAN	H01	5450	2	1192.4	(+0.9)	3.293	0.571	1.000	3	R.SVAGGFVYTYK.L
SW:S3B3_HUMAN	H01	5706	2	1277.4	(+0.7)	2.600	0.229	0.899	1	R.SWLSYSYQSR.F
SW:S3B3_HUMAN	H01	5516	2	1501.6	(-0.1)	2.902	0.511	0.982	1	R.TVL*DPVTGDL*SDTR.T
SW:S3B3_HUMAN	H02	5648	2	1501.6	(+0.6)	3.202	0.479	0.993	1	R.TVL*DPVTGDL*SDTR.T
SW:S3B3_HUMAN	H03	6510	2	1489.6	(+0.9)	4.293	0.558	1.000	1	R.TVLDPVTGDLSDTR.T
SW:S3B3_HUMAN	H01	6510	2	1927.1	(-0.4)	4.934	0.598	1.000	4	R.WVTASLLDYDTVAGADK.F
SW:S3B3_HUMAN	H04	7311	2	1316.5	(+0.9)	3.075	0.474	0.993	1	R.FL*AVGL*VDNTR.I
SW:SAT1_HUMAN	H07	7402	2	1559.8	(+0.8)	3.107	0.337	0.979		R.AMQNFL*QL*PEAER.D
SW:SAT1_HUMAN	H07	7410	2	1547.8	(+0.8)	2.335	0.286	0.899		R.AMQNFLQLPEAER.D
SW:SAT1_HUMAN	H07	6028	2	1453.5	(-0.0)	2.625	0.161	0.586		K.DNSGL*EVDVAEYK#.E
SW:SAT1_HUMAN	H08	6529	3	2328.6	(+0.4)	4.024	0.451	0.998		R.L*L*AQQSL*NQQYL*NHPPVSR.S
SW:SAT1_HUMAN	H07	6364	3	2524.9	(+0.5)	4.097	0.348	0.955		R.SL*NAASAM@GPAPL*ISTPPSRPPQVK#.T
SW:SAT1_HUMAN	H07	8180	2	1148.3	(+0.7)	2.620	0.255	0.938	2	R.TQGL*L*SEIL*R.K
SW:SAT1_HUMAN	H10	6525	3	2304.6	(+0.4)	4.260	0.339	0.992		R.LLAQQSLNQQYLNHPPVSR.S
SW:SBDS_HUMAN	H17	3962	2	878.1	(+0.9)	2.556	0.178	0.858	2	R.L*TNVAVVR.M
SW:SBDS_HUMAN	H17	6080	2	1266.5	(+0.3)	2.240	0.104	0.332		K.RPYTVIL*IER.A
SW:SC10_HUMAN	H09	7575	2	1470.7	(+0.6)	2.727	0.359	0.975	1	K.L*HL*IAQEL*PFDR.F
SW:SC10_HUMAN	H09	7459	2	1618.8	(+0.3)	2.714	0.472	0.974	1	K.QVGDIFSNPETVLAK.L
SW:SCD1_HUMAN	H11	6424	2	1453.7	(+0.2)	3.225	0.362	0.966	3	K.IHETIETINQL*K#.T
SW:SCD1_HUMAN	H11	4774	2	1005.2	(+0.8)	2.418	0.112	0.732	7	R.KLDQTIMR.K
SW:SCD1_HUMAN	H11	5588	3	2246.5	(+0.9)	6.330	0.527	1.000	4	R.KRPAPQQIQVQQQAVQNR.N
SW:SCD1_HUMAN	H11	5586	3	2254.5	(+0.9)	6.256	0.530	0.977	4	R.K#RPAPQQIQVQQQAVQNR.N
SW:SCD1_HUMAN	H11	9732	3	2519.0	(+0.2)	4.227	0.390	0.976	4	R.L*L*GIHTQTRPVIIQAL*WQYIK#.T
SW:SCD1_HUMAN	H11	6668	2	1313.5	(+0.9)	3.698	0.442	1.000	4	R.RQELEQALGIR.N
SW:SCD1_HUMAN	H11	6726	2	1728.8	(-0.0)	3.711	0.439	0.984	4	K.SDAEDGEGETVASWEL*R.V
SW:SCD1_HUMAN	H11	6722	2	1722.8	(+0.5)	3.403	0.525	1.000	4	K.SDAEDGEGETVASWELR.V
SW:SCD1_HUMAN	H11	4594	2	1434.5	(+0.8)	3.957	0.533	1.000	4	R.TATTQETDGFQVK#.R
SW:SCD1_HUMAN	H11	4516	2	1434.5	(+0.3)	3.348	0.412	0.976	4	R.TATTQETDGFQVK#.R
SW:SCD1_HUMAN	H11	4524	2	1426.5	(+0.4)	2.912	0.301	0.963	4	R.TATTQETDGFQVK.R
SW:SCD1_HUMAN	H11	4616	2	1434.5	(-0.4)	2.819	0.404	0.960	4	R.TATTQETDGFQVK#.R
SW:SCD1_HUMAN	H11	6664	2	1325.5	(+0.5)	2.416	0.363	0.959	4	R.RQEL*EQAL*GIR.N
SW:SEC8_HUMAN	H06	8486	2	1643.9	(+0.3)	4.076	0.493	1.000	4	R.FIQEIEHAL*GL*GPAK#.Q
SW:SEC8_HUMAN	H06	8738	2	1550.8	(+0.7)	4.272	0.326	0.991	2	K.HVLNLLDEIENIK.Q
SW:SEC8_HUMAN	H06	8734	2	1576.8	(+0.7)	3.338	0.416	0.990	2	K.HVL*NL*L*DEIENIK#.Q
SW:SEC8_HUMAN	H06	9030	2	1536.8	(+0.1)	2.328	0.375	0.901	4	K.NIFL*NQVL*AEINK#.E
SW:SEP1_HUMAN	H14	6183	2	1507.6	(+0.3)	3.020	0.359	0.962	3	K.EVTHDL*L*YEGYR.A
SW:SEP1_HUMAN	H14	6181	2	1495.6	(+0.2)	2.948	0.393	0.969	3	K.EVTHDLLYEGYR.A
SW:SEP1_HUMAN	H14	6943	2	1627.8	(+0.5)	3.426	0.451	0.993	2	K.EYVGFAAL*PNQL*HR.K
SW:SEP1_HUMAN	H14	6939	2	1615.8	(+0.3)	2.679	0.448	0.969	2	K.EYVGFAALPNQLHR.K
SW:SEP1_HUMAN	H14	6961	2	1615.8	(-1.0)	2.525	0.287	0.613	2	K.EYVGFAALPNQLHR.K
SW:SEP1_HUMAN	H13	7768	2	1508.7	(+0.8)	2.972	0.452	0.992	3	K.FIEEQFEQYL*R.D
SW:SEP1_HUMAN	H14	7713	2	1508.7	(+0.8)	4.010	0.420	1.000	3	K.FIEEQFEQYL*R.D
SW:SEP1_HUMAN	H13	7692	2	1275.5	(+0.7)	2.926	0.367	0.697	2	R.GL*RPL*DVAFL*R.A
SW:SEP1_HUMAN	H14	7659	2	1275.5	(+0.4)	2.818	0.381	0.694	2	R.GL*RPL*DVAFL*R.A
SW:SEP1_HUMAN	H14	5839	2	1368.6	(-0.3)	2.821	0.171	0.743	3	R.M@L*VQTHL*QDL*K#.E
SW:SEP1_HUMAN	H14	4123	2	1173.3	(+0.1)	2.692	0.240	0.852	2	R.RGVEIEEGGVK.V

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:SEP1_HUMAN	H14	9023	2	1900.1	(+0.5)	4.706	0.565	1.000	2	K.STLINSFLFLTNLYEDR.Q
SW:SEP1_HUMAN	H21	8618	2	1900.1	(+0.3)	3.102	0.498	0.979	2	K.STLINSFLFLTNLYEDR.Q
SW:SEP1_HUMAN	H22	8478	2	1900.1	(+0.5)	2.907	0.493	0.991	2	K.STLINSFLFLTNLYEDR.Q
SW:SEP1_HUMAN	H22	8466	2	1924.1	(+0.0)	2.873	0.495	0.981	2	K.STL*INSL*FL*TNL*YEDR.Q
SW:SEP2_HUMAN	H14	5853	2	1353.5	(+1.0)	3.113	0.178	0.925	3	R.ILDEIEEHNK.I
SW:SEP2_HUMAN	H14	8145	2	2286.5	(+0.3)	4.886	0.512	1.000	3	R.LYPWGVVEVENPEHNDFLK.L
SW:SEP2_HUMAN	H14	8155	2	2306.5	(+0.1)	4.714	0.444	0.999	3	R.L*YPWGVVEVENPEHNDFL*K#.L
SW:SEP2_HUMAN	H14	4373	3	2439.7	(+0.6)	5.538	0.478*	0.211	3	R.M@QAQM@QM@QM@QGGDGDGGAL*GHHV.-
SW:SEP2_HUMAN	H14	4149	3	2439.7	(+0.8)	5.085	0.411*	0.149	3	R.M@QAQM@QM@QM@QGGDGDGGAL*GHHV.-
SW:SEP2_HUMAN	H14	4455	3	2439.7	(+0.9)	4.732	0.547*	0.141	3	R.M@QAQM@QM@QM@QGGDGDGGAL*GHHV.-
SW:SEP2_HUMAN	H14	9093	2	1883.2	(+0.7)	3.631	0.375	0.989	4	K.STLINSFLFLTDLYPER.V
SW:SEP2_HUMAN	H14	7403	3	2914.2	(+0.6)	4.559	0.536	1.000	4	R.TM@L*ITHM@QDL*QEVTDQL*HYENFR.S
SW:SEP2_HUMAN	H14	8391	3	2882.2	(+0.6)	4.513	0.496	1.000	4	R.TML*ITHMQDL*QEVTDQL*HYENFR.S
SW:SEP2_HUMAN	H14	8079	3	2898.2	(-0.0)	4.370	0.545*	0.042	4	R.TM@L*ITHMQDL*QEVTDQL*HYENFR.S
SW:SEP2_HUMAN	H14	7553	2	1761.0	(+0.7)	2.742	0.429	0.942	3	K.ASIPFSVVGSNQLIEAK.G
SW:SEP6_HUMAN	H12	6160	2	2072.2	(+0.6)	3.870	0.614	0.998	12	K.DTDPDSKPFSLQETYEAK.R
SW:SEP6_HUMAN	H12	6154	2	2094.2	(-0.5)	2.279	0.206	0.039	12	K.DTDPDSK#PFSL*QETYEAK#.R
SW:SEP6_HUMAN	H11	6594	3	3147.3	(+0.2)	5.492	0.571	1.000	9	K.FEGEPATHTQPGVQLQSNTYDLQESNVR.L
SW:SEP6_HUMAN	H11	6596	3	3159.3	(-0.5)	4.669	0.451	0.995	9	K.FEGEPATHTQPGVQL*QSNTYDL*QESNVR.L
SW:SEP6_HUMAN	H12	6322	3	3147.3	(+0.7)	7.586	0.556	1.000	9	K.FEGEPATHTQPGVQLQSNTYDLQESNVR.L
SW:SEP6_HUMAN	H12	6324	3	3159.3	(+0.4)	6.732	0.630	0.999	9	K.FEGEPATHTQPGVQL*QSNTYDL*QESNVR.L
SW:SEP6_HUMAN	H12	6456	3	3159.3	(-0.5)	4.902	0.494	1.000	9	K.FEGEPATHTQPGVQL*QSNTYDL*QESNVR.L
SW:SEP6_HUMAN	H12	6344	2	3147.3	(+0.5)	3.980	0.566	1.000	9	K.FEGEPATHTQPGVQLQSNTYDLQESNVR.L
SW:SEP6_HUMAN	H13	6216	3	3147.3	(+0.6)	6.787	0.617	0.999	9	K.FEGEPATHTQPGVQLQSNTYDLQESNVR.L
SW:SEP6_HUMAN	H13	6220	3	3159.3	(+0.1)	6.242	0.587	1.000	9	K.FEGEPATHTQPGVQL*QSNTYDL*QESNVR.L
SW:SEP6_HUMAN	H12	5778	2	2104.3	(+0.9)	6.789	0.622	1.000	4	R.KTAAELLQSQGSQAGGSQTLK.R
SW:SEP6_HUMAN	H12	13084	2	1606.8	(+0.9)	2.229	0.385	0.942	8	K.L*TIVSTVGFQDQINK#.E
SW:SEP6_HUMAN	H12	6246	2	1234.4	(-0.6)	2.384	0.195	0.690	14	K.RNEFLGELQK.K
SW:SEP6_HUMAN	H13	6126	2	1254.4	(+0.1)	2.678	0.338	0.938	14	K.RNEFL*GEL*QK#.K
SW:SEP6_HUMAN	H12	6158	2	1138.2	(+0.7)	2.202	0.349	0.927	5	K.SLDDEVNAFK.Q
SW:SEP6_HUMAN	H13	6078	2	1138.2	(+1.0)	3.218	0.485	1.000	5	K.SLDDEVNAFK.Q
SW:SEP6_HUMAN	H12	7878	2	1271.5	(-0.7)	2.216	0.390	0.779	14	K.STLMDTLFNTK.F
SW:SEP6_HUMAN	H12	5624	2	1976.2	(+0.9)	5.314	0.603	0.997	4	K.TAAELLQSQGSQAGGSQTLK.R
SW:SEP6_HUMAN	H12	7536	2	2108.4	(+0.7)	5.265	0.589	0.997	9	R.TVPLAGHVGFDSLPLDQLVNK.S
SW:SEP6_HUMAN	H12	7524	2	2134.4	(-0.6)	3.280	0.465	0.980	9	R.TVPL*AGHVGFDSL*PDQL*VNK#.S
SW:SEP6_HUMAN	H12	1554	2	1134.2	(+0.9)	2.397	0.338	0.958	8	R.VL*HTYHDSR.I
SW:SEP6_HUMAN	H12	1556	2	1128.2	(+0.7)	2.291	0.210	0.847	8	R.VLHTYHDSR.I
SW:SEP6_HUMAN	H13	6124	2	1234.4	(+0.6)	2.383	0.238	0.889	14	K.RNEFLGELQK.K
SW:SEP7_HUMAN	H12	5766	2	1250.3	(+0.5)	2.544	0.213	0.892	3	K.FEDYL*NAESR.V
SW:SEP7_HUMAN	H13	1568	2	1075.2	(+0.9)	2.549	0.419	0.986	2	R.ILEQQNSSR.T
SW:SEP7_HUMAN	H12	5774	2	1766.8	(-0.2)	3.136	0.364	0.957	2	K.IYEFPETDDEEENK#.L
SW:SEP7_HUMAN	H13	4548	2	1529.7	(-0.8)	3.903	0.426	0.950	2	R.K#L*AAVTYNGVDNNK#.N
SW:SEP7_HUMAN	H13	4504	2	1507.7	(+0.9)	3.200	0.440	0.991	2	R.KLAAVTYNGVDNNK.N
SW:SEP7_HUMAN	H13	4084	2	1393.5	(+0.4)	4.042	0.463	1.000	2	K.L*AAVTYNGVDNNK#.N
SW:SEP7_HUMAN	H13	4078	2	1379.5	(+0.6)	3.265	0.469	0.993	2	K.LAAVTYNGVDNNK.N
SW:SEP7_HUMAN	H13	4162	2	1393.5	(+0.2)	3.097	0.505	0.985	2	K.L*AAVTYNGVDNNK#.N
SW:SEP7_HUMAN	H13	4240	2	1393.5	(-0.6)	2.830	0.216	0.792	2	K.L*AAVTYNGVDNNK#.N
SW:SEP7_HUMAN	H13	7760	2	1955.2	(+0.6)	4.036	0.582	1.000	2	K.NLEGYVGFANLPNQVYR.K
SW:SEP7_HUMAN	H13	7754	2	1967.2	(-0.3)	2.954	0.409	0.966	2	K.NL*EGYVGFANL*PNQVYR.K
SW:SEP7_HUMAN	H12	5240	2	1190.3	(-0.3)	3.420	0.391	0.984	2	K.SPLAQMEEER.R
SW:SEP7_HUMAN	H12	5180	2	1190.3	(+0.9)	3.068	0.462	0.991	2	K.SPLAQMEEER.R
SW:SEP7_HUMAN	H12	5194	2	1196.3	(+0.9)	2.879	0.239	0.951	2	K.SPL*AQMEEER.R
SW:SEP7_HUMAN	H13	5256	2	1196.3	(+0.8)	2.785	0.247	0.946	2	K.SPL*AQMEEER.R
SW:SEP7_HUMAN	H13	5088	2	1352.5	(+0.9)	3.051	0.349	0.694	2	K.SPL*AQMEEERR.E
SW:SEP7_HUMAN	H13	8994	2	2608.9	(-0.1)	3.619	0.437	0.984	2	K.STLINSFLFLTDLYSPEYPGPSHR.I
SW:SEP7_HUMAN	H13	9000	2	2632.9	(+0.4)	3.518	0.492	1.000	2	K.STL*INSL*FL*TDL*YSPEYPGPSHR.I
SW:SEP7_HUMAN	H13	1488	2	1075.2	(+0.6)	2.441	0.278	0.942	2	R.ILEQQNSSR.T
SW:SERA_HUMAN	H11	10318	3	2273.7	(+0.0)	3.809	0.380	0.992	4	R.TQTSDPAMPLPTMIGLAEAGVR.L
SW:SERA_HUMAN	H11	5176	2	1131.3	(-0.3)	2.834	0.440	0.978	1	K.VTADVINAEEK.L
SW:SET_HUMAN	H15	4796	2	1447.5	(+0.8)	2.851	0.434	0.987	3	K.EFHLNESGDPSSK.S
SW:SET_HUMAN	H15	4798	2	1461.5	(+0.7)	2.684	0.294	0.939	3	K.EFHL*NESGDPSSK#.S

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:SET_HUMAN	H15	7990	2	1842.0	(+0.8)	3.502	0.441	0.993	3	R.IDFYFDENPYFENK.V
SW:SET_HUMAN	H15	10126	3	3728.2	(+0.2)	7.070	0.663	0.990	2	K.IPNFWVTTFVNHQPVSALLGEEDEEALHYLTR.V
SW:SET_HUMAN	H15	5482	2	1274.4	(+1.0)	4.286	0.357	0.994	3	R.LNEQASEEILK.V
SW:SET_HUMAN	H15	5484	2	1294.4	(+0.1)	2.499	0.244	0.782	3	R.L*NEQASEEIL*K#.V
SW:SET_HUMAN	H16	5036	2	1274.4	(+0.9)	2.551	0.249	0.916	3	R.LNEQASEEILK.V
SW:SFPQ_HUMAN	H07	2074	1	715.9	(+0.1)	1.950	0.112*	0.000	4	R.ALAEIAK.A
SW:SFPQ_HUMAN	H06	5912	3	2471.6	(-0.0)	5.516	0.445	1.000	3	K.DK#L*ESEM@EDAYHEHQANL*L*R.Q
SW:SFPQ_HUMAN	H06	7050	3	2455.6	(-0.3)	5.124	0.342	0.764	3	K.DK#L*ESEMEDAYHEHQANL*L*R.Q
SW:SFPQ_HUMAN	H07	5780	3	2471.6	(+0.3)	5.233	0.492	0.997	3	K.DK#L*ESEM@EDAYHEHQANL*L*R.Q
SW:SFPQ_HUMAN	H07	7056	3	2455.6	(+0.2)	5.151	0.419	0.972	3	K.DK#L*ESEMEDAYHEHQANL*L*R.Q
SW:SFPQ_HUMAN	H07	7082	2	2429.6	(-0.9)	3.945	0.426	0.449	3	K.DKLESEMEDAYHEHQANLLR.Q
SW:SFPQ_HUMAN	H06	5332	2	1150.3	(+0.9)	2.552	0.335	0.964	4	R.FATHAAAL*SVR.N
SW:SFPQ_HUMAN	H07	5496	2	1150.3	(+0.7)	2.352	0.334	0.950	4	R.FATHAAAL*SVR.N
SW:SFPQ_HUMAN	H08	5339	2	1144.3	(+0.7)	2.548	0.321	0.958	4	R.FATHAAALSVR.N
SW:SFPQ_HUMAN	H08	5327	2	1150.3	(+0.6)	2.541	0.370	0.973	4	R.FATHAAAL*SVR.N
SW:SFPQ_HUMAN	H06	7864	2	1985.2	(-0.9)	2.649	0.236	0.037	3	R.L*FVGNL*PADITEDEFK#R.L
SW:SFPQ_HUMAN	H07	1912	2	1431.6	(+0.2)	2.484	0.312	0.884	3	R.MEEL*HNQEMQK#.R
SW:SFPQ_HUMAN	H07	1914	2	1417.6	(+0.7)	2.421	0.301	0.938	3	R.MEELHNQEMQK.R
SW:SFPQ_HUMAN	H07	1622	2	1447.6	(+0.1)	2.404	0.205	0.665	3	R.MEEL*HNQEM@QK#.R
SW:SFPQ_HUMAN	H07	4362	2	1797.0	(+0.6)	4.059	0.505*	0.721	3	R.M@GGGGAMNMGDPYGGGQK#.F
SW:SFPQ_HUMAN	H07	5164	2	1781.0	(-0.3)	3.161	0.340	0.945	3	R.MGGGGAMNMGDPYGGGQK#.F
SW:SFPQ_HUMAN	H07	5166	2	1773.0	(-0.4)	2.440	0.467	0.962	3	R.MGGGGAMNMGDPYGGGQK.F
SW:SFPQ_HUMAN	H07	5142	3	2393.7	(-0.1)	5.106	0.508	0.990	2	K.MPGGPK#PGGGPGL*STPGGHPK#PPHR.G
SW:SFPQ_HUMAN	H07	2322	3	2409.7	(+0.1)	4.096	0.399	0.965	2	K.M@PGGPK#PGGGPGL*STPGGHPK#PPHR.G
SW:SFPQ_HUMAN	H07	9900	2	2640.9	(-0.2)	4.283	0.497	1.000	4	R.NLSPYVSNELLEAFSQFGPIER.A
SW:SFPQ_HUMAN	H06	1860	2	1573.8	(+0.1)	2.607	0.274	0.865	3	R.RMEELHNQEMQK.R
SW:SFPQ_HUMAN	H07	1966	2	1587.8	(+0.1)	2.985	0.419	0.972	3	R.RMEEL*HNQEMQK#.R
SW:SFPQ_HUMAN	H07	1948	2	1573.8	(+0.4)	2.723	0.421	0.985	3	R.RMEELHNQEMQK.R
SW:SFPQ_HUMAN	H06	5996	2	1261.4	(+0.2)	3.100	0.503	0.973	4	K.YGEPGEVFIN#G
SW:SFPQ_HUMAN	H06	5970	2	1253.4	(-0.1)	2.278	0.362	0.910	4	K.YGEPGEVFIN#G
SW:SFPQ_HUMAN	H10	6127	2	1261.4	(+0.6)	2.873	0.412	0.986	4	K.YGEPGEVFIN#G
SW:SFPQ_HUMAN	H11	6322	2	1261.4	(+0.8)	2.248	0.357	0.946	4	K.YGEPGEVFIN#G
SW:SFR1_HUMAN	H16	6126	2	1257.5	(+0.9)	3.240	0.417	0.992	4	R.IYVGNLPPDIR.T
SW:SFR1_HUMAN	H16	6034	2	1263.5	(+0.8)	3.034	0.394	0.988	4	R.IYVGNL*PPDIR.T
SW:SFR1_HUMAN	H16	6206	2	1257.5	(+0.8)	2.561	0.390	0.976	4	R.IYVGNLPPDIR.T
SW:SFR1_HUMAN	H16	1610	2	1113.3	(+1.0)	2.688	0.206	0.916	3	R.KEDMTYAVR.K
SW:SFR1_HUMAN	H16	6486	2	1669.9	(-0.8)	2.839	0.332	0.787	4	R.VVVSGLPPSGSWQDLK.D
SW:SFR1_HUMAN	H16	6524	2	1689.9	(-0.1)	2.681	0.289	0.848	4	R.VVVSGL*PPSGSWQDL*K#.D
SW:SFR1_HUMAN	H16	6120	2	1263.5	(+0.5)	2.324	0.339	0.949	4	R.IYVGNL*PPDIR.T
SW:SFR3_HUMAN	H19	4126	2	1249.4	(+0.4)	2.819	0.296	0.960	1	K.VYVGNLGNNGNK.T
SW:SFR3_HUMAN	H19	4180	2	1263.4	(+0.9)	2.560	0.327	0.951	1	K.VYVGNL*GNNGNK#.T
SW:SFR3_HUMAN	H19	6168	2	1044.2	(-0.4)	2.503	0.338	0.937	1	R.AFGYYGLR.S
SW:SFR9_HUMAN	H17	5648	2	1247.4	(+0.8)	2.870	0.350	0.979		R.IYVGNLPTDVR.E
SW:SFR9_HUMAN	H17	5634	2	1253.4	(+0.8)	2.794	0.339	0.975		R.IYVGNL*PTDVR.E
SW:SFR9_HUMAN	H17	6418	2	1300.5	(+0.8)	2.477	0.331	0.450		R.EKDLEDLFYK.Y
SW:SMD1_HUMAN	H21	5654	2	1290.5	(+0.2)	2.349	0.206	0.643		K.L*SHETVTIEL*K#.N
SW:SMD1_HUMAN	H21	5320	2	2240.5	(+0.3)	4.715	0.486	0.999	1	K.NGTQVHGHTITGVDVSM@NTHL*K#.A
SW:SMD1_HUMAN	H21	5946	3	2224.5	(+0.8)	3.865	0.433	0.999	1	K.NGTQVHGHTITGVDVSMNTHL*K#.A
SW:SMD1_HUMAN	H21	11987	3	2240.5	(-0.9)	3.723	0.352	0.974	1	K.NGTQVHGHTITGVDVSM@NTHL*K#.A
SW:SMD1_HUMAN	H01	5764	2	1555.8	(+0.7)	2.645	0.220	0.221	1	K.NREPVQLETLSIR.G
SW:SMD1_HUMAN	H20	6342	2	1567.8	(+0.0)	3.070	0.325	0.412	1	K.NREPVQL*ETL*SIR.G
SW:SMD1_HUMAN	H20	6354	2	1555.8	(+0.6)	3.042	0.423	0.772	1	K.NREPVQLETLSIR.G
SW:SMD1_HUMAN	H21	6274	2	1555.8	(+0.9)	4.087	0.534	0.999	1	K.NREPVQLETLSIR.G
SW:SMD1_HUMAN	H21	6226	2	1567.8	(+0.5)	2.976	0.369	0.671	1	K.NREPVQL*ETL*SIR.G
SW:SMD1_HUMAN	H21	6340	2	1567.8	(+0.6)	2.971	0.329	0.586	1	K.NREPVQL*ETL*SIR.G
SW:SMD1_HUMAN	H22	6388	2	1567.8	(-0.1)	3.018	0.263	0.265	1	K.NREPVQL*ETL*SIR.G
SW:SMD1_HUMAN	H02	8498	2	2288.7	(+0.1)	2.911	0.509	0.983	1	R.YFILPDSLPLDTLLVDVEPK.V
SW:SMD1_HUMAN	H03	10604	2	2288.7	(+0.3)	3.571	0.490	0.749	1	R.YFILPDSLPLDTLLVDVEPK.V
SW:SMD1_HUMAN	H04	10573	2	2288.7	(-0.2)	2.394	0.306	0.828	1	R.YFILPDSLPLDTLLVDVEPK.V
SW:SMD1_HUMAN	H19	10136	2	2288.7	(+0.2)	2.637	0.501	0.977	1	R.YFILPDSLPLDTLLVDVEPK.V
SW:SMD1_HUMAN	H21	9962	2	2288.7	(+0.3)	5.844	0.528	0.997	1	R.YFILPDSLPLDTLLVDVEPK.V



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:SMD1_HUMAN	H21	9870	2	2288.7	(-0.3)	2.842	0.471	0.975	1	R.YFILPDSLPLDILLVDVEPK.V
SW:SMD1_HUMAN	H22	9794	2	2288.7	(+0.3)	2.640	0.514	0.979	1	R.YFILPDSLPLDILLVDVEPK.V
SW:SMD2_HUMAN	H21	7830	2	2008.2	(+0.8)	4.694	0.585	1.000		R.EEEEFNTGPLSVLTQSVK.N
SW:SMD2_HUMAN	H21	7800	2	2028.2	(-0.0)	3.835	0.379	0.977		R.EEEEFNTGPL*SVL*TSQSVK#.N
SW:SMD2_HUMAN	H20	2164	1	726.9	(+0.0)	1.947	0.137	0.000		R.NPL*IAGK#.-
SW:SMD2_HUMAN	H21	2228	1	712.9	(-0.0)	2.343	0.192	0.000		R.NPLIAGK.-
SW:SMD2_HUMAN	H21	2234	1	726.9	(-1.0)	2.144	0.135	0.000		R.NPL*IAGK#.-
SW:SMD2_HUMAN	H21	2134	1	726.9	(-0.9)	2.129	0.137	0.000		R.NPL*IAGK#.-
SW:SMD2_HUMAN	H21	2292	1	712.9	(-0.0)	2.085	0.108	0.000		R.NPLIAGK.-
SW:SMD2_HUMAN	H21	2154	1	712.9	(-0.8)	1.998	0.196	0.000		R.NPLIAGK.-
SW:SMD2_HUMAN	H21	2364	1	726.9	(+0.5)	1.976	0.137	0.000		R.NPL*IAGK#.-
SW:SMD2_HUMAN	H21	7596	2	2164.4	(+1.0)	6.083	0.631	1.000		K.REEEEFNTGPLSVLTQSVK.N
SW:SMD2_HUMAN	H21	7490	2	2164.4	(+0.1)	5.257	0.571	0.999		K.REEEEFNTGPLSVLTQSVK.N
SW:SMD2_HUMAN	H21	2300	1	726.9	(-0.0)	1.972	0.119	0.000		R.NPL*IAGK#.-
SW:SMF1_HUMAN	H03	6412	2	1224.5	(+0.0)	2.520	0.404	0.953	9	K.AMGMTNL*PAVGR.K
SW:SMF1_HUMAN	H03	4954	2	1059.2	(+0.8)	2.739	0.202	0.913	9	K.EIGGLTQVVK.N
SW:SMF1_HUMAN	H03	4874	2	1059.2	(-0.2)	2.628	0.391	0.962	9	K.EIGGLTQVVK.N
SW:SMF1_HUMAN	H03	6666	2	1538.6	(-0.1)	2.500	0.381	0.917	9	R.GEDPPPDIFAAADSK#.K
SW:SMF1_HUMAN	H03	8638	2	2114.4	(+0.1)	2.849	0.467	0.976	15	K.LSIQDNNVDLILATPPFSR.L
SW:SMF1_HUMAN	H03	1778	2	1314.5	(+0.9)	2.283	0.373	0.952	8	K.RPM@DGTGYPPAK#.R
SW:SMF1_HUMAN	H03	7412	2	1572.7	(+0.9)	3.355	0.510	1.000	10	R.SL*SFVPGNDFEMSK#.H
SW:SMF1_HUMAN	H03	7606	2	1487.7	(+0.5)	3.916	0.510	1.000	8	R.VQEFDSGLLHWR.I
SW:SMF1_HUMAN	H04	4317	2	1059.2	(+0.6)	2.370	0.302	0.940	9	K.EIGGLTQVVK.N
SW:SN21_HUMAN	H05	6564	2	1326.5	(+0.9)	2.337	0.328	0.946	2	R.K#ANYAVDAYFR.E
SW:SN21_HUMAN	H05	5622	2	1135.3	(+0.8)	2.988	0.250	0.952	2	R.L*DSIVIQQGR.L
SW:SN21_HUMAN	H05	5614	2	1129.3	(+0.8)	2.689	0.241	0.936	2	R.LDSIVIQQGR.L
SW:SN21_HUMAN	H08	5243	2	1129.3	(+0.7)	2.244	0.225	0.837	2	R.LDSIVIQQGR.L
SW:SN22_HUMAN	H04	9505	2	1617.9	(+0.5)	4.336	0.328	0.992	7	K.FNVLLTTYEYIHK.D
SW:SN22_HUMAN	H04	9501	2	1637.9	(+0.2)	2.794	0.342	0.930	7	K.FNVL*L*TTYEYIHK#.D
SW:SN22_HUMAN	H04	6623	2	1601.8	(-0.5)	3.827	0.316	0.966	5	K.HQEYL*NSIL*QHAK#.D
SW:SN22_HUMAN	H04	8209	2	1623.9	(+0.2)	3.266	0.339	0.957	7	R.L*MEEDEL*PSWIIK#.D
SW:SN22_HUMAN	H04	7887	2	1639.9	(-0.7)	3.212	0.172	0.546	7	R.L*M@EEDEL*PSWIIK#.D
SW:SN22_HUMAN	H04	7721	3	2454.7	(+0.9)	4.670	0.526	0.993	7	R.L*M@EEDEL*PSWIIK#DDAEVER.L
SW:SN22_HUMAN	H04	8009	3	2438.7	(-0.1)	3.884	0.303	0.811	7	R.L*MEEDEL*PSWIIK#DDAEVER.L
SW:SN22_HUMAN	H04	5887	2	1524.8	(+0.2)	3.835	0.461	1.000	6	K.L*TQVL*NTHYVAPR.R
SW:SN22_HUMAN	H04	5903	2	1512.8	(-0.1)	3.653	0.379	0.979	6	K.LTQVLNTHYVAPR.R
SW:SN22_HUMAN	H04	7467	2	1429.6	(+0.9)	2.313	0.304	0.921	8	R.QL*SEVFIQL*PSR.K
SW:SN22_HUMAN	H04	9367	2	1796.1	(+0.3)	3.842	0.510	0.997	5	K.TIQTIAL*ITYL*MEHK#.R
SW:SN22_HUMAN	H04	8051	2	1233.5	(+0.8)	2.225	0.400	0.970	7	K.TL*MNTIMQL*R.K
SW:SN22_HUMAN	H04	7777	2	1569.8	(+0.7)	3.029	0.334	0.970	7	R.VDL*NEEETIL*IIR.R
SW:SN22_HUMAN	H04	5645	2	1145.3	(+0.8)	3.226	0.370	0.988	7	K.VIQAGMFDQK#.S
SW:SN22_HUMAN	H04	5643	2	1137.3	(+0.7)	2.678	0.439	0.989	7	K.VIQAGMFDQK.S
SW:SN22_HUMAN	H04	2397	2	1161.3	(+0.5)	2.232	0.371	0.936	7	K.VIQAGM@FDQK#.S
SW:SN22_HUMAN	H05	6876	2	1601.8	(+0.2)	3.066	0.289	0.919	5	K.HQEYL*NSIL*QHAK#.D
SW:SN24_HUMAN	H04	7445	2	1269.4	(+0.4)	2.742	0.410	0.986	3	R.GLDPVEILQER.E
SW:SN24_HUMAN	H04	5981	2	1650.8	(-0.1)	3.976	0.431	0.986	3	R.GPTPFNQNQLHQLR.A
SW:SN24_HUMAN	H04	6103	2	1639.9	(-0.7)	3.532	0.527	1.000	3	R.GQPL*PDHL*QMAVQGK#.R
SW:SN24_HUMAN	H04	5687	2	1655.9	(-0.5)	2.757	0.428	0.959	3	R.GQPL*PDHL*QM@AVQGK#.R
SW:SN24_HUMAN	H04	6861	2	1375.5	(+0.6)	2.482	0.262	0.927	5	R.HEEFDL*FM@R.M
SW:SN24_HUMAN	H04	7679	2	1725.9	(+0.4)	4.697	0.552	1.000	2	R.IQELENLPGSLAGDLR.T
SW:SN24_HUMAN	H04	7707	2	1725.9	(-0.8)	4.642	0.525	1.000	2	R.IQELENLPGSLAGDLR.T
SW:SN24_HUMAN	H04	6189	3	3270.5	(-0.7)	4.588	0.404	0.995	3	K.K#AENAEGQTPAIGPDGEPL*DETSQM@SDL*PVK#.V
SW:SN24_HUMAN	H04	5067	2	1758.8	(-0.3)	2.893	0.466	0.977	3	K.KIPDPDSDVSEVDAR.H
SW:SN24_HUMAN	H04	5829	2	1672.7	(-0.1)	3.874	0.514	1.000	3	K.QDVDDEYGVVSQAL*AR.G
SW:SN24_HUMAN	H04	5839	2	1666.7	(-0.0)	3.081	0.280	0.910	3	K.QDVDDEYGVVSQALAR.G
SW:SN24_HUMAN	H04	7439	2	1281.4	(+0.6)	2.438	0.283	0.928	3	R.GL*DPVEIL*QER.E
SW:SNAA_HUMAN	H16	4588	3	2563.7	(+0.8)	6.389	0.529	1.000	5	K.AIAHYEQSADYYKGEESNSSANK.C
SW:SNAA_HUMAN	H16	4584	3	2579.7	(-0.3)	3.951	0.402	0.960	5	K.AIAHYEQSADYYK#GEESNSSANK#.C
SW:SNAA_HUMAN	H16	7612	2	1564.7	(-0.1)	3.483	0.458	0.982	2	K.NSQSFFSGL*FGSSK#.I
SW:SNAA_HUMAN	H16	6620	2	1454.7	(+0.4)	3.059	0.473	0.992	2	K.VAGYAALLEQYQK.A

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:SNAH_HUMAN	H16	6972	2	1461.6	(+0.7)	3.724	0.470	1.000	3	K.YEELFPAFSDSR.E
SW:SNAH_HUMAN	H16	7626	2	1550.7	(-0.2)	2.494	0.367	0.916	2	K.NSQSFFSGLFGGSSK.I
SW:SNF5_HUMAN	H13	6562	2	1562.6	(+0.2)	3.645	0.410	0.980	5	K.ASEVEEIL*DGNDK#.Y
SW:SNF5_HUMAN	H13	4934	2	1063.2	(+0.0)	2.547	0.272	0.881	3	R.L*DMEIDGQK#.L
SW:SNF5_HUMAN	H13	8188	2	1928.2	(+0.2)	4.138	0.524	1.000	3	K.TYAFSENPL*PTVEIAIR.N
SW:SNF5_HUMAN	H13	8206	2	1922.2	(+0.1)	2.583	0.238	0.758	3	K.TYAFSENPLPTVEIAIR.N
SW:SNF5_HUMAN	H13	4922	2	1049.2	(+0.6)	2.356	0.315	0.953	3	R.LDMEIDGQK.L
SW:SP22_HUMAN	H19	6864	2	1434.6	(+0.2)	2.700	0.337	0.924		K.NNAL*NQVVL*WDK#.I
SW:SP22_HUMAN	H19	7506	2	1337.4	(+0.7)	2.282	0.310	0.919		K.YFFFDDGNGL*K#.G
SW:SPCB_HUMAN	H03	6502	2	1270.4	(-0.2)	2.661	0.349	0.382	4	K.HRPDL*IDFDK#.L
SW:SPCB_HUMAN	H03	4688	2	989.1	(-0.0)	2.434	0.138	0.642	11	K.WVNSHL*AR.V
SW:SPCN_HUMAN	H03	8890	2	1214.5	(+0.7)	3.106	0.166	0.926	2	R.AALLELWELR.R
SW:SPCN_HUMAN	H05	8868	2	1214.5	(+0.7)	2.992	0.344	0.984	2	R.AALLELWELR.R
SW:SPCN_HUMAN	H05	6996	2	1233.4	(+0.5)	2.700	0.512	0.993	6	K.ADVVESWIGEK.E
SW:SPCN_HUMAN	H05	6992	2	1241.4	(+0.9)	2.464	0.348	0.959	6	K.ADVVESWIGEK#.E
SW:SPCN_HUMAN	H04	9049	3	2897.2	(-0.0)	4.864	0.420	0.997	5	R.AGTFQAFEQFGQQL*L*AHGHYASPEIK#.Q
SW:SPCN_HUMAN	H04	9055	3	2877.2	(+0.2)	3.708	0.557	1.000	5	R.AGTFQAFEQFGQQLLAHGHYASPEIK.Q
SW:SPCN_HUMAN	H05	9178	3	2877.2	(+0.7)	4.225	0.443	0.999	5	R.AGTFQAFEQFGQQLLAHGHYASPEIK.Q
SW:SPCN_HUMAN	H03	9784	3	2128.3	(+0.1)	4.073	0.449	0.989	2	K.ALINADELASDVAGAEALLDR.H
SW:SPCN_HUMAN	H03	9782	2	2128.3	(+0.4)	3.175	0.520	0.994	2	K.ALINADELASDVAGAEALLDR.H
SW:SPCN_HUMAN	H03	9766	2	2152.3	(-0.6)	2.575	0.142	0.488	2	K.AL*INADEL*ASDVAGAEAL*L*DR.H
SW:SPCN_HUMAN	H05	9782	2	2128.3	(+0.5)	3.862	0.510	1.000	2	K.ALINADELASDVAGAEALLDR.H
SW:SPCN_HUMAN	H05	2012	2	1280.5	(+0.9)	2.348	0.482	0.722	3	R.ALSSEGKPYVTK.E
SW:SPCN_HUMAN	H03	8342	2	1720.9	(-0.5)	4.032	0.383	0.984	2	R.AQL*ADSFHL*QQFFR.D
SW:SPCN_HUMAN	H04	8207	2	1720.9	(+0.1)	3.012	0.354	0.953	2	R.AQL*ADSFHL*QQFFR.D
SW:SPCN_HUMAN	H03	9256	2	2305.4	(+0.7)	4.266	0.249	0.978	6	K.ASAFNWFWENAEEDL*TDPV.R.C
SW:SPCN_HUMAN	H05	9252	2	2299.4	(-0.2)	2.321	0.344	0.867	6	K.ASAFNWFWENAEEDLTDV.R.C
SW:SPCN_HUMAN	H03	7658	2	1104.3	(+0.5)	2.729	0.406	0.986	2	R.DL*ASVQAL*L*R.K
SW:SPCN_HUMAN	H04	7505	2	1104.3	(+0.5)	2.589	0.435	0.987	2	R.DL*ASVQAL*L*R.K
SW:SPCN_HUMAN	H03	7866	2	1139.3	(-0.3)	2.271	0.120	0.368	4	K.DL*IGVQNL*L*K#.K
SW:SPCN_HUMAN	H03	6374	3	2282.4	(+0.0)	4.724	0.542	1.000	3	K.DL*NSQADSL*M@TSSAFDTSQV#.D
SW:SPCN_HUMAN	H03	7256	2	1231.4	(-0.4)	2.229	0.393	0.915	6	R.DL*SSVQTL*L*TK#.Q
SW:SPCN_HUMAN	H05	5486	2	1028.1	(+0.6)	2.374	0.387	0.977	5	R.DL*TGVQNL*R.K
SW:SPCN_HUMAN	H07	4642	2	1173.3	(+0.8)	2.759	0.266	0.955	3	K.DLTNVQNLQK.K
SW:SPCN_HUMAN	H03	6932	2	1240.4	(+0.1)	2.289	0.445	0.956	2	R.DL*TSWVTEM@K#.A
SW:SPCN_HUMAN	H04	7749	2	1224.4	(+1.0)	2.556	0.345	0.967	2	R.DL*TSWVTEMK#.A
SW:SPCN_HUMAN	H03	5726	2	1292.3	(-0.5)	3.035	0.326	0.956	5	R.DM@DDEESWIK#.E
SW:SPCN_HUMAN	H05	5738	2	1292.3	(+0.1)	2.379	0.327	0.892	5	R.DM@DDEESWIK#.E
SW:SPCN_HUMAN	H03	7166	2	1214.3	(+0.5)	3.156	0.425	0.991	2	R.DVDETISWIK#.E
SW:SPCN_HUMAN	H03	7822	3	2259.5	(+0.9)	4.615	0.331	0.996	6	K.EAALTSEEVGADLEQVEVLQK.K
SW:SPCN_HUMAN	H03	7188	2	1502.6	(+0.8)	3.440	0.429	0.993	6	R.EANELQQWINEK.E
SW:SPCN_HUMAN	H03	7182	2	1516.6	(+0.2)	2.761	0.213	0.787	6	R.EANEL*QQWINEK#.E
SW:SPCN_HUMAN	H04	6993	2	1502.6	(+0.6)	2.871	0.353	0.978	6	R.EANELQQWINEK.E
SW:SPCN_HUMAN	H05	7184	2	1516.6	(+0.7)	2.689	0.253	0.918	6	R.EANEL*QQWINEK#.E
SW:SPCN_HUMAN	H03	8134	2	1588.8	(+0.7)	3.658	0.478	1.000	3	R.ELPTAFDYVEFTR.S
SW:SPCN_HUMAN	H03	8146	2	1594.8	(+0.4)	3.397	0.478	0.994	3	R.EL*PTAFDYVEFTR.S
SW:SPCN_HUMAN	H04	8013	2	1594.8	(+0.5)	2.470	0.476	0.985	3	R.EL*PTAFDYVEFTR.S
SW:SPCN_HUMAN	H05	8086	2	1588.8	(+0.8)	3.470	0.506	1.000	3	R.ELPTAFDYVEFTR.S
SW:SPCN_HUMAN	H05	8096	2	1594.8	(+0.2)	2.591	0.428	0.962	3	R.EL*PTAFDYVEFTR.S
SW:SPCN_HUMAN	H06	8008	2	1594.8	(-0.3)	2.761	0.273	0.879	3	R.EL*PTAFDYVEFTR.S
SW:SPCN_HUMAN	H03	7060	2	1304.5	(+1.0)	3.041	0.465	0.992	3	R.GVIDMGNSLIER.G
SW:SPCN_HUMAN	H03	6152	2	1326.5	(+0.9)	2.996	0.308	0.967	3	R.GVIDM@GNSL*IER.G
SW:SPCN_HUMAN	H04	6841	2	1310.5	(+0.6)	2.347	0.408	0.972	3	R.GVIDMGNSL*IER.G
SW:SPCN_HUMAN	H05	5824	2	1615.7	(+0.0)	3.103	0.423	0.975	3	K.HQAFEAL*HANADR.I
SW:SPCN_HUMAN	H03	9382	2	1993.3	(+0.9)	4.167	0.532	1.000	5	K.IAAL*QAFADQL*IAAGHYAK#.G
SW:SPCN_HUMAN	H03	9380	2	1973.3	(-1.0)	3.918	0.491	1.000	5	K.IAALQAFADQLIAAGHYAK.G
SW:SPCN_HUMAN	H04	9249	2	1993.3	(-0.6)	3.822	0.550	1.000	5	K.IAAL*QAFADQL*IAAGHYAK#.G
SW:SPCN_HUMAN	H05	9360	2	1993.3	(-0.5)	3.904	0.536	0.998	5	K.IAAL*QAFADQL*IAAGHYAK#.G
SW:SPCN_HUMAN	H03	7450	2	1417.6	(+0.8)	4.163	0.511	1.000	4	K.KGDILTLNNTNK.D
SW:SPCN_HUMAN	H03	7430	2	1451.6	(-0.0)	3.153	0.417	0.973	4	K.K#GDIL*TL*L*NSTNK#.D
SW:SPCN_HUMAN	H04	7241	2	1451.6	(-0.1)	2.867	0.274	0.882	4	K.K#GDIL*TL*L*NSTNK#.D
SW:SPCN_HUMAN	H05	7410	2	1451.6	(-0.0)	2.557	0.376	0.928	4	K.K#GDIL*TL*L*NSTNK#.D

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:SPCN_HUMAN	H03	7818	3	2204.5	(+0.2)	4.557	0.525	1.000	4	K.K#HEAL*MSDL*SAYGSSIQAL*R.E
SW:SPCN_HUMAN	H04	7695	3	2204.5	(+0.5)	4.004	0.497	0.999	4	K.K#HEAL*MSDL*SAYGSSIQAL*R.E
SW:SPCN_HUMAN	H03	8102	2	1339.6	(+0.5)	3.254	0.466	0.993	4	R.K#VEDL*FL*TFAK#.K
SW:SPCN_HUMAN	H03	8124	2	1339.6	(-0.8)	2.767	0.112	0.278	4	R.K#VEDL*FL*TFAK#.K
SW:SPCN_HUMAN	H05	8058	2	1339.6	(+0.1)	2.614	0.349	0.931	4	R.K#VEDL*FL*TFAK#.K
SW:SPCN_HUMAN	H03	8402	2	1631.9	(+0.5)	4.395	0.486	1.000	3	R.LAALADQWQFLVQK.S
SW:SPCN_HUMAN	H03	8396	3	1657.9	(-0.2)	3.854	0.383	0.990	3	R.L*AAL*ADQWQFL*VQK#.S
SW:SPCN_HUMAN	H03	6632	2	1158.3	(+0.9)	3.069	0.373	0.989	6	R.LAQFVEHWK.E
SW:SPCN_HUMAN	H04	6371	2	1172.3	(+0.5)	2.437	0.475	0.988	6	R.L*AQFVEHWK#.E
SW:SPCN_HUMAN	H03	5694	2	997.1	(+0.6)	3.643	0.469	1.000	2	K.L*FGAAEVQR.F
SW:SPCN_HUMAN	H04	5351	2	997.1	(+0.9)	2.902	0.419	0.991	2	K.L*FGAAEVQR.F
SW:SPCN_HUMAN	H05	5710	2	997.1	(+1.0)	3.106	0.374	0.990	2	K.L*FGAAEVQR.F
SW:SPCN_HUMAN	H03	6010	2	1394.5	(+0.8)	4.006	0.511	1.000	4	K.LGESQTLQQFSR.D
SW:SPCN_HUMAN	H03	5996	2	1406.5	(+0.6)	3.747	0.443	0.999	4	K.L*GESQTL*QQFSR.D
SW:SPCN_HUMAN	H04	5697	2	1406.5	(+0.3)	3.425	0.470	1.000	4	K.L*GESQTL*QQFSR.D
SW:SPCN_HUMAN	H05	6052	2	1406.5	(+0.1)	3.148	0.123	0.733	4	K.L*GESQTL*QQFSR.D
SW:SPCN_HUMAN	H06	5778	2	1406.5	(+0.5)	3.322	0.409	0.991	4	K.L*GESQTL*QQFSR.D
SW:SPCN_HUMAN	H03	5478	2	1087.2	(+0.2)	2.563	0.229	0.826	2	K.L*IDVNHYAK#.D
SW:SPCN_HUMAN	H04	5089	2	1087.2	(+0.0)	2.295	0.275	0.824	2	K.L*IDVNHYAK#.D
SW:SPCN_HUMAN	H05	5470	2	1073.2	(+0.7)	2.498	0.238	0.922	2	K.LIDVNHYAK.D
SW:SPCN_HUMAN	H06	5030	2	1087.2	(+0.8)	2.374	0.314	0.947	2	K.L*IDVNHYAK#.D
SW:SPCN_HUMAN	H07	5054	2	1087.2	(+1.0)	2.382	0.332	0.950	2	K.L*IDVNHYAK#.D
SW:SPCN_HUMAN	H03	6096	2	1606.8	(+0.8)	4.356	0.376	0.994	2	K.LIQEQHPPEELIK.T
SW:SPCN_HUMAN	H03	6084	2	1626.8	(-0.0)	4.256	0.179	0.930	2	K.L*IQEQHPPEEL*IK#.T
SW:SPCN_HUMAN	H04	5787	2	1626.8	(-0.4)	3.734	0.293	0.959	2	K.L*IQEQHPPEEL*IK#.T
SW:SPCN_HUMAN	H03	5600	2	1121.2	(+0.6)	2.555	0.322	0.964	4	K.L*L*VGSSEDYGR.D
SW:SPCN_HUMAN	H05	5590	2	1121.2	(+0.5)	2.403	0.286	0.930	4	K.L*L*VGSSEDYGR.D
SW:SPCN_HUMAN	H05	5602	2	1109.2	(+0.8)	2.400	0.319	0.947	4	K.LLVGSEDYGR.D
SW:SPCN_HUMAN	H06	5206	2	1109.2	(+0.5)	2.231	0.233	0.846	4	K.LLVGSEDYGR.D
SW:SPCN_HUMAN	H03	5896	2	1698.9	(-0.6)	4.151	0.514	1.000	2	R.L*QQSHPL*SATQIQVK#.R
SW:SPCN_HUMAN	H03	5888	3	1698.9	(+0.8)	3.760	0.382	0.997	2	R.L*QQSHPL*SATQIQVK#.R
SW:SPCN_HUMAN	H03	4994	2	1760.9	(-0.4)	3.531	0.177	0.183	3	K.L*SDDNTIGK#EEIQQR.L
SW:SPCN_HUMAN	H03	7190	2	1150.4	(+0.7)	2.392	0.214	0.864	2	R.M@NEVISL*WK#.K
SW:SPCN_HUMAN	H04	7377	2	1134.4	(+0.6)	2.452	0.250	0.915	2	R.MNEVISL*WK#.K
SW:SPCN_HUMAN	H03	5072	2	1518.7	(-0.0)	3.050	0.410	0.976	4	R.M@QHNL*EQQIQAR.N
SW:SPCN_HUMAN	H06	2322	2	1518.7	(+0.6)	2.376	0.403	0.972	4	R.M@QHNL*EQQIQAR.N
SW:SPCN_HUMAN	H04	8717	3	2514.8	(-0.1)	4.387	0.389	0.600	6	K.QETFDAGL*QAFQQEGIANITAL*K#.D
SW:SPCN_HUMAN	H05	8836	3	2494.8	(+0.9)	5.249	0.569	1.000	6	K.QETFDAGLQAFQQEGIANITALK.D
SW:SPCN_HUMAN	H06	8754	3	2514.8	(+0.1)	4.681	0.410	0.993	6	K.QETFDAGL*QAFQQEGIANITAL*K#.D
SW:SPCN_HUMAN	H03	8252	2	1788.0	(+0.6)	2.557	0.304	0.932	3	K.QVEELYHSLLELGEK.R
SW:SPCN_HUMAN	H03	7644	3	3031.2	(+0.3)	6.687	0.556	0.967	4	R.RQDL*EDSL*QAQQYFADANEAESWM@R.E
SW:SPCN_HUMAN	H03	8290	3	3015.2	(+0.0)	6.661	0.505	0.988	4	R.RQDL*EDSL*QAQQYFADANEAESWMR.E
SW:SPCN_HUMAN	H03	8304	3	3003.2	(+0.9)	5.469	0.574	0.998	4	R.RQDLEDSLQAQQYFADANEAESWMR.E
SW:SPCN_HUMAN	H04	7509	3	3031.2	(+0.2)	5.968	0.497	0.999	4	R.RQDL*EDSL*QAQQYFADANEAESWM@R.E
SW:SPCN_HUMAN	H05	8272	3	3015.2	(+0.5)	5.918	0.592	0.991	4	R.RQDL*EDSL*QAQQYFADANEAESWMR.E
SW:SPCN_HUMAN	H06	8194	3	3003.2	(+0.3)	4.005	0.496	0.999	4	R.RQDLEDSLQAQQYFADANEAESWMR.E
SW:SPCN_HUMAN	H03	5714	2	1086.2	(+0.5)	2.761	0.345	0.980	6	R.SL*QQL*AEER.S
SW:SPCN_HUMAN	H03	5718	2	1074.2	(+0.5)	2.410	0.338	0.965	6	R.SLQQLAEER.S
SW:SPCN_HUMAN	H04	5347	2	1086.2	(+0.4)	2.330	0.252	0.906	6	R.SL*QQL*AEER.S
SW:SPCN_HUMAN	H04	5361	2	1074.2	(+0.7)	2.281	0.218	0.857	6	R.SLQQLAEER.S
SW:SPCN_HUMAN	H05	5720	2	1074.2	(+0.8)	2.764	0.279	0.966	6	R.SLQQLAEER.S
SW:SPCN_HUMAN	H05	5718	2	1086.2	(+0.9)	2.730	0.354	0.982	6	R.SL*QQL*AEER.S
SW:SPCN_HUMAN	H03	5036	2	1325.5	(+0.7)	2.612	0.447	0.986	6	R.SQLLGSAGEVQR.F
SW:SPCN_HUMAN	H04	4247	2	1325.5	(+0.2)	2.770	0.382	0.958	6	R.SQLLGSAGEVQR.F
SW:SPCN_HUMAN	H04	4171	2	1337.5	(+0.4)	2.497	0.349	0.962	6	R.SQL*L*GSAHEVQR.F
SW:SPCN_HUMAN	H04	4093	2	1337.5	(+0.3)	2.389	0.250	0.770	6	R.SQL*L*GSAHEVQR.F
SW:SPCN_HUMAN	H04	4327	2	1337.5	(+0.2)	2.255	0.352	0.888	6	R.SQL*L*GSAHEVQR.F
SW:SPCN_HUMAN	H05	4534	2	1325.5	(+0.2)	3.073	0.398	0.973	6	R.SQLLGSAGEVQR.F
SW:SPCN_HUMAN	H05	4392	2	1325.5	(+0.4)	2.972	0.357	0.981	6	R.SQLLGSAGEVQR.F
SW:SPCN_HUMAN	H05	4276	2	1325.5	(+0.3)	2.673	0.352	0.940	6	R.SQLLGSAGEVQR.F
SW:SPCN_HUMAN	H05	4358	2	1337.5	(+0.3)	2.442	0.409	0.950	6	R.SQL*L*GSAHEVQR.F
SW:SPCN_HUMAN	H03	7796	2	1953.1	(+0.5)	4.825	0.483	1.000	6	R.SSLSSAQADFNQLAELDR.Q
SW:SPCN_HUMAN	H04	7667	2	1971.1	(-0.7)	2.781	0.257	0.611	6	R.SSL*SSAQADFNQL*AEL*DR.Q
SW:SPCN_HUMAN	H06	7672	2	1971.1	(-0.5)	2.655	0.335	0.909	6	R.SSL*SSAQADFNQL*AEL*DR.Q
SW:SPCN_HUMAN	H04	2421	2	1454.6	(+0.1)	2.480	0.301	0.210	2	K.TK#QDEVNAAWQR.L
SW:SPCN_HUMAN	H05	4670	2	1303.4	(+0.4)	2.981	0.498	0.994	2	K.VLETAEDIQER.R

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:SPCN_HUMAN	H05	4678	2	1309.4	(+0.0)	2.819	0.255	0.892	2	K.VL*ETAEDIQER.R
SW:SPCN_HUMAN	H05	4756	2	1309.4	(+0.3)	2.698	0.469	0.979	2	K.VL*ETAEDIQER.R
SW:SPCN_HUMAN	H05	4752	2	1303.4	(-0.4)	2.511	0.267	0.849	2	K.VLETAEDIQER.R
SW:SPCN_HUMAN	H06	2424	2	1309.4	(+0.4)	2.357	0.345	0.946	2	K.VL*ETAEDIQER.R
SW:SPCN_HUMAN	H04	2277	2	1128.3	(+0.7)	2.675	0.403	0.983	2	R.VNEVNQFAAK#.L
SW:SPCN_HUMAN	H03	8052	3	2595.8	(-0.3)	4.813	0.335	0.991	4	K.YTEHSTVGL*AAQQWDQL*DQL*GMR.M
SW:SPCN_HUMAN	H05	7992	3	2595.8	(+0.6)	3.858	0.267	0.968	4	K.YTEHSTVGL*AAQQWDQL*DQL*GMR.M
SW:SPCN_HUMAN	H07	4610	2	1193.3	(+0.3)	2.380	0.371	0.927	3	K.DL*TNVQNL*QK#.K
SW:SPCO_HUMAN	H03	2118	2	1345.5	(+0.6)	2.938	0.445	0.773	1	K.AK#DEQSAVSM@L*K#.K
SW:SPCO_HUMAN	H03	1918	2	1311.4	(+0.8)	2.777	0.490	0.992	1	R.ALVADSHPESEI
SW:SPCO_HUMAN	H03	6732	2	1918.1	(+0.3)	3.849	0.549	1.000		R.AQTL*PTSVVITITSESSPGK#.R
SW:SPCO_HUMAN	H03	8532	2	2093.3	(+0.5)	3.721	0.572	1.000	1	R.DASVAEAWLLGQEPYLSR.E
SW:SPCO_HUMAN	H03	9914	2	2241.4	(+0.4)	3.396	0.505	1.000		K.DDEEMNTWQAISSAISDK.H
SW:SPCO_HUMAN	H03	10966	2	1969.1	(-0.4)	3.426	0.351	0.965	1	K.DGL*NEAWADL*L*EL*IDTR.T
SW:SPCO_HUMAN	H04	10995	2	1945.1	(-0.1)	3.310	0.318	0.949	1	K.DGLNEAWADLLELIDTR.T
SW:SPCO_HUMAN	H04	10989	2	1969.1	(-0.4)	2.700	0.237	0.788	1	K.DGL*NEAWADL*L*EL*IDTR.T
SW:SPCO_HUMAN	H05	11056	2	1945.1	(+0.2)	2.938	0.438	0.972	1	K.DGLNEAWADLLELIDTR.T
SW:SPCO_HUMAN	H03	8198	2	1394.5	(+0.6)	3.593	0.509	0.996	2	R.DL*DDFQSWL*SR.T
SW:SPCO_HUMAN	H04	8091	2	1394.5	(+0.7)	2.555	0.509	0.991	2	R.DL*DDFQSWL*SR.T
SW:SPCO_HUMAN	H04	8095	2	1382.5	(+0.7)	2.385	0.437	0.981	2	R.DLDDFQSWLSR.T
SW:SPCO_HUMAN	H05	8180	2	1382.5	(+0.7)	2.994	0.408	0.989	2	R.DLDDFQSWLSR.T
SW:SPCO_HUMAN	H05	8166	2	1394.5	(+0.4)	2.238	0.241	0.844	2	R.DL*DDFQSWL*SR.T
SW:SPCO_HUMAN	H03	7842	3	3822.1	(-0.4)	5.895	0.566	1.000	2	K.DVAEEIANRPTL*DTL*HEQASAL*PQEHAESPDR.V
SW:SPCO_HUMAN	H03	7844	2	1460.6	(+0.6)	3.066	0.434	0.991	2	R.DVEDEILWVGER.M
SW:SPCO_HUMAN	H04	7725	2	1460.6	(+0.8)	2.428	0.195	0.805	2	R.DVEDEILWVGER.M
SW:SPCO_HUMAN	H03	5124	2	1375.5	(+0.0)	2.321	0.163	0.379	2	R.EL*EAENYHDIK#.R
SW:SPCO_HUMAN	H03	5138	2	1361.5	(+0.2)	2.294	0.293	0.834	2	R.ELEAENYHDIK.R
SW:SPCO_HUMAN	H04	2335	2	1517.6	(+0.5)	2.677	0.252	0.323	2	R.ELEAENYHDIK.I
SW:SPCO_HUMAN	H03	7734	2	1558.7	(+0.9)	4.311	0.434	0.998	2	R.EQWANLEQLSAIR.K
SW:SPCO_HUMAN	H05	7688	2	1570.7	(+0.4)	2.714	0.237	0.910	2	R.EQWANL*EQL*SAIR.K
SW:SPCO_HUMAN	H04	7789	2	1509.6	(+0.6)	2.834	0.393	0.984	1	R.EVDDL*EQWIAER.E
SW:SPCO_HUMAN	H05	7856	2	1509.6	(+0.5)	2.580	0.368	0.972	1	R.EVDDL*EQWIAER.E
SW:SPCO_HUMAN	H03	6570	3	2556.8	(+0.7)	5.258	0.468	1.000	1	R.EVVAGSHEL*GQDYEHVTM@L*QER.F
SW:SPCO_HUMAN	H03	6830	3	2540.8	(+0.5)	5.208	0.458	0.999	1	R.EVVAGSHEL*GQDYEHVTML*QER.F
SW:SPCO_HUMAN	H04	6335	3	2556.8	(+0.5)	4.274	0.343	0.994	1	R.EVVAGSHEL*GQDYEHVTM@L*QER.F
SW:SPCO_HUMAN	H03	8326	2	2185.4	(+0.0)	4.672	0.543	1.000	2	K.FANSLVGVQQQLQAFNTYR.T
SW:SPCO_HUMAN	H03	8310	3	2197.4	(+1.0)	4.093	0.515	1.000	2	K.FANSL*VGVQQQL*QAFNTYR.T
SW:SPCO_HUMAN	H03	5052	2	1674.8	(-0.6)	2.931	0.346	0.945	2	R.FESL*EPEM@NNQASR.V
SW:SPCO_HUMAN	H03	7994	2	1409.6	(+0.8)	3.167	0.344	0.985	2	K.FMEL*L*EPL*NER.K
SW:SPCO_HUMAN	H03	7138	2	1425.6	(+0.1)	2.566	0.102	0.469	2	K.FM@EL*L*EPL*NER.K
SW:SPCO_HUMAN	H05	7950	2	1409.6	(+1.0)	2.227	0.420	0.972	2	K.FMEL*L*EPL*NER.K
SW:SPCO_HUMAN	H05	7642	2	1265.5	(+0.9)	2.543	0.294	0.946	2	K.HLLGVEDLLQK.H
SW:SPCO_HUMAN	H04	8543	3	2359.6	(+0.9)	6.072	0.414	1.000	1	K.HQIL*EQAVEDYAETVHQL*SK#.T
SW:SPCO_HUMAN	H03	6528	2	1110.3	(+0.8)	2.445	0.399	0.981	1	R.ITDLYTDLR.D
SW:SPCO_HUMAN	H03	5942	2	2066.2	(-0.6)	4.211	0.361	0.979	2	K.IVSSSDVGHDEYSTQSL*VK#.K
SW:SPCO_HUMAN	H03	6928	2	1480.6	(+0.3)	3.713	0.384	0.981	2	R.L*AEISDVWEEM@K#.T
SW:SPCO_HUMAN	H04	7773	2	1450.6	(+0.5)	2.900	0.478	0.992	2	R.LAEISDVWEEMK.T
SW:SPCO_HUMAN	H03	6116	2	1264.4	(-0.5)	2.595	0.294	0.908	2	K.L*EDL*EVIQHR.F
SW:SPCO_HUMAN	H03	2182	1	816.9	(-0.1)	2.206	0.193	0.000	3	K.L*ISDINK#.A
SW:SPCO_HUMAN	H03	6540	2	1742.8	(-0.0)	4.409	0.512	1.000	1	K.L*L*DPEDISVDHPDEK#.S
SW:SPCO_HUMAN	H03	6898	3	2665.8	(+0.2)	6.234	0.394	0.995	2	K.L*L*TQHENIK#NEIDNYEEDYQK#.M
SW:SPCO_HUMAN	H04	6679	3	2637.8	(+0.3)	5.327	0.545	1.000	2	K.LLTQHENIKNEIDNYEEDYQK.M
SW:SPCO_HUMAN	H04	6677	3	2665.8	(-0.4)	4.733	0.268	0.852	2	K.L*L*TQHENIK#NEIDNYEEDYQK#.M
SW:SPCO_HUMAN	H03	6346	2	1432.5	(-0.4)	3.091	0.426	0.976		R.L*NDGNEYL*FQAK#.D
SW:SPCO_HUMAN	H05	6400	2	1432.5	(+0.7)	3.420	0.502	1.000		R.L*NDGNEYL*FQAK#.D
SW:SPCO_HUMAN	H03	6858	2	1525.7	(+0.6)	3.136	0.311	0.974	2	R.LQALDTGWNELHK.M
SW:SPCO_HUMAN	H04	6627	2	1525.7	(+0.5)	3.943	0.355	0.991	2	R.LQALDTGWNELHK.M
SW:SPCO_HUMAN	H04	6615	2	1551.7	(-0.8)	2.722	0.284	0.667	2	R.L*QAL*DTGWNEL*HK#.M
SW:SPCO_HUMAN	H03	8218	2	2023.2	(+0.9)	4.866	0.488	0.998	2	R.LVSQDNFGFDLPAVEAATK.K
SW:SPCO_HUMAN	H03	10428	2	1348.6	(+0.3)	3.353	0.250	0.948	2	R.LWEYLLELLR.A
SW:SPCO_HUMAN	H04	6813	3	2007.2	(+0.5)	4.155	0.472	0.999	1	R.M@HTTFEHDIQAL*GTQVR.Q
SW:SPCO_HUMAN	H03	7220	3	2366.7	(-0.6)	3.775	0.289	0.958	2	R.M@PL*ATSTDHGHNL*QTVQL*L*IK#.K
SW:SPCO_HUMAN	H03	7516	3	2350.7	(-0.4)	3.742	0.448	0.998	2	R.MPL*ATSTDHGHNL*QTVQL*L*IK#.K
SW:SPCO_HUMAN	H03	6480	2	1483.7	(+0.4)	3.925	0.451	1.000	2	K.M@WEVL*ESTTQTK#.A
SW:SPCO_HUMAN	H03	7012	2	1467.7	(+0.1)	3.770	0.535	1.000	2	K.MWEVL*ESTTQTK#.A

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:SPCO_HUMAN	H03	6986	2	1453.7	(-0.1)	2.274	0.206	0.609	2	K.MWEVLESTTQTK.A
SW:SPCO_HUMAN	H03	5340	2	1560.6	(+0.8)	3.080	0.421	0.698	2	K.NEIDNYEEDYQK.M
SW:SPCO_HUMAN	H03	5336	2	1568.6	(-0.3)	2.803	0.263	0.870	2	K.NEIDNYEEDYQK#.M
SW:SPCO_HUMAN	H03	8588	2	1485.7	(+0.2)	2.218	0.332	0.839	1	K.QL*WGL*L*IEETEK#.R
SW:SPCO_HUMAN	H03	8416	2	1615.9	(+0.5)	2.584	0.270	0.310	1	K.QLWGLLIEETEK.R.H
SW:SPCO_HUMAN	H03	8496	3	2516.7	(-0.2)	6.585	0.514	1.000	1	K.SNAHYNL*QNAFNL*AEQHL*GL*TK#.L
SW:SPCO_HUMAN	H04	8343	3	2484.7	(-0.9)	3.836	0.407	0.836	1	K.SNAHYNLQNAFNLAEQHLGLTK.L
SW:SPCO_HUMAN	H05	8462	3	2516.7	(+0.7)	6.462	0.515	0.928	1	K.SNAHYNL*QNAFNL*AEQHL*GL*TK#.L
SW:SPCO_HUMAN	H06	8356	3	2516.7	(+0.0)	5.866	0.470	1.000	1	K.SNAHYNL*QNAFNL*AEQHL*GL*TK#.L
SW:SPCO_HUMAN	H04	6279	2	1784.9	(+0.1)	3.076	0.378	0.961	1	R.SQNVITDSSSL*SAEAIR.Q
SW:SPCO_HUMAN	H03	6600	2	1771.0	(-0.8)	2.951	0.379	0.851		K.TAASGIPYHSEVPVSL*K#.E
SW:SPCO_HUMAN	H03	5640	2	1380.6	(-0.6)	2.804	0.443	0.972		K.TAL*PAQSAATL*PAR.T
SW:SPCO_HUMAN	H03	5638	2	1368.6	(+0.5)	2.572	0.264	0.823		K.TALPAQSAATL*PAR.T
SW:SPCO_HUMAN	H04	5289	2	1380.6	(-0.1)	2.934	0.501	0.982		K.TAL*PAQSAATL*PAR.T
SW:SPCO_HUMAN	H04	5297	2	1368.6	(+0.8)	2.886	0.305	0.960		K.TALPAQSAATL*PAR.T
SW:SPCO_HUMAN	H05	5648	2	1380.6	(+0.1)	2.766	0.425	0.954		K.TAL*PAQSAATL*PAR.T
SW:SPCO_HUMAN	H06	5302	2	1380.6	(-0.3)	2.637	0.407	0.954		K.TAL*PAQSAATL*PAR.T
SW:SPCO_HUMAN	H03	6312	2	1394.6	(-0.1)	2.942	0.276	0.902	1	R.TQIL*AASYEL*HK#.F
SW:SPCO_HUMAN	H03	5482	2	2081.2	(+0.6)	4.133	0.449	0.999	2	R.TQTAIASEDM@PNTL*TEAEK#.L
SW:SPCO_HUMAN	H03	8548	3	2808.0	(+0.7)	7.815	0.503	0.992	1	R.VDTVNHLADELINSGHSDAATIAEWK.D
SW:SPCO_HUMAN	H03	8544	3	2828.0	(-0.1)	6.730	0.514	0.767	1	R.VDTVNHL*ADEL*INSGHSDAATIAEWK#.D
SW:SPCO_HUMAN	H06	8454	3	2808.0	(+1.0)	5.013	0.523	1.000	1	R.VDTVNHLADELINSGHSDAATIAEWK.D
SW:SPCO_HUMAN	H06	8446	3	2828.0	(+0.3)	4.301	0.474	0.979	1	R.VDTVNHL*ADEL*INSGHSDAATIAEWK#.D
SW:SPCO_HUMAN	H03	8178	3	2149.4	(+0.6)	3.800	0.420	0.998	2	K.VIESTQDL*GNDL*AGVMAL*QR.K
SW:SPCO_HUMAN	H03	4434	2	1146.3	(+0.5)	2.631	0.504	0.992	2	K.VL*DNAIETEK#.M
SW:SPCO_HUMAN	H03	4560	2	1146.3	(+0.3)	2.586	0.465	0.975	2	K.VL*DNAIETEK#.M
SW:SPCO_HUMAN	H03	4556	2	1132.3	(+0.9)	2.449	0.356	0.969	2	K.VLDNAIETEK.M
SW:SPCO_HUMAN	H04	2381	2	1132.3	(+0.0)	2.232	0.335	0.886	2	K.VLDNAIETEK.M
SW:SPCO_HUMAN	H06	5812	2	1142.3	(+0.7)	2.269	0.213	0.802	2	K.VL*VL*SQDYGK#.H
SW:SPCO_HUMAN	H03	5048	2	1109.3	(-0.0)	3.124	0.324	0.545	2	R.YKEVAELTR.L
SW:SPCO_HUMAN	H03	5038	2	1123.3	(+0.5)	2.714	0.351	0.662	2	R.YK#EVAEL*TR.L
SW:SPCO_HUMAN	H04	4465	2	1109.3	(+0.6)	2.448	0.246	0.265	2	R.YKEVAELTR.L
SW:SPCO_HUMAN	H04	4367	2	1123.3	(+0.8)	2.244	0.189	0.129	2	R.YK#EVAEL*TR.L
SW:SPCO_HUMAN	H04	4383	2	1109.3	(+0.7)	2.210	0.354	0.464	2	R.YKEVAELTR.L
SW:SPCO_HUMAN	H08	8395	3	2516.7	(-0.3)	5.069	0.388	0.998	1	K.SNAHYNL*QNAFNL*AEQHL*GL*TK#.L
SW:SPK_HUMAN	H05	8586	3	3460.9	(+0.3)	3.943	0.643	1.000		K.EAPAGPLEEDDLEPLTAPAPAPRPPQDLIGLR.L
SW:SPK_HUMAN	H05	9750	3	3309.7	(+0.5)	4.849	0.452	1.000		R.LLGTQHGEGNSALSPLNPGELLIALHNIDSVK.C
SW:SPK_HUMAN	H05	1982	2	1275.4	(+0.6)	2.307	0.416	0.977	1	R.RQEHDISL*DR.I
SW:SPK_HUMAN	H05	8254	3	2522.9	(+0.8)	4.552	0.453	0.999		R.SFTPHQQAHPNSIMTIL*EASGK#.Q
SW:SPK_HUMAN	H05	8256	3	2508.9	(+0.6)	3.843	0.317	0.988		R.SFTPHQQAHPNSIMTILEASGK.Q
SW:SPK_HUMAN	H05	8984	2	1269.5	(+0.7)	2.223	0.218	0.704		R.FL*IPVL*NGL*EK#.K
SW:SPS1_HUMAN	H13	6106	2	1458.5	(+0.9)	2.568	0.329	0.959	1	R.ESFNPESYELDK.S
SW:SPS1_HUMAN	H13	8314	2	1681.0	(+0.8)	3.870	0.452	0.994	2	R.NEVSFVIHNL*PVLAK.M
SW:SPS1_HUMAN	H14	8291	2	1701.0	(-0.3)	3.686	0.403*	0.429	2	R.NEVSFVIHNL*PVL*AK#.M
SW:SR14_HUMAN	H20	6984	2	1255.5	(+0.7)	2.597	0.384	0.981	2	K.FQMAYSNL*L*.R.A
SW:SR14_HUMAN	H20	4430	2	1272.3	(+0.8)	2.414	0.309	0.928	2	K.GTVEGFEPADNK#.C
SW:SR14_HUMAN	H20	4358	2	1408.5	(+0.7)	2.610	0.327	0.898	2	K.K#GTVEGFEPADNK#.C
SW:SR14_HUMAN	H20	4484	2	1408.5	(+0.1)	2.460	0.262	0.775	2	K.K#GTVEGFEPADNK#.C
SW:SR14_HUMAN	H20	5746	2	1083.2	(+0.5)	2.749	0.421	0.922	2	R.TSGSVYITL*K#.K
SW:SR14_HUMAN	H20	4354	2	1392.5	(+0.3)	2.250	0.244	0.681	2	K.KGTVEGFEPADNK.C
SW:SR54_HUMAN	H12	4100	2	850.0	(+1.0)	2.321	0.196	0.858		R.AGAFDQLK.Q
SW:SR54_HUMAN	H12	2234	2	1017.1	(+0.5)	3.074	0.409	0.987		K.GGGAL*SAVAATK#.S
SW:SR54_HUMAN	H12	2226	2	1003.1	(+1.0)	2.913	0.416	0.988		K.GGGALSAVAATK.S
SW:SR54_HUMAN	H12	3946	2	850.0	(+0.8)	2.309	0.160	0.792		R.AGAFDQLK.Q
SW:SR68_HUMAN	H09	5281	2	1135.2	(+0.9)	2.517	0.381	0.974	4	R.DYIL*EGEPGK#.V
SW:SR68_HUMAN	H09	5493	2	1057.2	(+0.8)	2.369	0.367*	0.302	2	K.L*EAL*ITQTR.A
SW:SR68_HUMAN	H09	4421	2	1082.2	(-0.1)	2.719	0.340	0.935	2	R.SGGTEGL*L*AEK#.L
SW:SR68_HUMAN	H09	5027	2	1190.3	(+0.9)	3.387	0.413	0.993	2	K.VTEELLTDNR.Y
SW:SR68_HUMAN	H09	4447	2	1394.5	(+0.4)	3.495	0.484	1.000	4	K.YANEVNSDAGAFK#.N
SW:SR68_HUMAN	H09	4435	2	1386.5	(-0.0)	3.383	0.506	0.999	4	K.YANEVNSDAGAFK.N
SW:SR68_HUMAN	H09	8355	2	1526.7	(+0.8)	2.353	0.244	0.852	4	K.DLPDVQELITQVR.S



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:T2D7_HUMAN	H16	7484	3	2181.5	(+0.7)	4.082	0.258	0.969	1	K.ASIPATSAVQNVLINPSLIGSK.N
SW:T2D7_HUMAN	H16	7774	2	1374.6	(+0.8)	2.938	0.508	0.993	3	R.VINQML*EFAFR.Y
SW:TAG2_HUMAN	H19	7862	2	1595.7	(+0.0)	3.198	0.433	0.979	2	R.DDGLFSGDPNWFVK.K
SW:TAG2_HUMAN	H19	3692	2	1280.3	(+0.7)	3.307	0.411	0.992	2	R.NFSDNQLQEGK.N
SW:TAG2_HUMAN	H19	8928	2	2101.3	(+0.4)	4.222	0.504	1.000	2	R.YGINTTDIFQTVDLWEGK.N
SW:TAG2_HUMAN	H19	3680	2	1294.3	(+0.3)	2.634	0.425	0.964	2	R.NFSDNQL*QEGK#.N
SW:TBA1_HUMAN	H12	8054	2	1702.9	(+1.0)	4.737	0.499	1.000	5	R.AVFVDLEPTVIDEVR.T
SW:TBA1_HUMAN	H12	8058	2	1708.9	(+0.6)	4.208	0.421	0.994	5	R.AVFVDL*EPTVIDEVR.T
SW:TBA1_HUMAN	H12	8852	2	2428.7	(+0.7)	4.379	0.531	1.000	16	R.FDGAL*NVDL*TEFQTNL*VPYPR.I
SW:TBA1_HUMAN	H12	8848	2	2410.7	(-0.9)	3.112	0.371	0.878	16	R.FDGALNVDLTEFQTNLVPYPR.I
SW:TBA1_HUMAN	H12	9022	2	2410.7	(+0.4)	2.281	0.201	0.713	16	R.FDGALNVDLTEFQTNLVPYPR.I
SW:TBA1_HUMAN	H12	7782	2	1772.1	(-0.3)	2.791	0.373	0.938	15	R.IHFPL*ATYAPVISAEEK#.A
SW:TBA1_HUMAN	H12	9640	2	1500.8	(+0.1)	3.675	0.566	1.000	9	R.L*ISQIVSSITASL*R.F
SW:TBA1_HUMAN	H12	11852	2	1488.8	(+0.7)	3.221	0.498	0.994	9	R.LISQIVSSITASL.R.F
SW:TBA1_HUMAN	H12	9746	2	1500.8	(+0.9)	3.111	0.548	1.000	9	R.L*ISQIVSSITASL*R.F
SW:TBA1_HUMAN	H12	11248	2	1488.8	(+0.1)	3.004	0.487	0.983	9	R.LISQIVSSITASL.R.F
SW:TBA1_HUMAN	H12	12270	2	1488.8	(+0.8)	3.000	0.490	0.992	9	R.LISQIVSSITASL.R.F
SW:TBA1_HUMAN	H12	13390	2	1488.8	(+0.6)	2.969	0.468	0.991	9	R.LISQIVSSITASL.R.F
SW:TBA1_HUMAN	H12	11696	2	1488.8	(+0.5)	2.958	0.504	0.993	9	R.LISQIVSSITASL.R.F
SW:TBA1_HUMAN	H12	10994	2	1488.8	(+0.9)	2.930	0.478	0.991	9	R.LISQIVSSITASL.R.F
SW:TBA1_HUMAN	H12	13234	2	1488.8	(+0.8)	2.805	0.435	0.986	9	R.LISQIVSSITASL.R.F
SW:TBA1_HUMAN	H12	12970	2	1488.8	(+0.8)	2.792	0.441	0.913	9	R.LISQIVSSITASL.R.F
SW:TBA1_HUMAN	H12	11726	2	1500.8	(+0.3)	2.771	0.518	0.926	9	R.L*ISQIVSSITASL*R.F
SW:TBA1_HUMAN	H12	9560	2	1488.8	(-0.8)	2.739	0.464	0.918	9	R.LISQIVSSITASL.R.F
SW:TBA1_HUMAN	H12	13086	2	1488.8	(+0.7)	2.647	0.467	0.981	9	R.LISQIVSSITASL.R.F
SW:TBA1_HUMAN	H12	9534	2	1500.8	(+0.8)	2.628	0.586	0.994	9	R.L*ISQIVSSITASL*R.F
SW:TBA1_HUMAN	H12	11800	2	1500.8	(+0.3)	2.609	0.522	0.981	9	R.L*ISQIVSSITASL*R.F
SW:TBA1_HUMAN	H12	13506	2	1488.8	(+0.5)	2.562	0.490	0.987	9	R.LISQIVSSITASL.R.F
SW:TBA1_HUMAN	H12	11086	2	1488.8	(+0.6)	2.549	0.430	0.980	9	R.LISQIVSSITASL.R.F
SW:TBA1_HUMAN	H12	13030	2	1500.8	(+0.9)	2.380	0.531	0.989	9	R.L*ISQIVSSITASL*R.F
SW:TBA1_HUMAN	H12	12520	2	1488.8	(+0.8)	2.296	0.433	0.973	9	R.LISQIVSSITASL.R.F
SW:TBA1_HUMAN	H13	9594	2	1488.8	(+0.2)	2.440	0.469	0.965	9	R.LISQIVSSITASL.R.F
SW:TBA1_HUMAN	H12	6188	2	1719.9	(+0.8)	2.730	0.230	0.249	16	R.NLDIERPTYTNLNR.L
SW:TBA1_HUMAN	H12	6190	2	1731.9	(+0.6)	2.520	0.185	0.120	16	R.NL*DIERPTYTNL*NR.L
SW:TBA1_HUMAN	H17	6154	2	1826.1	(+1.0)	2.684	0.341	0.960	19	K.VGINYQPPTVPPGGDLAK.V
SW:TBA1_HUMAN	H18	7894	2	1708.9	(+0.5)	3.770	0.518	0.999	5	R.AVFVDL*EPTVIDEVR.T
SW:TBB1_HUMAN	H12	7400	2	1616.9	(+0.8)	3.403	0.366	0.985	13	R.AILVDLEPGTMDSVR.S
SW:TBB1_HUMAN	H12	7438	2	1616.9	(-0.9)	2.959	0.524	0.952	13	R.AILVDLEPGTMDSVR.S
SW:TBB1_HUMAN	H12	6890	2	1644.9	(+0.1)	2.896	0.340	0.935	13	R.AIL*VDL*EPGTM@DSVR.S
SW:TBB1_HUMAN	H12	5066	2	1447.6	(+0.6)	3.415	0.221	0.961	16	K.EVDEQMLNVQNK.N
SW:TBB1_HUMAN	H14	5313	2	1447.6	(+0.1)	3.263	0.259	0.932	16	K.EVDEQMLNVQNK.N
SW:TBB1_HUMAN	H12	7668	3	3104.3	(+1.0)	5.467	0.537*	0.225	4	K.FWEVISDEHGIDPTGTGYHGSDQLQDR.I
SW:TBB1_HUMAN	H12	7592	3	3116.3	(+0.7)	5.447	0.487*	0.221	4	K.FWEVISDEHGIDPTGTGYHGSDL*QL*DR.I
SW:TBB1_HUMAN	H12	7588	3	3104.3	(+0.9)	4.612	0.541*	0.112	4	K.FWEVISDEHGIDPTGTGYHGSDQLQDR.I
SW:TBB1_HUMAN	H12	8828	2	1960.2	(-0.7)	4.646	0.490	0.994	19	K.GHYTEGAELVDSVLDVVR.K
SW:TBB1_HUMAN	H13	8828	2	1960.2	(+0.7)	5.381	0.584	1.000	19	K.GHYTEGAELVDSVLDVVR.K
SW:TBB1_HUMAN	H13	8830	2	1972.2	(-0.0)	3.585	0.424	0.982	19	K.GHYTEGAEL*VDSVL*DVVR.K
SW:TBB1_HUMAN	H15	8916	2	1972.2	(+0.8)	2.996	0.301	0.961	19	K.GHYTEGAEL*VDSVL*DVVR.K
SW:TBB1_HUMAN	H21	8388	2	1960.2	(+0.3)	4.486	0.480	0.998	19	K.GHYTEGAELVDSVLDVVR.K
SW:TBB1_HUMAN	H12	6196	2	1344.6	(+0.5)	3.435	0.341	0.985	17	R.IM@NTFSVVPSPK#.V
SW:TBB1_HUMAN	H12	6668	2	1328.6	(-0.3)	2.861	0.417	0.967	17	R.IMNTFSVVPSPK#.V
SW:TBB1_HUMAN	H12	6686	2	1320.6	(-0.9)	2.599	0.387	0.852	17	R.IMNTFSVVPSPK#.V
SW:TBB1_HUMAN	H11	5646	2	1302.4	(+0.9)	2.784	0.438	0.988	4	R.ISVYYNEATGGK.Y
SW:TBB1_HUMAN	H12	4848	2	1310.4	(+0.4)	3.403	0.476	1.000	4	R.ISVYYNEATGGK#.Y
SW:TBB1_HUMAN	H12	5336	2	1310.4	(+0.6)	2.575	0.477	0.987	4	R.ISVYYNEATGGK#.Y
SW:TBB1_HUMAN	H12	4890	2	1302.4	(+0.8)	2.248	0.386	0.960	4	R.ISVYYNEATGGK.Y
SW:TBB1_HUMAN	H12	6608	2	1166.4	(+0.9)	3.024	0.467	0.993	31	K.L*AVNM@VPFPR.L
SW:TBB1_HUMAN	H12	7252	2	1144.4	(-0.7)	2.602	0.342	0.825	31	K.LAVNMVFPFR.L
SW:TBB1_HUMAN	H12	8542	2	1621.9	(-0.1)	3.907	0.530	0.999	20	R.LHFFMPGFAPLTSR.G
SW:TBB1_HUMAN	H12	8574	2	1633.9	(-0.1)	3.755	0.417	0.985	20	R.L*HFFMPGFAPL*TSR.G
SW:TBB1_HUMAN	H12	7828	2	1649.9	(-0.2)	3.235	0.328	0.954	20	R.L*HFFM@PGFAPL*TSR.G
SW:TBB1_HUMAN	H13	8542	2	1621.9	(+0.7)	2.650	0.429	0.982	20	R.LHFFMPGFAPLTSR.G

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:TBB1_HUMAN	H12	9084	2	1871.2	(+0.6)	2.986	0.435	0.988	7	K.MAVTFIGNSTAIQELFK.R
SW:TBB1_HUMAN	H12	8710	2	1901.2	(+0.1)	2.284	0.208	0.521	7	K.M@AVTFIGNSTAIQEL*FK#.R
SW:TBB1_HUMAN	H12	8578	2	2808.1	(-0.9)	3.963	0.387	0.357	13	R.SGPFQIFRPDNFVFGQSGAGNNWAK#.G
SW:TBB1_HUMAN	H16	8026	3	2800.1	(+0.2)	3.855	0.479	0.989	13	R.SGPFQIFRPDNFVFGQSGAGNNWAK.G
SW:TBB1_HUMAN	H21	8384	2	1972.2	(-0.1)	2.954	0.403	0.964	19	K.GHYTEGAEL*VDSVL*DVVR.K
SW:TBB2_HUMAN	H12	7124	2	1614.8	(+0.1)	3.219	0.226	0.872	8	R.AVL*VDL*EPGTMDSVR.S
SW:TBB2_HUMAN	H12	4860	2	1329.5	(-0.5)	3.041	0.397	0.971	4	R.INVYYNEATGGK.Y
SW:TBB2_HUMAN	H12	6620	2	1630.8	(+0.3)	2.640	0.227	0.752	8	R.AVL*VDL*EPGTM@DSVR.S
SW:TBL3_HUMAN	H01	5290	2	1362.5	(+0.8)	3.489	0.501	1.000	2	R.GTQLLSSGSDGLVK.L
SW:TBL3_HUMAN	H02	4604	2	1257.4	(+0.3)	2.719	0.348	0.941	2	K.DINSVAIAPNDK.L
SW:TCE1_HUMAN	H15	2966	2	1436.6	(+0.8)	3.757	0.392	0.992	3	R.KQSTDEEVTSLAK.S
SW:TCE1_HUMAN	H15	3248	2	1436.6	(+0.2)	3.498	0.436	0.985	3	R.KQSTDEEVTSLAK.S
SW:TCE1_HUMAN	H15	3214	2	1458.6	(-0.0)	3.336	0.492	1.000	3	R.K#QSTDEEVTSL*AK#.S
SW:TCE1_HUMAN	H15	3138	2	1458.6	(+0.2)	3.193	0.429	0.977	3	R.K#QSTDEEVTSL*AK#.S
SW:TCE1_HUMAN	H15	3296	2	1458.6	(+0.0)	3.155	0.404	0.969	3	R.K#QSTDEEVTSL*AK#.S
SW:TCE1_HUMAN	H15	3024	2	1458.6	(+0.3)	3.109	0.464	0.981	3	R.K#QSTDEEVTSL*AK#.S
SW:TCE1_HUMAN	H15	3124	2	1436.6	(+0.3)	3.086	0.327	0.950	3	R.KQSTDEEVTSLAK.S
SW:TCE1_HUMAN	H15	2922	2	1458.6	(+0.3)	2.666	0.421	0.958	3	R.K#QSTDEEVTSL*AK#.S
SW:TCE1_HUMAN	H15	5994	2	1355.5	(+0.3)	2.905	0.488	0.984	3	R.MTAEEMASDELK.E
SW:TCE1_HUMAN	H15	4776	2	1308.4	(+0.9)	2.302	0.387	0.964	3	K.QSTDEEVTSLAK.S
SW:TCOF_HUMAN	H03	2074	2	907.0	(+0.9)	2.446	0.326	0.953	3	R.GPASVPSVGK#.A
SW:TCOF_HUMAN	H03	5678	2	1302.5	(-0.1)	2.561	0.340	0.896	3	K.GSL*GQGTAPVL*PGK#.T
SW:TCOF_HUMAN	H03	1446	2	910.1	(-0.0)	2.307	0.369	0.917	3	R.K#GAAPAPPK#.T
SW:TCOF_HUMAN	H03	1518	2	873.0	(+0.1)	2.401	0.154	0.565	3	R.K#GAAPAPPR.K
SW:TCOF_HUMAN	H03	1514	2	940.1	(+0.1)	2.521	0.370	0.941	3	R.K#GAAPTTPGK#.T
SW:TCOF_HUMAN	H04	6265	2	1452.7	(+0.7)	3.466	0.427	0.992	2	K.KNPASLPLTQAALK.V
SW:TCOF_HUMAN	H04	1869	2	1271.5	(+0.8)	2.672	0.478	0.987	3	R.K#TGPAAAQVQVGK#.Q
SW:TCOF_HUMAN	H03	6812	2	1805.0	(+0.2)	3.115	0.454	0.976	3	R.L*ASTNSSVL*GADL*PSSMK#.E
SW:TCOF_HUMAN	H04	4925	2	1363.5	(+0.7)	2.217	0.281	0.857	1	K.LDSSPSVSSTLAAK.D
SW:TCOF_HUMAN	H03	1942	2	1106.2	(+1.0)	2.412	0.267	0.921	3	R.NPQNSTVL*AR.G
SW:TCOF_HUMAN	H04	1873	2	1100.2	(+0.6)	2.606	0.422	0.986	3	R.NPQNSTVLAR.G
SW:TCOF_HUMAN	H03	5320	2	1059.2	(+0.6)	3.247	0.539	1.000	3	K.TGL*AVTVGQAK#.S
SW:TCOF_HUMAN	H04	4907	2	1045.2	(+0.9)	3.277	0.445	0.993	3	K.TGLAVTVGQAK.S
SW:TCOF_HUMAN	H04	4903	2	1059.2	(+0.5)	2.628	0.336	0.964	3	K.TGL*AVTVGQAK#.S
SW:TCOF_HUMAN	H03	2030	2	1127.3	(+0.8)	3.257	0.386	0.986	3	K.TGPAAAQVQVGK.Q
SW:TCOF_HUMAN	H04	1941	2	1127.3	(+0.8)	2.978	0.360	0.982	3	K.TGPAAAQVQVGK.Q
SW:TCOF_HUMAN	H04	1943	2	1135.3	(+0.7)	2.978	0.478	0.981	3	K.TGPAAAQVQVGK#.Q
SW:TCOF_HUMAN	H05	1918	2	1135.3	(+0.5)	2.864	0.430	0.977	3	K.TGPAAAQVQVGK#.Q
SW:TCOF_HUMAN	H03	6882	2	1248.4	(+0.5)	2.748	0.225	0.931	1	K.VL*TEL*L*EQER.K
SW:TCOF_HUMAN	H05	5706	2	1302.5	(+0.2)	2.211	0.169	0.379	3	K.GSL*GQGTAPVL*PGK#.T
SW:TCP4_HUMAN	H20	4568	2	1092.2	(-1.0)	2.901	0.419	0.902	2	R.DDNM@FQIGK#.M
SW:TCP4_HUMAN	H20	4702	2	1092.2	(-0.0)	2.856	0.300	0.940	2	R.DDNM@FQIGK#.M
SW:TCP4_HUMAN	H20	5790	2	1068.2	(-0.3)	2.714	0.316	0.945	2	R.DDNMFQIGK.M
SW:TCP4_HUMAN	H20	4534	2	1092.2	(+0.3)	2.697	0.286	0.913	2	R.DDNM@FQIGK#.M
SW:TCP4_HUMAN	H21	4390	2	1092.2	(+0.8)	2.728	0.259	0.951	2	R.DDNM@FQIGK#.M
SW:TCP4_HUMAN	H20	5762	2	1749.9	(+0.5)	3.204	0.496*	0.039	2	R.EYWMDPEGEM@K#PGR.K
SW:TCP4_HUMAN	H21	7210	2	1500.7	(-0.8)	2.686	0.230	0.532	2	K.GISLNPEQWSQLK.E
SW:TCP4_HUMAN	H20	7020	2	1656.9	(+0.0)	3.443	0.356	0.965	2	R.K#GISL*NPEQWSQL*K#.E
SW:TCP4_HUMAN	H21	7180	2	1500.7	(+0.8)	2.406	0.271	0.897	2	K.GISLNPEQWSQLK.E
SW:TCPB_HUMAN	H11	9486	2	1518.8	(+0.7)	2.729	0.507	0.991	1	R.LTSFIGAIAIGDLVK.S
SW:TCPB_HUMAN	H11	8750	2	1914.1	(-0.8)	2.376	0.474	0.880		K.LGGSLADSYLDEGFLLDK.K
SW:TCPD_HUMAN	H11	9308	2	1489.7	(-0.8)	2.666	0.106	0.184	2	R.DAL*SDL*AL*HFL*NK#.M
SW:TCPD_HUMAN	H11	6536	2	1479.6	(+0.7)	4.040	0.538	1.000	1	R.ETLLNSATTSLNSK.V
SW:TCPD_HUMAN	H11	6818	2	1457.7	(+0.9)	3.370	0.420	0.991	1	K.GIHPTIISESFQK.A
SW:TCPD_HUMAN	H11	6466	2	1364.5	(+0.8)	3.118	0.552	1.000	1	K.VIDPATATSVDL*R.D
SW:TCPD_HUMAN	H11	5116	2	959.1	(+0.7)	2.439	0.342	0.971	2	K.LVIEEAER.S
SW:TCPH_HUMAN	H10	9395	2	2253.5	(-0.6)	3.218	0.434	0.974	1	K.SQDAEVDGTTSVTLAAEFLK.Q
SW:TCPH_HUMAN	H11	7840	2	1566.8	(+0.9)	2.682	0.539	0.993		K.LPIGDVATQYFADR.D



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:TCPZ_HUMAN	H11	3144	2	938.1	(-0.3)	2.400	0.251	0.804	2	R.GLVLDHGAR.H
SW:TCPZ_HUMAN	H11	11544	2	2207.6	(+0.9)	6.130	0.683	1.000	2	K.VHAELADVLTEAVVDSILAIK.K
SW:TCPZ_HUMAN	H11	3024	2	938.1	(+0.5)	2.233	0.310	0.901	2	R.GLVLDHGAR.H
SW:TCTP_HUMAN	H19	7114	2	1713.9	(+0.8)	5.184	0.489	0.999	3	R.DLISHDEMFSDIYK.I
SW:TCTP_HUMAN	H19	7110	2	1727.9	(+0.2)	4.420	0.397	1.000	3	R.DL*ISHDEMFSDIYK#.I
SW:TCTP_HUMAN	H19	7144	2	1713.9	(-0.5)	3.148	0.470	0.983	3	R.DLISHDEMFSDIYK.I
SW:TCTP_HUMAN	H19	6404	2	1743.9	(-0.2)	2.802	0.271	0.858	3	R.DL*ISHDEM@FSDIYK#.I
SW:TCTP_HUMAN	H19	5456	2	843.0	(-0.0)	2.461	0.288	0.925	5	K.HILANFK.N
SW:TCTP_HUMAN	H19	5422	1	857.0	(-0.3)	1.961	0.130	0.000	5	K.HIL*ANFK#.N
SW:TCTP_HUMAN	H19	5706	2	1420.7	(+0.2)	3.208	0.344	0.489	5	R.VKPFMTGAAEQIK.H
SW:TCTP_HUMAN	H19	5418	1	843.0	(-0.3)	1.939	0.177	0.000	5	K.HILANFK.N
SW:TE2I_HUMAN	H11	9676	2	1623.9	(+0.3)	3.330	0.475	0.983	1	K.FNL*DL*STVTQAFL*K#.N
SW:TE2I_HUMAN	H11	9692	2	1623.9	(-0.9)	2.416	0.100	0.102	1	K.FNL*DL*STVTQAFL*K#.N
SW:TE2I_HUMAN	H11	6046	3	2770.0	(+0.2)	4.848	0.500	1.000	1	R.L*GPASADTGSEAK#PGAL*AEGAAEPEPQR.H
SW:TE2I_HUMAN	H11	6050	3	2750.0	(+0.6)	4.438	0.508	1.000	1	R.LGPASADTGSEAKPGALAEAAEPEPQR.H
SW:TE2I_HUMAN	H11	6224	2	1422.5	(+0.0)	2.204	0.247	0.659	3	K.SSL*TQHSWQSL*K#.D
SW:TE2I_HUMAN	H11	4684	2	1107.3	(+0.2)	2.967	0.456	0.980	1	K.VSQPEVGAAIK#.I
SW:TE2I_HUMAN	H21	8858	2	1623.9	(-0.1)	3.175	0.311	0.934	1	K.FNL*DL*STVTQAFL*K#.N
SW:TEM2_HUMAN	H21	4874	2	957.2	(+0.9)	2.575	0.467	0.854		K.ITLVSAAPGK.V
SW:TEM2_HUMAN	H21	6394	2	1330.5	(-0.5)	3.183	0.411	0.976		K.TL*AFTSVDL*TNK#.A
SW:TEM2_HUMAN	H21	4888	2	971.2	(+0.5)	2.517	0.402	0.979		K.ITL*VSAAPGK#.V
SW:TF1B_HUMAN	H06	6710	2	1527.6	(+0.9)	4.565	0.539	0.998	2	K.DHQYQFL*EDAVR.N
SW:TF1B_HUMAN	H06	6712	2	1521.6	(+0.7)	4.323	0.496	0.999	2	K.DHQYQFLEDAVR.N
SW:TF1B_HUMAN	H06	7814	3	3696.0	(-0.0)	3.708	0.457	0.983	5	K.EEETEAAIGAPPTATEGPETK#PVL*MAL*AEGPGAEGPR.L
SW:TF1B_HUMAN	H06	8026	2	1309.5	(+0.7)	2.702	0.392	0.984	2	K.FQWDLNAWTK.S
SW:TF1B_HUMAN	H06	7492	2	1685.9	(-0.7)	2.375	0.227	0.329	5	R.L*DL*DL*TADSQPPVFK#.V
SW:TF1B_HUMAN	H07	7570	2	1659.9	(+0.4)	2.601	0.369	0.966	5	R.LDLDLTADSQPPVFK.V
SW:TF1B_HUMAN	H06	6322	3	3583.7	(-0.0)	7.021	0.603	1.000	2	K.QSGSSSQPM@EVQEGYGFSGDDPYSSAEPHVSQVK#.R
SW:TF1B_HUMAN	H06	6566	3	3567.7	(-0.1)	6.141	0.561	1.000	2	K.QSGSSSQPM@EVQEGYGFSGDDPYSSAEPHVSQVK#.R
SW:TF1B_HUMAN	H06	6570	3	3559.7	(+0.1)	5.473	0.572	0.996	2	K.QSGSSSQPM@EVQEGYGFSGDDPYSSAEPHVSQVK#.R
SW:TF1B_HUMAN	H06	5058	2	1122.2	(+0.9)	2.751	0.310	0.964	4	R.SGEGEVSGLMR.K
SW:TF1B_HUMAN	H06	5052	2	1128.2	(+0.1)	2.461	0.246	0.804	4	R.SGEGEVSGL*MR.K
SW:TF1B_HUMAN	H06	7698	2	1960.2	(+0.3)	2.319	0.260	0.716	5	K.VFPGSTTEDYNL*IVIER.G
SW:TF1B_HUMAN	H07	7566	2	1685.9	(+0.0)	2.383	0.206	0.565	5	R.L*DL*DL*TADSQPPVFK#.V
SW:TFH4_HUMAN	H13	4920	2	1434.5	(-0.5)	2.885	0.466	0.976		K.AWSDDTSQL*GPKD#.H
SW:TFH4_HUMAN	H13	10774	2	2225.5	(+0.2)	2.551	0.445	0.961		K.DYSVEGMSDSSLNLFQHLR.E
SW:THO1_HUMAN	H08	6203	2	1675.9	(+0.6)	5.474	0.561	0.998	1	R.DKPVTGEQIEVFANK.L
SW:THO1_HUMAN	H08	6191	2	1691.9	(-0.1)	4.991	0.589	1.000	1	R.DK#PVTGEQIEVFANK#.L
SW:THO1_HUMAN	H08	8195	2	1404.6	(+0.6)	2.687	0.444	0.989	1	R.K#FWSL*QDYFR.N
SW:THO1_HUMAN	H08	6545	2	1473.6	(+0.1)	2.896	0.227	0.859	1	K.L*M@DL*QL*SDSNFR.R
SW:THO1_HUMAN	H08	6933	2	1704.8	(+0.8)	3.373	0.447	0.992	1	K.SVYQLLENPPDGER.F
SW:THO1_HUMAN	H08	5449	3	2640.6	(+0.1)	5.888	0.565	0.999	1	K.TGEDEDEEDNDAL*L*K#ENESPDVR.R
SW:THO1_HUMAN	H08	7263	2	1439.6	(+0.7)	2.489	0.333	0.955	1	K.LMDLQLSDSNFR.R
SW:THO2_HUMAN	H04	5745	2	1271.3	(+0.6)	3.387	0.237	0.974	1	K.ADQLDYENFR.H
SW:THO2_HUMAN	H04	5739	2	1277.3	(+0.7)	2.597	0.301	0.959	1	K.ADQL*DYENFR.H
SW:THO2_HUMAN	H04	5241	2	1142.3	(+0.3)	2.239	0.285	0.822	1	R.FVEL*VHQQK#.T
SW:THO2_HUMAN	H05	8130	2	1428.7	(+0.9)	2.539	0.312	0.945		R.LDPETLESGLIK.Q
SW:THO2_HUMAN	H04	10001	2	2218.6	(+0.2)	3.710	0.358	0.974		K.LSHSNPTILFDYILSQIK.Y
SW:THO2_HUMAN	H04	5457	2	1415.6	(+0.9)	3.794	0.405	0.993		K.NETYNSHPLLVK.V
SW:THO2_HUMAN	H04	5445	2	1435.6	(+0.1)	3.166	0.363	0.964		K.NETYNSHPL*L*VK#.V
SW:THO2_HUMAN	H05	6936	2	1113.3	(+0.9)	2.617	0.378	0.976	1	K.VLNLGQALER.R
SW:THO2_HUMAN	H04	7921	2	1477.7	(+0.7)	2.864	0.506	0.992		K.YDNLITPVVDSLK.Y
SW:THO2_HUMAN	H04	11283	2	1920.3	(+0.2)	4.020	0.485	0.999	1	K.YPIDLAGLLQYVANQLK.A
SW:THO2_HUMAN	H04	11289	2	1952.3	(-0.8)	2.381	0.261	0.427	1	K.YPIDL*AGL*L*QYVANQL*K#.A
SW:THO2_HUMAN	H05	6090	2	1271.3	(+0.4)	2.322	0.137	0.674	1	K.ADQLDYENFR.H
SW:THO4_HUMAN	H17	5488	2	1227.4	(+0.1)	2.596	0.230	0.812		K.M@DM@SL*DDIHK#.L
SW:THO4_HUMAN	H17	6402	2	1211.4	(+0.6)	2.396	0.388*	0.250		K.M@DMSL*DDIHK#.L

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:THO4_HUMAN	H17	6876	3	2704.9	(+0.8)	4.169	0.443	0.992	1	K.QLPDKWQHDLFDSGFGGGAGVETGGK.L
SW:THO4_HUMAN	H17	6238	3	2054.2	(+0.7)	4.560	0.503	0.996	1	K.QQL*SAEEL*DAQL*DAYNAR.M
SW:THO4_HUMAN	H17	6248	2	2036.2	(+1.0)	4.383	0.515	1.000	1	K.QQLSAEELDAQLDAYNAR.M
SW:THO4_HUMAN	H16	5220	2	1238.3	(+0.5)	3.207	0.510	1.000		R.SL*GTADVHFER.K
SW:THO4_HUMAN	H16	5230	2	1232.3	(+0.9)	3.202	0.489	0.999		R.SLGTADVHFER.K
SW:THO4_HUMAN	H17	6548	3	2137.2	(+0.8)	4.381	0.505	1.000	1	K.WQHDL*FDSGFGGGAGVETGGK#.L
SW:THO4_HUMAN	H17	6628	3	2137.2	(+1.0)	4.362	0.499	0.999	1	K.WQHDL*FDSGFGGGAGVETGGK#.L
SW:THO4_HUMAN	H20	5482	2	1232.3	(+1.0)	2.699	0.458	0.979		R.SLGTADVHFER.K
SW:THPA_HUMAN	H08	9157	2	2320.6	(+0.1)	4.508	0.521	1.000	3	R.DSGSFVAFQNPISGSELMSSFAK.T
SW:THPA_HUMAN	H08	9149	2	2334.6	(+0.8)	3.292	0.418	0.987	3	R.DSGSFVAFQNPISGSEL*MSSFAK#.T
SW:THPA_HUMAN	H08	6777	2	1351.5	(+1.0)	2.487	0.365	0.970	3	K.FQETEFSPPR.K
SW:THPA_HUMAN	H08	6691	2	1357.5	(-0.4)	2.250	0.291	0.816	3	K.FQETEFLL*SPPR.K
SW:THPA_HUMAN	H08	6669	2	1357.5	(+0.9)	2.226	0.227	0.816	3	K.FQETEFLL*SPPR.K
SW:THPA_HUMAN	H08	6327	3	2577.7	(+0.6)	5.583	0.455	0.987	7	K.GPPDFSSDEEREPTPVL*GSGAAAAGR.S
SW:THPA_HUMAN	H11	6504	3	2571.7	(+0.9)	5.380	0.531	0.997	7	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S
SW:THPA_HUMAN	H11	6500	3	2577.7	(+0.9)	4.550	0.459	0.997	7	K.GPPDFSSDEEREPTPVL*GSGAAAAGR.S
SW:THPA_HUMAN	H15	6118	3	2571.7	(+0.9)	4.430	0.507	0.998	7	K.GPPDFSSDEEREPTPVLGSGAAAAGR.S
SW:THPA_HUMAN	H08	1825	2	1252.4	(+0.1)	2.492	0.300	0.211	7	R.NRPPLPAGTNSK.G
SW:THPA_HUMAN	H08	1841	2	1266.4	(-0.6)	2.392	0.308	0.176	7	R.NRPPL*PAGTNSK#.G
SW:THPA_HUMAN	H08	7087	2	1375.6	(-0.6)	2.631	0.345	0.932	1	-.PEFLEDPSVLTK.D
SW:THPA_HUMAN	H08	7063	2	1395.6	(+0.3)	2.349	0.349	0.888	1	-.PEFL*EDPSVL*TK#.D
SW:THPA_HUMAN	H11	7236	2	1395.6	(+0.4)	3.031	0.405	0.986	1	-.PEFL*EDPSVL*TK#.D
SW:THPA_HUMAN	H12	5966	2	1698.9	(+0.7)	4.807	0.559	1.000	7	K.SELVANNVTLPAGEQR.K
SW:THPA_HUMAN	H08	5581	2	1654.8	(+0.1)	2.207	0.189	0.314	7	R.SSTPL*PTISSAENTR.Q
SW:THPA_HUMAN	H08	5467	2	1648.8	(+0.5)	2.205	0.273	0.837	7	R.SSTPLPTISSAENTR.Q
SW:THPA_HUMAN	H11	5990	2	1654.8	(+0.2)	3.353	0.311	0.948	7	R.SSTPL*PTISSAENTR.Q
SW:THPA_HUMAN	H11	5980	2	1648.8	(+0.1)	3.153	0.396	0.969	7	R.SSTPLPTISSAENTR.Q
SW:THPA_HUMAN	H08	5687	2	1088.3	(-0.4)	2.427	0.333	0.905	2	R.THQAL*GIL*SK#.T
SW:THPA_HUMAN	H08	7339	2	1681.9	(-0.5)	4.478	0.392	0.985	3	K.TVVSHSL*TTL*GL*EVAK#.Q
SW:THPA_HUMAN	H15	5870	2	1698.9	(+0.6)	3.714	0.552	1.000	7	K.SELVANNVTLPAGEQR.K
SW:THPB_HUMAN	H11	8300	2	1800.1	(+1.0)	2.307	0.474	0.980	1	K.HASPIL*PIFEFSDIPR.R
SW:THPB_HUMAN	H15	5752	3	2683.8	(+0.4)	5.763	0.593	0.974	1	R.RVEHNQSYSQAGITETEWTSGSSK.G
SW:TM21_HUMAN	H19	7530	2	1305.6	(+0.8)	3.042	0.399	0.974	2	R.IPDQL*VIL*DMK#.H
SW:TM21_HUMAN	H19	5002	2	1305.5	(-0.0)	4.272	0.470	1.000	3	K.ITDSAGHILYSK.E
SW:TM21_HUMAN	H19	4990	2	1319.5	(+0.3)	4.217	0.519	0.985	3	K.ITDSAGHIL*YSK#.E
SW:TM21_HUMAN	H19	6686	2	1321.6	(-0.0)	2.331	0.162	0.500	2	R.IPDQL*VIL*DM@K#.H
SW:TOP1_HUMAN	H07	6568	2	1121.3	(+0.8)	2.954	0.420	0.989	4	K.AEEVATFFAK#.M
SW:TOP1_HUMAN	H07	7162	2	1382.6	(+0.2)	2.906	0.126	0.630	6	K.HL*QDL*MEGL*TAK#.V
SW:TOP1_HUMAN	H07	1756	2	1446.5	(+0.4)	2.843	0.307	0.485	7	K.L*EVQATDREENK#.Q
SW:TOP1_HUMAN	H07	6096	2	1508.7	(+0.5)	4.133	0.478	1.000	6	R.TYNASITLQQQLK.E
SW:TOP1_HUMAN	H07	6088	2	1528.7	(-0.0)	2.986	0.305	0.923	6	R.TYNASITL*QQQL*K#.E
SW:TOP1_HUMAN	H07	6562	2	1622.8	(+0.8)	4.744	0.425	0.997	4	K.WWEEERYPEGIK.W
SW:TOP1_HUMAN	H07	6550	2	1630.8	(-0.0)	4.051	0.477	1.000	4	K.WWEEERYPEGIK#.W
SW:TOP1_HUMAN	H07	6564	2	1113.3	(+0.3)	2.458	0.403	0.956	4	K.AEEVATFFAK.M
SW:TP2A_HUMAN	H04	8305	2	1336.6	(+0.8)	2.274	0.289	0.910	3	R.FLEEFITPIVK.V
SW:TP2A_HUMAN	H04	7511	2	1469.7	(+0.1)	2.767	0.273	0.902	7	R.KEWLTNFMEDR.R
SW:TP2A_HUMAN	H05	7400	2	1462.6	(+0.9)	2.421	0.304	0.928	9	K.IFDEILVNAADNK.Q
SW:TP2B_HUMAN	H04	8169	2	1853.0	(+0.5)	2.448	0.465	0.982	5	K.SQDFGNLFSFPSYSQK.S
SW:TP2B_HUMAN	H04	5589	2	1008.2	(+0.9)	2.230	0.385	0.969	4	K.TPALISDYK.E
SW:TPIS_HUMAN	H18	7824	2	1603.9	(+0.7)	3.548	0.463	0.994	3	K.VVLAYEPVVAIGTGK.T
SW:TPIS_HUMAN	H18	1526	2	1467.6	(+0.7)	2.874	0.349	0.975	3	K.TATPQQAQEVHEK.L
SW:TPM1_HUMAN	H17	5714	2	1244.4	(+0.4)	2.959	0.364	0.985	27	R.IQLVEEELDR.A
SW:TPM1_HUMAN	H02	5304	2	1460.7	(+0.9)	2.642	0.123*	0.006	11	K.MEIQEIQLK.E
SW:TPM1_HUMAN	H17	5932	2	1132.4	(+0.6)	2.377	0.103*	0.306	11	K.MEIQEIQLK.E
SW:TPR_HUMAN	H03	6380	2	1510.7	(-1.0)	3.611	0.359	0.924	2	K.AIQDHILLEVEQSK.D
SW:TPR_HUMAN	H03	6418	2	1464.6	(+0.7)	4.309	0.419	0.989	3	K.FLADQQSEIDGLK.G
SW:TPR_HUMAN	H03	10226	2	2025.4	(+0.8)	4.914	0.569	1.000	2	R.GQNLLLTNLQTIQGILER.S

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:TPR_HUMAN	H04	10179	2	2025.4	(+0.4)	3.236	0.469	0.992	2	R.GQNLLLTNLQTIQGILER.S
SW:TPR_HUMAN	H03	8494	3	2154.5	(+0.4)	4.877	0.462	0.999	3	R.KLELDILPLQEANAELSEK.S
SW:TPR_HUMAN	H03	5738	2	1324.4	(-0.4)	3.386	0.382	0.975	3	K.L*DEL*QASDVSVK#.Y
SW:TPR_HUMAN	H03	5164	2	1102.2	(+0.9)	3.021	0.276	0.975	2	K.LQEQVTDLR.S
SW:TPR_HUMAN	H03	5152	2	1114.2	(+0.4)	2.394	0.277	0.936	2	K.L*QEQVTDL*R.S
SW:TPR_HUMAN	H03	2244	2	1406.5	(+0.9)	2.268	0.303	0.921	2	R.NIEEL*QQQNQR.L
SW:TPR_HUMAN	H03	7154	3	2697.0	(+0.7)	5.430	0.460	1.000	2	K.RPSTSQTVSTPAPVPIESTEAIK.A
SW:TPR_HUMAN	H03	6248	2	1275.4	(+0.8)	3.343	0.346	0.987	2	K.SLESQVENLQK.T
SW:TPR_HUMAN	H08	5395	2	1304.4	(+0.2)	2.314	0.131	0.304	3	K.LDELQASDVSVK.Y
SW:TRF2_HUMAN	H10	4955	2	1396.5	(+0.1)	3.733	0.522	1.000	1	K.TLSGAQDSEAAFAK.L
SW:TRF2_HUMAN	H10	4935	2	1410.5	(-0.1)	2.867	0.394	0.955	1	K.TL*SGAQDSEAAFAK#.L
SW:TRF2_HUMAN	H10	8359	2	1480.8	(+0.1)	2.365	0.334	0.198	1	R.DIMQAL*L*VRPL*GK#.E
SW:U2AF_HUMAN	H11	7368	2	2134.4	(+0.4)	4.427	0.575	1.000	1	R.LGGLTQAPGNPVLAVQINQDK.N
SW:U2AF_HUMAN	H11	7362	2	2160.4	(-0.7)	3.273	0.374	0.884	1	R.L*GGL*TQAPGNPVL*AVQINQDK#.N
SW:U2AF_HUMAN	H11	7726	3	3592.0	(-0.7)	5.617	0.537	0.998	1	R.RPHDYQPL*PGM@SENPSVYVPGVVSTVVPDSAHK#.L
SW:U2AF_HUMAN	H11	8132	3	3576.0	(-0.3)	4.693	0.425	0.998	1	R.RPHDYQPL*PGMSENPSVYVPGVVSTVVPDSAHK#.L
SW:U2AF_HUMAN	H11	8134	3	3562.0	(-0.1)	4.495	0.531	1.000	1	R.RPHDYQPLPGMSENPSVYVPGVVSTVVPDSAHK.L
SW:U2AF_HUMAN	H11	8358	2	1807.1	(-0.8)	2.477	0.231	0.416	1	K.LFIGGLPNYLNDQVK.E
SW:U520_HUMAN	H03	7708	2	1755.0	(+0.2)	2.318	0.334	0.828	7	R.EEEVTGPVIAPLFPQK.R
SW:U520_HUMAN	H04	8887	3	2842.2	(-0.2)	4.793	0.542	1.000	2	K.GL*FYFDNSFRPVPL*EQTYVGITEK#.K
SW:U520_HUMAN	H03	5528	2	1072.2	(+0.6)	2.871	0.318	0.976	3	K.GNIIISTPEK.W
SW:U520_HUMAN	H03	5530	2	1080.2	(-0.4)	2.350	0.230	0.732	3	K.GNIIISTPEK#.W
SW:U520_HUMAN	H04	5149	2	1072.2	(+0.8)	2.661	0.327	0.971	3	K.GNIIISTPEK.W
SW:U520_HUMAN	H03	6002	2	1190.4	(+0.9)	3.667	0.499	1.000	3	R.IVALSSSLNAK.D
SW:U520_HUMAN	H04	9383	2	2094.4	(+0.1)	2.202	0.353	0.853	3	R.LIGLSATLPNYEDVATFLR.V
SW:U520_HUMAN	H03	7592	2	1699.9	(+0.6)	4.344	0.494	1.000	3	R.LYDLNHNEIGELIR.M
SW:U520_HUMAN	H03	7920	2	1746.9	(-0.5)	2.654	0.132	0.492	7	R.NAL*L*QL*TDSQIADVAR.F
SW:U520_HUMAN	H03	6356	2	1316.4	(+0.2)	3.177	0.471	0.985	2	R.NSAFESL*YQDK#.F
SW:U520_HUMAN	H03	8170	2	1296.5	(+1.0)	3.538	0.582	0.997	4	R.SL*VQEMVGSFGK#.R
SW:U520_HUMAN	H03	6132	2	1222.3	(+0.9)	3.264	0.241	0.965	4	K.TGNFQVTELR.I
SW:U520_HUMAN	H03	8040	2	1721.9	(+0.4)	3.094	0.469	0.992	3	K.VELTITPDFQWDEK.V
SW:U520_HUMAN	H03	8034	2	1735.9	(+0.0)	2.610	0.215	0.705	3	K.VEL*TITPDFQWDEK#.V
SW:U520_HUMAN	H03	10198	2	1717.0	(+1.0)	4.258	0.595	1.000	3	R.WTELGALDILQMLGR.A
SW:U520_HUMAN	H03	9586	2	1757.0	(+0.0)	2.309	0.385	0.907	3	R.WTEL*GAL*DIL*QM@L*GR.A
SW:U520_HUMAN	H03	9110	2	2120.5	(+0.1)	3.505	0.513	0.999	3	K.YPPPTLDDLQPLPVSALR.N
SW:U520_HUMAN	H05	6186	2	1228.3	(+0.6)	2.813	0.489	0.993	4	K.TGNFQVTEL*GR.I
SW:U5S1_HUMAN	H06	8846	2	1800.0	(+0.3)	2.350	0.457	0.954	2	K.AFIPAIDSFGFETDLR.T
SW:U5S1_HUMAN	H06	4544	2	1049.1	(+0.7)	2.598	0.227	0.903	2	K.GL*SEDVSISK#.F
SW:U5S1_HUMAN	H06	6360	2	1402.6	(+0.7)	3.458	0.249	0.522	2	R.GNEEAQIFRPLK.F
SW:U5S1_HUMAN	H06	6352	2	1416.6	(+0.3)	2.698	0.280	0.208	2	R.GNEEAQIFRPL*K#.F
SW:U5S1_HUMAN	H06	7504	2	1595.8	(+0.5)	2.854	0.473	0.989	2	K.IL*AQVVGVDVDTSL*PR.T
SW:U5S1_HUMAN	H06	7508	2	1583.8	(+0.6)	2.295	0.348	0.934	2	K.ILAQVVGVDVDTSLPR.T
SW:U5S1_HUMAN	H06	9632	2	1505.8	(+0.7)	2.900	0.435	0.987	2	R.SFVEFIL*EPL*YK#.I
SW:U5S1_HUMAN	H06	4038	2	1321.5	(+0.1)	2.608	0.357	0.922	2	R.VL*SGTIHAGQPVK#.V
SW:U5S1_HUMAN	H06	4206	2	1321.5	(+0.7)	2.607	0.316	0.945	2	R.VL*SGTIHAGQPVK#.V
SW:U5S1_HUMAN	H06	3928	2	1307.5	(+0.6)	2.444	0.434	0.979	2	R.VLSGTIHAGQPVK.V
SW:U5S1_HUMAN	H06	3960	2	1321.5	(-0.2)	2.313	0.403	0.922	2	R.VL*SGTIHAGQPVK#.V
SW:U5S1_HUMAN	H06	4116	2	1321.5	(-0.7)	2.298	0.197	0.256	2	R.VL*SGTIHAGQPVK#.V
SW:U5S1_HUMAN	H06	3008	2	1307.5	(+0.4)	2.258	0.289	0.888	2	R.VLSGTIHAGQPVK.V
SW:UBCE_HUMAN	H17	6386	2	1502.6	(-0.0)	3.622	0.464	1.000	3	R.L*L*L*ENYEEYAAR.A
SW:UBCE_HUMAN	H17	5030	2	1457.6	(+0.5)	3.068	0.515	0.994	3	K.EVTTLTADPPDGIK.V
SW:UBCI_HUMAN	H19	6372	2	1323.5	(+0.8)	3.211	0.418	0.989	4	K.DHPFGFVAVPTK#.N
SW:UBCI_HUMAN	H19	6390	2	1315.5	(+0.1)	2.313	0.388	0.918	4	K.DHPFGFVAVPTK.N
SW:UBCI_HUMAN	H20	6446	2	1323.5	(+0.7)	2.729	0.300	0.951	4	K.DHPFGFVAVPTK#.N
SW:UBCI_HUMAN	H19	6266	2	1459.7	(-0.4)	4.149	0.470	0.941	4	R.K#DHPFGFVAVPTK#.N
SW:UBCI_HUMAN	H19	6256	3	1459.7	(+0.6)	4.085	0.417	0.999	4	R.K#DHPFGFVAVPTK#.N
SW:UBCI_HUMAN	H19	6258	2	1443.7	(+0.9)	3.288	0.370	0.986	4	R.KDHPFGFVAVPTK.N
SW:UBCI_HUMAN	H20	6292	2	1459.7	(-0.2)	3.748	0.454	0.999	4	R.K#DHPFGFVAVPTK#.N
SW:UBCI_HUMAN	H20	6290	3	1459.7	(+0.1)	3.707	0.457	0.985	4	R.K#DHPFGFVAVPTK#.N
SW:UBCI_HUMAN	H20	6308	2	1443.7	(-0.2)	2.957	0.443	0.977	4	R.KDHPFGFVAVPTK.N

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:UBCI_HUMAN	H20	6626	2	1242.4	(+0.3)	3.512	0.417	0.981	5	K.K#GTPWEGGL*FK#.L
SW:UBCI_HUMAN	H20	5508	2	1563.8	(-0.8)	2.558	0.345	0.100	5	R.M@L*FK#DDYPSSPPK#.C
SW:UBCN_HUMAN	H20	7488	2	2197.5	(+0.1)	4.936	0.551	1.000	1	R.YFHVVIAGPQDSPFEGGTFK.L
SW:UBCN_HUMAN	H20	7484	2	2205.5	(+0.7)	3.986	0.450	0.999	1	R.YFHVVIAGPQDSPFEGGTFK#.L
SW:UBCN_HUMAN	H20	6004	2	1057.3	(+0.4)	2.294	0.335	0.943	1	R.L*L*AEPVPGIK#.A
SW:UBF1_HUMAN	H07	5932	2	1505.6	(+0.8)	3.290	0.263	0.969	2	R.FLESLPEEEQQR.V
SW:UBF1_HUMAN	H07	8214	2	2035.3	(-0.0)	2.776	0.404	0.957	2	K.RAEEIWQQSVIGDYLAR.F
SW:UBF1_HUMAN	H07	5754	2	1431.6	(+0.3)	2.509	0.397	0.953	2	K.TPQQLWYTHEK.K
SW:UNRI_HUMAN	H14	5065	2	1417.6	(+1.0)	3.504	0.407	0.831	2	R.IYDLNKPEAEPK.E
SW:UNRI_HUMAN	H14	5469	2	1611.6	(-0.0)	4.040	0.450	1.000	2	K.YDYNSGEEL*ESYK#.G
SW:UNRI_HUMAN	H14	5475	2	1597.6	(-0.6)	3.809	0.551	1.000	2	K.YDYNSGEELESYK.G
SW:UNRI_HUMAN	H14	5063	2	1439.6	(-0.2)	2.844	0.266	0.222	2	R.IYDL*NK#PEAEPK#.E
SW:VAPA_HUMAN	H17	6576	2	1589.8	(+0.9)	2.848	0.380	0.608	2	K.FK#GPFTDVVTTNL*K#.L
SW:VAPA_HUMAN	H17	6530	2	1618.9	(-0.7)	2.873	0.323	0.568	1	K.HEQILVLDPPDLDK.F
SW:VAPA_HUMAN	H17	6498	2	1618.9	(+0.8)	2.534	0.100	0.550	1	K.HEQILVLDPPDLDK.F
SW:VAPA_HUMAN	H18	6652	2	1306.5	(-0.0)	2.762	0.381	0.952	5	K.GPFTDVVTTNL*K#.L
SW:VAT1_HUMAN	H13	10252	2	2177.5	(-0.1)	4.138	0.455	1.000	5	R.TWWNQFSVTALQLLQANR.A
SW:VAT1_HUMAN	H13	7006	2	1575.8	(+0.5)	3.844	0.527	1.000	5	K.GVDIVMDPLGGSDTAK.G
SW:VIME_HUMAN	H11	2392	2	1843.9	(-0.6)	3.651	0.315	0.955	5	R.DGQVINETSQHHDLL*E.-
SW:VIME_HUMAN	H12	2114	2	1843.9	(+0.6)	2.856	0.436	0.984	5	R.DGQVINETSQHHDLL*E.-
SW:VIME_HUMAN	H12	2112	2	1837.9	(+0.1)	2.315	0.271	0.581	5	R.DGQVINETSQHHDLE.-
SW:VIME_HUMAN	H12	4552	2	1099.2	(-0.5)	2.328	0.261	0.830	6	R.DNL*AEDIM@R.L
SW:VIME_HUMAN	H12	5364	2	1324.4	(+0.7)	2.539	0.186	0.839	6	R.EEAENTLQSF.R.Q
SW:VIME_HUMAN	H12	5382	2	1324.4	(-0.8)	2.301	0.415	0.838	6	R.EEAENTLQSF.R.Q
SW:VIME_HUMAN	H11	5818	2	1304.5	(+0.8)	2.553	0.390	0.657	6	R.EKLQEEMLR.E
SW:VIME_HUMAN	H11	6906	2	1669.8	(-0.6)	2.796	0.474	0.975	5	R.ETNLDLPLVDTHSK.R
SW:VIME_HUMAN	H11	6888	2	1695.8	(+0.5)	2.456	0.216	0.787	5	R.ETNL*DSL*PL*VDTHSK#.R
SW:VIME_HUMAN	H11	5322	2	1094.2	(-0.7)	3.688	0.367	0.949	7	K.FADLSEANR.N
SW:VIME_HUMAN	H11	5298	2	1100.2	(+0.7)	2.983	0.377	0.987	7	K.FADL*SEANR.N
SW:VIME_HUMAN	H11	5216	2	871.0	(+0.7)	2.252	0.242	0.916	5	R.FANYIDK.V
SW:VIME_HUMAN	H12	7918	2	1202.4	(-0.2)	2.466	0.241	0.796	5	K.IL*L*AEL*EQL*K#.G
SW:VIME_HUMAN	H17	7270	2	1170.4	(+0.9)	3.415	0.301	0.985	5	K.ILLAELEQLK.G
SW:VIME_HUMAN	H11	9196	2	1571.9	(-1.0)	2.292	0.393	0.763	6	R.ISLPLPNFSSLNLR.E
SW:VIME_HUMAN	H12	7512	2	1562.8	(-0.2)	3.492	0.334	0.964	7	R.K#VESL*QEEIAFL*K#.K
SW:VIME_HUMAN	H17	6938	2	1534.8	(+0.3)	5.247	0.451	1.000	7	R.KVESLQEEIAFLK.K
SW:VIME_HUMAN	H19	7348	2	1534.8	(+0.7)	3.069	0.315	0.968	7	R.KVESLQEEIAFLK.K
SW:VIME_HUMAN	H11	6302	2	1267.4	(+0.4)	3.068	0.445	0.993	5	R.L*GDL*YEEEMR.E
SW:VIME_HUMAN	H11	6324	2	1255.4	(+0.0)	2.958	0.322	0.956	5	R.LGDLYEEMR.E
SW:VIME_HUMAN	H11	5494	2	1283.4	(+0.4)	2.922	0.445	0.992	5	R.L*GDL*YEEEM@R.E
SW:VIME_HUMAN	H12	6018	2	1267.4	(+0.4)	2.712	0.448	0.990	5	R.L*GDL*YEEEMR.E
SW:VIME_HUMAN	H12	4532	2	1283.4	(+0.3)	2.392	0.273	0.847	5	R.L*GDL*YEEEM@R.E
SW:VIME_HUMAN	H12	4610	2	1283.4	(+0.1)	2.333	0.396	0.945	5	R.L*GDL*YEEEM@R.E
SW:VIME_HUMAN	H11	10196	2	2153.4	(+0.4)	2.988	0.379	0.978	5	R.L*L*QDSVDFSL*ADAINTEFK#.N
SW:VIME_HUMAN	H11	13598	2	2153.4	(+0.9)	2.504	0.368	0.955	5	R.L*L*QDSVDFSL*ADAINTEFK#.N
SW:VIME_HUMAN	H11	10308	2	2153.4	(+0.8)	2.392	0.270	0.861	5	R.L*L*QDSVDFSL*ADAINTEFK#.N
SW:VIME_HUMAN	H11	9872	2	2127.4	(+0.8)	2.382	0.490	0.984	5	R.LLQDSVDFSLADAINTEFK.N
SW:VIME_HUMAN	H11	12734	2	2153.4	(+0.9)	2.365	0.383	0.953	5	R.L*L*QDSVDFSL*ADAINTEFK#.N
SW:VIME_HUMAN	H11	13500	2	2127.4	(+0.8)	2.325	0.373	0.951	5	R.LLQDSVDFSLADAINTEFK.N
SW:VIME_HUMAN	H11	4826	2	1133.3	(-0.2)	2.686	0.264	0.896	7	R.L*QDEIQNMK#.E
SW:VIME_HUMAN	H11	4762	2	1119.3	(+0.7)	2.455	0.178	0.842	7	R.LQDEIQNMK.E
SW:VIME_HUMAN	H11	4746	2	1133.3	(+0.0)	2.334	0.119	0.346	7	R.L*QDEIQNMK#.E
SW:VIME_HUMAN	H11	5014	2	1059.2	(+0.9)	2.656	0.151	0.855	7	K.L*QEEML*QR.E
SW:VIME_HUMAN	H11	4892	2	1047.2	(+1.0)	2.368	0.216	0.895	7	K.LQEEMLR.E
SW:VIME_HUMAN	H11	5866	2	1429.6	(+0.8)	3.543	0.452	0.990	3	R.SLYASSPGGVYATR.S
SW:VIME_HUMAN	H11	5864	2	1435.6	(+0.2)	3.212	0.416	0.959	3	R.SL*YASSPGGVYATR.S
SW:VIME_HUMAN	H11	5886	2	1429.6	(-0.9)	2.419	0.425	0.843	3	R.SLYASSPGGVYATR.S
SW:VIME_HUMAN	H12	5270	2	1435.6	(-0.0)	3.140	0.510	0.987	3	R.SL*YASSPGGVYATR.S
SW:VIME_HUMAN	H17	4784	2	1429.6	(+0.7)	2.632	0.329	0.955	3	R.SLYASSPGGVYATR.S
SW:VIME_HUMAN	H12	6074	2	1508.7	(+0.1)	2.370	0.286	0.111	2	R.TYSL*GSAL*RPSTSR.S
SW:VIME_HUMAN	H22	5230	2	1435.6	(-0.4)	2.323	0.466	0.958	3	R.SL*YASSPGGVYATR.S

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:VP35_HUMAN	H08	8277	2	1576.9	(+0.1)	3.457	0.434	0.983	7	K.IFSFAHQTISALIK.A
SW:VP35_HUMAN	H08	5347	2	1244.4	(+0.8)	3.247	0.379	0.989	5	R.LSQLEGVNVVER.Y
SW:VP35_HUMAN	H08	5359	2	1256.4	(+0.7)	2.915	0.482	0.992	5	R.L*SQL*EGVNVVER.Y
SW:VP35_HUMAN	H08	8319	2	1623.9	(-0.4)	2.523	0.323	0.872	6	K.IPVDTYNNIL*TVL*K#.L
SW:VRK1_HUMAN	H13	6118	3	3137.3	(+0.7)	6.404	0.585	0.993	1	K.EIEESKEPGVEDTEWSNTQTEEEAIQTR.S
SW:VRK1_HUMAN	H13	6122	3	3145.3	(+0.6)	5.607	0.518	0.991	1	K.EIEESK#EPGVEDTEWSNTQTEEEAIQTR.S
SW:VRK1_HUMAN	H13	8470	2	1874.2	(+0.6)	4.413	0.571	1.000	1	R.HLAEQFAVGEIITDMAK.K
SW:VRK1_HUMAN	H13	6944	2	1800.0	(-0.7)	3.049	0.262	0.091	1	K.L*L*DYTEK#PL*YENL*R.D
SW:VRK1_HUMAN	H13	7514	2	1799.0	(-0.9)	2.605	0.374	0.802	1	K.NPDQVYL*VDYGL*AYR.Y
SW:VRK1_HUMAN	H13	6212	2	1354.5	(+0.5)	2.362	0.320	0.359	1	R.YRENIASL*MDK#.C
SW:WDR5_HUMAN	H14	6279	2	1610.7	(-0.1)	2.942	0.499	0.979	1	K.FSPNGEWL*ASSSADK#.L
SW:WDR5_HUMAN	H14	6893	2	1574.7	(-0.1)	2.666	0.343	0.912	1	K.TL*IDDDNPPVSVFK#.F
SW:WDR5_HUMAN	H15	6922	2	1560.7	(+1.0)	2.828	0.535	0.993	1	K.TLIDDDNPPVSVFK.F
SW:WDR5_HUMAN	H14	7471	2	1362.6	(+0.3)	2.393	0.284	0.806	1	K.YIL*AATL*DNLT*K#.L
SW:WDR5_HUMAN	H15	6262	2	1596.7	(+0.4)	2.466	0.202	0.741	1	K.FSPNGEWLASSSADK.L
SW:XRC1_HUMAN	H08	7707	2	1614.8	(+0.7)	3.805	0.356	0.990	1	K.HFFLYGEFPGDER.R
SW:XRC1_HUMAN	H08	7701	2	1620.8	(+0.2)	2.853	0.388	0.961	1	K.HFFL*YGEFPGDER.R
SW:XRC1_HUMAN	H08	1451	2	1330.5	(+1.0)	2.280	0.339	0.359	1	R.AIGSTSKPQESPK.G
SW:Y056_HUMAN	H04	10865	2	1642.0	(-0.1)	3.182	0.370	0.961	2	R.NFIENIPIIISL*K#.T
SW:Y056_HUMAN	H04	10285	2	1675.9	(+0.1)	3.063	0.396	0.966		R.NQAVQFISALVDELK.E
SW:Y056_HUMAN	H04	8669	2	1432.7	(+0.5)	3.241	0.395	0.987		R.TFAAQL*VQL*L*SK#.L
SW:Y056_HUMAN	H04	10289	2	1695.9	(-0.5)	2.857	0.266	0.850		R.NQAVQFISAL*VDEL*K#.E
SW:Y101_HUMAN	H20	4506	2	1516.6	(+0.6)	2.885	0.293	0.951		K.ENQIPEEAGSSGLGK.A
SW:Y101_HUMAN	H21	4416	2	1976.1	(+0.9)	5.059	0.529	1.000		K.DSEKENQIPEEAGSSGLGK.A
SW:Y539_HUMAN	H03	8282	2	1437.6	(+0.6)	3.098	0.357	0.981		R.EDVYDVVEGYIK#.I
SW:Y539_HUMAN	H03	8274	2	1429.6	(+0.6)	3.042	0.479	0.993		R.EDVYDVVEGYIK.I
SW:Y539_HUMAN	H03	10614	2	1786.0	(+0.8)	2.338	0.218	0.776	1	K.TAADDLVLVADLVVNILK.V
SW:YZX5_HUMAN	H20	6426	2	1361.5	(-0.1)	3.599	0.389	0.978	1	K.FGGVQELLNQK.K
SW:YZX5_HUMAN	H20	6372	2	1517.7	(+0.3)	2.555	0.286	0.840	1	K.K#FGGVQEL*L*NQK#.K
SW:YZX5_HUMAN	H20	3862	2	802.9	(+0.7)	2.279	0.192	0.840	1	K.SGEVAVLK.R
SW:YZX5_HUMAN	H21	6348	2	1361.5	(+0.9)	3.736	0.418	0.994	1	K.FGGVQELLNQK.K
SW:ZAP3_HUMAN	H03	5756	2	1157.2	(+0.9)	2.541	0.380	0.978	1	R.GHEEFPLDGR.N
SW:ZAP3_HUMAN	H03	6782	2	1245.4	(+0.5)	2.897	0.450	0.986	2	R.HFDQFWSAAK#.T
SW:ZAP3_HUMAN	H03	5142	3	2358.5	(+0.2)	4.424	0.494	0.996	3	K.SQAEPL*SGNK#EPL*ADTSSNQK#.N
SW:ZAP3_HUMAN	H03	5154	3	2330.5	(+0.6)	4.254	0.536	0.998	3	K.SQAEPLSGNKEPLADTSSNQK#.N
SW:ZAP3_HUMAN	H04	4613	3	2358.5	(-0.8)	3.702	0.182	0.107	3	K.SQAEPL*SGNK#EPL*ADTSSNQK#.N
SW:ZAP3_HUMAN	H03	10912	2	2083.3	(-0.1)	2.794	0.436	0.968	2	K.TLDDGFFPFIILDAINDR.V
SW:ZAP3_HUMAN	H05	4960	3	2330.5	(+0.6)	4.211	0.556	1.000	3	K.SQAEPLSGNKEPLADTSSNQK#.N
SW:ZN22_HUMAN	H17	5984	2	1470.6	(+0.4)	3.128	0.436	0.989	1	K.SFFQSSNL*IQHR.R
SW:ZN22_HUMAN	H17	5140	2	1539.7	(-0.4)	3.098	0.322	0.941	1	K.SFSQSSTL*FQHQK#.I
SWN:A32E_HUMAN	H16	8170	2	2029.3	(+0.5)	4.032	0.504	0.988	2	R.KLELSDNIISGGLEVLAEK.C
SWN:A32E_HUMAN	H16	6452	2	1357.5	(+0.4)	2.698	0.363	0.971	2	K.DL*STVEAL*QNL*K#.N
SWN:ANC5_HUMAN	H08	9399	3	2561.7	(+0.1)	3.998	0.411	0.996	6	K.DMEQFFDDLSDSFSGTEPEVHK.T
SWN:ANC5_HUMAN	H08	9381	2	1977.4	(+0.6)	3.868	0.406	0.992	5	R.LNQLLLPLQGPDITLSK.L
SWN:CC16_HUMAN	H09	9537	3	3228.5	(-0.5)	3.995	0.508	0.995	3	K.YNK#PSETVIPESVDGL*QENL*DVVSL*AER.H
SWN:CC16_HUMAN	H09	4453	2	986.1	(+0.8)	2.681	0.334	0.966	2	K.IYDAL*DNR.T
SWN:DOC2_HUMAN	H04	9799	2	1663.0	(+0.4)	3.156	0.367	0.979	1	K.DL*IAWQIPFL*GAGIK#.I
SWN:DOC2_HUMAN	H04	6507	2	1336.5	(+1.0)	2.946	0.428	0.988	1	K.GDSGGQLWVVTM.K
SWN:DOC2_HUMAN	H04	6503	2	1350.5	(+0.6)	2.542	0.298	0.712	1	K.GDSGGQL*WVVTM#.M
SWN:DOC2_HUMAN	H04	6955	2	1593.8	(+0.6)	2.275	0.112	0.352	1	R.ISSSPHSLYVFR.N
SWN:DOC2_HUMAN	H04	8311	2	1450.7	(+0.7)	2.564	0.376	0.971	1	K.L*GFPEIIMPGDVR.N
SWN:DOC2_HUMAN	H04	6457	2	1614.8	(-0.4)	2.647	0.300	0.200	1	R.L*SQTFL*QL*SDGDK#K#.T

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SWN:DOC2_HUMAN	H04	8291	2	1269.6	(+0.0)	3.200	0.291	0.945	2	K.LTQNVGLLGLLK.W
SWN:DOC2_HUMAN	H04	7207	2	1180.4	(+0.9)	2.544	0.407	0.983	1	K.M@L*VGDIQIR.K
SWN:DOC2_HUMAN	H04	6947	2	1576.8	(-0.3)	2.941	0.366	0.465	1	K.NKPVPDQIINFYK.S
SWN:DOC2_HUMAN	H04	8399	2	1700.0	(+0.3)	3.643	0.295	0.947	1	R.RPFGVAVM@DITDIK#.G
SWN:DOC2_HUMAN	H04	7425	2	1651.9	(+0.5)	3.997	0.435	1.000	2	K.VQSMNEIVQSNL*FK#.K
SWN:DOC2_HUMAN	H04	6465	2	1667.9	(-0.4)	3.613	0.496	1.000	2	K.VQSM@NEIVQSNL*FK#.K
SWN:DOC2_HUMAN	H04	7409	2	1637.9	(+0.9)	3.297	0.496	0.994	2	K.VQSMNEIVQSNLFLK.K
SWN:DOC2_HUMAN	H04	9007	2	1894.2	(+0.1)	3.536	0.449	0.895	2	K.YIPSVL*HDVEM@VFDAK#.L
SWN:DOC2_HUMAN	H04	7415	2	1229.4	(+1.0)	2.230	0.173	0.643	2	R.L*FESINNL*MK#.S
SWN:FNB3_HUMAN	H05	6980	2	1536.6	(+0.9)	2.290	0.287	0.894	3	K.EPAFEDITLESER.K
SWN:FNB3_HUMAN	H05	5518	2	987.1	(+0.8)	2.535	0.337	0.972	6	K.TPAEQLLSK.C
SWN:FNB3_HUMAN	H06	5126	2	987.1	(+0.7)	2.304	0.364	0.964	6	K.TPAEQLLSK.C
SWN:FNB3_HUMAN	H06	5070	2	1007.1	(+0.5)	2.224	0.395	0.968	6	K.TPAEQL*L*SK#.C
SWN:FUB1_HUMAN	H08	6507	3	2666.0	(+0.5)	4.755	0.525	1.000	3	K.GRPAPGFHHGDGPGNAVQEIM@IPASK#.A
SWN:FUB1_HUMAN	H09	6375	3	2666.0	(+0.8)	4.652	0.429	0.996	3	K.GRPAPGFHHGDGPGNAVQEIM@IPASK#.A
SWN:FUB1_HUMAN	H09	6787	3	2650.0	(+0.8)	4.401	0.550	1.000	3	K.GRPAPGFHHGDGPGNAVQEIMIPASK#.A
SWN:FUB1_HUMAN	H08	5045	2	1989.0	(-0.5)	3.750	0.477	1.000	3	K.IGGDAGTSL*NSNDYGYGGQK#.R
SWN:FUB1_HUMAN	H08	5051	2	1975.0	(-0.5)	3.414	0.425	0.980	3	K.IGGDAGTSLNSNDYGYGGQK.R
SWN:FUB1_HUMAN	H09	5127	2	1975.0	(-0.5)	3.424	0.495	0.987	3	K.IGGDAGTSLNSNDYGYGGQK.R
SWN:FUB1_HUMAN	H08	4475	2	1504.6	(-0.2)	2.926	0.324	0.367	3	R.IQFKPDDGTTPER.I
SWN:FUB1_HUMAN	H08	4467	2	1512.6	(-0.1)	2.880	0.294	0.291	3	R.IQFK#PDDGTTPER.I
SWN:FUB1_HUMAN	H08	2469	2	1512.6	(+1.0)	2.679	0.304	0.428	3	R.IQFK#PDDGTTPER.I
SWN:FUB1_HUMAN	H08	4593	2	1512.6	(-0.6)	2.378	0.136	0.027	3	R.IQFK#PDDGTTPER.I
SWN:FUB1_HUMAN	H08	4555	2	1504.6	(+0.0)	2.275	0.323	0.176	3	R.IQFKPDDGTTPER.I
SWN:FUB1_HUMAN	H09	4791	2	1512.6	(+0.1)	2.722	0.250	0.171	3	R.IQFK#PDDGTTPER.I
SWN:FUB1_HUMAN	H09	4797	2	1504.6	(-0.1)	2.546	0.271	0.163	3	R.IQFKPDDGTTPER.I
SWN:FUB1_HUMAN	H08	5685	2	1359.5	(+0.1)	2.743	0.333	0.928	3	K.IQIAPDSGGL*PER.S
SWN:FUB1_HUMAN	H09	5681	2	1359.5	(+0.7)	3.690	0.500	1.000	3	K.IQIAPDSGGL*PER.S
SWN:FUB1_HUMAN	H09	5691	2	1353.5	(+0.8)	2.370	0.270	0.890	3	K.IQIAPDSGGLPER.S
SWN:FUB1_HUMAN	H08	1423	2	1009.1	(+0.9)	2.225	0.243	0.875	12	K.K#IQNDAGVR.I
SWN:FUB1_HUMAN	H08	5781	2	978.1	(+0.5)	2.374	0.365	0.972	3	R.L*L*DQIVEK#.G
SWN:FUB1_HUMAN	H09	1621	2	1341.4	(+0.9)	2.607	0.509	0.991	3	K.RPLEDGDQPDAK.K
SWN:FUB1_HUMAN	H09	1639	2	1355.4	(+0.2)	2.556	0.341	0.911	3	K.RPL*EDGDQPDAK#.K
SWN:FUB1_HUMAN	H10	4983	2	1504.6	(+0.0)	3.233	0.404	0.611	3	R.IQFKPDDGTTPER.I
SWN:FUB2_HUMAN	H07	7802	2	1185.4	(-0.7)	3.188	0.295	0.871	2	R.IINDLLQSLR.S
SWN:FUB2_HUMAN	H07	6264	3	2206.5	(+0.5)	3.762	0.469	0.999	2	K.K#L*ASQGDSISSQL*GPIHPPPR.T
SWN:FUB2_HUMAN	H08	6429	3	2206.5	(+0.7)	4.936	0.419	0.999	2	K.K#L*ASQGDSISSQL*GPIHPPPR.T
SWN:FUB2_HUMAN	H07	4634	2	1317.5	(+0.3)	2.449	0.269	0.747	2	R.SVSL*TGAPESVQK#.A
SWN:FUB2_HUMAN	H07	5058	2	1317.5	(+0.7)	2.360	0.190	0.726	2	R.SVSL*TGAPESVQK#.A
SWN:FUB2_HUMAN	H08	4675	2	1317.5	(-0.5)	2.218	0.311	0.730	2	R.SVSL*TGAPESVQK#.A
SWN:FUB2_HUMAN	H07	7982	2	1227.5	(+0.9)	2.263	0.460	0.980	3	R.VPDGMVGLIIGR.G
SWN:FUB2_HUMAN	H07	5138	2	1355.5	(+0.8)	3.618	0.316	0.985	2	K.VQISPDSSGGLPER.S
SWN:FUB2_HUMAN	H07	5136	2	1361.5	(+0.7)	3.526	0.421	0.992	2	K.VQISPDSSGGL*PER.S
SWN:FUB2_HUMAN	H08	5135	2	1355.5	(+0.9)	3.169	0.313	0.975	2	K.VQISPDSSGGLPER.S
SWN:FUB2_HUMAN	H08	5131	2	1361.5	(+0.1)	2.810	0.353	0.945	2	K.VQISPDSSGGL*PER.S
SWN:FUB2_HUMAN	H08	5155	2	1355.5	(-0.3)	2.758	0.276	0.882	2	K.VQISPDSSGGLPER.S
SWN:FUB2_HUMAN	H13	4660	2	1317.5	(+0.1)	2.246	0.214	0.395	2	R.SVSL*TGAPESVQK#.A
SWN:MED8_HUMAN	H17	9878	3	2418.8	(+0.2)	4.883	0.447	0.998		R.LTWPSVLDSFALLSGQLNTLNK.V
SWN:MED8_HUMAN	H01	6088	2	2224.6	(+0.9)	2.710	0.222	0.212	1	R.NQVIPLVLSPPDRDEDLMR.Q
SWN:MED8_HUMAN	H02	6188	2	2224.6	(+0.9)	2.614	0.124	0.064	1	R.NQVIPLVLSPPDRDEDLMR.Q
SWN:MED8_HUMAN	H22	6768	2	2224.6	(+1.0)	2.583	0.109	0.039	1	R.NQVIPLVLSPPDRDEDLMR.Q
SWN:N133_HUMAN	H05	11818	3	2376.8	(+0.6)	4.763	0.552	0.995	3	R.SDLLSPLLSLGQYLWAASLAEK.Y
SWN:N133_HUMAN	H05	8706	2	1905.1	(+0.6)	2.238	0.492	0.981	3	R.EYEIPSNL*TPADVFFR.E
SWN:NEK7_HUMAN	H16	6522	2	1752.0	(-0.1)	3.015	0.375	0.466	1	K.AL*RPDMGYNTL*ANFR.I
SWN:NEK7_HUMAN	H16	5642	2	1434.6	(+0.1)	4.688	0.428	1.000	1	K.RPDVTVYVDVAK#.R
SWN:NEK7_HUMAN	H16	5644	2	1426.6	(+0.9)	4.332	0.560	0.996	1	K.RPDVTVYVDVAK#.R
SWN:NEK7_HUMAN	H16	7226	2	1180.4	(+0.5)	2.852	0.366	0.984	1	K.VQIFDLMDAK.A
SWN:PPIH_HUMAN	H19	5222	2	1033.1	(+0.7)	2.264	0.163	0.720		R.GPFADENFK#.L
SWN:PPIH_HUMAN	H19	2314	1	694.8	(-0.2)	2.017	0.381	0.001	9	K.HVVFVK#.I

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SWN:PPIH_HUMAN	H19	2248	1	694.8	(-0.2)	2.008	0.390	0.002	9	K.HVVFVK#.I
SWN:PPIH_HUMAN	H19	2016	2	1536.8	(+0.9)	2.761	0.222	0.242		R.KIENVPTGPNKPK.L
SWN:PPIH_HUMAN	H19	2014	2	1560.8	(-0.8)	2.651	0.281	0.057		R.K#IENVPTGPNK#PK#.L
SWN:PPIH_HUMAN	H19	2446	1	694.8	(-0.1)	1.968	0.391	0.000	9	K.HVVFVK#.I
SWN:PRP3_HUMAN	H07	2470	2	1272.4	(+0.6)	2.843	0.548	1.000	2	R.VL*GTEAVQDPTK#.V
SWN:PRP3_HUMAN	H08	2389	2	1272.4	(-0.0)	3.428	0.590	1.000	2	R.VL*GTEAVQDPTK#.V
SWN:PRP3_HUMAN	H08	5369	2	1220.4	(+0.8)	3.238	0.529	1.000	1	K.DVNVVVVEGGPK#.A
SWN:SA1_HUMAN	H05	9688	3	3210.4	(+0.7)	3.704	0.465	0.999		R.FNHSVEDLLQEGEEADDDDIYNVLSTLK.R
SWN:SA1_HUMAN	H05	6396	2	1272.4	(+0.5)	2.923	0.357	0.981	7	K.YYNDYGDIIK#.E
SWN:SA1_HUMAN	H05	5428	2	1066.2	(-0.3)	2.238	0.328	0.892		K.ALQSLYTNR.E
SWN:SA2_HUMAN	H05	8410	2	1279.5	(-0.1)	2.537	0.214	0.742	5	R.FAL*TFGL*DQL*K#.T
SWN:SA2_HUMAN	H05	9526	2	1628.0	(+0.6)	2.224	0.279	0.851	5	K.ITELFAVALPQLLAK.Y
SWN:SELH_HUMAN	H21	6936	2	1594.8	(+0.8)	2.970	0.370	0.639	1	K.FPEPQEVVEEL*K#K#.Y
SWN:SELH_HUMAN	H21	4370	2	1202.4	(+0.4)	3.399	0.572	0.998	2	R.K#AEAAVVAEAK#.R
SWN:SELH_HUMAN	H21	4466	2	1186.4	(+0.9)	2.909	0.557	1.000	2	R.KAEAAVVAEAK#.R
SWN:SELH_HUMAN	H21	4368	2	1186.4	(+1.0)	2.794	0.518	0.993	2	R.KAEAAVVAEAK#.R
SWN:SM1A_HUMAN	H04	4365	2	1098.2	(+0.6)	2.473	0.318	0.957	3	K.L*EEYITTSK#.Q
SWN:SM1A_HUMAN	H05	3998	2	1259.4	(+0.9)	2.294	0.231	0.825	3	K.NM@DAIIVDSEK#.T
SWN:SM1A_HUMAN	H05	2368	2	1105.2	(-0.2)	2.411	0.218	0.677	2	K.SGVISGGASDL*K#.A
SWN:SM1A_HUMAN	H05	4574	2	1098.2	(+0.5)	2.266	0.346	0.952	3	K.L*EEYITTSK#.Q
SWN:SMC2_HUMAN	H05	6312	2	1345.5	(+0.3)	2.674	0.310	0.910	1	K.AL*NHEIEEL*EK#.R
SWN:SMC2_HUMAN	H05	5514	2	1285.4	(+0.3)	3.544	0.301	0.966	1	R.AM@NVL*TEAEER.C
SWN:SMC2_HUMAN	H05	5754	2	1217.4	(+0.5)	2.295	0.421	0.976		K.EVITAQDQTVIK.L
SWN:SMC2_HUMAN	H05	5758	2	1225.4	(+0.5)	2.239	0.287	0.889		K.EVITAQDQTVIK#.L
SWN:SMC2_HUMAN	H05	6702	2	1289.5	(+0.8)	2.622	0.429	0.985	1	K.ILTTIEDLDQK.K
SWN:SMC2_HUMAN	H05	1766	2	1333.4	(+0.7)	2.629	0.230	0.281	1	K.LQEELSENDKK.I
SWN:SMC2_HUMAN	H05	6412	2	1203.3	(+0.9)	3.255	0.307	0.981	1	R.SLEDALAEAR.V
SWN:SMC2_HUMAN	H06	4748	2	1148.3	(+0.9)	2.635	0.406	0.984		K.TEEADLLQTK.L
SWN:SMC2_HUMAN	H05	6852	2	1529.7	(+0.7)	2.688	0.385	0.974	3	K.TIL*EEEITPTIQK#.L
SWN:SMC2_HUMAN	H06	5064	2	1285.4	(-0.2)	2.382	0.262	0.809	1	R.AM@NVL*TEAEER.C
SWN:SMC3_HUMAN	H05	7070	2	1426.6	(+0.9)	3.343	0.465	0.993	2	K.ALDQFVNFSEQK.E
SWN:SMC3_HUMAN	H05	7064	2	1440.6	(+0.4)	2.949	0.465	0.990	2	K.AL*DQFVNFSEQK#.E
SWN:SMC3_HUMAN	H05	5594	2	1487.5	(+0.3)	3.703	0.409	0.984	1	K.DL*QDEL*AGNSEQR.K
SWN:SMC3_HUMAN	H05	5588	2	1475.5	(+0.5)	3.366	0.377	0.988	1	K.DLQDELAGNSEQR.K
SWN:SMC3_HUMAN	H05	6654	2	1348.5	(+0.9)	2.523	0.505	0.990	2	R.ELGSLPQEAPEK.Y
SWN:SMC3_HUMAN	H05	5606	2	1374.5	(+0.4)	3.597	0.409	0.991	1	R.K#AEEL*GEL*EAK#.L
SWN:SMC3_HUMAN	H05	6890	2	1241.5	(+0.9)	2.987	0.377	0.987	2	R.KYEAQLTFK.Q
SWN:SMC3_HUMAN	H05	6888	2	1263.5	(+0.9)	2.326	0.385	0.967	2	R.K#YEAQL*TFK#.Q
SWN:SMC3_HUMAN	H05	6116	2	1164.3	(+0.8)	2.700	0.477	0.990	1	R.LALLHEGTGPR.V
SWN:SMC3_HUMAN	H05	8178	2	1573.9	(+0.9)	3.626	0.363	0.988	1	K.MNLPGEVTFPLPLNK.L
SWN:SMC3_HUMAN	H05	7904	2	1581.7	(+0.7)	2.569	0.538	0.992	1	K.NDVM@NL*L*ESAGFSR.S
SWN:SMC3_HUMAN	H05	7380	2	1660.8	(+0.0)	2.614	0.128	0.512	2	K.RL*DQVEQEL*NEL*R.E
SWN:SMC3_HUMAN	H05	5248	2	1122.3	(+0.4)	2.664	0.418	0.985	1	R.SMEVSTQLAR.A
SWN:SMC3_HUMAN	H05	5048	2	1045.1	(+0.7)	3.129	0.311	0.984	1	R.VDALNDEIR.Q
SWN:SMC3_HUMAN	H05	8182	2	1599.9	(-0.3)	2.314	0.231	0.625	1	K.MNL*PGEVTF*PL*NK#.L
SWN:SMC4_HUMAN	H04	5565	2	1432.5	(+0.7)	4.358	0.516	1.000	3	R.DTLVADNLDQATR.V
SWN:SMC4_HUMAN	H04	5567	2	1444.5	(-0.4)	3.336	0.447	0.984	3	R.DTL*VADNL*DQATR.V
SWN:SMC4_HUMAN	H04	6935	2	1463.6	(+0.8)	3.907	0.529*	0.796	2	K.FTQLDLEDVQVR.E
SWN:SMC4_HUMAN	H04	6931	2	1475.6	(+0.5)	2.487	0.381	0.971	2	K.FTQL*DL*EDVQVR.E
SWN:SMC4_HUMAN	H04	1987	2	1099.2	(+0.1)	2.262	0.392	0.936	3	R.HNTAVSQLTK.A
SWN:SMC4_HUMAN	H04	6913	3	2474.7	(+0.7)	4.324	0.360	0.977	3	K.IIDKEGDDYVIPNSNFYVSR.T
SWN:SMC4_HUMAN	H04	5391	2	1544.7	(+0.7)	4.297	0.474	1.000	2	K.NTNAEEESLPEIQK.E
SWN:SMC4_HUMAN	H04	1891	2	1309.5	(+0.8)	3.132	0.306	0.978	2	K.VIQENEHALQK.D
SWN:SMC4_HUMAN	H05	7168	2	1463.6	(+0.7)	2.657	0.251	0.921	2	K.FTQLDLEDVQVR.E
SWN:XRN2_HUMAN	H06	9114	3	3124.6	(-0.5)	3.884	0.366	0.921	4	K.GTK#PFK#PL*EQL*M@GVFPAASGNFL*PPSWR.K
SWN:XRN2_HUMAN	H07	5838	2	1469.7	(+0.6)	2.720	0.399	0.592	1	R.KPAAVLKPSDWEK.S

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GP:AB000516_1	R07	7705	2	1686.0	(-0.4)	3.909	0.397	0.987	2	K.FIAYQFTDTPQLQIK.S
GP:AB000516_1	R07	7717	2	1700.0	(-0.8)	3.601	0.303	0.886	2	K.FIAYQFTDTPQLQIK#.S
GP:AB000516_1	R07	6411	2	1507.8	(-0.5)	2.644	0.231	0.815	2	R.L*GYWNQQM@VPIK#.E
GP:AB000516_1	R07	8263	3	2266.6	(-0.1)	4.251	0.314	0.936	2	K.SFAMSAVITEGVK#PTL*SEL*EK#.F
GP:AB000516_1	R07	5809	2	1113.3	(+0.8)	2.512	0.375	0.973	2	R.FEGDTGL*IVR.V
GP:AB002330_1	R07	5629	3	1741.9	(+0.1)	3.918	0.441	0.999	1	K.K#PGQSFQEVEHYR.D
GP:AB002330_1	R07	7499	2	1598.8	(-0.3)	4.033	0.382	0.983	1	R.L*YL*VSDVL*YNSAK#.V
GP:AB002330_1	R07	6137	2	1342.5	(+0.0)	3.259	0.272	0.940	1	K.L*YSIL*QGDSPTK#.W
GP:AB002330_1	R07	7149	2	968.2	(+0.3)	2.203	0.275	0.911	1	R.NL*L*AL*IHR.M
GP:AB002330_1	R11	10212	2	1744.1	(+0.4)	3.629	0.491	1.000	1	K.LQNIFLGLVNIIEK.E
GP:AB007510_1	R05	7934	3	3181.5	(+0.2)	4.160	0.463	0.999	1	R.ASEM@AGPPQM@PNDFL*SFQDIATEAAHPIR.L
GP:AB007510_1	R01	10195	2	2084.4	(-0.6)	3.082	0.477	0.985	1	K.ATEPQMVLFLNLYDDWLK.T
GP:AB007510_1	R05	9636	2	2084.4	(-0.2)	3.374	0.536	1.000	1	K.ATEPQMVLFLNLYDDWLK.T
GP:AB007510_1	R01	6363	2	1417.5	(+0.4)	3.496	0.447	1.000	1	K.DGVWNL*QNEVTK#.E
GP:AB007510_1	R06	6452	2	1403.5	(-0.2)	2.707	0.225	0.858	1	K.DGVWNLQNEVTK.E
GP:AB007510_1	R05	7254	2	2137.2	(-0.8)	4.234	0.407	1.000	1	R.DINL*QDEDWNEFNINDINK#.I
GP:AB007510_1	R04	10314	3	2534.9	(+0.8)	3.839	0.376	0.998	1	R.LANQLLTDLVDDNYFYFLDLK.A
GP:AB007510_1	R05	10178	3	2534.9	(+0.4)	4.981	0.465	1.000	1	R.LANQLLTDLVDDNYFYFLDLK.A
GP:AB007510_1	R01	11721	3	3099.5	(+0.9)	5.661	0.569	1.000	1	R.LGNVDAFQLADGLQYIFAHVGLTGMRY.Y
GP:AB007510_1	R01	6913	2	1604.9	(-0.3)	3.329	0.508	1.000	1	R.LIVDHNIADYMTAK.N
GP:AB007510_1	R05	6982	2	1604.9	(+0.9)	2.850	0.301	0.952	1	R.LIVDHNIADYMTAK.N
GP:AB007510_1	R03	5889	2	1079.2	(+0.1)	2.920	0.325	0.966	1	K.TAEVAAL*IR.S
GP:AB007510_1	R05	6278	2	1079.2	(+0.6)	3.824	0.429	1.000	1	K.TAEVAAL*IR.S
GP:AB007510_1	R05	6286	2	1073.2	(+0.9)	3.684	0.308	0.987	1	K.TAEVAALIR.S
GP:AB007510_1	R01	10987	2	2173.5	(+0.0)	4.793	0.496	0.989	1	R.TDMIQALGGVEGILEHTLFG.K
GP:AB007510_1	R02	8906	3	2215.5	(+0.0)	4.133	0.441	0.999	1	R.TDM@IQAL*GGVEGIL*EHTL*FK#.G
GP:AB007510_1	R03	10256	3	2173.5	(+1.0)	3.715	0.476	0.999	1	R.TDMIQALGGVEGILEHTLFG.K
GP:AB007510_1	R01	8517	2	1562.9	(+0.0)	2.681	0.403	0.960	1	K.VPGL*PTPIENMIL*Y
GP:AB007510_1	R05	7426	2	1578.9	(-0.2)	2.229	0.273	0.784	1	K.VPGL*PTPIENM@IL*Y
GP:AB007510_1	R01	4389	2	1096.2	(-0.1)	2.594	0.355	0.950	1	K.YEL*QL*ANPK#.E
GP:AB007510_1	R01	4301	2	1096.2	(-0.4)	2.428	0.242	0.832	1	K.YEL*QL*ANPK#.E
GP:AB007510_1	R05	5554	2	1096.2	(+0.3)	2.357	0.367	0.958	1	K.YEL*QL*ANPK#.E
GP:AB007510_1	R02	5392	3	2232.4	(+0.6)	5.749	0.509	0.998	1	R.YLTEHPDPNNENIVGYNNK.K
GP:AB007510_1	R02	5386	3	2246.4	(+0.4)	5.311	0.401	1.000	1	R.YL*TEHPDPNNENIVGYNNK#.K
GP:AB007510_1	R03	5189	3	2246.4	(+0.1)	5.385	0.453	0.990	1	R.YL*TEHPDPNNENIVGYNNK#.K
GP:AB007510_1	R03	5191	3	2232.4	(+0.6)	4.897	0.428	0.983	1	R.YLTEHPDPNNENIVGYNNK.K
GP:AB007510_1	R04	5484	3	2246.4	(+0.4)	4.893	0.371	0.985	1	R.YL*TEHPDPNNENIVGYNNK#.K
GP:AB007510_1	R05	5620	3	2246.4	(+0.7)	5.302	0.484	0.993	1	R.YL*TEHPDPNNENIVGYNNK#.K
GP:AB007510_1	R18	10835	3	2534.9	(-0.0)	3.923	0.469	0.999	1	R.LANQLLTDLVDDNYFYFLDLK.A
GP:AB019494_1	R04	10370	2	1682.0	(+0.6)	4.684	0.450	1.000	1	R.AFLISLLNLFDDTAK.T
GP:AB019494_1	R05	10244	2	1682.0	(-0.2)	4.085	0.410	1.000	1	R.AFLISLLNLFDDTAK.T
GP:AB019494_1	R05	10254	2	1714.0	(-0.9)	2.292	0.249	0.415	1	R.AFL*ISL*L*NL*FDDTAK#.T
GP:AB019494_1	R06	10552	2	1682.0	(+0.2)	4.401	0.444	1.000	1	R.AFLISLLNLFDDTAK.T
GP:AB019494_1	R06	7204	3	2067.3	(+0.6)	3.913	0.432	0.998	1	K.FHL*QNTL*YPQYDPVYR.L
GP:AB019494_1	R04	6358	2	1214.3	(+0.2)	2.472	0.365	0.943	1	K.NL*YNNIL*SDK#.N
GP:AB019494_1	R04	10064	2	1533.8	(+0.8)	3.644	0.407	0.991	1	R.QLILEEIFTSLAR.L
GP:AB019494_1	R04	10052	2	1551.8	(+0.1)	2.972	0.426	0.975	1	R.QL*IL*EEIFTSL*AR.L
GP:AB019494_1	R05	9944	2	1533.8	(-0.2)	3.573	0.465	1.000	1	R.QLILEEIFTSLAR.L
GP:AB019494_1	R05	9938	2	1551.8	(-0.2)	3.006	0.435	0.982	1	R.QL*IL*EEIFTSL*AR.L
GP:AB019494_1	R04	8592	2	1299.6	(-0.7)	2.389	0.123	0.482	1	K.VL*EL*L*M@YFTK#.H
GP:AB019494_1	R04	5212	2	1048.2	(+0.7)	2.376	0.133	0.662	1	R.VL*GENAIAVR.T
GP:AB020713_1	R01	5869	2	1448.6	(+0.8)	4.168	0.547	0.964	1	K.AVDPTSGQLYGLAR.E
GP:AB020713_1	R01	5871	2	1460.6	(-0.0)	3.867	0.473	1.000	1	K.AVDPTSGQL*YGL*AR.E
GP:AB020713_1	R01	5883	2	1448.6	(-0.6)	2.285	0.212	0.658	1	K.AVDPTSGQLYGLAR.E
GP:AB020713_1	R02	5806	2	1448.6	(-0.8)	3.598	0.577	0.999	1	K.AVDPTSGQLYGLAR.E
GP:AB020713_1	R02	5802	2	1460.6	(-0.2)	3.460	0.418	0.985	1	K.AVDPTSGQL*YGL*AR.E
GP:AB020713_1	R03	5675	2	1460.6	(+0.1)	3.354	0.369	0.977	1	K.AVDPTSGQL*YGL*AR.E
GP:AB020713_1	R04	6034	2	1460.6	(+0.2)	3.305	0.512	0.999	1	K.AVDPTSGQL*YGL*AR.E
GP:AB020713_1	R01	1912	2	930.0	(+0.6)	2.329	0.361	0.960	1	R.DDFVQIGK#.G
GP:AB020713_1	R01	1056	2	940.0	(+0.8)	2.388	0.314	0.950	1	R.DGAASLSYR.V
GP:AB020713_1	R03	1094	2	940.0	(+0.9)	2.753	0.336	0.977	1	R.DGAASLSYR.V



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GP:AB020713_1	R01	5555	2	1547.7	(-0.8)	3.862	0.469	1.000	1	R.GVAIGQTSLTASVTNK.A
GP:AB020713_1	R03	5477	2	1561.7	(-0.2)	3.756	0.417	0.977	1	R.GVAIGQTSL*TASVTNK#.A
GP:AB020713_1	R01	7693	2	1622.9	(-0.1)	3.263	0.489	1.000	1	R.L*PSQYNFAMNVL*GR.V
GP:AB020713_1	R02	7194	2	1622.9	(-0.2)	3.843	0.559	0.994	1	R.L*PSQYNFAMNVL*GR.V
GP:AB020713_1	R03	6773	2	1059.3	(+0.4)	2.660	0.310	0.962	1	R.TVSVGLTLR.V
GP:AB020713_1	R01	1218	2	1022.2	(+0.6)	2.916	0.503	1.000	1	K.VPVVHVDEK.G
GP:AB020713_1	R01	1214	2	1030.2	(+0.4)	2.721	0.503	1.000	1	K.VPVVHVDEK#.G
GP:AB023196_1	R06	6018	2	1657.9	(-0.2)	3.540	0.502	1.000	4	K.TTNVLGAVNKPLSSAGK.Q
GP:AB023196_1	R06	6016	2	1685.9	(-0.2)	2.749	0.205	0.054	4	K.TTNVL*GAVNK#PL*SSAGK#.Q
GP:AB023196_1	R06	730	2	1069.1	(+0.3)	2.578	0.279	0.935	3	K.TPVTEQEEK#.L
GP:AB023482_13	R05	7976	2	1407.7	(+0.3)	2.284	0.186	0.553	2	K.FSPIFPPL*SYK#.H
GP:AB023482_13	R05	7980	2	1393.7	(+0.6)	2.276	0.188	0.655	2	K.FSPIFPPLSYK.H
GP:AB023482_13	R05	8138	2	1427.6	(+0.5)	2.324	0.375	0.954	2	R.FTL*WWSPTINR.A
GP:AB023482_13	R01	9135	2	1762.0	(+0.5)	2.289	0.466	0.976	2	K.GTYFPTWEGLFWEK.A
GP:AB023482_13	R02	8336	2	1776.0	(-0.1)	2.345	0.249	0.723	2	K.GTYFPTWEGL*FWEK#.A
GP:AB023482_13	R01	802	2	810.9	(+0.4)	2.391	0.273	0.940	2	K.HDVNLGR.S
GP:AB023482_13	R03	834	2	816.9	(+0.4)	2.570	0.354	0.981	2	K.HDVNL*GR.S
GP:AB023482_13	R05	904	2	816.9	(+0.6)	2.656	0.408	0.989	2	K.HDVNL*GR.S
GP:AB023482_13	R03	6427	2	958.1	(+0.9)	2.569	0.129	0.810	2	K.IDLTLNLR.L
GP:AB023482_13	R05	8062	2	996.2	(+0.9)	3.063	0.212	0.960	2	K.ISL*IQIFR.A
GP:AB023482_13	R01	8003	2	1510.6	(-0.4)	2.338	0.222	0.747	2	R.L*TL*EDL*EDSWDR.G
GP:AB023482_13	R05	6592	2	1093.2	(+0.9)	2.674	0.292	0.959	2	K.LWNLNNYR.T
GP:AB023482_13	R05	6578	2	1105.2	(+0.3)	2.351	0.228	0.894	2	K.L*WNL*NNYR.T
GP:AB023482_13	R05	7644	3	2146.4	(-0.5)	3.916	0.486	1.000	2	K.NL*NYL*HL*DYNFNL*K#PVK#.T
GP:AB023482_13	R01	7585	2	1354.6	(+0.8)	3.228	0.385	0.986	2	R.TILQHLSEAWR.C
GP:AB023482_13	R03	7229	2	1354.6	(+0.8)	2.610	0.372	0.973	2	R.TILQHLSEAWR.C
GP:AB023482_13	R05	7554	2	1366.6	(+0.3)	2.824	0.256	0.915	2	R.TIL*QHL*SEAWR.C
GP:AB023482_13	R05	5338	2	962.2	(-0.5)	2.381	0.265	0.871	2	K.VQMLLSDR.F
GP:AB023482_13	R05	7796	2	1510.6	(-0.7)	2.202	0.205	0.639	2	R.L*TL*EDL*EDSWDR.G
GP:AB029028_1	R06	6570	2	1443.6	(-0.6)	3.256	0.315	0.954	2	K.AGVQEFVDGL*HEK#.L
GP:AB029028_1	R06	5598	2	1001.1	(+0.8)	2.222	0.367	0.954	2	R.L*SEFIYSK#.T
GP:AB033061_1	R05	6504	2	1044.2	(+0.2)	2.407	0.371	0.946	5	K.FPFGIQQA#.S
GP:AB033061_1	R05	5272	2	1442.6	(+0.5)	2.824	0.482	0.983	4	K.SSIAL*TAPDAAADPK#.E
GP:AB043584_1	R08	7047	2	1145.3	(+0.2)	2.402	0.339	0.938	1	K.DPFL*GFTDAR.Q
GP:AB043584_1	R09	6490	2	1139.3	(+0.9)	2.786	0.245	0.941	1	K.DPFLGFTDAR.Q
GP:AB043584_1	R09	6484	2	1145.3	(+0.4)	2.583	0.183	0.848	1	K.DPFL*GFTDAR.Q
GP:AB043584_1	R08	8163	2	1704.9	(+0.5)	3.991	0.458	1.000	1	R.GGGFAPGTEPFPGFLFPR.K
GP:AB043584_1	R08	8171	2	1710.9	(-0.1)	3.312	0.398	0.974	1	R.GGGFAPGTEPFPGFL*FPR.K
GP:AB043584_1	R09	7734	2	1704.9	(-0.3)	3.792	0.424	0.987	1	R.GGGFAPGTEPFPGFLFPR.K
GP:AB043584_1	R09	5904	2	1600.8	(+0.1)	2.561	0.399	0.956	1	R.IYL*EPGPASSL*TPR.L
GP:AB058705_1	R08	2348	2	1088.3	(+0.5)	3.029	0.280	0.969	2	K.GAVLHHLVKN.H
GP:AB058705_1	R08	5719	2	1098.3	(+1.0)	2.675	0.406	0.983	1	R.KPALFPEPAK.T
GP:AB058705_1	R08	7073	2	1250.4	(+0.8)	2.668	0.415	0.983	2	K.LLEDTLFPSSK.K
GP:AB058705_1	R08	7069	2	1276.4	(+0.8)	2.649	0.458	0.983	2	K.L*L*EDTL*FPSSK#.K
GP:AB058705_1	R08	6097	2	1108.2	(+0.8)	2.380	0.388	0.974	2	R.NVLQFTEEK.E
GP:AB058705_1	R08	1850	2	997.1	(-0.5)	2.478	0.393	0.969	1	K.SALFSESQK.A
GP:AB058705_1	R08	2330	2	1108.3	(+0.1)	2.296	0.171	0.580	2	K.GAVL*HHL*VKN#.H
GP:AB065003_1	R07	7227	3	2567.6	(+1.0)	5.195	0.525	0.996	2	K.LEFFGFEDHETGGDEGGSSNYK.I
GP:AB065003_1	R07	8287	2	1763.9	(+0.5)	3.073	0.464	0.990	2	R.TGL*FEWDNDFEDIR.S
GP:AB088099_1	R04	5480	3	2471.6	(-0.3)	5.288	0.462	1.000	2	R.GPGAPGL*AHL*QESQAGSDTDVEEGK#.A
GP:AB088099_1	R04	4778	2	1168.3	(+0.1)	2.629	0.480	0.978	2	K.TPETL*VPTAPK#.L
GP:AB088099_1	R05	4782	2	1168.3	(-0.1)	2.665	0.287	0.904	2	K.TPETL*VPTAPK#.L
GP:AB088099_1	R04	6422	2	1083.3	(+0.7)	2.556	0.347	0.884	2	K.VL*FTGVVDAR.G
GP:AB088099_1	R05	4858	2	1168.3	(+0.6)	2.358	0.351	0.936	2	K.TPETL*VPTAPK#.L
GP:AC004611_2	R07	5395	2	2126.2	(-0.9)	3.531	0.322	0.888	2	K.AIEDEGGNPDEIEITSEGNK#.K
GP:AC004611_2	R07	5305	2	2262.3	(-0.9)	3.042	0.118	0.010	2	K.AIEDEGGNPDEIEITSEGNK#.K#.T

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GP:AF072718_1	R04	6242	2	1363.6	(+0.7)	2.684	0.344*	0.311	1	K.FLDQSLGEQVVK.N
GP:AF072718_1	R04	7708	2	1370.6	(+1.0)	2.262	0.421	0.955	1	K.FL*GAVAMDL*GIDK#.V
GP:AF072718_1	R04	10258	2	1868.2	(-0.3)	3.192	0.436	0.977	1	K.K#DWL*FDMVTTWFGAK#.K
GP:AF072718_1	R04	1056	2	1135.3	(+0.5)	3.829	0.499	0.941	1	K.L*AVSAQSEPAR.V
GP:AF072718_1	R04	9852	2	1296.6	(+0.8)	3.866	0.532	0.999	1	R.LLFSFLTITK.L
GP:AF072718_1	R04	9838	2	1328.6	(-0.5)	2.876	0.378	0.966	1	R.L*L*FSFL*TL*ITK#.L
GP:AF072718_1	R04	6708	2	1197.4	(+0.8)	2.237	0.152	0.302	1	K.YILDYPLGDK.L
GP:AF073771_1	R07	6757	2	1730.8	(+0.6)	2.967	0.443	0.982	1	R.DSEPSSTVSL*NGTFFK#.M
GP:AF073771_1	R07	5803	2	1240.4	(+0.5)	2.454	0.195	0.796	1	R.VAL*EFGSEEPH.H
GP:AF112222_1	R08	5545	3	2916.9	(+0.3)	6.636	0.523	0.999	1	R.EEEELEETGNQHNDVEIEEAGEEEEEK.E
GP:AF112222_1	R08	5707	3	2916.9	(+0.4)	5.683	0.505	1.000	1	R.EEEELEETGNQHNDVEIEEAGEEEEEK.E
GP:AF112222_1	R08	5549	3	2930.9	(+0.6)	5.334	0.572	1.000	1	R.EEEL*EETGNQHNDVEIEEAGEEEEEK#.E
GP:AF112222_1	R08	5627	3	2916.9	(+0.7)	4.455	0.411	0.779	1	R.EEEELEETGNQHNDVEIEEAGEEEEEK.E
GP:AF112222_1	R08	1128	2	1304.4	(+0.7)	2.909	0.333	0.430	2	K.FK#QESTVATER.Q
GP:AF112222_1	R08	1130	2	1296.4	(+0.2)	2.572	0.203	0.062	2	K.FKQESTVATER.Q
GP:AF112222_1	R08	5495	2	1100.2	(-0.3)	3.206	0.406	0.983	2	R.IEFAEQINK#.M
GP:AF112222_1	R08	5479	2	1092.2	(-0.3)	2.755	0.293	0.952	2	R.IEFAEQINK.M
GP:AF112222_1	R08	1234	2	1109.2	(-0.2)	2.591	0.219	0.877	2	K.L*EVQAEER.K
GP:AF112222_1	R08	1236	2	1103.2	(-0.3)	2.550	0.195	0.834	2	K.LEVQAEER.K
GP:AF112222_1	R08	5535	2	998.2	(+0.7)	2.643	0.239	0.912	2	R.LLALSGPGGGGR.G
GP:AF112222_1	R08	5559	2	1016.2	(-0.6)	2.600	0.327	0.943	2	R.L*L*AL*SGPGGGGR.G
GP:AF112222_1	R08	5661	2	938.1	(+0.9)	2.828	0.315	0.973	1	K.MNALFEGR.R
GP:AF112222_1	R08	5655	2	944.1	(+0.0)	2.673	0.394	0.979	1	K.MNAL*FEGR.R
GP:AF112222_1	R08	5815	2	1256.4	(+0.5)	2.720	0.212	0.885	2	R.RIEFAEQINK#.M
GP:AF112222_1	R08	7723	2	1263.5	(-0.1)	2.546	0.213	0.774	2	R.IFGL*L*M@GTL*QK#.F
GP:AF113534_1	R11	1356	2	974.1	(+0.8)	2.656	0.278*	0.362	1	R.GQLEQITGK.G
GP:AF113534_1	R11	1362	2	988.1	(+0.4)	2.344	0.264	0.888	1	R.GQL*EQITGK#.G
GP:AF113534_1	R12	7444	2	1602.8	(+0.9)	2.668	0.357	0.961		K.TIPSWATLSASQLAR.A
GP:AF144074_1	R09	5694	2	1637.7	(+0.9)	3.530	0.418	0.661	2	K.AEKDEPGAWEEFTK.T
GP:AF144074_1	R09	732	2	978.1	(+0.3)	2.762	0.537	1.000	3	R.AHAHLDTGR.R
GP:AF144074_1	R09	5776	2	1683.8	(-1.0)	3.493	0.487	1.000	2	R.DENSVELTMAEGPYK.I
GP:AF144074_1	R09	5782	2	1697.8	(-0.4)	2.818	0.273	0.873	2	R.DENSVEL*TMAEGPYK#.I
GP:AF144074_1	R10	6345	2	1683.8	(+0.5)	3.001	0.517	1.000	2	R.DENSVELTMAEGPYK.I
GP:AF144074_1	R09	5768	2	1309.4	(+0.8)	2.331	0.289	0.911	2	K.DEPGAWEETFK.T
GP:AF144074_1	R09	7776	3	2158.4	(+0.5)	3.878	0.445	0.999	3	R.DVHNIYGL*YVHMATADGL*R.Q
GP:AF144074_1	R09	6986	2	1962.1	(+1.0)	4.253	0.488	1.000	3	R.FGAVWTGDNTAEWDHL*K#.I
GP:AF144074_1	R09	6980	2	1948.1	(-0.5)	3.934	0.469	1.000	3	R.FGAVWTGDNTAEWDHLK.I
GP:AF144074_1	R09	6162	2	1175.3	(-0.2)	3.238	0.210	0.258	2	R.FRIDELEPR.R
GP:AF144074_1	R09	6150	2	1181.3	(+0.6)	2.515	0.240	0.180	2	R.FRIDELE*EPR.R
GP:AF144074_1	R10	6927	2	1175.3	(+0.4)	2.666	0.194	0.123	2	R.FRIDELEPR.R
GP:AF144074_1	R10	7165	2	1175.3	(+0.5)	2.648	0.291	0.318	2	R.FRIDELEPR.R
GP:AF144074_1	R10	6845	2	1175.3	(+0.6)	2.604	0.150	0.086	2	R.FRIDELEPR.R
GP:AF144074_1	R10	7089	2	1175.3	(+0.4)	2.336	0.158	0.054	2	R.FRIDELEPR.R
GP:AF144074_1	R09	5664	2	1129.3	(+0.6)	2.345	0.139	0.612	2	R.GLLEFEHQR.A
GP:AF144074_1	R09	5668	2	1141.3	(+0.2)	2.259	0.185	0.701	2	R.GL*L*EFEHQR.A
GP:AF144074_1	R10	6237	2	1129.3	(+0.5)	2.641	0.250	0.940	2	R.GLLEFEHQR.A
GP:AF144074_1	R10	6417	2	1233.5	(+0.6)	3.269	0.331	0.982	2	R.KLVAIVDPHIK.V
GP:AF144074_1	R09	5792	2	1105.4	(+0.9)	2.884	0.288	0.966	2	K.LVAIVDPHIK.V
GP:AF144074_1	R10	6363	2	1105.4	(+1.0)	2.544	0.333	0.963	2	K.LVAIVDPHIK.V
GP:AF144074_1	R10	10027	3	3649.2	(-0.6)	4.029	0.526	0.999	2	R.LYNLDVFQYELYNPMALYGSVPVLLAHNPHR.D
GP:AF144074_1	R09	5580	2	1935.1	(+0.9)	4.423	0.544	1.000	2	K.MMDYL*QGSGETPQTDV.R.W
GP:AF144074_1	R09	5574	2	1929.1	(-0.8)	4.345	0.495	1.000	2	K.MMDYLQGSGETPQTDV.R.W
GP:AF144074_1	R10	6151	2	1929.1	(+0.3)	4.431	0.591	0.998	2	K.MMDYLQGSGETPQTDV.R.W
GP:AF144074_1	R08	6017	2	1067.2	(+0.8)	2.291	0.254	0.883	3	K.NPEPELLV.R.W
GP:AF144074_1	R09	5292	2	1067.2	(+0.7)	2.461	0.326	0.930	3	K.NPEPELLV.R.W
GP:AF144074_1	R09	7988	2	2536.8	(-0.2)	2.903	0.461	0.977	2	R.QYASLTGTQALPPLFSLGYHQS.R.W
GP:AF144074_1	R09	2110	2	1146.3	(+0.6)	2.312	0.206	0.062	2	R.SIRPGLSPYR.A
GP:AF144074_1	R09	7294	2	1246.4	(+0.9)	4.149	0.487	1.000		K.VNLTLSIWDK.I
GP:AF144074_1	R09	7292	2	1266.4	(-0.1)	2.941	0.192	0.841		K.VNL*TL*GSIWDK#.I
GP:AF144074_1	R09	6394	2	1368.6	(+0.7)	3.868	0.511	0.998	2	R.VPDVL*VADPPIAR.L
GP:AF144074_1	R09	6386	2	1362.6	(-0.1)	2.383	0.294	0.871	2	R.VPDVLVADPPIAR.L
GP:AF144074_1	R10	6361	2	1119.4	(+0.2)	2.207	0.259	0.769	2	K.L*VAIVDPHIK#.V

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GP:AF155827_1	R10	8265	3	2171.6	(+0.8)	4.320	0.503	0.975	1	R.K#GTL*QIHPVVITSFEIAM@R.D
GP:AF155827_1	R09	6228	2	1482.7	(-0.4)	2.799	0.234	0.885	1	K.KQEIFYTAIVNR.T
GP:AF155827_1	R10	7407	2	1490.7	(-0.2)	4.066	0.496	1.000	1	K.K#QEIFYTAIVNR.T
GP:AF155827_1	R10	7427	2	1482.7	(+0.2)	3.734	0.409	0.999	1	K.KQEIFYTAIVNR.T
GP:AF155827_1	R10	6099	2	1185.3	(+0.0)	2.623	0.292	0.924	1	R.TIANMFGSSEK.E
GP:AF155827_1	R10	6109	2	1193.3	(-0.4)	2.361	0.291	0.853	1	R.TIANMFGSSEK#.E
GP:AF155827_1	R10	8501	2	1503.7	(+0.3)	3.377	0.345	0.985	1	R.WYQVEGMEWL*R.M
GP:AF155827_1	R10	2314	2	1102.2	(+0.4)	2.459	0.265	0.929	1	K.YLIVDEGHR.I
GP:AF155827_1	R10	2296	2	1108.2	(-0.6)	2.380	0.290	0.893	1	K.YL*IVDEGHR.I
GP:AF155827_1	R11	6452	2	1482.7	(-0.4)	3.032	0.320	0.961	1	K.KQEIFYTAIVNR.T
GP:AF173937_1	R25	7958	2	1294.4	(+0.1)	2.459	0.377	0.955		K.ELEALDEVFTK.V
GP:AF173937_1	R25	7756	3	2669.9	(+0.7)	5.317	0.390	0.996		R.ILNEDGSPNLDFKPEDQPHFDIK.D
GP:AF173937_1	R25	7760	3	2697.9	(+0.2)	3.910	0.313	0.899		R.IL*NEDGSPNL*DFK#PEDQPHFDIK#.D
GP:AF173937_1	R25	7190	2	1725.9	(-0.3)	4.190	0.504	1.000		R.YGGEEEDQPIYL*AVK#.G
GP:AF173937_1	R25	7186	2	1711.9	(+0.9)	4.107	0.482	0.999		R.YGGEEEDQPIYLAVK.G
GP:AF173937_1	R25	6282	2	1017.1	(+0.7)	2.385	0.484	0.982		K.GVVFVDTSGK#.E
GP:AF177387_1	R06	1546	2	1456.5	(+0.0)	3.611	0.522	0.990	6	K.SEDSSGAAGL*SGL*HR.T
GP:AF177387_1	R06	1706	2	1080.1	(-0.3)	2.559	0.265	0.916	5	R.AEDNFNLEK.E
GP:AF180425_1	R06	6636	2	1553.7	(+0.7)	3.894	0.491	1.000	1	K.ALGLSTDDAYEELR.Q
GP:AF180425_1	R06	6622	2	1571.7	(-1.0)	3.110	0.327	0.886	1	K.AL*GL*STDDAYEEL*R.Q
GP:AF180425_1	R06	8700	2	1535.7	(+0.4)	3.034	0.393	0.972	1	R.LFNWLSETLANAR.H
GP:AF418569_1	R07	9259	2	1242.4	(+0.6)	2.630	0.216	0.890	3	K.FPEL*FNWFK#.N
GP:AF418569_1	R07	6271	2	1309.4	(-0.3)	2.997	0.274	0.922	3	K.HGGGTESL*FFDK#.V
GP:AF418569_1	R07	8859	3	2164.4	(+0.5)	4.068	0.422	1.000	3	K.L*QFGSQPVYNDFL*DIMK#.E
GP:AF418569_1	R07	8779	3	1593.7	(+0.9)	3.777	0.319	0.997	3	K.SL*L*NEIESIYDER.Q
GP:AJ006778_1	R04	9840	3	2110.5	(+0.3)	4.309	0.422	0.996		K.DKEQSSVLITLLLPFLHR.G
GP:AJ006778_1	R04	7668	3	2546.8	(-0.4)	4.319	0.451*	0.090		K.DL*VQL*THYHDPEDFFENM@K#.H
GP:AJ006778_1	R04	7240	3	2562.8	(-0.9)	3.703	0.162	0.408		K.DL*VQL*THYHDPED@DFFENM@K#.H
GP:AJ006778_1	R04	7648	2	1478.7	(-0.5)	3.539	0.441	0.999		R.FETFQTITSYIK.E
GP:AJ006778_1	R04	6480	3	3505.6	(+0.3)	3.715	0.460	0.999		K.GMVAEEIEEPAAGDDEEL*EEEAVPQDESSQK#.K
GP:AJ006778_1	R05	10962	3	2185.5	(+1.0)	4.291	0.426	0.999		R.GNIAEDTEVDILVTQNLK.H
GP:AJ006778_1	R04	8354	2	1586.8	(-0.2)	2.676	0.151	0.591		K.GPL*SQEAL*MEL*FPK#.L
GP:AJ006778_1	R04	9114	3	2448.8	(-0.2)	3.800	0.315	0.985		R.GYQVHVL*TFTVHM@L*L*QGL*TNK#.L
GP:AJ006778_1	R04	6842	3	2083.3	(+0.8)	3.825	0.363	0.997		R.HDVVQTAVPDGPL*QEVPL*R.Y
GP:AJ006778_1	R04	6290	2	1244.3	(+0.9)	2.208	0.417	0.970		R.HLDDINFVDR.F
GP:AJ006778_1	R05	6356	2	1244.3	(+0.1)	2.372	0.324	0.925		R.HLDDINFVDR.F
GP:AJ006778_1	R04	9232	2	1814.1	(-0.2)	2.939	0.289	0.905		K.IIEDL*GVHFL*QYVL*K#.E
GP:AJ006778_1	R04	7388	3	2463.7	(+0.3)	3.868	0.432	0.999		R.IL*NHFVDVQL*PESMEDDGL*SER.Q
GP:AJ006778_1	R04	6420	2	1264.5	(+0.2)	2.971	0.368	0.974		R.LGNVNDIHR.I
GP:AJ006778_1	R04	8904	3	1973.2	(+0.9)	3.924	0.431	0.999		K.M@VTDIFL*DWESYQFR.T
GP:AJ006778_1	R04	9638	2	1767.1	(+0.8)	3.043	0.367	0.961		R.NEQFPVLDHLLSIK.L
GP:AJ006778_1	R04	8288	2	1440.7	(+0.6)	3.136	0.440	0.990		R.NFAAESFTFL*MR.K
GP:AJ006778_1	R04	6780	2	1398.6	(+0.7)	3.150	0.435	0.983		K.NIQGTITGDILPR.L
GP:AJ006778_1	R04	6772	2	1404.6	(+0.4)	2.326	0.407	0.965		K.NIQGTITGDIL*PR.L
GP:AJ006778_1	R05	10270	3	1972.3	(-0.1)	4.105	0.463	1.000		K.NSFAYQPL*L*DL*VVQL*AR.D
GP:AJ006778_1	R05	10290	3	1948.3	(+0.8)	3.747	0.386	0.999		K.NSFAYQPLLDLVVQLAR.D
GP:AJ006778_1	R06	10584	3	1972.3	(+0.1)	3.817	0.384	0.997		K.NSFAYQPL*L*DL*VVQL*AR.D
GP:AJ006778_1	R04	7232	3	2917.1	(-0.6)	4.327	0.470	1.000		K.SVGDESWEQTQEGDVGL*YHEQL*AL*K#.T
GP:AJ006778_1	R04	7236	3	2891.1	(+0.6)	4.136	0.510	0.999		K.SVGDESWEQTQEGDVGL*YHEQLALK.T
GP:AJ006778_1	R04	8366	2	1820.2	(-0.6)	2.998	0.297	0.917		K.YPL*VFSPQM@VGFYK#.Q
GP:AJ006778_1	R04	8928	2	1804.2	(-0.4)	2.213	0.186	0.449		K.YPL*VFSPQM@VGFYK#.Q
GP:AJ006778_1	R06	6350	2	1250.3	(+0.9)	2.574	0.309	0.942		R.HL*DDINFVDR.F
GP:AK001461_1	R04	6914	3	2608.8	(+0.4)	4.932	0.521	0.996	1	K.FDGSENRPFSPL*NNISSTVTK#.N
GP:AK001461_1	R06	7118	3	2608.8	(+0.2)	5.444	0.520	0.997	1	K.FDGSENRPFSPL*NNISSTVTK#.N
GP:AK001461_1	R04	6698	3	1668.9	(-0.1)	3.730	0.222	0.821		K.L*IAEQL*QENL*IEK#.G
GP:AK001461_1	R04	6694	2	1668.9	(+0.4)	3.466	0.345	0.977		K.L*IAEQL*QENL*IEK#.G
GP:AK001461_1	R04	6790	2	1345.5	(-0.2)	2.447	0.284	0.850	1	K.STDFVFIPEPK#.D
GP:AK001461_1	R04	5514	2	1315.5	(-0.3)	2.419	0.182	0.035	1	K.VK#GEIL*L*EEEK#.S
GP:AK001461_1	R06	6852	2	1668.9	(-0.7)	3.286	0.288	0.938		K.L*IAEQL*QENL*IEK#.G

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GP:AK001599_1	R03	6833	2	1434.6	(+0.7)	2.752	0.237	0.915	3	R.GLEMEGWVVER.R
GP:AK001599_1	R14	9219	2	2124.4	(-0.2)	3.655	0.475	1.000	4	K.GWGEL*EFGAGDL*QGPL*FGL*K#.L
GP:AK001599_1	R14	8783	2	2131.4	(+0.2)	2.209	0.279	0.777	3	R.LFNLVHQAYEVLSDPQTR.A
GP:AK022932_1	R03	7245	3	1895.1	(+1.0)	4.466	0.569	1.000		K.HANTL*ITAVHDSFVAVGK#.D
GP:AK022932_1	R04	7492	3	1895.1	(+0.8)	4.324	0.526	1.000		K.HANTL*ITAVHDSFVAVGK#.D
GP:AK022932_1	R04	6830	2	1324.6	(-0.2)	2.722	0.329	0.931		K.L*VIPL*VVHSAQK#.V
GP:AK022932_1	R04	9664	2	1911.2	(+0.4)	4.131	0.478	1.000		R.SGSFINSLQLLEELGFR.S
GP:AK022932_1	R05	9508	2	1935.2	(-0.7)	2.795	0.223	0.835		R.SGSFINSL*L*QL*EEL*GFR.S
GP:AK022932_1	R06	7632	3	1895.1	(+0.9)	5.753	0.570	1.000		K.HANTL*ITAVHDSFVAVGK#.D
GP:AK023383_1	R15	5959	3	1870.1	(+0.4)	5.334	0.527	1.000	1	K.SM@L*QATAEANNL*AAAASAK#.D
GP:AK023383_1	R15	9021	3	2495.7	(-0.1)	3.894	0.369	0.949	1	R.DWSFPYEYSYGL*QGGMAFL*DK#.R
GP:AK074587_1	R01	7219	2	1365.5	(+0.4)	2.518	0.331	0.943		R.FYSL*WDTGYAK#.I
GP:AK074587_1	R01	8907	3	2494.7	(+1.0)	5.057	0.539	1.000		R.STHHLASHGFYEFLNWFDER.A
GP:AK074587_1	R01	8909	3	2506.7	(-0.3)	4.952	0.439	0.997		R.STHHL*ASHGFYEFL*NWFDER.A
GP:AK074587_1	R02	8182	3	2506.7	(+0.6)	5.907	0.510	0.999		R.STHHL*ASHGFYEFL*NWFDER.A
GP:AK090435_1	R04	6954	3	2531.7	(+0.2)	4.100	0.482	0.990	2	R.HYEM@QQQQFQHL*YQEWER.E
GP:AK090435_1	R04	8146	2	1671.9	(-0.3)	2.452	0.263	0.832	2	R.VLSLDDYFITEVEK.E
GP:AK093060_1	R02	5086	2	1477.7	(+0.1)	3.327	0.119*	0.505	5	R.FLEQQNQVLETK.W
GP:AK093060_1	R25	7060	2	1359.5	(+0.6)	3.042	0.120	0.754	3	R.DLDLDSIAEVR.A
GP:AL022398_2	R14	11541	3	2281.6	(-0.2)	4.378	0.162	0.837	1	K.MVIL*QDL*L*STL*IQASDSSWK#.G
GP:AL022398_2	R14	5315	2	1125.3	(+0.4)	2.216	0.216	0.773	1	K.VL*L*EMEDQK#.N
GP:AL022398_2	R20	7088	3	2353.6	(+0.7)	5.906	0.530	1.000	1	R.VQQLQGLLQNQSLQLQEKEK.L
GP:AL161797_1	R12	6142	3	2360.5	(+0.4)	5.129	0.520	0.992		K.DIELHLESSSHQETLDHIQK.Q
GP:AL161797_1	R12	5686	3	2954.9	(+0.5)	5.636	0.438	0.999		K.GENPFIEIQDHSQDQQIEGDEEDEEK#.I
GP:AL161797_1	R12	6140	3	2386.5	(-0.6)	4.662	0.460	1.000		K.DIEL*HL*ESSSHQETL*DHIQK#.Q
GP:AL832200_1	R05	5098	3	2558.8	(+0.1)	4.370	0.411	0.994		R.IPQNPSPTHQQQNAPVTVIQSK#.A
GP:AL832200_1	R05	10556	3	2356.7	(+0.6)	3.797	0.312	0.987		R.QLGLDTLGNIAAELLDPVDFK.T
GP:AL834470_1	R09	7840	3	2828.0	(+0.9)	4.681	0.481	0.999		K.DEEEDQTLVNLDTYTSDLHFQVSK.D
GP:AL834470_1	R09	7252	2	1836.1	(-0.3)	2.518	0.153	0.498		K.EVEGDDVPESIML*EMK#.A
GP:AL834470_1	R09	6644	2	1041.2	(+0.9)	2.815	0.302	0.971		K.FPTL*WSGAR.S
GP:AL834470_1	R10	7909	2	1041.2	(+1.0)	2.482	0.299	0.931		K.FPTL*WSGAR.S
GP:AL834470_1	R09	922	2	1175.3	(+0.3)	2.826	0.496	0.999		K.GL*EEPEM@DPK#.S
GP:AL834470_1	R09	6956	2	1950.2	(-0.3)	2.250	0.200	0.585		R.KEVEGDDVPESIMLEMK.A
GP:AL834470_1	R09	6116	2	1557.8	(+0.3)	4.926	0.513	0.929		R.K#VVVVVPNEEDWK#.K
GP:AL834470_1	R09	870	2	1383.4	(+0.1)	3.193	0.454	0.974		R.SGDETPGSEVPGDK#.A
GP:AL834470_1	R09	6260	2	1413.6	(+0.4)	2.334	0.118	0.276		K.VVVVVPNEEDWK.K
GP:AL834470_1	R09	4646	2	1126.3	(-0.1)	3.474	0.471	0.998		R.YGGQPLFSEK.F
GP:AL834470_1	R09	4724	2	1126.3	(+0.9)	3.357	0.438	0.997		R.YGGQPLFSEK.F
GP:AL834470_1	R09	4566	2	1126.3	(+0.2)	3.113	0.422	0.984		R.YGGQPLFSEK.F
GP:AL834470_1	R11	4744	2	1126.3	(+0.2)	2.778	0.334	0.962		R.YGGQPLFSEK.F
GP:AL834470_1	R09	7238	2	1620.9	(+0.8)	2.895	0.252	0.927		R.YNVL*GAETVL*NQMR.M
GP:AL834470_1	R09	6322	2	1636.9	(+0.6)	2.499	0.303	0.922		R.YNVL*GAETVL*NQM@R.M
GP:AL834470_1	R10	8227	2	1620.9	(-1.0)	2.505	0.231	0.551		R.YNVL*GAETVL*NQMR.M
GP:AL834470_1	R11	7374	2	1608.9	(-0.3)	3.017	0.299	0.943		R.YNVLGAETVLNQM.R.M
GP:AL834470_1	R12	4712	2	1126.3	(+0.6)	2.283	0.365	0.957		R.YGGQPLFSEK.F
GP:AY186731_1	R12	5350	2	1302.4	(+0.7)	3.119	0.461	0.990		R.GEGLVGDGPVDMR.T
GP:AY186731_1	R12	6004	2	1478.6	(+0.7)	3.877	0.582	0.999		R.GLLASDLNTDGDGM.R.V
GP:AY186731_1	R12	5338	2	1308.4	(-0.4)	2.539	0.247	0.840		R.GEGL*VGDGPVDMR.T
GP:BC039843_1	R07	7031	3	2805.1	(+0.3)	4.147	0.477	1.000	1	K.ASHHIYPYSSSQDDEEWRPVMR.K
GP:BC039843_1	R07	6601	3	2827.1	(+0.9)	4.145	0.411	0.993	1	K.ASHHIYPYSSSQDDEEWR*RPVM@R.K
GP:BC039843_1	R07	7793	2	2023.3	(-0.7)	2.706	0.441	0.972	1	K.DMEDPTPVPNIEEVVLPK.N
GP:BC039843_1	R07	7789	2	2037.3	(-0.7)	2.438	0.243	0.720	1	K.DMEDPTPVPNIEEVV*L*PK#.N
GP:BC039843_1	R07	7575	2	2053.3	(-0.7)	2.361	0.273	0.767	1	K.DM@EDPTPVPNIEEVV*L*PK#.N
GP:BC039843_1	R07	1950	2	983.1	(+0.3)	2.686	0.273	0.962	1	R.FDL*QNPSR.M

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GP:BC039843_1	R07	1958	2	977.1	(+0.9)	2.520	0.304	0.955	1	R.FDLQNPSR.M
GP:BC039843_1	R07	6891	2	1780.9	(+0.6)	4.013	0.554	1.000	1	K.FWESPETVSQLDSVR.V
GP:BC039843_1	R07	4785	2	1993.0	(-0.8)	4.405	0.391	0.999	1	K.GGTVADLDEQDEETVTAGGK.E
GP:BC039843_1	R07	4753	3	1993.0	(+0.8)	4.209	0.539	1.000	1	K.GGTVADLDEQDEETVTAGGK.E
GP:BC039843_1	R07	4767	2	1993.0	(+0.4)	4.064	0.406	1.000	1	K.GGTVADLDEQDEETVTAGGK.E
GP:BC039843_1	R07	4759	2	2007.0	(-0.6)	3.484	0.216	0.896	1	K.GGTVADL*DEQDEETVTAGGK#.E
GP:BC039843_1	R07	992	2	1071.1	(+0.9)	3.159	0.259	0.951	1	R.HQGTFTDEK#.S
GP:BC039843_1	R07	1340	2	1015.2	(+0.7)	2.695	0.380	0.982	1	K.HVTNPAFTK.L
GP:BC039843_1	R07	1060	2	974.1	(-0.1)	2.608	0.457	0.978	1	K.K#GQASL*YQG#.R
GP:BC039843_1	R07	6357	2	1279.5	(+0.5)	2.653	0.262*	0.256	1	R.NVEMFM@NIEK#.T
GP:BC039843_1	R07	4473	2	1295.5	(-0.2)	2.440	0.171	0.659	1	R.NVEM@FM@NIEK#.T
GP:BC039843_1	R07	4319	2	1295.5	(-0.8)	2.285	0.109	0.163	1	R.NVEM@FM@NIEK#.T
GP:BC039843_1	R07	4395	2	1295.5	(-0.8)	2.228	0.137	0.198	1	R.NVEM@FM@NIEK#.T
GP:BC039843_1	R07	4243	2	1295.5	(-0.9)	2.219	0.112	0.146	1	R.NVEM@FM@NIEK#.T
GP:BC039843_1	R07	2122	2	1133.3	(+0.6)	2.906	0.256	0.962	1	R.RFDLQNPSR.M
GP:BC039843_1	R07	2104	2	1139.3	(+0.2)	2.516	0.275	0.918	1	R.RFDL*QNPSR.M
GP:BC039843_1	R07	5873	2	1816.1	(-0.5)	3.683	0.466	0.999	1	R.SPQVPAQQM@L*NFPEK#.N
GP:BC039843_1	R04	10736	3	2110.4	(-0.3)	4.536	0.477	1.000	1	K.TL*AGL*VVQL*L*QFQEDAFGK#.H
GP:BC039843_1	R05	10640	3	2110.4	(-0.0)	4.776	0.456	0.999	1	K.TL*AGL*VVQL*L*QFQEDAFGK#.H
GP:BC039843_1	R06	10938	3	2110.4	(-0.3)	4.428	0.429	0.999	1	K.TL*AGL*VVQL*L*QFQEDAFGK#.H
GP:BC039843_1	R06	10948	2	2110.4	(-0.8)	2.226	0.255	0.400	1	K.TL*AGL*VVQL*L*QFQEDAFGK#.H
GP:BC039843_1	R07	11019	3	2078.4	(+0.9)	6.148	0.595	0.961	1	K.TLAGLVVQLLQFQEDAFGK.H
GP:BC039843_1	R07	11033	2	2078.4	(+0.8)	5.859	0.628	1.000	1	K.TLAGLVVQLLQFQEDAFGK.H
GP:BC039843_1	R07	11017	3	2110.4	(+0.2)	5.150	0.577	1.000	1	K.TL*AGL*VVQL*L*QFQEDAFGK#.H
GP:BC039843_1	R07	11023	2	2110.4	(-0.3)	3.599	0.398	0.977	1	K.TL*AGL*VVQL*L*QFQEDAFGK#.H
GP:BC039843_1	R08	11037	3	2110.4	(-0.8)	4.046	0.377	0.990	1	K.TL*AGL*VVQL*L*QFQEDAFGK#.H
GP:BC039843_1	R10	11163	3	2078.4	(+0.2)	3.963	0.438	0.996	1	K.TLAGLVVQLLQFQEDAFGK.H
GP:BC039843_1	R11	10992	3	2110.4	(-0.0)	5.028	0.407	0.997	1	K.TL*AGL*VVQL*L*QFQEDAFGK#.H
GP:BC039843_1	R11	11008	2	2078.4	(+0.3)	2.243	0.388	0.946	1	K.TLAGLVVQLLQFQEDAFGK.H
GP:BC039843_1	R13	11413	3	2078.4	(+0.2)	5.523	0.536	0.998	1	K.TLAGLVVQLLQFQEDAFGK.H
GP:BC039843_1	R20	11116	3	2078.4	(+0.7)	5.917	0.578	0.977	1	K.TLAGLVVQLLQFQEDAFGK.H
GP:BC039843_1	R20	11108	3	2110.4	(+0.2)	4.397	0.401	0.998	1	K.TL*AGL*VVQL*L*QFQEDAFGK#.H
GP:BC039843_1	R21	10801	3	2078.4	(+0.9)	4.587	0.513	0.964	1	K.TLAGLVVQLLQFQEDAFGK.H
GP:BC039843_1	R07	7117	2	1748.0	(-0.8)	3.594	0.438	0.329	1	R.VREEVPLELVEAHVK.K
GP:BC039843_1	R07	974	2	1124.2	(+0.8)	2.857	0.390	0.980	1	K.YVHADAPTNK#.T
GP:BC039843_1	R21	10803	3	2110.4	(-0.3)	3.789	0.383	0.996	1	K.TL*AGL*VVQL*L*QFQEDAFGK#.H
GP:BC044255_1	R06	7172	2	1177.3	(+0.2)	2.788	0.302	0.935	1	K.L*L*DIEGL*YSK#.V
GP:BC044255_1	R06	7168	2	1151.3	(+0.3)	2.677	0.204	0.896	1	K.LLDIEGLYSK.V
GP:BC044255_1	R05	6778	2	1655.8	(-0.8)	2.736	0.375	0.886	1	R.L*QDSFASSETNL*DFR.S
GP:BC044255_1	R02	8552	3	2970.3	(+0.5)	3.793	0.485	1.000	1	R.SGLAIVSQHDLDDLQADAINAFGESLQK.K
GP:BC044255_1	R03	8871	3	2970.3	(+0.9)	4.074	0.463	0.999	1	R.SGLAIVSQHDLDDLQADAINAFGESLQK.K
GP:BC044255_1	R06	8654	3	3107.5	(+0.4)	6.812	0.595	1.000	1	R.THLYGSLLYLQIAQRPEPDTLEAAK.K
GP:BC044255_1	R06	7848	2	1549.9	(-0.6)	2.268	0.177	0.439	1	R.TLQSLLTPQPLLK.A
GP:BC044255_1	R05	6214	2	1272.4	(-0.2)	2.955	0.363	0.970	1	K.VL*VDSL*VEDDR.T
GP:BC044255_1	R05	6218	2	1260.4	(+0.9)	2.503	0.428	0.981	1	K.VLVDSLVEDDR.T
GP:BC044255_1	R06	6204	2	1260.4	(+0.0)	3.211	0.499	1.000	1	K.VLVDSLVEDDR.T
GP:BC044255_1	R05	7794	2	1097.3	(+0.9)	3.747	0.424	0.993	1	R.YSFIQALVR.R
GP:BC044255_1	R05	7790	2	1103.3	(+1.0)	3.025	0.439	1.000	1	R.YSFIQAL*VR.R
GP:BC044255_1	R06	7894	2	1097.3	(+0.9)	3.596	0.434	0.991	1	R.YSFIQALVR.R
GP:BC044255_1	R06	6236	2	1272.4	(-0.8)	2.262	0.210	0.442	1	K.VL*VDSL*VEDDR.T
GP:BX248076_1	R09	4110	2	1197.2	(+0.8)	2.335	0.309*	0.246		R.AL*WEEEEER.L
GP:BX248076_1	R09	6036	2	1199.4	(+1.0)	3.343	0.404	0.986		K.RVDLLEQVAR.E
GP:BX248076_1	R09	4104	2	1191.2	(+0.2)	2.259	0.306	0.904		R.ALWEEEEER.L
GP:D79984_1	R05	5632	2	1453.5	(+0.5)	3.743	0.453	1.000	1	K.DVDEAHYAYSFK#.Y
GP:D79984_1	R05	5486	3	3143.0	(+0.1)	5.907	0.460	1.000		K.FVEEEDDDEEEEEENLDDQDEQGNLK.G
GP:D79984_1	R05	5490	3	3163.0	(+0.1)	5.836	0.480	0.992		K.FVEEEDDDEEEEEENL*DDQDEQGNL*K#.G
GP:D79984_1	R05	5462	3	1589.7	(+0.3)	3.970	0.517	1.000	1	R.K#DVDEAHYAYSFK#.Y
GP:D79984_1	R05	5602	3	3271.2	(-0.3)	7.169	0.544	1.000		K.KFVEEEDDDEEEEEENLDDQDEQGNLK.G
GP:D79984_1	R05	5598	3	3299.2	(-1.0)	6.309	0.457	1.000		K.K#FVEEEDDDEEEEEENL*DDQDEQGNL*K#.G
GP:D79984_1	R05	5512	2	1164.3	(+1.0)	2.205	0.333	0.242	2	K.ELRDDQFLK.I
GP:D86978_1	R06	10292	2	1688.0	(-0.2)	4.526	0.417	0.989		R.DLEHMLLIGELYK.K
GP:D86978_1	R06	6860	2	1575.8	(-0.1)	5.164	0.444	1.000		R.FTDELMEQGLTYK.V

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta M$	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GP:D86978_1	R06	6854	2	1595.8	(-1.0)	3.497	0.493	1.000		R.FTDEL*MEQGL*TYK#.V
GP:D86978_1	R06	1460	2	1100.3	(+0.6)	3.019	0.412	0.989		K.KADNVVNIAR.Y
GP:D86978_1	R06	7554	2	914.1	(+1.0)	2.812	0.431	0.990		R.LAWALALR.G
GP:D86978_1	R06	7550	2	932.1	(+0.3)	2.361	0.446	0.979		R.L*AWAL*AL*R.G
GP:D86978_1	R01	8109	3	2927.3	(+0.5)	3.951	0.445	0.995		R.LLHLLDDMPVKPYSDGEGGIEDENR.S
GP:D86978_1	R06	5358	2	967.1	(+0.5)	2.464	0.326	0.961		K.L*PGL*QATVR.L
GP:D86978_1	R06	5450	2	967.1	(+0.9)	2.396	0.296	0.894		K.L*PGL*QATVR.L
GP:D86978_1	R06	5228	2	1589.7	(-0.3)	3.998	0.465	0.999		K.L*VGDFTHDQSSISQK#.L
GP:D86978_1	R06	5576	2	1326.5	(-0.7)	2.566	0.296	0.896		R.RQPEAVHL*L*DK#.I
GP:D86978_1	R06	6964	2	1410.6	(+0.6)	4.431	0.383	0.992		R.SVSGFLHFDATK.V
GP:D86978_1	R06	6952	2	1424.6	(-0.3)	3.170	0.393	0.973		R.SVSGFL*HFDATK.V
GP:D86978_1	R06	8972	2	2164.4	(-0.3)	2.982	0.336	0.954		R.TSQDFLFSQLQLPFSNK.E
GP:D86978_1	R05	5038	2	816.0	(+0.4)	2.390	0.234	0.924		K.VGNALWR.R
GP:D86978_1	R01	10623	2	1770.2	(+0.1)	3.508	0.392	0.976		R.VHNL*ITDFL*AL*MPMK#.V
GP:D86978_1	R06	10376	2	1744.2	(+0.4)	3.062	0.424	0.985		R.VHNLITDFLALMPMK.V
GP:D86978_1	R06	8776	2	1802.2	(-0.9)	2.832	0.367	0.851		R.VHNL*ITDFL*AL*M@PM@K#.V
GP:D86978_1	R06	7464	2	1433.6	(+0.4)	2.305	0.265	0.869		K.EDTL*L*L*IGHL*ER.V
GP:U66618_1	R14	1296	2	959.1	(-0.3)	2.360	0.167	0.745		R.K#L*DQTIAR.K
GP:U66618_1	R14	5961	2	1257.4	(+0.7)	2.239	0.236	0.821		R.IYISNTFSPSK.A
GPN:AK000010_1	R16	6730	3	2657.9	(+0.8)	3.732	0.503	1.000		R.L*PVIEPVSINEENEGFEHNTQVR.N
GPN:AK000010_1	R16	6058	2	1141.3	(+0.8)	2.682	0.447	0.988		R.NQGIAL*SYR.D
GPN:AK000261_1	R12	8256	2	1637.9	(+1.0)	3.250	0.363	0.981	4	R.LQIQLPDSVNQLLR.Y
GPN:AK000261_1	R12	8264	2	1661.9	(-0.4)	2.864	0.283	0.921	4	R.L*QIQL*PDSVNQL*L*R.Y
GPN:AK000261_1	R12	1802	2	987.1	(+0.9)	2.384	0.178	0.836	4	K.LTNQELLR.K
GPN:AK000261_1	R12	1908	2	1278.4	(+0.6)	2.571	0.519	0.990	3	R.SHSSFQASLTGR.L
GPN:AK000261_1	R12	1900	2	1284.4	(+0.3)	2.216	0.388	0.955	3	R.SHSSFQASL*TGR.L
GPN:AK000261_1	R12	8378	3	2481.8	(+0.1)	4.358	0.386	0.980	3	K.VL*AFGAK#PDSTL*HTYFSPFL*SR.A
GPN:AK000261_1	R12	5154	2	815.0	(+0.9)	2.212	0.387	0.960	3	K.GFGMIGPK#.D
GPN:AK000304_1	R11	7858	2	1466.7	(+0.9)	4.263	0.569	1.000	1	K.FDFPVSYPGPVK.A
GPN:AK000304_1	R11	7872	2	1466.7	(-0.5)	3.443	0.435	0.987	1	K.FDFPVSYPGPVK.A
GPN:AK000304_1	R11	7860	2	1480.7	(-0.8)	2.714	0.406	0.889	1	K.FDFPVSYP*PGPVK#.A
GPN:AK000304_1	R11	7828	2	1796.1	(+0.3)	3.301	0.338	0.977	4	K.GEQL*FL*EPEL*VIPHR.Q
GPN:AK000304_1	R11	2202	2	986.2	(+0.6)	3.266	0.352	0.988	5	R.LAQLITQAK.H
GPN:AK000304_1	R11	2158	2	1006.2	(-0.1)	3.025	0.442	1.000	5	R.L*AQL*ITQAK#.H
GPN:AK000304_1	R11	7930	2	1777.1	(+0.1)	2.854	0.405	0.963	3	K.WAPFVQENL*L*M@YTK#.L
GPN:AK000304_1	R11	6354	2	1044.2	(+0.7)	2.315	0.267	0.910	4	R.SYEIASL*VR.T
GPN:AK000349_1	R13	7587	2	1574.7	(+0.2)	3.180	0.483	1.000	1	R.GNL*ASYPIDEL*VDR.A
GPN:AK000349_1	R13	8373	2	1371.6	(+0.9)	2.868	0.420	0.985	1	R.DIGNLPTLLWK.L
GPN:AK003493_1	R01	7351	3	2643.0	(+0.9)	5.115	0.630	1.000	1	K.DVIGIAHHPHQNLTIATYSEDGLLK.L
GPN:AK003493_1	R01	7345	3	2669.0	(-0.3)	4.638	0.482	1.000	1	K.DVIGIAHHPHQNL*TIATYSEDGL*L*K#.L
GPN:AK003493_1	R01	7303	2	1242.5	(+0.9)	2.521	0.397	0.970	2	R.YIHLENLLAR.S
GPN:AK003493_1	R02	6540	2	1674.8	(+0.4)	2.480	0.152	0.389	1	K.DSSQIL*SASFDQTR.I
GPN:AK004558_1	R20	6364	2	1575.7	(-0.6)	2.952	0.247	0.882	7	K.EQL*DNQL*DAYMSK#.T
GPN:AK004558_1	R20	5606	2	1785.1	(-0.7)	3.935	0.278	0.378	6	R.LAQQMENRPSVQAALK.L
GPN:AK004558_1	R20	6362	2	1555.7	(-0.1)	2.684	0.368	0.955	7	K.EQLDNQLDAYMSK.T
GPN:AK004766_1	R10	6905	2	1304.5	(+0.2)	2.644	0.371	0.943	2	K.AGSFITGIDVTSK#.E
GPN:AK004766_1	R10	7107	2	1372.5	(-0.4)	2.448	0.113	0.382	6	R.AL*IGDDVGL*TSYK#.H
GPN:AK010310_1	R16	9968	3	1950.3	(+0.5)	4.064	0.329	0.997	3	K.TGAFAL*PIL*NAL*L*ETPQR.L
GPN:AK010310_1	R16	1868	2	1118.2	(+0.1)	2.338	0.194	0.759	5	K.YL*VMDEADR.I
GPN:AK026042_1	R01	6725	2	1531.7	(+0.6)	4.785	0.619	1.000		K.AVDPSSVALVTLGSSK.E
GPN:AK026042_1	R01	6721	2	1551.7	(-0.9)	2.645	0.412	0.872		K.AVDPSSVAL*VTL*GSSK#.E
GPN:AK026042_1	R02	6514	2	1531.7	(+1.0)	4.946	0.608	0.996		K.AVDPSSVALVTLGSSK.E
GPN:AK026042_1	R03	6409	2	1531.7	(+0.8)	3.505	0.496	1.000		K.AVDPSSVALVTLGSSK.E
GPN:AK026042_1	R03	7419	2	1123.4	(+0.1)	2.343	0.446	0.964		K.ITIAAYL*PL*K#.A
GPN:AK026042_1	R02	6396	2	1096.3	(-0.4)	2.514	0.191	0.791		R.VGQALELPLR.I
GPN:AK026042_1	R03	6283	2	1114.3	(+0.4)	2.635	0.254	0.933		R.VGQAL*EL*PL*R.I

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GPN:AK026042_1	R03	6279	2	1096.3	(+0.2)	2.543	0.128	0.649		R.VGQALELPLR.I
GPN:AK026042_1	R04	6566	2	1096.3	(+1.0)	2.963	0.256	0.959		R.VGQALELPLR.I
GPN:AK026042_1	R04	6570	2	1114.3	(+0.0)	2.819	0.293	0.949		R.VGQAL*EL*PL*R.I
GPN:AK026042_1	R05	6702	2	1114.3	(+0.7)	2.912	0.387	0.985		R.VGQAL*EL*PL*R.I
GPN:AK026042_1	R06	6688	2	1114.3	(+0.7)	2.766	0.351	0.977		R.VGQAL*EL*PL*R.I
GPN:AK030781_1	R06	6056	3	2161.3	(+0.5)	3.860	0.273	0.988	7	R.HYNEEGSQVYNDAHIL*EK#.L
GPN:AK030781_1	R06	1928	2	1065.2	(+0.7)	3.126	0.330	0.984	7	K.LNEVYEAVK.N
GPN:AK030781_1	R06	8324	3	1981.3	(+0.3)	3.762	0.343	0.997	7	R.RL*DL*FQEHMFVL*ER.A
GPN:AK030781_1	R06	4876	2	1636.7	(-0.7)	2.502	0.372	0.916	7	K.EL*GPL*PDDDDM@ASP#.L
GPN:AK039567_1	R01	7575	2	1164.3	(+0.6)	2.511	0.133	0.759	2	R.DIDAFWLQR.Q
GPN:AK039567_1	R01	7565	2	1170.3	(+0.7)	2.326	0.361	0.964	2	R.DIDAFWL*QR.Q
GPN:AK039567_1	R01	6765	2	1507.6	(+0.2)	2.854	0.387	0.970	2	R.EIDL*L*L*GQTDDTR.Y
GPN:AK039567_1	R02	9907	3	2151.4	(+0.8)	3.752	0.475	1.000	2	R.ETYEVLISFIQAALGDQPR.D
GPN:AK039567_1	R01	2044	2	1194.3	(+0.5)	3.572	0.274	0.976	2	R.FYDDAIVSQK#.K
GPN:AK039567_1	R01	2046	2	1186.3	(+1.0)	3.405	0.408	1.000	2	R.FYDDAIVSQK.K
GPN:AK039567_1	R02	4830	2	1194.3	(-0.1)	3.293	0.427	1.000	2	R.FYDDAIVSQK#.K
GPN:AK039567_1	R02	4842	2	1186.3	(-0.1)	2.727	0.499	0.998	2	R.FYDDAIVSQK.K
GPN:AK039567_1	R03	4597	2	1186.3	(-0.0)	3.062	0.445	0.987	2	R.FYDDAIVSQK.K
GPN:AK039567_1	R01	5785	2	1043.3	(+0.9)	2.328	0.296	0.934	2	R.YHVLVNLGK.K
GPN:AK039567_1	R04	4892	2	1194.3	(+0.0)	2.438	0.371	0.943	2	R.FYDDAIVSQK#.K
GPN:AK041594_1	R12	5968	3	2514.8	(+0.7)	5.065	0.396	0.999	2	K.TPVVQNAASIVQPSPAHVGQQGLSK.L
GPN:AK041594_1	R12	6814	3	2284.5	(+0.5)	3.764	0.510	1.000	2	R.TTSSAIYM@NL*ASHIQPGTVNR.V
GPN:AK041594_1	R12	4378	2	1398.6	(-0.2)	3.229	0.482	1.000	2	R.VIAPNPAQL*QGQR.G
GPN:AK041594_1	R12	4442	2	1392.6	(-0.3)	3.184	0.416	0.981	2	R.VIAPNPAQLQGQR.G
GPN:AK041594_1	R12	4364	2	1392.6	(-0.3)	3.135	0.468	0.987	2	R.VIAPNPAQLQGQR.G
GPN:AK041594_1	R12	4302	2	1398.6	(-0.2)	2.944	0.484	0.985	2	R.VIAPNPAQL*QGQR.G
GPN:AK041594_1	R12	4456	2	1398.6	(-0.6)	2.878	0.429	0.979	2	R.VIAPNPAQL*QGQR.G
GPN:AK045159_1	R06	7498	2	1588.8	(+0.9)	3.866	0.432	0.999	3	K.ETQFAQIFELHK.S
GPN:AK045159_1	R06	7510	2	1602.8	(-0.6)	3.241	0.488	1.000	3	K.ETQFAQIFEL*HK#.S
GPN:AK045159_1	R06	5002	2	913.0	(-0.1)	2.294	0.312	0.876	5	K.L*GMDDL*TK#.L
GPN:AK045159_1	R06	6180	2	1115.4	(+0.9)	2.457	0.135	0.573	4	R.SALLPVLHKK.S
GPN:AK045159_1	R06	10750	3	3507.1	(+0.0)	4.362	0.481	0.907	4	K.SLDPSNLEHLITPLVTIGHIALLAPDQFAAPLK.S
GPN:AK045159_1	R06	6948	2	1104.3	(+0.5)	3.347	0.312	0.977	4	K.VAEAAL*QIF#.N
GPN:AK045159_1	R06	4924	2	913.0	(+0.6)	2.230	0.421	0.960	5	K.L*GMDDL*TK#.L
GPN:AK047081_1	R04	6484	2	1403.6	(+0.0)	2.334	0.296	0.826	2	K.AL*EFVTNPDIAAK#.K
GPN:AK047081_1	R04	6170	3	1576.8	(+0.6)	3.731	0.344	0.995	2	K.K#TNM@HIFIESGL*R.L
GPN:AK047081_1	R04	7978	3	2456.8	(+1.0)	5.196	0.446	1.000	2	K.L*RPNL*EFML*AQL*NYEHETGR.E
GPN:AK047081_1	R04	8676	2	1723.0	(-0.2)	3.367	0.385	0.972	2	K.L*VGL*ESFSL*AFASVQK#.Q
GPN:AK047081_1	R04	8954	2	1326.5	(+0.3)	2.907	0.352	0.970	2	K.NL*SQEIIEL*L*K#.K
GPN:AK047081_1	R04	1132	2	913.0	(+0.5)	2.214	0.198	0.812	2	K.L*EAAYSPR.N
GPN:AK088011_1	R09	7818	2	1396.6	(-0.0)	3.535	0.440*	0.482	4	K.NSMVAL*VENL*ASK#.E
GPN:AK088011_1	R09	5884	2	1099.3	(+0.2)	3.183	0.391	0.982	4	K.VAAMGAL*QGL*R.Q
GPN:AK125781_1	R07	7315	2	1497.7	(-0.5)	3.114	0.296	0.952	1	K.AGYPQYVSEILEK.V
GPN:AK125781_1	R07	7483	2	1381.6	(+0.9)	4.519	0.513	1.000	1	K.ISNQFDWALMR.L
GPN:AK125781_1	R07	9549	3	2249.4	(+0.4)	5.161	0.393	1.000		K.NNDIDAAIENIENMLTSENK.V
GPN:AK125781_1	R07	10319	2	1997.3	(+0.2)	3.408	0.503	0.996	1	R.SM@NINL*WSEITEL*L*YK#.D
GPN:AK125781_1	R07	7347	2	1511.7	(-0.8)	2.461	0.219	0.449	1	K.AGYPQYVSEIL*EK#.V
GPN:AK126214_1	R02	8340	3	2450.7	(+1.0)	3.798	0.394	0.986	1	K.ADKDQANDGLSSALLILYLD SAR.N
GPN:AK126214_1	R10	9301	3	2450.7	(+0.6)	3.771	0.542	1.000	1	K.ADKDQANDGLSSALLILYLD SAR.N
GPN:AK126214_1	R01	6173	2	1399.6	(+0.6)	3.568	0.437	1.000	1	R.IHFIEAQLDQK.G
GPN:AK126214_1	R01	8187	2	1667.0	(+0.3)	2.383	0.340	0.932	1	R.ITVPLVSEVQIAQLR.F
GPN:AK126214_1	R02	7834	2	1605.8	(+0.8)	3.673	0.370	0.988	1	R.LLDEWFTLDEV PK.G
GPN:AK126214_1	R10	8857	2	1605.8	(-0.4)	3.196	0.292	0.954	1	R.LLDEWFTLDEV PK.G
GPN:AK127872_1	R05	1320	2	1081.2	(-0.2)	2.750	0.395	0.969	5	K.VAIESAVQK#.Q
GPN:AK127872_1	R05	6792	2	1250.4	(+0.5)	2.456	0.171	0.695	6	R.FSFITHL*QDK#.H
GPN:AK128368_1	R05	5572	2	1329.5	(+0.9)	2.465	0.448	0.980		R.AAAVQADDVEVLK.V

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GPN:AK128368_1	R05	6950	2	1151.4	(-0.2)	2.280	0.287	0.876	2	R.STIMSHLFSK.L
GPN:AK131089_1	R09	6894	3	2262.5	(-0.5)	4.665	0.447	1.000		K.AAVSAL*L*EQHGL*QGDAVFGHSHK#.L
GPN:AK131089_1	R09	6906	3	2236.5	(+0.4)	4.544	0.390	0.987		K.AAVSALLEQHGGLQGDAVFGHSHK.L
GPN:AK131089_1	R09	7222	2	1512.8	(-0.1)	3.661	0.466	1.000	2	R.HQVAYLGLLENVR.V
GPN:AK131089_1	R09	5240	2	1311.5	(-0.1)	2.309	0.373	0.941	2	R.L*L*YNSTDPTL*R.A
GPN:AY358088_1	R01	11621	3	1974.4	(+0.9)	4.226	0.450	0.999	1	R.VGLAVVGSVLGAFLTFPGLR.L
GPN:AY358088_1	R01	9807	2	1512.9	(+0.8)	3.785	0.392	0.989	1	R.IAGALGGLLTPLFLR.G
GPN:AY358445_1	R22	6258	2	1091.2	(+0.7)	2.553	0.386	0.970	2	K.SSGPPSYFIK#.R
GPN:AY358445_1	R22	7208	2	1695.0	(-0.3)	2.296	0.411	0.249	2	R.AVVPGVKPDWISAAR.V
GPN:AY358463_1	R14	6045	2	1291.4	(+0.7)	3.182	0.385	0.961	2	R.FDGILTEGEGPR.R
GPN:AY358463_1	R15	5891	2	1291.4	(+1.0)	2.774	0.419	0.984	2	R.FDGILTEGEGPR.R
GPN:AY358463_1	R15	2056	2	1506.6	(-0.3)	3.721	0.450	1.000	2	R.LGAVDESLSEETQK.A
GPN:AY358463_1	R14	8817	2	1400.7	(-0.8)	2.421	0.122	0.217	2	K.M@*L*L*EIL*HEIK#.S
GPN:AY358463_1	R14	8369	2	1381.6	(+0.9)	2.588	0.411	0.978	2	R.QEIVSLFNAFGR.I
GPN:AY358463_1	R15	8111	2	1387.6	(+0.7)	3.570	0.436	0.998	2	R.QEIVSL*FNAFGR.I
GPN:AY358463_1	R14	7567	2	1349.5	(-0.6)	2.206	0.144	0.439	2	R.YL*L*QETWL*EK#.K
GPN:AY358463_1	R15	7315	2	1323.5	(+1.0)	3.886	0.395	0.997	2	R.YLLQETWLEK.K
GPN:AY358463_1	R15	5905	2	1291.4	(-0.2)	2.602	0.300	0.919	2	R.FDGILTEGEGPR.R
GPN:AY358691_1	R01	1586	2	1237.4	(+0.7)	3.905	0.424	0.992	2	K.RGDTYELQVR.G
GPN:AY358691_1	R01	1588	2	1243.4	(+0.8)	3.555	0.428	0.997	2	K.RGDTYEL*QVR.G
GPN:AY358691_1	R01	2140	2	1266.4	(+0.2)	2.313	0.303	0.872		K.VSQL*M@EWTNK#.R
GPN:AY358793_1	R15	11219	3	2406.7	(+0.9)	4.880	0.571	1.000	4	K.TATALLESPLSATVEDALQSFLK.A
GPN:AY358793_1	R15	8113	2	1229.4	(+0.2)	2.425	0.154	0.665	3	K.DLEELEVLIR.D
GPN:AY359059_1	R23	7892	2	1419.6	(-0.6)	2.682	0.164	0.683	3	K.AAL*EYL*EDIDL*K#.T
GPN:AY359059_1	R01	8669	2	1634.0	(+0.0)	3.414	0.378	0.977	4	K.SMLDQLGVPLYAVVK.E
GPN:AY359059_1	R01	8469	2	1157.4	(+0.9)	2.795	0.391	0.982	4	K.VNLLSVLEAAK.M
GPN:AY359059_1	R23	8642	2	1183.4	(+0.1)	2.372	0.332	0.901	4	K.VNL*L*SVL*EAAK#.M
GPN:AY359091_1	R05	9554	3	3135.3	(+0.3)	3.966	0.506	1.000		R.DDFHNYNVEELLGFLELYNSAATDSEK.A
GPN:AY359091_1	R05	5480	2	1685.7	(-0.5)	3.990	0.495	1.000		K.FGSTADALVSDDETTR.L
GPN:AY359091_1	R05	7724	3	2936.2	(+0.4)	5.600	0.461	1.000		K.QGKQSATDYSDPDNDVDDGLFIVDIPK.T
GPN:AY359091_1	R05	7720	3	2958.2	(+0.1)	5.239	0.262	0.906		K.QGK#PQSATDYSDPDNDVDDGL*FIVDIPK#.T
GPN:AY359091_1	R05	10770	2	2311.6	(-0.9)	2.243	0.444	0.873		K.NILTTWGDITFISVTGGEETR.D
GPN:AY359102_1	R24	9150	3	1876.1	(+0.3)	3.867	0.345	0.998	1	R.AL*VDEL*EWEIAQVDPK#.K
GPN:AY359102_1	R24	9144	2	1856.1	(+1.0)	3.128	0.276	0.953	1	R.ALVDELEWEIAQVDPK.K
GPN:AY359102_1	R24	5078	2	1063.2	(+0.3)	2.875	0.174	0.867		R.IDSDISGTL*K#.F
GPN:AY359102_1	R24	5074	2	1049.2	(+0.9)	2.853	0.203	0.920		R.IDSDISGTLK.F
GPN:AY359102_1	R24	5096	2	1049.2	(-0.7)	2.769	0.230	0.903		R.IDSDISGTLK.F
GPN:AY359102_1	R24	6182	2	1418.5	(+0.4)	2.665	0.251	0.907		R.NGESSELDLQGR.I
GPN:AY363225_1	R18	6675	2	1884.1	(+0.5)	5.326	0.578	0.999		K.IFVGGIKEDTEEYNLR.D
GPN:AY363225_1	R18	6699	3	1884.1	(-0.5)	4.469	0.505	1.000		K.IFVGGIKEDTEEYNLR.D
GPN:AY363225_1	R18	6659	3	1898.1	(+0.8)	3.756	0.273	0.919		K.IFVGGIK#EDTEEYNLR.D
GPN:AY363225_1	R18	7339	2	1714.8	(-0.2)	3.690	0.427	0.986		R.GFAFVTFDDHDTVDK.I
GPN:BC000001_1	R18	7937	3	2478.7	(+0.5)	6.161	0.500	0.998	4	R.HFAGDVL*GYVTPWNSHGYDVTK#.V
GPN:BC000001_1	R18	6819	2	1620.7	(+0.7)	4.793	0.431	0.988	6	R.NVL DSEDEIEELSK.T
GPN:BC000001_1	R18	6817	2	1640.7	(-0.1)	3.489	0.282	0.947	6	R.NVL*DSEDEIEEL*SK#.T
GPN:BC000001_1	R18	8263	2	1480.8	(+0.3)	3.029	0.384	0.979	7	K.FTQISPVWL*QL*K#.R
GPN:BC000041_1	R17	7978	3	2632.9	(+1.0)	3.933	0.464	0.999	2	K.NDTGFQEGYPYPHPTLYLLDK.A
GPN:BC000041_1	R17	8152	2	1634.9	(+0.6)	3.767	0.477	1.000	2	R.VYEIPGLEPITFAGK.M
GPN:BC000041_1	R17	8154	2	1648.9	(+0.2)	3.603	0.518	0.999	2	R.VYEIPGL*EPITFAGK#.M
GPN:BC000041_1	R17	5788	2	1026.2	(+0.4)	2.631	0.192	0.891	2	K.VL*SL*VDDPR.N
GPN:BC000416_1	R17	2448	2	985.1	(+0.1)	2.345	0.231	0.833	1	R.DLAVENPVK.Y
GPN:BC000416_1	R17	6394	3	1684.9	(+0.5)	3.723	0.272	0.988	1	R.RPL*NSVVL*QQGL*ADR.I
GPN:BC000416_1	R17	5986	3	1985.1	(+0.4)	3.863	0.587	1.000	1	R.TQHL*SVETSYL*QHESGR.I



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GPN:BC000416_1	R17	7260	2	1208.5	(-0.2)	2.262	0.331	0.906	1	R.K#GVQL*GL*VAFR.R
GPN:BC000488_1	R12	4886	2	1568.8	(+1.0)	2.291	0.320	0.166	2	R.AIEAL*HGHEL*RPGR.A
GPN:BC000488_1	R12	1800	2	1206.3	(+0.1)	3.041	0.422	0.982	1	R.AQPSASLVGYR.T
GPN:BC000488_1	R12	4828	2	1246.4	(+0.7)	2.385	0.360	0.954	1	R.AQPSVSLGAPYR.G
GPN:BC000488_1	R12	1012	2	1179.3	(-0.3)	2.888	0.401	0.969	1	K.K#GPGL*AVQSGDK#.T
GPN:BC000488_1	R12	5218	2	1067.2	(+0.9)	2.676	0.333	0.973	1	R.LSESQLSFR.R
GPN:BC000488_1	R12	5216	2	1079.2	(+0.3)	2.395	0.290	0.938	1	R.L*SESQL*SFR.R
GPN:BC000488_1	R12	4896	2	1556.8	(-0.4)	2.284	0.261	0.065	2	R.AIEALHGHEL RPGR.A
GPN:BC000591_1	R11	8366	2	1556.8	(+0.7)	4.215	0.554	1.000	1	K.NQIALWDQLLEGR.I
GPN:BC000591_1	R11	8368	2	1574.8	(+0.1)	3.416	0.351	0.977	1	K.NQIAL*WDQL*L*EGR.I
GPN:BC000591_1	R11	6970	2	1542.7	(+0.3)	3.879	0.507	1.000	1	K.TPGFSVQSISDFEK.F
GPN:BC000591_1	R11	8866	2	1563.8	(+0.5)	2.488	0.314	0.917	1	R.SIL*TQIDHIL*M@DK#.E
GPN:BC000697_1	R13	7277	2	1431.7	(+0.8)	4.809	0.503	0.975	3	K.IMLGDEAALLEQK.E
GPN:BC000697_1	R12	7486	2	1631.9	(-0.4)	2.656	0.349	0.938	2	K.LFNESHGIFLGLQR.I
GPN:BC000697_1	R12	1662	3	2414.5	(+0.4)	6.583	0.586	1.000	2	R.RPVHGESDTEQLQDDDIETTK.V
GPN:BC000697_1	R13	1988	3	2414.5	(+0.4)	5.198	0.585	1.000	2	R.RPVHGESDTEQLQDDDIETTK.V
GPN:BC000697_1	R13	1978	3	2428.5	(+0.2)	4.644	0.466	1.000	2	R.RPVHGESDTEQL*QDDDIETTK#.V
GPN:BC000697_1	R13	8157	2	2087.4	(+0.7)	4.041	0.519	0.998	3	R.TMPILSPGNTQTLTELELK.W
GPN:BC000697_1	R13	7667	2	2051.3	(+0.8)	5.038	0.511	0.999	2	R.YLQDSTFATSPHLESLLK.I
GPN:BC000697_1	R13	9245	2	1696.9	(-0.0)	3.073	0.387	0.976	3	K.EL*L*SNWYHFL*VTR.L
GPN:BC000875_1	R19	10486	2	1505.8	(+0.4)	3.510	0.457	1.000		R.EEGILGFFAGLVPR.L
GPN:BC000875_1	R20	4768	3	2356.6	(+0.4)	6.443	0.443	0.998		K.VLQHYQESDKGEELGPGNVQK.E
GPN:BC000875_1	R20	4846	3	2356.6	(+0.4)	5.602	0.423	0.995		K.VLQHYQESDKGEELGPGNVQK.E
GPN:BC000875_1	R20	4690	3	2356.6	(+0.6)	5.214	0.521	1.000		K.VLQHYQESDKGEELGPGNVQK.E
GPN:BC000875_1	R20	4784	3	2384.6	(-0.5)	5.022	0.527	1.000		K.VL*QHYQESDK#GEEL*GPGNVQK#.E
GPN:BC000875_1	R20	5602	2	1256.4	(-0.1)	2.349	0.250	0.782		K.EVSSSFHDVHK#.E
GPN:BC001107_1	R18	5173	2	1269.3	(+0.7)	4.129	0.391	0.999	2	R.DAEDALHNLDR.K
GPN:BC001107_1	R22	5760	2	1269.3	(-0.2)	2.991	0.370	0.975	2	R.DAEDALHNLDR.K
GPN:BC001107_1	R22	5758	2	1281.3	(-0.5)	2.385	0.210	0.760	2	R.DAEDAL*HNL*DR.K
GPN:BC001107_1	R18	8993	2	1918.2	(+0.9)	3.366	0.490	1.000	2	R.YGPIVDVYVPLDFYTR.R
GPN:BC001107_1	R18	8991	2	1924.2	(+0.9)	3.134	0.531	1.000	2	R.YGPIVDVYVPL*DFYTR.R
GPN:BC001107_1	R19	9124	2	1918.2	(+0.8)	3.889	0.503	0.996	2	R.YGPIVDVYVPLDFYTR.R
GPN:BC001107_1	R22	9024	2	1918.2	(+0.9)	4.353	0.567	1.000	2	R.YGPIVDVYVPLDFYTR.R
GPN:BC001107_1	R23	8988	2	1918.2	(+0.8)	3.424	0.519	0.992	2	R.YGPIVDVYVPLDFYTR.R
GPN:BC001107_1	R18	6865	2	1475.7	(-0.1)	2.739	0.342	0.292	2	R.YL*RPPNTSL*FVR.N
GPN:BC001107_1	R22	7030	2	1463.7	(+0.6)	3.002	0.360	0.449	2	R.YLRPPNTSLFVR.N
GPN:BC001107_1	R22	7038	2	1475.7	(-0.8)	2.857	0.344	0.137	2	R.YL*RPPNTSL*FVR.N
GPN:BC001107_1	R22	7044	2	1463.7	(-0.7)	2.732	0.317	0.244	2	R.YLRPPNTSLFVR.N
GPN:BC001107_1	R24	9002	2	1918.2	(+0.1)	2.977	0.466	0.982	2	R.YGPIVDVYVPLDFYTR.R
GPN:BC001191_1	R15	5869	2	1368.6	(+0.6)	3.713	0.320	0.983	2	K.FVQLEGAPLEK.S
GPN:BC001191_1	R15	6199	2	1360.5	(+0.1)	3.091	0.375	0.978	1	K.HNL*EYPDFYR.K
GPN:BC001191_1	R15	6189	2	1354.5	(+0.2)	2.798	0.244	0.918	1	K.HNLEYPDFYR.K
GPN:BC001191_1	R15	6705	2	1205.4	(+0.5)	2.582	0.194	0.884	2	K.RAELWDTWK.V
GPN:BC001191_1	R15	2518	2	1015.2	(-0.3)	2.731	0.333	0.965	1	R.RLEAVLASR.S
GPN:BC001191_1	R15	2464	2	1015.2	(+0.9)	2.616	0.279	0.943	1	R.RLEAVLASR.S
GPN:BC001191_1	R15	2538	2	1027.2	(+0.6)	2.613	0.183	0.877	1	R.RL*EAVL*ASR.S
GPN:BC001191_1	R15	6137	3	3010.2	(-0.0)	3.740	0.243	0.563	1	R.VL*VHRPHGPEL*DADPYDPGEEDPAQSR.A
GPN:BC001191_1	R15	2460	2	1027.2	(-0.3)	2.521	0.160	0.738	1	R.RL*EAVL*ASR.S
GPN:BC001309_1	R24	1606	2	875.0	(+1.0)	2.831	0.307	0.973		R.ASGAQLEAK.V
GPN:BC001309_1	R24	1454	2	875.0	(+0.8)	2.617	0.312	0.964		R.ASGAQLEAK.V
GPN:BC001309_1	R24	1688	2	875.0	(+0.0)	2.440	0.363	0.958		R.ASGAQLEAK.V
GPN:BC001309_1	R23	7370	2	1304.5	(+0.9)	2.532	0.362	0.965		R.EAPVDVL*TIQGR.S
GPN:BC001309_1	R24	7338	2	1298.5	(-0.4)	3.354	0.385	0.982		R.EAPVDVLTQIGR.S
GPN:BC001309_1	R24	4772	2	1152.3	(-0.0)	2.644	0.321	0.935		R.RDFAPPGQQK#.R
GPN:BC001309_1	R24	2204	2	1152.3	(+1.0)	2.480	0.377	0.961		R.RDFAPPGQQK#.R
GPN:BC001309_1	R24	4760	2	1144.3	(+0.8)	2.382	0.154	0.723		R.RDFAPPGQQK.R
GPN:BC001309_1	R25	7780	2	1304.5	(+0.5)	2.405	0.360	0.956		R.EAPVDVL*TIQGR.S
GPN:BC001364_1	R22	4530	2	1209.3	(+0.0)	3.082	0.333	0.973		R.DLQQYQSQAK.Q

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta M$	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GPN:BC001364_1	R22	1848	2	1223.3	(+0.0)	2.342	0.168	0.599		R.DL*QQYQSQAQ#.Q
GPN:BC001364_1	R22	5000	2	1011.1	(+0.4)	2.972	0.436	0.987		R.GEAL*SAL*DSK#.A
GPN:BC001364_1	R22	4902	2	1011.1	(+0.5)	2.538	0.359	0.961		R.GEAL*SAL*DSK#.A
GPN:BC001364_1	R22	4908	2	991.1	(+0.7)	2.399	0.516	0.989		R.GEALSALDSK.A
GPN:BC001364_1	R22	5418	2	1011.1	(-0.1)	2.392	0.386	0.946		R.GEAL*SAL*DSK#.A
GPN:BC001364_1	R22	5084	2	1011.1	(+0.3)	2.386	0.353	0.949		R.GEAL*SAL*DSK#.A
GPN:BC001364_1	R22	5104	2	991.1	(+0.4)	2.285	0.329	0.930		R.GEALSALDSK.A
GPN:BC001364_1	R22	7994	2	1421.7	(+0.2)	4.180	0.449	1.000		R.IMVANIEEVL*QR.G
GPN:BC001364_1	R22	7596	2	1437.7	(-0.5)	3.690	0.401	1.000		R.IM@VANIEEVL*QR.G
GPN:BC001364_1	R22	1444	2	1073.2	(+0.3)	2.676	0.267	0.946		R.KLNEQSPTR.C
GPN:BC001364_1	R02	6080	2	1587.7	(-0.9)	2.300	0.323	0.642		R.NLGSINTELQDVQR.I
GPN:BC001364_1	R22	6608	2	1599.7	(-0.2)	3.468	0.359	0.799		R.NL*GSINTEL*QDVQR.I
GPN:BC001364_1	R22	6754	3	1987.1	(+0.6)	4.520	0.412	0.999		R.VADGL*PL*AASMQEDEQSGR.D
GPN:BC001364_1	R22	6726	2	1975.1	(+0.8)	4.328	0.590	1.000		R.VADGLPLAASMQEDEQSGR.D
GPN:BC001364_1	R23	5076	2	991.1	(+0.7)	2.402	0.358	0.962		R.GEALSALDSK.A
GPN:BC001403_1	R21	6182	3	1910.1	(+0.7)	3.885	0.575*	0.014		K.LPGGELNPGEDEVEGLKR.L
GPN:BC001403_1	R21	6364	2	945.2	(+0.3)	2.569	0.234	0.933	1	R.L*MTEIL*GR.Q
GPN:BC001568_1	R10	6439	3	2025.2	(+0.7)	3.708	0.450	0.999	1	K.GGL*NTPL*HESDFSGVTPQR.Q
GPN:BC001568_1	R10	6573	2	1390.5	(+0.6)	3.440	0.462	1.000	1	R.GVDYNAEIPFEK#.K
GPN:BC001568_1	R10	6571	2	1382.5	(+0.6)	2.836	0.319	0.965	1	R.GVDYNAEIPFEK.K
GPN:BC001568_1	R10	5075	2	1007.2	(+0.5)	2.652	0.240	0.935	2	K.ILLGGYQSR.A
GPN:BC001568_1	R10	8201	3	2571.7	(+0.4)	4.151	0.520	0.993	1	K.K#PAL*GFYDTSEENYQAL*DADFR.K
GPN:BC001568_1	R10	5099	2	1007.2	(-0.7)	2.352	0.155	0.669	2	K.ILLGGYQSR.A
GPN:BC001623_1	R24	5004	3	1741.9	(+0.5)	4.237	0.441	0.996	1	R.TQHHVEAL*VEHQNGK#.V
GPN:BC001623_1	R24	4874	3	1741.9	(+0.6)	3.717	0.521	1.000	1	R.TQHHVEAL*VEHQNGK#.V
GPN:BC001623_1	R24	7044	2	1033.2	(+0.2)	2.472	0.196	0.777	1	R.NL*EL*L*SVAR.K
GPN:BC002457_1	R01	11843	3	2270.7	(+0.5)	4.320	0.359	0.974		K.LGLISPAYLFLWPEAFLYR.F
GPN:BC002457_1	R01	11859	2	2270.7	(-0.8)	3.125	0.462	0.954		K.LGLISPAYLFLWPEAFLYR.F
GPN:BC002457_1	R01	7641	2	1386.6	(-0.3)	2.855	0.248	0.917	1	R.NFLSTPQFLYR.W
GPN:BC002457_1	R01	7623	2	1386.6	(+0.9)	2.724	0.209	0.894	1	R.NFLSTPQFLYR.W
GPN:BC002457_1	R01	8463	2	1522.8	(+0.6)	3.642	0.526	1.000		R.YWFAATVAVPLVVGK.L
GPN:BC002457_1	R01	8461	2	1536.8	(+0.0)	2.307	0.237	0.676		R.YWFAATVAVPL*VGK#.L
GPN:BC002457_1	R02	7162	2	1386.6	(+0.6)	2.402	0.208	0.822	1	R.NFLSTPQFLYR.W
GPN:BC002583_1	R24	6808	2	1656.8	(-0.2)	3.530	0.542	1.000	2	R.GSGQGDSLYPVGYLDK.Q
GPN:BC002583_1	R24	6774	2	1676.8	(-0.6)	2.804	0.279	0.877	2	R.GSGQGDSL*YPVGYL*DK#.Q
GPN:BC002583_1	R24	6816	2	1293.4	(+0.7)	2.555	0.195	0.770	2	K.WAIEL*SGPGGSR.G
GPN:BC002748_1	R24	6348	2	1114.3	(+0.9)	2.427	0.301	0.946	2	K.HVFTTFYAK.T
GPN:BC002748_1	R01	7753	2	1387.6	(+0.1)	2.347	0.204	0.707	2	K.SL*L*VNPVL*FPNR.E
GPN:BC002748_1	R24	6360	2	1122.3	(-0.3)	2.326	0.426	0.961	2	K.HVFTTFYAK#.T
GPN:BC003082_1	R01	2158	2	1590.8	(+0.5)	3.306	0.468	1.000	3	K.KLNSPEETAFTQPK.S
GPN:BC003082_1	R01	5347	2	1420.6	(+1.0)	3.916	0.482	1.000	3	K.LILYQAAAATNGR.V
GPN:BC003082_1	R01	4031	2	1192.4	(+0.1)	2.681	0.325	0.948	4	K.VLNSNPPPIIK.Y
GPN:BC003082_1	R01	4151	2	1192.4	(+0.4)	2.665	0.339	0.961	4	K.VLNSNPPPIIK.Y
GPN:BC003082_1	R01	4073	2	1206.4	(+0.0)	2.602	0.337	0.933	4	K.VL*NSNPPPIIK#.Y
GPN:BC003082_1	R01	3991	2	1206.4	(-0.1)	2.250	0.178	0.383	4	K.VL*NSNPPPIIK#.Y
GPN:BC003082_1	R02	5940	3	2918.1	(+0.4)	3.937	0.435	0.999	2	R.L*WTSASDQQM@TEFSNPSPTSISAEK#.T
GPN:BC003413_1	R21	6614	2	1083.2	(+0.7)	3.217	0.283	0.979		K.VDEIFGQL*R.D
GPN:BC003413_1	R22	7362	2	1554.8	(+0.4)	3.235	0.321	0.976		K.VPYFNAPVYLENK.E
GPN:BC003413_1	R22	6840	2	1083.2	(+0.6)	2.657	0.340	0.974		K.VDEIFGQL*R.D
GPN:BC003696_1	R05	7448	2	1460.7	(-0.4)	3.667	0.404	1.000	3	R.AL*QQFL*YVQMAK#.E
GPN:BC003696_1	R05	6806	2	1476.7	(-0.3)	2.640	0.177	0.699	3	R.AL*QQFL*YVQM@AK#.E
GPN:BC003696_1	R05	6130	2	1332.5	(+0.1)	2.586	0.362	0.306	2	R.DAQLM*IEDVK#.R.I
GPN:BC003696_1	R05	6516	2	994.2	(+0.4)	2.543	0.250	0.940	5	K.FLLGYQPR.G
GPN:BC003696_1	R05	7834	2	1355.6	(+0.2)	2.502	0.271	0.852	5	R.GQIFPTVNGL*FR.W
GPN:BC003696_1	R05	7952	2	1355.6	(+0.8)	2.476	0.232	0.863	5	R.GQIFPTVNGL*FR.W
GPN:BC003696_1	R05	6538	2	1857.9	(-0.4)	3.531	0.403	0.976	3	K.GVEGYGNDQTYFEEIK#.Q
GPN:BC003696_1	R05	6542	2	1849.9	(-0.5)	2.431	0.274	0.833	3	K.GVEGYGNDQTYFEEIK.Q

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GPN:BC003696_1	R06	6540	2	1857.9	(+0.9)	4.039	0.491	1.000	3	K.GVEGYGNDQTYFEEIK#.Q
GPN:BC003696_1	R05	6326	2	1262.4	(+0.3)	3.033	0.401	0.986	3	R.LDNGVTGFIPTK.F
GPN:BC003696_1	R05	6334	2	1276.4	(+0.1)	2.735	0.492	0.981	3	R.L*DNGVTGFIPTK#.F
GPN:BC003696_1	R06	6344	2	1262.4	(+0.6)	2.563	0.211	0.853	3	R.LDNGVTGFIPTK.F
GPN:BC003696_1	R06	8250	3	1778.0	(+0.9)	3.979	0.280	0.948	3	R.LKDLDLDAFAEELER.Q
GPN:BC003696_1	R05	7206	2	1554.7	(-0.2)	3.035	0.199	0.836	3	R.SPNTEEIFNM@L*TK#.E
GPN:BC003696_1	R06	8018	2	1538.7	(+0.4)	2.539	0.266	0.877	3	R.SPNTEEIFNML*TK#.E
GPN:BC003696_1	R05	7268	2	1966.2	(+0.8)	3.968	0.528	1.000	4	R.TPASINATPANINL*ADL*TR.A
GPN:BC003696_1	R05	5426	3	2750.8	(+0.5)	5.655	0.538	0.999	2	R.VAPYRPDQQVEEDDDFM@DENQ GK#.G
GPN:BC003696_1	R05	6082	3	2734.8	(+0.5)	5.014	0.444	1.000	2	R.VAPYRPDQQVEEDDDFM@DENQ GK#.G
GPN:BC003696_1	R05	6554	2	1027.2	(+0.6)	3.015	0.332	0.979	2	R.VL*GIAFSSAR.D
GPN:BC003696_1	R06	7178	2	1554.7	(+0.6)	2.517	0.295	0.842	3	R.SPNTEEIFNM@L*TK#.E
GPN:BC004169_1	R22	6054	2	1139.3	(+0.8)	2.541	0.349	0.968		R.SQ LNDISSFK.N
GPN:BC004169_1	R22	8084	2	1457.6	(+0.5)	2.295	0.389	0.964		K.DQWYNVLEFSR.T
GPN:BC004951_1	R18	5149	2	1295.5	(+0.2)	3.222	0.455	1.000	3	K.L*HGVNINVEASK#.N
GPN:BC004951_1	R18	5839	2	1230.3	(+0.6)	2.703	0.440	0.983	3	K.NYGFVHIEDK#.T
GPN:BC004951_1	R18	5847	2	1222.3	(+0.4)	2.689	0.420	0.944	3	K.NYGFVHIEDK.T
GPN:BC005102_1	R23	6970	2	1225.5	(+0.8)	3.688	0.484	0.990		K.GKPLALVEEIR.N
GPN:BC005102_1	R23	6966	2	1245.5	(-0.2)	2.412	0.383	0.292		K.GK#PL*AL*VEEIR.N
GPN:BC005102_1	R23	2324	2	894.1	(+0.2)	2.323	0.314	0.921		R.VGLEPPPGK.R
GPN:BC005102_1	R23	7398	2	1271.5	(+0.7)	2.296	0.410	0.967		R.IGFDVVTL*SGTR.G
GPN:BC005190_1	R18	5247	2	1275.4	(+0.5)	3.608	0.503	1.000	1	R.AGIATHFVDSEK.L
GPN:BC005190_1	R18	5243	2	1283.4	(+0.4)	3.393	0.414	0.641	1	R.AGIATHFVDSEK#.L
GPN:BC005190_1	R18	8861	2	1276.5	(-0.1)	2.763	0.302	0.943		K.L*GYFL*AL*TGFR.L
GPN:BC005405_1	R10	8657	3	3012.3	(+0.4)	4.534	0.533	1.000	4	R.FSFGNTLVSSADPEGHFETPIWIER.V
GPN:BC005405_1	R11	8234	3	3012.3	(+0.3)	4.370	0.462	0.999	4	R.FSFGNTLVSSADPEGHFETPIWIER.V
GPN:BC005405_1	R09	8334	2	2391.8	(-0.1)	4.337	0.500	1.000	4	K.HHGPQTL*YLPVTLSSIPVFQR.G
GPN:BC005405_1	R10	8817	3	2409.8	(-0.0)	4.714	0.267	0.981	4	K.HHGPQTL*YL*PVTL*SSIPVFQR.G
GPN:BC005405_1	R26	7444	3	1693.9	(+1.0)	4.426	0.455	1.000	4	R.KPGINVASDWSIHLR.-
GPN:BC005405_1	R01	7085	2	1742.0	(+0.7)	2.279	0.275	0.846	4	R.LSFQHDPEPETSVLVLR.K
GPN:BC005405_1	R09	6856	2	1760.0	(-0.3)	3.321	0.366	0.974	4	R.L*SFQHDPEPETS*VL*R.K
GPN:BC005405_1	R10	8011	3	1742.0	(+0.8)	3.983	0.304	0.971	4	R.LSFQHDPEPETSVLVLR.K
GPN:BC005405_1	R10	8015	3	1760.0	(+0.4)	3.763	0.395	0.999	4	R.L*SFQHDPEPETS*VL*R.K
GPN:BC005405_1	R10	8023	2	1742.0	(-0.2)	3.738	0.396	0.985	4	R.LSFQHDPEPETSVLVLR.K
GPN:BC005405_1	R26	8670	3	3012.3	(+0.0)	3.926	0.458	0.999	4	R.FSFGNTLVSSADPEGHFETPIWIER.V
GPN:BC005934_1	R21	6584	2	1433.6	(-0.0)	2.436	0.207	0.730		R.ELLSISSESLQAR.K
GPN:BC005934_1	R22	5666	2	1058.2	(+0.3)	2.362	0.106	0.612		K.LAQLELENK.E
GPN:BC006487_1	R23	7352	2	1103.3	(+0.9)	2.833	0.460	0.990		K.LYALGLVPTR.G
GPN:BC006487_1	R23	7044	3	2015.3	(+0.4)	5.266	0.414	1.000		R.M@AQHL*QAAVAFVEQGHVR.V
GPN:BC006487_1	R23	7298	2	1555.7	(-0.1)	2.667	0.281	0.877		R.SM@EDFVTWVDSSK#.I
GPN:BC006504_1	R20	6822	2	1106.3	(+0.8)	3.080	0.352	0.984	3	R.GEVGLLFTNR.T
GPN:BC006504_1	R20	6816	2	1118.3	(+0.6)	2.564	0.337	0.964	3	R.GEVGL*L*FTNR.T
GPN:BC006504_1	R20	6228	2	1427.6	(+0.0)	3.617	0.445	1.000	3	R.TK#EEVNEWFTK#.Y
GPN:BC007087_1	R27	5825	2	1350.5	(-0.0)	3.047	0.448	0.986		K.KYFNSTLTGR.M
GPN:BC007087_1	R27	5845	2	1222.3	(+0.0)	2.762	0.425	0.981		K.YFNSTLTGR.M
GPN:BC007087_1	R27	5847	2	1228.3	(+0.0)	2.400	0.398	0.963		K.YFNSTLT*TGR.M
GPN:BC007875_1	R24	2370	2	1070.2	(+0.3)	2.362	0.228	0.853		K.INQLPEAER.N
GPN:BC007875_1	R24	4470	2	1198.4	(-0.6)	2.489	0.220	0.835		R.KINQLPEAER.N
GPN:BC007875_1	R24	10605	2	2627.1	(+0.7)	2.678	0.375	0.967		R.SGLTGLVIGGLYPVFLAIPVNGGLAAR.Y
GPN:BC007875_1	R24	5314	2	1057.2	(+0.7)	2.546	0.253	0.932		R.YQSALLPHK.G
GPN:BC007875_1	R24	4452	2	1212.4	(+0.5)	2.257	0.103	0.362		R.K#INQL*PEAER.N
GPN:BC008212_1	R25	7470	2	1163.4	(+0.6)	2.410	0.505	0.985	2	R.GMITFESIEK#.A
GPN:BC008212_1	R25	6236	2	1493.7	(+0.7)	2.405	0.347	0.243	2	R.MKGEAEDILETEK.S
GPN:BC008700_1	R01	2566	2	1393.6	(-0.2)	2.900	0.298	0.275		K.ILDKLEDYQQK.V

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta M$	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GPN:BC008700_1	R01	5177	2	1015.2	(+0.8)	2.513	0.333	0.966		K.KVDAAELLR.L
GPN:BC008905_1	R14	6137	2	1250.4	(+0.8)	3.200	0.441	1.000	4	R.L*AQAWFNTHR.E
GPN:BC008905_1	R14	6141	2	1244.4	(+0.2)	2.739	0.383	0.973	4	R.LAQAWFNTHR.E
GPN:BC008905_1	R14	1582	2	958.1	(+0.6)	2.594	0.284	0.960	4	R.RLEEAALR.R
GPN:BC008905_1	R15	1378	2	958.1	(-0.1)	2.332	0.264	0.846	4	R.RLEEAALR.R
GPN:BC010102_1	R25	8812	2	1236.5	(+0.8)	3.655	0.420	1.000	1	R.GYIVIEDLWK.E
GPN:BC010102_1	R24	6468	2	1290.4	(+0.7)	3.025	0.439	0.989	1	R.SQLEESISQLR.H
GPN:BC010102_1	R24	6570	2	1651.8	(+0.8)	2.902	0.461	0.987	1	K.VDELSLYSVEGQSK.Y
GPN:BC010102_1	R25	6914	2	1302.4	(+0.2)	2.959	0.428	0.981	1	R.SQL*EESISQL*R.H
GPN:BC010457_1	R06	8032	2	1501.8	(-0.7)	2.353	0.119	0.417	5	R.L*L*PQVL*NSWSIGR.D
GPN:BC010457_1	R07	7977	2	1483.8	(+0.7)	4.288	0.490	0.999	5	R.LLPQVLNSWSIGR.D
GPN:BC010457_1	R06	6956	2	1301.5	(-0.1)	2.980	0.336	0.946	4	R.L*PSL*GAGFSQGL*K#.H
GPN:BC010457_1	R07	6831	2	1301.5	(-0.6)	2.848	0.262	0.884	4	R.L*PSL*GAGFSQGL*K#.H
GPN:BC010457_1	R07	9057	3	2509.9	(-0.2)	3.808	0.287	0.965	4	R.SIQQVLQTQDPPATMELAVAVLR.D
GPN:BC010457_1	R07	7973	2	1501.8	(+0.1)	2.593	0.289	0.901	5	R.L*L*PQVL*NSWSIGR.D
GPN:BC010736_1	R18	7697	2	1913.1	(+0.6)	4.596	0.562	1.000	2	K.IPDEFDNDPILVQQLR.R
GPN:BC010736_1	R18	8179	2	1933.2	(+0.9)	4.745	0.637	1.000	2	R.TVLEHYALEDPLAAFK.Q
GPN:BC010736_1	R18	7701	2	1925.1	(-0.9)	2.750	0.356	0.860	2	K.IPDEFDNDPIL*VQQL*R.R
GPN:BC011017_1	R16	842	2	1111.1	(+0.3)	2.985	0.346	0.980	2	R.AEAAL*EEESR.Q
GPN:BC011017_1	R16	6146	2	1564.7	(+0.5)	3.812	0.411	1.000	2	K.FL*ESTDSFNEL*K#.R
GPN:BC011017_1	R16	6596	2	1497.7	(+0.6)	3.085	0.366	0.982	2	R.K#*EAEL*L*QIEER.H
GPN:BC011017_1	R16	840	2	1105.1	(+0.7)	2.772	0.438	0.988	2	R.AEAAL*EEESR.Q
GPN:BC011596_1	R21	4698	2	946.0	(-0.7)	2.622	0.274	0.924		R.LSENVIDR.M
GPN:BC011596_1	R21	4730	2	952.0	(+0.9)	2.367	0.379	0.975		R.L*SENVIDR.M
GPN:BC011596_1	R21	6170	2	1716.9	(+0.9)	2.421	0.307	0.886		R.VTFEADENENITVVK#.G
GPN:BC011596_1	R21	5390	2	1576.7	(-0.5)	4.086	0.554	1.000		R.YSGAYGASVSDEELK.R
GPN:BC011596_1	R21	5392	2	1590.7	(-0.5)	3.606	0.480	0.999		R.YSGAYGASVSDEEL*K#.R
GPN:BC011596_1	R22	5498	2	1576.7	(+0.5)	4.219	0.529	1.000		R.YSGAYGASVSDEELK.R
GPN:BC011684_1	R12	6240	2	1731.9	(+0.5)	2.807	0.238	0.896	3	R.DWSNGAVL*QASSQL*SR.G
GPN:BC011684_1	R11	2110	2	942.1	(-0.5)	2.257	0.381	0.952	2	R.MSAATVL*SR.E
GPN:BC011684_1	R12	2104	2	936.1	(+0.7)	2.791	0.332	0.976	2	R.MSAATVLSR.E
GPN:BC011684_1	R12	2100	2	942.1	(+0.2)	2.387	0.434	0.975	2	R.MSAATVL*SR.E
GPN:BC011684_1	R13	4849	2	947.2	(+0.2)	2.507	0.203	0.800	1	R.IIQQGL*IR.V
GPN:BC011719_1	R18	7513	2	1147.3	(-0.7)	2.251	0.346	0.901	5	R.FFL*SSGL*IDK#.V
GPN:BC011719_1	R18	5881	2	1213.4	(+0.0)	2.757	0.384	0.971	6	K.L*EDPHVDIIR.R
GPN:BC011719_1	R18	7761	3	2381.6	(+1.0)	6.436	0.588	0.993	5	K.SGDTLLLLHHGDFSAEEVFHR.E
GPN:BC011719_1	R18	2290	2	1122.2	(+0.9)	2.374	0.332	0.949	3	K.TSSQPGFLER.L
GPN:BC011719_1	R18	5879	2	1207.4	(-0.3)	2.235	0.364	0.935	6	K.LEDPHVDIIR.R
GPN:BC011993_1	R18	12229	3	2348.7	(+0.9)	4.933	0.572	1.000	1	K.NWSLIGSVLGALIGVAGSTYVNR.V
GPN:BC011993_1	R18	12231	3	2366.7	(+0.8)	3.819	0.351	0.996	1	K.NWSL*IGSVL*GAL*IGVAGSTYVNR.V
GPN:BC011993_1	R18	5007	2	886.1	(+0.6)	2.200	0.233	0.863	1	K.ALLLEAQK.G
GPN:BC012043_1	R20	4954	2	1262.4	(+0.5)	3.326	0.336	0.536	1	K.DKLDQVSSEIK.E
GPN:BC012043_1	R20	4874	2	1262.4	(-0.5)	2.609	0.207	0.085	1	K.DKLDQVSSEIK.E
GPN:BC012043_1	R20	4860	2	1284.4	(+0.1)	2.461	0.284	0.113	1	K.DK#*DQVSSEIK#.E
GPN:BC012043_1	R20	5826	3	1587.9	(-0.5)	4.138	0.429	0.993	2	R.KPTLDKPSPETFVK.S
GPN:BC012043_1	R20	5824	2	1587.9	(-0.4)	4.015	0.470	1.000	2	R.KPTLDKPSPETFVK.S
GPN:BC012043_1	R20	1720	2	1019.1	(+0.9)	2.672	0.193	0.899	1	K.LDQVSSEIK.E
GPN:BC012043_1	R20	1694	2	1033.1	(-0.2)	2.346	0.204	0.733	1	K.L*DQVSSEIK#.E
GPN:BC012306_1	R24	9518	2	1722.0	(+0.8)	3.616	0.411	0.989	1	R.DSHLTLNQLLQGLR.Q
GPN:BC012306_1	R24	6844	2	956.2	(+0.7)	2.929	0.396	0.989	1	K.L*FQVL*APR.Y
GPN:BC012565_1	R23	6674	2	1374.6	(-0.1)	3.670	0.386	0.986	3	K.EVLLAQDMAVR.D
GPN:BC012565_1	R23	5312	2	1354.6	(-0.6)	2.924	0.361	0.966	2	K.LVEGPPPPPEPPK.T
GPN:BC012565_1	R23	5318	2	1368.6	(-0.1)	2.854	0.280	0.903	2	K.L*VEGPPPPPEPPK#.T
GPN:BC012565_1	R23	5248	2	1304.4	(-0.7)	2.646	0.257	0.886	1	R.SNL*YIAESTSGR.G

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GPN:BC012565_1	R23	5246	2	1298.4	(-0.2)	2.421	0.398	0.957	1	R.SNLYIAESTSGR.G
GPN:BC013283_1	R15	7821	3	2401.6	(+0.1)	4.697	0.485	0.991	5	R.AAQL*VVK#DSTFL*STL*EHHL*SR.Y
GPN:BC013283_1	R15	7317	2	1401.6	(+0.8)	4.111	0.456	1.000	6	R.DPEFVFDYDQLK.Q
GPN:BC013283_1	R15	7311	2	1415.6	(+0.2)	3.598	0.488	0.999	6	R.DPEFVFDYDQL*K#.Q
GPN:BC013283_1	R15	2326	2	887.1	(+0.5)	2.725	0.199	0.928	5	R.IIAEALTR.V
GPN:BC013283_1	R15	6587	2	1434.6	(+0.4)	3.945	0.469	0.996	2	R.LLDFSYEQYQK.A
GPN:BC013283_1	R15	6579	2	1454.6	(-0.3)	3.479	0.508	0.999	2	R.L*L*DFSYEYQYQK#.A
GPN:BC013283_1	R15	4879	2	984.2	(+0.6)	2.725	0.307	0.964	2	R.TMAAEVL*SR.R
GPN:BC013283_1	R15	4817	2	978.2	(-0.1)	2.576	0.199	0.847	2	R.TMAAEVLSR.R
GPN:BC013283_1	R15	4801	2	984.2	(+0.5)	2.527	0.272	0.939	2	R.TMAAEVL*SR.R
GPN:BC013587_1	R26	5696	2	1561.7	(-0.4)	3.778	0.446	0.999		R.IL*ANGEIVQDDDP.R.V
GPN:BC013587_1	R26	6460	2	1415.5	(-0.0)	4.300	0.442	0.999		R.L*GAAQSPFNDL*NR.Q
GPN:BC013587_1	R26	6462	2	1403.5	(-0.5)	3.626	0.398	0.985		R.LGAAQSPFNDLNR.Q
GPN:BC013587_1	R26	5690	2	1555.7	(-0.6)	3.598	0.481	0.997		R.ILANGEIVQDDDP.R.V
GPN:BC014545_1	R10	5757	3	4061.8	(-0.2)	7.635	0.631	0.973	1	K.EVL*PDQVEEEEEENDDQEEEEDEDEDDEEEDR.M
GPN:BC014545_1	R10	7939	2	1483.6	(-0.3)	3.979	0.537	1.000	2	K.L*L*DVTGGL*GTDEL*R.L
GPN:BC014545_1	R10	7941	2	1459.6	(+0.3)	3.347	0.475	0.623	2	K.LLDVTGGLGTDEL.R.L
GPN:BC014766_1	R19	7226	2	1189.4	(+0.4)	2.203	0.230	0.817	1	K.DLQMVNISLR.V
GPN:BC014766_1	R19	6472	2	1184.3	(+0.6)	3.045	0.214	0.945	1	K.FNASQL*ITQR.A
GPN:BC014766_1	R19	7830	2	1855.1	(-0.3)	3.935	0.489	0.996		R.IGGVQQDTILAEGLHFR.I
GPN:BC014766_1	R19	4476	2	1224.3	(+0.0)	3.351	0.439	1.000	1	K.IVQAEGEAEAAK#.M
GPN:BC014766_1	R19	1200	2	1224.3	(+0.6)	3.077	0.411	0.980	1	K.IVQAEGEAEAAK#.M
GPN:BC014766_1	R19	4472	2	1216.3	(-0.6)	2.599	0.432	0.974	1	K.IVQAEGEAEAAK.M
GPN:BC014766_1	R19	8836	3	2250.5	(+0.2)	5.212	0.465	1.000	2	R.IYL*TADNL*VL*NL*QDESFR.G
GPN:BC014766_1	R19	8842	2	2226.5	(+0.7)	4.114	0.418	1.000	2	R.IYLTADNLVNLQDESFR.G
GPN:BC014766_1	R20	8570	3	2250.5	(-0.1)	3.919	0.243	0.944	2	R.IYL*TADNL*VL*NL*QDESFR.G
GPN:BC014766_1	R19	2490	2	1007.1	(+0.6)	2.304	0.363	0.968	1	R.L*GL*DYEER.V
GPN:BC014766_1	R19	7254	2	1260.5	(+0.1)	4.103	0.527	0.999		K.LLLGAGAVAYGVR.E
GPN:BC014766_1	R19	7248	2	1278.5	(+0.0)	2.921	0.523	1.000		K.L*L*L*GAGAVAYGVR.E
GPN:BC014766_1	R21	8394	3	2226.5	(+0.2)	3.806	0.382	0.996	2	R.IYLTADNLVNLQDESFR.G
GPN:BC014918_1	R14	8973	3	3050.5	(-0.7)	6.819	0.554	1.000	2	K.ATRPEELLELLGGSHDLDSNQAAMVLIR.L
GPN:BC014918_1	R14	1910	2	1217.3	(+0.3)	2.367	0.259	0.899	2	K.ELQSVEQEV.R.W
GPN:BC014918_1	R14	7745	3	2251.4	(-0.5)	3.927	0.406	0.998	4	R.L*NFHPDQEDQFFSL*VHEK#.L
GPN:BC014918_1	R14	1912	2	1223.3	(+0.5)	2.205	0.259	0.863	2	K.EL*QSVEQEV.R.W
GPN:BC014987_1	R09	6172	2	1172.3	(-0.6)	2.545	0.371	0.928	2	K.L*L*EAISSL*DGK#.N
GPN:BC014987_1	R09	8154	2	1210.5	(+0.7)	3.856	0.388	1.000	2	K.LVLADLLEPVK.T
GPN:BC014987_1	R09	1646	2	918.0	(+0.6)	2.629	0.135*	0.474	1	R.SDLSVIQR.N
GPN:BC014987_1	R09	8704	2	1608.8	(+0.4)	2.863	0.442	0.982	2	R.TPL*EQEIFNL*L*HK#.N
GPN:BC015060_1	R25	6468	2	1285.4	(+0.8)	4.135	0.469	1.000	2	R.HETLTSLNLEK.K
GPN:BC015060_1	R25	6472	2	1311.4	(-0.6)	2.573	0.187	0.725	2	R.HETL*TSL*NL*EK#.K
GPN:BC015060_1	R25	6484	2	1285.4	(-0.9)	2.570	0.396	0.906	2	R.HETLTSLNLEK.K
GPN:BC015060_1	R25	5576	2	1349.6	(-0.7)	2.482	0.318	0.198	2	R.VPLHKPTDWQK.K
GPN:BC015109_1	R19	9620	3	2373.7	(+0.3)	3.765	0.253	0.976	2	K.NVEPFTSVL*SL*PYPFASEINK#.V
GPN:BC015109_1	R19	5210	2	1302.4	(-0.6)	2.387	0.368	0.924	3	K.VAVFTENASEVK#.I
GPN:BC015408_1	R01	8477	3	2554.0	(+0.8)	6.143	0.602	1.000	1	K.NELHNLLDKPQLQGIPVVLGNK.R
GPN:BC015408_1	R23	8604	3	2554.0	(+0.9)	7.256	0.615	1.000	1	K.NELHNLLDKPQLQGIPVVLGNK.R
GPN:BC015408_1	R23	5710	2	1054.2	(+0.4)	2.222	0.293	0.916	1	K.MNL*SAIQDR.E
GPN:BC015477_1	R10	1490	2	1205.3	(-0.4)	2.701	0.414	0.976	6	K.IDEELVTNSGK.F
GPN:BC015477_1	R10	5383	2	1304.5	(-0.0)	2.981	0.328	0.963	4	K.L*ISIQIPEVDR.E
GPN:BC015477_1	R10	1326	2	1117.3	(+0.5)	2.661	0.428	0.981	6	R.L*VTANTIDQK#.I
GPN:BC015477_1	R10	4277	2	1519.7	(+0.0)	3.886	0.418	1.000	6	R.SDL*IDQM@NASGPIK#.E
GPN:BC015477_1	R10	4355	2	1519.7	(-0.4)	3.570	0.466	1.000	6	R.SDL*IDQM@NASGPIK#.E
GPN:BC015477_1	R10	4131	2	1519.7	(+0.2)	3.162	0.416	0.975	6	R.SDL*IDQM@NASGPIK#.E
GPN:BC015477_1	R10	6599	2	1503.7	(-0.8)	3.156	0.245	0.741	6	R.SDL*IDQMNASGPIK#.E
GPN:BC015477_1	R10	4203	2	1519.7	(-0.4)	2.916	0.344	0.943	6	R.SDL*IDQM@NASGPIK#.E
GPN:BC015477_1	R10	6601	2	1489.7	(+0.2)	2.891	0.395	0.971	6	R.SDLIDQMNASGPIK.E

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta M$	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GPN:BC015477_1	R10	4059	2	1519.7	(-0.5)	2.844	0.427	0.969	6	R.SDL*IDQM@NASGPIK#.E
GPN:BC015477_1	R10	3969	2	1519.7	(+0.1)	2.461	0.411	0.945	6	R.SDL*IDQM@NASGPIK#.E
GPN:BC015477_1	R10	8333	2	1529.8	(+0.5)	4.277	0.496	0.997	6	K.VISDKDLELLDR.S
GPN:BC015477_1	R10	1484	2	1219.3	(-0.4)	2.356	0.220	0.718	6	K.IDEEL*VTNSGK#.F
GPN:BC015693_1	R08	6789	2	1315.6	(-0.3)	2.425	0.252	0.849	2	R.ALLLTDQHLYK.L
GPN:BC015693_1	R09	6208	2	1315.6	(+0.2)	3.154	0.450	0.988	2	R.ALLLTDQHLYK.L
GPN:BC015693_1	R09	7450	2	1164.3	(+0.6)	2.323	0.212	0.825	2	R.GSFTLLWPSR.-
GPN:BC015880_1	R01	6827	2	1143.3	(-0.3)	3.297	0.396	0.987		R.FGEMQLDFR.T
GPN:BC015880_1	R01	5759	2	1165.3	(+0.5)	2.774	0.417	0.988		R.FGEM@QL*DFR.T
GPN:BC015880_1	R01	7113	2	1766.9	(-1.0)	3.424	0.407	0.950		K.HL*EEAFTSEHWL*VR.I
GPN:BC016707_1	R15	7557	2	1942.2	(+0.4)	2.429	0.351	0.926	3	K.EQL*AQAMFDHIPVGVGSK#.G
GPN:BC016707_1	R15	6793	2	1406.5	(-0.5)	2.544	0.151	0.617	3	R.SYNDEL*QFL*EK#.I
GPN:BC016707_1	R15	2118	2	1235.4	(-0.5)	2.270	0.387	0.928	1	R.IASPEGQDYL*K#.G
GPN:BC017408_1	R20	6350	3	2704.9	(+0.2)	3.958	0.414	0.997		R.LTGSSAQEAASGVALGEAPDHSYESLR.V
GPN:BC017408_1	R20	5504	2	1481.7	(+0.4)	3.925	0.566	1.000	2	K.M@M@ADEAL*GSGL*VSR.V
GPN:BC017408_1	R20	6442	2	1449.7	(-0.4)	3.658	0.439	1.000	2	K.MMADEAL*GSGL*VSR.V
GPN:BC017408_1	R20	1176	2	925.1	(+0.3)	2.606	0.294	0.945	2	K.SPVAVQSTK#.V
GPN:BC017408_1	R20	1178	2	917.1	(+1.0)	2.493	0.306	0.955	2	K.SPVAVQSTK.V
GPN:BC017408_1	R21	7512	2	1733.0	(-0.2)	3.348	0.414	0.982	1	K.VIGNQSLVNELAFTAR.K
GPN:BC017693_1	R21	6004	2	1105.2	(+0.0)	2.728	0.315	0.946		K.DSNFQNPFK#.I
GPN:BC017693_1	R21	7450	2	2014.2	(-0.7)	2.457	0.301	0.876		R.TVLTAAADVLPDGPFPQDEK.L
GPN:BC017693_1	R21	6438	2	1266.4	(+0.9)	2.344	0.456	0.979		R.TSLDPSLEIYK.K
GPN:BC017732_1	R11	4644	2	965.1	(+0.3)	2.905	0.331	0.970	5	K.ASAAL*AAL*EK#.L
GPN:BC017732_1	R11	5862	2	1359.6	(+0.7)	2.893	0.392	0.522	2	K.DKPTETLLNTVK.D
GPN:BC017732_1	R11	5852	2	1387.6	(+0.3)	2.484	0.385	0.318	2	K.DK#PTETL*L*NTVK#.D
GPN:BC017732_1	R11	5396	2	1069.2	(+0.7)	2.302	0.159	0.720	2	K.DNLPIQIK.L
GPN:BC017732_1	R11	5654	2	1344.4	(-0.0)	3.795	0.483	1.000	2	K.HVSDWLDETNIK.G
GPN:BC017732_1	R11	5638	2	1358.4	(+0.5)	3.373	0.471	1.000	2	K.HVSDWL*DETNIK#.G
GPN:BC017732_1	R11	4944	2	1350.6	(+0.1)	3.041	0.195	0.111	5	R.L*NQIRPGL*QYK#.L
GPN:BC017732_1	R11	4724	2	965.1	(-0.5)	2.223	0.320	0.866	5	K.ASAAL*AAL*EK#.L
GPN:BC017734_1	R12	8080	2	1457.7	(+0.1)	2.682	0.336	0.944		R.FGQDIISPL*L*SVR.E
GPN:BC017734_1	R12	8598	2	2153.3	(+0.3)	3.742	0.580	1.000	6	K.GSPFPEVAESVQQUELESYR.A
GPN:BC017734_1	R12	8072	3	2100.4	(+0.0)	4.189	0.442	0.993	5	R.SK#L*EDIANAAL*AASAVTQVAK#.V
GPN:BC017734_1	R12	5030	2	1551.8	(-0.6)	2.525	0.384	0.937	6	R.VMNTGSQFVM@EGVK#.N
GPN:BC017734_1	R13	8291	2	1457.7	(+0.6)	3.131	0.307	0.970		R.FGQDIISPL*L*SVR.E
GPN:BC017895_1	R26	7890	2	1577.7	(-0.1)	3.093	0.304	0.950		R.GL*GWVQFSSEGL*R.N
GPN:BC017895_1	R26	6272	2	1579.8	(-0.1)	3.098	0.430	0.982		R.NALQQENHIIDGVK.V
GPN:BC017895_1	R26	6546	2	1372.6	(-0.2)	2.717	0.391	0.959		R.RIPWTAASSQL*K#.E
GPN:BC017959_1	R22	6648	2	1342.5	(+0.9)	3.222	0.312	0.978	1	K.QLLSASYEFQR.E
GPN:BC017959_1	R23	8762	2	1177.4	(+0.9)	3.420	0.360	0.988	1	K.FDLLEELVAK.E
GPN:BC018698_1	R15	7261	3	2616.9	(+0.3)	4.651	0.525	1.000		K.K#VTSVVFHPSQDL*VFSASPDATIR.I
GPN:BC018698_1	R15	6057	2	1110.3	(-0.3)	2.697	0.183	0.787		K.SSEQIL*ATL*K#.G
GPN:BC018698_1	R15	7801	3	3617.9	(+0.1)	5.518	0.543	0.870		R.TNVANFPGHSGPITSIAFSENGYYL*ATAADDSSVK#.L
GPN:BC018698_1	R15	6187	2	1341.5	(+0.5)	2.625	0.298	0.934		K.TL*QL*DNNFEVK#.S
GPN:BC019069_1	R13	10149	2	2202.6	(+0.7)	3.984	0.551	1.000	4	R.IGHVGMQIEHIIENIVAVTK.G
GPN:BC019069_1	R13	9785	2	2071.3	(+0.4)	3.090	0.413	0.984	4	K.SAALPIFSSFVSNWDEATK.R
GPN:BC019104_1	R23	2048	2	1097.2	(+0.4)	2.797	0.426	0.983	1	R.M@ESGL*SDVTK#.D
GPN:BC019104_1	R23	8920	3	3074.4	(+0.3)	5.071	0.504	0.645	1	R.RVEPPEL*PADL*QHWISYNEASSQL*L*R.M
GPN:BC019104_1	R23	8914	3	3050.4	(+0.1)	4.535	0.419	0.998	1	R.RVEPPELPADLQHWISYNEASSQLLR.M
GPN:BC019104_1	R23	7032	2	1015.2	(+0.8)	2.269	0.296	0.937	1	R.L*L*EPFEVR.T
GPN:BC020166_1	R15	1582	2	1105.2	(+1.0)	3.001	0.345	0.982	1	R.NPALYASNVR.R
GPN:BC020166_1	R15	1584	2	1111.2	(+0.7)	2.852	0.437	0.989	1	R.NPAL*YASNVR.R
GPN:BC020166_1	R15	9335	3	1624.9	(+0.8)	4.265	0.384	0.998	3	K.TAL*GVAEL*TVTDL*FR.A

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GPN:BC020166_1	R15	9345	2	1606.9	(-0.4)	3.687	0.489	1.000	3	K.TALGVAELTVTDLFR.A
GPN:BC020166_1	R15	9337	2	1624.9	(-0.1)	3.383	0.513	0.999	3	K.TAL*GVAEL*TVTDL*FR.A
GPN:BC020166_1	R15	9331	2	1606.9	(+1.0)	2.989	0.402	0.886	3	K.TALGVAELTVTDLFR.A
GPN:BC020166_1	R15	7025	2	1170.4	(+0.5)	2.390	0.458	0.978	3	R.TL*DTIQL*AFK#.M
GPN:BC020832_1	R21	8912	3	3474.9	(+0.5)	4.232	0.507	1.000		R.DLVPTGVLVTNGDYDQEQFADNQIPLLIGTK.L
GPN:BC020832_1	R21	5868	2	1064.2	(-0.3)	2.404	0.373	0.935		K.VL*VL*GDSGVGK#.S
GPN:BC021143_1	R01	10065	3	2588.9	(-0.2)	3.805	0.377	0.994	4	R.QWVEEFFPSVSL*GDPTL*ETL*L*R.Q
GPN:BC021143_1	R01	12701	3	2393.9	(+0.6)	5.014	0.408	1.000	3	R.SQLSPLEAPALLWGLLMAVGAVR.F
GPN:BC021143_1	R01	9095	2	2055.3	(+0.2)	3.798	0.265	0.961	3	R.WQQLWETPTLLWEAPR.L
GPN:BC021143_1	R03	8597	2	2055.3	(+1.0)	3.149	0.422	0.986	3	R.WQQLWETPTLLWEAPR.L
GPN:BC021208_1	R11	6974	2	1663.9	(-0.3)	3.649	0.441	1.000		R.AMYLPDTLSPADQLK.S
GPN:BC021208_1	R11	6054	2	1387.6	(+1.0)	2.927	0.561	1.000		K.LIAEEGVDSLNVK.E
GPN:BC021208_1	R11	7760	2	1642.9	(-0.5)	2.703	0.243	0.857		K.L*L*EL*QSIGTNNFL*R.F
GPN:BC021208_1	R11	6292	2	1246.4	(-0.4)	2.736	0.418	0.974		K.LTSLAAALDENK.D
GPN:BC021208_1	R11	6538	2	1320.5	(-0.0)	2.771	0.157	0.698		K.STL*QTL*PEIVAK#.E
GPN:BC021208_1	R11	924	2	1325.4	(+0.9)	4.609	0.472	1.000		K.VAEVEGEQVDNK#.A
GPN:BC021208_1	R11	8896	3	2867.3	(+0.2)	5.982	0.613	1.000		K.VIELVDKEDVHISTSQVAEIVATLEK.E
GPN:BC021208_1	R11	9116	3	2531.9	(+1.0)	6.184	0.551	1.000		R.VQQMIGQIDGLISQLEMDQQAGK.L
GPN:BC021208_1	R11	9088	3	2567.9	(-0.0)	5.484	0.556	1.000		R.VQQMIGQIDGL*ISQL*EM@DQQAGK#.L
GPN:BC021208_1	R11	6598	3	2920.3	(+0.5)	6.012	0.488	0.998		R.VVAAPQRPQTEPQPEMPDVTVLQSETLK.D
GPN:BC021208_1	R11	6602	3	2940.3	(-0.4)	4.700	0.394	0.987		R.VVAAPQRPQTEPQPEMPDVTVL*QSETL*K#.D
GPN:BC021208_1	R11	6288	2	1272.4	(-0.4)	2.541	0.378	0.943		K.L*TSL*AAAL*DENK#.D
GPN:BC021973_1	R22	7056	2	1294.5	(+0.1)	2.947	0.500	1.000	2	R.VNFL*VNAAGINR.D
GPN:BC021973_1	R22	4990	2	860.1	(+0.4)	2.218	0.300	0.932	2	R.AVAQLMAR.K
GPN:BC022352_1	R20	2290	2	1313.4	(-0.0)	2.696	0.164	0.766	1	K.ISNYGWDQSDK.F
GPN:BC022352_1	R20	6966	3	2565.9	(-0.8)	4.313	0.431	0.970	1	K.K#AEL*L*DNEK#PAAVVAPITTYGTVK#.I
GPN:BC022352_1	R20	6970	3	2529.9	(+0.6)	4.267	0.468	1.000	1	K.KAELLDNEKPAAVVAPITTYGTVK.I
GPN:BC022352_1	R20	6386	2	1196.3	(+0.3)	2.392	0.288	0.917	1	R.WDYLL*TQVEK#.E
GPN:BC022352_1	R21	6896	3	2529.9	(+0.6)	5.697	0.547	0.999	1	K.KAELLDNEKPAAVVAPITTYGTVK.I
GPN:BC022807_1	R20	7850	2	1852.0	(+1.0)	4.814	0.522	0.999		R.SIYSLILGQDNAADQSR.M
GPN:BC022807_1	R20	7420	2	1541.7	(+0.1)	4.168	0.549	1.000		K.YYFNNPEDGFFK.K
GPN:BC022807_1	R20	7422	2	1549.7	(-0.2)	3.247	0.416	0.979		K.YYFNNPEDGFFK#.K
GPN:BC023144_1	R08	5923	2	1060.2	(+0.6)	2.348	0.360	0.949		K.DIDIL*NSAGK#.M
GPN:BC023144_1	R08	7193	2	1740.8	(+0.8)	4.244	0.491	1.000		K.ESEITDEDIDGIL*ER.G
GPN:BC023144_1	R07	1590	2	1080.2	(+0.4)	2.479	0.189	0.756		R.FEDSPSYVK#.W
GPN:BC023144_1	R08	1592	2	1080.2	(+0.6)	2.681	0.329	0.963		R.FEDSPSYVK#.W
GPN:BC023144_1	R08	7677	2	1487.7	(+0.3)	2.665	0.376	0.382		K.IAFTEWIEPPK#.E
GPN:BC023144_1	R07	5069	2	1763.8	(-0.7)	3.782	0.457	1.000		K.IDEAESLNDEELEEK.E
GPN:BC023144_1	R08	5299	2	1763.8	(+0.9)	5.597	0.380	1.000		K.IDEAESLNDEELEEK.E
GPN:BC023144_1	R08	892	2	1174.2	(+0.3)	2.316	0.183	0.764		R.L*DGQTPHDER.Q
GPN:BC023144_1	R08	6903	2	1618.8	(-0.3)	3.145	0.292	0.281		K.L*GFDK#ENVYDEL*R.Q
GPN:BC023144_1	R07	6655	2	1342.5	(-0.1)	3.027	0.320	0.954		K.L*L*TQGFTNWNK#.R
GPN:BC023144_1	R08	6941	2	1342.5	(+0.1)	2.976	0.355	0.963		K.L*L*TQGFTNWNK#.R
GPN:BC023144_1	R08	1114	2	964.1	(-0.1)	2.584	0.222	0.870		R.L*VDQNL*NK#.I
GPN:BC023144_1	R08	5137	2	1944.0	(-0.6)	3.785	0.452	1.000		R.RTEQEEDEEL*L*TESSK#.A
GPN:BC023144_1	R08	7357	2	1380.6	(+0.6)	3.578	0.440	1.000		K.STLHNWMSEFK.R
GPN:BC023144_1	R08	7351	2	1394.6	(+0.2)	3.148	0.255	0.924		K.STL*HNWMSEFK#.R
GPN:BC023144_1	R08	4867	2	1767.8	(-0.6)	3.808	0.530	1.000		R.TEQEEDEELLTESSK.A
GPN:BC023144_1	R08	4945	2	1767.8	(+0.5)	3.690	0.523	1.000		R.TEQEEDEELLTESSK.A
GPN:BC023144_1	R08	4855	2	1787.8	(-0.5)	3.558	0.462	0.986		R.TEQEEDEEL*L*TESSK#.A
GPN:BC023144_1	R08	4789	2	1767.8	(-0.6)	2.866	0.423	0.975		R.TEQEEDEELLTESSK.A
GPN:BC023144_1	R08	8097	2	1394.7	(-0.4)	2.287	0.337	0.881		K.TL*QTISL*L*GYMK#.H
GPN:BC023247_1	R15	1966	3	2184.4	(+0.1)	4.282	0.247	0.965	1	R.L*QQQHSEQPPL*QPSPVTTTR.R
GPN:BC023247_1	R14	1688	2	949.1	(+0.6)	2.230	0.189	0.800	2	R.MQNDSILK.S
GPN:BC023247_1	R15	1462	2	949.1	(+1.0)	2.477	0.155	0.826	2	R.MQNDSILK.S
GPN:BC023247_1	R14	1034	2	1350.4	(+0.7)	3.492	0.539	1.000	2	K.SELGNQSPSTSSR.Q
GPN:BC023247_1	R14	1032	2	1356.4	(+0.2)	2.608	0.344	0.942	2	K.SEL*GNQSPSTSSR.Q
GPN:BC023247_1	R15	2104	3	2757.7	(-0.1)	3.944	0.428	0.997	3	K.VNFSEEGETEEDDQDSSHSSVTTVK.A

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GPN:BC023247_1	R14	978	2	1054.1	(+0.6)	2.610	0.448	0.987	3	R.YEATSVMQK.V
GPN:BC023247_1	R14	974	2	1062.1	(+0.3)	2.425	0.396	0.970	3	R.YEATSVMQK#.V
GPN:BC023532_1	R10	6009	3	2121.5	(+0.3)	5.761	0.542	1.000		R.K#PPGPPPPPPPPVQVM@YGR.K
GPN:BC023532_1	R10	7743	2	1284.4	(+0.3)	2.346	0.500	0.982		R.AQL*SQYFDAVK#.N
GPN:BC024240_1	R26	5322	2	1023.1	(-0.4)	3.324	0.344	0.983		R.LNDFASTVR.I
GPN:BC024240_1	R26	5326	2	1029.1	(-0.8)	2.940	0.377	0.942		R.L*NDFASTVR.I
GPN:BC024240_1	R26	5712	2	1185.3	(+0.5)	2.444	0.267	0.919		R.RL*NDFASTVR.I
GPN:BC025279_1	R07	6603	2	1321.5	(+0.8)	3.702	0.500	1.000	1	R.NLWVSGLSSTTR.A
GPN:BC025279_1	R07	6595	2	1333.5	(+0.2)	3.345	0.525	0.999	1	R.NL*WVSGL*SSTTR.A
GPN:BC025279_1	R07	5821	2	1274.4	(+0.1)	2.760	0.327	0.940	1	K.NTL*ETSSL*NFK#.V
GPN:BC025279_1	R08	6921	2	1321.5	(-0.0)	2.454	0.271	0.868	1	R.NLWVSGLSSTTR.A
GPN:BC026185_1	R17	10076	2	1568.8	(+0.2)	3.323	0.408	0.979	2	K.FPWFFSFGYFSK#.Q
GPN:BC026185_1	R17	9060	3	2401.7	(+0.4)	3.703	0.445	0.999	2	K.GVYIIGSSGFDSIPADLGVYTR.N
GPN:BC026185_1	R17	6236	2	1434.5	(+0.5)	2.532	0.359	0.960	2	K.SAIYGFQDQSNL*R.K
GPN:BC026222_1	R06	6426	2	2214.3	(-0.9)	3.673	0.428	0.960	3	K.ADPAFGL*ESSGIAGTTSDEPER.I
GPN:BC026222_1	R06	6760	3	3315.4	(-0.1)	5.041	0.639	1.000	3	K.ADPAFGL*ESSGIAGTTSDEPERIEESGNDEAR.V
GPN:BC026222_1	R06	8082	3	1906.1	(+0.9)	5.094	0.596	1.000	4	R.DIGEGNL*STAAAAAL*AAAAVK#.A
GPN:BC026222_1	R06	8098	2	1886.1	(-0.4)	4.401	0.580	1.000	4	R.DIGEGNLSTAAAAALAAAAVK.A
GPN:BC026222_1	R06	8088	2	1906.1	(-0.2)	3.683	0.335	0.956	4	R.DIGEGNL*STAAAAAL*AAAAVK#.A
GPN:BC026222_1	R06	6992	2	2011.2	(-0.9)	2.564	0.293	0.657	3	K.DMDEPSPVNVVEEVT*PK#.T
GPN:BC026222_1	R06	7040	2	1426.6	(-0.1)	3.549	0.327	0.980	4	R.HFEEL*ETIMDR.E
GPN:BC026222_1	R06	7048	2	1420.6	(+0.1)	3.452	0.511	0.994	4	R.HFEELETIMDR.E
GPN:BC026222_1	R07	6913	2	1420.6	(+0.8)	3.900	0.468	1.000	4	R.HFEELETIMDR.E
GPN:BC026222_1	R07	5903	2	1442.6	(-0.0)	3.441	0.351	0.828	4	R.HFEEL*ETIM@DR.E
GPN:BC026222_1	R07	6911	2	1426.6	(+0.6)	3.306	0.299	0.976	4	R.HFEEL*ETIMDR.E
GPN:BC026222_1	R08	7211	2	1426.6	(+0.2)	3.286	0.283	0.964	4	R.HFEEL*ETIMDR.E
GPN:BC026222_1	R06	996	2	925.0	(+0.5)	2.219	0.244	0.883	3	K.HLAAVEER.K
GPN:BC026222_1	R08	1180	2	931.0	(+0.6)	2.377	0.134	0.745	3	K.HL*AAVEER.K
GPN:BC026222_1	R06	6448	2	1724.0	(-0.2)	3.456	0.418	0.546	3	K.MK#EEVPTAL*VEAHVR.K
GPN:BC026222_1	R06	4688	2	1282.5	(-0.1)	2.248	0.108	0.291	3	R.NVEM@FM@TIEK#.S
GPN:BC026222_1	R07	6149	2	1266.5	(+0.5)	2.229	0.409*	0.131	3	R.NVEMFM@TIEK#.S
GPN:BC026222_1	R06	11142	3	2184.5	(-0.7)	4.239	0.462	1.000	3	K.SL*SSL*VVQL*L*QFQEEVFGK#.H
GPN:BC026222_1	R06	11158	2	2152.5	(+0.4)	3.947	0.598	1.000	3	K.SLSSLVVQLLQFQEEVFGK.H
GPN:BC026222_1	R07	11243	3	2184.5	(+0.3)	4.994	0.552	1.000	3	K.SL*SSL*VVQL*L*QFQEEVFGK#.H
GPN:BC026222_1	R07	11259	2	2152.5	(+0.5)	3.743	0.528	1.000	3	K.SLSSLVVQLLQFQEEVFGK.H
GPN:BC026222_1	R07	11247	2	2184.5	(-0.8)	2.283	0.241	0.385	3	K.SL*SSL*VVQL*L*QFQEEVFGK#.H
GPN:BC026222_1	R11	11266	3	2184.5	(-0.3)	4.124	0.381	0.997	3	K.SL*SSL*VVQL*L*QFQEEVFGK#.H
GPN:BC026222_1	R06	8346	2	1358.6	(+0.2)	2.874	0.343	0.950	5	K.SL*VAL*L*VETQMK#.K
GPN:BC026222_1	R07	8301	2	1332.6	(+0.7)	4.171	0.527	1.000	5	K.SLVALLVETQMK.K
GPN:BC026222_1	R07	8297	2	1358.6	(-0.2)	3.023	0.256	0.911	5	K.SL*VAL*L*VETQMK#.K
GPN:BC026222_1	R07	7671	2	1374.6	(+0.5)	2.549	0.159	0.694	5	K.SL*VAL*L*VETQM@K#.K
GPN:BC026222_1	R03	6025	2	1126.3	(+0.1)	2.304	0.197	0.753	5	K.TPEIYLAYR.N
GPN:BC026222_1	R06	6404	2	1126.3	(+0.1)	3.135	0.462	0.999	5	K.TPEIYLAYR.N
GPN:BC026222_1	R06	6386	2	1132.3	(+0.6)	2.735	0.307	0.969	5	K.TPEIYL*AYR.N
GPN:BC026222_1	R07	6289	2	1126.3	(+0.9)	3.411	0.464	1.000	5	K.TPEIYLAYR.N
GPN:BC026222_1	R07	6285	2	1132.3	(+0.6)	2.983	0.400	0.989	5	K.TPEIYL*AYR.N
GPN:BC026222_1	R08	6591	2	1126.3	(-0.0)	2.914	0.507	0.994	5	K.TPEIYLAYR.N
GPN:BC026222_1	R10	6541	2	1126.3	(+0.6)	3.091	0.548	1.000	5	K.TPEIYLAYR.N
GPN:BC030129_1	R12	5152	2	1286.4	(+0.5)	3.467	0.360	0.987		R.VQGLLEEEAAAR.G
GPN:BC030129_1	R12	5150	2	1298.4	(+0.4)	3.406	0.347	0.984		R.VQGL*L*EEEAAR.G
GPN:BC030129_1	R12	6496	2	1075.3	(+0.9)	2.511	0.348	0.965	2	R.TDVLTGLSIR.L
GPN:BC030652_1	R10	8897	3	1976.2	(+0.9)	4.315	0.485	1.000	2	R.NPEL*STQL*IDIHTAAAR.A
GPN:BC030652_1	R10	9097	2	1839.2	(+0.5)	2.380	0.242	0.818	2	K.VL*DIL*L*EQYPAL*ITGR.S
GPN:BC030652_1	R10	5639	2	1165.3	(+0.9)	2.329	0.182	0.692	2	K.FLQALADGSSR.L
GPN:BC031791_1	R17	7984	2	1630.9	(+0.7)	3.809	0.405	0.990		K.DL*NL*MAPGL*TIQAVR.V
GPN:BC031791_1	R17	7994	2	1612.9	(-0.2)	3.058	0.303	0.944		K.DLNLMAPGLTIQAVR.V
GPN:BC031791_1	R17	2454	2	1542.7	(+0.5)	3.115	0.458	0.986		K.EAL*EPSENVQNK#.E
GPN:BC031791_1	R17	6954	2	1335.5	(+0.6)	4.489	0.531	1.000	2	R.ISEIEDAAFLAR.E



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GPN:BC031791_1	R17	6958	2	1341.5	(+0.3)	4.058	0.526	1.000	2	R.ISEIEDAAFL*AR.E
GPN:BC031791_1	R17	7998	2	1630.9	(-0.8)	3.002	0.329	0.863		K.DL*NL*MAPGL*TIQAVR.V
GPN:BC032300_1	R25	7532	2	1620.8	(-0.2)	4.808	0.589	0.999	1	K.HNELTGDNVGPLILK.K
GPN:BC032300_1	R25	13251	3	3397.2	(+0.6)	3.745	0.336	0.957	1	R.LTVSEWLRLPFLGLVALLGYLAVRPFLPK.K
GPN:BC032638_1	R16	6704	2	1622.8	(-0.5)	3.749	0.539	1.000	1	R.L*QGL*SASDVTEQIIK#.T
GPN:BC032638_1	R20	9376	3	3722.1	(-0.3)	4.764	0.607	0.984	1	K.GLQGVGPGSNDETLLSAVASALHTSSAPITGQVSAAVEK.N
GPN:BC032643_1	R11	8960	2	1594.8	(+0.1)	2.520	0.264	0.859	6	R.DLFEDELVPLFEK.A
GPN:BC032643_1	R12	9128	2	1594.8	(+0.6)	2.574	0.308	0.939	6	R.DLFEDELVPLFEK.A
GPN:BC032643_1	R12	9146	2	1594.8	(-0.6)	2.388	0.218	0.738	6	R.DLFEDELVPLFEK.A
GPN:BC032643_1	R13	9275	2	1594.8	(+0.6)	3.240	0.365	0.964	6	R.DLFEDELVPLFEK.A
GPN:BC032643_1	R14	9105	2	1594.8	(+0.3)	3.131	0.413	0.980	6	R.DLFEDELVPLFEK.A
GPN:BC032643_1	R12	8392	2	1709.9	(-0.2)	3.809	0.428	1.000	5	K.EFNEDGALAVLQQFK.D
GPN:BC032643_1	R12	8386	2	1729.9	(-0.5)	2.570	0.164	0.561	5	K.EFNEDGAL*AVL*QQFK#.D
GPN:BC032643_1	R13	8569	2	1729.9	(-0.1)	2.439	0.167	0.507	5	K.EFNEDGAL*AVL*QQFK#.D
GPN:BC032643_1	R12	7146	2	1279.5	(-0.2)	2.643	0.374	0.961	6	R.L*MMDPL*TGL*NR.G
GPN:BC032643_1	R12	7166	2	1261.5	(+0.9)	2.426	0.241	0.877	6	R.LMMDPLTGLNR.G
GPN:BC032643_1	R12	7596	2	1474.7	(+0.5)	4.425	0.527	1.000	6	R.NLANTVTEEILEK.A
GPN:BC032643_1	R12	7586	2	1494.7	(-0.3)	3.294	0.159	0.823	6	R.NL*ANTVTEEIL*EK#.A
GPN:BC032643_1	R13	7789	2	1494.7	(+0.4)	2.902	0.317	0.953	6	R.NL*ANTVTEEIL*EK#.A
GPN:BC032643_1	R12	6006	2	1374.5	(-0.3)	2.706	0.243	0.111	5	K.TK#EQIL*EEFSK#.V
GPN:BC032643_1	R14	9091	2	1620.8	(+0.1)	3.041	0.306	0.938	6	R.DL*FEDEL*VPL*FEK#.A
GPN:BC032797_1	R20	6666	2	1153.3	(+0.8)	2.807	0.342	0.976	1	K.AMVEFATLDR.Q
GPN:BC032797_1	R20	6662	2	1159.3	(+0.8)	2.737	0.336	0.973	1	K.AMVEFATL*DR.Q
GPN:BC032797_1	R19	9390	3	2357.5	(-0.4)	3.755	0.423	0.998	1	R.SSSNSGSTGFISFSGVESAL*SSL*K#.N
GPN:BC032797_1	R20	5958	2	1175.3	(+0.3)	2.468	0.332	0.958	1	K.AM@VEFATL*DR.Q
GPN:BC032847_1	R09	9848	3	1762.1	(+0.5)	4.037	0.380	0.999		R.FL*NWIPL*GYIFETK#.L
GPN:BC032847_1	R09	7444	2	1292.5	(+0.1)	2.506	0.120	0.538		R.IYL*DML*NVYK#.C
GPN:BC032847_1	R09	5412	2	924.1	(+0.7)	2.642	0.412	0.987		K.L*ISGWVSR.S
GPN:BC032847_1	R09	6082	3	2142.4	(+0.5)	5.089	0.413	0.997		R.MAKPEEVLVENDQGEVVR.E
GPN:BC032847_1	R09	5438	2	1371.6	(+0.0)	2.957	0.468	0.578		K.NVDILKDPETVK.Q
GPN:BC032847_1	R09	9560	3	2169.5	(+0.3)	3.945	0.428	0.999		K.YML*L*PNQVWDSIIQQATK#.N
GPN:BC032847_1	R09	9562	3	2149.5	(+0.8)	3.855	0.486	1.000		K.YMLLPNQVWDSIIQQATK.N
GPN:BC032847_1	R09	6728	2	1758.8	(+0.1)	2.495	0.179	0.636		K.EFAGEDTSDLFLEER.E
GPN:BC032893_1	R26	7456	2	1398.5	(+0.7)	2.742	0.261	0.932	2	K.FSL*DTVINPDDR.V
GPN:BC032893_1	R26	7846	2	1407.6	(+0.7)	3.808	0.333	0.988	2	R.LLEITEGSEFLR.L
GPN:BC032893_1	R26	7850	2	1425.6	(-0.1)	2.267	0.247	0.684	2	R.L*L*EITEGSEFL*R.L
GPN:BC033074_1	R05	4408	2	1193.3	(-0.1)	2.744	0.347	0.959	5	K.M@AEQWL*QEK#.E
GPN:BC033074_1	R05	4494	2	1193.3	(-0.6)	2.556	0.262	0.889	5	K.M@AEQWL*QEK#.E
GPN:BC033074_1	R05	4336	2	1193.3	(-0.7)	2.375	0.194	0.724	5	K.M@AEQWL*QEK#.E
GPN:BC033074_1	R05	1930	2	1186.3	(+0.4)	3.351	0.462	1.000	5	K.SNSHAAIDWGK.M
GPN:BC033074_1	R05	1926	2	1194.3	(-0.2)	3.114	0.372	0.972	5	K.SNSHAAIDWGK#.M
GPN:BC033074_1	R05	6052	2	1087.3	(-0.0)	2.626	0.268	0.926	2	R.YM@VAL*QIAR.E
GPN:BC033074_1	R05	1178	2	1058.1	(-0.2)	2.290	0.222	0.799	2	R.AL*DTDMER.L
GPN:BC033113_1	R24	9038	3	2596.0	(+0.5)	4.456	0.488	1.000		K.LYLHELLEGSEIYLPEVVKPPR.N
GPN:BC033113_1	R24	5302	2	1225.3	(+0.8)	2.614	0.385	0.974		R.ALGPGELEPER.L
GPN:BC033299_1	R23	5940	2	1486.6	(-0.8)	2.871	0.362	0.870	1	R.HVL*DNSGEWSVTK#.R
GPN:BC033299_1	R22	6068	2	1113.3	(+0.5)	2.629	0.397	0.978	1	R.INAQLPLTDK.A
GPN:BC033299_1	R22	6064	2	1133.3	(-0.3)	2.331	0.184	0.641	1	R.INAQL*PL*TDK#.A
GPN:BC033299_1	R23	7444	2	1399.6	(+0.6)	2.987	0.470	0.991	2	K.VL*GDL*IFNQPDR.R
GPN:BC033299_1	R23	7448	2	1387.6	(+0.0)	2.928	0.364	0.965	2	K.VLGDILFNQPDR.R
GPN:BC033299_1	R22	9952	2	1564.9	(+0.3)	3.701	0.384	0.989	1	R.YVILDIPLLFETK.K
GPN:BC033299_1	R22	9956	2	1590.9	(-0.4)	3.324	0.132	0.778	1	R.YVIL*DIPL*L*FETK#.K
GPN:BC033299_1	R23	9924	2	1564.9	(+0.9)	3.470	0.441	0.995	1	R.YVILDIPLLFETK.K
GPN:BC033299_1	R23	9950	2	1564.9	(-0.4)	2.766	0.325	0.944	1	R.YVILDIPLLFETK.K
GPN:BC033299_1	R23	5936	2	1472.6	(-0.1)	2.444	0.478	0.976	1	R.HVLDNSGEWSVTK.R
GPN:BC033775_1	R24	6028	2	2057.0	(-0.8)	3.897	0.350	0.944	1	K.YPDLYPQEDEDEEEER.E

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GPN:BC033775_1	R24	4808	2	1886.1	(-0.8)	3.838	0.568	1.000	1	K.KPAEQAEETAPEIATATK.E
GPN:BC034346_1	R10	1530	2	1058.2	(+1.0)	2.331	0.308	0.942		R.AQHQLGEFK.T
GPN:BC034346_1	R10	8109	2	1318.4	(+0.7)	3.478	0.451	1.000		K.DNALLSAIEESR.K
GPN:BC034346_1	R10	8105	2	1330.4	(+0.1)	2.888	0.414	0.978		K.DNAL*L*SAIEESR.K
GPN:BC034346_1	R01	4387	2	1197.3	(+0.1)	2.363	0.293	0.898		K.DSQGENMFLR.C
GPN:BC034346_1	R01	2126	2	1126.3	(+0.7)	3.045	0.339	0.981		R.GLDISHISQR.L
GPN:BC034346_1	R01	2124	2	1132.3	(+0.4)	2.966	0.258	0.960		R.GL*DISHISQR.L
GPN:BC034346_1	R02	5132	2	1132.3	(+0.3)	2.221	0.422	0.972		R.GL*DISHISQR.L
GPN:BC034346_1	R10	5087	2	1132.3	(+0.1)	3.099	0.351	0.977		R.GL*DISHISQR.L
GPN:BC034346_1	R10	5071	2	1126.3	(+0.7)	2.763	0.323	0.970		R.GLDISHISQR.L
GPN:BC034346_1	R01	8449	3	3416.7	(+0.2)	4.974	0.519	1.000		R.ILHTLLASGEDALDFTQESEPSYISDVGPGR.S
GPN:BC034346_1	R02	7660	3	3416.7	(-0.0)	4.075	0.367	0.993		R.ILHTLLASGEDALDFTQESEPSYISDVGPGR.S
GPN:BC034346_1	R03	7937	3	3416.7	(-0.1)	5.256	0.596	0.997		R.ILHTLLASGEDALDFTQESEPSYISDVGPGR.S
GPN:BC034346_1	R10	8663	3	3416.7	(-0.0)	4.472	0.500	1.000		R.ILHTLLASGEDALDFTQESEPSYISDVGPGR.S
GPN:BC034346_1	R11	8424	3	2851.2	(+0.8)	3.734	0.434	0.979		R.LESLSAATTFEPLPVKDTDIQGLK.N
GPN:BC034346_1	R11	5616	2	985.1	(+0.1)	2.285	0.361	0.938		R.L*TL*SQFQK#.Q
GPN:BC034346_1	R01	1296	2	1292.4	(-0.3)	3.031	0.195	0.890		R.NL*QEIQQAGER.L
GPN:BC034346_1	R03	1414	2	1286.4	(+0.7)	3.497	0.306	0.977		R.NLQEIQQAGER.L
GPN:BC034346_1	R10	1528	2	1292.4	(+0.4)	3.402	0.209	0.957		R.NL*QEIQQAGER.L
GPN:BC034346_1	R01	4615	2	1005.2	(+0.5)	2.333	0.192	0.807		K.NMALSAIER.Y
GPN:BC034346_1	R01	4605	2	1011.2	(-0.6)	2.266	0.244	0.830		K.NMAL*SAIER.Y
GPN:BC034346_1	R10	5629	2	1011.2	(+1.0)	2.306	0.208	0.835		K.NMAL*SAIER.Y
GPN:BC034346_1	R10	6463	2	1370.5	(+0.7)	3.710	0.421	0.999		R.SSLDNIEMAYAR.Q
GPN:BC034346_1	R10	6077	2	1392.5	(+0.7)	3.407	0.347	0.984		R.SSL*DNIEM@AYAR.Q
GPN:BC034346_1	R01	8325	2	1383.7	(+0.8)	3.128	0.491	1.000		R.TLITFAGMIPYR.T
GPN:BC034346_1	R01	8319	2	1389.7	(+0.7)	2.782	0.346	0.969		R.TL*ITFAGMIPYR.T
GPN:BC034346_1	R03	7881	2	1389.7	(+0.9)	2.481	0.278	0.915		R.TL*ITFAGMIPYR.T
GPN:BC034346_1	R10	8689	2	1389.7	(+0.8)	3.846	0.393	1.000		R.TL*ITFAGMIPYR.T
GPN:BC034346_1	R10	8691	2	1383.7	(+0.8)	3.387	0.418	0.990		R.TLITFAGMIPYR.T
GPN:BC034346_1	R10	8221	2	1405.7	(+0.9)	2.963	0.484	0.989		R.TL*ITFAGM@IPYR.T
GPN:BC034346_1	R24	4688	2	1286.4	(-0.2)	3.308	0.241	0.949		R.NLQEIQQAGER.L
GPN:BC034525_1	R24	4416	2	1700.8	(-0.4)	3.240	0.357	0.666	1	R.SSPSGPSNPSNPSVEEK.L
GPN:BC034525_1	R24	8248	2	2088.2	(+0.2)	3.612	0.549	1.000		R.TVNTFSQSVSSLFGEDNVR.A
GPN:BC034525_1	R24	8246	2	2094.2	(+0.0)	3.038	0.382	0.970		R.TVNTFSQSVSSL*FGEDNVR.A
GPN:BC034525_1	R24	1774	2	1708.8	(-0.2)	2.703	0.279	0.861	1	R.SSPSGPSNPSNPSVEEK#.L
GPN:BC034589_1	R01	9975	2	2138.5	(-0.8)	3.323	0.435	0.953	1	R.ALVQTEDHLLFLQQLAGK.V
GPN:BC034589_1	R01	8347	3	2020.3	(+0.9)	3.850	0.406	0.984	1	K.DKESGMSSLYVFNPIFGK.W
GPN:BC034589_1	R02	5978	2	1170.3	(+0.6)	2.656	0.334	0.965		K.FASLEFSPGSK.K
GPN:BC034589_1	R02	6826	2	1221.4	(+0.4)	2.367	0.220	0.850	1	K.VLLLIDDEYK.V
GPN:BC034589_1	R02	5836	2	1159.3	(+0.4)	2.232	0.246	0.852	1	K.NEINIDTLAR.D
GPN:BC036379_1	R10	5961	2	1342.5	(+0.6)	3.379	0.378	0.984	1	K.FFADDTQAAL*TK#.H
GPN:BC036379_1	R10	10785	3	2699.1	(+1.0)	5.220	0.537	1.000	1	K.HIQDAPEEFISELAELYLIKPLNK.T
GPN:BC036379_1	R10	5453	2	1259.4	(+0.6)	2.806	0.320	0.968	1	R.IISGHIDL*DNR.G
GPN:BC036379_1	R10	5207	2	1263.5	(+0.7)	2.498	0.213	0.856	1	K.IPEDQHALLVK.Y
GPN:BC036379_1	R10	9463	3	2295.6	(+0.3)	4.600	0.409*	0.047	1	K.K#K#PEISFMFQDEIEDFL*R.K
GPN:BC036379_1	R10	6663	2	1522.7	(-0.2)	2.680	0.354	0.950	1	K.NNPVHLITEEDLK.Q
GPN:BC036379_1	R10	6393	3	2701.8	(-0.6)	4.207	0.447	0.991	1	K.TGQGDYPL*NNEL*DK#EQEDVASTTR.K
GPN:BC036379_1	R10	8839	2	1857.1	(-0.4)	2.490	0.233	0.774	1	K.TYDL*PGNFL*QTAL*QTR.L
GPN:BC036379_1	R10	9533	3	2345.7	(+0.7)	4.272	0.300	0.994	1	R.VNIVDLQQVINVDLIHIENR.I
GPN:BC036391_1	R16	10810	3	4055.6	(-0.4)	5.585	0.520	1.000	5	K.EGPEGANLIYHLPQFEGDQDILQMFMPFGNVISAK.V
GPN:BC036391_1	R15	5561	3	1549.8	(+0.1)	4.114	0.438	1.000	7	R.K#AAL*EAQNAL*HNIK#.T
GPN:BC036391_1	R16	5442	2	1413.6	(+0.6)	2.918	0.321	0.956	7	K.AAL*EAQNAL*HNIK#.T
GPN:BC039256_1	R06	8468	2	1682.0	(+0.8)	4.666	0.573	1.000	2	K.DILLVNDHLLNFVR.E
GPN:BC039256_1	R06	6810	2	1261.5	(+0.5)	3.667	0.428	1.000	3	R.HDVIVSIVTAAK#.K
GPN:BC039256_1	R06	4966	2	1452.6	(-0.2)	2.769	0.316	0.939	3	R.IYAPEAPYTSPDK.L
GPN:BC039256_1	R06	8022	3	1810.1	(+0.9)	4.176	0.454	1.000	2	K.KDILLVNDHLLNFVR.E
GPN:BC039256_1	R06	10510	3	2435.8	(+0.1)	3.846	0.404	0.997	3	R.TAQAIEPYITNFFNQVL*M@L*GK#.T
GPN:BC039256_1	R06	10582	3	2435.8	(-0.1)	3.735	0.331	0.988	3	R.TAQAIEPYITNFFNQVL*M@L*GK#.T
GPN:BC039256_1	R07	8433	2	1682.0	(+0.5)	2.410	0.419	0.970	2	K.DILLVNDHLLNFVR.E

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GPN:BC039828_1	R08	8423	3	2631.8	(+0.8)	5.365	0.537	0.992	1	K.AFQNKQENSVNQEIEQFQQAIEK#.D
GPN:BC039828_1	R08	9685	2	1874.1	(+0.2)	2.706	0.475	0.979	1	R.FGPNVPAL*L*EAIDDAYR.Q
GPN:BC039828_1	R08	8473	3	2913.2	(+0.8)	4.394	0.512	0.996	2	K.INQLSELADPLKDELNLADSEVDNQK.R
GPN:BC039828_1	R08	7681	2	1269.4	(+1.0)	2.785	0.208	0.915	2	K.LYFDNLLSQR.A
GPN:BC039828_1	R08	5527	2	1573.7	(-0.3)	3.147	0.425	0.981	2	K.NETLSISVQPGEGNK.A
GPN:BC039828_1	R08	5731	2	1342.5	(+0.5)	2.252	0.298	0.906	1	R.AYNEAEVLYNR.S
GPN:BC040035_1	R26	7966	2	1094.3	(+0.9)	2.825	0.509	0.999		K.GIGFLTSGWR.F
GPN:BC040035_1	R26	9818	3	3565.1	(+0.6)	3.707	0.414	0.989		K.LKPYVSYLAPSEETPLTAAQLFSEAVAPAIEK.D
GPN:BC040035_1	R26	4724	2	1156.2	(+0.1)	2.241	0.372	0.940	2	K.YGFQPTQEGK.L
GPN:BC040185_1	R11	7612	3	2387.6	(+0.7)	3.847	0.455	1.000	1	R.NVTEDLVPIEDIPDVHPDLQK.Q
GPN:BC040185_1	R11	10594	2	1628.0	(-0.1)	2.273	0.250	0.736	1	K.TLAFVIPVVQALLSR.V
GPN:BC041098_1	R06	8268	3	2919.2	(-0.1)	4.537	0.515	1.000	1	R.AYNYVAQEVDDYHAFQTL*THIYNK#.V
GPN:BC041098_1	R06	1666	2	1050.2	(+0.7)	2.486	0.191	0.859	1	K.DLSQNFPTK.A
GPN:BC041098_1	R06	7794	2	1329.5	(+0.7)	4.148	0.471	1.000	2	K.FL*FVDADQIVR.T
GPN:BC041098_1	R06	7780	2	1323.5	(-0.2)	3.640	0.421	1.000	2	K.FLFVDADQIVR.T
GPN:BC041098_1	R06	5526	2	1009.1	(+0.8)	2.431	0.399	0.978	1	R.FTILDSQGK.T
GPN:BC041098_1	R06	7764	3	3465.8	(+0.7)	5.277	0.584	1.000	2	R.GQYQGLSQDPNSLSNLDQDLPNMNIHQVPIK.S
GPN:BC041098_1	R06	5602	2	1469.7	(+0.3)	3.564	0.549	1.000	1	K.HLVESTNEMAPLK.V
GPN:BC041098_1	R06	9402	2	1483.9	(+0.7)	4.592	0.537	1.000	1	R.ILASPVELALVVMK.D
GPN:BC041098_1	R06	9404	2	1509.9	(-0.2)	3.002	0.391	0.961	1	R.IL*ASPVEL*AL*VVMK#.D
GPN:BC041098_1	R06	10784	2	1632.0	(-0.2)	4.042	0.447	0.993	2	K.IFLDLVLFPLVVDK.F
GPN:BC041098_1	R06	1642	2	988.2	(+0.8)	2.738	0.302	0.968	2	R.ISMINNPAK.E
GPN:BC041098_1	R06	1652	2	996.2	(+0.1)	2.422	0.313	0.913	2	R.ISMINNPAK#.E
GPN:BC041098_1	R06	8036	3	2923.1	(+0.5)	3.936	0.409	0.999	2	K.KADMVNEDLLSDGTSENESEGFWDSEFK.W
GPN:BC041098_1	R06	7412	2	1795.1	(-0.9)	3.088	0.482	0.943	1	R.K#EPVYL*SGYGVEL*AIK#.S
GPN:BC041098_1	R06	5506	3	1597.9	(+0.9)	4.087	0.308	0.997	1	R.KHLVESTNEMAPLK.V
GPN:BC041098_1	R06	6642	2	1704.9	(+0.9)	2.985	0.392	0.980	1	K.LNIQPSEADYAVDIR.S
GPN:BC041098_1	R06	5792	2	1211.3	(+0.3)	2.586	0.452	0.985	2	K.SGYWASHL*AGR.K
GPN:BC041098_1	R06	6076	2	1349.5	(+0.8)	3.602	0.475	1.000	2	R.VEEDVASDL*VMK#.V
GPN:BC041098_1	R06	7750	2	1663.9	(+0.9)	4.010	0.524	0.999	1	K.VWQLQDLSFQTAAR.I
GPN:BC041098_1	R06	7746	3	1675.9	(+0.8)	3.991	0.468	0.995	1	K.VWQL*QDL*SFQTAAR.I
GPN:BC043619_1	R20	5786	2	1301.5	(+0.3)	2.213	0.431	0.381	1	K.GK#PDL*NTAL*PVR.Q
GPN:BC043619_1	R20	8840	2	1782.0	(-0.3)	4.587	0.481	0.998	1	K.K#L*SGL*NAFDIAEEL*VK#.T
GPN:BC043619_1	R19	10030	3	2066.4	(+0.9)	3.723	0.431	0.999	1	R.L*EEAL*MADML*AHVEEL*AR.D
GPN:BC043619_1	R19	9466	3	1645.9	(+0.5)	3.988	0.266	0.990	1	K.L*SGL*NAFDIAEEL*VK#.T
GPN:BC043619_1	R19	9462	2	1645.9	(-0.3)	3.687	0.411	0.981	1	K.L*SGL*NAFDIAEEL*VK#.T
GPN:BC043619_1	R20	9182	3	1645.9	(+0.2)	4.462	0.321	0.990	1	K.L*SGL*NAFDIAEEL*VK#.T
GPN:BC043619_1	R20	9180	2	1619.9	(+1.0)	3.383	0.533	0.999	1	K.LSGLNAFDIAEELVK.T
GPN:BC043619_1	R21	8984	2	1619.9	(+0.9)	4.090	0.541	0.997	1	K.LSGLNAFDIAEELVK.T
GPN:BC043619_1	R20	9600	3	2222.6	(+0.1)	4.223	0.490	0.999	1	K.RL*EEAL*MADML*AHVEEL*AR.D
GPN:BC043619_1	R21	8988	2	1645.9	(-0.9)	2.660	0.241	0.555	1	K.L*SGL*NAFDIAEEL*VK#.T
GPN:BC045623_1	R06	5300	2	1695.7	(-0.4)	3.694	0.463	1.000	2	K.ASSSSASSAGAL*ESSL*DR.K
GPN:BC045623_1	R06	8540	2	1386.7	(-0.1)	2.869	0.350	0.948	2	K.ISSIL*SSL*TSVMK#.N
GPN:BC045623_1	R06	6000	2	1184.3	(+0.2)	2.950	0.445	0.982	2	K.L*EEFVNGL*DK#.Q
GPN:BC045623_1	R06	8600	2	1420.7	(+0.0)	4.511	0.428	1.000	2	R.SQALIEELLYK.R
GPN:BC045623_1	R06	8598	2	1452.7	(-0.9)	2.994	0.238	0.728	2	R.SQAL*IEEL*L*L*YK#.R
GPN:BC045623_1	R06	9088	2	1487.7	(+0.6)	2.852	0.249	0.917	2	K.VEITPESILSLSK.T
GPN:BC045623_1	R06	7470	2	1402.7	(+0.2)	2.534	0.374	0.936	2	K.ISSIL*SSL*TSVM@K#.N
GPN:BC047029_1	R18	5621	2	1366.6	(-0.8)	3.011	0.236	0.050	1	R.ISTMRPL*ATAYK#.A
GPN:BC047029_1	R18	1116	2	928.0	(+0.3)	2.306	0.445	0.979		K.K#DESL*VSK#.A
GPN:BC047029_1	R18	1442	2	1319.5	(-0.0)	2.425	0.457	0.972	1	K.TL*GTPTQPGSTPR.I
GPN:BC047880_1	R09	7198	2	1259.4	(+0.6)	3.091	0.360	0.977	5	K.FL*INL*EGGDIR.E
GPN:BC047880_1	R09	5578	2	1172.3	(+0.1)	2.725	0.381	0.960	5	K.SGDL*YVL*AADK#.V
GPN:BC047880_1	R09	4988	2	1096.2	(+0.5)	2.435	0.425	0.984	4	R.TFYQMYDK.G
GPN:BC048134_1	R09	6616	3	2206.3	(+0.4)	4.825	0.585	1.000	6	K.HWDQDDDFEFTGSHLTVR.N
GPN:BC048134_1	R09	7650	2	1596.9	(+0.5)	2.679	0.321	0.950	6	R.IADQFLGAMYTLPR.Q
GPN:BC048134_1	R09	6758	2	1176.4	(+0.6)	2.677	0.572	1.000	5	R.HGL*INFGIYK#.R

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GPN:BC049850_1	R09	5500	2	1329.4	(-0.1)	2.221	0.236	0.746		R.EFEEGLVSQYK.F
GPN:BC049850_1	R10	7737	3	2306.6	(-0.3)	4.023	0.297	0.862	2	R.FAAHL*IAGAPSEGSAL*K#PEL*SR.R
GPN:BC049850_1	R09	5118	2	1006.2	(+0.1)	2.754	0.328	0.947	1	K.L*GQASL*GVIK#.V
GPN:BC049850_1	R09	5108	2	986.2	(+0.6)	2.686	0.307	0.962	1	K.LGQASLGVIK.V
GPN:BC049850_1	R10	5619	2	986.2	(+0.9)	3.378	0.314	0.984	1	K.LGQASLGVIK.V
GPN:BC050528_1	R17	7812	3	2286.5	(+0.3)	5.791	0.392	1.000	2	R.LKQDITYGDIYNFPIHAFDK.A
GPN:BC050528_1	R17	6938	2	1370.6	(+0.8)	3.695	0.423	0.999	2	K.ALIAAQLDNAIEK.E
GPN:BC050546_1	R07	7751	2	1174.4	(+0.9)	4.683	0.442	1.000	2	K.ALVDILSEVSK.A
GPN:BC050546_1	R07	7739	2	1194.4	(+0.3)	3.219	0.532	0.997	2	K.AL*VDIL*SEVSK#.A
GPN:BC050546_1	R07	8179	2	1354.6	(+0.7)	3.561	0.358	0.988	2	K.ATLQEILPEVLK.A
GPN:BC050546_1	R06	10794	2	2105.4	(+0.3)	2.469	0.339	0.937	2	R.EAVSSAFFSLLQLTSTQFK.Q
GPN:BC050546_1	R07	6621	2	1443.6	(+0.2)	2.254	0.309	0.873	2	K.HPFSFPLENQAR.E
GPN:BC050546_1	R07	7405	2	1330.6	(-0.0)	3.332	0.386	0.977	2	R.K#AL*VDIL*SEVSK#.A
GPN:BC050546_1	R06	5604	2	898.1	(+0.4)	2.763	0.318	0.966	1	R.L*ITGL*GVGR.E
GPN:BC050546_1	R07	5521	2	898.1	(+0.5)	2.709	0.418	0.986	1	R.L*ITGL*GVGR.E
GPN:BC050546_1	R07	5519	2	886.1	(+0.0)	2.615	0.274	0.928	1	R.LITGLGVGR.E
GPN:BC050546_1	R07	8499	2	1254.5	(-0.7)	2.689	0.350	0.946	3	R.VL*DL*VEVL*VTK#.Q
GPN:BC050546_1	R07	952	2	1119.2	(+0.6)	2.248	0.316	0.929	2	K.EL*EAHSAEAR.A
GPN:BC050557_1	R07	8093	3	2611.9	(-0.2)	4.137	0.189	0.861	3	R.TFHFIEQNL*TNYEM@M@L*TDR.K
GPN:BC050557_1	R07	7259	2	1055.3	(+0.3)	2.775	0.426	0.986	2	K.LLALGLVAER.R
GPN:BC051803_1	R15	7429	3	3465.8	(-0.3)	4.111	0.502	1.000		R.AEPWLSQPASGSAYATPGAYGDIRPSAASWVGSR.G
GPN:BC051803_1	R15	7425	3	3471.8	(-0.6)	3.824	0.299	0.825		R.AEPWL*SQPASGSAYATPGAYGDIRPSAASWVGSR.G
GPN:BC051803_1	R15	4949	2	1223.3	(+0.5)	3.002	0.441	0.990		R.AVEFLASNESR.I
GPN:BC051803_1	R15	1754	2	1421.5	(+0.8)	2.960	0.489	0.991		K.GEDQSELVTTVDK.V
GPN:BC051803_1	R15	1740	2	1435.5	(+0.3)	2.825	0.332	0.955		K.GEDQSEL*VTTVDK#.V
GPN:BC051803_1	R15	1188	2	970.1	(+0.5)	2.493	0.275	0.211		R.LREDAPLR.A
GPN:BC051803_1	R15	4861	2	1229.3	(+0.9)	2.375	0.368	0.961		R.AVEFL*ASNESR.I
GPN:BC051893_1	R07	7103	2	1495.8	(-0.9)	2.666	0.162	0.439	3	K.M@QVTITL*TSPPIR.E
GPN:BC051893_1	R07	6201	2	1464.7	(+0.9)	2.847	0.276	0.921	1	K.STPVTSAVQIPEVK#.Q
GPN:BC051893_1	R08	6495	2	1456.7	(+0.0)	2.235	0.233	0.640	1	K.STPVTSAVQIPEVK.Q
GPN:BC051913_1	R11	8970	2	1783.0	(-0.2)	2.976	0.446	0.980	2	K.DPSTWSVDEVIQFMK.H
GPN:BC051913_1	R11	8008	2	1667.9	(-0.3)	2.311	0.397	0.938	2	K.HTDPQISGPLADLFR.Q
GPN:BC051913_1	R11	7212	3	1999.3	(+0.7)	3.984	0.465	1.000	1	R.IQQL*PDHFGPGPVNVVL*R.R
GPN:BC051913_1	R11	7964	2	1679.9	(+0.3)	2.299	0.287	0.868	2	K.HTDPQISGPL*ADL*FR.Q
GPN:BC052279_1	R19	8016	2	2314.6	(-0.8)	4.611	0.513	0.999		R.DKLDGNELDLSLSDLNEVPVK.E
GPN:BC052279_1	R19	6008	2	1145.3	(+0.7)	2.615	0.269	0.940		K.LQQLPADFGR.L
GPN:BC052279_1	R19	7606	2	1534.8	(-0.4)	3.318	0.307	0.964		R.LVNLQHLDLLNNK.L
GPN:BC052279_1	R19	7938	2	1882.1	(-0.3)	4.960	0.523	1.000	1	R.RHEILQWVLQTDSQQ.-
GPN:BC052279_1	R20	8032	2	1316.6	(+0.9)	2.756	0.406	0.982		K.LVTLPVSFQQLK.N
GPN:BC052641_1	R21	6216	2	1342.5	(+0.5)	2.736	0.266*	0.373	3	R.QLLDQVEQIQK.E
GPN:BC052641_1	R21	6582	3	2219.5	(+1.0)	4.930	0.594	1.000	3	R.VHLDIQVGEHANNYPEIAAK.D
GPN:BC052641_1	R22	6816	3	2233.5	(+0.6)	3.845	0.474	1.000	3	R.VHL*DIQVGEHANNYPEIAAK#.D
GPN:BC052641_1	R22	6204	2	1116.3	(+0.8)	2.851	0.257	0.315	3	K.DKLTQLR.A
GPN:BC053660_1	R11	8914	3	2342.6	(-0.2)	4.207	0.349	0.957	2	K.EK#FPEADPYEIIIESFNVVAK#.E
GPN:BC053660_1	R11	9260	2	2069.3	(+0.0)	5.086	0.474	1.000	2	K.FPEADPYEIIIESFNVVAK.E
GPN:BC053660_1	R11	9268	2	2077.3	(-0.2)	4.579	0.501	1.000	2	K.FPEADPYEIIIESFNVVAK#.E
GPN:BC053660_1	R11	7802	2	1661.0	(+1.0)	5.403	0.538	0.998	2	K.YTQQIIQGIQQLVK.E
GPN:BC053660_1	R11	7804	2	1675.0	(+0.2)	3.657	0.385	0.979	2	K.YTQQIIQGIQQL*VK#.E
GPN:BC058912_1	R01	8935	3	2653.0	(+1.0)	4.151	0.477	1.000	4	K.GDNVYEFHLEFLDLVKPEPVYK.L
GPN:BC058912_1	R01	5295	2	1546.7	(-0.2)	3.896	0.461	1.000	5	R.LESEGSPETLTNLR.K
GPN:BC058912_1	R01	5297	2	1564.7	(-0.8)	2.990	0.410	0.927	5	R.L*ESEGSPETL*TNL*R.K
GPN:BC058912_1	R02	5534	2	1564.7	(-0.0)	3.201	0.472	0.987	5	R.L*ESEGSPETL*TNL*R.K
GPN:BC058912_1	R03	5371	2	1546.7	(-0.3)	3.202	0.363	0.972	5	R.LESEGSPETLTNLR.K
GPN:BC058912_1	R01	7177	2	1347.6	(-0.2)	3.207	0.357	0.978	6	K.RPLFLAPDFDR.W
GPN:BC058912_1	R01	7151	2	1359.6	(+0.5)	2.381	0.170	0.734	6	K.RPL*FL*APDFDR.W
GPN:BC058912_1	R02	6888	2	1347.6	(+0.7)	2.250	0.345	0.937	6	K.RPLFLAPDFDR.W

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GPN:BC058912_1	R03	6887	2	1359.6	(-0.0)	2.521	0.235	0.847	6	K.RPL*FL*APDFDR.W
GPN:BC058912_1	R03	6319	2	1506.6	(+0.8)	2.280	0.312	0.915	6	R.WL*DESDAEMEL*R.A
GPN:BX640786_1	R08	9567	3	2591.0	(+0.9)	5.840	0.556	1.000	2	K.DIIHNPQALSPQFTGILQLLQSR.T
GPN:BX640786_1	R08	6299	3	1690.9	(+0.9)	4.185	0.361	0.999	1	R.L*IVDHHGTAQL*QAL*R.Q
GPN:BX640786_1	R08	9099	3	2561.8	(+0.7)	3.939	0.434	0.998	2	K.ETVVEEPVDITPYLDQLDESLR.D
GPN:BX640952_1	R08	6079	3	3388.5	(-0.1)	4.929	0.466	0.999	3	K.AAEAAPTQEAQGETEPTAQAPDAL*EQAADTSR.R
GPN:BX640952_1	R08	6087	3	3382.5	(-0.3)	4.153	0.546	1.000	3	K.AAEAAPTQEAQGETEPTAQAPDALEQAADTSR.R
GPN:BX640952_1	R08	8305	2	1589.9	(-0.0)	2.708	0.343	0.945	2	K.VLLLSSPGLEELYR.C
PIR1:S64732	R08	6567	2	916.1	(+0.9)	2.679	0.404	0.985	4	K.ADSSLAVVK.R
PIR1:S64732	R07	1530	2	1050.0	(+0.6)	2.360	0.372	0.952	3	R.DGWGGYGSDK#.R
PIR1:S64732	R07	5733	2	1699.8	(-0.5)	3.433	0.188	0.870	2	K.EL*PEQL*QEHAIEDK#.E
PIR1:S64732	R07	6871	3	3430.5	(-0.1)	6.557	0.571	0.987	4	K.LAEEDLFDLSAHPEEGDLDLASESTAHQSSK.A
PIR1:S64732	R07	6865	3	3462.5	(-0.5)	5.349	0.526	1.000	4	K.L*AEEDL*FDSAHPPEEGDL*DL*ASESTAHQSSK#.A
PIR1:S64732	R08	7157	3	3430.5	(+0.6)	7.264	0.636	0.999	4	K.LAEEDLFDLSAHPEEGDLDLASESTAHQSSK.A
PIR1:S64732	R07	6825	2	1355.5	(+0.9)	3.330	0.330	0.981	2	R.NFWVWGLSSTTR.A
PIR1:S64732	R07	4583	2	1259.3	(-0.8)	2.565	0.291	0.755	2	R.RDDAYWPEAK#.R
PIR1:S64732	R06	6284	3	2864.0	(+0.2)	4.228	0.382	0.973	4	K.SEPVK#EESSEL*EQPFAQDTSSVGPDR.K
PIR1:S64732	R07	6169	3	2864.0	(+0.5)	6.620	0.489	1.000	4	K.SEPVK#EESSEL*EQPFAQDTSSVGPDR.K
PIR1:S64732	R07	6189	2	2864.0	(-0.1)	4.853	0.540	1.000	4	K.SEPVK#EESSEL*EQPFAQDTSSVGPDR.K
PIR1:S64732	R08	6453	3	2850.0	(+0.1)	4.594	0.544	1.000	4	K.SEPVKEESSELEQPFAQDTSSVGPDR.K
PIR1:S64732	R09	5916	3	2850.0	(+0.1)	4.043	0.305	0.871	4	K.SEPVKEESSELEQPFAQDTSSVGPDR.K
PIR1:S64732	R09	5948	2	916.1	(+1.0)	2.349	0.427	0.980	4	K.ADSSLAVVK.R
PIR1:UQHUB	R01	6119	2	1068.3	(+0.9)	2.228	0.264	0.890	65	K.ESTLHLVLR.L
PIR1:UQHUB	R03	5975	2	1068.3	(-0.0)	2.667	0.208	0.873	65	K.ESTLHLVLR.L
PIR1:UQHUB	R06	6354	2	1068.3	(+0.6)	2.571	0.287	0.953	65	K.ESTLHLVLR.L
PIR1:UQHUB	R20	6400	2	1068.3	(+0.8)	2.283	0.259	0.896	65	K.ESTLHLVLR.L
PIR1:UQHUB	R03	6347	2	1789.0	(+0.3)	3.132	0.473*	0.417	58	K.TITLEVEPSDTIENVK.A
PIR1:UQHUB	R22	6954	2	1803.0	(-0.5)	2.560	0.390	0.939	58	K.TITL*EVEPSDTIENVK#.A
PIR1:UQHUB	R23	6908	2	1803.0	(-0.6)	2.654	0.406	0.952	58	K.TITL*EVEPSDTIENVK#.A
PIR1:UQHUB	R25	7424	2	1789.0	(+0.5)	2.917	0.348*	0.328	58	K.TITLEVEPSDTIENVK.A
PIR1:UQHUB	R27	6329	2	1803.0	(+1.0)	4.675	0.560	1.000	58	K.TITL*EVEPSDTIENVK#.A
PIR1:UQHUB	R27	6185	2	1803.0	(-0.5)	3.256	0.406	0.971	58	K.TITL*EVEPSDTIENVK#.A
PIR1:UQHUB	R01	1310	2	1082.2	(+0.9)	2.342	0.260	0.908	67	R.TLSDYNIQK.E
PIR1:UQHUB	R07	1670	2	1082.2	(+0.5)	2.481	0.281	0.942	67	R.TLSDYNIQK.E
PIR1:UQHUB	R17	1950	2	1082.2	(+0.6)	2.433	0.342	0.936	67	R.TLSDYNIQK.E
PIR1:UQHUB	R26	4578	2	1096.2	(+0.7)	2.323	0.317	0.930	67	R.TL*SDYNIQK#.E
PIR1:UQHUB	R27	4821	2	1096.2	(+0.9)	2.774	0.369	0.977	67	R.TL*SDYNIQK#.E
PIR1:UQHUB	R27	4629	2	1096.2	(-0.1)	2.612	0.428	0.974	67	R.TL*SDYNIQK#.E
PIR1:UQHUB	R27	4697	2	1082.2	(+0.7)	2.563	0.265	0.940	67	R.TLSDYNIQK.E
PIR1:UQHUB	R27	4617	2	1082.2	(+0.6)	2.523	0.324	0.964	67	R.TLSDYNIQK.E
PIR1:UQHUB	R27	5913	2	1304.6	(-0.9)	2.208	0.289*	0.001	15	-.M@QIFVK#TL*TKG#.T
PIR2:A42184	R05	1648	2	1017.1	(+0.5)	2.241	0.154	0.687	2	R.AEELGQELK.A
PIR2:A42184	R05	834	2	958.1	(+0.5)	2.275	0.251	0.875		R.AL*QQVQEK#.E
PIR2:A42184	R05	6350	2	1314.5	(+0.2)	3.846	0.290	0.976		K.DQLQEQLQALK.E
PIR2:A42184	R05	6910	2	1561.7	(+0.7)	3.779	0.358	0.988	2	R.DSALETLLQGQLEEK.A
PIR2:A42184	R05	6896	2	1587.7	(-0.8)	2.624	0.156	0.314	2	R.DSAL*ETL*QGQL*EEK#.A
PIR2:A42184	R05	8260	3	2568.8	(+0.9)	6.022	0.509	1.000	2	R.EFASHLQQLQDALNELTEEHSK.A
PIR2:A42184	R05	8254	3	2600.8	(-0.6)	5.451	0.421	0.999	2	R.EFASHL*QQL*QDAL*NEL*TEEHSK#.A
PIR2:A42184	R06	8552	3	2568.8	(+0.8)	6.393	0.454	1.000	2	R.EFASHLQQLQDALNELTEEHSK.A
PIR2:A42184	R06	8546	3	2600.8	(-0.7)	4.847	0.416	0.997	2	R.EFASHL*QQL*QDAL*NEL*TEEHSK#.A
PIR2:A42184	R05	7176	2	1058.2	(+0.5)	2.318	0.289	0.928	2	R.EL*GEL*IPL*R.Q
PIR2:A42184	R04	8736	3	2503.7	(+0.0)	4.295	0.387	0.997	3	K.FVLHDHEDGLNLNEDLENFLQK.A
PIR2:A42184	R06	8832	3	2503.7	(-0.0)	4.144	0.302	0.869	3	K.FVLHDHEDGLNLNEDLENFLQK.A
PIR2:A42184	R05	7902	2	1546.8	(-0.1)	2.557	0.206	0.671		K.GEVL*GDVL*QL*ETL*K#.Q
PIR2:A42184	R06	8096	2	1514.8	(+0.8)	4.659	0.450	1.000		K.GEVLGDVLQLETLK.Q
PIR2:A42184	R06	8084	2	1546.8	(-0.3)	3.300	0.273	0.932		K.GEVL*GDVL*QL*ETL*K#.Q
PIR2:A42184	R05	1712	2	1256.4	(+0.6)	2.594	0.291	0.932		R.HQVEQLSSSLK.Q
PIR2:A42184	R05	1772	2	1367.5	(-0.0)	2.625	0.434	0.968	3	R.IHGTEEGQQL*K#.Q
PIR2:A42184	R06	1714	2	1367.5	(+0.2)	2.282	0.191	0.574	3	R.IHGTEEGQQL*K#.Q
PIR2:A42184	R04	4998	2	1259.4	(-0.2)	2.234	0.168	0.501	1	K.L*ADDL*STL*QEK#.M
PIR2:A42184	R05	6914	3	1772.0	(-0.2)	4.216	0.423	0.994		K.L*EIL*QQQL*QVANEAR.D

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
PIR2:A42184	R05	6924	2	1772.0	(-0.0)	4.102	0.366	0.985		K.L*EIL*QQQL*QVANEAR.D
PIR2:A42184	R05	1030	2	1098.2	(+0.3)	2.491	0.171	0.829	2	R.L*QNAL*NEQR.V
PIR2:A42184	R05	9034	2	1822.0	(+0.0)	2.313	0.288	0.825	2	K.NSL*ISSL*EEVSIL*NR.Q
PIR2:A42184	R05	6072	2	1578.7	(+0.6)	4.092	0.505	0.699	4	R.SL*EAQVAHADQQL*R.D
PIR2:A42184	R05	8646	2	2218.4	(-0.9)	3.581	0.342	0.927	4	R.SQAPL*ESSL*DSL*GDVFL*DSGR.K
PIR2:A42184	R06	8890	2	1898.1	(-0.0)	3.038	0.433	0.974	2	R.VEFATL*QEAL*AHAL*TEK#.E
PIR2:A42184	R06	5194	2	1233.4	(+0.3)	2.227	0.416	0.968	1	K.LADDLSTLQEK.M
PIR2:A54857	R01	11371	3	3000.5	(+0.1)	4.472	0.531	1.000	1	R.FPGFEPLTPWILDLLGHYAVMNNPTR.Q
PIR2:A54857	R17	11102	3	3000.5	(+0.8)	5.131	0.589	1.000	1	R.FPGFEPLTPWILDLLGHYAVMNNPTR.Q
PIR2:A54857	R17	7800	3	1790.1	(+0.3)	3.844	0.382	0.999		K.GTMTTGHNVDL*VVIL*K#.I
PIR2:A54857	R17	7806	2	1790.1	(-0.9)	2.600	0.228	0.486		K.GTMTTGHNVDL*VVIL*K#.I
PIR2:A54857	R17	6986	2	1249.5	(+0.2)	2.646	0.209	0.838	1	K.IL*ITTVPPNL*R.K
PIR2:A54857	R17	6972	2	1237.5	(+0.9)	2.414	0.324	0.945	1	K.ILITTVPPNL.R.K
PIR2:A54857	R17	8008	2	1410.7	(+0.9)	3.540	0.506	1.000		K.ILPTLEAVAALGNK.V
PIR2:A54857	R17	8030	2	1436.7	(-0.8)	3.288	0.336	0.885		K.IL*PTL*EAVAAL*GNK#.V
PIR2:A54857	R17	9396	3	2583.9	(+0.8)	5.134	0.390	0.998		K.INNVIDNLIVAPGTFEVQIEEVR.Q
PIR2:A54857	R17	9376	3	2589.9	(+0.9)	5.007	0.419	1.000		K.INNVIDNL*IVAPGTFEVQIEEVR.Q
PIR2:A54857	R17	9294	3	2589.9	(+0.7)	4.427	0.451	1.000		K.INNVIDNL*IVAPGTFEVQIEEVR.Q
PIR2:A54857	R17	9300	3	2583.9	(+0.7)	4.236	0.470	1.000		K.INNVIDNLIVAPGTFEVQIEEVR.Q
PIR2:A54857	R17	9324	2	2589.9	(-0.4)	3.853	0.325	0.976		K.INNVIDNL*IVAPGTFEVQIEEVR.Q
PIR2:A54857	R18	9453	3	2583.9	(+0.4)	3.961	0.421	0.999		K.INNVIDNLIVAPGTFEVQIEEVR.Q
PIR2:A54857	R18	9449	3	2589.9	(+0.8)	3.826	0.377	0.998		K.INNVIDNL*IVAPGTFEVQIEEVR.Q
PIR2:A54857	R17	10702	3	3309.8	(+0.1)	3.906	0.196	0.355	1	R.IRFPGFPEPL*TPWIL*DL*L*GHYAVM@NNPTR.Q
PIR2:A54857	R17	6628	2	1355.6	(-0.3)	2.510	0.134	0.546	1	R.K#L*DPEL*HL*DIK#.V
PIR2:A54857	R17	6704	2	1219.4	(-0.0)	2.416	0.167	0.635	1	K.L*DPEL*HL*DIK#.V
PIR2:A54857	R17	7920	2	2100.3	(+0.8)	4.520	0.612	1.000		R.NQDLAPNSAEQASILSLVTK.I
PIR2:A54857	R17	7720	3	2256.5	(+1.0)	3.955	0.460	0.997		K.RNQDLAPNSAEQASILSLVTK.I
PIR2:A54857	R17	6764	3	1761.0	(+0.3)	4.162	0.518	1.000		R.VK#PAPDETSFSEAL*L*K#.R
PIR2:A54857	R17	6786	2	1733.0	(-0.5)	2.986	0.537	0.997		R.VKPAPDETSFSEALLK.R
PIR2:A54857	R17	6460	2	1054.3	(+0.5)	2.501	0.366	0.971	1	K.VL*QSAL*AAIR.H
PIR2:A54857	R17	5292	2	1434.5	(-0.1)	3.618	0.508	1.000	1	R.WFEENASQSTVK#.V
PIR2:A54857	R17	5294	2	1426.5	(+0.7)	3.405	0.448	1.000	1	R.WFEENASQSTVK.V
PIR2:A54857	R17	5392	2	1434.5	(-0.9)	2.419	0.412	0.861	1	R.WFEENASQSTVK#.V
PIR2:A54857	R17	5462	2	1426.5	(-0.0)	2.377	0.378	0.945	1	R.WFEENASQSTVK.V
PIR2:A54857	R19	9568	3	2589.9	(+0.7)	3.809	0.305	0.990		K.INNVIDNL*IVAPGTFEVQIEEVR.Q
PIR2:I38968	R09	2000	2	1649.7	(-0.6)	2.949	0.396	0.971	3	R.EADGSETPEPFAAEAK.F
PIR2:I38968	R09	8086	2	2307.6	(+0.6)	4.920	0.537	1.000	3	R.NLPGLVQEGEPFSEEATLFTK.E
PIR2:I38968	R09	1950	2	1019.1	(+0.3)	2.672	0.178	0.864	2	K.SLLSAEAAK.Q
PIR2:I38968	R09	5478	2	1474.6	(-0.6)	3.664	0.457	1.000	4	R.SSHYDEL*L*AAEAR.A
PIR2:I38968	R09	798	2	1042.1	(+0.6)	2.662	0.368	0.970	3	R.VADISGDTQK#.A
PIR2:I38968	R09	5190	2	1480.6	(-0.5)	2.889	0.321	0.927	3	K.VITEYL*NAQESAK#.S
PIR2:I38968	R09	5952	2	1430.7	(+0.8)	3.124	0.449	0.986	3	K.VM@QVL*NADAVVVK#.L
PIR2:I38968	R09	6524	3	2472.7	(+0.2)	4.514	0.252	0.976	3	K.VWAHYEEQPVEEVM@PVL*EEK#.E
PIR2:I38968	R09	7334	2	2442.7	(-0.3)	3.414	0.427	0.982	3	K.VWAHYEEQPVEEVM@PVL*EEK#.E
PIR2:JC4775	R15	9223	3	3240.6	(+0.6)	5.284	0.603	0.999	2	K.LLAAGQLADALSQFHAAVDGDNDNYIAYYR.R
PIR2:JC4775	R15	9225	3	3264.6	(-0.6)	4.376	0.471	0.999	2	K.L*L*AAGQL*ADAL*SQFHAAVDGDNDNYIAYYR.R
PIR2:JC4775	R15	6501	2	1185.4	(+0.6)	3.476	0.410	1.000	1	K.L*IESAEEL*IR.D
PIR2:JC5279	R16	1770	2	1152.3	(+0.2)	2.636	0.392	0.947		K.KGEEALFTTR.E
PIR2:JC5279	R16	1790	2	1166.3	(-0.1)	2.325	0.388	0.954		K.K#GEEAL*FTTR.E
PIR2:JC5279	R16	4798	2	951.1	(+0.8)	2.395	0.442	0.981	2	R.VDYFIASK#.A
PIR2:JC5279	R16	4858	2	943.1	(+0.6)	2.380	0.435	0.984	2	R.VDYFIASK.A
PIR2:JC5279	R16	4878	2	951.1	(+0.5)	2.279	0.444	0.978	2	R.VDYFIASK#.A
PIR2:JC5279	R16	4778	2	943.1	(+0.5)	2.266	0.365	0.967	2	R.VDYFIASK.A
PIR2:JC7168	R12	1198	2	853.0	(+0.9)	2.423	0.432	0.980	5	K.AVDITTPK#.A
PIR2:JC7168	R12	7176	2	1273.5	(+0.3)	2.285	0.381	0.265	6	R.DFK#PGDL*IFAK#.M
PIR2:JC7168	R12	722	2	976.1	(+0.5)	2.214	0.458	0.975	5	K.FSSQQAATK#.Q
PIR2:JC7168	R12	6826	2	1647.8	(-0.2)	3.149	0.320	0.942	5	K.GFNEGL*WEIDNNPK#.V
PIR2:JC7168	R13	2510	2	1074.3	(+0.4)	2.380	0.402	0.977	3	K.HTEMITTLK.K
PIR2:JC7168	R12	8924	2	1923.3	(+0.2)	3.718	0.544	1.000	5	K.LPIFFFGTHETAFLGPK.D
PIR2:JC7168	R12	8952	2	1943.3	(+0.9)	2.225	0.373	0.918	5	K.L*PIFFFGTHETAFL*GPK#.D
PIR2:JC7168	R12	8914	2	1965.3	(+0.9)	6.385	0.558	0.978	3	K.NMFLVGEVGDVITQVLNK.S

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PIR2:JC7168	R12	8246	2	2001.3	(-0.6)	4.618	0.528	1.000	3	K.NM@FL*VGEEDSVITQVL*NK#.S
PIR2:JC7168	R13	7441	2	1251.5	(+0.8)	2.279	0.292	0.158	6	R.DFKPGDLIFAK.M
PIR2:JC7599	R03	5759	3	1891.1	(+0.8)	3.754	0.489	1.000	2	K.K#PTSAL*DEPVSHWRPR.L
PIR2:JC7599	R01	8595	3	2507.8	(-0.5)	3.803	0.363	0.992	2	R.L*AL*NVMADNFVFDGSSL*PADVHR.Y
PIR2:JC7599	R03	7473	3	2523.8	(+0.0)	4.560	0.366	0.996	2	R.L*AL*NVM@ADNFVFDGSSL*PADVHR.Y
PIR2:JC7599	R02	7550	3	2558.8	(+0.7)	4.637	0.410	0.812	1	R.SHLGAENNIDLVLNVEDFDVESK.F
PIR2:JC7599	R01	6187	2	1474.6	(+0.0)	2.470	0.334	0.494	4	R.STTEL*PL*TVSYDK#.V
PIR2:JC7599	R01	9105	2	1948.3	(+0.4)	3.186	0.496	1.000	4	K.TVHYL*PIL*FIDQL*SNR.V
PIR2:JC7599	R01	1338	2	1331.4	(+0.6)	3.351	0.194	0.947	2	R.VNEFGESYEEK.A
PIR2:JC7599	R01	1342	2	1339.4	(+0.2)	3.280	0.422	0.981	2	R.VNEFGESYEEK#.A
PIR2:JC7599	R02	1716	2	1331.4	(+0.8)	3.232	0.363	0.978	2	R.VNEFGESYEEK.A
PIR2:JC7599	R03	1522	2	1331.4	(+0.5)	3.021	0.301	0.969	2	R.VNEFGESYEEK.A
PIR2:JC7599	R03	1528	2	1339.4	(+0.2)	2.924	0.363	0.963	2	R.VNEFGESYEEK#.A
PIR2:JC7599	R04	1644	2	1331.4	(-0.0)	2.670	0.330	0.950	2	R.VNEFGESYEEK.A
PIR2:JC7977	R20	7956	3	2855.3	(+0.7)	6.422	0.619	1.000	4	R.KVPILVAQEGESSQQLNDSSVIISALK.T
PIR2:JC7977	R20	7964	3	2889.3	(-0.7)	5.121	0.481	1.000	4	R.K#VPIL*VAQEGESSQQL*NDSSVIISAL*K#.T
PIR2:JC7977	R20	7862	2	1589.8	(+0.1)	4.520	0.426	0.863	4	R.TPTEAL*ASFYIVR.E
PIR2:JC7977	R20	7352	2	1319.6	(+0.7)	2.909	0.475	0.990	4	K.YMGAAAMYLIISK.R
PIR2:JE0326	R21	4492	2	1176.3	(+1.0)	3.466	0.477	0.991	1	R.LGNSADALESAR.R
PIR2:JE0326	R22	7434	2	926.2	(+0.9)	3.066	0.124	0.911	1	R.LQVLLLAR.V
PIR2:JW0079	R19	9014	2	2218.5	(+0.7)	4.029	0.434	1.000	3	K.EYFGAFGEIENIEL*PMDTK#.T
PIR2:JW0079	R19	9020	2	2204.5	(+0.2)	3.915	0.497	1.000	3	K.EYFGAFGEIENIELPMDTK.T
PIR2:JW0079	R19	8554	2	2234.5	(-0.1)	3.191	0.365	0.962	3	K.EYFGAFGEIENIEL*PM@DTK#.T
PIR2:JW0079	R19	5932	2	1125.3	(+0.7)	2.756	0.190	0.910	3	K.KDLTEYLSR.F
PIR2:JW0079	R19	7794	2	1356.6	(+0.0)	3.021	0.402	0.935	3	K.MFIGGL*SWDTSK#.K
PIR2:JW0079	R16	6080	2	1720.9	(-0.1)	3.552	0.396	0.976	3	K.VFVGG*SPDTSEEQIK#.E
PIR2:JW0079	R19	6506	2	1720.9	(-0.8)	3.382	0.306	0.857	3	K.VFVGG*SPDTSEEQIK#.E
PIR2:JW0079	R20	6322	2	1706.9	(-0.4)	4.605	0.505	1.000	3	K.VFVGG*SPDTSEEQIK#.E
PIR2:JW0079	R20	6318	2	1720.9	(-0.5)	3.516	0.375	0.968	3	K.VFVGG*SPDTSEEQIK#.E
PIR2:S33377	R13	5163	2	1097.2	(+0.3)	2.543	0.314	0.943	3	K.DL*SDGIHVVK#.D
PIR2:S33377	R13	5627	3	2023.2	(+0.6)	4.713	0.445	0.985	2	K.VQEQVHTLLSQDQAQAAR.L
PIR2:S33377	R13	9353	2	1798.0	(-0.3)	3.902	0.609*	0.603	2	K.VQSLQATFGTFESILR.S
PIR2:S33377	R13	9335	2	1810.0	(-0.1)	2.381	0.489*	0.097	2	K.VQSL*QATFGTFESIL*R.S
PIR2:S33377	R13	2600	2	1288.4	(+0.1)	2.200	0.426	0.956	2	R.HSEAFEALQK.S
PIR2:S49618	R08	5633	2	1173.3	(+0.6)	2.982	0.498	0.996	3	R.AGGVGLNLSAASR.V
PIR2:S49618	R08	5369	2	1032.1	(+0.5)	2.546	0.339	0.960	3	K.AVLDLESER.R
PIR2:S49618	R08	6755	3	2015.2	(+0.2)	5.146	0.495	1.000	3	K.DRPENVHGGIL*ADDMGL*GK#.T
PIR2:S49618	R08	6049	2	1158.4	(+0.4)	2.307	0.403	0.399	3	K.GK#PVL*EL*PER.K
PIR2:S49618	R08	7055	2	1736.8	(+0.3)	4.227	0.577	1.000	4	R.NDL*YNTITNFSEK#.D
PIR2:S49618	R08	11265	3	2136.6	(+1.0)	3.907	0.301	0.982	3	K.SLVVSQFTTFLSLIEIPLK.A
PIR2:S49618	R08	7601	2	1481.6	(+0.4)	3.747	0.542	1.000	4	K.TLGFNLESGWGSGR.A
PIR2:S49618	R08	6713	2	1593.8	(-0.7)	2.398	0.283	0.860	3	K.VFIQHITL*SDEER.K
PIR2:S49618	R10	5413	2	1173.3	(+0.7)	2.379	0.270	0.881	3	R.AGGVGLNLSAASR.V
PIR2:T00034	R09	5072	3	2395.6	(+0.6)	4.389	0.443	0.991	1	R.VSEVEEEK#EPVPQPL*PSDDTR.V
PIR2:T00034	R09	5070	3	2381.6	(+0.7)	4.207	0.428	0.993	1	R.VSEVEEEK#EPVPQPLPSDDTR.V
PIR2:T00034	R09	1880	2	1269.4	(+0.8)	2.872	0.505	1.000	1	R.L*QAQSL*STVGPR.L
PIR2:T00074	R06	7938	3	2232.5	(+1.0)	3.811	0.462	1.000	3	K.DHSSLLQGTLAEHFGLVPGPR.D
PIR2:T00074	R06	6054	2	1505.7	(+0.2)	2.477	0.401	0.938	3	K.ASIGQSPGL*PSTTFK#.L
PIR2:T00333	R06	8982	3	2596.8	(+0.3)	3.763	0.511	1.000	1	R.AAFAPPEL*YDFAL*SNVAEVDTR.E
PIR2:T00333	R06	6108	2	1121.3	(+0.7)	2.869	0.294	0.954	1	R.ADVITINL*NVR.D
PIR2:T00333	R06	6908	2	1325.5	(+0.7)	2.559	0.291	0.936	2	K.K#IFTQL*EEFR.A
PIR2:T00333	R06	8658	3	2490.8	(+0.4)	4.295	0.436	0.911	1	K.M@PNQIATL*DFNDTFL*SIEHL*K#.A
PIR2:T00333	R06	7384	3	1983.2	(+0.2)	3.929	0.461	0.999	1	R.TL*IVTHSNQAL*NQL*FEK#.I
PIR2:T00333	R06	5924	2	1327.5	(+0.7)	2.224	0.303	0.811	2	R.VGVPTVDLDAQGR.A
PIR2:T00356	R07	1582	2	1024.1	(-0.1)	2.446	0.342	0.935	1	R.AVEEGL*TYK#.F
PIR2:T00356	R07	5607	2	1255.5	(-0.3)	2.819	0.403	0.970	1	K.HVQL*VM@EAIGK#.L

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PIR2:T00356	R07	6425	2	1239.5	(+0.3)	2.256	0.238	0.787	1	K.HVQL*VMEAIK#.L
PIR2:T00356	R07	1892	2	1254.4	(+0.2)	2.554	0.354	0.952	1	K.LHNELQSGSLR.L
PIR2:T00356	R07	1870	2	1272.4	(-0.3)	2.333	0.160	0.602	1	K.L*HNEL*QSGSL*R.L
PIR2:T00356	R07	1084	2	996.2	(+0.9)	2.758	0.398	0.984	3	R.VLATQPGPGR.G
PIR2:T00356	R07	1082	2	1002.2	(+0.3)	2.285	0.381	0.964	3	R.VL*ATQPGPGR.G
PIR2:T00356	R07	5019	2	1208.3	(+0.7)	2.212	0.386	0.842	1	K.VLDPASSDFTR.L
PIR2:T00374	R07	8251	2	1530.8	(+0.3)	3.171	0.383	0.983	1	K.EVQLAQIFEPLSR.S
PIR2:T00374	R07	8221	2	1542.8	(-0.6)	2.774	0.330	0.946	1	K.EVQL*AQIFEPL*SR.S
PIR2:T00374	R07	7479	2	1678.0	(-0.8)	2.743	0.409	0.881	1	R.IAPVHIDSEAISL*VK#.L
PIR2:T00374	R07	6935	2	1719.9	(-0.1)	2.823	0.282	0.884	1	K.L*WSPDEEVSPEVL*AK#.V
PIR2:T00374	R07	4977	3	2356.4	(+0.8)	5.152	0.464	0.997	2	R.STGTETGSNINVNSEL*NPSTGNR.S
PIR2:T00374	R07	4989	3	2350.4	(+0.1)	4.361	0.440	0.998	2	R.STGTETGSNINVNSELNPSTGNR.S
PIR2:T00374	R07	1782	2	876.1	(+0.4)	2.213	0.348	0.936	1	R.L*AAGSAIMK#.L
PIR2:T02246	R18	6211	2	1671.8	(+0.4)	4.144	0.592	1.000	4	K.AEQINQAAGEASAVLAK.A
PIR2:T02246	R18	8257	3	2331.6	(+0.9)	4.516	0.544	1.000	3	K.ASYGVEDPEYAVTQLAQTTMR.S
PIR2:T02246	R18	1394	2	1063.2	(+0.8)	2.546	0.315	0.957	3	R.ATVLESEGR.E
PIR2:T02246	R18	10645	2	3052.5	(-0.1)	2.917	0.293	0.927	3	K.DSNITLLPSNPGDVTSMVAQAMGVYGALTK.A
PIR2:T02246	R18	5429	2	1675.7	(+0.0)	4.358	0.512	0.998	3	R.DVQGTDSL*DEEL*DR.V
PIR2:T02246	R18	5435	2	1663.7	(+0.9)	3.947	0.513	1.000	3	R.DVQGTDSLDEELDR.V
PIR2:T02246	R18	8205	2	2015.3	(+0.8)	4.726	0.512	1.000	3	R.NTVVLFVFPQQEAWVVER.M
PIR2:T02246	R18	9517	2	1700.1	(-0.5)	2.433	0.186	0.631	3	R.IL*EPGL*NIL*IPVL*DR.I
PIR2:T03030	R07	7085	3	2584.8	(-0.5)	4.148	0.365	0.995	3	K.NTPSPDVTL*GTNPGTEDIQFPIQK#.I
PIR2:T03030	R07	7081	3	2570.8	(+0.7)	4.066	0.448	0.977	3	K.NTPSPDVTLTGTPGTEDIQFPIQK.I
PIR2:T03030	R07	6857	2	1483.7	(+0.8)	2.224	0.298	0.840	3	R.AL*NIVDQEGSL*L*GK#.G
PIR2:T08745	R08	5159	2	1187.3	(+0.3)	2.837	0.454	0.989	2	K.ANAEELANLQ.K
PIR2:T08745	R08	5809	2	1100.2	(+0.7)	2.366	0.297	0.931	5	K.DSNFAGDL*VR.N
PIR2:T08745	R08	6987	2	1320.4	(-0.2)	3.548	0.502	1.000	3	R.VSYL*VFDEADR.M
PIR2:T08767	R14	7991	2	1607.8	(+0.2)	3.478	0.604	1.000	3	R.FESFPAGSTLIFYK.Y
PIR2:T08767	R14	7179	2	1685.0	(+0.3)	3.289	0.337	0.969	4	R.ISHL*VL*PVQPENAL*K#.R
PIR2:T08767	R14	6153	2	1399.5	(+0.2)	3.941	0.461	1.000	3	K.L*EVDQEL*SNQFK#.N
PIR2:T08767	R14	6159	2	1379.5	(+0.3)	3.458	0.412	0.990	3	K.LEVDQELSNQFK.N
PIR2:T08767	R14	7605	2	1254.5	(+0.4)	2.877	0.356	0.976	3	R.SQPAILLTAAR.D
PIR2:T08767	R14	7959	2	1621.8	(-0.3)	2.373	0.185	0.553	3	R.FESFPAGSTL*IFYK#.Y
PIR2:T08769	R08	8571	2	1310.6	(+1.0)	3.273	0.502	1.000	4	R.ALTLGALTPLAR.L
PIR2:T08769	R09	8190	2	1310.6	(+0.9)	2.761	0.332	0.963	4	R.ALTLGALTPLAR.L
PIR2:T08769	R08	8607	2	1715.0	(-0.6)	2.530	0.248	0.768	5	R.DPPDPYVSL*L*L*PDK#.N
PIR2:T08769	R08	8061	2	1533.7	(+0.5)	2.561	0.266	0.915	5	R.FEWELPLDEAQR.R
PIR2:T08769	R08	7411	2	1922.1	(-0.5)	4.737	0.461	0.978	4	R.FFLQDPQSQELDVQVK.D
PIR2:T08769	R08	7183	3	2343.6	(+0.8)	6.595	0.555	0.994	4	K.GNKEPNPMVQLSIQDVTQESK.A
PIR2:T08769	R08	7167	3	2365.6	(+0.3)	5.418	0.492	1.000	4	K.GNK#EPNPMVQL*SIQDVTQESK#.A
PIR2:T08769	R08	6597	3	2381.6	(+0.8)	4.571	0.368	0.964	4	K.GNK#EPNPM@VQL*SIQDVTQESK#.A
PIR2:T08769	R08	6159	3	1733.9	(+0.3)	3.713	0.447	1.000	5	K.HL*SPYATL*TVGDSSHK#.T
PIR2:T08769	R08	6949	2	1370.6	(-0.4)	2.843	0.185	0.785	4	R.IHVL*EAQDL*IAK#.D
PIR2:T08769	R08	5733	3	1457.6	(+0.7)	3.880	0.398	0.999	5	R.K#PHTESL*EL*QVR.G
PIR2:T08769	R13	8985	2	1404.6	(+0.8)	4.219	0.507	1.000	4	R.LEWLSLLSDEAK.L
PIR2:T08769	R08	7399	2	1360.5	(+0.8)	2.941	0.429	0.986	5	K.LTLWYSEER.K
PIR2:T08769	R08	8267	2	2115.3	(+0.8)	3.240	0.553	1.000	5	K.TISQTSAPVWDESASF*IR.K
PIR2:T08769	R08	8269	2	2109.3	(+0.1)	2.469	0.367	0.935	5	K.TISQTSAPVWDESASF*IR.K
PIR2:T08769	R08	8783	3	2588.9	(-0.2)	4.573	0.418	0.999	4	K.VL*QASVL*DDWFPL*QGGQGVHL*R.L
PIR2:T08769	R08	8779	3	2564.9	(+0.6)	4.116	0.505	0.999	4	K.VLQASVLDLDDWFPLQGGQGVHLR.L
PIR2:T08769	R12	8748	3	2564.9	(+0.5)	4.088	0.537	0.999	4	K.VLQASVLDLDDWFPLQGGQGVHLR.L
PIR2:T08769	R08	6975	2	1715.9	(+0.9)	4.542	0.580	0.969	5	K.VQLDLAETDLSQGVAR.W
PIR2:T08769	R08	6971	2	1733.9	(-1.0)	2.904	0.198	0.594	5	K.VQL*DL*AETDL*SQGVAR.W
PIR2:T08769	R08	7933	2	1592.8	(-0.3)	4.523	0.519	0.999	5	R.WFTLSSGQGVLLR.A
PIR2:T08769	R08	7927	2	1610.8	(-0.8)	3.185	0.319	0.887	5	R.WFTL*SSGQGVLL*R.A
PIR2:T08769	R08	6649	2	1085.2	(+0.7)	2.262	0.359	0.964	5	R.WYDLMDNK.D
PIR2:T08769	R15	8587	2	1404.6	(+0.3)	2.236	0.210	0.725	4	R.LEWLSLLSDEAK.L
PIR2:T12471	R20	7508	2	1107.2	(+0.8)	2.701	0.347	0.968	3	K.DFINFISDK#.E
PIR2:T12471	R21	7436	2	1099.2	(+0.9)	3.149	0.306	0.981	3	K.DFINFISDK#.E



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
PIR2:T12471	R22	7672	2	1099.2	(+0.3)	2.571	0.259	0.938	3	K.DFINFISDK.E
PIR2:T12471	R20	8030	2	1558.7	(-0.6)	3.338	0.404	0.485	3	K.DFINFISDK#EWK#.S
PIR2:T12471	R20	7020	2	1227.4	(+0.5)	2.843	0.311	0.971	3	K.KDFINFISDK.E
PIR2:T12471	R20	7018	2	1243.4	(+0.2)	2.495	0.424	0.965	3	K.K#DFINFISDK#.E
PIR2:T12471	R20	5184	2	1214.4	(+0.1)	2.637	0.342	0.952	3	K.KLLESQAQLK.K
PIR2:T12471	R20	2534	2	1086.3	(+0.7)	2.554	0.247	0.918	3	K.LLESQAQLK.K
PIR2:T12471	R20	2450	2	1112.3	(+0.1)	2.338	0.399	0.947	3	K.L*L*SESAQPL*K#.K
PIR2:T12471	R20	2454	2	1086.3	(-0.2)	2.263	0.290	0.876	3	K.LLESQAQLK.K
PIR2:T12471	R21	5222	2	1086.3	(+0.7)	2.525	0.191	0.817	3	K.LLESQAQLK.K
PIR2:T12471	R20	1660	2	1233.4	(+0.2)	2.363	0.263	0.864	3	R.RPQYPYPSK.K
PIR2:T12471	R20	2132	2	1009.1	(+0.2)	2.232	0.358	0.911	3	R.SL*GPSL*ATDK#.S
PIR2:T12471	R19	1906	2	1076.2	(+0.5)	2.541	0.478	0.603	3	R.SLGPLATDKS.-
PIR2:T12471	R20	2064	2	1076.2	(+0.7)	2.854	0.472	0.667	3	R.SLGPLATDKS.-
PIR2:T12471	R20	2052	2	1096.2	(+0.1)	2.329	0.357	0.219	3	R.SL*GPSL*ATDK#.S.-
PIR2:T12471	R19	1698	2	1264.4	(+0.2)	3.509	0.514	1.000	3	K.VDVTEQPGL*SGR.F
PIR2:T12471	R20	1850	2	1264.4	(+0.5)	3.286	0.491	1.000	3	K.VDVTEQPGL*SGR.F
PIR2:T12471	R20	1820	2	1258.4	(+0.6)	2.936	0.431	0.987	3	K.VDVTEQPGLSGR.F
PIR2:T12471	R21	4626	2	1258.4	(-0.0)	3.314	0.430	0.985	3	K.VDVTEQPGLSGR.F
PIR2:T12471	R20	4722	3	2311.2	(+0.0)	5.614	0.530	0.989	3	K.VEEEQEADEEDVSEEEAESK.E
PIR2:T12518	R04	5020	2	2033.2	(-0.9)	2.643	0.339	0.820	1	R.EL*DPSL*VSANDSPSGM@QTR.C
PIR2:T12518	R05	7684	2	1490.7	(+0.3)	2.598	0.399	0.966	2	R.GL*EEIPVFDISEK#.T
PIR2:T12518	R04	8536	2	1823.2	(-0.3)	2.508	0.348	0.926	2	R.LVSDIIDPVALEIPLSK.N
PIR2:T12518	R04	790	2	1109.2	(+0.1)	2.300	0.255	0.609	1	R.SHSSNSSPIGK#.S
PIR2:T12518	R04	1150	2	1341.4	(+0.3)	3.562	0.404	0.988	1	R.SQEDEISSPVNK#.V
PIR2:T12518	R04	7472	2	1973.1	(+0.8)	5.205	0.586	1.000	2	R.VSFADPIYQAGL*ADDIDR.R
PIR2:T12518	R06	8664	3	1849.2	(+0.5)	4.022	0.244	0.985	2	R.L*VSDIIDPVAL*EIPL*SK#.N
PIR2:T13155	R01	6627	2	1274.4	(-0.1)	2.266	0.325	0.875	2	R.AFHPDL*EFVGK#.F
PIR2:T13155	R01	9365	3	2588.0	(+0.8)	4.461	0.472	1.000	3	K.DPDVNMLHVFLGEWQPIEYGK.K
PIR2:T13155	R01	4975	2	1483.7	(-0.2)	2.755	0.436	0.476	4	K.HGIEYQEKLPLR.A
PIR2:T13155	R01	7487	2	1159.4	(+0.9)	2.801	0.340	0.978	4	K.LWLDAYLHK.-
PIR2:T13156	R08	8143	2	1517.7	(+0.9)	2.760	0.430	0.984	2	R.ELPAWVSFPDVEK.A
PIR2:T13156	R09	7720	2	1517.7	(+0.6)	2.592	0.387	0.971	2	R.ELPAWVSFPDVEK.A
PIR2:T13156	R12	7992	2	1517.7	(+0.3)	3.135	0.440	0.989	2	R.ELPAWVSFPDVEK.A
PIR2:T13156	R08	5865	2	1023.2	(-0.0)	2.285	0.198	0.746	2	K.GMQL*HGVL*R.V
PIR2:T13156	R08	5919	2	1140.4	(+0.8)	2.509	0.304	0.943	2	K.LLAETVAPAVR.G
PIR2:T13156	R08	9193	2	1790.2	(+0.5)	2.519	0.425	0.970	3	R.LLVPLVPDLQDVAQLR.S
PIR2:T13156	R13	9367	2	1790.2	(+0.7)	2.463	0.390	0.947	3	R.LLVPLVPDLQDVAQLR.S
PIR2:T17244	R09	7344	2	1181.4	(+0.8)	2.480	0.322	0.955	6	R.DFIL*PISDVR.A
PIR2:T17244	R09	7336	2	1175.4	(+0.9)	2.296	0.297	0.878	6	R.DFILPISDVR.A
PIR2:T17244	R09	5222	2	1246.4	(+1.0)	3.933	0.488	0.996	3	K.DVDGVTDINLKG.L
PIR2:T17244	R09	7730	2	1583.8	(-0.1)	3.562	0.402	0.974	3	K.EIGL*L*ADEIEIYGK#.S
PIR2:T17244	R09	8188	2	1712.0	(+0.1)	5.374	0.565	1.000	4	R.FQFLYDVQVPIVDK.I
PIR2:T17244	R09	1864	2	1022.2	(+0.7)	2.326	0.281	0.913	4	R.TIAQAVYGAK.D
PIR2:T17244	R09	6890	2	1615.9	(+0.8)	4.320	0.508*	0.781	2	K.YVLVAGITPTPLGEGK.S
PIR2:T17244	R09	6884	2	1635.9	(-0.4)	2.813	0.329	0.923	2	K.YVL*VAGITPTPL*GEGK#.S
PIR2:T17244	R10	8765	2	1726.0	(+1.0)	2.876	0.430	0.979	4	R.FQFL*YDVQVPIVDK#.I
PIR2:T17289	R01	5723	3	2518.8	(+0.1)	4.713	0.284	0.976	2	R.ASPGHSPHYFAASSPTSPNALPPAR.K
PIR2:T17289	R02	5670	3	2524.8	(+0.4)	3.878	0.291	0.983	2	R.ASPGHSPHYFAASSPTSPNAL*PPAR.K
PIR2:T17289	R03	5527	3	2524.8	(+0.6)	4.251	0.348	0.997	2	R.ASPGHSPHYFAASSPTSPNAL*PPAR.K
PIR2:T17289	R03	5535	3	2518.8	(+0.3)	4.073	0.376	0.998	2	R.ASPGHSPHYFAASSPTSPNALPPAR.K
PIR2:T17289	R03	6071	2	1124.3	(+0.8)	2.715	0.222	0.907	2	R.DLAVPAALTPR.A
PIR2:T17289	R01	7987	2	1544.8	(+0.0)	4.043	0.351	0.971	2	R.VFGAPEVLENLEVK.S
PIR2:T17289	R01	7985	2	1564.8	(-0.6)	3.604	0.290	0.955	2	R.VFGAPEVL*ENL*EVK#.S
PIR2:T17289	R03	7573	3	1564.8	(+0.2)	4.118	0.389	0.998	2	R.VFGAPEVL*ENL*EVK#.S
PIR2:T17289	R03	7569	2	1564.8	(+0.3)	3.363	0.403	0.983	2	R.VFGAPEVL*ENL*EVK#.S
PIR2:T17289	R04	6366	2	1136.3	(+0.1)	2.217	0.165	0.550	2	R.DL*AVPAAL*TPR.A
PIR2:T17316	R11	7788	2	1403.6	(+0.1)	3.188	0.491	0.995	2	R.DLLMNLGQEITR.A
PIR2:T17316	R11	7786	2	1421.6	(-0.3)	2.638	0.196	0.795	2	R.DL*L*MNL*GQEITR.A
PIR2:T17316	R11	5838	2	1027.2	(+0.4)	2.420	0.159	0.782	2	K.VDL*AAFQTR.G
PIR2:T17316	R11	6956	2	1073.3	(+0.0)	2.290	0.196	0.660	2	R.L*YAAIQL*R.W

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
PIR2:T17320	R15	7233	2	1368.6	(+0.4)	2.523	0.306	0.933		K.AL*ASIL*L*QDHIR.D
PIR2:T17320	R15	7901	3	2402.5	(+0.5)	5.418	0.429	1.000	2	K.ESGHSNWLGDPEEPLTGFWSR.G
PIR2:T17320	R15	7911	3	2414.5	(+0.3)	5.178	0.479	1.000	2	K.ESGHSNWL*GDPEEPL*TGFSWR.G
PIR2:T17320	R15	6271	3	2178.5	(+0.3)	4.055	0.496	1.000	1	R.GADDAMESSK#PGPVQVVL*VQK#.D
PIR2:T17320	R15	5903	3	2194.5	(+0.0)	3.870	0.373	0.968	1	R.GADDAM@ESSK#PGPVQVVL*VQK#.D
PIR2:T17320	R15	1850	2	1297.5	(+0.7)	2.903	0.421	0.986	2	K.IYQGEDLPHPK.S
PIR2:T17320	R15	6811	3	2125.4	(+0.8)	4.719	0.499	1.000	2	K.KVAVVLMDTQGAFFDSQSTVK.D
PIR2:T17320	R15	2240	2	1309.4	(-0.0)	2.888	0.229	0.917	2	R.YQQELEEEIK.E
PIR2:T17320	R15	2246	2	1323.4	(+0.1)	2.427	0.209	0.748	2	R.YQQEL*EEEEIK#.E
PIR2:T17320	R15	1614	2	1248.3	(+0.7)	2.239	0.318	0.929	1	K.DQHSFELDEK.A
PIR2:T42680	R07	878	2	1193.3	(+0.8)	2.970	0.333	0.966	4	K.VPAQANGTPPTK#.S
PIR2:T42680	R06	7448	2	1337.5	(-0.1)	2.811	0.369	0.956	4	R.VYSTAL*SSFL*TK#.R
PIR2:T42680	R07	7335	2	1317.5	(+0.7)	2.918	0.384	0.981	4	R.VYSTALSSFLTK.R
PIR2:T42680	R07	7329	2	1337.5	(-0.4)	2.457	0.439	0.962	4	R.VYSTAL*SSFL*TK#.R
PIR2:T46333	R11	9248	3	2491.8	(-0.1)	4.980	0.463	0.983	9	R.IWGL*GFL*PQVSTDL*TPQTFSEK#.V
PIR2:T46333	R11	5574	2	916.1	(+0.9)	2.618	0.456*	0.405	9	K.AIAALISEK.L
PIR2:T46429	R05	7760	3	2168.4	(+0.5)	4.201	0.401	0.971	6	K.HADPLHDLSDNSDLVMLK.S
PIR2:T46429	R05	9936	3	2168.4	(+0.5)	4.091	0.401	0.971	6	R.GQTVEDL*L*EVL*SDIDEMSR.R
PIR2:T46447	R01	5677	2	1307.5	(+0.7)	3.879	0.513	1.000	4	R.HFDSQVYIYGK.Q
PIR2:T46447	R01	1142	2	1181.2	(+0.1)	2.385	0.182	0.698	4	K.L*EEQDEFEK#.I
PIR2:T46447	R02	8174	3	2919.2	(+0.7)	3.996	0.422	0.999	4	R.QDSIDLFLGNYSVDELESHSPLSVPR.D
PIR2:T46447	R01	8405	2	1757.1	(+0.1)	3.455	0.461	1.000	4	R.THL*GL*IMDGWNSMIR.Y
PIR2:T46447	R02	7192	2	1127.3	(+0.6)	2.769	0.186	0.892	4	R.TNVIQSL*L*AR.R
PIR2:T46447	R03	7281	2	1127.3	(+0.8)	2.597	0.311	0.890	4	R.TNVIQSL*L*AR.R
PIR2:T46935	R18	5177	2	1341.5	(+0.7)	3.567	0.279	0.971	4	K.IFQGNVHNFEK#.N
PIR2:T46935	R18	7349	3	2803.1	(+0.0)	3.950	0.420	0.998	2	K.LPGHAGSINEVAFHPDEPIIASSSDK.R
PIR2:T46935	R18	5203	2	1341.5	(-0.6)	3.004	0.319	0.952	4	K.IFQGNVHNFEK#.N
PIR2:T51878	R12	7302	3	2010.3	(+0.3)	4.566	0.419	0.999	4	K.TPL*STGGTL*AFVSPSL*AVHK#.S
PIR2:T51878	R12	1120	2	1372.5	(+0.3)	3.561	0.364	0.989	6	-.ALQQEQEIEQR.L
SW:143B_HUMAN	R20	8466	2	1208.4	(+0.2)	2.565	0.146	0.708	20	K.DSTL*IMQL*L*R.D
SW:143B_HUMAN	R21	8586	3	2180.3	(+0.8)	3.717	0.262	0.983	1	K.TAFDEAIAEL*DTL*NEESYK#.D
SW:2AAA_HUMAN	R14	1180	2	1161.3	(+0.7)	2.897	0.409	0.985	5	K.LTQDQDQVDVK.Y
SW:2AAA_HUMAN	R14	5105	2	930.1	(+0.9)	2.723	0.196	0.925	5	K.VLELDNVK.S
SW:3MG_HUMAN	R19	8710	2	1692.0	(+0.1)	2.834	0.407	0.970	8	R.L*GL*EFFDQPAVPL*AR.A
SW:3MG_HUMAN	R19	6134	2	1470.7	(-0.6)	2.351	0.188	0.598	9	R.GPL*EPSEPAVVAAR.V
SW:4F2_HUMAN	R11	5516	2	1189.3	(+0.0)	2.294	0.148	0.540	3	K.ADL*L*L*STQPGR.E
SW:4F2_HUMAN	R11	7272	2	1977.1	(+0.6)	4.100	0.431	1.000	3	K.DDVAQTDLLQIDPNFGSK.E
SW:4F2_HUMAN	R10	8769	2	1524.7	(-0.2)	2.414	0.155	0.546	3	K.GQSEDPGSL*L*SL*FR.R
SW:4F2_HUMAN	R11	8258	2	1524.7	(-0.1)	3.018	0.454	0.975	3	K.GQSEDPGSL*L*SL*FR.R
SW:4F2_HUMAN	R12	8428	2	1506.7	(-0.2)	3.919	0.501	0.999	3	K.GQSEDPGSLLSLFR.R
SW:4F2_HUMAN	R10	9113	2	1372.7	(+0.5)	3.708	0.503	1.000	3	R.LLTSFLPAQLLR.L
SW:4F2_HUMAN	R11	8700	2	1372.7	(-0.2)	2.515	0.311	0.918	3	R.LLTSFLPAQLLR.L
SW:4F2_HUMAN	R12	8658	3	2311.6	(-0.1)	4.842	0.471	1.000	2	R.SL*L*HGDFHAFSAGPGL*FSYIR.H
SW:4F2_HUMAN	R12	8420	2	1524.7	(+0.5)	3.510	0.418	0.990	3	K.GQSEDPGSL*L*SL*FR.R
SW:AAAS_HUMAN	R01	6893	2	1508.6	(+0.4)	3.070	0.402	0.976	3	R.GGGVTNL*L*WSPDGSK#.I
SW:AAAS_HUMAN	R15	6915	2	1488.6	(+0.9)	3.921	0.494	0.999	3	R.GGGVTNLLWSPDGSK.I
SW:AAAS_HUMAN	R01	8701	2	1536.8	(+0.1)	2.908	0.195	0.797	2	R.GQWINL*PVL*QL*TK#.D
SW:AAAS_HUMAN	R01	6305	2	1176.4	(+1.0)	3.173	0.435	0.988	3	K.ILATTPSAVFR.V
SW:AAAS_HUMAN	R01	6303	2	1182.4	(+0.7)	2.748	0.379	0.979	3	K.IL*ATTPSAVFR.V
SW:AAAS_HUMAN	R15	6301	2	1182.4	(+0.4)	2.623	0.418	0.982	3	K.IL*ATTPSAVFR.V
SW:AAAS_HUMAN	R01	10551	2	2195.6	(+0.4)	3.053	0.514	1.000	3	R.LLFTVLGEPLIYLSFPER.C
SW:AAAS_HUMAN	R01	5951	2	1225.4	(+0.3)	2.390	0.294	0.914	3	R.L*L*SASPVDAAIR.V
SW:AAAS_HUMAN	R01	5969	2	1213.4	(+0.5)	2.347	0.324	0.918	3	R.LLSASPVDAAIR.V
SW:AAAS_HUMAN	R15	6065	2	1225.4	(+0.3)	3.043	0.287	0.964	3	R.L*L*SASPVDAAIR.V

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:AAAS_HUMAN	R15	6069	2	1213.4	(+0.8)	2.653	0.239	0.903	3	R.LLSASPVDAAIR.V
SW:AAAS_HUMAN	R15	6901	2	1508.6	(+0.1)	2.575	0.202	0.675	3	R.GGGVTNL*L*WSPDGSK#.I
SW:AATM_HUMAN	R18	6255	2	1557.7	(+0.5)	3.797	0.418	0.988	1	K.ASAEL*AL*GENSEVL*K#.S
SW:AATM_HUMAN	R18	6269	2	1531.7	(+0.7)	3.566	0.268	0.967	1	K.ASAELALGENSEVLK.S
SW:AATM_HUMAN	R18	2108	2	1139.3	(+0.2)	2.531	0.317	0.938	1	R.DAGMQLQGYR.Y
SW:AATM_HUMAN	R18	5593	2	1460.6	(+0.1)	3.316	0.446	0.596	1	R.DDNGKPYVLPVSR.K
SW:AATM_HUMAN	R18	6621	2	1456.7	(+0.7)	4.108	0.573	0.991	1	R.FVTVQTISGTGAL*R.I
SW:AATM_HUMAN	R18	6633	2	1450.7	(+0.6)	3.412	0.552	0.998	1	R.FVTVQTISGTGALR.I
SW:AATM_HUMAN	R18	6721	2	1280.5	(+0.2)	2.307	0.390	0.945	1	R.IAAAIL*NTPDL*R.K
SW:AATM_HUMAN	R18	1006	2	946.1	(+0.8)	3.040	0.522	1.000	1	R.K#AEAQIAAK#.N
SW:AATM_HUMAN	R18	5431	2	981.2	(+0.8)	2.556	0.414	0.984	1	K.MNLGVGAYR.D
SW:AATM_HUMAN	R18	2110	2	1145.3	(+0.4)	2.259	0.313	0.928	1	R.DAGMQL*QGYR.Y
SW:ABD3_HUMAN	R01	10073	3	2558.1	(+0.1)	3.873	0.341	0.990	1	K.GIEGVQVIPL*IPGAGEIIIADNIIK#.F
SW:ABD3_HUMAN	R03	9447	3	2558.1	(+0.5)	4.048	0.453	0.999	1	K.GIEGVQVIPL*IPGAGEIIIADNIIK#.F
SW:ABD3_HUMAN	R01	8989	2	1362.6	(+0.5)	2.819	0.369	0.975	2	R.VL*GEL*WPL*FGGR.L
SW:ABD3_HUMAN	R03	8503	2	1344.6	(+0.4)	3.389	0.238	0.962	2	R.VLGELWPLFGGR.L
SW:ACDM_HUMAN	R17	5850	2	1466.7	(-0.2)	2.954	0.361	0.331	1	K.TRPVVAAGAVGLAQR.A
SW:ACDM_HUMAN	R17	8352	2	1166.4	(+0.3)	2.366	0.343	0.959	1	K.ANWYFL*L*AR.S
SW:ACDV_HUMAN	R13	6741	2	1306.5	(+0.9)	3.982	0.459	1.000	2	R.ALEQFATVVEAK.L
SW:ACDV_HUMAN	R13	5131	2	1196.3	(+0.4)	3.231	0.431	1.000	2	R.FFEEVNDPAK.N
SW:ACDV_HUMAN	R13	5127	2	1204.3	(+0.5)	3.123	0.350	0.979	2	R.FFEEVNDPAK#.N
SW:ACDV_HUMAN	R13	7095	2	1317.5	(+0.9)	2.356	0.362	0.958	2	K.GIVNEQFLLQR.L
SW:ACDV_HUMAN	R13	6443	2	1178.3	(+1.0)	2.557	0.362	0.972	2	R.IFEGTNDILR.L
SW:ACDV_HUMAN	R13	7641	2	1458.7	(+0.7)	3.859	0.483	0.990	2	K.NPFGNAGLLLGEAGK.Q
SW:ACDV_HUMAN	R13	7037	2	1519.7	(+0.8)	4.848	0.523	1.000	2	R.VPSENVLGEVGSFGK.V
SW:ACDV_HUMAN	R13	7033	2	1533.7	(+0.1)	3.878	0.442	1.000	2	R.VPSENVL*GEVGSFGK#.V
SW:ACIN_HUMAN	R06	5820	2	1326.5	(-0.5)	2.403	0.171	0.515	4	K.K#PSISITTESL*K#.S
SW:ACIN_HUMAN	R11	5730	2	1326.5	(+0.1)	3.216	0.417	0.979	4	K.K#PSISITTESL*K#.S
SW:ACIN_HUMAN	R06	6612	2	1358.6	(-0.3)	2.216	0.270	0.755	2	K.VPEESVL*PL*VQK#.S
SW:ACLY_HUMAN	R08	8509	3	2599.1	(+0.4)	5.366	0.413	0.981	2	R.LLQDHPWLLSQNLVVKPDQLIK.R
SW:ACLY_HUMAN	R08	2378	2	873.0	(+0.2)	2.595	0.271	0.936	2	K.LLVGVDEK.L
SW:ACOD_HUMAN	R01	9293	2	1565.9	(+0.7)	4.240	0.436	1.000	5	R.GFFFHVGVWLLVR.K
SW:ACOD_HUMAN	R01	6335	2	1378.5	(+0.7)	3.821	0.448	1.000	5	K.GSTLDLSDLEAEK.L
SW:ACOD_HUMAN	R01	8205	3	3207.6	(-0.1)	5.177	0.466	0.982	4	K.L*ETMPL*YL*EDDIRPDIK#DDIYDPTYK#.D
SW:ACOD_HUMAN	R01	8201	3	3173.6	(-0.1)	4.797	0.458	1.000	4	K.LETMPLYLEDDIRPDIKDDIYDPTYK.D
SW:ACOD_HUMAN	R02	6148	2	1378.5	(+0.4)	3.220	0.388	0.985	5	K.GSTLDLSDLEAEK.L
SW:ACON_HUMAN	R11	4710	2	936.1	(+0.8)	2.655	0.274	0.960	4	R.DGYAQILR.D
SW:ACON_HUMAN	R11	4826	2	936.1	(-0.0)	2.468	0.294	0.937	4	R.DGYAQILR.D
SW:ACON_HUMAN	R11	8582	3	1768.9	(+0.9)	4.497	0.462	1.000	2	K.DINQEVYNFL*ATAGAK#.Y
SW:ACON_HUMAN	R11	5806	2	1558.6	(+0.4)	3.102	0.378	0.975	2	K.FNPETDYLTGTDGK.K
SW:ACON_HUMAN	R11	7944	3	2246.5	(+0.3)	4.122	0.266	0.972	5	R.GHL*DNISNNL*L*IGAINIENGK#.A
SW:ACON_HUMAN	R11	5690	2	1220.4	(+0.3)	3.277	0.469	1.000	2	K.LTGSLSGWSSPK.D
SW:ACON_HUMAN	R11	7400	3	2336.6	(+0.4)	5.494	0.431	1.000	2	K.VAMSHFEPNEYIHYDLLEK.N
SW:ACON_HUMAN	R11	7390	3	2356.6	(+0.9)	5.416	0.306	0.733	2	K.VAMSHFEPNEYIHYDL*L*EK#.N
SW:ACON_HUMAN	R11	7096	3	2372.6	(+0.0)	3.879	0.347	0.993	2	K.VAM@SHFEPNEYIHYDL*L*EK#.N
SW:ACON_HUMAN	R11	7984	2	1790.0	(-0.8)	2.204	0.330	0.607	4	K.QGL*L*PL*TFADPADYNK#.I
SW:ACTA_HUMAN	R17	1226	2	1207.2	(+0.8)	3.527	0.444	1.000	12	K.DSYVGDEAQS#.R
SW:ACTA_HUMAN	R17	4162	2	1199.2	(+0.6)	2.687	0.406	0.982	12	K.DSYVGDEAQS#.R
SW:ACTA_HUMAN	R17	1224	2	1199.2	(+0.7)	2.504	0.328	0.950	12	K.DSYVGDEAQS#.R
SW:ACTA_HUMAN	R17	7218	2	1792.0	(+0.9)	4.874	0.502	1.000	16	K.SYELPDGQVITIGNER.F
SW:ACTA_HUMAN	R17	6812	2	1792.0	(+0.8)	4.337	0.570	1.000	16	K.SYELPDGQVITIGNER.F
SW:ACTA_HUMAN	R18	7207	2	1792.0	(+1.0)	2.723	0.420	0.979	16	K.SYELPDGQVITIGNER.F
SW:ACTA_HUMAN	R17	7154	3	1962.2	(-0.7)	4.143	0.245	0.967	6	K.YPIEHGIITNWDDMEK.I
SW:ACTA_HUMAN	R17	7138	2	1962.2	(-0.7)	3.316	0.238	0.922	6	K.YPIEHGIITNWDDMEK.I
SW:ACTA_HUMAN	R17	7142	2	1970.2	(-0.7)	2.706	0.344	0.923	6	K.YPIEHGIITNWDDMEK#.I
SW:ACTA_HUMAN	R18	5403	2	1162.4	(+1.0)	2.348	0.361	0.957	18	K.EITALAPSTMK.I

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta M$	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ACTB_HUMAN	R17	7062	2	2244.5	(+0.2)	3.646	0.553	1.000	11	K.DL*YANTVL*SGGTTM@YPGIADR.M
SW:ACTB_HUMAN	R17	7554	2	2216.5	(-0.1)	2.798	0.453	0.978	11	K.DLYANTVLSGGTTMYPGIADR.M
SW:ACTB_HUMAN	R17	6532	2	1516.7	(-0.1)	2.319	0.383	0.947	10	K.IWHHTFYNELR.V
SW:ACTB_HUMAN	R17	8108	3	3185.6	(+0.3)	6.133	0.522	1.000	7	R.TTGIVMDSGDGVTHTVPIYEGYALPHAILR.L
SW:ACTB_HUMAN	R17	8104	3	3197.6	(-0.2)	5.613	0.479	0.972	7	R.TTGIVMDSGDGVTHTVPIYEGYAL*PHAIL*R.L
SW:ACTB_HUMAN	R17	6772	2	1955.3	(+0.4)	4.582	0.621	1.000	5	R.VAPEEHPVLLTEAPLNPK.A
SW:ACTB_HUMAN	R27	6529	3	2244.5	(+0.2)	4.520	0.541	0.949	11	K.DL*YANTVL*SGGTTM@YPGIADR.M
SW:ADAS_HUMAN	R13	9205	2	1980.2	(+0.5)	4.803	0.531	1.000		K.GFDPNQLSVATLLFEGDR.E
SW:ADAS_HUMAN	R13	9209	2	1998.2	(-0.7)	3.492	0.361	0.977		K.GFDPNQL*SVATL*L*FEGDR.E
SW:ADAS_HUMAN	R13	8331	2	1806.0	(+0.8)	4.778	0.645	1.000		R.GISDPLTVFEQTEAAAR.E
SW:ADAS_HUMAN	R13	8349	2	1812.0	(+0.2)	2.785	0.317	0.932		R.GISDPL*TVFEQTEAAAR.E
SW:ADAS_HUMAN	R13	8711	2	1627.9	(-0.6)	3.680	0.472	1.000		K.NIYGNIEDLVVHIK.M
SW:ADNP_HUMAN	R07	1434	2	980.1	(+0.5)	2.610	0.160	0.820	2	R.IGSL*ASGNVR.S
SW:ADNP_HUMAN	R07	7823	3	3048.3	(+0.3)	4.961	0.322	0.981	2	R.KLDDSDSPSFFEEKPEEPVVLALDPK.G
SW:ADNP_HUMAN	R07	7813	3	3090.3	(-0.1)	4.414	0.511	1.000	2	R.K#L*DDSDSPSFFEEK#PEEPVVL*AL*DPK#.G
SW:ADNP_HUMAN	R07	6143	2	1901.1	(-0.4)	2.578	0.344	0.909	2	R.L*GL*GGNAPVSIQQSQSVK#.Q
SW:ADNP_HUMAN	R07	7901	2	1863.0	(+0.3)	3.293	0.351	0.979	1	K.NTTWEDVGLWDPSTLK.N
SW:ADNP_HUMAN	R07	1602	2	1114.2	(+0.2)	2.727	0.358	0.956	2	K.SDIASHFSNK#.R
SW:ADNP_HUMAN	R07	5679	2	1130.4	(+0.8)	2.551	0.377	0.967	2	K.VPAVANYIM@K#.I
SW:ADNP_HUMAN	R07	5791	2	1741.9	(+0.8)	2.962	0.558	0.999	2	R.YSLQSANASSLSSGQLK.S
SW:ADNP_HUMAN	R07	8139	2	1114.3	(+0.7)	2.272	0.227	0.811	2	K.L*AASL*WL*WK#.S
SW:ADT1_HUMAN	R01	2206	2	1137.4	(-0.3)	2.751	0.270	0.931	6	K.LLLQVQHASK.Q
SW:ADT1_HUMAN	R02	5224	2	1163.4	(+0.4)	2.223	0.229	0.776	6	K.L*L*L*QVQHASK#.Q
SW:ADT1_HUMAN	R03	4967	2	1137.4	(-0.3)	2.473	0.196	0.786	6	K.LLLQVQHASK.Q
SW:ADT1_HUMAN	R02	7522	2	1447.7	(+1.0)	2.882	0.477	0.990	9	R.YFPTQALNFAFK.D
SW:ADT1_HUMAN	R03	7733	2	1447.7	(+0.8)	2.760	0.496	0.990	9	R.YFPTQALNFAFK.D
SW:ADT1_HUMAN	R04	7990	2	1447.7	(+0.8)	2.478	0.526	0.989	9	R.YFPTQALNFAFK.D
SW:ADT1_HUMAN	R20	8200	2	1461.7	(+0.5)	3.282	0.480	1.000	9	R.YFPTQAL*NFAFK#.D
SW:ADT2_HUMAN	R01	6233	2	1220.4	(+0.8)	2.680	0.518	1.000	3	R.AAYFGIYDTAK.G
SW:ADT2_HUMAN	R01	6993	2	1234.4	(+0.4)	4.146	0.439	1.000	2	K.DFL*AGGVAAAISK#.T
SW:ADT2_HUMAN	R01	6989	2	1220.4	(+0.3)	4.107	0.525*	0.789	2	K.DFLAGGVAAAISK.T
SW:ADT2_HUMAN	R02	6694	2	1234.4	(+0.5)	3.830	0.501	1.000	2	K.DFL*AGGVAAAISK#.T
SW:ADT2_HUMAN	R03	6637	2	1234.4	(+0.5)	2.752	0.513*	0.255	2	K.DFL*AGGVAAAISK#.T
SW:ADT2_HUMAN	R04	6912	2	1220.4	(+0.7)	2.681	0.465*	0.280	2	K.DFLAGGVAAAISK.T
SW:ADT2_HUMAN	R04	6926	2	1220.4	(-0.8)	2.452	0.190	0.425	2	K.DFLAGGVAAAISK.T
SW:ADT2_HUMAN	R05	7062	2	1220.4	(-0.6)	3.002	0.164	0.811	2	K.DFLAGGVAAAISK.T
SW:AF32_HUMAN	R11	1660	2	1069.2	(+0.8)	2.716	0.153	0.750	1	K.GAILTGPPGTGK.T
SW:AF32_HUMAN	R11	1060	2	1090.2	(+0.6)	2.579	0.308	0.955	1	R.ITTGAQDDLK.K
SW:AF32_HUMAN	R11	9456	2	1403.7	(+0.4)	3.326	0.333	0.976	1	K.L*EIMEFVNFL*K#.N
SW:AF32_HUMAN	R11	8688	2	1419.7	(+0.0)	2.811	0.374	0.962	1	K.L*EIM@EFVNFL*K#.N
SW:AF32_HUMAN	R11	6656	2	1132.3	(+0.9)	3.610	0.457	1.000	1	K.VGQISFDLPR.Q
SW:AF32_HUMAN	R11	6660	2	1138.3	(+0.7)	2.247	0.284	0.902	1	K.VGQISFDL*PR.Q
SW:AHNK_HUMAN	R03	5347	2	1282.4	(-0.0)	2.531	0.374	0.941	5	K.AEGPEVDVNL*PK#.A
SW:AHNK_HUMAN	R04	5668	2	1282.4	(-0.7)	2.773	0.197	0.789	5	K.AEGPEVDVNL*PK#.A
SW:AHNK_HUMAN	R04	5508	2	1254.4	(+0.1)	2.638	0.420	0.956	3	K.GEGPDVDVNL*PK#.A
SW:ALFA_HUMAN	R17	5494	2	1347.5	(-0.1)	2.931	0.288	0.910	3	K.GIL*AADESTGSIK#.R
SW:ALFA_HUMAN	R17	5492	2	1333.5	(-0.1)	2.434	0.351	0.925	3	K.GILAADESTGSIK.R
SW:ALFA_HUMAN	R18	5147	2	1333.5	(+0.2)	4.013	0.561	1.000	3	K.GILAADESTGSIK.R
SW:ALFA_HUMAN	R18	5139	2	1347.5	(-0.5)	3.921	0.513	1.000	3	K.GIL*AADESTGSIK#.R
SW:ALFA_HUMAN	R18	5377	2	1435.6	(+0.1)	3.606	0.384	0.984		-.PYQYPALTPEQK.K
SW:ALFA_HUMAN	R18	5371	2	1449.6	(-0.1)	3.275	0.360	0.970		-.PYQYPAL*TPEQK#.K
SW:AMPL_HUMAN	R15	1960	2	1009.2	(+0.6)	2.705	0.421	0.987	3	K.ASANMDLMR.A
SW:AMPL_HUMAN	R15	6161	2	1245.4	(+0.4)	3.047	0.253	0.951	3	K.GVL*FASGQNL*AR.Q
SW:AMPL_HUMAN	R15	6707	2	1195.4	(+0.8)	2.535	0.420	0.979	3	K.GITFDSGGISIK.A
SW:ANX2_HUMAN	R18	6597	2	1422.6	(+0.5)	2.362	0.388	0.967	6	K.SLYYYIQQDTK.G
SW:ANX2_HUMAN	R18	1708	2	1237.3	(-0.2)	2.959	0.238	0.898	6	K.TPAQYDASEL*K#.A
SW:ANX2_HUMAN	R18	6583	2	1436.6	(+0.2)	2.307	0.194	0.625	6	K.SL*YYYIQQDTK#.G

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:APE1_HUMAN	R18	7969	3	2499.7	(-0.1)	5.470	0.469	1.000	7	K.L*PAEL*QEL*PGL*SHQYWSAPSDK#.E
SW:APE1_HUMAN	R19	8120	3	2467.7	(+0.1)	5.194	0.513	1.000	7	K.LPAELQELPGLSHQYWSAPSDK.E
SW:APE1_HUMAN	R19	8126	3	2499.7	(-0.1)	5.072	0.457	0.999	7	K.L*PAEL*QEL*PGL*SHQYWSAPSDK#.E
SW:APE1_HUMAN	R19	9320	2	1849.1	(+0.0)	3.299	0.612	0.999	5	R.QGFGELLQAVPLADSF.R.H
SW:APE1_HUMAN	R19	9338	2	1867.1	(-0.3)	2.225	0.302	0.825	5	R.QGFGEL*L*QAVPL*ADSF.R.H
SW:APMA_HUMAN	R17	7602	2	1104.3	(+0.5)	2.308	0.387	0.961	2	K.GL*FEVNPWK#.R
SW:APMA_HUMAN	R17	2090	2	1048.1	(+0.9)	2.280	0.212	0.711	3	K.IYFTDSSSK.W
SW:APMA_HUMAN	R16	4150	2	1251.4	(+0.4)	3.559	0.337	0.978	2	K.L*ENGEIETIAR.F
SW:APMA_HUMAN	R16	3692	2	1245.4	(+0.8)	3.511	0.405	0.991	2	K.LENGEIETIAR.F
SW:APMA_HUMAN	R16	3548	2	1245.4	(+0.5)	3.347	0.373	0.988	2	K.LENGEIETIAR.F
SW:APMA_HUMAN	R16	3626	2	1245.4	(+0.8)	3.327	0.244	0.965	2	K.LENGEIETIAR.F
SW:APMA_HUMAN	R16	4256	2	1245.4	(+0.6)	3.252	0.384	0.988	2	K.LENGEIETIAR.F
SW:APMA_HUMAN	R16	3740	2	1251.4	(+0.9)	3.175	0.323	0.975	2	K.L*ENGEIETIAR.F
SW:APMA_HUMAN	R16	3854	2	1245.4	(-0.6)	3.165	0.372	0.979	2	K.LENGEIETIAR.F
SW:APMA_HUMAN	R16	3844	2	1251.4	(-0.3)	3.101	0.337	0.972	2	K.L*ENGEIETIAR.F
SW:APMA_HUMAN	R16	4168	2	1245.4	(+0.5)	3.082	0.362	0.983	2	K.LENGEIETIAR.F
SW:APMA_HUMAN	R16	3916	2	1251.4	(+0.0)	3.055	0.364	0.975	2	K.L*ENGEIETIAR.F
SW:APMA_HUMAN	R16	3992	2	1251.4	(+0.1)	3.005	0.308	0.960	2	K.L*ENGEIETIAR.F
SW:APMA_HUMAN	R16	2210	2	1245.4	(+0.8)	2.767	0.281	0.952	2	K.LENGEIETIAR.F
SW:APMA_HUMAN	R16	3928	2	1245.4	(-0.6)	2.754	0.312	0.940	2	K.LENGEIETIAR.F
SW:APMA_HUMAN	R16	4336	2	1245.4	(+0.4)	2.665	0.319	0.961	2	K.LENGEIETIAR.F
SW:APMA_HUMAN	R16	3596	2	1251.4	(-0.2)	2.530	0.282	0.904	2	K.L*ENGEIETIAR.F
SW:APMA_HUMAN	R16	3526	2	1251.4	(+0.5)	2.503	0.370	0.969	2	K.L*ENGEIETIAR.F
SW:APMA_HUMAN	R16	2246	2	1251.4	(+0.8)	2.335	0.327	0.939	2	K.L*ENGEIETIAR.F
SW:APMA_HUMAN	R17	5386	2	1245.4	(+0.2)	2.587	0.322	0.939	2	K.LENGEIETIAR.F
SW:APMA_HUMAN	R17	5422	2	1251.4	(+0.4)	2.485	0.313	0.945	2	K.L*ENGEIETIAR.F
SW:APMA_HUMAN	R16	8842	3	2888.2	(+0.1)	4.293	0.481	1.000	2	R.L*FENQL*VGPESIAHIGDVMFTGTADGR.V
SW:APMA_HUMAN	R16	8852	3	2876.2	(+0.5)	3.760	0.338	0.933	2	R.LFENQLVGPESIAHIGDVMFTGTADGR.V
SW:APMA_HUMAN	R17	5640	2	1097.3	(-0.3)	2.302	0.172	0.628	3	K.L*FSQETVMK#.F
SW:APMA_HUMAN	R16	4170	2	1110.3	(-0.1)	2.662	0.344	0.958	3	R.LLEYDTVTR.E
SW:APMA_HUMAN	R16	4070	2	1122.3	(+0.2)	2.579	0.382	0.971	3	R.L*L*EYDTVTR.E
SW:APMA_HUMAN	R16	4248	2	1110.3	(+0.3)	2.482	0.250	0.878	3	R.LLEYDTVTR.E
SW:APMA_HUMAN	R16	4000	2	1110.3	(+0.2)	2.359	0.349	0.946	3	R.LLEYDTVTR.E
SW:APMA_HUMAN	R16	4092	2	1110.3	(+0.3)	2.349	0.414	0.977	3	R.LLEYDTVTR.E
SW:APMA_HUMAN	R16	3696	2	1122.3	(+0.3)	2.266	0.389	0.969	3	R.L*L*EYDTVTR.E
SW:APMA_HUMAN	R17	5356	2	1110.3	(+0.6)	2.878	0.390	0.987	3	R.LLEYDTVTR.E
SW:APMA_HUMAN	R17	5362	2	1122.3	(+0.4)	2.705	0.407	0.984	3	R.L*L*EYDTVTR.E
SW:APMA_HUMAN	R16	5952	2	1313.5	(+0.8)	2.885	0.489	0.988	2	K.L*L*L*SSETPIEGK#.N
SW:APMA_HUMAN	R17	6288	2	1313.5	(-0.8)	2.293	0.208	0.359	2	K.L*L*L*SSETPIEGK#.N
SW:APMA_HUMAN	R17	2416	3	2093.3	(+0.8)	3.932	0.419	0.994	1	R.RPLRPQVVTTDDGGQAPEAK.D
SW:APMA_HUMAN	R17	2414	3	2107.3	(+0.5)	3.756	0.350	0.979	1	R.RPL*RPQVVTTDDGGQAPEAK#.D
SW:APMA_HUMAN	R26	5358	3	2107.3	(+0.1)	3.782	0.265	0.786	1	R.RPL*RPQVVTTDDGGQAPEAK#.D
SW:APMA_HUMAN	R26	5368	3	2093.3	(+0.7)	3.764	0.454	0.992	1	R.RPLRPQVVTTDDGGQAPEAK.D
SW:ARF1_HUMAN	R24	7600	2	1090.3	(+0.2)	3.565	0.482	0.995	4	R.DAVLLVFANK.Q
SW:ARF1_HUMAN	R24	7604	2	1110.3	(-0.4)	3.061	0.451	0.998	4	R.DAVL*L*VFANK#.Q
SW:ARF1_HUMAN	R24	7802	2	1574.7	(-0.8)	3.024	0.497	0.951	2	K.NISFTVWDVGGQDK#.I
SW:ARF1_HUMAN	R24	6246	2	1124.4	(-0.7)	2.722	0.227	0.845	6	R.IL*M@VGL*DAAGK#.T
SW:ARME_HUMAN	R24	8192	2	1949.2	(-0.5)	4.213	0.460	0.999	3	K.DRDVTFSPATIENELIK.F
SW:ARME_HUMAN	R24	5540	2	973.2	(-0.1)	2.862	0.142	0.811	3	R.KINELMPK.Y
SW:ARME_HUMAN	R25	6766	3	1925.3	(+0.8)	4.078	0.383	0.992	3	K.IINEVSKPLAHHIPVEK.I
SW:ARS2_HUMAN	R08	8387	2	1516.7	(+0.1)	3.626	0.539	1.000	7	K.EVAFFNNFLTDAK.R
SW:ARS2_HUMAN	R08	8381	2	1530.7	(-0.7)	2.717	0.417	0.960	7	K.EVAFFNNFL*TDAK#.R
SW:ARS2_HUMAN	R08	1452	2	1132.3	(+0.6)	2.680	0.322	0.960	6	R.VAL*SEPQPER.R
SW:ART1_HUMAN	R01	5143	2	1405.6	(-0.8)	2.324	0.312	0.707	6	R.ILASTQFEPTAAR.M
SW:ART1_HUMAN	R01	5151	2	1411.6	(-0.1)	2.275	0.241	0.701	6	R.IL*ASTQFEPTAAR.M
SW:ART1_HUMAN	R02	7960	2	1516.8	(+0.8)	3.741	0.485	0.999	6	K.TQEFPQILTLIGR.N
SW:ATA1_HUMAN	R03	1752	2	1400.6	(+0.2)	3.012	0.359	0.941	12	K.AEIGIAM@GSGTAVAK#.T
SW:ATA1_HUMAN	R01	7727	2	1534.7	(+0.1)	2.730	0.306	0.894	9	R.DIVPGDIVEVAVGDK#.V
SW:ATA1_HUMAN	R01	7725	2	1526.7	(+0.7)	2.323	0.318	0.907	9	R.DIVPGDIVEVAVGDK.V

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ATA1_HUMAN	R03	7297	2	1526.7	(+0.5)	2.735	0.535	0.990	9	R.DIVPGDIVEVAVGDK.V
SW:ATA1_HUMAN	R01	5057	2	1504.8	(-0.2)	3.697	0.494	0.999	12	K.KAEIGIAMGSGTAVAK.T
SW:ATA1_HUMAN	R01	5045	2	1520.8	(-0.6)	3.501	0.433	0.981	12	K.K#AEIGIAMGSGTAVAK#.T
SW:ATA1_HUMAN	R01	6269	2	1171.3	(+0.8)	2.262	0.474	0.984	12	K.K#EFTL*EFSR.D
SW:ATA1_HUMAN	R01	2316	2	1166.3	(+0.9)	2.967	0.272	0.964	5	K.LDEFGEQLSK.V
SW:ATA1_HUMAN	R01	2322	2	1186.3	(+0.1)	2.898	0.407	0.975	5	K.L*DEFGEQL*SK#.V
SW:ATA1_HUMAN	R01	4597	2	1073.2	(+0.4)	2.962	0.413	0.988	6	R.NAENAIEALK.E
SW:ATA1_HUMAN	R01	4677	2	1073.2	(-0.1)	2.953	0.394	0.981	6	R.NAENAIEALK.E
SW:ATA1_HUMAN	R01	4687	2	1087.2	(-0.0)	2.590	0.300	0.915	6	R.NAENAIEAL*K#.E
SW:ATA1_HUMAN	R01	4573	2	1087.2	(+0.1)	2.353	0.293	0.867	6	R.NAENAIEAL*K#.E
SW:ATA1_HUMAN	R01	4517	2	1073.2	(+0.3)	2.244	0.303	0.918	6	R.NAENAIEALK.E
SW:ATA1_HUMAN	R04	5476	2	1073.2	(+0.1)	2.745	0.241	0.908	6	R.NAENAIEALK.E
SW:ATA1_HUMAN	R01	6419	2	1324.5	(-0.0)	3.025	0.360	0.969	6	K.NMLFSGTNIAGK.A
SW:ATA1_HUMAN	R01	5419	2	1354.5	(-0.4)	2.347	0.309	0.613	6	K.NM@L*FSGTNIAGK#.A
SW:ATA1_HUMAN	R03	5465	2	1354.5	(+0.1)	2.454	0.361	0.920	6	K.NM@L*FSGTNIAGK#.A
SW:ATA1_HUMAN	R02	8482	3	2426.7	(+0.7)	4.792	0.350	0.998	6	K.TASEMVLADDFSTIVAAVEEGR.A
SW:ATA1_HUMAN	R02	8038	3	2448.7	(+0.8)	3.763	0.325	0.991	6	K.TASEM@VL*ADDFSTIVAAVEEGR.A
SW:ATA1_HUMAN	R03	8809	3	2426.7	(+0.5)	4.548	0.420	0.995	6	K.TASEMVLADDFSTIVAAVEEGR.A
SW:ATA1_HUMAN	R01	6573	2	1575.8	(-0.9)	2.746	0.432	0.922	6	R.VDQSILTGESVSVIK.H
SW:ATA1_HUMAN	R02	6362	2	1575.8	(-0.8)	3.198	0.269	0.822	6	R.VDQSILTGESVSVIK.H
SW:ATA1_HUMAN	R03	6261	2	1589.8	(-0.3)	2.439	0.230	0.695	6	R.VDQSIL*TGESVSVIK#.H
SW:ATA1_HUMAN	R04	5466	2	1087.2	(-0.3)	2.640	0.334	0.941	6	R.NAENAIEAL*K#.E
SW:ATA2_HUMAN	R02	5390	2	1570.8	(-0.9)	2.907	0.426	0.910	1	K.AM@GVVATGVNTEIGK#.I
SW:ATA2_HUMAN	R01	8191	2	1548.8	(+0.6)	3.721	0.433	1.000	1	K.DIVPGDIVEIAVGDK#.V
SW:ATA2_HUMAN	R01	8185	2	1540.8	(+0.3)	2.608	0.421	0.976	1	K.DIVPGDIVEIAVGDK.V
SW:ATA2_HUMAN	R02	7496	2	1548.8	(+0.5)	4.240	0.530	0.999	1	K.DIVPGDIVEIAVGDK#.V
SW:ATA2_HUMAN	R02	7492	2	1540.8	(+0.7)	2.612	0.331	0.947	1	K.DIVPGDIVEIAVGDK.V
SW:ATA2_HUMAN	R03	7705	2	1548.8	(-0.0)	3.174	0.320	0.944	1	K.DIVPGDIVEIAVGDK#.V
SW:ATA2_HUMAN	R04	7966	2	1540.8	(+0.6)	2.603	0.458	0.982	1	K.DIVPGDIVEIAVGDK.V
SW:ATA2_HUMAN	R04	7982	2	1548.8	(+0.7)	2.589	0.458	0.976	1	K.DIVPGDIVEIAVGDK#.V
SW:ATA2_HUMAN	R01	1784	2	1312.4	(+0.0)	2.689	0.386	0.969	1	R.EFDEL*NPSAQR.D
SW:ATA2_HUMAN	R01	1780	2	1306.4	(+0.3)	2.563	0.265	0.923	1	R.EFDELNPSAQR.D
SW:ATA2_HUMAN	R02	4312	2	1306.4	(-0.5)	3.081	0.298	0.960	1	R.EFDELNPSAQR.D
SW:ATA2_HUMAN	R02	4242	2	1306.4	(-0.3)	2.517	0.232	0.841	1	R.EFDELNPSAQR.D
SW:ATA2_HUMAN	R02	4198	2	1312.4	(-0.1)	2.361	0.222	0.776	1	R.EFDEL*NPSAQR.D
SW:ATA2_HUMAN	R02	4270	2	1312.4	(-0.1)	2.304	0.315	0.898	1	R.EFDEL*NPSAQR.D
SW:ATA2_HUMAN	R02	4350	2	1312.4	(+0.5)	2.223	0.427	0.971	1	R.EFDEL*NPSAQR.D
SW:ATA2_HUMAN	R03	3995	2	1312.4	(+0.4)	3.034	0.382	0.985	1	R.EFDEL*NPSAQR.D
SW:ATA2_HUMAN	R03	4077	2	1306.4	(+0.4)	3.027	0.406	0.987	1	R.EFDELNPSAQR.D
SW:ATA2_HUMAN	R03	3925	2	1312.4	(-0.1)	2.677	0.372	0.962	1	R.EFDEL*NPSAQR.D
SW:ATA2_HUMAN	R03	3933	2	1306.4	(-0.7)	2.431	0.234	0.822	1	R.EFDELNPSAQR.D
SW:ATA2_HUMAN	R03	3865	2	1306.4	(-0.0)	2.368	0.305	0.900	1	R.EFDELNPSAQR.D
SW:ATA2_HUMAN	R03	3857	2	1312.4	(-0.1)	2.241	0.312	0.884	1	R.EFDEL*NPSAQR.D
SW:ATA2_HUMAN	R04	4300	2	1312.4	(-0.1)	2.672	0.320	0.942	1	R.EFDEL*NPSAQR.D
SW:ATA2_HUMAN	R04	4320	2	1306.4	(+0.0)	2.646	0.384	0.967	1	R.EFDELNPSAQR.D
SW:ATA2_HUMAN	R04	4248	2	1306.4	(-0.2)	2.538	0.260	0.883	1	R.EFDELNPSAQR.D
SW:ATA2_HUMAN	R04	4228	2	1312.4	(-0.0)	2.534	0.333	0.939	1	R.EFDEL*NPSAQR.D
SW:ATA2_HUMAN	R04	4374	2	1312.4	(-0.0)	2.310	0.287	0.869	1	R.EFDEL*NPSAQR.D
SW:ATA2_HUMAN	R01	6115	2	1417.5	(+0.8)	3.647	0.474	1.000	1	R.IGIFGQDEDTVSK#.A
SW:ATA2_HUMAN	R01	6139	2	1417.5	(-0.7)	3.334	0.429	0.981	1	R.IGIFGQDEDTVSK#.A
SW:ATA2_HUMAN	R02	6048	2	1409.5	(+0.1)	3.581	0.415	0.987	1	R.IGIFGQDEDTVSK.A
SW:ATA2_HUMAN	R02	6046	2	1417.5	(-0.6)	3.256	0.360	0.968	1	R.IGIFGQDEDTVSK#.A
SW:ATA2_HUMAN	R03	5921	2	1417.5	(-0.8)	2.679	0.274	0.688	1	R.IGIFGQDEDTVSK#.A
SW:ATA2_HUMAN	R04	6260	2	1409.5	(+0.1)	2.201	0.382	0.925	1	R.IGIFGQDEDTVSK.A
SW:ATA2_HUMAN	R01	8999	2	1472.8	(+0.6)	2.958	0.257	0.942	4	K.ISLPVILMDETLK.F
SW:ATA2_HUMAN	R03	8523	2	1472.8	(+0.9)	2.883	0.375	0.978	4	K.ISLPVILMDETLK.F
SW:ATA2_HUMAN	R03	6147	2	1111.3	(+0.6)	2.305	0.280	0.876	2	K.MNVFDTL*K#.G
SW:ATA2_HUMAN	R02	7370	3	2473.7	(+0.9)	4.563	0.399	0.998	1	K.TVEEVLGHFGVNESTGLSLEQVK.K
SW:ATA2_HUMAN	R03	7607	3	2473.7	(+0.8)	4.169	0.328	0.994	1	K.TVEEVLGHFGVNESTGLSLEQVK.K
SW:ATA2_HUMAN	R06	6334	2	1417.5	(+0.3)	2.833	0.339	0.600	1	R.IGIFGQDEDTVSK#.A
SW:ATA3_HUMAN	R01	6519	2	1336.5	(-0.1)	3.085	0.350	0.959	5	R.L*GIFGDTEDVAGK#.A
SW:ATA3_HUMAN	R03	6255	2	1336.5	(+0.1)	2.788	0.256	0.868	5	R.L*GIFGDTEDVAGK#.A
SW:ATA3_HUMAN	R01	7625	2	1510.7	(+0.9)	4.572	0.524*	0.861	4	K.MNVFDTDLQALSR.V
SW:ATA3_HUMAN	R02	7150	2	1510.7	(+0.6)	3.620	0.493	1.000	4	K.MNVFDTDLQALSR.V

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ATA3_HUMAN	R03	8653	3	2404.6	(+0.8)	4.115	0.460	0.999	5	K.SAAEM@VL*SDDNFASIVAAVEEGR.A
SW:ATA3_HUMAN	R03	5403	2	1046.2	(+0.9)	2.635	0.252	0.931	4	R.NAESAIEALK.E
SW:ATPA_HUMAN	R21	6232	2	1027.2	(+0.6)	2.215	0.221	0.804	7	K.AVDSLVPPIGR.G
SW:ATPA_HUMAN	R15	6571	2	1554.7	(-0.1)	2.741	0.424	0.975	7	R.EAYPGDVFYHLHSR.L
SW:ATPA_HUMAN	R16	6410	2	1554.7	(+0.8)	2.778	0.383	0.977	7	R.EAYPGDVFYHLHSR.L
SW:ATPA_HUMAN	R15	8685	2	1311.5	(+1.0)	3.911	0.561	0.999	6	K.EIVTNFLAGFEA.-
SW:ATPA_HUMAN	R15	8817	2	1317.5	(+0.9)	3.266	0.406	0.989	6	K.EIVTNFL*AGFEA.-
SW:ATPA_HUMAN	R15	12111	2	1311.5	(+0.7)	3.211	0.567	1.000	6	K.EIVTNFLAGFEA.-
SW:ATPA_HUMAN	R15	11741	2	1311.5	(+1.0)	3.101	0.574	1.000	6	K.EIVTNFLAGFEA.-
SW:ATPA_HUMAN	R15	11663	2	1311.5	(+0.8)	2.981	0.527	1.000	6	K.EIVTNFLAGFEA.-
SW:ATPA_HUMAN	R15	11485	2	1311.5	(+0.4)	2.919	0.526	1.000	6	K.EIVTNFLAGFEA.-
SW:ATPA_HUMAN	R15	12471	2	1311.5	(+0.6)	2.853	0.463	0.989	6	K.EIVTNFLAGFEA.-
SW:ATPA_HUMAN	R15	8739	2	1317.5	(+0.6)	2.819	0.580	1.000	6	K.EIVTNFL*AGFEA.-
SW:ATPA_HUMAN	R15	8935	2	1311.5	(+0.9)	2.800	0.545	1.000	6	K.EIVTNFLAGFEA.-
SW:ATPA_HUMAN	R15	12195	2	1311.5	(+0.6)	2.776	0.487	0.990	6	K.EIVTNFLAGFEA.-
SW:ATPA_HUMAN	R15	8661	2	1317.5	(+1.0)	2.683	0.563	1.000	6	K.EIVTNFL*AGFEA.-
SW:ATPA_HUMAN	R15	12333	2	1311.5	(+0.5)	2.593	0.509	0.989	6	K.EIVTNFLAGFEA.-
SW:ATPA_HUMAN	R15	11559	2	1311.5	(+0.2)	2.420	0.497	0.980	6	K.EIVTNFLAGFEA.-
SW:ATPA_HUMAN	R15	11413	2	1311.5	(+0.7)	2.412	0.406	0.971	6	K.EIVTNFLAGFEA.-
SW:ATPA_HUMAN	R15	8699	2	1311.5	(-0.9)	2.307	0.344	0.782	6	K.EIVTNFLAGFEA.-
SW:ATPA_HUMAN	R15	9421	2	2339.6	(+0.2)	5.282	0.562	0.990	7	R.EVAFAQFGSDLDAATQQLLSR.G
SW:ATPA_HUMAN	R15	9429	2	2357.6	(+0.7)	4.991	0.482	1.000	7	R.EVAFAQFGSDL*DAATQQL*L*SR.G
SW:ATPA_HUMAN	R15	10833	3	2339.6	(+0.7)	4.735	0.409	0.999	7	R.EVAFAQFGSDLDAATQQLLSR.G
SW:ATPA_HUMAN	R15	11999	3	2339.6	(+0.8)	4.641	0.439	1.000	7	R.EVAFAQFGSDLDAATQQLLSR.G
SW:ATPA_HUMAN	R15	11649	3	2339.6	(+0.8)	4.341	0.446	1.000	7	R.EVAFAQFGSDLDAATQQLLSR.G
SW:ATPA_HUMAN	R15	12415	3	2339.6	(+0.4)	4.227	0.440	0.998	7	R.EVAFAQFGSDLDAATQQLLSR.G
SW:ATPA_HUMAN	R15	10661	3	2339.6	(+0.4)	4.030	0.470	1.000	7	R.EVAFAQFGSDLDAATQQLLSR.G
SW:ATPA_HUMAN	R15	11433	3	2339.6	(+0.5)	4.027	0.377	0.998	7	R.EVAFAQFGSDLDAATQQLLSR.G
SW:ATPA_HUMAN	R15	11833	3	2339.6	(+0.7)	3.978	0.277	0.983	7	R.EVAFAQFGSDLDAATQQLLSR.G
SW:ATPA_HUMAN	R15	13053	3	2339.6	(+0.5)	3.973	0.364	0.998	7	R.EVAFAQFGSDLDAATQQLLSR.G
SW:ATPA_HUMAN	R15	12341	3	2339.6	(-0.4)	3.945	0.392	0.996	7	R.EVAFAQFGSDLDAATQQLLSR.G
SW:ATPA_HUMAN	R15	12545	3	2339.6	(-0.0)	3.897	0.384	0.996	7	R.EVAFAQFGSDLDAATQQLLSR.G
SW:ATPA_HUMAN	R15	11209	3	2339.6	(+0.4)	3.889	0.401	0.999	7	R.EVAFAQFGSDLDAATQQLLSR.G
SW:ATPA_HUMAN	R15	10997	3	2339.6	(+0.4)	3.886	0.380	0.998	7	R.EVAFAQFGSDLDAATQQLLSR.G
SW:ATPA_HUMAN	R15	12191	3	2339.6	(+0.6)	3.884	0.325	0.993	7	R.EVAFAQFGSDLDAATQQLLSR.G
SW:ATPA_HUMAN	R15	11281	3	2339.6	(+0.5)	3.874	0.381	0.998	7	R.EVAFAQFGSDLDAATQQLLSR.G
SW:ATPA_HUMAN	R15	11577	3	2339.6	(+0.6)	3.734	0.347	0.996	7	R.EVAFAQFGSDLDAATQQLLSR.G
SW:ATPA_HUMAN	R01	8239	3	2368.7	(+0.9)	5.103	0.554	1.000	6	K.FENAFLSHVVSQHQALLGTIR.A
SW:ATPA_HUMAN	R15	8101	3	2368.7	(+1.0)	6.977	0.561	0.997	6	K.FENAFLSHVVSQHQALLGTIR.A
SW:ATPA_HUMAN	R15	8037	2	2368.7	(+0.4)	6.324	0.625	0.986	6	K.FENAFLSHVVSQHQALLGTIR.A
SW:ATPA_HUMAN	R15	8049	2	2386.7	(+0.2)	5.366	0.489	1.000	6	K.FENAFL*SHVVSQHQAL*L*GTIR.A
SW:ATPA_HUMAN	R15	7867	3	2386.7	(+0.5)	4.129	0.557	1.000	6	K.FENAFL*SHVVSQHQAL*L*GTIR.A
SW:ATPA_HUMAN	R16	7862	3	2386.7	(+0.8)	5.179	0.590	1.000	6	K.FENAFL*SHVVSQHQAL*L*GTIR.A
SW:ATPA_HUMAN	R15	6395	2	1439.7	(-0.3)	2.909	0.404	0.420	7	K.GIRPAINVGLSVSR.V
SW:ATPA_HUMAN	R15	7927	3	2125.4	(+0.9)	4.172	0.455	1.000	5	K.GMSL*NL*EPDNVGVVVFVGNDK#.L
SW:ATPA_HUMAN	R15	7931	2	2105.4	(+0.3)	3.949	0.386	0.990	5	K.GMSLNLEPDNVGVVVFVGNDK.L
SW:ATPA_HUMAN	R21	7988	2	2105.4	(+0.3)	2.622	0.346	0.954	5	K.GMSLNLEPDNVGVVVFVGNDK.L
SW:ATPA_HUMAN	R15	5499	2	1150.3	(+0.7)	2.367	0.301	0.216	7	R.GYLDKLEPSK.I
SW:ATPA_HUMAN	R15	6503	2	1288.5	(+0.3)	4.203	0.436	0.999	7	K.HALIYDDL*SK.Q
SW:ATPA_HUMAN	R15	6621	2	1288.5	(+0.8)	2.817	0.262	0.946	7	K.HALIYDDL*SK.Q
SW:ATPA_HUMAN	R16	6352	2	1288.5	(+0.8)	3.493	0.384	0.990	7	K.HALIYDDL*SK.Q
SW:ATPA_HUMAN	R16	6354	2	1308.5	(-0.2)	2.488	0.329	0.915	7	K.HAL*IIYDDL*SK#.Q
SW:ATPA_HUMAN	R19	6862	2	1308.5	(+0.3)	2.883	0.413	0.982	7	K.HAL*IIYDDL*SK#.Q
SW:ATPA_HUMAN	R15	5971	2	1588.7	(-0.9)	3.203	0.366	0.917	3	R.IL*GADTSVDL*EETGR.V
SW:ATPA_HUMAN	R15	6051	2	1588.7	(-0.5)	2.780	0.263	0.885	3	R.IL*GADTSVDL*EETGR.V
SW:ATPA_HUMAN	R15	12837	2	1576.7	(+0.3)	2.749	0.335	0.957	3	R.ILGADTSVDLEETGR.V
SW:ATPA_HUMAN	R15	12051	2	1576.7	(+0.2)	2.602	0.343	0.932	3	R.ILGADTSVDLEETGR.V
SW:ATPA_HUMAN	R15	13011	2	1588.7	(-0.5)	2.579	0.347	0.932	3	R.IL*GADTSVDL*EETGR.V
SW:ATPA_HUMAN	R15	10809	2	1576.7	(+0.1)	2.526	0.359	0.935	3	R.ILGADTSVDLEETGR.V
SW:ATPA_HUMAN	R15	10549	2	1576.7	(-0.6)	2.364	0.236	0.737	3	R.ILGADTSVDLEETGR.V
SW:ATPA_HUMAN	R15	12141	2	1576.7	(+0.5)	2.283	0.339	0.914	3	R.ILGADTSVDLEETGR.V
SW:ATPA_HUMAN	R15	11497	2	1588.7	(+0.1)	2.264	0.237	0.700	3	R.IL*GADTSVDL*EETGR.V
SW:ATPA_HUMAN	R15	616	2	877.9	(+0.7)	2.216	0.228	0.833	7	K.ISEQSDAK.L
SW:ATPA_HUMAN	R15	2508	2	905.0	(+0.1)	2.310	0.217	0.806	7	K.L*EL*AQYR.E
SW:ATPA_HUMAN	R15	2424	2	905.0	(+0.7)	2.253	0.258	0.905	7	K.L*EL*AQYR.E

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ATPA_HUMAN	R15	8591	2	1552.8	(+0.7)	3.733	0.551	1.000	6	K.LKEIVTNFLAGFEA.-
SW:ATPA_HUMAN	R15	8819	2	1552.8	(-0.3)	3.301	0.482	0.999	6	K.LKEIVTNFLAGFEA.-
SW:ATPA_HUMAN	R15	8609	2	1572.8	(-0.6)	2.602	0.274	0.124	6	K.L*K#EIVTNFL*AGFEA.-
SW:ATPA_HUMAN	R15	12323	2	1668.9	(+0.5)	3.670	0.458	0.996	3	R.NVQAEEMVEFSSGLK.G
SW:ATPA_HUMAN	R15	13021	2	1668.9	(-0.1)	3.580	0.444	0.987	3	R.NVQAEEMVEFSSGLK.G
SW:ATPA_HUMAN	R15	12687	2	1668.9	(-0.2)	3.528	0.501	0.999	3	R.NVQAEEMVEFSSGLK.G
SW:ATPA_HUMAN	R15	12603	2	1668.9	(+0.1)	3.523	0.345	0.974	3	R.NVQAEEMVEFSSGLK.G
SW:ATPA_HUMAN	R15	12525	2	1668.9	(-0.3)	3.435	0.352	0.973	3	R.NVQAEEMVEFSSGLK.G
SW:ATPA_HUMAN	R15	12885	2	1668.9	(-0.2)	3.304	0.398	0.979	3	R.NVQAEEMVEFSSGLK.G
SW:ATPA_HUMAN	R15	12463	2	1698.9	(+0.7)	2.685	0.482	0.982	3	R.NVQAEEM@VEFSSGL*K#.G
SW:ATPA_HUMAN	R15	12275	2	1698.9	(+0.0)	2.418	0.209	0.605	3	R.NVQAEEM@VEFSSGL*K#.G
SW:ATPA_HUMAN	R15	9861	2	1668.9	(-0.2)	2.264	0.311	0.761	3	R.NVQAEEMVEFSSGLK.G
SW:ATPA_HUMAN	R15	13093	2	1698.9	(-0.1)	2.224	0.428	0.930	3	R.NVQAEEM@VEFSSGL*K#.G
SW:ATPA_HUMAN	R15	744	2	1076.1	(+0.3)	2.534	0.173	0.767	7	K.RFNDGSDEK#.K
SW:ATPA_HUMAN	R15	1106	2	1021.2	(+1.0)	3.040	0.197	0.934	7	K.RLTDADAMK.Y
SW:ATPA_HUMAN	R15	1114	2	1035.2	(-0.2)	2.376	0.179	0.686	7	K.RL*TDADAMK#.Y
SW:ATPA_HUMAN	R15	7525	2	1625.9	(+0.5)	3.495	0.365	0.984	5	R.TGAIVDVPVGEELLGR.V
SW:ATPA_HUMAN	R16	7288	2	1625.9	(-0.0)	3.848	0.459	1.000	5	R.TGAIVDVPVGEELLGR.V
SW:ATPA_HUMAN	R19	7942	2	1625.9	(-0.1)	3.767	0.478	1.000	5	R.TGAIVDVPVGEELLGR.V
SW:ATPA_HUMAN	R15	6305	2	1430.6	(+0.7)	3.259	0.371	0.984	3	K.TGTAEMSSIL*EER.I
SW:ATPA_HUMAN	R15	6313	2	1424.6	(+0.3)	2.237	0.448	0.972	3	K.TGTAEMSSILEER.I
SW:ATPA_HUMAN	R15	6639	2	1325.5	(+0.3)	3.557	0.343	0.974	7	K.TSIAIDTIINQK#.R
SW:ATPA_HUMAN	R15	6813	2	1317.5	(+0.8)	3.443	0.399	0.990	7	K.TSIAIDTIINQK.R
SW:ATPA_HUMAN	R15	5751	2	1001.2	(-0.2)	2.944	0.328	0.968	3	R.VLSIGDGIAR.V
SW:ATPA_HUMAN	R15	5349	2	1007.2	(+0.9)	2.772	0.252	0.944	3	R.VL*SIGDGIAR.V
SW:ATPA_HUMAN	R15	5369	2	1001.2	(+1.0)	2.527	0.413	0.980	3	R.VLSIGDGIAR.V
SW:ATPA_HUMAN	R15	2312	2	1186.3	(+0.0)	3.458	0.430	1.000	6	R.VVDAL*GNAIDGK#.G
SW:ATPA_HUMAN	R15	2458	2	1186.3	(+0.8)	3.282	0.448	1.000	6	R.VVDAL*GNAIDGK#.G
SW:ATPA_HUMAN	R15	5347	2	1186.3	(+0.3)	3.276	0.442	0.988	6	R.VVDAL*GNAIDGK#.G
SW:ATPA_HUMAN	R15	4425	2	1172.3	(+0.3)	3.123	0.506	1.000	6	R.VVDALGNAIDGK.G
SW:ATPA_HUMAN	R15	2480	2	1186.3	(-0.7)	2.950	0.360	0.960	6	R.VVDAL*GNAIDGK#.G
SW:ATPA_HUMAN	R15	4403	2	1186.3	(-0.0)	2.803	0.446	0.975	6	R.VVDAL*GNAIDGK#.G
SW:ATPA_HUMAN	R15	4479	2	1186.3	(-0.3)	2.774	0.427	0.971	6	R.VVDAL*GNAIDGK#.G
SW:ATPA_HUMAN	R15	5443	2	1172.3	(+0.8)	2.621	0.534	0.991	6	R.VVDALGNAIDGK.G
SW:ATPA_HUMAN	R15	5361	2	1186.3	(-1.0)	2.468	0.380	0.831	6	R.VVDAL*GNAIDGK#.G
SW:ATPA_HUMAN	R15	5363	2	1172.3	(-0.9)	2.439	0.528	0.953	6	R.VVDALGNAIDGK.G
SW:ATPA_HUMAN	R15	4991	2	1186.3	(+0.1)	2.348	0.338	0.888	6	R.VVDAL*GNAIDGK#.G
SW:ATPA_HUMAN	R15	2490	2	1172.3	(-0.5)	2.268	0.508	0.978	6	R.VVDALGNAIDGK.G
SW:ATPA_HUMAN	R15	2332	2	1172.3	(-0.6)	2.202	0.300	0.848	6	R.VVDALGNAIDGK.G
SW:ATPA_HUMAN	R16	5154	2	1172.3	(+0.3)	3.380	0.523	1.000	6	R.VVDALGNAIDGK.G
SW:ATPA_HUMAN	R16	5166	2	1186.3	(+0.1)	2.887	0.465	0.980	6	R.VVDAL*GNAIDGK#.G
SW:ATPA_HUMAN	R19	5722	2	1172.3	(+1.0)	3.091	0.476	0.999	6	R.VVDALGNAIDGK.G
SW:ATPA_HUMAN	R23	6336	2	1027.2	(+0.7)	2.377	0.330	0.922	7	K.AVDSLVPPIGR.G
SW:ATPB_HUMAN	R15	7621	2	1989.2	(+0.8)	3.306	0.521	0.999	3	R.AIAELGIYPAVDPLDSTSR.I
SW:ATPB_HUMAN	R15	10381	2	1923.1	(+0.9)	4.237	0.413	1.000	3	R.DQEGQDVLLFIDNIFR.F
SW:ATPB_HUMAN	R15	10383	2	1935.1	(-0.4)	3.195	0.447	0.984	3	R.DQEGQDVL*L*FIDNIFR.F
SW:ATPB_HUMAN	R16	10460	3	1935.1	(+1.0)	4.370	0.445	0.998	3	R.DQEGQDVL*L*FIDNIFR.F
SW:ATPB_HUMAN	R16	10458	2	1935.1	(+0.1)	3.784	0.452	1.000	3	R.DQEGQDVL*L*FIDNIFR.F
SW:ATPB_HUMAN	R16	10470	2	1923.1	(-0.9)	2.496	0.388	0.856	3	R.DQEGQDVLLFIDNIFR.F
SW:ATPB_HUMAN	R16	10380	2	1935.1	(-0.2)	2.402	0.279	0.801	3	R.DQEGQDVL*L*FIDNIFR.F
SW:ATPB_HUMAN	R18	10727	2	1923.1	(+0.6)	2.915	0.457	0.987	3	R.DQEGQDVLLFIDNIFR.F
SW:ATPB_HUMAN	R18	10741	2	1923.1	(-0.6)	2.504	0.427	0.963	3	R.DQEGQDVLLFIDNIFR.F
SW:ATPB_HUMAN	R16	7596	2	2062.3	(+0.2)	3.461	0.354	0.975	3	R.EGNDLYHEMIESGVINLK.D
SW:ATPB_HUMAN	R16	8232	2	2024.3	(-0.6)	2.795	0.484	0.982	3	R.FLSQPFQVAEVTGHHMGK.L
SW:ATPB_HUMAN	R15	6949	2	1436.6	(+0.8)	4.614	0.421	1.000	3	R.FTQAGSEVSALLGR.I
SW:ATPB_HUMAN	R15	6953	2	1448.6	(-0.1)	3.153	0.428	0.982	3	R.FTQAGSEVSAL*L*GR.I
SW:ATPB_HUMAN	R16	6740	2	1436.6	(+0.9)	3.867	0.408	1.000	3	R.FTQAGSEVSALLGR.I
SW:ATPB_HUMAN	R16	6710	2	1448.6	(+0.7)	3.531	0.537	1.000	3	R.FTQAGSEVSAL*L*GR.I
SW:ATPB_HUMAN	R18	7115	2	1436.6	(+0.7)	2.932	0.442	0.986	3	R.FTQAGSEVSALLGR.I
SW:ATPB_HUMAN	R15	8837	3	3388.8	(-0.2)	4.154	0.290	0.979	3	K.GFQQIL*AGEYDHL*PEQAFYM@VGPIEEAVAK#.A
SW:ATPB_HUMAN	R16	8756	3	3388.8	(-0.4)	4.239	0.430	0.999	3	K.GFQQIL*AGEYDHL*PEQAFYM@VGPIEEAVAK#.A
SW:ATPB_HUMAN	R16	9676	2	3352.8	(+0.2)	3.956	0.453	1.000	3	K.GFQQILAGEYDHLPEQAFYMVGPIEEAVAK.A
SW:ATPB_HUMAN	R16	13712	3	3717.1	(-0.3)	3.949	0.389	0.996	2	K.GSITSVQAIYVPADLTDPA PATTFAHL DATTVLSR.A
SW:ATPB_HUMAN	R16	11114	3	3717.1	(-0.1)	3.766	0.258	0.929	2	K.GSITSVQAIYVPADLTDPA PATTFAHL DATTVLSR.A
SW:ATPB_HUMAN	R16	8330	3	3717.1	(+0.2)	3.700	0.467	0.999	2	K.GSITSVQAIYVPADLTDPA PATTFAHL DATTVLSR.A



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ATPB_HUMAN	R15	6329	2	990.2	(+0.2)	2.455	0.442	0.965	2	K.IGL*FGGAGVGK#.T
SW:ATPB_HUMAN	R16	6592	2	2273.6	(+0.2)	4.315	0.562	1.000	3	R.IPSAVGYQPTL*ATDMGTMQER.I
SW:ATPB_HUMAN	R16	6034	2	2289.6	(-0.9)	3.105	0.390*	0.134	3	R.IPSAVGYQPTL*ATDM@GTMQER.I
SW:ATPB_HUMAN	R16	4884	2	1045.2	(+0.7)	2.491	0.327	0.943	2	K.IPVGPETL*GR.I
SW:ATPB_HUMAN	R16	4720	2	1045.2	(+0.8)	2.401	0.367	0.958	2	K.IPVGPETL*GR.I
SW:ATPB_HUMAN	R16	4802	2	1045.2	(+0.8)	2.330	0.357	0.958	2	K.IPVGPETL*GR.I
SW:ATPB_HUMAN	R16	4640	2	1045.2	(-0.8)	2.214	0.409	0.874	2	K.IPVGPETL*GR.I
SW:ATPB_HUMAN	R16	8052	3	3845.3	(+0.2)	7.952	0.688	1.000	2	K.KGSITSVQAIYVPADDLTDPAPATTF AHL DATTVLSR.A
SW:ATPB_HUMAN	R15	7017	2	1651.9	(-0.3)	4.627	0.615	1.000	2	R.LVLEVAQHLGESTVR.T
SW:ATPB_HUMAN	R15	7009	2	1669.9	(-0.5)	2.912	0.343	0.953	2	R.L*VL*EVAQHL*GESTVR.T
SW:ATPB_HUMAN	R16	7150	2	1651.9	(+0.3)	2.676	0.466	0.984	2	R.LVLEVAQHLGESTVR.T
SW:ATPB_HUMAN	R16	7382	2	1651.9	(-0.1)	2.580	0.414	0.963	2	R.LVLEVAQHLGESTVR.T
SW:ATPB_HUMAN	R16	9666	3	2146.4	(+0.4)	4.439	0.476	0.999	2	K.SL*QDI IAIL*GMDDEL*SEEDK#.L
SW:ATPB_HUMAN	R16	9678	2	2120.4	(+0.6)	2.246	0.335	0.911	2	K.SLQDI IAILGMDDELSEEDK.L
SW:ATPB_HUMAN	R15	5825	2	1269.5	(-0.5)	2.391	0.344	0.927	2	R.TIAMDGTEGL*VR.G
SW:ATPB_HUMAN	R16	5638	2	1263.5	(-0.2)	3.298	0.423	0.982	2	R.TIAMDGTEGLVR.G
SW:ATPB_HUMAN	R16	5858	2	1263.5	(+0.4)	3.221	0.456	1.000	2	R.TIAMDGTEGLVR.G
SW:ATPB_HUMAN	R16	5266	2	1269.5	(-0.1)	2.992	0.391	0.976	2	R.TIAMDGTEGL*VR.G
SW:ATPB_HUMAN	R16	1572	2	1285.5	(+1.0)	2.982	0.448	0.989	2	R.TIAM@DGTEGL*VR.G
SW:ATPB_HUMAN	R16	5252	2	1263.5	(+0.4)	2.721	0.392	0.978	2	R.TIAMDGTEGLVR.G
SW:ATPB_HUMAN	R16	1376	2	1285.5	(+0.8)	2.643	0.344	0.953	2	R.TIAM@DGTEGL*VR.G
SW:ATPB_HUMAN	R18	5877	2	1263.5	(-0.0)	2.458	0.297	0.897	2	R.TIAMDGTEGLVR.G
SW:ATPB_HUMAN	R15	9171	2	1478.8	(-0.3)	4.070	0.314	0.976	2	K.TVL*IMEL*INNVAK#.A
SW:ATPB_HUMAN	R16	9114	2	1478.8	(+0.2)	4.192	0.465	1.000	2	K.TVL*IMEL*INNVAK#.A
SW:ATPB_HUMAN	R16	8144	2	1494.8	(-0.2)	2.972	0.212	0.838	2	K.TVL*IM@EL*INNVAK#.A
SW:ATPB_HUMAN	R18	9565	2	1458.8	(+0.8)	4.160	0.437	0.999	2	K.TVLIMELINNVAK.A
SW:ATPB_HUMAN	R18	9563	2	1478.8	(+0.7)	3.462	0.362	0.981	2	K.TVL*IMEL*INNVAK#.A
SW:ATPB_HUMAN	R19	9684	2	1478.8	(-0.4)	3.588	0.305	0.963	2	K.TVL*IMEL*INNVAK#.A
SW:ATPB_HUMAN	R16	7750	2	1452.7	(+0.8)	2.767	0.537	1.000	3	R.VAL*TGL*TVAEYFR.D
SW:ATPB_HUMAN	R16	5790	2	1602.8	(+0.4)	4.280	0.434	1.000	1	K.VALVYQGMNEPPGAR.A
SW:ATPB_HUMAN	R16	5706	2	1602.8	(-0.2)	4.278	0.473*	0.701	1	K.VALVYQGMNEPPGAR.A
SW:ATPB_HUMAN	R16	1734	2	1624.8	(+0.3)	3.220	0.433	0.988	1	K.VAL*VYQGM@NEPPGAR.A
SW:ATPB_HUMAN	R20	10566	2	1923.1	(+0.3)	2.535	0.288	0.909	3	R.DQEGQDVLFFIDNIFR.F
SW:ATPD_HUMAN	R25	2508	2	1432.5	(-0.0)	2.760	0.429	0.975		K.AQAELVGTADAEATR.A
SW:ATPD_HUMAN	R25	5546	2	1432.5	(-0.4)	2.475	0.385	0.948		K.AQAELVGTADAEATR.A
SW:ATPD_HUMAN	R25	2432	2	1001.1	(+0.5)	2.592	0.258	0.907		R.IEANEAL*VK#.A
SW:ATPD_HUMAN	R25	2518	2	1438.5	(-0.1)	2.234	0.328	0.867		K.AQAEL*VGTADAEATR.A
SW:ATPF_HUMAN	R22	6494	2	1451.6	(-0.2)	2.728	0.366	0.955	2	K.EQEHMINWVEK#.H
SW:ATPF_HUMAN	R22	6490	2	1443.6	(-0.0)	2.511	0.351	0.853	2	K.EQEHMINWVEK.H
SW:ATPF_HUMAN	R22	1902	2	1392.5	(+0.7)	3.152	0.436	0.986	2	K.HVVQSISTQQEK#.E
SW:ATPF_HUMAN	R22	1900	2	1384.5	(+0.1)	2.934	0.547	1.000	2	K.HVVQSISTQQEK.E
SW:ATPF_HUMAN	R22	6580	2	1084.2	(+1.0)	2.441	0.333	0.967	2	R.HYL*FDVQR.N
SW:ATPF_HUMAN	R23	6472	2	1078.2	(+0.5)	2.571	0.365	0.979	2	R.HYLFDVQR.N
SW:ATPF_HUMAN	R22	2086	2	902.0	(+0.2)	2.328	0.165	0.725	2	K.LAQLEEAK.Q
SW:ATPF_HUMAN	R23	2156	2	922.0	(-0.0)	2.256	0.233	0.791	2	K.L*AQL*EEAK#.Q
SW:ATPF_HUMAN	R22	1524	2	902.0	(+0.8)	2.697	0.220	0.938	2	K.SQQALVQK.R
SW:ATPF_HUMAN	R22	1612	2	902.0	(+0.8)	2.285	0.149	0.737	2	K.SQQALVQK.R
SW:ATPF_HUMAN	R22	1522	2	916.0	(+0.3)	2.206	0.271	0.873	2	K.SQQAL*VQK#.R
SW:ATPF_HUMAN	R23	1578	2	902.0	(+0.1)	2.607	0.180	0.853	2	K.SQQALVQK.R
SW:ATPF_HUMAN	R23	10162	2	2024.4	(-0.1)	3.259	0.471*	0.379	1	K.TGVTGPYVLGTGLILYALSK.E
SW:ATPF_HUMAN	R22	7074	2	1230.4	(+0.0)	2.628	0.490	0.985	2	K.YGPFVADFADK.L
SW:ATPF_HUMAN	R23	7062	2	1230.4	(-0.3)	2.247	0.344	0.915	2	K.YGPFVADFADK.L
SW:ATPG_HUMAN	R19	5764	2	1109.3	(+0.6)	2.563	0.310	0.956	3	K.HL*L*IGVSSDR.G
SW:ATPG_HUMAN	R20	5790	2	1097.3	(+0.7)	3.133	0.197	0.942	3	K.HLLIGVSSDR.G
SW:ATPG_HUMAN	R20	5792	2	1109.3	(+0.1)	2.451	0.212	0.810	3	K.HL*L*IGVSSDR.G
SW:ATPG_HUMAN	R19	7802	2	1327.6	(+0.6)	3.105	0.494	1.000	3	R.IYGLGSLALYEK.A
SW:ATPG_HUMAN	R20	7556	2	1353.6	(-0.0)	3.125	0.297	0.944	3	R.IYGL*GSL*AL*YEK#.A
SW:ATPG_HUMAN	R20	1376	2	908.0	(+1.0)	2.272	0.329	0.951	3	K.NASEMIDK.L
SW:ATPG_HUMAN	R20	1388	2	916.0	(+1.0)	2.224	0.158	0.671	3	K.NASEMIDK#.L
SW:ATPG_HUMAN	R19	1740	2	1062.2	(+0.1)	2.383	0.334	0.905	3	K.SEVATL*TAAGK#.E
SW:ATPG_HUMAN	R20	1898	2	1062.2	(+0.3)	2.722	0.538	1.000	3	K.SEVATL*TAAGK#.E
SW:ATPG_HUMAN	R19	6980	2	1293.5	(+0.5)	2.415	0.228	0.857	3	R.THSDQFLVAFK.E
SW:ATPG_HUMAN	R21	7508	2	1327.6	(+0.6)	2.268	0.493	0.983	3	R.IYGLGSLALYEK.A

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ATPJ_HUMAN	R27	7389	2	1489.7	(+0.5)	3.093	0.479	0.991	2	R.YSALFLGVAYGATR.Y
SW:ATPJ_HUMAN	R27	7371	2	1501.7	(+0.4)	2.945	0.389	0.979	2	R.YSAL*FL*GVAYGATR.Y
SW:ATPJ_HUMAN	R27	6239	2	1191.5	(+0.6)	2.829	0.370	0.973		-.VPPVQVSPL*IK#.L
SW:ATPN_HUMAN	R26	6656	3	1588.8	(+0.7)	3.846	0.566	1.000	2	K.TPALVNAAVTYSKPR.L
SW:ATPN_HUMAN	R26	6708	2	1588.8	(-0.3)	3.136	0.482	0.589	2	K.TPALVNAAVTYSKPR.L
SW:ATPN_HUMAN	R26	7680	2	1177.4	(+0.5)	2.234	0.375	0.951	2	R.L*ATFWYYAK#.V
SW:ATPO_HUMAN	R23	9314	2	1874.1	(+0.7)	2.725	0.306	0.942		R.FSPLTTNLLINLLAENGR.L
SW:ATPO_HUMAN	R23	9480	2	1898.1	(+0.1)	2.669	0.345	0.939		R.FSPL*TTNL*INL*L*AENGR.L
SW:ATPO_HUMAN	R23	9470	2	1874.1	(-0.1)	2.537	0.250	0.820		R.FSPLTTNLLINLLAENGR.L
SW:ATPO_HUMAN	R23	6606	3	1583.9	(+0.9)	3.796	0.372	0.990		K.LVRPPVQVYGIAGR.Y
SW:ATPO_HUMAN	R23	6652	2	1583.9	(-0.8)	3.150	0.344	0.156		K.LVRPPVQVYGIAGR.Y
SW:ATPO_HUMAN	R23	6656	2	1589.9	(-0.2)	2.603	0.274	0.124		K.L*VRPPVQVYGIAGR.Y
SW:ATPO_HUMAN	R23	7412	2	1259.5	(+1.0)	2.592	0.371	0.970		K.TDPSILGGMIVR.I
SW:ATPO_HUMAN	R23	6386	2	1127.3	(+0.3)	2.339	0.318	0.923		K.SFL*SQGQVL*K#.L
SW:ATPQ_HUMAN	R23	7362	2	1685.9	(-0.2)	2.766	0.449	0.967	2	K.KYPYWPHQPIENL.-
SW:ATPQ_HUMAN	R23	7982	3	1953.2	(-0.6)	4.396	0.442	1.000	2	R.L*AAL*PENPPAIDWAYYK#.A
SW:ATPQ_HUMAN	R23	7968	2	1953.2	(+1.0)	3.618	0.411	0.986	2	R.L*AAL*PENPPAIDWAYYK#.A
SW:ATPQ_HUMAN	R23	9248	2	2466.8	(-0.4)	3.017	0.387	0.971	2	K.NLIPFDQMTIEDLNEAFPETK.L
SW:ATPQ_HUMAN	R23	5472	2	1094.2	(+0.4)	2.683	0.283	0.958	2	K.SWNETLTSR.L
SW:ATPQ_HUMAN	R23	5478	2	1100.2	(-0.0)	2.483	0.274	0.905	2	K.SWNETL*TSR.L
SW:ATPQ_HUMAN	R23	7962	2	1933.2	(+0.6)	2.443	0.370	0.953	2	R.LAALPENPPAIDWAYYK.A
SW:ATY2_HUMAN	R01	7523	2	1370.6	(+0.7)	2.209	0.195	0.634	2	K.AML*TAVDWTL*TK#.D
SW:ATY2_HUMAN	R03	8461	2	1526.8	(+0.7)	2.251	0.129	0.292	2	K.AEMVVPDFSEL*FK#.E
SW:B53A_HUMAN	R16	6438	2	1330.5	(+0.2)	2.757	0.235	0.848	4	K.IPEGL*FDPSNVK#.G
SW:B53A_HUMAN	R17	6792	2	1330.5	(-0.2)	2.833	0.317	0.880	4	K.IPEGL*FDPSNVK#.G
SW:B53A_HUMAN	R16	968	2	1137.3	(+0.7)	2.902	0.397	0.986	2	K.L*IANNTTVER.R
SW:B53A_HUMAN	R16	972	2	1131.3	(+1.0)	2.862	0.342	0.978	2	K.LIANNTTVER.R
SW:B53A_HUMAN	R17	1546	2	1137.3	(+0.4)	2.967	0.323	0.977	2	K.L*IANNTTVER.R
SW:B53A_HUMAN	R16	6236	2	1575.7	(+0.8)	2.965	0.484	0.989	2	K.QGGPTYIDTNAL*R.V
SW:B53A_HUMAN	R16	7118	3	3093.5	(-0.4)	4.461	0.455	0.999	2	R.STGLILDGATHTTAIPVHDGYVLQQGIVK.S
SW:B53A_HUMAN	R17	7592	3	3093.5	(+0.1)	6.441	0.435	0.999	2	R.STGLILDGATHTTAIPVHDGYVLQQGIVK.S
SW:B53A_HUMAN	R17	5644	2	1396.5	(+0.3)	2.308	0.486	0.982	2	R.DDGSTLMEIDGDK.G
SW:BA1A_HUMAN	R06	8662	2	1404.6	(+0.6)	4.192	0.453	0.999	2	R.DFIEDYVDIL*R.Q
SW:BA1A_HUMAN	R06	5382	2	1078.3	(-0.2)	2.235	0.285	0.826	3	R.IYQGTL*GAIK#.V
SW:BA1A_HUMAN	R07	8675	2	1398.6	(+0.6)	3.965	0.456	1.000	2	R.DFIEDYVDILR.Q
SW:BA1B_HUMAN	R06	5542	2	1004.1	(+0.7)	2.750	0.334	0.975	4	R.SDLIEVATR.L
SW:BA1B_HUMAN	R06	9308	2	1844.1	(+0.6)	3.935	0.631	1.000	4	R.YWLFSDVEVPGLFIEK.G
SW:BA1B_HUMAN	R06	6960	2	1198.4	(+0.5)	2.270	0.293	0.909	4	R.SVQEFLTDMK.Q
SW:BA31_HUMAN	R21	5196	2	1032.2	(+0.7)	3.088	0.408	0.990	3	K.AENQVLAMR.K
SW:BA31_HUMAN	R22	5152	2	1032.2	(+0.9)	3.216	0.386	0.990	3	K.AENQVLAMR.K
SW:BA31_HUMAN	R21	4766	2	1159.3	(+0.1)	2.919	0.306	0.939	3	K.L*QAAVDGPMK#.K
SW:BA31_HUMAN	R21	4800	2	1175.3	(-0.6)	2.702	0.305	0.922	3	K.L*QAAVDGPM@DK#.K
SW:BA31_HUMAN	R21	4764	2	1145.3	(+0.0)	2.629	0.308	0.935	3	K.LQAAVDGPMK.K
SW:BA31_HUMAN	R21	3902	2	1170.3	(+0.7)	2.335	0.380	0.967	3	K.YMEENDQLK.K
SW:BA31_HUMAN	R22	5174	2	1032.2	(-0.4)	2.236	0.173	0.600	3	K.AENQVLAMR.K
SW:BAF_HUMAN	R27	7231	3	2445.8	(-0.5)	4.165	0.335	0.941	1	R.DFVAEPM@GEK#PVGSL*AGIGEVL*GK#.K
SW:BAF_HUMAN	R27	7511	3	2429.8	(+0.1)	4.020	0.438	0.990	1	R.DFVAEPMGEK#PVGSL*AGIGEVL*GK#.K
SW:BAF_HUMAN	R27	8115	2	1376.7	(-0.3)	2.324	0.194	0.606	1	K.AYVVL*GQFL*VL*K#.K
SW:BAG2_HUMAN	R22	2516	2	930.1	(-0.0)	2.670	0.196	0.864		R.IIDEVVNK.F
SW:BAG2_HUMAN	R22	2452	2	938.1	(+0.7)	2.482	0.160	0.658		R.IIDEVVNK#.F
SW:BAG2_HUMAN	R23	7698	2	1329.5	(+0.8)	3.642	0.442	1.000	1	R.LLESLDQLELR.V
SW:BAXA_HUMAN	R24	6108	2	1520.7	(+0.9)	3.280	0.296	0.972	4	R.IGDELDSNMELQR.M
SW:BAXA_HUMAN	R23	8230	2	1432.7	(+0.3)	4.461	0.454	1.000	4	K.TGALLLQGFQDR.A
SW:BAXA_HUMAN	R24	8276	2	1432.7	(+0.8)	4.427	0.473	1.000	4	K.TGALLLQGFQDR.A

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:BAXA_HUMAN	R24	8266	2	1450.7	(+0.0)	2.660	0.369	0.957	4	K.TGAL*L*L*QGFIQDR.A
SW:BP28_HUMAN	R05	7958	2	1302.4	(+0.5)	3.524	0.401	0.988		R.GWEEAL*ENVIK#.S
SW:BP28_HUMAN	R01	6625	2	1371.6	(+0.4)	2.765	0.492	0.989		R.LALPQSDASLLSR.D
SW:BP28_HUMAN	R05	10554	3	1999.3	(+0.7)	4.029	0.426	0.999	2	R.L*L*ETVL*GYISAVAQSMER.N
SW:BP28_HUMAN	R05	10558	3	1981.3	(+0.9)	3.871	0.492	1.000	2	R.LLETVLGYISAVAQSMER.N
SW:BP28_HUMAN	R04	9892	3	2237.6	(+0.9)	4.006	0.331	0.996	2	K.NTSELVVSSEVYLLSALAALQK.V
SW:BP28_HUMAN	R01	8573	2	1684.0	(+0.4)	2.534	0.344	0.948	2	K.VNALLPTETFIPVIR.G
SW:BP28_HUMAN	R01	8867	2	1542.9	(+0.2)	3.135	0.369	0.974		K.VSLLNEQFLPLIR.L
SW:BP28_HUMAN	R03	8365	2	1566.9	(-0.4)	2.658	0.189	0.767		K.VSL*L*NEQFL*PL*IR.L
SW:BP28_HUMAN	R03	8363	2	1542.9	(+0.0)	2.558	0.316	0.919		K.VSLLNEQFLPLIR.L
SW:BP28_HUMAN	R02	4502	2	1142.3	(+0.1)	2.479	0.329	0.913	2	K.VVESGGPEIL*K#.G
SW:BP28_HUMAN	R03	4193	2	1142.3	(+0.6)	2.447	0.273	0.890	2	K.VVESGGPEIL*K#.G
SW:BP28_HUMAN	R05	4436	2	1142.3	(-0.8)	2.286	0.296	0.635	2	K.VVESGGPEIL*K#.G
SW:BP28_HUMAN	R05	8160	2	1255.5	(-0.3)	2.286	0.278	0.851	2	K.L*VPDL*L*AIVQR.K
SW:BRD4_HUMAN	R06	6276	2	1435.8	(+0.8)	3.498	0.329	0.981		R.AASVVQPQPLVVVK.E
SW:BRD4_HUMAN	R06	6258	2	1449.8	(-0.4)	2.785	0.270	0.874		R.AASVVQPQPL*VVVK#.E
SW:BRD4_HUMAN	R06	7288	3	1973.3	(+0.7)	4.559	0.396	0.999	4	K.INEL*PTEETEIMIVQAK#.G
SW:BRD4_HUMAN	R06	6870	2	1235.4	(-0.1)	2.580	0.305	0.906	1	K.NMGSWASL*VQK#.H
SW:CA00_HUMAN	R22	8078	2	1394.6	(+0.3)	2.414	0.385	0.955	2	K.L*EDIL*ESINSIK#.S
SW:CA00_HUMAN	R23	8074	2	1374.6	(+1.0)	4.226	0.387	0.996	2	K.LEDILESINSIK.S
SW:CA00_HUMAN	R23	8072	2	1394.6	(+0.3)	3.336	0.403	0.950	2	K.L*EDIL*ESINSIK#.S
SW:CA00_HUMAN	R23	7252	2	1284.5	(+0.3)	2.823	0.409	0.980	2	K.YITGTDIL*DMK#.L
SW:CA00_HUMAN	R23	8094	2	1374.6	(-0.8)	2.513	0.164	0.402	2	K.LEDILESINSIK.S
SW:CABI_HUMAN	R05	5838	3	2509.5	(-0.4)	5.737	0.441	1.000	2	R.K#L*DPEEEDDSFNYYEVQSEAK#.L
SW:CABI_HUMAN	R05	4876	3	2377.7	(-0.4)	3.756	0.378	0.805	5	R.QQPTPL*TPAQAPAPAPATTTGTR.A
SW:CABI_HUMAN	R21	5952	2	900.1	(-0.7)	2.560	0.202	0.817	5	K.LVIPSAAATK.F
SW:CALM_HUMAN	R25	6982	3	1755.9	(+1.0)	4.151	0.318	0.975	5	R.VFDKDGNGYISAAELR.H
SW:CALM_HUMAN	R25	7552	2	1846.0	(-0.4)	3.380	0.428	0.549	4	K.EAFSLFDKDGDTITTK.E
SW:CALU_HUMAN	R17	9402	3	3361.5	(+0.9)	4.719	0.445	0.999	3	K.NADGFIDLEEYIGDMYSHDGNTEPEWVK.T
SW:CALU_HUMAN	R17	6582	3	2480.6	(+0.6)	4.890	0.524	1.000	4	K.VHNDAQSFYDHDHDAFLGAEAK.T
SW:CALU_HUMAN	R18	6517	3	2494.6	(+0.6)	4.807	0.523	1.000	4	K.VHNDAQSFYDHDHDAFL*GAEAK#.T
SW:CALX_HUMAN	R11	1410	2	1089.1	(+0.9)	2.595	0.396	0.981	2	K.AEEDEILNR.S
SW:CALX_HUMAN	R14	1738	2	1089.1	(+0.3)	2.336	0.378	0.969	2	K.AEEDEILNR.S
SW:CALX_HUMAN	R17	1960	2	1089.1	(+0.3)	2.504	0.310	0.956	2	K.AEEDEILNR.S
SW:CALX_HUMAN	R19	1800	2	1089.1	(+0.6)	2.529	0.373	0.976	2	K.AEEDEILNR.S
SW:CALX_HUMAN	R11	792	2	1022.0	(+0.9)	2.380	0.174	0.757	2	K.DDTDDEIAK.Y
SW:CALX_HUMAN	R11	610	2	1410.3	(+0.1)	2.836	0.411	0.384	2	K.DK#GDEEEEGEEK#.L
SW:CALX_HUMAN	R11	598	2	1394.3	(+0.1)	2.561	0.351	0.259	2	K.DKGDEEEEGEEK.L
SW:CALX_HUMAN	R11	7010	2	1062.3	(-0.6)	2.575	0.243	0.838	2	R.GTLSGWILSK.A
SW:CALX_HUMAN	R10	6395	3	2125.3	(+0.3)	5.051	0.529	1.000	3	K.IPDPEAVK#PDDWDEDAPAK#.I
SW:CALX_HUMAN	R10	6407	3	2109.3	(+0.7)	4.986	0.568	0.998	3	K.IPDPEAVK#PDDWDEDAPAK.I
SW:CALX_HUMAN	R11	5982	3	2125.3	(+0.0)	4.704	0.496	1.000	3	K.IPDPEAVK#PDDWDEDAPAK#.I
SW:CALX_HUMAN	R11	6122	3	2125.3	(-0.4)	4.191	0.534	1.000	3	K.IPDPEAVK#PDDWDEDAPAK#.I
SW:CALX_HUMAN	R11	5978	3	2109.3	(-0.1)	4.152	0.484	0.999	3	K.IPDPEAVK#PDDWDEDAPAK.I
SW:CALX_HUMAN	R11	6164	2	2125.3	(-0.8)	3.510	0.391	0.205	3	K.IPDPEAVK#PDDWDEDAPAK#.I
SW:CALX_HUMAN	R11	6148	2	2109.3	(-0.8)	2.956	0.480	0.287	3	K.IPDPEAVK#PDDWDEDAPAK.I
SW:CALX_HUMAN	R12	5982	3	2109.3	(+1.0)	4.664	0.498	1.000	3	K.IPDPEAVK#PDDWDEDAPAK.I
SW:CALX_HUMAN	R12	5986	3	2125.3	(+0.2)	3.892	0.391	0.980	3	K.IPDPEAVK#PDDWDEDAPAK#.I
SW:CALX_HUMAN	R13	6365	3	2109.3	(+0.6)	4.608	0.478	1.000	3	K.IPDPEAVK#PDDWDEDAPAK.I
SW:CALX_HUMAN	R13	6363	3	2125.3	(+0.1)	3.945	0.245	0.744	3	K.IPDPEAVK#PDDWDEDAPAK#.I
SW:CALX_HUMAN	R14	6387	3	2109.3	(+0.6)	4.695	0.558	0.988	3	K.IPDPEAVK#PDDWDEDAPAK.I
SW:CALX_HUMAN	R17	6360	3	2125.3	(-0.3)	4.812	0.550	1.000	3	K.IPDPEAVK#PDDWDEDAPAK#.I
SW:CALX_HUMAN	R11	8690	2	1742.9	(+0.8)	3.498	0.445	1.000	2	K.IPNPDFFEDL*EPFR.M
SW:CALX_HUMAN	R11	8692	2	1736.9	(-0.7)	3.108	0.372	0.972	2	K.IPNPDFFEDLEPFR.M
SW:CALX_HUMAN	R11	8624	2	1736.9	(+0.6)	2.916	0.453	0.987	2	K.IPNPDFFEDLEPFR.M
SW:CALX_HUMAN	R12	8876	2	1736.9	(-0.2)	3.618	0.486	1.000	2	K.IPNPDFFEDLEPFR.M
SW:CALX_HUMAN	R13	9045	2	1736.9	(+0.7)	4.209	0.476	1.000	2	K.IPNPDFFEDLEPFR.M
SW:CALX_HUMAN	R13	9025	2	1742.9	(+0.7)	2.588	0.440	0.980	2	K.IPNPDFFEDL*EPFR.M
SW:CALX_HUMAN	R11	7076	2	1489.6	(+0.8)	3.525	0.553	1.000	2	R.IVDDWANDGWGLK.K

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:CALX_HUMAN	R11	6978	2	1503.6	(+0.3)	3.418	0.448	0.992	2	R.IVDDWANDGWGL*K#.K
SW:CALX_HUMAN	R12	7184	2	1503.6	(+0.2)	2.719	0.359	0.942	2	R.IVDDWANDGWGL*K#.K
SW:CALX_HUMAN	R11	762	2	1150.2	(+0.8)	3.864	0.276	0.695	2	K.KDDTDDEIAK.Y
SW:CALX_HUMAN	R11	760	2	1166.2	(+0.1)	3.133	0.266	0.841	2	K.K#DDTDDEIAK#.Y
SW:CALX_HUMAN	R11	8354	2	1865.1	(-0.5)	3.350	0.460	0.987	2	R.KIPNPDDFFEDLEPFR.M
SW:CALX_HUMAN	R20	8528	3	1879.1	(+1.0)	3.939	0.212	0.969	2	R.K#PNPDDFFEDL*EPFR.M
SW:CALX_HUMAN	R11	1088	2	1300.4	(-0.3)	3.575	0.434	1.000	4	R.KPEDWDERPK.I
SW:CALX_HUMAN	R11	836	2	1099.2	(+0.8)	2.895	0.377	0.981	2	K.KTDAPQPDKV.K
SW:CALX_HUMAN	R11	834	2	1115.2	(-0.6)	2.403	0.355	0.931	2	K.K#TDAPQPDKV#.E
SW:CALX_HUMAN	R11	852	2	971.1	(+0.7)	2.330	0.368	0.967	2	K.TDAPQPDKV.E
SW:CALX_HUMAN	R10	6441	2	1457.6	(-0.1)	3.298	0.400	0.982	1	K.TPELNLDQFHDK.T
SW:CALX_HUMAN	R11	6154	2	1457.6	(+0.5)	3.368	0.462	1.000	1	K.TPELNLDQFHDK.T
SW:CALX_HUMAN	R11	6156	2	1477.6	(-0.8)	2.609	0.261	0.656	1	K.TPEL*NL*DQFHDK#.T
SW:CALX_HUMAN	R16	6070	2	1457.6	(+0.5)	3.655	0.459	0.998	1	K.TPELNLDQFHDK.T
SW:CALX_HUMAN	R11	6680	2	1278.5	(+0.6)	3.329	0.521	1.000	3	K.TPYTIMFGPDK#.C
SW:CALX_HUMAN	R11	6676	2	1270.5	(+0.4)	3.300	0.510	0.999	3	K.TPYTIMFGPDK.C
SW:CALX_HUMAN	R11	6102	2	1294.5	(+0.4)	3.017	0.498	0.685	3	K.TPYTIM@FGPDK#.C
SW:CALX_HUMAN	R11	4700	2	951.1	(+0.5)	2.214	0.254	0.879	2	K.WEVEEMK.E
SW:CALX_HUMAN	R20	1964	2	1089.1	(+0.9)	3.072	0.313	0.981	2	K.AEEDEILNR.S
SW:CAO1_HUMAN	R16	8396	2	1698.9	(+0.5)	2.725	0.372	0.968	6	R.EFGIADPDEIMWFK.K
SW:CAO1_HUMAN	R23	8030	2	1502.7	(+0.9)	4.953	0.444	1.000	8	K.EVAWNLTSDVLR.A
SW:CAO1_HUMAN	R23	8028	2	1514.7	(+0.2)	2.219	0.376	0.923	8	K.EVAWNLT*TSVDL*VR.A
SW:CATA_HUMAN	R14	7835	2	1529.8	(+0.2)	2.705	0.362	0.948	3	R.DPILFSPFIHSQK.R
SW:CATA_HUMAN	R14	7359	3	2205.4	(+0.4)	3.818	0.383	0.999	4	K.NFTEVHPDYGSHIQAL*L*DK#.Y
SW:CATA_HUMAN	R14	2062	2	1415.5	(+0.3)	2.455	0.355	0.947	2	K.ADVLTGAGNPVGDK.L
SW:CB80_HUMAN	R11	7420	2	1251.4	(+1.0)	2.744	0.351	0.973		K.ATNDEIFSILK.D
SW:CB80_HUMAN	R11	4400	2	1188.3	(+0.1)	2.406	0.180	0.725		K.DGVLEEQUIER.L
SW:CB80_HUMAN	R11	4406	2	1194.3	(+0.2)	2.402	0.222	0.813		K.DGVL*EEQUIER.L
SW:CB80_HUMAN	R11	8934	2	1514.8	(+0.9)	4.420	0.404	0.999		R.LFVWEILHSTIR.K
SW:CB80_HUMAN	R11	8924	2	1526.8	(+0.3)	3.739	0.459	1.000		R.L*FVWEIL*HSTIR.K
SW:CB80_HUMAN	R11	8776	2	1162.4	(+0.7)	3.239	0.313	0.979		K.NL*FL*VIFQR.F
SW:CB80_HUMAN	R11	5980	2	1186.4	(+0.2)	2.345	0.126	0.535		R.IFANTESYLK.R
SW:CBF_HUMAN	R07	1772	2	1082.2	(-0.6)	2.403	0.418	0.964	1	K.AIVSSGTL*GDR.M
SW:CBF_HUMAN	R07	5929	2	1004.2	(+0.2)	2.384	0.275	0.870	1	K.AL*L*VQVVK#.L
SW:CBF_HUMAN	R07	8249	2	1412.6	(+0.6)	3.283	0.396	0.988	1	K.ELLITDLLPDNR.K
SW:CBF_HUMAN	R07	10657	3	2513.9	(-0.5)	6.883	0.478	1.000	1	K.HL*VAEFVQVL*ETL*SHDTL*VTTK#.T
SW:CBF_HUMAN	R07	10641	3	2481.9	(+0.9)	6.641	0.444	0.998	1	K.HLVAEFVQVLETL*SHDTL*VTTK#.T
SW:CBF_HUMAN	R09	10419	3	2481.9	(+0.4)	4.481	0.393	0.999	1	K.HLVAEFVQVLETL*SHDTL*VTTK#.T
SW:CBF_HUMAN	R07	6579	2	1305.5	(+0.0)	2.270	0.220	0.761	1	K.LYQHEINLFK.S
SW:CBF_HUMAN	R10	10739	3	2513.9	(+0.1)	4.200	0.369	0.996	1	K.HL*VAEFVQVL*ETL*SHDTL*VTTK#.T
SW:CBP2_HUMAN	R16	7504	3	2406.7	(+1.0)	4.716	0.449	1.000	4	K.AVLSAEQLRDEEVHAGLGELLR.S
SW:CBP2_HUMAN	R16	10268	3	2553.0	(+0.6)	4.797	0.570	1.000	4	K.DQAVENILVSPVVVASSLGLVSLGGK.A
SW:CBP2_HUMAN	R16	1624	2	1225.4	(+0.9)	3.503	0.266	0.966	4	K.GVVEVTHDLQK.H
SW:CBP2_HUMAN	R16	6400	2	1338.5	(+0.2)	3.370	0.340	0.974	4	K.HLAGLGLTEAIDK.N
SW:CBP2_HUMAN	R16	7184	2	1660.8	(+0.1)	4.018	0.562	1.000	5	R.LYGPSVSVFADDFVR.S
SW:CBP2_HUMAN	R17	6760	2	1338.5	(+0.8)	3.672	0.311	0.982	4	K.HLAGLGLTEAIDK.N
SW:CBX3_HUMAN	R23	6064	2	1662.8	(-0.5)	4.946	0.443	0.999	2	K.KVEEAPEEFVVEK.V
SW:CBX3_HUMAN	R23	6108	2	1542.7	(-0.4)	3.285	0.416	0.979	2	K.VEEAEPEEFVVEK#.V
SW:CBX3_HUMAN	R23	6380	2	1490.7	(-0.2)	2.783	0.381	0.359	3	K.WKDSDEADLVLAKE
SW:CBX3_HUMAN	R23	6112	2	1534.7	(-0.4)	2.563	0.289	0.897	2	K.VEEAEPEEFVVEK.V
SW:CBX5_HUMAN	R21	4288	2	1206.2	(+0.1)	3.043	0.341	0.962	1	K.SNFSNSADDIK#.S
SW:CBX5_HUMAN	R21	4328	2	1198.2	(+0.5)	2.872	0.419	0.986	1	K.SNFSNSADDIK.S
SW:CBX5_HUMAN	R22	5796	2	1190.3	(+0.5)	2.362	0.240	0.861	1	K.DTDEADLVLAKE
SW:CD3D_HUMAN	R23	5906	2	1590.7	(-0.3)	3.078	0.408	0.978		R.DDAQYSHLGGNWAR.N
SW:CD3D_HUMAN	R23	5904	2	1596.7	(-0.5)	2.994	0.271	0.925		R.DDAQYSHL*GGNWAR.N
SW:CD3D_HUMAN	R23	5884	2	1861.9	(-0.7)	3.496	0.367	0.464		R.DRDAQYSHLGGNWAR.N
SW:CD3D_HUMAN	R24	6166	2	1114.2	(+0.4)	2.678	0.277	0.956		K.IPIEELEDR.V
SW:CD3D_HUMAN	R22	6098	2	1216.4	(+0.0)	3.472	0.376	0.983		R.LSGAADTQALLR.N

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:CD3D_HUMAN	R23	5948	2	1216.4	(+0.9)	2.988	0.354	0.978		R.LSGAADTQALLR.N
SW:CD3D_HUMAN	R23	5946	2	1234.4	(+0.6)	2.793	0.351	0.972		R.L*SGAADTQAL*L*R.N
SW:CD3D_HUMAN	R24	6058	2	1216.4	(+0.8)	3.206	0.311	0.976		R.LSGAADTQALLR.N
SW:CD3D_HUMAN	R23	4942	2	1139.2	(-1.0)	3.519	0.264	0.925		R.NDQVYQPL*R.D
SW:CD3D_HUMAN	R23	4990	2	1133.2	(-0.3)	3.133	0.376*	0.582		R.NDQVYQPLR.D
SW:CD3D_HUMAN	R23	4928	2	1139.2	(+0.2)	2.645	0.428	0.980		R.NDQVYQPL*R.D
SW:CD3D_HUMAN	R24	6162	2	1120.2	(+0.2)	2.477	0.267	0.906		K.IPIEEL*EDR.V
SW:CD3E_HUMAN	R22	5218	2	1078.2	(-0.1)	2.459	0.380	0.959		R.DL*YSGL*NQR.R
SW:CD3E_HUMAN	R23	5348	2	1078.2	(-0.1)	2.619	0.349	0.964		R.DL*YSGL*NQR.R
SW:CD3E_HUMAN	R23	5546	2	1078.2	(-0.5)	2.556	0.376	0.963		R.DL*YSGL*NQR.R
SW:CD3E_HUMAN	R23	5254	2	1078.2	(+0.1)	2.399	0.322	0.902		R.DL*YSGL*NQR.R
SW:CD3E_HUMAN	R01	5133	3	1905.2	(+0.7)	3.849	0.385	0.991		K.ERPPVPNPDYEPiRK.G
SW:CD3E_HUMAN	R01	5053	3	1905.2	(+0.8)	3.813	0.375	0.989		K.ERPPVPNPDYEPiRK.G
SW:CD3E_HUMAN	R22	6026	3	1905.2	(+1.0)	3.966	0.397	0.991		K.ERPPVPNPDYEPiRK.G
SW:CD3E_HUMAN	R23	7322	2	1673.9	(-0.3)	3.180	0.544	1.000	1	R.GSKPEDANFYLYLR.A
SW:CD3E_HUMAN	R23	7320	2	1693.9	(-0.9)	2.498	0.310	0.055	1	R.GSK#PEDANFYLYL*R.A
SW:CD3E_HUMAN	R24	7350	2	1673.9	(-0.4)	2.902	0.507	0.596	1	R.GSKPEDANFYLYLR.A
SW:CD3E_HUMAN	R01	5257	2	2272.3	(+0.6)	4.930	0.561	1.000		K.NIGGDEDDKNIGSDEDHLSLK.E
SW:CD3E_HUMAN	R01	5273	2	2272.3	(-1.0)	4.062	0.457	1.000		K.NIGGDEDDKNIGSDEDHLSLK.E
SW:CD3E_HUMAN	R02	5502	3	2272.3	(+0.3)	4.508	0.466	1.000		K.NIGGDEDDKNIGSDEDHLSLK.E
SW:CD3E_HUMAN	R03	5333	3	2300.3	(-0.1)	3.844	0.365	0.962		K.NIGGDEDDK#NIGSDEDHL*SL*K#.E
SW:CD3E_HUMAN	R04	5660	3	2300.3	(-0.3)	4.333	0.421	0.948		K.NIGGDEDDK#NIGSDEDHL*SL*K#.E
SW:CD3E_HUMAN	R22	6082	3	2272.3	(+0.8)	4.587	0.526	1.000		K.NIGGDEDDKNIGSDEDHLSLK.E
SW:CD3E_HUMAN	R22	6078	3	2300.3	(-0.4)	4.361	0.420	0.991		K.NIGGDEDDK#NIGSDEDHL*SL*K#.E
SW:CD3E_HUMAN	R23	5756	3	2300.3	(+0.3)	4.876	0.278	0.969		K.NIGGDEDDK#NIGSDEDHL*SL*K#.E
SW:CD3E_HUMAN	R23	5760	3	2272.3	(+0.7)	4.632	0.510	0.996		K.NIGGDEDDKNIGSDEDHLSLK.E
SW:CD3E_HUMAN	R23	5900	3	2272.3	(+0.6)	3.973	0.573	1.000		K.NIGGDEDDKNIGSDEDHLSLK.E
SW:CD3E_HUMAN	R24	5874	3	2300.3	(-0.1)	4.935	0.281	0.934		K.NIGGDEDDK#NIGSDEDHL*SL*K#.E
SW:CD3E_HUMAN	R24	5968	3	2272.3	(+0.9)	4.191	0.474	1.000		K.NIGGDEDDKNIGSDEDHLSLK.E
SW:CD3E_HUMAN	R24	5868	3	2272.3	(-0.8)	3.829	0.397	0.924		K.NIGGDEDDKNIGSDEDHLSLK.E
SW:CD3E_HUMAN	R24	5752	2	1348.4	(-0.7)	2.826	0.257	0.886	1	K.NIGSDEDHL*SL*K#.E
SW:CD3E_HUMAN	R24	5294	2	1078.2	(-0.1)	2.269	0.323	0.920		R.DL*YSGL*NQR.R
SW:CD3G_HUMAN	R23	5074	3	1975.0	(+0.6)	4.169	0.440	0.997		K.DREDDQYSHLQGNQLR.R
SW:CD3G_HUMAN	R23	5070	3	1987.0	(+0.4)	4.114	0.513	0.999		K.DREDDQYSHL*QGNQL*R.R
SW:CD3G_HUMAN	R23	4980	2	1703.8	(-0.3)	2.998	0.310	0.947		R.EDDQYSHLQGNQLR.R
SW:CD3G_HUMAN	R22	6458	2	1084.2	(+0.8)	2.574	0.344	0.963		K.M@IGFL*TEDK#.K
SW:CD3G_HUMAN	R23	6314	2	1084.2	(+0.7)	2.292	0.320	0.928		K.M@IGFL*TEDK#.K
SW:CD3G_HUMAN	R22	7142	2	1703.9	(-0.7)	2.469	0.231	0.727		K.QLT*L*PNDQL*YQPL*K#.D
SW:CD3G_HUMAN	R23	5524	2	1154.4	(+0.8)	2.332	0.356	0.338		K.SKPLQVYYR.M
SW:CD3G_HUMAN	R24	5042	3	1975.0	(+0.7)	4.131	0.386	0.993		K.DREDDQYSHLQGNQLR.R
SW:CD3Z_HUMAN	R25	7638	3	2469.6	(+0.7)	4.904	0.456	0.997	2	R.SADAPAYQQGNQL*YNEL*NL*GR.R
SW:CD3Z_HUMAN	R25	5946	2	1448.6	(-0.2)	2.789	0.562	1.000	2	K.GHDGLYQGLSTATK.D
SW:CD45_HUMAN	R06	5982	2	1381.5	(+0.4)	3.082	0.369	0.984	5	K.DLQYSTDYTFK.A
SW:CD45_HUMAN	R05	7602	3	2823.1	(-0.6)	3.809	0.349	0.991	4	R.EVTHIQFTSWPDHGVPEPDPHL*L*L*K#.L
SW:CD45_HUMAN	R06	7724	3	2823.1	(+0.1)	4.166	0.459	0.999	4	R.EVTHIQFTSWPDHGVPEPDPHL*L*L*K#.L
SW:CD45_HUMAN	R02	7306	2	1321.6	(+1.0)	2.770	0.436	0.986	3	R.LFLAEFQSIPR.V
SW:CD45_HUMAN	R02	7302	2	1333.6	(-0.4)	2.524	0.150	0.668	3	R.L*FL*AEFQSIPR.V
SW:CD45_HUMAN	R03	7461	2	1333.6	(-0.1)	2.626	0.163	0.743	3	R.L*FL*AEFQSIPR.V
SW:CD45_HUMAN	R05	7746	2	1321.6	(+0.9)	3.922	0.470	1.000	3	R.LFLAEFQSIPR.V
SW:CD45_HUMAN	R05	7742	2	1333.6	(+0.7)	3.432	0.281	0.977	3	R.L*FL*AEFQSIPR.V
SW:CD45_HUMAN	R06	7874	2	1333.6	(+0.2)	3.598	0.324	0.980	3	R.L*FL*AEFQSIPR.V
SW:CD45_HUMAN	R06	6266	3	1856.0	(+0.2)	4.467	0.509	0.999	4	K.RDPPSEPSLEAEFQR.L
SW:CD45_HUMAN	R06	6816	2	1301.5	(+0.0)	2.729	0.331	0.934	5	K.TL*IL*DVPPGVEK#.F
SW:CD45_HUMAN	R06	6250	2	1050.2	(+0.5)	2.363	0.341	0.947	4	K.VDVYGYVVK#.L
SW:CD45_HUMAN	R05	7562	3	2591.8	(+0.9)	4.792	0.471	0.511	5	R.VEL*SEINGDAGSNYINASYIDGFK#.E
SW:CD45_HUMAN	R06	7656	3	2591.8	(+0.6)	5.050	0.544	0.993	5	R.VEL*SEINGDAGSNYINASYIDGFK#.E
SW:CD45_HUMAN	R06	7296	2	1066.4	(-0.1)	2.540	0.382	0.960	4	K.VIVML*TEL*K#.H
SW:CD45_HUMAN	R06	6278	2	1513.7	(-0.2)	2.851	0.248	0.898	5	R.YHL*EVEAGNTL*VR.N
SW:CDC2_HUMAN	R19	5162	2	1186.4	(+0.3)	2.621	0.271	0.934	5	K.IGEGTYGVVYK.G
SW:CDC2_HUMAN	R19	7048	2	1331.5	(+0.7)	3.146	0.315	0.975	2	K.NLDENGLDLLSK.M
SW:CDC2_HUMAN	R19	5192	2	1029.2	(+0.8)	2.797	0.417	0.986	2	R.SPEVLLGSAR.Y

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW: CDC2_HUMAN	R19	11270	2	2213.5	(-0.6)	2.615	0.447	0.972	2	R.YSTPVDIWSIGTIFAELATK.K
SW: CEB1_HUMAN	R11	8486	3	2732.1	(+0.5)	5.667	0.545	0.977		K.LDSHAELLDATQHTLQQQIQTLVK.E
SW: CEB1_HUMAN	R11	4820	2	1003.1	(+0.7)	2.600	0.351	0.971		K.LGTGLLESGR.H
SW: CEB1_HUMAN	R11	5198	3	2093.3	(+0.6)	4.969	0.483	1.000		R.L*VEAQATHFQQGHEEL*SR.L
SW: CEB1_HUMAN	R11	5200	3	2081.3	(+0.2)	3.758	0.397	0.997		R.LVEAQATHFQQGHEELSR.L
SW: CEB1_HUMAN	R11	4812	2	1021.1	(+0.1)	2.385	0.252	0.854		K.L*GTGL*L*ESGR.H
SW: CENF_HUMAN	R04	7968	3	2424.6	(+0.1)	4.105	0.323	0.990	1	K.L*QEDTSAHQNVVAETL*SAL*ENK#.E
SW: CENF_HUMAN	R04	4598	2	1354.4	(+0.3)	2.557	0.320	0.935	3	K.TAEL*QEEL*SGEK#.N
SW: CES5_HUMAN	R17	2058	2	1053.2	(+0.0)	2.304	0.189	0.726	3	K.LFSEYHEK.R
SW: CES5_HUMAN	R17	1390	2	1015.2	(+0.3)	2.627	0.371	0.979	3	R.LVNSQGQLR.V
SW: CES5_HUMAN	R17	5570	2	1051.2	(+0.5)	2.305	0.321	0.946	3	R.NVTVDEL*R.M
SW: CES5_HUMAN	R17	1394	2	1027.2	(-0.0)	2.250	0.303	0.900	3	R.L*VNSQGQL*R.V
SW: CG51_HUMAN	R15	5017	2	1303.5	(+0.0)	2.770	0.377	0.961	5	K.SSLSHAMVIDSR.N
SW: CG51_HUMAN	R15	6767	2	1799.0	(+0.2)	3.860	0.469	0.999	5	K.VNQELAGYTGDDVFSFIK.E
SW: CG51_HUMAN	R15	6319	2	1178.3	(+0.4)	2.643	0.467	0.989	5	K.VTFQFSYGTK.E
SW: CH10_HUMAN	R26	2502	2	1014.2	(+0.5)	2.889	0.249	0.951	3	K.GGEIQVSVK.V
SW: CH10_HUMAN	R26	2600	2	1022.2	(+0.5)	2.700	0.293	0.935	3	K.GGEIQVSVK#.V
SW: CH10_HUMAN	R26	2508	2	1022.2	(-0.3)	2.666	0.306	0.914	3	K.GGEIQVSVK#.V
SW: CH10_HUMAN	R26	5164	2	1022.2	(+0.1)	2.661	0.342	0.947	3	K.GGEIQVSVK#.V
SW: CH10_HUMAN	R26	5158	2	1014.2	(+0.8)	2.611	0.144	0.790	3	K.GGEIQVSVK.V
SW: CH10_HUMAN	R26	2522	2	1014.2	(-0.8)	2.437	0.275	0.730	3	K.GGEIQVSVK.V
SW: CH10_HUMAN	R26	5758	2	1316.5	(+0.8)	3.152	0.646	1.000	3	K.VLQATVVAVGSGSK.G
SW: CH10_HUMAN	R26	5786	2	1330.5	(+0.3)	2.281	0.353	0.915	3	K.VL*QATVVAVGSGSK#.G
SW: CH10_HUMAN	R27	5407	2	1330.5	(-0.3)	3.506	0.392	0.976	3	K.VL*QATVVAVGSGSK#.G
SW: CH10_HUMAN	R26	7958	2	1530.8	(+1.0)	3.482	0.524	1.000	3	K.VVLDKDYFLFR.D
SW: CH10_HUMAN	R27	5485	2	1316.5	(-0.0)	2.712	0.466	0.979	3	K.VLQATVVAVGSGSK.G
SW: CH60_HUMAN	R06	10594	3	2146.6	(-0.4)	3.853	0.359	0.994	1	R.AL*ML*QGVDL*L*ADAVAVTMGPK#.G
SW: CH60_HUMAN	R12	10818	3	2114.6	(+0.9)	3.932	0.546	1.000	1	R.ALMLQGVDLLADAVAVTMGPK.G
SW: CH60_HUMAN	R13	10941	3	2114.6	(+0.5)	3.857	0.485	1.000	1	R.ALMLQGVDLLADAVAVTMGPK.G
SW: CH60_HUMAN	R14	9743	3	2162.6	(+0.2)	5.148	0.567	1.000	1	R.AL*ML*QGVDL*L*ADAVAVTM@GPK#.G
SW: CH60_HUMAN	R14	12825	3	2114.6	(+0.7)	4.563	0.550	1.000	1	R.ALMLQGVDLLADAVAVTMGPK.G
SW: CH60_HUMAN	R14	13371	3	2114.6	(+0.8)	4.458	0.514	0.863	1	R.ALMLQGVDLLADAVAVTMGPK.G
SW: CH60_HUMAN	R14	12905	3	2114.6	(+1.0)	4.448	0.530	1.000	1	R.ALMLQGVDLLADAVAVTMGPK.G
SW: CH60_HUMAN	R14	12207	3	2114.6	(+0.8)	4.407	0.576	0.999	1	R.ALMLQGVDLLADAVAVTMGPK.G
SW: CH60_HUMAN	R14	12655	3	2114.6	(+0.9)	4.314	0.572	0.988	1	R.ALMLQGVDLLADAVAVTMGPK.G
SW: CH60_HUMAN	R14	12505	3	2114.6	(+0.7)	4.275	0.603	1.000	1	R.ALMLQGVDLLADAVAVTMGPK.G
SW: CH60_HUMAN	R14	12281	3	2114.6	(+1.0)	4.155	0.552	1.000	1	R.ALMLQGVDLLADAVAVTMGPK.G
SW: CH60_HUMAN	R14	12581	3	2114.6	(+0.9)	4.147	0.576	1.000	1	R.ALMLQGVDLLADAVAVTMGPK.G
SW: CH60_HUMAN	R14	11603	3	2114.6	(+0.9)	4.076	0.543	0.998	1	R.ALMLQGVDLLADAVAVTMGPK.G
SW: CH60_HUMAN	R14	12429	3	2114.6	(+0.8)	3.935	0.564	1.000	1	R.ALMLQGVDLLADAVAVTMGPK.G
SW: CH60_HUMAN	R14	11621	3	2162.6	(+1.0)	3.931	0.517*	0.117	1	R.AL*M@L*QGVDL*L*ADAVAVTMGPK#.G
SW: CH60_HUMAN	R14	13687	3	2162.6	(+0.4)	3.808	0.472*	0.101	1	R.AL*M@L*QGVDL*L*ADAVAVTMGPK#.G
SW: CH60_HUMAN	R14	10771	2	2114.6	(+0.1)	3.368	0.408	0.982	1	R.ALMLQGVDLLADAVAVTMGPK.G
SW: CH60_HUMAN	R14	10865	2	2114.6	(-0.3)	2.227	0.226	0.652	1	R.ALMLQGVDLLADAVAVTMGPK.G
SW: CH60_HUMAN	R15	9509	3	2162.6	(+0.1)	4.392	0.478	1.000	1	R.AL*ML*QGVDL*L*ADAVAVTM@GPK#.G
SW: CH60_HUMAN	R16	9898	3	2162.6	(+0.0)	3.846	0.303	0.982	1	R.AL*M@L*QGVDL*L*ADAVAVTMGPK#.G
SW: CH60_HUMAN	R16	9580	3	2162.6	(+0.0)	3.766	0.471	0.998	1	R.AL*ML*QGVDL*L*ADAVAVTM@GPK#.G
SW: CH60_HUMAN	R17	10770	3	2146.6	(+0.0)	3.919	0.402	0.998	1	R.AL*ML*QGVDL*L*ADAVAVTMGPK#.G
SW: CH60_HUMAN	R14	998	2	689.8	(+0.9)	2.289	0.347	0.960	2	K.DGVTVAK.S
SW: CH60_HUMAN	R14	12787	3	3147.4	(+0.9)	4.229	0.361	0.998	1	K.DM@AIATGGAVFGEEGL*TL*NL*EDVQPHDL*GK#.V
SW: CH60_HUMAN	R14	12405	3	3099.4	(-0.0)	4.055	0.449	0.993	1	K.DMAIATGGAVFGEEGLTLNLEDVQPHDLGK.V
SW: CH60_HUMAN	R14	12817	3	3099.4	(+0.2)	3.986	0.401	0.993	1	K.DMAIATGGAVFGEEGLTLNLEDVQPHDLGK.V
SW: CH60_HUMAN	R14	13467	3	3147.4	(-0.8)	3.746	0.324	0.948	1	K.DM@AIATGGAVFGEEGL*TL*NL*EDVQPHDL*GK#.V
SW: CH60_HUMAN	R14	12075	3	3147.4	(-0.4)	3.738	0.414	0.997	1	K.DM@AIATGGAVFGEEGL*TL*NL*EDVQPHDL*GK#.V
SW: CH60_HUMAN	R14	9733	2	1429.8	(+1.0)	4.806	0.441	1.000	2	R.GVMLAVDAVIAELK.K
SW: CH60_HUMAN	R14	9599	2	1449.8	(-0.2)	4.196	0.443	1.000	2	R.GVML*AVDAVIAEL*K#.K
SW: CH60_HUMAN	R14	9677	2	1449.8	(-0.2)	4.031	0.401	1.000	2	R.GVML*AVDAVIAEL*K#.K
SW: CH60_HUMAN	R14	8919	2	1465.8	(+0.5)	3.767	0.392	0.986	2	R.GVM@L*AVDAVIAEL*K#.K
SW: CH60_HUMAN	R14	8811	2	1465.8	(+0.2)	3.696	0.440	0.996	2	R.GVM@L*AVDAVIAEL*K#.K
SW: CH60_HUMAN	R14	9631	2	1429.8	(+1.0)	3.342	0.506	1.000	2	R.GVMLAVDAVIAELK.K

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:CH60_HUMAN	R14	12001	2	1429.8	(+0.4)	3.173	0.347	0.974	2	R.GVMLAVDAVIAELK.K
SW:CH60_HUMAN	R14	11571	2	1429.8	(+0.5)	2.990	0.327	0.963	2	R.GVMLAVDAVIAELK.K
SW:CH60_HUMAN	R14	13573	2	1429.8	(+0.6)	2.983	0.326	0.937	2	R.GVMLAVDAVIAELK.K
SW:CH60_HUMAN	R14	12921	2	1429.8	(+0.4)	2.900	0.340	0.959	2	R.GVMLAVDAVIAELK.K
SW:CH60_HUMAN	R14	13831	2	1429.8	(+0.4)	2.210	0.270	0.830	2	R.GVMLAVDAVIAELK.K
SW:CH60_HUMAN	R15	9401	2	1449.8	(+0.4)	4.827	0.518	1.000	2	R.GVML*AVDAVIAEL*K#K
SW:CH60_HUMAN	R15	9393	2	1429.8	(+0.9)	4.618	0.481	1.000	2	R.GVMLAVDAVIAELK.K
SW:CH60_HUMAN	R14	9263	2	1585.9	(-0.1)	4.588	0.576	1.000	2	R.GVML*AVDAVIAEL*K#K#.Q
SW:CH60_HUMAN	R14	6863	2	1390.6	(+0.8)	3.369	0.466	0.999	1	R.GYISPYFINTSK.G
SW:CH60_HUMAN	R14	6853	2	1398.6	(-0.4)	3.211	0.485	1.000	1	R.GYISPYFINTSK#.G
SW:CH60_HUMAN	R14	6879	2	1390.6	(-0.5)	2.288	0.333	0.904	1	R.GYISPYFINTSK.G
SW:CH60_HUMAN	R15	6269	2	794.0	(+0.7)	2.350	0.161	0.696	1	K.IGIEIK#.R
SW:CH60_HUMAN	R14	8367	3	2517.8	(+0.6)	5.144	0.547	1.000	1	K.IMQSSSEVGYDAMAGDFVNMVEK#.G
SW:CH60_HUMAN	R14	6635	3	2565.8	(-0.1)	4.301	0.436	0.999	1	K.IM@QSSSEVGYDAM@AGDFVNM@VEK#.G
SW:CH60_HUMAN	R14	6767	3	2549.8	(+0.3)	4.200	0.465*	0.140	1	K.IMQSSSEVGYDAM@AGDFVNM@VEK#.G
SW:CH60_HUMAN	R14	12597	3	2533.8	(+0.2)	3.906	0.302*	0.043	1	K.IMQSSSEVGYDAM@AGDFVNMVEK#.G
SW:CH60_HUMAN	R14	13359	3	2533.8	(+0.6)	3.877	0.331*	0.096	1	K.IMQSSSEVGYDAM@AGDFVNMVEK#.G
SW:CH60_HUMAN	R14	7627	2	2053.2	(+0.9)	5.613	0.594	0.999	1	R.IQEIIQL*DVTTSEYEK#.E
SW:CH60_HUMAN	R14	7623	2	2039.2	(+0.8)	5.177	0.475	1.000	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	12917	2	2039.2	(+0.6)	4.974	0.446	1.000	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	12739	3	2039.2	(+0.3)	4.747	0.478	1.000	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	11455	2	2039.2	(-0.1)	4.717	0.515	1.000	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	12265	2	2039.2	(+0.0)	4.583	0.497	0.999	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	13177	2	2039.2	(+1.0)	4.483	0.482	1.000	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	13941	3	2039.2	(+0.9)	4.459	0.462	0.998	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	11691	2	2039.2	(-0.3)	4.445	0.504	1.000	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	13411	2	2039.2	(+0.0)	4.329	0.446	1.000	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	12089	2	2039.2	(+0.7)	4.320	0.524	1.000	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	12011	2	2039.2	(+0.1)	4.130	0.426	1.000	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	10953	2	2039.2	(+0.6)	4.058	0.526	1.000	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	11733	3	2039.2	(+0.4)	4.009	0.479	1.000	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	12761	2	2039.2	(-0.2)	3.972	0.480	1.000	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	12823	3	2053.2	(+0.7)	3.972	0.492	1.000	1	R.IQEIIQL*DVTTSEYEK#.E
SW:CH60_HUMAN	R14	12159	3	2053.2	(+0.4)	3.948	0.474	0.999	1	R.IQEIIQL*DVTTSEYEK#.E
SW:CH60_HUMAN	R14	12487	3	2053.2	(+0.7)	3.903	0.442	1.000	1	R.IQEIIQL*DVTTSEYEK#.E
SW:CH60_HUMAN	R14	12233	3	2053.2	(+0.8)	3.891	0.425	0.999	1	R.IQEIIQL*DVTTSEYEK#.E
SW:CH60_HUMAN	R14	12167	2	2039.2	(-0.1)	3.877	0.385	0.985	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	13569	2	2039.2	(+0.2)	3.783	0.431	1.000	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	12841	2	2039.2	(+0.1)	3.772	0.396	0.985	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	11977	2	2053.2	(+0.6)	3.772	0.589	1.000	1	R.IQEIIQL*DVTTSEYEK#.E
SW:CH60_HUMAN	R14	11213	2	2039.2	(-0.4)	3.748	0.429	1.000	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	12897	3	2053.2	(+0.4)	3.746	0.452	0.998	1	R.IQEIIQL*DVTTSEYEK#.E
SW:CH60_HUMAN	R14	13279	2	2039.2	(+0.8)	3.745	0.466	1.000	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	12431	2	2039.2	(-0.1)	3.731	0.467	0.998	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	8835	2	2039.2	(+0.1)	3.707	0.412	0.986	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	13549	2	2053.2	(-0.2)	3.565	0.451	1.000	1	R.IQEIIQL*DVTTSEYEK#.E
SW:CH60_HUMAN	R14	11123	2	2039.2	(+0.0)	3.555	0.521	1.000	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	11531	2	2039.2	(-0.4)	3.553	0.448	0.987	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	11319	2	2039.2	(+0.1)	3.453	0.340	0.970	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	12939	2	2053.2	(+0.1)	3.362	0.292	0.941	1	R.IQEIIQL*DVTTSEYEK#.E
SW:CH60_HUMAN	R14	12935	2	2039.2	(-0.7)	3.302	0.431	0.983	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	11921	2	2039.2	(+0.1)	3.297	0.457	0.986	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	12599	2	2039.2	(-0.0)	3.174	0.392	0.976	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	12201	2	2053.2	(-0.1)	3.172	0.472	0.981	1	R.IQEIIQL*DVTTSEYEK#.E
SW:CH60_HUMAN	R14	11845	2	2039.2	(-0.1)	3.066	0.403	0.976	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	12053	2	2053.2	(-1.0)	3.027	0.252	0.705	1	R.IQEIIQL*DVTTSEYEK#.E
SW:CH60_HUMAN	R14	13747	2	2039.2	(-0.0)	2.997	0.462	0.983	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	13283	2	2053.2	(-0.0)	2.997	0.468	0.975	1	R.IQEIIQL*DVTTSEYEK#.E
SW:CH60_HUMAN	R14	11769	2	2039.2	(-0.8)	2.996	0.401	0.923	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	13329	2	2039.2	(-0.6)	2.937	0.391	0.970	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	12483	2	2053.2	(+0.2)	2.883	0.427	0.968	1	R.IQEIIQL*DVTTSEYEK#.E
SW:CH60_HUMAN	R14	10737	2	2039.2	(+0.4)	2.840	0.438	0.984	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	13977	2	2039.2	(+0.1)	2.759	0.401	0.966	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	8043	2	2039.2	(+0.8)	2.698	0.192	0.775	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	13013	2	2039.2	(+0.1)	2.668	0.392	0.960	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	13895	2	2039.2	(+0.0)	2.643	0.382	0.955	1	R.IQEIIQLDVTTSEYEK.E

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:CH60_HUMAN	R14	12775	2	2053.2	(-0.7)	2.549	0.359	0.918	1	R.IQEIIQL*DVTTSEYEK#.E
SW:CH60_HUMAN	R14	9383	2	2039.2	(+0.5)	2.362	0.192	0.417	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	12861	2	2053.2	(-0.8)	2.222	0.364	0.690	1	R.IQEIIQL*DVTTSEYEK#.E
SW:CH60_HUMAN	R15	12981	3	2039.2	(+0.8)	3.877	0.378	0.999	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R15	12639	2	2039.2	(+0.4)	2.384	0.382	0.955	1	R.IQEIIQLDVTTSEYEK.E
SW:CH60_HUMAN	R14	7947	2	1926.2	(+1.0)	5.026	0.583	0.991	1	K.ISSIQSIVPAL*EIANAH.R.K
SW:CH60_HUMAN	R14	8025	2	1920.2	(+0.9)	4.274	0.580	0.998	1	K.ISSIQSIVPALEIANAH.R.K
SW:CH60_HUMAN	R14	7941	3	1920.2	(-0.6)	3.874	0.349	0.993	1	K.ISSIQSIVPALEIANAH.R.K
SW:CH60_HUMAN	R14	7943	2	1920.2	(-0.6)	3.277	0.459	0.986	1	K.ISSIQSIVPALEIANAH.R.K
SW:CH60_HUMAN	R14	4759	2	902.1	(+0.4)	3.241	0.394	0.991	1	K.LSDGVAVLK.V
SW:CH60_HUMAN	R14	4353	2	902.1	(+1.0)	3.222	0.377	0.989	1	K.LSDGVAVLK.V
SW:CH60_HUMAN	R14	4431	2	902.1	(+0.8)	3.131	0.386	0.987	1	K.LSDGVAVLK.V
SW:CH60_HUMAN	R14	4197	2	902.1	(+0.9)	3.118	0.379	0.987	1	K.LSDGVAVLK.V
SW:CH60_HUMAN	R14	4673	2	902.1	(+0.7)	3.057	0.370	0.987	1	K.LSDGVAVLK.V
SW:CH60_HUMAN	R14	4591	2	902.1	(+0.8)	2.930	0.383	0.987	1	K.LSDGVAVLK.V
SW:CH60_HUMAN	R14	4899	2	902.1	(+0.6)	2.880	0.350	0.982	1	K.LSDGVAVLK.V
SW:CH60_HUMAN	R14	4985	2	902.1	(+0.7)	2.815	0.339	0.978	1	K.LSDGVAVLK.V
SW:CH60_HUMAN	R14	4515	2	922.1	(-0.2)	2.699	0.270	0.917	1	K.L*SDGVAVL*K#.V
SW:CH60_HUMAN	R14	4709	2	922.1	(-0.0)	2.551	0.286	0.910	1	K.L*SDGVAVL*K#.V
SW:CH60_HUMAN	R14	4423	2	922.1	(-0.2)	2.518	0.280	0.900	1	K.L*SDGVAVL*K#.V
SW:CH60_HUMAN	R14	4593	2	922.1	(+0.2)	2.496	0.370	0.953	1	K.L*SDGVAVL*K#.V
SW:CH60_HUMAN	R14	4333	2	922.1	(-0.2)	2.293	0.326	0.904	1	K.L*SDGVAVL*K#.V
SW:CH60_HUMAN	R14	5071	2	902.1	(+0.7)	2.276	0.267	0.903	1	K.LSDGVAVLK.V
SW:CH60_HUMAN	R14	2424	2	902.1	(+0.8)	2.271	0.393	0.970	1	K.LSDGVAVLK.V
SW:CH60_HUMAN	R14	4087	2	922.1	(+0.2)	2.246	0.405	0.948	1	K.L*SDGVAVL*K#.V
SW:CH60_HUMAN	R17	5194	2	902.1	(+0.9)	2.983	0.309	0.974	1	K.LSDGVAVLK.V
SW:CH60_HUMAN	R18	4623	2	902.1	(+0.8)	2.681	0.299	0.962	1	K.LSDGVAVLK.V
SW:CH60_HUMAN	R18	4709	2	902.1	(+0.9)	2.269	0.297	0.881	1	K.LSDGVAVLK.V
SW:CH60_HUMAN	R14	5699	2	2573.7	(+0.1)	5.532	0.557	0.999	1	K.L*VQDVANNTNEEAGDGTTTATVL*AR.S
SW:CH60_HUMAN	R14	5625	3	2561.7	(+0.7)	5.180	0.567	0.999	1	K.LVQDVANNTNEEAGDGTTTATVLAR.S
SW:CH60_HUMAN	R14	5811	2	2573.7	(+0.5)	4.742	0.512	0.998	1	K.L*VQDVANNTNEEAGDGTTTATVL*AR.S
SW:CH60_HUMAN	R14	5619	3	2573.7	(+0.8)	4.653	0.531	1.000	1	K.L*VQDVANNTNEEAGDGTTTATVL*AR.S
SW:CH60_HUMAN	R14	5921	2	2561.7	(-0.4)	4.439	0.586	0.999	1	K.LVQDVANNTNEEAGDGTTTATVLAR.S
SW:CH60_HUMAN	R14	5769	3	2573.7	(+0.6)	4.387	0.524	0.999	1	K.L*VQDVANNTNEEAGDGTTTATVL*AR.S
SW:CH60_HUMAN	R14	5899	3	2561.7	(+0.9)	4.206	0.492	1.000	1	K.LVQDVANNTNEEAGDGTTTATVLAR.S
SW:CH60_HUMAN	R14	5759	2	1216.4	(+1.0)	3.962	0.461	1.000	1	K.NAGVEGLIVEK.I
SW:CH60_HUMAN	R14	5595	2	1216.4	(+0.2)	3.523	0.467	1.000	1	K.NAGVEGLIVEK.I
SW:CH60_HUMAN	R14	5541	2	1230.4	(+0.6)	3.321	0.379	0.983	1	K.NAGVEGSL*IVEK#.I
SW:CH60_HUMAN	R14	5363	2	1216.4	(+0.9)	3.176	0.473	1.000	1	K.NAGVEGLIVEK.I
SW:CH60_HUMAN	R14	5281	2	1216.4	(+0.7)	2.999	0.482	0.991	1	K.NAGVEGLIVEK.I
SW:CH60_HUMAN	R14	5623	2	1230.4	(+0.3)	2.949	0.394	0.978	1	K.NAGVEGSL*IVEK#.I
SW:CH60_HUMAN	R14	5201	2	1216.4	(-0.1)	2.917	0.349	0.965	1	K.NAGVEGLIVEK.I
SW:CH60_HUMAN	R14	5241	2	1230.4	(+0.5)	2.817	0.393	0.975	1	K.NAGVEGSL*IVEK#.I
SW:CH60_HUMAN	R14	5715	2	1230.4	(+0.3)	2.622	0.360	0.958	1	K.NAGVEGSL*IVEK#.I
SW:CH60_HUMAN	R14	5503	2	1216.4	(+0.2)	2.622	0.387	0.964	1	K.NAGVEGLIVEK.I
SW:CH60_HUMAN	R14	5349	2	1230.4	(+0.2)	2.526	0.358	0.932	1	K.NAGVEGSL*IVEK#.I
SW:CH60_HUMAN	R14	5461	2	1230.4	(+0.2)	2.301	0.332	0.879	1	K.NAGVEGSL*IVEK#.I
SW:CH60_HUMAN	R15	4971	2	1216.4	(+0.2)	2.335	0.470	0.973	1	K.NAGVEGLIVEK.I
SW:CH60_HUMAN	R14	6945	2	2385.6	(+0.3)	2.765	0.464	0.573	1	K.QSKPVTTPEEIAQVATISANGDK.E
SW:CH60_HUMAN	R14	8685	3	3558.0	(+0.6)	5.169	0.506	1.000	1	K.QSKPVTTPEEIAQVATISANGDK#EIGNIISDAMK.K
SW:CH60_HUMAN	R14	8689	3	3582.0	(+0.2)	4.251	0.496*	0.009	1	K.QSK#PVTTPEEIAQVATISANGDK#EIGNIISDAMK#.K
SW:CH60_HUMAN	R14	9057	2	1585.9	(-0.2)	3.773	0.353	0.980	2	R.RGVM LAVDAVIAELK.K
SW:CH60_HUMAN	R01	12097	3	2483.9	(+0.4)	4.328	0.467	0.999	2	R.TALLDAAGVASLLTTAEVVVTEIPK.E
SW:CH60_HUMAN	R02	10900	3	2483.9	(+0.7)	3.852	0.468	0.999	2	R.TALLDAAGVASLLTTAEVVVTEIPK.E
SW:CH60_HUMAN	R07	11628	3	2483.9	(+0.7)	4.304	0.345	0.996	2	R.TALLDAAGVASLLTTAEVVVTEIPK.E
SW:CH60_HUMAN	R08	11613	3	2515.9	(+0.9)	3.998	0.369	0.998	2	R.TAL*L*DAAGVASL*L*TTAEVVVTEIPK#.E
SW:CH60_HUMAN	R08	11609	3	2483.9	(+0.8)	3.973	0.468	1.000	2	R.TALLDAAGVASLLTTAEVVVTEIPK.E
SW:CH60_HUMAN	R10	11763	3	2483.9	(+0.5)	4.539	0.443	1.000	2	R.TALLDAAGVASLLTTAEVVVTEIPK.E
SW:CH60_HUMAN	R13	12001	3	2483.9	(+0.4)	4.670	0.470	0.997	2	R.TALLDAAGVASLLTTAEVVVTEIPK.E
SW:CH60_HUMAN	R14	12661	3	2483.9	(+0.9)	5.428	0.526	1.000	2	R.TALLDAAGVASLLTTAEVVVTEIPK.E
SW:CH60_HUMAN	R14	13779	3	2483.9	(+1.0)	5.395	0.532	1.000	2	R.TALLDAAGVASLLTTAEVVVTEIPK.E
SW:CH60_HUMAN	R14	12735	3	2483.9	(+0.9)	5.356	0.573	1.000	2	R.TALLDAAGVASLLTTAEVVVTEIPK.E
SW:CH60_HUMAN	R14	12957	3	2483.9	(+0.9)	5.310	0.582	0.998	2	R.TALLDAAGVASLLTTAEVVVTEIPK.E
SW:CH60_HUMAN	R14	12883	3	2483.9	(+0.7)	5.218	0.555	1.000	2	R.TALLDAAGVASLLTTAEVVVTEIPK.E
SW:CH60_HUMAN	R14	11795	2	2483.9	(-0.1)	4.729	0.464	1.000	2	R.TALLDAAGVASLLTTAEVVVTEIPK.E
SW:CH60_HUMAN	R14	12127	3	2515.9	(+0.7)	4.719	0.483	1.000	2	R.TAL*L*DAAGVASL*L*TTAEVVVTEIPK#.E



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:CH60_HUMAN	R14	12809	3	2483.9	(+1.0)	4.667	0.517	1.000	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R14	13487	3	2483.9	(+0.3)	4.639	0.489	0.999	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R14	11865	3	2515.9	(-0.0)	4.515	0.445	0.999	2	R.TAL*L*DAAGVASL*L*TTAEVWVTEIPK#.E
SW:CH60_HUMAN	R14	12411	3	2515.9	(+0.0)	4.483	0.481	0.998	2	R.TAL*L*DAAGVASL*L*TTAEVWVTEIPK#.E
SW:CH60_HUMAN	R14	13671	3	2515.9	(+0.2)	4.283	0.444	0.997	2	R.TAL*L*DAAGVASL*L*TTAEVWVTEIPK#.E
SW:CH60_HUMAN	R14	13501	3	2515.9	(+0.6)	4.211	0.428	0.999	2	R.TAL*L*DAAGVASL*L*TTAEVWVTEIPK#.E
SW:CH60_HUMAN	R14	13961	3	2483.9	(-0.6)	4.152	0.468	0.999	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R14	13419	3	2515.9	(+0.3)	4.136	0.333	0.995	2	R.TAL*L*DAAGVASL*L*TTAEVWVTEIPK#.E
SW:CH60_HUMAN	R14	12791	3	2515.9	(+0.4)	3.918	0.423	0.999	2	R.TAL*L*DAAGVASL*L*TTAEVWVTEIPK#.E
SW:CH60_HUMAN	R14	13765	3	2515.9	(+0.8)	3.875	0.356	0.997	2	R.TAL*L*DAAGVASL*L*TTAEVWVTEIPK#.E
SW:CH60_HUMAN	R14	11987	2	2483.9	(-0.9)	2.951	0.372	0.900	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R15	12183	3	2483.9	(+0.9)	6.222	0.524	0.999	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R15	12331	3	2483.9	(+0.7)	5.367	0.515	1.000	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R15	13173	3	2483.9	(+0.9)	5.020	0.472	1.000	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R15	12621	3	2483.9	(+0.8)	4.756	0.508	1.000	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R15	12257	3	2483.9	(+0.4)	4.709	0.463	1.000	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R15	11915	3	2515.9	(+0.4)	4.685	0.507	1.000	2	R.TAL*L*DAAGVASL*L*TTAEVWVTEIPK#.E
SW:CH60_HUMAN	R15	12477	3	2483.9	(+0.4)	4.678	0.420	0.999	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R15	11865	2	2483.9	(-0.0)	4.590	0.453	1.000	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R15	13321	3	2483.9	(-0.8)	4.455	0.362	0.985	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R15	13533	3	2483.9	(+0.6)	4.330	0.469	0.999	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R15	12549	3	2483.9	(-0.4)	4.172	0.394	0.997	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R15	12405	3	2483.9	(+0.7)	4.162	0.459	0.997	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R15	13059	3	2483.9	(+0.6)	3.961	0.446	0.993	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R15	13391	3	2483.9	(+0.8)	3.904	0.415	0.997	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R15	12089	3	2515.9	(-0.5)	3.873	0.390	0.996	2	R.TAL*L*DAAGVASL*L*TTAEVWVTEIPK#.E
SW:CH60_HUMAN	R15	12949	3	2515.9	(+0.2)	3.836	0.320	0.984	2	R.TAL*L*DAAGVASL*L*TTAEVWVTEIPK#.E
SW:CH60_HUMAN	R15	11725	3	2483.9	(-0.2)	3.711	0.359	0.990	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R15	12213	3	2515.9	(-0.6)	3.708	0.413	0.997	2	R.TAL*L*DAAGVASL*L*TTAEVWVTEIPK#.E
SW:CH60_HUMAN	R16	13674	3	2483.9	(+0.8)	4.400	0.364	0.998	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R16	11830	3	2483.9	(+0.5)	4.350	0.490	0.999	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R16	12070	3	2483.9	(+0.9)	3.900	0.463	0.999	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R16	11816	3	2515.9	(-0.5)	3.705	0.407	0.997	2	R.TAL*L*DAAGVASL*L*TTAEVWVTEIPK#.E
SW:CH60_HUMAN	R16	11732	2	2483.9	(-0.1)	3.694	0.461	1.000	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R16	11736	2	2515.9	(-0.9)	2.953	0.419	0.909	2	R.TAL*L*DAAGVASL*L*TTAEVWVTEIPK#.E
SW:CH60_HUMAN	R17	11878	3	2483.9	(+0.5)	4.921	0.520	1.000	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R17	11808	3	2483.9	(-0.5)	4.343	0.457	0.999	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R17	11696	3	2483.9	(+0.3)	4.063	0.499	1.000	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R18	12109	3	2483.9	(+0.6)	4.131	0.413	0.986	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R19	12104	3	2483.9	(+0.7)	4.465	0.490	1.000	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R20	11828	3	2483.9	(+0.9)	5.047	0.514	1.000	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R20	11730	3	2483.9	(+0.9)	3.721	0.342	0.994	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R20	11738	3	2515.9	(-0.4)	3.712	0.364	0.992	2	R.TAL*L*DAAGVASL*L*TTAEVWVTEIPK#.E
SW:CH60_HUMAN	R20	11768	2	2483.9	(-0.3)	2.249	0.212	0.621	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R21	11369	3	2483.9	(+0.9)	3.819	0.509	1.000	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R21	11393	2	2483.9	(+0.0)	2.961	0.366	0.963	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R22	11804	3	2483.9	(+0.8)	3.864	0.440	0.999	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R23	11757	3	2483.9	(+0.7)	4.448	0.466	0.999	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R24	11784	3	2483.9	(+0.3)	4.005	0.447	0.999	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R25	12116	3	2483.9	(+0.9)	5.046	0.570	0.977	2	R.TALLDAAGVASLLTTAEVWVTEIPK.E
SW:CH60_HUMAN	R14	7931	2	1505.7	(+0.1)	4.489	0.539	0.999	2	K.TLNDELEIIEGMK.F
SW:CH60_HUMAN	R14	7251	2	1541.7	(-0.3)	3.480	0.385	0.969	2	K.TL*NDEL*EIIIEGM@K#.F
SW:CH60_HUMAN	R14	7961	2	1525.7	(+0.1)	3.382	0.382	0.975	2	K.TL*NDEL*EIIIEGMK#.F
SW:CH60_HUMAN	R17	7982	2	1505.7	(+0.2)	3.932	0.544	1.000	2	K.TLNDELEIIEGMK.F
SW:CH60_HUMAN	R20	7882	2	1525.7	(-0.6)	2.420	0.256	0.779	2	K.TL*NDEL*EIIIEGMK#.F
SW:CH60_HUMAN	R14	6275	2	1345.5	(+0.9)	3.601	0.441	1.000		R.TVIIEQSWGSPK.V
SW:CH60_HUMAN	R14	6189	2	1345.5	(+0.8)	3.164	0.429	0.989		R.TVIIEQSWGSPK.V
SW:CH60_HUMAN	R14	6193	2	1353.5	(+0.7)	2.639	0.412	0.974		R.TVIIEQSWGSPK#.V
SW:CH60_HUMAN	R20	6216	2	1353.5	(+0.7)	2.297	0.168	0.599		R.TVIIEQSWGSPK#.V
SW:CH60_HUMAN	R14	1460	2	853.0	(+0.4)	2.705	0.294	0.960	2	K.VGEVIVTK#.D
SW:CH60_HUMAN	R14	1474	1	853.0	(-0.4)	2.011	0.244	0.000	2	K.VGEVIVTK#.D
SW:CH60_HUMAN	R18	1600	2	853.0	(+0.6)	2.747	0.392	0.982	2	K.VGEVIVTK#.D
SW:CH60_HUMAN	R20	1690	2	845.0	(+1.0)	2.398	0.283	0.944	2	K.VGEVIVTK.D
SW:CH60_HUMAN	R14	4361	2	1234.3	(-0.0)	3.193	0.434	0.985	1	K.VGGTSDVEVNEK.K
SW:CH60_HUMAN	R14	4439	2	1234.3	(-0.6)	2.717	0.346	0.955	1	K.VGGTSDVEVNEK.K
SW:CH60_HUMAN	R14	4363	2	1242.3	(-0.7)	2.708	0.311	0.919	1	K.VGGTSDVEVNEK#.K

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:CH60_HUMAN	R14	1124	2	1242.3	(-0.5)	2.464	0.167	0.595	1	K.VGGTSDVEVNEK#.K
SW:CH60_HUMAN	R14	1122	2	1234.3	(+0.2)	2.314	0.403	0.951	1	K.VGGTSDVEVNEK.K
SW:CH60_HUMAN	R14	5667	2	913.1	(-0.6)	3.147	0.324	0.974	1	K.VGLQVVAVK.A
SW:CH60_HUMAN	R14	5651	2	913.1	(+0.6)	2.973	0.277	0.970	1	K.VGLQVVAVK.A
SW:CH60_HUMAN	R14	5741	2	927.1	(+0.0)	2.712	0.327	0.950	1	K.VGL*QVVAVK#.A
SW:CH60_HUMAN	R14	5845	2	927.1	(+0.5)	2.413	0.218	0.842	1	K.VGL*QVVAVK#.A
SW:CH60_HUMAN	R14	5771	2	913.1	(-0.6)	2.246	0.306	0.901	1	K.VGLQVVAVK.A
SW:CH60_HUMAN	R17	5938	2	913.1	(+0.5)	2.272	0.331	0.948	1	K.VGLQVVAVK.A
SW:CH60_HUMAN	R14	1266	2	961.1	(+0.9)	3.558	0.418	1.000	2	R.VTDALNATR.A
SW:CH60_HUMAN	R14	4585	2	967.1	(+0.5)	2.881	0.424	0.987	2	R.VTDAL*NATR.A
SW:CH60_HUMAN	R14	1258	2	967.1	(+0.6)	2.419	0.345	0.964	2	R.VTDAL*NATR.A
SW:CH60_HUMAN	R25	12118	3	2515.9	(+0.4)	4.694	0.428	1.000	2	R.TAL*L*DAAGVASL*L*TTAEVVTIPEK#.E
SW:CHD3_HUMAN	R05	8278	2	2041.3	(+0.7)	3.983	0.568	1.000	6	R.FSWAQGTDTILADEMGLGK.T
SW:CHD3_HUMAN	R05	8276	2	2061.3	(-0.9)	2.802	0.373	0.853	6	R.FSWAQGTDTIL*ADEMGL*GK#.T
SW:CHD3_HUMAN	R01	9499	2	1901.2	(+0.5)	4.741	0.595	1.000	3	K.GPFLVSAPLSTIINWER.E
SW:CHD3_HUMAN	R02	8652	2	1913.2	(+0.1)	3.408	0.430	0.984	3	K.GPFL*VSAPL*STIINWER.E
SW:CHD3_HUMAN	R03	8967	2	1901.2	(+1.0)	4.671	0.612	1.000	3	K.GPFLVSAPLSTIINWER.E
SW:CHD3_HUMAN	R05	7776	2	1578.8	(-0.7)	3.040	0.263	0.930	7	K.L*L*EQAL*VIEEQL*R.R
SW:CHD3_HUMAN	R01	1344	2	932.1	(+0.9)	2.345	0.157	0.740	3	R.VELSPMQK.K
SW:CHD3_HUMAN	R03	6503	2	1081.3	(+0.4)	2.500	0.234	0.885	7	R.VL*IFSQMTK#.M
SW:CHD3_HUMAN	R03	6505	2	1067.3	(+0.9)	2.459	0.192	0.823	7	R.VLIFSQMTK.M
SW:CHD3_HUMAN	R05	6902	2	1067.3	(+0.9)	2.545	0.395	0.981	7	R.VLIFSQMTK.M
SW:CHD3_HUMAN	R05	6892	2	1081.3	(+0.1)	2.243	0.285	0.843	7	R.VL*IFSQMTK#.M
SW:CHD4_HUMAN	R01	9739	2	1881.1	(-0.1)	4.850	0.541	1.000	1	R.FHNLEGFLEEFADIAK.E
SW:CHD4_HUMAN	R01	9715	3	1901.1	(+1.0)	4.641	0.316	0.994	1	R.FHNL*EGFL*EEFADIAK#.E
SW:CHD4_HUMAN	R01	9719	2	1901.1	(-0.8)	2.986	0.311	0.804	1	R.FHNL*EGFL*EEFADIAK#.E
SW:CHD4_HUMAN	R02	8890	3	1901.1	(+0.6)	4.317	0.350	0.995	1	R.FHNL*EGFL*EEFADIAK#.E
SW:CHD4_HUMAN	R03	9179	3	1901.1	(+0.2)	4.316	0.280	0.988	1	R.FHNL*EGFL*EEFADIAK#.E
SW:CHD4_HUMAN	R03	9175	2	1881.1	(+0.8)	3.310	0.440	0.989	1	R.FHNLEGFLEEFADIAK.E
SW:CHD4_HUMAN	R04	9416	3	1901.1	(+0.6)	4.575	0.294	0.996	1	R.FHNL*EGFL*EEFADIAK#.E
SW:CHD4_HUMAN	R05	9222	2	1881.1	(-0.1)	4.702	0.558	1.000	1	R.FHNLEGFLEEFADIAK.E
SW:CHD4_HUMAN	R06	9536	2	1881.1	(+0.6)	5.279	0.551	0.996	1	R.FHNLEGFLEEFADIAK.E
SW:CHD4_HUMAN	R06	9524	2	1901.1	(-0.9)	4.052	0.420	1.000	1	R.FHNL*EGFL*EEFADIAK#.E
SW:CHD4_HUMAN	R05	9274	3	2522.8	(+0.5)	3.856	0.496	1.000	1	R.FHNL*EGFL*EEFADIAK#EDQIK#.K
SW:CHD4_HUMAN	R01	9047	2	1644.9	(+0.3)	4.100	0.474	0.999	1	R.GGGNQVSL*NVVMDL*K#.K
SW:CHD4_HUMAN	R01	9021	2	1670.9	(-0.3)	2.505	0.147	0.474	1	R.GGGNQVSL*L*NVVMDL*K#.K
SW:CHD4_HUMAN	R03	7989	2	1686.9	(+0.4)	2.559	0.188	0.710	1	R.GGGNQVSL*L*NVVMDL*K#.K
SW:CHD4_HUMAN	R05	8654	3	1670.9	(-0.7)	4.131	0.307	0.992	1	R.GGGNQVSL*L*NVVMDL*K#.K
SW:CHD4_HUMAN	R05	8126	3	1686.9	(+0.4)	3.965	0.351	0.998	1	R.GGGNQVSL*L*NVVMDL*K#.K
SW:CHD4_HUMAN	R05	8122	2	1686.9	(+0.2)	3.194	0.233	0.881	1	R.GGGNQVSL*L*NVVMDL*K#.K
SW:CHD4_HUMAN	R05	8658	2	1644.9	(+0.2)	2.796	0.491	0.983	1	R.GGGNQVSL*NVVMDL*K#.K
SW:CHD4_HUMAN	R05	8642	2	1670.9	(-0.0)	2.328	0.141	0.364	1	R.GGGNQVSL*L*NVVMDL*K#.K
SW:CHD4_HUMAN	R06	8922	2	1644.9	(+0.5)	3.043	0.368	0.975	1	R.GGGNQVSL*NVVMDL*K#.K
SW:CHD4_HUMAN	R06	8928	2	1670.9	(+0.8)	2.615	0.360	0.947	1	R.GGGNQVSL*L*NVVMDL*K#.K
SW:CHD4_HUMAN	R06	8368	2	1686.9	(-0.3)	2.533	0.203	0.648	1	R.GGGNQVSL*L*NVVMDL*K#.K
SW:CHD4_HUMAN	R01	11593	3	3765.3	(+0.2)	4.046	0.386	0.974	1	K.GSSGASVAAAAAIVAVVESMTATEVAPPPPPVEVPIRK#.A
SW:CHD4_HUMAN	R01	8359	3	1912.1	(+0.8)	4.318	0.494	1.000	1	R.HDYWL*L*AGIINHGYAR.W
SW:CHD4_HUMAN	R05	8088	3	1912.1	(+0.9)	4.966	0.456	1.000	1	R.HDYWL*L*AGIINHGYAR.W
SW:CHD4_HUMAN	R06	8332	3	1912.1	(+0.7)	4.717	0.442	1.000	1	R.HDYWL*L*AGIINHGYAR.W
SW:CHD4_HUMAN	R05	4584	3	1864.0	(+0.9)	4.291	0.478	1.000	1	K.IEENSLKEEESIEGEK.E
SW:CHD4_HUMAN	R05	4598	3	1886.0	(+0.6)	3.807	0.437	0.997	1	K.IEENSL*K#EEESIEGEK#.E
SW:CHD4_HUMAN	R06	4528	3	1864.0	(+0.9)	3.832	0.464	1.000	1	K.IEENSLKEEESIEGEK.E
SW:CHD4_HUMAN	R05	1774	3	1984.0	(+0.5)	4.114	0.409	0.999	1	R.K#NDMDEPPSGDFGGDEEK#.S
SW:CHD4_HUMAN	R03	8623	2	1901.1	(-1.0)	2.569	0.361	0.794	1	K.M@L*DL*L*EDFL*EHGYK#.Y
SW:CHD4_HUMAN	R05	4886	2	1463.7	(-0.2)	2.896	0.166	0.788	1	K.M@PNGM@YDGSAL*IR.A
SW:CHD4_HUMAN	R05	4810	2	1463.7	(+0.6)	2.850	0.373	0.976	1	K.M@PNGM@YDGSAL*IR.A
SW:CHD4_HUMAN	R05	4734	2	1463.7	(+0.7)	2.383	0.117	0.453	1	K.M@PNGM@YDGSAL*IR.A
SW:CHD4_HUMAN	R06	1872	2	941.0	(-0.3)	2.526	0.251	0.915	1	R.NFEAL*NAR.G
SW:CHD4_HUMAN	R02	6248	3	2515.6	(+0.3)	4.991	0.495	1.000	1	R.NQDETEDTEL*QGM@NEYL*SSFK#.V
SW:CHD4_HUMAN	R03	6163	3	2515.6	(-0.6)	4.254	0.488	1.000	1	R.NQDETEDTEL*QGM@NEYL*SSFK#.V
SW:CHD4_HUMAN	R05	7728	3	2479.6	(+0.9)	4.389	0.305	0.995	1	R.NQDETEDTELQGMNEYLSSFK.V
SW:CHD4_HUMAN	R05	7722	3	2499.6	(-0.3)	4.197	0.363	0.991	1	R.NQDETEDTEL*QGMNEYL*SSFK#.V
SW:CHD4_HUMAN	R06	7868	3	2499.6	(-0.5)	4.115	0.467	1.000	1	R.NQDETEDTEL*QGMNEYL*SSFK#.V
SW:CHD4_HUMAN	R05	5526	2	1533.6	(+0.9)	2.662	0.309	0.936	1	K.QEESVDPDYWEK#.L

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:CHD4_HUMAN	R05	6974	2	1400.6	(+0.9)	3.537	0.405	0.990	1	K.SAIDLTPIVVEDK.E
SW:CHD4_HUMAN	R03	8815	3	2873.0	(+0.7)	3.841	0.389	0.997	1	K.SSAQLLEDWGMEDIDHVFSEEDYR.T
SW:CHD4_HUMAN	R05	8858	3	2873.0	(+0.8)	3.706	0.425	0.999	1	K.SSAQLLEDWGMEDIDHVFSEEDYR.T
SW:CHD4_HUMAN	R02	5264	3	2594.8	(+0.3)	4.702	0.386	0.999	1	K.TPTPSTPGDTPNTAPVPPAEDGIK#.I
SW:CHD4_HUMAN	R01	8091	2	1533.8	(+0.4)	3.269	0.491	1.000	1	K.TVQTAVFLYSLYK.E
SW:CHD4_HUMAN	R02	7468	2	1553.8	(-0.3)	2.806	0.380	0.957	1	K.TVQTAVFL*YSL*YK#.E
SW:CHD4_HUMAN	R06	8072	2	1533.8	(-0.0)	3.933	0.529	0.999	1	K.TVQTAVFLYSLYK.E
SW:CHD4_HUMAN	R01	6783	2	1346.5	(+0.9)	3.190	0.436	0.989	5	R.VGGNIEVLGFNAR.Q
SW:CHD4_HUMAN	R03	6499	2	1352.5	(+0.4)	2.460	0.428	0.976	5	R.VGGNIEVL*GFNAR.Q
SW:CHD4_HUMAN	R05	6898	2	1346.5	(-0.3)	2.747	0.439	0.973	5	R.VGGNIEVLGFNAR.Q
SW:CHD4_HUMAN	R05	6886	2	1352.5	(+0.8)	2.519	0.258	0.893	5	R.VGGNIEVL*GFNAR.Q
SW:CHD4_HUMAN	R06	6896	2	1352.5	(+0.7)	4.286	0.518	1.000	5	R.VGGNIEVL*GFNAR.Q
SW:CHD4_HUMAN	R02	6408	2	1109.3	(+0.1)	2.303	0.230	0.773	1	R.YAIL*NEPFK#.G
SW:CHD4_HUMAN	R05	6672	2	1109.3	(+0.3)	2.690	0.431	0.984	1	R.YAIL*NEPFK#.G
SW:CHD4_HUMAN	R01	8075	2	1917.2	(+0.2)	2.241	0.442	0.954	1	R.YGMPPQDAFTTQWL*VR.D
SW:CHD4_HUMAN	R05	7596	2	1933.2	(-0.5)	3.283	0.498	1.000	1	R.YGM@PPQDAFTTQWL*VR.D
SW:CHD4_HUMAN	R06	6682	2	1109.3	(-0.2)	2.345	0.384	0.947	1	R.YAIL*NEPFK#.G
SW:CIRP_HUMAN	R24	8132	2	1568.7	(-0.5)	2.410	0.147	0.448	2	R.GFGVTFENIDDAK#.D
SW:CIRP_HUMAN	R24	8958	3	2372.6	(-0.2)	3.825	0.413	0.997	2	K.L*FVGGL*SFDTNEQSL*EQVFSK#.Y
SW:CIRP_HUMAN	R24	6352	2	1221.4	(+0.9)	2.345	0.436	0.977	2	K.YGQISEVWVK.D
SW:CISY_HUMAN	R16	8724	2	1327.6	(+1.0)	3.430	0.528	1.000	3	R.ALGVLAQLIWSR.A
SW:CISY_HUMAN	R16	6688	2	1339.5	(-0.0)	3.149	0.370	0.975	3	R.DYIWNTLNSGR.V
SW:CISY_HUMAN	R16	5310	2	1099.3	(+1.0)	2.212	0.311	0.929	3	K.HLPNDPMFK.L
SW:CLPP_HUMAN	R21	5956	3	2022.2	(+0.1)	4.557	0.485	1.000		K.VL*VHPPQDGEDEPTL*VQK#.E
SW:CLPP_HUMAN	R21	6700	2	1391.6	(+0.7)	2.662	0.567	1.000		K.QLQVIESAMER.D
SW:CN01_HUMAN	R01	11047	2	1505.8	(+0.0)	2.811	0.301	0.921	3	R.TFGIWTL*L*SSVIR.C
SW:CN01_HUMAN	R25	11198	2	1505.8	(+0.8)	3.228	0.333	0.978	3	R.TFGIWTL*L*SSVIR.C
SW:CN01_HUMAN	R25	5656	2	1092.2	(-0.3)	2.650	0.385	0.916	3	R.YLEVEPVS.R.Q
SW:CNG6_HUMAN	R21	6672	2	1134.3	(+0.9)	3.000	0.368	0.986		R.HDDYLVMLK.A
SW:CNG6_HUMAN	R21	6458	2	1023.2	(+1.0)	2.666	0.310	0.972		R.LLHIEELR.E
SW:CNG6_HUMAN	R21	7258	2	1834.0	(-0.1)	2.415	0.316	0.855		K.NAEPL*INL*DVNNPDFK#.A
SW:COF1_HUMAN	R24	8018	2	2181.4	(+0.5)	5.489	0.571	0.992	1	K.EIL*VGDVGQTVDDPYATFVK#.M
SW:COF1_HUMAN	R24	9122	2	1991.3	(-0.0)	5.036	0.500	1.000	2	K.KEDLVFIFWAPESAPLK.S
SW:COF1_HUMAN	R24	6018	2	1338.5	(+0.7)	3.520	0.534	0.986	2	R.YALYDATYETK.E
SW:COF1_HUMAN	R24	6020	2	1352.5	(+0.4)	2.404	0.386	0.959	2	R.YAL*YDATYETK#.E
SW:COXJ_HUMAN	R27	6209	2	1035.2	(-0.1)	3.632	0.362	0.986		K.GGVADALLYR.A
SW:COXJ_HUMAN	R27	7197	2	1649.8	(-1.0)	3.104	0.139	0.480		K.L*FQEDDEIPL*YL*K#.G
SW:CPT1_HUMAN	R02	6854	2	1187.4	(+0.2)	2.279	0.176	0.588	1	K.YL*AVESPFL*K#.E
SW:CPT1_HUMAN	R03	1304	2	888.0	(-0.4)	2.526	0.425*	0.273	1	R.LAALTAGDR.V
SW:CPT2_HUMAN	R13	8909	3	2471.7	(+0.9)	5.256	0.566	0.999	1	K.YILSDSSPAPEFPLAYLTSEN.R.D
SW:CPT2_HUMAN	R13	8315	2	1359.5	(-0.3)	2.873	0.460	0.979		K.AL*EDMFDAL*EGK#.S
SW:CRN1_HUMAN	R11	8596	2	1492.7	(+0.8)	4.252	0.473	1.000	6	K.FAELETILGDIDR.A
SW:CRN1_HUMAN	R11	8600	2	1504.7	(+0.1)	3.093	0.416	0.979	6	K.FAEL*ETIL*GDIDR.A
SW:CRN1_HUMAN	R12	5882	2	1068.3	(-0.3)	2.206	0.243	0.760	6	R.FVL*VHPDVK#.N
SW:CRTC_HUMAN	R15	8267	3	2589.8	(+0.5)	3.878	0.382	0.970		K.DDEFTHL*YTL*IVRPDNTYEVK#.I
SW:CRTC_HUMAN	R15	1118	3	2709.6	(+0.5)	3.716	0.383	0.983		K.DEDEEDEDKEEDEDVPGQAK.D
SW:CRTC_HUMAN	R16	958	3	2709.6	(+0.5)	4.247	0.443	0.996		K.DEDEEDEDKEEDEDVPGQAK.D
SW:CRTC_HUMAN	R15	520	2	1056.1	(-0.1)	2.433	0.209	0.100		K.DK#QDEEQR.L
SW:CRTC_HUMAN	R15	938	2	1475.5	(-0.3)	2.645	0.354	0.950		K.EEDEDVPGQAK.D
SW:CRTC_HUMAN	R16	814	2	1475.5	(+0.8)	3.501	0.385	0.983		K.EEDEDVPGQAK.D
SW:CRTC_HUMAN	R15	2362	2	1832.8	(-0.7)	3.324	0.317	0.332		K.EEDEDVPGQAKDEL.-
SW:CRTC_HUMAN	R15	2440	2	1832.8	(-0.6)	2.906	0.363	0.323		K.EEDEDVPGQAKDEL.-
SW:CRTC_HUMAN	R15	2528	2	1832.8	(-0.7)	2.598	0.198	0.051		K.EEDEDVPGQAKDEL.-
SW:CRTC_HUMAN	R15	6247	2	1411.5	(+0.8)	2.588	0.475	0.987		K.EQFLDGDGWT.SR.W
SW:CRTC_HUMAN	R15	6119	2	1411.5	(-0.6)	2.550	0.460	0.978		K.EQFLDGDGWT.SR.W

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:CRTC_HUMAN	R16	5964	2	1417.5	(+0.4)	2.665	0.318	0.956		K.EQFL*DGDGWTSR.W
SW:CRTC_HUMAN	R19	6592	2	1411.5	(+0.9)	2.307	0.348	0.943		K.EQFLDGDGWTSR.W
SW:CRTC_HUMAN	R20	6392	2	1417.5	(+0.8)	2.337	0.327	0.933		K.EQFL*DGDGWTSR.W
SW:CRTC_HUMAN	R21	6406	2	1411.5	(+0.7)	2.539	0.467	0.985		K.EQFLDGDGWTSR.W
SW:CRTC_HUMAN	R26	6688	2	1411.5	(-0.6)	2.545	0.391	0.961		K.EQFLDGDGWTSR.W
SW:CRTC_HUMAN	R14	7903	2	1608.8	(+0.6)	4.606	0.559	1.000		R.FYALSASFEPFSNK.G
SW:CRTC_HUMAN	R15	7605	2	1622.8	(-0.5)	3.233	0.260	0.829		R.FYAL*SASFEPFSNK#.G
SW:CRTC_HUMAN	R15	7831	2	1608.8	(+0.4)	2.812	0.499	0.808		R.FYALSASFEPFSNK.G
SW:CRTC_HUMAN	R15	7749	2	1608.8	(+0.1)	2.439	0.268	0.833		R.FYALSASFEPFSNK.G
SW:CRTC_HUMAN	R16	7498	2	1608.8	(+0.3)	4.692	0.537	0.999		R.FYALSASFEPFSNK.G
SW:CRTC_HUMAN	R16	7412	2	1622.8	(+0.1)	3.944	0.281	0.533		R.FYAL*SASFEPFSNK#.G
SW:CRTC_HUMAN	R21	7746	2	1622.8	(+0.5)	3.732	0.507	1.000		R.FYAL*SASFEPFSNK#.G
SW:CRTC_HUMAN	R23	8024	2	1608.8	(-0.0)	2.705	0.341	0.943		R.FYALSASFEPFSNK.G
SW:CRTC_HUMAN	R24	8068	2	1608.8	(+0.4)	2.416	0.372	0.951		R.FYALSASFEPFSNK.G
SW:CRTC_HUMAN	R26	8182	2	1608.8	(+1.0)	2.748	0.538	0.970		R.FYALSASFEPFSNK.G
SW:CRTC_HUMAN	R15	776	2	976.0	(+0.8)	2.866	0.457	0.991		K.GLQTSQDAR.F
SW:CRTC_HUMAN	R15	6791	2	1220.5	(+0.6)	3.282	0.442	1.000		K.GQTLVVQFTVK.H
SW:CRTC_HUMAN	R15	6733	2	1234.5	(+0.4)	2.783	0.479	0.987		K.GQTL*VVQFTVK#.H
SW:CRTC_HUMAN	R16	6528	2	1220.5	(+0.7)	3.618	0.522	1.000		K.GQTLVVQFTVK.H
SW:CRTC_HUMAN	R27	6479	2	1220.5	(+0.8)	2.879	0.453	0.989		K.GQTLVVQFTVK.H
SW:CRTC_HUMAN	R15	5979	2	2761.9	(-0.1)	3.278	0.287	0.265		K.IDDPTDSKPEDWDKPEHIPDPAK.K
SW:CRTC_HUMAN	R16	5880	2	2761.9	(-0.5)	2.828	0.350	0.280		K.IDDPTDSKPEDWDKPEHIPDPAK.K
SW:CRTC_HUMAN	R15	7601	2	2392.5	(+0.1)	4.279	0.492	0.995		K.IDNSQVESGSLEDDWDFLPPK.K
SW:CRTC_HUMAN	R15	7791	2	2392.5	(+0.0)	3.963	0.427	1.000		K.IDNSQVESGSLEDDWDFLPPK.K
SW:CRTC_HUMAN	R15	7441	3	2548.7	(+0.2)	4.093	0.490	1.000		K.IDNSQVESGSL*EDDWDFL*PPK#K#.I
SW:CRTC_HUMAN	R15	7449	3	2520.7	(+0.9)	4.046	0.283	0.926		K.IDNSQVESGSLEDDWDFLPPK.I
SW:CRTC_HUMAN	R15	7361	3	2548.7	(-0.1)	3.733	0.410	0.980		K.IDNSQVESGSL*EDDWDFL*PPK#K#.I
SW:CRTC_HUMAN	R16	7200	3	2520.7	(+0.6)	3.909	0.299	0.937		K.IDNSQVESGSLEDDWDFLPPK.I
SW:CRTC_HUMAN	R15	1792	2	1801.9	(+0.4)	3.455	0.508	1.000		K.IKDPDASKPEDWDER.A
SW:CRTC_HUMAN	R16	1392	2	1801.9	(+1.0)	4.024	0.503	1.000		K.IKDPDASKPEDWDER.A
SW:CRTC_HUMAN	R15	7389	3	2962.2	(+0.5)	5.669	0.510	0.949		K.KPEDWDEEMDGEWEPPVIQNPEYK.G
SW:CRTC_HUMAN	R15	6909	3	2994.2	(+0.0)	5.423	0.438	1.000		K.K#PEDWDEEM@DGEWEPPVIQNPEYK#.G
SW:CRTC_HUMAN	R15	6991	3	2994.2	(+0.1)	5.408	0.428	0.996		K.K#PEDWDEEM@DGEWEPPVIQNPEYK#.G
SW:CRTC_HUMAN	R15	7243	3	2978.2	(+0.2)	4.514	0.389	0.997		K.K#PEDWDEEMDGEWEPPVIQNPEYK#.G
SW:CRTC_HUMAN	R15	7379	2	2962.2	(+0.3)	4.498	0.582	1.000		K.KPEDWDEEMDGEWEPPVIQNPEYK.G
SW:CRTC_HUMAN	R15	7355	3	2978.2	(-0.4)	4.106	0.386	0.997		K.K#PEDWDEEMDGEWEPPVIQNPEYK#.G
SW:CRTC_HUMAN	R15	7403	2	2978.2	(-0.1)	3.956	0.534	1.000		K.K#PEDWDEEMDGEWEPPVIQNPEYK#.G
SW:CRTC_HUMAN	R16	7168	2	2962.2	(-0.3)	4.524	0.532	1.000		K.KPEDWDEEMDGEWEPPVIQNPEYK.G
SW:CRTC_HUMAN	R20	7550	3	2962.2	(+0.1)	4.558	0.393	0.998		K.KPEDWDEEMDGEWEPPVIQNPEYK.G
SW:CRTC_HUMAN	R15	5895	2	1164.4	(+0.3)	2.857	0.445	0.985		K.K#VHVIFNYK#.G
SW:CRTC_HUMAN	R16	5746	2	1148.4	(-0.1)	2.457	0.259	0.895		K.KVHVIFNYK.G
SW:CRTC_HUMAN	R15	9341	3	3284.5	(+0.3)	3.970	0.512	0.996		K.SGTIFDNFL*ITNDEAYAEFFGNETWGVTK#.A
SW:CRTC_HUMAN	R15	11357	3	3270.5	(+0.9)	3.854	0.484	1.000		K.SGTIFDNFLITNDEAYAEFFGNETWGVTK.A
SW:CRTC_HUMAN	R15	9351	2	3270.5	(+0.4)	3.523	0.552	1.000		K.SGTIFDNFLITNDEAYAEFFGNETWGVTK.A
SW:CRTC_HUMAN	R15	9359	2	3284.5	(+0.8)	3.468	0.432	0.987		K.SGTIFDNFL*ITNDEAYAEFFGNETWGVTK#.A
SW:CRTC_HUMAN	R16	9394	2	3270.5	(+0.5)	3.486	0.538	1.000		K.SGTIFDNFLITNDEAYAEFFGNETWGVTK.A
SW:CRTC_HUMAN	R15	5911	2	1020.2	(+0.7)	2.541	0.414	0.985		K.VHVIFNYK.G
SW:CRTC_HUMAN	R15	5937	2	1020.2	(-0.9)	2.481	0.397	0.925		K.VHVIFNYK.G
SW:CRTC_HUMAN	R21	6200	2	1020.2	(+0.9)	2.227	0.172	0.579		K.VHVIFNYK.G
SW:CRTC_HUMAN	R27	6115	2	1411.5	(-0.2)	2.282	0.454	0.967		K.EQFLDGDGWTSR.W
SW:CSE1_HUMAN	R09	7546	2	1072.3	(+0.9)	3.062	0.463	1.000	4	K.IPGLLGVFQK.L
SW:CSE1_HUMAN	R09	10130	2	1676.1	(+0.3)	4.418	0.565	1.000	5	K.LVLDAFALPLTNLFK.A
SW:CSE1_HUMAN	R10	9151	2	1764.0	(+1.0)	4.294	0.543	1.000	5	K.YGALALQEIFDGIQPK.M
SW:CSE1_HUMAN	R10	11269	3	2896.3	(-0.9)	4.144	0.468	0.996	4	K.HGITQANEL*VNL*TEFFVNHL*PDL*K#.S
SW:CT77_HUMAN	R18	8789	2	1706.9	(+0.3)	4.128	0.578	1.000	3	R.EFESVLVDAFASHVAR.E
SW:CT77_HUMAN	R18	2036	2	1268.4	(-0.8)	2.399	0.165	0.349	2	R.ML*VEYTQNK#.D
SW:CT77_HUMAN	R18	6971	2	1369.6	(+0.8)	2.963	0.312	0.869	3	R.SVYGGFEFIQQLK.L
SW:CT77_HUMAN	R18	6973	2	1383.6	(+0.5)	2.735	0.396	0.972	3	R.SVYGGFEFIQQL*K#.L
SW:CT77_HUMAN	R19	9098	2	1766.0	(-0.2)	2.721	0.245	0.815	7	K.L*TFL*YL*ANDVIQNSK#.R
SW:CTOG_HUMAN	R05	5316	2	1136.3	(+0.1)	3.377	0.384	0.981	2	K.GEAVQEEL*L*K#.G
SW:CTOG_HUMAN	R05	5544	2	1435.6	(+0.3)	3.170	0.456	0.986	2	R.IEDL*EEGQQVIR.S
SW:CTOG_HUMAN	R05	8020	2	1645.9	(-0.7)	3.270	0.255	0.917	2	K.L*DDIFEPVL*IPEPK#.I
SW:CTOG_HUMAN	R05	8158	3	2432.7	(-0.5)	4.315	0.396*	0.013	1	R.M@FFEDEK#PAL*L*SQIDAEFEK#.M

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:CTOG_HUMAN	R05	6862	2	1312.4	(+0.7)	3.618	0.369*	0.682	2	K.YSDADIEPFL*K#.N
SW:CTOG_HUMAN	R10	5233	2	1116.3	(+0.4)	3.261	0.344	0.983	2	K.GEAVQEELK.G
SW:CU4A_HUMAN	R10	5365	2	1008.2	(+0.7)	2.200	0.204	0.817	10	K.RIESL*IDR.D
SW:CU4A_HUMAN	R10	9411	2	1467.8	(+0.3)	4.064	0.504	0.915	1	R.SLLGMLSDLQVYK.D
SW:CU4A_HUMAN	R11	9058	2	1467.8	(+0.7)	4.748	0.517	0.945	1	R.SLLGMLSDLQVYK.D
SW:CU4A_HUMAN	R10	6581	2	1298.5	(-0.0)	2.672	0.294	0.900	2	K.TFGTAIVINPEK#.D
SW:CU4A_HUMAN	R11	6326	2	1298.5	(+0.5)	3.182	0.508	0.966	2	K.TFGTAIVINPEK#.D
SW:CU4A_HUMAN	R10	9249	2	1256.5	(+0.8)	3.878	0.383	1.000	7	K.TIDGILLIER.E
SW:CX41_HUMAN	R25	6496	2	1241.4	(+0.4)	2.804	0.307	0.964	1	K.ASWSSLSMDEK.V
SW:CX41_HUMAN	R25	7120	2	1565.7	(-0.9)	3.457	0.408	0.942		K.HYVYGPL*PQSFDK#.E
SW:CX41_HUMAN	R25	7832	3	2165.5	(-0.3)	4.411	0.496	1.000		K.HYVYGPLPQSFDKEWVAK.Q
SW:CX41_HUMAN	R25	6504	2	1255.4	(+0.2)	2.515	0.398	0.955	1	K.ASWSSL*SMDEK#.V
SW:CYB5_HUMAN	R25	6522	2	1512.7	(-0.2)	3.393	0.342	0.974	3	K.FLEEHPGGEEVLR.E
SW:CYB5_HUMAN	R25	7410	2	1652.9	(-0.4)	4.275	0.456	0.996	3	K.TFIIGEL*HPDDRPK#.L
SW:CYB5_HUMAN	R25	7408	2	1638.9	(+0.8)	4.053	0.469	1.000	3	K.TFIIGELHPDDRPK.L
SW:CYC_HUMAN	R26	9486	2	2009.3	(+1.0)	3.695	0.500	1.000	3	K.GIIWGEDTLMEYLENPK.K
SW:CYC_HUMAN	R26	6962	2	1181.3	(+0.4)	2.644	0.337	0.966	3	K.TGPNL*HGL*FGR.K
SW:CYM5_HUMAN	R23	8410	3	3629.8	(-0.0)	7.185	0.675	0.972	2	R.FLNEHPGGEEVLEQAGVDASESFEDVGHSSDAR.E
SW:CYM5_HUMAN	R24	8426	3	3629.8	(-0.0)	7.110	0.629	1.000	2	R.FLNEHPGGEEVLEQAGVDASESFEDVGHSSDAR.E
SW:CYM5_HUMAN	R24	8424	3	3647.8	(-0.7)	6.535	0.602	0.997	2	R.FL*NEHPGGEEVL*L*EQAGVDASESFEDVGHSSDAR.E
SW:CYM5_HUMAN	R24	6594	2	2135.3	(+0.0)	2.320	0.287	0.085	2	K.QYYIGDIHPSDLKPESGSK.D
SW:CYM5_HUMAN	R24	7392	2	1135.3	(+0.2)	2.293	0.354	0.941	2	K.EL*WL*VIHGR.V
SW:D3HI_HUMAN	R19	9334	2	1252.4	(+0.9)	2.258	0.514	0.987		K.DFSSVFQFL*R.E
SW:D3HI_HUMAN	R19	9352	3	2391.8	(+0.9)	4.097	0.495	0.998		R.IITMLPTSINAIEAYSGANGILK.K
SW:D3HI_HUMAN	R19	7994	2	1586.9	(+0.5)	2.735	0.419	0.980		K.SPIL*L*GSL*AHQIYR.M
SW:D3HI_HUMAN	R19	9328	2	1246.4	(+0.9)	2.235	0.373	0.958		K.DFSSVFQFLR.E
SW:DAPT_HUMAN	R13	8509	2	1890.1	(+0.9)	3.745	0.583	0.999	1	R.EVFDTYLVPISISYDK.I
SW:DAPT_HUMAN	R13	7623	3	2429.6	(+0.7)	4.031	0.435	0.999	1	K.YLLSEEDHFSEEQYLA AVR.K
SW:DAPT_HUMAN	R13	8903	2	1606.8	(+0.6)	2.591	0.355	0.958	1	R.NGYAPVEFFL*EGTR.S
SW:DB83_HUMAN	R02	7254	2	1214.5	(+0.6)	2.503	0.389	0.971	1	R.ALLANALTSALR.L
SW:DB83_HUMAN	R02	7252	2	1238.5	(+0.2)	2.320	0.400	0.950	1	R.AL*L*ANAL*TSAL*R.L
SW:DB83_HUMAN	R03	5787	2	957.1	(+0.0)	2.598	0.230	0.869	1	R.GSNSLPLLR.S
SW:DB83_HUMAN	R01	1488	2	1149.3	(+0.2)	2.733	0.355	0.949	1	K.L*SANQQNIL*K#.F
SW:DB83_HUMAN	R01	1490	2	1129.3	(+0.5)	2.683	0.354	0.975	1	K.LSANQQNILK.F
SW:DB83_HUMAN	R02	1966	2	1149.3	(-0.0)	2.547	0.196	0.765	1	K.L*SANQQNIL*K#.F
SW:DB83_HUMAN	R03	1754	2	1149.3	(-0.5)	2.453	0.225	0.791	1	K.L*SANQQNIL*K#.F
SW:DBPA_HUMAN	R16	4630	2	1287.5	(-1.0)	2.669	0.425	0.932	15	K.EDVFNHQTAIK.K
SW:DBPA_HUMAN	R16	6220	2	1796.9	(+0.7)	2.371	0.430	0.970	14	R.SVGDGETVEFDVVEGEK.G
SW:DD15_HUMAN	R10	8527	2	1748.0	(-0.1)	2.277	0.102	0.279	1	K.AL*VTGYFMQVAHL*ER.T
SW:DD15_HUMAN	R01	5535	2	1386.5	(+0.4)	2.798	0.172	0.646	2	R.EVDDLGPVGDIIK.I
SW:DD15_HUMAN	R03	5505	2	1386.5	(-0.0)	2.642	0.169	0.607	2	R.EVDDLGPVGDIIK.I
SW:DD15_HUMAN	R10	6033	2	1386.5	(+0.6)	3.701	0.501	0.999	2	R.EVDDLGPVGDIIK.I
SW:DD15_HUMAN	R10	6031	2	1400.5	(+0.1)	3.108	0.362	0.963	2	R.EVDDL*GPEVGDIIK#.I
SW:DD15_HUMAN	R10	5827	2	1460.6	(-0.1)	3.623	0.514	1.000	1	R.HQSFLV*VGETGSGK#.T
SW:DD15_HUMAN	R10	4089	2	1214.3	(+0.5)	2.928	0.435	0.985	1	R.L*DL*GEDYPSGK#.K
SW:DD15_HUMAN	R10	4013	2	1194.3	(+0.6)	2.907	0.391	0.984	1	R.LDLGEDYPSGK.K
SW:DD15_HUMAN	R10	4091	2	1194.3	(+0.7)	2.900	0.432	0.988	1	R.LDLGEDYPSGK.K
SW:DD15_HUMAN	R10	4175	2	1194.3	(+0.7)	2.809	0.443	0.988	1	R.LDLGEDYPSGK.K
SW:DD15_HUMAN	R10	2516	2	1194.3	(+0.1)	2.736	0.401	0.974	1	R.LDLGEDYPSGK.K
SW:DD15_HUMAN	R10	3945	2	1194.3	(+0.7)	2.701	0.389	0.979	1	R.LDLGEDYPSGK.K
SW:DD15_HUMAN	R10	3879	2	1194.3	(+0.9)	2.583	0.415	0.981	1	R.LDLGEDYPSGK.K
SW:DD15_HUMAN	R10	4171	2	1214.3	(+0.0)	2.583	0.482	0.963	1	R.L*DL*GEDYPSGK#.K
SW:DD15_HUMAN	R10	2624	2	1214.3	(-0.6)	2.474	0.415	0.958	1	R.L*DL*GEDYPSGK#.K
SW:DD15_HUMAN	R10	2502	2	1214.3	(-0.0)	2.372	0.364	0.904	1	R.L*DL*GEDYPSGK#.K
SW:DD15_HUMAN	R10	2700	2	1214.3	(-0.3)	2.353	0.408	0.947	1	R.L*DL*GEDYPSGK#.K
SW:DD15_HUMAN	R10	3951	2	1214.3	(+0.2)	2.329	0.308	0.868	1	R.L*DL*GEDYPSGK#.K

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:DD15_HUMAN	R10	4269	2	1214.3	(-1.0)	2.325	0.275	0.597	1	R.L*DL*GEDYPSGK#.K
SW:DD15_HUMAN	R10	4245	2	1214.3	(+0.7)	2.296	0.475	0.977	1	R.L*DL*GEDYPSGK#.K
SW:DD15_HUMAN	R10	3809	2	1194.3	(+0.8)	2.210	0.422	0.969	1	R.LDLGEDYPSGK.K
SW:DD15_HUMAN	R10	4019	2	1214.3	(+0.1)	2.208	0.411	0.936	1	R.L*DL*GEDYPSGK#.K
SW:DD15_HUMAN	R10	9333	3	2564.9	(-0.3)	4.667	0.387	0.998	1	K.L*GIDDL*VHFDFM@DPPAPETL*MR.A
SW:DD15_HUMAN	R10	9757	3	2548.9	(+0.1)	4.316	0.428	0.996	1	K.L*GIDDL*VHFDFMDPPAPETL*MR.A
SW:DD15_HUMAN	R10	7927	2	1184.4	(-0.5)	2.297	0.355	0.909	1	R.SNL*GSVVL*QL*K#.K
SW:DD15_HUMAN	R10	6465	2	1616.8	(-0.2)	2.671	0.284	0.833	1	K.TEMQDNTYPEIL*R.S
SW:DD15_HUMAN	R10	6037	2	1632.8	(-0.4)	2.310	0.112	0.361	1	K.TEM@QDNTYPEIL*R.S
SW:DD15_HUMAN	R10	9421	2	1301.6	(-0.7)	2.783	0.357	0.950	2	R.TL*ATDIL*MGVL*K#.E
SW:DD15_HUMAN	R10	9089	2	1317.6	(+0.1)	2.683	0.394	0.959	2	R.TL*ATDIL*M@GVL*K#.E
SW:DD15_HUMAN	R10	7845	2	1180.4	(+0.1)	2.444	0.352	0.925	1	R.VESL*L*VTAISK#.A
SW:DD15_HUMAN	R10	6887	2	1421.6	(+0.1)	3.229	0.386	0.977	1	R.YGVIL*DEAHER.T
SW:DD15_HUMAN	R10	6777	2	1415.6	(-0.1)	3.207	0.274	0.952	1	R.YGVILDEAHER.T
SW:DD15_HUMAN	R10	6753	2	1421.6	(+0.2)	2.426	0.334	0.924	1	R.YGVIL*DEAHER.T
SW:DD15_HUMAN	R11	6402	2	1415.6	(+0.6)	2.908	0.184	0.884	1	R.YGVILDEAHER.T
SW:DD17_HUMAN	R11	6186	2	1233.4	(+0.8)	3.642	0.518	1.000	5	K.APIL*IATDVASR.G
SW:DD17_HUMAN	R11	6188	2	1227.4	(+0.9)	2.636	0.527	0.991	5	K.APIL IATDVASR.G
SW:DD17_HUMAN	R12	6054	2	1233.4	(+0.8)	3.262	0.532	1.000	5	K.APIL*IATDVASR.G
SW:DD17_HUMAN	R14	6399	2	1227.4	(+0.6)	3.816	0.513	0.999	5	K.APIL IATDVASR.G
SW:DD17_HUMAN	R14	6393	2	1233.4	(+0.8)	3.068	0.467	0.991	5	K.APIL*IATDVASR.G
SW:DD17_HUMAN	R13	1728	2	1172.3	(+0.4)	2.488	0.432	0.973	1	R.DMVGI AQTGSGK#.T
SW:DD17_HUMAN	R13	6625	2	1706.8	(-1.0)	3.098	0.424	0.922	1	R.EL*AQQVQQVADDYGK#.C
SW:DD17_HUMAN	R13	7337	2	1417.6	(+0.8)	2.341	0.404	0.959	1	K.GTAYTFFTPGNLQ
SW:DD17_HUMAN	R12	8628	2	1448.8	(+0.6)	3.774	0.410	0.998	1	K.LIQLMEEIMAEK.E
SW:DD17_HUMAN	R12	8614	2	1468.8	(-0.0)	3.702	0.314	0.971	1	K.L*IQL*MEEIMAEK#.E
SW:DD17_HUMAN	R13	8761	2	1468.8	(-0.4)	2.658	0.106	0.496	1	K.L*IQL*MEEIMAEK#.E
SW:DD17_HUMAN	R12	5596	2	1375.6	(+0.1)	2.837	0.260	0.924	10	R.M@L*DM@GFEPQIR.K
SW:DD17_HUMAN	R13	7281	2	1337.6	(+0.8)	3.617	0.459	0.998	10	R.MLDMGFEPQIR.K
SW:DD17_HUMAN	R13	6023	2	1375.6	(+0.3)	3.294	0.347	0.985	10	R.M@L*DM@GFEPQIR.K
SW:DD17_HUMAN	R13	7275	2	1343.6	(+0.0)	2.761	0.403	0.975	10	R.ML*DMGFEPQIR.K
SW:DD17_HUMAN	R12	1492	2	1340.5	(-0.6)	2.219	0.193	0.544	1	K.VL*EEANQAINPK#.L
SW:DD17_HUMAN	R13	1810	2	1340.5	(-0.2)	2.937	0.439	0.977	1	K.VL*EEANQAINPK#.L
SW:DD17_HUMAN	R15	7049	2	1343.6	(+0.9)	2.643	0.178	0.804	10	R.ML*DMGFEPQIR.K
SW:DD18_HUMAN	R11	9062	3	2304.7	(-0.6)	3.743	0.290	0.977	6	K.YHYEL*L*NYIDL*PVL*AIHGK#.Q
SW:DD18_HUMAN	R11	1994	2	1161.3	(+0.1)	2.310	0.184	0.691	3	K.ISDIQSQLEK.L
SW:DD21_HUMAN	R01	6069	2	1177.4	(-0.2)	2.229	0.324	0.894	3	R.APQVL*VL*APTR.E
SW:DD21_HUMAN	R02	7410	2	1235.5	(+0.2)	2.658	0.437	0.972	3	R.GVTFL*FPIQAK#.T
SW:DD21_HUMAN	R02	6388	2	1212.4	(+0.7)	2.301	0.232	0.817	4	R.NGIDILVGT PGR.I
SW:DD48_HUMAN	R16	754	2	1199.3	(+0.4)	3.481	0.467	1.000	2	R.DVIAQSQSGTGK#.T
SW:DD48_HUMAN	R16	5462	2	1213.4	(+0.9)	2.452	0.294	0.931	2	R.ETQALILAPTR.E
SW:DD48_HUMAN	R16	6188	2	1837.1	(-0.3)	4.024	0.371	0.562	7	R.GIYAYGF EK#PSAIQQR.A
SW:DD48_HUMAN	R16	6186	2	1829.1	(-0.2)	3.878	0.487	1.000	7	R.GIYAYGF EKPSAIQQR.A
SW:DD48_HUMAN	R16	1466	2	1612.8	(-0.3)	4.455	0.447	1.000	2	R.K#L*DYGQHVVAGTPGR.V
SW:DD48_HUMAN	R16	5216	2	1019.2	(+0.9)	2.540	0.385	0.981	10	R.KVDWLTEK.M
SW:DD48_HUMAN	R01	7787	2	1521.8	(+0.2)	2.898	0.469	0.984	2	K.MLVLDEADEMLNK.G
SW:DD48_HUMAN	R16	7452	2	1547.8	(-0.3)	3.600	0.388	0.979	2	K.ML*VL*DEADEML*NK#.G
SW:DD48_HUMAN	R16	5750	2	1174.3	(+1.0)	3.233	0.342*	0.655	2	K.RDEL TLEGIK.Q
SW:DD48_HUMAN	R16	5722	2	1194.3	(+0.0)	2.667	0.360	0.953	2	K.RDEL*TL*EGIK#.Q
SW:DD48_HUMAN	R16	5132	2	1041.2	(+1.0)	2.265	0.144	0.562	10	R.K#VDWL*TEK#.M
SW:DDB1_HUMAN	R07	8385	2	1820.1	(+0.8)	2.446	0.237	0.526	2	K.ICYQEV SQCFGLSSR.I
SW:DDB1_HUMAN	R07	8229	2	1820.1	(+0.2)	2.277	0.141	0.149	2	K.ICYQEV SQCFGLSSR.I
SW:DDB1_HUMAN	R01	5961	3	2954.2	(+0.3)	5.803	0.487	1.000	2	R.IEVQDTSGGTALRPSASTQALSSSVSSSK.L
SW:DDB1_HUMAN	R01	5945	3	2974.2	(-0.5)	4.848	0.507	1.000	2	R.IEVQDTSGGTAL*RPSASTQAL*SSSVSSSK#.L
SW:DDB1_HUMAN	R02	5716	3	2954.2	(+0.0)	5.227	0.506	1.000	2	R.IEVQDTSGGTALRPSASTQALSSSVSSSK.L
SW:DDB1_HUMAN	R02	5718	3	2974.2	(-0.9)	4.503	0.439	0.977	2	R.IEVQDTSGGTAL*RPSASTQAL*SSSVSSSK#.L
SW:DDB1_HUMAN	R03	5617	3	2954.2	(+0.4)	5.774	0.616	0.984	2	R.IEVQDTSGGTALRPSASTQALSSSVSSSK.L
SW:DDB1_HUMAN	R01	5585	2	1156.3	(+0.7)	2.824	0.479	0.984	2	R.IVVFQYSDGK.L
SW:DDB1_HUMAN	R01	5591	2	1164.3	(-0.1)	2.217	0.224	0.692	2	R.IVVFQYSDGK#.L
SW:DDB1_HUMAN	R02	5758	2	1156.3	(+0.2)	2.661	0.478	0.985	2	R.IVVFQYSDGK.L
SW:DDB1_HUMAN	R02	5754	2	1164.3	(+0.8)	2.484	0.401	0.971	2	R.IVVFQYSDGK#.L

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta M$	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:DDB1_HUMAN	R02	8828	3	2679.0	(+0.6)	4.010	0.484	1.000	2	R.K#TEPATGFIDGDL*IESFL*DISRPK#.M
SW:DDB1_HUMAN	R12	8436	2	1820.1	(+0.7)	2.273	0.163	0.258	2	K.ICYQEVSQCFGLSSR.I
SW:DDX3_HUMAN	R12	8880	2	1161.3	(+0.7)	2.288	0.157	0.622	4	K.DL*L*DL*L*VEAK#.Q
SW:DDX3_HUMAN	R12	2598	2	800.0	(+0.5)	2.207	0.296	0.923	4	K.HAIPIIK#.E
SW:DDX3_HUMAN	R13	8379	3	2084.3	(+0.9)	4.850	0.497	0.998	4	K.HVINFDLPSDIEEYVHR.I
SW:DDX3_HUMAN	R12	10336	2	2333.7	(-0.5)	2.541	0.355*	0.126	2	K.TAAFLLPILSQIYSDGPGEALR.A
SW:DDX3_HUMAN	R12	10334	2	2357.7	(+0.9)	2.408	0.407	0.965	2	K.TAAFL*L*PIL*SQIYSDGPGEAL*R.A
SW:DDX3_HUMAN	R12	5358	2	1094.2	(+0.4)	2.906	0.256	0.962	8	K.YLVLDEADR.M
SW:DDX3_HUMAN	R14	9083	2	1292.5	(+0.4)	3.868	0.506	1.000	2	R.SFLDLLLNATGK.D
SW:DDX5_HUMAN	R13	5203	2	1390.5	(-0.1)	3.268	0.317	0.972	3	K.NFYQEHPDLAR.R
SW:DDX5_HUMAN	R13	8591	3	3396.8	(-0.4)	4.489	0.563	1.000	3	R.QNFTEPTAIQAQGWVVAL*SGL*DM@VGVAQTGSGK#.T
SW:DDX5_HUMAN	R13	6361	2	1296.4	(+0.7)	4.156	0.502	1.000	2	R.TTYLVLDEADR.M
SW:DDX5_HUMAN	R13	6357	2	1308.4	(-0.2)	2.592	0.281	0.912	2	R.TTYL*VL*DEADR.M
SW:DDX5_HUMAN	R14	6151	2	1004.2	(+0.9)	2.356	0.319	0.957	1	K.L*L*QL*VEDR.G
SW:DDX6_HUMAN	R15	1568	3	2367.6	(+0.2)	5.305	0.430	1.000	3	R.GPVKPTGGPGGGGTQTQQQMNQLK.N
SW:DDX6_HUMAN	R15	12361	3	2217.7	(+0.6)	4.208	0.349	0.998	2	K.LLSQDFVQIMEDIILTLPK.N
SW:DEK_HUMAN	R16	6412	2	1419.7	(+0.8)	3.725	0.520	1.000		K.LLASANLEEVTK.Q
SW:DEK_HUMAN	R16	6406	2	1445.7	(-0.2)	3.373	0.543	1.000		K.L*L*ASANL*EEVTK#.Q
SW:DEK_HUMAN	R16	5444	2	1474.7	(+0.0)	3.124	0.369	0.358	2	K.L*L*YNRPGTVSSL*K#.K
SW:DEK_HUMAN	R16	5096	2	1163.4	(+0.7)	3.676	0.437	1.000	1	R.LTMQVSSLR.E
SW:DEK_HUMAN	R16	6876	2	1357.5	(+0.4)	3.098	0.424	0.846	2	K.NVGQFSGFPFEK.G
SW:DEK_HUMAN	R16	5082	2	1175.4	(+0.5)	2.587	0.332	0.964	1	R.L*TMQVSSL*QR.E
SW:DESM_HUMAN	R15	2106	2	1116.2	(+0.6)	2.959	0.265	0.967	21	K.VELQELNDR.F
SW:DESM_HUMAN	R15	2024	2	1116.2	(-0.6)	2.587	0.327	0.954	21	K.VELQELNDR.F
SW:DESM_HUMAN	R15	2116	2	1128.2	(+0.1)	2.424	0.154	0.702	21	K.VEL*QEL*NDR.F
SW:DESM_HUMAN	R15	2034	2	1128.2	(-0.6)	2.282	0.267	0.867	21	K.VEL*QEL*NDR.F
SW:DESM_HUMAN	R24	6368	2	1674.9	(-0.4)	2.476	0.287	0.729	14	R.FLEQQNAALAAEVNR.L
SW:DHB4_HUMAN	R02	6296	2	1283.5	(+0.7)	3.034	0.366	0.980	1	R.IDVVVNNAGILR.D
SW:DHB4_HUMAN	R01	7401	2	1426.6	(+0.6)	2.719	0.420	0.980		K.LQSTFVFEEIGR.R
SW:DHB4_HUMAN	R11	7280	2	1432.6	(+0.2)	2.637	0.383	0.962		K.L*QSTFVFEEIGR.R
SW:DHB4_HUMAN	R03	6835	3	2537.8	(+0.4)	3.793	0.473	0.984		K.VQETGDIVISNAYVDLAPTSGETSAK.T
SW:DHB4_HUMAN	R19	6096	2	1170.4	(+0.7)	3.444	0.577	1.000		R.VVLVTGAGAGLGR.A
SW:DHB4_HUMAN	R19	6098	2	1182.4	(+0.2)	3.129	0.494	1.000		R.VVL*VTGAGAGL*GR.A
SW:DHB4_HUMAN	R19	8902	2	1497.8	(-0.4)	2.284	0.407	0.941		K.LGLLGLANSLAIEGR.K
SW:DHC7_HUMAN	R01	7107	2	2188.5	(+0.8)	5.568	0.680	0.998	2	K.FL*PGYVGGIQEGAVTPAGVVNK#.Y
SW:DHC7_HUMAN	R01	7101	2	2174.5	(+0.1)	5.363	0.615	0.999	2	K.FLPGYVGGIQEGAVTPAGVVNK.Y
SW:DHC7_HUMAN	R01	7089	3	2188.5	(+0.2)	3.809	0.353	0.876	2	K.FL*PGYVGGIQEGAVTPAGVVNK#.Y
SW:DHC7_HUMAN	R01	7927	2	1205.4	(+0.9)	3.138	0.270	0.967	3	K.LLVSGFWGVAR.H
SW:DHC7_HUMAN	R01	7925	2	1217.4	(+0.2)	2.758	0.135	0.725	3	K.L*L*VSGFWGVAR.H
SW:DHC7_HUMAN	R01	928	2	977.0	(+0.9)	2.277	0.436	0.979	1	K.SLDGVTNDR.T
SW:DHC7_HUMAN	R03	938	2	977.0	(+0.9)	2.342	0.325	0.943	1	K.SLDGVTNDR.T
SW:DHCR_HUMAN	R01	6727	3	1988.3	(+0.1)	3.776	0.443	0.999	2	K.L*YEQHHVQDML*VPMK#.C
SW:DHCR_HUMAN	R01	10843	2	2313.7	(-0.1)	2.785	0.403	0.968	2	R.SIFWEL*QDIIPFGNNPIFR.Y
SW:DHCR_HUMAN	R02	6452	2	1102.3	(+0.5)	2.266	0.218	0.805	2	R.EGL*EYIPL*R.H
SW:DHE3_HUMAN	R15	6517	2	1498.7	(+0.3)	3.709	0.553	1.000	3	K.DIVHSGL*AYTMER.S
SW:DHE3_HUMAN	R15	6801	3	2257.5	(+0.1)	3.791	0.477	0.988	5	K.IIAEGANGPTTPEADK#IFL*ER.N
SW:DHE3_HUMAN	R15	6475	2	1197.4	(+1.0)	2.851	0.398	0.984	6	K.LQHGSILGFPA.A
SW:DHE3_HUMAN	R15	6493	2	1197.4	(-0.3)	2.515	0.407	0.954	6	K.LQHGSILGFPA.A
SW:DHE3_HUMAN	R15	1704	2	1242.3	(+0.6)	2.626	0.454	0.986	6	R.YSTDVSVDEVK.A
SW:DHE3_HUMAN	R15	1706	2	1250.3	(+0.5)	2.261	0.420	0.961	6	R.YSTDVSVDEVK#.A
SW:DHSA_HUMAN	R13	2270	2	1330.4	(+0.5)	4.068	0.442	0.991	3	R.GEGGILINSQGER.F
SW:DHSA_HUMAN	R13	2284	2	1336.4	(-0.1)	3.301	0.329	0.970	3	R.GEGGIL*INSQGER.F
SW:DHSA_HUMAN	R13	9863	3	3800.2	(-0.2)	5.522	0.512	1.000	2	K.GSDWLGDDQDAIHYMTEQAPAAVVELENYGMPFSR.T
SW:DHSA_HUMAN	R13	6679	3	2845.1	(-0.9)	3.840	0.432	0.988	3	R.HVNGQDQIVPGL*YACGEAACASVHGANR.L
SW:DHSA_HUMAN	R13	2020	2	1813.0	(-0.4)	3.752	0.316	0.417	2	R.IDEYDYSKPIQQQK.K
SW:DHSA_HUMAN	R13	2026	2	1829.0	(+0.1)	3.483	0.427	0.496	2	R.IDEYDYSK#PIQQQK#.K

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:DHSA_HUMAN	R13	9699	2	1498.7	(-0.3)	3.173	0.326	0.962	3	R.L*GANSL*L*DL*VVFGR.A
SW:DHSA_HUMAN	R13	6151	2	1333.6	(-0.1)	3.062	0.309	0.338	2	K.VTLEYRVIDK.T
SW:DHSA_HUMAN	R13	6147	2	1347.6	(+0.1)	3.036	0.304	0.262	2	K.VTL*EYRVIDK#.T
SW:DHSA_HUMAN	R13	9713	2	1474.7	(-0.1)	2.380	0.404	0.942	3	R.LGANSLDLLVVFGR.A
SW:DHSB_HUMAN	R21	7888	3	1693.9	(+0.9)	3.843	0.381	0.999	5	K.DL*VPDL*SNFYAQYK#.S
SW:DHSB_HUMAN	R21	6136	2	1437.6	(-0.9)	2.920	0.320	0.122	4	K.IK#NEVDSTL*TFR.R
SW:DHSB_HUMAN	R21	2486	2	974.1	(+0.9)	2.602	0.141	0.786	3	R.RIDTNLNK.V
SW:DHSB_HUMAN	R21	7554	2	1382.7	(+0.6)	2.255	0.468	0.979	5	K.YLGPVAVLMQAYR.W
SW:DHX9_HUMAN	R07	7073	2	1261.5	(+0.8)	3.253	0.341	0.835	3	R.AAMEALVVEVTK.Q
SW:DHX9_HUMAN	R07	7079	2	1275.5	(+0.2)	3.075	0.236	0.899	3	R.AAMEAL*VVEVTK#.Q
SW:DHX9_HUMAN	R02	6702	2	1032.2	(+0.3)	2.368	0.303	0.951	3	R.DFVNYL*VR.I
SW:DHX9_HUMAN	R03	6629	2	1032.2	(+0.5)	2.800	0.287	0.972	3	R.DFVNYL*VR.I
SW:DHX9_HUMAN	R01	6905	2	1742.9	(+0.4)	2.321	0.194	0.686	3	R.ELDALDANDELTPPLGR.I
SW:DHX9_HUMAN	R07	6859	2	1742.9	(+0.1)	2.869	0.251	0.885	3	R.ELDALDANDELTPPLGR.I
SW:DHX9_HUMAN	R04	10456	2	1403.7	(+0.4)	2.694	0.426	0.983	3	K.ETPFELIEALLK.Y
SW:DHX9_HUMAN	R06	10646	2	1403.7	(+0.9)	2.985	0.294	0.964	3	K.ETPFELIEALLK.Y
SW:DHX9_HUMAN	R02	8434	3	2090.3	(+0.2)	4.965	0.424	0.999	2	R.FSDHVAL*L*SVFQAWDDAR.M
SW:DHX9_HUMAN	R04	9024	3	2078.3	(+0.8)	3.865	0.474	0.999	2	R.FSDHVALLSVFQAWDDAR.M
SW:DHX9_HUMAN	R07	9173	3	2090.3	(+0.7)	4.273	0.387	0.994	2	R.FSDHVAL*L*SVFQAWDDAR.M
SW:DHX9_HUMAN	R02	8104	3	2190.5	(+0.5)	4.231	0.456	1.000	3	K.K#FESEIL*EAIQNSVVIIR.G
SW:DHX9_HUMAN	R07	1616	2	1076.2	(+0.2)	2.588	0.355	0.964	3	K.LAQFEPSQR.Q
SW:DHX9_HUMAN	R01	6847	2	1024.2	(+0.0)	2.255	0.217	0.692	3	R.L*GGIGQFL*AK#.A
SW:DHX9_HUMAN	R03	6571	2	1024.2	(+0.7)	2.931	0.320	0.968	3	R.L*GGIGQFL*AK#.A
SW:DHX9_HUMAN	R01	8295	3	2511.7	(+0.2)	4.494	0.368	0.997	3	K.NEL*MYQL*EQDHDL*QAIL*QER.E
SW:DHX9_HUMAN	R02	7596	3	2511.7	(-0.0)	4.063	0.421	0.998	3	K.NEL*MYQL*EQDHDL*QAIL*QER.E
SW:DHX9_HUMAN	R03	7849	3	2487.7	(+0.7)	4.976	0.508	1.000	3	K.NELMYQLEQDHDLQAILQER.E
SW:DHX9_HUMAN	R03	7851	3	2511.7	(+0.2)	4.089	0.410	0.998	3	K.NEL*MYQL*EQDHDL*QAIL*QER.E
SW:DHX9_HUMAN	R01	8739	2	2051.3	(+0.5)	2.710	0.510	0.989	3	K.TTQVPQFILDFFIQNDR.A
SW:DHX9_HUMAN	R02	7950	3	2051.3	(+0.7)	4.453	0.471	0.999	3	K.TTQVPQFILDFFIQNDR.A
SW:DHX9_HUMAN	R07	8617	3	2051.3	(+1.0)	3.764	0.468	1.000	3	K.TTQVPQFILDFFIQNDR.A
SW:DHX9_HUMAN	R07	8649	2	2057.3	(+0.1)	2.419	0.351	0.919	3	K.TTQVPQFIL*DDFIQNDR.A
SW:DHX9_HUMAN	R07	7855	2	1729.9	(-0.1)	3.952	0.440	0.997	3	K.VQSDGQIVL*VDDWIK#.L
SW:DHX9_HUMAN	R01	8145	2	1326.5	(+0.6)	2.605	0.319	0.936	1	K.YPSPFFVFGEK#.I
SW:DHX9_HUMAN	R03	7745	2	1326.5	(+0.7)	2.337	0.196	0.725	1	K.YPSPFFVFGEK#.I
SW:DHX9_HUMAN	R07	8071	2	1326.5	(+0.4)	3.273	0.400	0.974	1	K.YPSPFFVFGEK#.I
SW:DHX9_HUMAN	R12	10880	2	1403.7	(+0.6)	2.269	0.312	0.913	3	K.ETPFELIEALLK.Y
SW:DIL2_HUMAN	R09	1722	3	1921.1	(-0.1)	3.804	0.322	0.936	4	R.M@PTK#EDEEEDEPVIK#.A
SW:DIL2_HUMAN	R09	7558	3	2217.4	(+0.1)	4.496	0.290	0.988	5	K.SVAEGL*SGSL*VQEPFQL*ATEK#.R
SW:DIL2_HUMAN	R09	7584	3	2191.4	(+0.8)	3.958	0.445	0.999	5	K.SVAEGLSGSLVQEPFQLATEK.R
SW:DIL2_HUMAN	R09	7660	3	2455.7	(+0.4)	4.085	0.491	1.000	4	R.TFDETVSTYVPLAQQVEDFHK.R
SW:DIL2_HUMAN	R09	7658	3	2469.7	(+0.4)	3.998	0.456	1.000	4	R.TFDETVSTYVPL*AAQQVEDFHK#.R
SW:DIL2_HUMAN	R09	4518	2	1349.4	(+0.2)	2.542	0.207	0.787	4	K.STAELEAELEK.L
SW:DJA1_HUMAN	R16	8874	3	2130.4	(+0.9)	4.165	0.360*	0.158	4	K.NVVHQLSVTLEDLYNGATR.K
SW:DJA1_HUMAN	R16	5592	2	1401.7	(+0.5)	3.181	0.461	0.987	4	R.TIVITSHPGQIVK#.H
SW:DJA1_HUMAN	R16	6046	2	1452.6	(-0.3)	2.713	0.493	0.984	4	K.QISQAYEVLSDAK.K
SW:DJBB_HUMAN	R17	7508	2	1772.9	(+0.4)	4.583	0.559	0.998	2	K.FQDLGAAYEVLSDSEK.R
SW:DJBB_HUMAN	R17	7518	3	1792.9	(+0.9)	3.740	0.388	0.998	2	K.FQDL*GAAYEVL*SDSEK#.R
SW:DJBB_HUMAN	R17	7522	2	1792.9	(-0.8)	3.019	0.337	0.844	2	K.FQDL*GAAYEVL*SDSEK#.R
SW:DJBB_HUMAN	R17	5840	2	1063.2	(+0.1)	2.515	0.261	0.907	2	K.LALQLHPDR.N
SW:DJBB_HUMAN	R17	5950	3	2186.4	(+0.7)	5.049	0.504	1.000	2	K.LALQLHPDRNPDDPQAQEK.F
SW:DJBB_HUMAN	R17	6270	2	1248.4	(+0.9)	3.778	0.566	1.000	2	R.TL*EVEIEPGVR.D
SW:DJBB_HUMAN	R18	6171	2	1242.4	(+0.8)	3.635	0.238	0.974	2	R.TLEVEIEPGVR.D
SW:DLDH_HUMAN	R15	990	2	1113.2	(+0.2)	2.984	0.340	0.959	3	K.ADGGTQVIDTK#.N
SW:DLDH_HUMAN	R15	994	2	1105.2	(+0.6)	2.663	0.378	0.976	3	K.ADGGTQVIDTK.N
SW:DLDH_HUMAN	R15	7007	2	1148.4	(+0.2)	2.574	0.468	0.975	3	K.AL*TGGIAHL*FK#.Q
SW:DLDH_HUMAN	R15	4287	2	1147.3	(+0.9)	3.646	0.516	0.951	3	K.IDVSIEAASGGK.A
SW:DLDH_HUMAN	R15	4119	2	1147.3	(+0.7)	3.470	0.542	1.000	3	K.IDVSIEAASGGK.A
SW:DLDH_HUMAN	R15	2542	2	1155.3	(+0.2)	3.341	0.480	1.000	3	K.IDVSIEAASGGK#.A
SW:DLDH_HUMAN	R15	4363	2	1147.3	(+0.2)	3.233	0.529	0.999	3	K.IDVSIEAASGGK.A
SW:DLDH_HUMAN	R15	4273	2	1155.3	(+0.2)	3.199	0.422	0.980	3	K.IDVSIEAASGGK#.A



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:DLDH_HUMAN	R15	4193	2	1147.3	(+0.4)	3.123	0.557	1.000	3	K.IDVSIEAASGGK.A
SW:DLDH_HUMAN	R15	3957	2	1155.3	(+0.0)	3.097	0.387	0.972	3	K.IDVSIEAASGGK#.A
SW:DLDH_HUMAN	R15	2540	2	1147.3	(-0.5)	3.075	0.452	0.986	3	K.IDVSIEAASGGK.A
SW:DLDH_HUMAN	R15	4535	2	1147.3	(+0.4)	3.069	0.553	1.000	3	K.IDVSIEAASGGK.A
SW:DLDH_HUMAN	R15	4443	2	1147.3	(+0.7)	3.064	0.537	0.996	3	K.IDVSIEAASGGK.A
SW:DLDH_HUMAN	R15	3973	2	1147.3	(+0.8)	3.041	0.479	1.000	3	K.IDVSIEAASGGK.A
SW:DLDH_HUMAN	R15	4043	2	1147.3	(+0.1)	2.930	0.530	1.000	3	K.IDVSIEAASGGK.A
SW:DLDH_HUMAN	R15	3905	2	1147.3	(+0.7)	2.848	0.495	0.991	3	K.IDVSIEAASGGK.A
SW:DLDH_HUMAN	R15	3891	2	1155.3	(+0.5)	2.841	0.478	0.987	3	K.IDVSIEAASGGK#.A
SW:DLDH_HUMAN	R15	4025	2	1155.3	(+0.2)	2.589	0.424	0.963	3	K.IDVSIEAASGGK#.A
SW:DLDH_HUMAN	R15	2454	2	1155.3	(-0.4)	2.571	0.334	0.921	3	K.IDVSIEAASGGK#.A
SW:DLDH_HUMAN	R15	4619	2	1147.3	(-0.1)	2.544	0.377	0.957	3	K.IDVSIEAASGGK.A
SW:DLDH_HUMAN	R15	4455	2	1155.3	(+0.0)	2.522	0.418	0.958	3	K.IDVSIEAASGGK#.A
SW:DLDH_HUMAN	R15	4105	2	1155.3	(+0.4)	2.518	0.451	0.977	3	K.IDVSIEAASGGK#.A
SW:DLDH_HUMAN	R15	3764	2	1147.3	(+1.0)	2.373	0.368	0.955	3	K.IDVSIEAASGGK.A
SW:DLDH_HUMAN	R15	4699	2	1147.3	(+0.4)	2.353	0.300	0.915	3	K.IDVSIEAASGGK.A
SW:DLDH_HUMAN	R15	8483	3	1994.4	(+0.6)	5.410	0.427	1.000	3	K.IPNIYAIGDVGPMPL*AHK#.A
SW:DLDH_HUMAN	R15	8023	2	1568.8	(+0.3)	3.652	0.496	1.000	3	K.NLGLLEELGIELDPR.G
SW:DLDH_HUMAN	R15	8009	2	1592.8	(-0.2)	2.509	0.192	0.572	3	K.NL*GL*EEL*GIEL*DPR.G
SW:DLDH_HUMAN	R15	1762	3	1582.7	(+0.6)	4.240	0.208	0.853	3	K.SEEQLKEEGIEYK.V
SW:DLDH_HUMAN	R15	3805	2	1155.3	(+0.6)	2.322	0.413	0.959	3	K.IDVSIEAASGGK#.A
SW:DM3A_HUMAN	R08	8291	2	1163.4	(+0.5)	3.174	0.399	0.988	2	R.GFGIGELVWGK.L
SW:DM3A_HUMAN	R08	6751	2	1517.7	(+0.3)	2.720	0.286	0.920	1	R.L*TFQAGDPYISK#.R
SW:DM3A_HUMAN	R11	7980	2	1177.4	(+0.2)	2.904	0.481	0.983	2	R.GFGIGEL*VWGK#.L
SW:DNM1_HUMAN	R06	5516	2	1054.3	(+0.5)	3.205	0.356	0.983	2	R.AIILAAAPGEK.L
SW:DNM1_HUMAN	R06	7436	2	1280.4	(-0.1)	2.966	0.367	0.969	2	R.FYFL*EAYNAK#.S
SW:DNM1_HUMAN	R06	6122	2	997.2	(+1.0)	2.550	0.320	0.944	3	R.ISWVGEAVK#.T
SW:DNM1_HUMAN	R06	8496	2	1630.9	(-0.4)	3.448	0.418	0.981		K.L*NL*L*HEFL*QTEIK#.N
SW:DNM1_HUMAN	R06	5208	3	2200.4	(+0.4)	4.947	0.444	1.000	3	K.YGQHPPDAVDEPQM@L*TNEK#.L
SW:DNM1_HUMAN	R06	2108	2	915.1	(+0.2)	2.503	0.369	0.964	3	K.LAGVTLGQR.R
SW:DP1_HUMAN	R24	5992	2	1074.2	(-0.1)	3.015	0.397	0.982	2	K.ATVNLLGEEK.K
SW:DP1_HUMAN	R24	5848	2	1202.4	(+0.7)	3.339	0.518	1.000	2	K.KATVNLLGEEK.K
SW:DP1_HUMAN	R24	5840	2	1230.4	(-0.5)	2.482	0.247	0.817	2	K.K#ATVNL*L*GEEK#.K
SW:DP1_HUMAN	R24	2218	2	1160.3	(+0.8)	2.310	0.369	0.960	2	K.HESQMDSVVK.D
SW:DP30_HUMAN	R25	11594	3	2126.6	(-0.3)	4.652	0.439	0.999		R.AYLDQTVVPILLQGLAVLAK.E
SW:DP30_HUMAN	R25	10836	2	1914.2	(+0.4)	2.339	0.280	0.089		K.ERPPNPIEFL*ASYL*L*K#.N
SW:DPM1_HUMAN	R21	10126	2	1437.8	(+0.6)	2.947	0.446	0.986	3	R.ENLPLIVWLLVK.S
SW:DPM1_HUMAN	R21	6382	3	2164.4	(+0.9)	4.546	0.519	1.000	2	K.HATGNYYIIM@DADL*SHHPK#.F
SW:DPM1_HUMAN	R20	7530	2	1177.4	(+0.9)	2.615	0.340	0.965	2	K.LGGNEIVSFLK.G
SW:DPM1_HUMAN	R21	7432	2	1197.4	(+0.1)	2.372	0.371	0.930	2	K.L*GGNEIVSFL*K#.G
SW:DSRA_HUMAN	R09	7156	2	1737.0	(+0.2)	3.833	0.480	0.999	4	R.AIMEMPSFYSHGLPR.C
SW:DSRA_HUMAN	R09	1966	2	1073.1	(+0.2)	2.989	0.356	0.975	4	R.DGSAFEDGL*R.H
SW:DSRA_HUMAN	R09	1830	2	1067.1	(-0.3)	2.802	0.183	0.855	4	R.DGSAFEDGLR.H
SW:DSRA_HUMAN	R09	1886	2	1073.1	(-0.1)	2.336	0.300	0.900	4	R.DGSAFEDGL*R.H
SW:DSRA_HUMAN	R08	7685	2	1289.5	(+0.5)	2.761	0.291	0.955	5	R.DINAVLIDMER.Q
SW:DSRA_HUMAN	R09	7202	2	1295.5	(+0.8)	3.473	0.306	0.982	5	R.DINAVL*IDMER.Q
SW:DSRA_HUMAN	R09	7206	2	1289.5	(+0.5)	3.111	0.407	0.988	5	R.DINAVLIDMER.Q
SW:DSRA_HUMAN	R09	5718	2	1311.5	(+0.5)	3.049	0.436	0.990	5	R.DINAVL*IDM@ER.Q
SW:DSRA_HUMAN	R09	6530	2	887.2	(+0.2)	2.434	0.280	0.902	4	K.IL*AAIMK#.K
SW:DSRA_HUMAN	R09	916	2	1304.4	(+0.9)	2.558	0.195	0.708	5	K.LVDQSGPPHEPK.F
SW:DSRA_HUMAN	R09	5958	2	1588.8	(-0.3)	3.875	0.514	1.000	3	R.M@GFTEVTPVTGASL*R.R
SW:DSRA_HUMAN	R09	6470	2	1566.8	(+0.2)	2.750	0.431	0.973	3	R.MGFTEVTPVTGASLR.R
SW:DSRA_HUMAN	R09	1916	2	1748.9	(-0.6)	2.438	0.372	0.916	1	R.NTNSVPETAPAAIPETK#.R
SW:DSRA_HUMAN	R09	640	2	1292.3	(+0.5)	2.688	0.379	0.970	5	K.SEESSHYTEK#.E
SW:DSRA_HUMAN	R09	4324	2	1002.1	(+1.0)	2.289	0.246	0.787	5	R.SHGFAAEFK#.L
SW:DSRA_HUMAN	R09	7394	2	1697.9	(-0.5)	3.439	0.403	0.982	5	K.SVTL*GYL*FSQGH*TR.A
SW:DSRA_HUMAN	R09	6002	2	1853.0	(+0.8)	4.553	0.551	1.000	5	K.TAESQTTPSATSFFSFGK#.S
SW:DSRA_HUMAN	R09	6006	2	1845.0	(-0.4)	2.946	0.502	0.986	5	K.TAESQTTPSATSFFSFGK.S
SW:DSRA_HUMAN	R09	1004	2	1121.3	(+0.4)	2.921	0.377	0.979	5	K.VENGQEPVIK#.L
SW:DSRA_HUMAN	R07	7803	2	1698.9	(-0.4)	3.145	0.320	0.940	5	R.YL*NTNPVGG*LY*EYAR.S

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:DSRA_HUMAN	R08	8029	2	1698.9	(-0.7)	2.851	0.274	0.906	5	R.YL*NTNPVGGGL*L*EYAR.S
SW:DSRA_HUMAN	R09	7572	3	1680.9	(+0.5)	3.981	0.434	0.999	5	R.YLNTNPVGGGLLEYAR.S
SW:DSRA_HUMAN	R09	7566	2	1698.9	(-0.2)	3.030	0.350	0.961	5	R.YL*NTNPVGGGL*L*EYAR.S
SW:DSRA_HUMAN	R09	5548	2	903.2	(+0.7)	2.211	0.266	0.877	4	K.IL*AAIIM@K#.K
SW:ECHA_HUMAN	R11	9638	3	1701.0	(+0.1)	4.965	0.428	0.998	2	K.ADMVIEAVFEDL*SL*K#.H
SW:ECHA_HUMAN	R11	9642	2	1681.0	(-0.4)	3.667	0.478	1.000	2	K.ADMVIEAVFEDLSLK.H
SW:ECHA_HUMAN	R11	9636	2	1701.0	(-0.9)	2.221	0.167	0.174	2	K.ADMVIEAVFEDL*SL*K#.H
SW:ECHA_HUMAN	R11	1884	2	976.1	(+0.7)	2.791	0.279	0.963	2	K.DATLTALDR.G
SW:ECHA_HUMAN	R12	1898	2	976.1	(+0.7)	2.508	0.332	0.950	2	K.DATLTALDR.G
SW:ECHA_HUMAN	R11	8936	3	1548.7	(+0.9)	3.911	0.286	0.995	2	K.DL*NSDMDSIL*ASL*K#.L
SW:ECHA_HUMAN	R11	8928	2	1522.7	(+0.4)	3.454	0.293	0.973	2	K.DLNSDMDSILASLK.L
SW:ECHA_HUMAN	R12	9116	2	1548.7	(-0.8)	3.121	0.491	0.999	2	K.DL*NSDMDSIL*ASL*K#.L
SW:ECHA_HUMAN	R11	8202	2	2063.2	(-0.7)	3.877	0.425	1.000	2	R.DSIFSNLTGQLDYQGFEK.A
SW:ECHA_HUMAN	R11	8204	2	2083.2	(-0.8)	2.317	0.110	0.106	2	R.DSIFSNL*TGQL*DYQGFEK#.A
SW:ECHA_HUMAN	R11	1758	2	1133.3	(-0.1)	3.370	0.390	0.978	2	K.DTSASAVAVGL*K#.Q
SW:ECHA_HUMAN	R11	1760	2	1119.3	(-0.4)	2.961	0.378	0.973	2	K.DTSASAVAVGLK.Q
SW:ECHA_HUMAN	R12	1772	2	1119.3	(+0.5)	3.266	0.489	1.000	2	K.DTSASAVAVGLK.Q
SW:ECHA_HUMAN	R12	1778	2	1133.3	(-0.5)	2.933	0.334	0.949	2	K.DTSASAVAVGL*K#.Q
SW:ECHA_HUMAN	R11	8886	3	2421.6	(+0.4)	3.807	0.371	0.998	2	K.ELHSEFSEVMNEIWASDQIR.S
SW:ECHA_HUMAN	R11	5558	2	939.1	(+0.2)	2.327	0.435	0.968	2	K.FGEL*VMTK#.E
SW:ECHA_HUMAN	R12	5360	2	925.1	(+1.0)	2.676	0.444	0.990	2	K.FGELVMTK.E
SW:ECHA_HUMAN	R11	6934	2	1598.8	(-0.3)	3.190	0.280	0.922	2	R.FGGNPPEL*L*TQMVSK#.G
SW:ECHA_HUMAN	R11	6034	2	1614.8	(+0.5)	2.796	0.200	0.809	2	R.FGGNPPEL*L*TQM@VSK#.G
SW:ECHA_HUMAN	R11	5074	2	1041.2	(+0.9)	2.867	0.294	0.971	2	R.FVDLYGAQK.I
SW:ECHA_HUMAN	R11	5128	2	1055.2	(+0.0)	2.444	0.320	0.922	2	R.FVDL*YGAQK#.I
SW:ECHA_HUMAN	R11	6160	2	1204.4	(+0.8)	3.349	0.467	0.995	2	K.GFYIQEGVK.R
SW:ECHA_HUMAN	R11	6162	2	1212.4	(+1.0)	2.203	0.376	0.943	2	K.GFYIQEGVK#.R
SW:ECHA_HUMAN	R12	5988	2	1212.4	(+0.5)	2.904	0.453	0.986	2	K.GFYIQEGVK#.R
SW:ECHA_HUMAN	R11	1168	2	999.2	(+0.9)	2.857	0.322	0.943	2	R.ILQEGVDPK.K
SW:ECHA_HUMAN	R11	1164	2	1013.2	(+0.4)	2.621	0.332	0.962	2	R.IL*QEGVDPK#.K
SW:ECHA_HUMAN	R11	9148	3	2838.2	(+0.6)	3.809	0.386	0.998	1	K.KLDSLTTSGFPGVGAATLVDEVGVDVAK.H
SW:ECHA_HUMAN	R11	7568	3	2323.7	(-0.4)	4.144	0.393	0.979	2	K.M@GL*VDQL*VEPL*GPGL*K#PPEER.T
SW:ECHA_HUMAN	R11	7708	2	1319.6	(+1.0)	4.533	0.387	1.000	2	K.MQLLEIITTEK.T
SW:ECHA_HUMAN	R11	7726	2	1339.6	(+0.4)	2.657	0.332	0.954	2	K.MQL*L*EIIITTEK#.T
SW:ECHA_HUMAN	R12	7834	2	1319.6	(+0.9)	3.213	0.376	0.987	2	K.MQLLEIITTEK.T
SW:ECHA_HUMAN	R11	8100	2	2008.3	(+0.9)	3.597	0.553	1.000	1	K.TVLGTPEVLLGALPGAGGTQR.L
SW:ECHA_HUMAN	R11	8116	2	2008.3	(-0.6)	2.760	0.477	0.981	1	K.TVLGTPEVLLGALPGAGGTQR.L
SW:ECHA_HUMAN	R11	8110	2	2032.3	(-0.2)	2.547	0.304	0.894	1	K.TVL*GTPEVL*L*GAL*PGAGGTQR.L
SW:ECHA_HUMAN	R12	4942	2	1055.2	(+0.2)	2.435	0.297	0.902	2	R.FVDL*YGAQK#.I
SW:ECHB_HUMAN	R16	6178	2	1443.6	(+0.5)	2.967	0.403	0.978	3	K.DQL*L*L*GPTYATPK#.V
SW:ECHB_HUMAN	R16	1432	2	1066.2	(+1.0)	2.306	0.267	0.859	3	R.EAALGAGFSDK.T
SW:ECHB_HUMAN	R16	4310	2	906.1	(+0.3)	3.071	0.405	0.990	4	R.LAAAFAVSR.L
SW:ECHB_HUMAN	R16	4232	2	906.1	(+0.7)	2.798	0.422	0.988	4	R.LAAAFAVSR.L
SW:ECHB_HUMAN	R16	4320	2	912.1	(+0.9)	2.666	0.314	0.968	4	R.L*AAAFAVSR.L
SW:ECHB_HUMAN	R16	4502	2	906.1	(+0.0)	2.628	0.291	0.941	4	R.LAAAFAVSR.L
SW:ECHB_HUMAN	R16	4414	2	906.1	(-0.3)	2.276	0.188	0.718	4	R.LAAAFAVSR.L
SW:ECHB_HUMAN	R16	1358	2	1137.2	(+0.7)	3.158	0.238	0.967	3	R.LEQDEYALR.S
SW:ECHB_HUMAN	R16	6442	2	1214.4	(+0.6)	3.372	0.432	1.000	2	R.TPFLSGTSYK.D
SW:ECHB_HUMAN	R16	6432	2	1234.4	(+0.4)	2.810	0.341	0.965	2	R.TPFL*L*SGTSYK#.D
SW:ECHB_HUMAN	R16	1278	2	979.2	(-0.1)	2.227	0.248	0.083	3	K.ALAMGYKPK.A
SW:ECHM_HUMAN	R21	7620	2	2126.4	(+0.6)	3.891	0.554	1.000	3	K.AQFAQPEILIGTIPGAGGTQR.L
SW:ECHM_HUMAN	R21	5444	2	1367.6	(-0.3)	2.711	0.237	0.874	2	K.SL*AM@EM@VL*TGDR.I
SW:EF11_HUMAN	R01	5291	2	996.2	(+0.2)	2.246	0.258	0.831	11	R.L*PL*QDVYK#.I
SW:EF11_HUMAN	R04	5720	2	996.2	(+0.1)	2.409	0.201	0.787	11	R.L*PL*QDVYK#.I
SW:EF11_HUMAN	R05	5832	2	976.2	(+0.8)	2.673	0.271	0.961	11	R.LPLQDVYK.I
SW:EF11_HUMAN	R06	5828	2	976.2	(+0.7)	2.627	0.173	0.890	11	R.LPLQDVYK.I
SW:EF11_HUMAN	R03	6115	3	1597.8	(+0.7)	4.382	0.402	0.998	4	K.THINIVIGHVDSGK#.S
SW:EF11_HUMAN	R01	7897	2	2517.0	(-0.5)	4.378	0.555	1.000	9	R.VETGVLKPGMVVTFAPVNVTTTEVK.S
SW:EF11_HUMAN	R03	7475	3	2517.0	(+0.6)	3.701	0.344	0.959	9	R.VETGVLKPGMVVTFAPVNVTTTEVK.S
SW:EF11_HUMAN	R16	7140	3	2555.0	(-0.1)	4.080	0.388	0.977	9	R.VETGVL*K#PGM@VVTFAPVNVTTTEVK#.S
SW:EF1B_HUMAN	R20	6456	2	1348.5	(+0.8)	2.775	0.466	0.681	2	R.SIQADGLVWGSSK.L

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:EF1B_HUMAN	R21	6472	2	1348.5	(+0.7)	3.766	0.478	1.000	2	R.SIQADGLVWGSSK.L
SW:EF1B_HUMAN	R20	7784	2	1604.8	(-0.1)	3.504	0.551	0.999	2	K.SPAGLQVLNDYLADK.S
SW:EF1B_HUMAN	R20	7782	2	1630.8	(-0.7)	2.727	0.228	0.784	2	K.SPAGL*QVL*NDYL*ADK#.S
SW:EF1B_HUMAN	R21	7700	2	1604.8	(+1.0)	4.286	0.520	1.000	2	K.SPAGLQVLNDYLADK.S
SW:EF1B_HUMAN	R20	7614	2	2064.3	(-0.3)	4.168	0.506	1.000	2	K.SSILLDVKPWDDETDMAK.L
SW:EF1B_HUMAN	R21	6486	2	1362.5	(-0.5)	2.544	0.172	0.621	2	R.SIQADGL*VWGSSK#.L
SW:EF1D_HUMAN	R19	5834	2	1359.5	(+0.0)	3.623	0.383	0.985	5	R.IASLEVENQSLR.G
SW:EF1D_HUMAN	R19	5838	2	1371.5	(-0.7)	2.765	0.296	0.933	5	R.IASL*EVENQSL*R.G
SW:EF1D_HUMAN	R19	10046	3	3063.4	(+0.4)	3.850	0.346	0.959	4	K.VGTDLLEEEITKFEEHVQSVDAIAFNK.I
SW:EF1D_HUMAN	R20	7618	2	1300.5	(+0.7)	2.877	0.402	0.983	5	R.GVVQELQQAISK.L
SW:EF1G_HUMAN	R16	5074	2	1348.5	(+0.0)	3.780	0.445	1.000	2	K.ALIAAQYSGAQVR.V
SW:EF1G_HUMAN	R16	5068	2	1354.5	(-0.1)	3.396	0.432	0.986	2	K.AL*IAAQYSGAQVR.V
SW:EF1G_HUMAN	R16	7350	2	1468.6	(+0.7)	2.905	0.451	0.989	4	K.DGWSL*WYSEYR.F
SW:EF1G_HUMAN	R16	7186	2	1685.8	(+1.0)	3.667	0.490	0.997	4	R.EYFSWEGAFQHVKG.A
SW:EF1G_HUMAN	R16	8712	2	2688.9	(-1.0)	2.981	0.450	0.945	4	R.GQELAFPLSPDWQVDYESYTW.R.K
SW:EF1G_HUMAN	R16	8090	2	1151.4	(-0.2)	2.621	0.176	0.748	4	R.IL*GL*L*DAYL*K#.T
SW:EF1G_HUMAN	R16	1732	2	1573.7	(+0.6)	3.044	0.310	0.965	4	R.KLDPGSEETQTLV.R.E
SW:EF1G_HUMAN	R16	1726	2	1593.7	(-0.3)	2.467	0.228	0.750	4	R.K#L*DPGSEETQTL*VR.E
SW:EF1G_HUMAN	R16	8542	3	2590.9	(+0.4)	5.533	0.514	1.000	4	R.KYSNEDTSLVALPYRWEHFDK.D
SW:EF1G_HUMAN	R16	1666	2	1445.6	(-0.1)	2.631	0.242	0.853	4	K.LDPGSEETQTLV.R.E
SW:EF1G_HUMAN	R16	8892	2	2482.7	(-0.9)	2.932	0.421	0.909	4	K.YSNEDTL*SVAL*PYFWEHFDK#.D
SW:EF1G_HUMAN	R16	5342	2	1124.3	(+0.9)	2.310	0.292	0.184	4	K.AKDPFAHLPK.S
SW:EF2_HUMAN	R10	9239	3	2221.5	(+0.6)	4.519	0.584	1.000	2	R.ALLELQLEPEELYQTFQR.I
SW:EF2_HUMAN	R10	7823	3	2144.3	(+0.7)	6.142	0.544	0.999	3	K.ARPFPDGLAEDIDKGEVSAR.Q
SW:EF2_HUMAN	R10	5841	2	1064.2	(+0.4)	2.254	0.355	0.957	3	K.GVQYLNEIK.D
SW:EFG1_HUMAN	R11	7254	3	2316.6	(+0.9)	4.959	0.514	1.000	1	R.FVLQDGAHMMVDSNEISFIR.A
SW:EFG1_HUMAN	R11	5578	2	1048.2	(+0.6)	3.002	0.398	0.989	1	R.YGEIPAELR.A
SW:EFG1_HUMAN	R11	5610	2	1219.4	(+0.5)	3.197	0.285	0.972	1	K.YLEATGQLPVK.K
SW:EFG1_HUMAN	R11	5614	2	1239.4	(+0.0)	2.917	0.299	0.938	1	K.YL*EATGQL*PVK#.K
SW:EFG1_HUMAN	R11	7472	2	1708.9	(+0.8)	2.894	0.293	0.902	1	K.VIGVL*EPL*DPEDYTK#.L
SW:EFTU_HUMAN	R16	5470	2	1198.3	(+0.2)	2.724	0.269	0.910	4	R.AEAGDNL*GAL*VR.G
SW:EFTU_HUMAN	R16	7096	2	1555.8	(-0.4)	3.086	0.340	0.961	3	K.L*L*DAVDTYIPV.PAR.D
SW:EFTU_HUMAN	R16	7092	2	1543.8	(+0.8)	2.822	0.409	0.976	3	K.LLDAVDTYIPV.PAR.D
SW:EFTU_HUMAN	R16	7154	2	1909.2	(+1.0)	4.537	0.547	0.999	3	R.TIGTGLVTNTLAMTEEEK.N
SW:EFTU_HUMAN	R16	6294	2	1270.5	(+0.1)	2.626	0.327	0.929	4	R.TVVTGIEMFHK#.S
SW:EFTU_HUMAN	R16	5490	2	1186.3	(+0.8)	2.568	0.168	0.777	4	R.AEAGDNLGALV.R.G
SW:ELV1_HUMAN	R19	5006	2	984.1	(+0.6)	2.218	0.300	0.916	10	R.AINTL*NGL*R.L
SW:ELV1_HUMAN	R19	2226	2	984.1	(-0.3)	2.201	0.370	0.941	10	R.AINTL*NGL*R.L
SW:ELV1_HUMAN	R19	1044	2	1004.1	(+0.9)	2.603	0.272	0.944		K.FAANPNQNK.N
SW:ELV1_HUMAN	R19	7312	2	1569.8	(+0.6)	3.404	0.481	1.000		K.NVALLSQLYHSPAR.R
SW:ELV1_HUMAN	R19	7308	2	1587.8	(-0.3)	2.450	0.258	0.823		K.NVAL*L*SQL*YHSPAR.R
SW:ELV1_HUMAN	R19	6660	3	2613.8	(+0.6)	4.676	0.417	0.996		R.SEAEAAITSFNGHKPPGSSEPITVK.F
SW:ELV1_HUMAN	R19	6780	3	2629.8	(+0.9)	4.085	0.470	0.998		R.SEAEAAITSFNGHK#PPGSSEPITVK#.F
SW:ELV1_HUMAN	R19	7330	2	1368.5	(+0.8)	3.993	0.499	1.000		R.SL*FSSIGEVESAK#.L
SW:ELV1_HUMAN	R19	8116	2	2181.5	(+0.7)	4.439	0.457*	0.789		R.TNL*IVNYL*PQNMTQDEL*R.S
SW:ELV1_HUMAN	R19	7506	2	2197.5	(-0.2)	2.701	0.353*	0.181		R.TNL*IVNYL*PQNMTQDEL*R.S
SW:ELV1_HUMAN	R19	2106	2	1189.4	(+0.8)	3.352	0.466	1.000		R.VLVDQTTGLSR.G
SW:ELV1_HUMAN	R19	2102	2	1201.4	(-0.3)	2.460	0.300	0.910		R.VL*VDQTTGL*SR.G
SW:ELV1_HUMAN	R19	2124	2	1189.4	(-0.9)	2.394	0.493	0.942		R.VLVDQTTGLSR.G
SW:ELV1_HUMAN	R20	2398	2	1201.4	(+0.8)	2.235	0.437	0.973		R.VL*VDQTTGL*SR.G
SW:EMD_HUMAN	R20	1272	2	942.0	(+1.0)	2.534	0.503	0.990	1	R.APGAGLGQDR.Q
SW:EMD_HUMAN	R19	5022	2	1139.2	(-0.3)	2.622	0.225	0.839	1	R.GDADMYDL*PK#.K
SW:EMD_HUMAN	R20	5232	2	1125.2	(-0.4)	2.666	0.310	0.944	1	R.GDADMYDL.PK.K
SW:EMD_HUMAN	R20	5268	2	1139.2	(+0.5)	2.509	0.174	0.770	1	R.GDADMYDL*PK#.K
SW:EMD_HUMAN	R20	2110	2	1195.4	(-0.7)	3.624	0.365	0.985	1	K.KEDALLYQSK.G
SW:EMD_HUMAN	R20	4714	2	1222.4	(+0.3)	2.826	0.365	0.983	1	K.K#IFEYETQR.R
SW:EMD_HUMAN	R20	4668	2	1214.4	(+0.2)	2.417	0.331	0.942	1	K.KIFEYETQR.R
SW:EMD_HUMAN	R20	4574	2	1214.4	(+0.1)	2.388	0.297	0.918	1	K.KIFEYETQR.R
SW:EMD_HUMAN	R20	6366	2	2162.3	(+0.1)	3.548	0.575	1.000	1	R.LSPPSSSAASSYSFSDLNSTR.G

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:EMD_HUMAN	R20	6374	2	2174.3	(-1.0)	2.216	0.369	0.760	1	R.L*SPPSSSAASSYSFSDL*NSTR.G
SW:ENPL_HUMAN	R10	1366	2	1290.4	(+0.6)	2.838	0.475	0.990	2	K.DISTNYYASQK.K
SW:ENPL_HUMAN	R10	7753	2	1526.6	(-0.6)	3.750	0.400	0.987	3	K.EEASDYLELDTIK.N
SW:ENPL_HUMAN	R10	7673	2	1526.6	(-0.6)	3.208	0.272	0.945	3	K.EEASDYLELDTIK.N
SW:ENPL_HUMAN	R10	6763	2	1786.9	(+0.9)	4.959	0.457	0.999	3	R.EEEAIQLDGLNASQIR.E
SW:ENPL_HUMAN	R10	6865	2	1786.9	(+0.7)	4.363	0.456	1.000	3	R.EEEAIQLDGLNASQIR.E
SW:ENPL_HUMAN	R10	7019	3	1786.9	(+0.6)	3.843	0.411	0.999	3	R.EEEAIQLDGLNASQIR.E
SW:ENPL_HUMAN	R10	6735	2	1798.9	(+0.1)	3.818	0.497	1.000	3	R.EEEAIQL*DGL*NASQIR.E
SW:ENPL_HUMAN	R10	6945	3	1786.9	(+0.9)	3.809	0.324	0.996	3	R.EEEAIQLDGLNASQIR.E
SW:ENPL_HUMAN	R10	7635	2	1786.9	(-0.6)	2.878	0.348	0.954	3	R.EEEAIQLDGLNASQIR.E
SW:ENPL_HUMAN	R10	4635	2	1867.8	(-0.7)	2.923	0.352	0.957	2	K.EESDDEAAVEEEEEEEK.K
SW:ENPL_HUMAN	R10	1268	2	2221.2	(-0.8)	2.599	0.280	0.044	2	K.EESDDEAAVEEEEEEEKPK.T
SW:ENPL_HUMAN	R10	5491	2	1276.4	(+0.7)	3.309	0.465	1.000	8	R.ELISNASDALDK.I
SW:ENPL_HUMAN	R10	5947	2	1276.4	(+0.9)	2.366	0.334	0.941	8	R.ELISNASDALDK.I
SW:ENPL_HUMAN	R11	5206	2	1276.4	(-0.0)	2.315	0.409	0.954	8	R.ELISNASDALDK.I
SW:ENPL_HUMAN	R13	5479	2	1276.4	(-0.5)	2.654	0.420	0.973	8	R.ELISNASDALDK.I
SW:ENPL_HUMAN	R04	6558	3	2261.4	(+0.6)	3.880	0.533	1.000	2	R.FQSSHPTDITSLDQYVER.M
SW:ENPL_HUMAN	R05	6678	3	2261.4	(+0.7)	3.980	0.447	1.000	2	R.FQSSHPTDITSLDQYVER.M
SW:ENPL_HUMAN	R09	6318	3	2261.4	(+0.7)	5.419	0.462	0.968	2	R.FQSSHPTDITSLDQYVER.M
SW:ENPL_HUMAN	R10	7697	3	2261.4	(+0.6)	5.045	0.537	1.000	2	R.FQSSHPTDITSL*DQYVER.M
SW:ENPL_HUMAN	R10	7627	2	2261.4	(+0.2)	4.484	0.506	1.000	2	R.FQSSHPTDITSLDQYVER.M
SW:ENPL_HUMAN	R11	6520	3	2261.4	(+0.5)	5.292	0.444	1.000	2	R.FQSSHPTDITSLDQYVER.M
SW:ENPL_HUMAN	R10	5789	2	1016.1	(+0.5)	2.395	0.276	0.929	2	R.GLFDEYGSK.K
SW:ENPL_HUMAN	R10	5887	2	1030.1	(+0.5)	2.265	0.542	0.987	2	R.GL*FDEYGSK#.K
SW:ENPL_HUMAN	R10	5807	2	1030.1	(+0.4)	2.233	0.507	0.983	2	R.GL*FDEYGSK#.K
SW:ENPL_HUMAN	R09	5980	2	1486.6	(+0.5)	4.453	0.441	0.999	2	K.GVVDSDDLPLNVS.R.E
SW:ENPL_HUMAN	R10	6487	2	1486.6	(+0.2)	3.216	0.407	0.980	2	K.GVVDSDDLPLNVS.R.E
SW:ENPL_HUMAN	R10	6491	2	1498.6	(-0.2)	3.156	0.150	0.803	2	K.GVVDSDDL*PL*NVS.R.E
SW:ENPL_HUMAN	R11	6260	2	1486.6	(+0.4)	4.640	0.502	1.000	2	K.GVVDSDDLPLNVS.R.E
SW:ENPL_HUMAN	R10	6343	2	1516.7	(-0.9)	3.815	0.510	0.999	2	K.IADDKYNDTFWK.E
SW:ENPL_HUMAN	R10	6347	2	1532.7	(-0.3)	3.420	0.348	0.405	2	K.IADDK#YNDTFWK#.E
SW:ENPL_HUMAN	R10	1508	2	1279.4	(-0.3)	3.067	0.241	0.929	2	R.KEAESSPFVER.L
SW:ENPL_HUMAN	R10	1506	2	1287.4	(-0.9)	2.230	0.256	0.554	2	R.K#EAESSPFVER.L
SW:ENPL_HUMAN	R10	1862	2	1005.2	(+0.6)	2.338	0.308	0.913	2	K.KTFEINPR.H
SW:ENPL_HUMAN	R10	8879	2	2008.3	(+0.7)	5.596	0.520	1.000	3	K.KYSQFINFPIYVWSSK.T
SW:ENPL_HUMAN	R10	8885	2	2024.3	(-0.6)	4.361	0.385	1.000	3	K.K#YSQFINFPIYVWSSK#.T
SW:ENPL_HUMAN	R10	8867	3	2024.3	(+0.7)	4.259	0.205	0.976	3	K.K#YSQFINFPIYVWSSK#.T
SW:ENPL_HUMAN	R10	1350	2	1146.2	(+0.9)	2.764	0.322	0.969	2	K.L*GVIEDHSNR.T
SW:ENPL_HUMAN	R10	1348	2	1140.2	(-0.2)	2.627	0.291	0.924	2	K.LGVIEDHSNR.T
SW:ENPL_HUMAN	R10	7399	2	964.2	(-0.9)	2.640	0.161	0.620	3	K.LIINSLYK.N
SW:ENPL_HUMAN	R10	7385	2	984.2	(+0.1)	2.516	0.347	0.952	3	K.L*IINSL*YK#.N
SW:ENPL_HUMAN	R10	12435	3	2047.3	(+0.9)	5.105	0.395	0.977	3	R.LISLTDENALSGNEELTVK.I
SW:ENPL_HUMAN	R10	11449	3	2047.3	(+0.7)	4.988	0.429	0.718	3	R.LISLTDENALSGNEELTVK.I
SW:ENPL_HUMAN	R10	12851	3	2079.3	(+0.9)	4.625	0.448	1.000	3	R.L*ISL*TDENAL*SGNEEL*TVK#.I
SW:ENPL_HUMAN	R10	13245	3	2047.3	(+0.7)	4.617	0.485	0.990	3	R.LISLTDENALSGNEELTVK.I
SW:ENPL_HUMAN	R10	13605	3	2047.3	(+0.8)	4.546	0.440	0.999	3	R.LISLTDENALSGNEELTVK.I
SW:ENPL_HUMAN	R10	11597	3	2047.3	(+0.7)	4.506	0.412	0.998	3	R.LISLTDENALSGNEELTVK.I
SW:ENPL_HUMAN	R10	12073	3	2047.3	(-0.7)	4.489	0.428	0.964	3	R.LISLTDENALSGNEELTVK.I
SW:ENPL_HUMAN	R10	12579	3	2047.3	(-0.0)	4.432	0.420	0.999	3	R.LISLTDENALSGNEELTVK.I
SW:ENPL_HUMAN	R10	13673	3	2047.3	(+0.6)	4.430	0.456	0.995	3	R.LISLTDENALSGNEELTVK.I
SW:ENPL_HUMAN	R10	11121	3	2047.3	(+0.5)	4.370	0.407	0.943	3	R.LISLTDENALSGNEELTVK.I
SW:ENPL_HUMAN	R10	13537	3	2047.3	(-0.2)	4.334	0.449	0.977	3	R.LISLTDENALSGNEELTVK.I
SW:ENPL_HUMAN	R10	13741	3	2047.3	(+0.1)	4.033	0.360	0.993	3	R.LISLTDENALSGNEELTVK.I
SW:ENPL_HUMAN	R10	12209	3	2079.3	(+0.8)	4.022	0.374	0.999	3	R.L*ISL*TDENAL*SGNEEL*TVK#.I
SW:ENPL_HUMAN	R10	10645	3	2047.3	(+0.8)	3.977	0.369	0.998	3	R.LISLTDENALSGNEELTVK.I
SW:ENPL_HUMAN	R10	13467	3	2047.3	(+0.3)	3.964	0.375	0.985	3	R.LISLTDENALSGNEELTVK.I
SW:ENPL_HUMAN	R10	11893	3	2079.3	(-0.5)	3.953	0.312	0.988	3	R.L*ISL*TDENAL*SGNEEL*TVK#.I
SW:ENPL_HUMAN	R10	13807	3	2047.3	(+0.3)	3.907	0.413	0.995	3	R.LISLTDENALSGNEELTVK.I
SW:ENPL_HUMAN	R10	13305	3	2079.3	(+0.6)	3.885	0.387	0.998	3	R.L*ISL*TDENAL*SGNEEL*TVK#.I
SW:ENPL_HUMAN	R10	11491	3	2079.3	(+0.5)	3.881	0.449	1.000	3	R.L*ISL*TDENAL*SGNEEL*TVK#.I
SW:ENPL_HUMAN	R10	12453	3	2079.3	(+0.3)	3.880	0.154	0.861	3	R.L*ISL*TDENAL*SGNEEL*TVK#.I
SW:ENPL_HUMAN	R10	11043	3	2047.3	(+1.0)	3.855	0.415	0.995	3	R.LISLTDENALSGNEELTVK.I
SW:ENPL_HUMAN	R10	11967	3	2079.3	(+0.8)	3.833	0.414	0.999	3	R.L*ISL*TDENAL*SGNEEL*TVK#.I
SW:ENPL_HUMAN	R10	12245	2	2047.3	(+1.0)	3.543	0.473	1.000	3	R.LISLTDENALSGNEELTVK.I
SW:ENPL_HUMAN	R10	11367	2	2047.3	(+1.0)	3.534	0.469	1.000	3	R.LISLTDENALSGNEELTVK.I

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ENPL_HUMAN	R10	13399	2	2047.3	(+1.0)	3.184	0.471	0.990	3	R.LISLTDENALSGNEELTVK.I
SW:ENPL_HUMAN	R10	12675	2	2047.3	(+0.9)	2.925	0.463	0.987	3	R.LISLTDENALSGNEELTVK.I
SW:ENPL_HUMAN	R10	11999	2	2047.3	(+0.0)	2.810	0.398	0.967	3	R.LISLTDENALSGNEELTVK.I
SW:ENPL_HUMAN	R10	11207	2	2047.3	(-0.8)	2.452	0.429	0.890	3	R.LISLTDENALSGNEELTVK.I
SW:ENPL_HUMAN	R10	11283	2	2047.3	(-0.6)	2.346	0.295	0.844	3	R.LISLTDENALSGNEELTVK.I
SW:ENPL_HUMAN	R10	12823	2	2047.3	(+0.4)	2.314	0.324	0.911	3	R.LISLTDENALSGNEELTVK.I
SW:ENPL_HUMAN	R10	11059	2	2047.3	(-0.4)	2.276	0.394	0.932	3	R.LISLTDENALSGNEELTVK.I
SW:ENPL_HUMAN	R10	11133	2	2047.3	(-0.8)	2.243	0.327	0.676	3	R.LISLTDENALSGNEELTVK.I
SW:ENPL_HUMAN	R11	13492	3	2047.3	(+1.0)	3.980	0.441	0.999	3	R.LISLTDENALSGNEELTVK.I
SW:ENPL_HUMAN	R12	12618	3	2047.3	(+0.9)	3.804	0.164	0.860	3	R.LISLTDENALSGNEELTVK.I
SW:ENPL_HUMAN	R08	6309	2	1086.2	(+0.4)	2.499	0.276	0.932	2	R.LSLNIDPDAK.V
SW:ENPL_HUMAN	R10	6219	2	1086.2	(+0.5)	3.223	0.304	0.979	2	R.LSLNIDPDAK.V
SW:ENPL_HUMAN	R10	6495	2	1526.7	(+0.4)	4.521	0.496	1.000	3	K.NL*L*HVTDTGVGMTR.E
SW:ENPL_HUMAN	R10	6519	2	1526.7	(-0.9)	3.697	0.391	0.954	3	K.NL*L*HVTDTGVGMTR.E
SW:ENPL_HUMAN	R10	6493	2	1514.7	(-0.2)	3.064	0.480	0.986	3	K.NLLHVTDTGVGMTR.E
SW:ENPL_HUMAN	R10	5975	2	1542.7	(-0.4)	2.844	0.390	0.968	3	K.NL*L*HVTDTGVGM@TR.E
SW:ENPL_HUMAN	R10	4993	2	994.1	(+0.9)	3.473	0.306	0.917	2	R.SGYLLPDTK.A
SW:ENPL_HUMAN	R10	4753	2	994.1	(-0.9)	2.792	0.337	0.909	2	R.SGYLLPDTK.A
SW:ENPL_HUMAN	R10	4823	2	1014.1	(+0.2)	2.346	0.297	0.885	2	R.SGYL*L*PDTK#.A
SW:ENPL_HUMAN	R10	4831	2	994.1	(+0.8)	2.213	0.265	0.888	2	R.SGYLLPDTK.A
SW:ENPL_HUMAN	R11	4432	2	994.1	(+0.7)	2.423	0.131	0.718	2	R.SGYLLPDTK.A
SW:ENPL_HUMAN	R17	5444	2	994.1	(+0.9)	2.872	0.245	0.956	2	R.SGYLLPDTK.A
SW:ENPL_HUMAN	R10	1688	2	1730.8	(-0.6)	2.620	0.271	0.834	3	K.TETVEEPMEEEEAAK#.E
SW:ENPL_HUMAN	R10	1674	2	1722.8	(-0.6)	2.243	0.200	0.519	3	K.TETVEEPMEEEEAAK.E
SW:ENPL_HUMAN	R10	6335	2	1636.9	(-0.5)	4.019	0.464	1.000	1	R.VFITDDFHDM@M@PK#.Y
SW:ENPL_HUMAN	R10	7749	2	1620.9	(+0.1)	3.986	0.529*	0.573	1	R.VFITDDFHDM@PK#.Y
SW:ENPL_HUMAN	R10	6063	2	974.1	(+0.2)	2.251	0.127	0.571	2	K.YNDTFWK.E
SW:ENPL_HUMAN	R04	8778	2	1880.2	(-0.2)	3.000	0.309	0.943	3	K.YSQFINFPIYVWSSK.T
SW:ENPL_HUMAN	R10	9159	2	1888.2	(+0.2)	3.709	0.458	1.000	3	K.YSQFINFPIYVWSSK#.T
SW:ENPL_HUMAN	R11	8846	2	1888.2	(-0.1)	3.623	0.508	1.000	3	K.YSQFINFPIYVWSSK#.T
SW:ENPL_HUMAN	R12	9024	2	1880.2	(+0.6)	4.377	0.492	1.000	3	K.YSQFINFPIYVWSSK.T
SW:ENPL_HUMAN	R17	6268	2	1086.2	(+0.7)	2.653	0.238	0.923	2	R.LSLNIDPDAK.V
SW:ER25_HUMAN	R01	2288	2	1650.7	(-0.4)	3.454	0.385	0.981		R.IFGTDSQYNAYNEK.R
SW:ER25_HUMAN	R02	5164	2	1658.7	(-0.4)	4.522	0.478	1.000		R.IFGTDSQYNAYNEK#.R
SW:ER25_HUMAN	R02	5162	2	1650.7	(-0.4)	4.187	0.525	0.985		R.IFGTDSQYNAYNEK.R
SW:ER25_HUMAN	R03	4925	2	1658.7	(-0.5)	4.259	0.466	1.000		R.IFGTDSQYNAYNEK#.R
SW:ER25_HUMAN	R01	7081	2	1546.7	(+0.3)	2.779	0.268	0.921		K.NAWNYML*NNYTK#.F
SW:ER25_HUMAN	R03	4921	2	1650.7	(-0.6)	3.689	0.486	0.998		R.IFGTDSQYNAYNEK.R
SW:ER29_HUMAN	R21	6100	2	1617.7	(+1.0)	4.576	0.380	1.000		R.DGDFENPVPTGAVK#.V
SW:ER29_HUMAN	R20	7394	2	1325.5	(+0.7)	2.629	0.352	0.966		K.GALPLDVTTFYK.V
SW:ER29_HUMAN	R21	6306	2	1709.9	(-0.5)	3.830	0.540	1.000		K.ILDQGEDFPASEMTR.I
SW:ER29_HUMAN	R21	6086	2	1609.7	(-0.9)	2.855	0.238	0.682		R.DGDFENPVPTGAVK.V
SW:ER53_HUMAN	R15	2120	2	979.1	(+0.3)	2.680	0.228	0.941	2	R.DIDNL*VQR.N
SW:ER53_HUMAN	R15	2036	2	973.1	(+0.6)	2.657	0.156	0.876	2	R.DIDNLVQR.N
SW:ER53_HUMAN	R15	7139	2	2182.3	(+0.6)	5.449	0.581	1.000	2	K.GHPDLQGQPAEEIFESVGDR.E
SW:ER53_HUMAN	R15	7203	3	2188.3	(+0.9)	4.424	0.518	1.000	2	K.GHPDL*QGQPAEEIFESVGDR.E
SW:ER53_HUMAN	R15	7307	3	2959.3	(+0.3)	6.591	0.554	1.000	2	K.GPHLVQSDGTVPFWAHAGNAIPSSDQIR.V
SW:ER53_HUMAN	R15	7115	3	2688.0	(+0.8)	5.233	0.385	0.999	2	R.L*VSGMQHPGSAGGVYETTQHFIDIK#.E
SW:ER53_HUMAN	R15	7113	3	2674.0	(+0.5)	4.438	0.400	0.999	2	R.LVSGMQHPGSAGGVYETTQHFIDIK.E
SW:ER53_HUMAN	R15	6913	3	2704.0	(+0.3)	4.195	0.407	0.999	2	R.L*VSGM@QHPGSAGGVYETTQHFIDIK#.E
SW:ER53_HUMAN	R15	6265	2	1261.4	(+0.8)	2.426	0.207	0.847	2	R.QLDMILDEQR.R
SW:ER53_HUMAN	R15	5809	2	1426.6	(+0.0)	2.468	0.133	0.325	2	R.RYVSSL*TEEISK#.R
SW:ER53_HUMAN	R15	6563	2	1871.0	(+0.8)	4.912	0.514	1.000	2	K.YQEFEHFQQLDK.K
SW:ER53_HUMAN	R15	5557	2	1256.4	(+0.2)	2.722	0.485	0.985	2	R.YVSSLTEEISK.R
SW:ER53_HUMAN	R16	5368	2	1256.4	(+0.7)	2.620	0.341	0.949	2	R.YVSSLTEEISK.R
SW:ERG7_HUMAN	R11	6872	2	1609.8	(+0.3)	2.919	0.532	1.000	2	R.EQTGLEAYALGLDTK.N
SW:ERG7_HUMAN	R12	6876	2	1635.8	(-0.9)	2.891	0.330	0.814	2	R.EQTGL*EAYAL*GL*DTK#.N
SW:ERG7_HUMAN	R11	6542	2	1399.6	(+0.9)	3.842	0.424	1.000	2	R.LSAAEDPLVQSLR.Q
SW:ERG7_HUMAN	R12	5600	2	914.1	(+0.6)	2.455	0.108	0.664	2	K.AVLLLQEK.C
SW:ES1_HUMAN	R22	2224	2	1555.6	(-0.2)	3.226	0.414	0.980	4	R.GVEVTVGHEQEEGGK.W
SW:ES1_HUMAN	R21	7642	3	2463.7	(-0.1)	4.220	0.183	0.831	4	K.ITDL*ANL*SAANHDAAIFFGGFGAAK#.N

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ES1_HUMAN	R21	7654	3	2443.7	(+1.0)	3.713	0.275	0.975	4	K.ITDLANLSAANHDAIFPGGFGAAK.N
SW:ES1_HUMAN	R22	6438	2	1215.4	(-0.5)	2.405	0.146	0.529	4	K.WPYAGTAEAIK#.A
SW:ETFA_HUMAN	R19	10508	2	2209.5	(+0.4)	6.252	0.703	1.000		K.DPEAIFQVADYGVADLFK.V
SW:ETFA_HUMAN	R19	10506	3	2223.5	(+0.9)	5.535	0.589	1.000		K.DPEAIFQVADYGVADL*FK#.V
SW:ETFA_HUMAN	R19	10500	3	2209.5	(+0.7)	4.679	0.534	0.999		K.DPEAIFQVADYGVADLFK.V
SW:ETFA_HUMAN	R19	10512	2	2223.5	(-0.4)	4.464	0.506	1.000		K.DPEAIFQVADYGVADL*FK#.V
SW:ETFA_HUMAN	R19	1886	2	1172.4	(+0.3)	2.685	0.434	0.986		K.VLVAQHVDVYK.G
SW:ETFB_HUMAN	R21	5858	2	1103.2	(+0.6)	2.407	0.250	0.896	1	R.EIDGGLETLR.L
SW:ETFB_HUMAN	R21	6394	2	1067.3	(+0.4)	2.641	0.319*	0.367	1	K.L*PAVVVTADL*R.L
SW:ETFB_HUMAN	R21	6024	2	1340.5	(+0.9)	2.516	0.355	0.961		K.LSVISVEDPPQR.T
SW:ETFB_HUMAN	R21	5640	2	866.0	(+0.2)	2.399	0.155	0.734		R.L*GPL*QVAR.V
SW:FAC1_HUMAN	R01	9911	3	1929.2	(+0.4)	3.800	0.440	1.000	2	R.IVL*FDTL*L*EEYSVL*NK#.D
SW:FAC1_HUMAN	R02	9032	3	1929.2	(+0.1)	3.718	0.315	0.988	2	R.IVL*FDTL*L*EEYSVL*NK#.D
SW:FAC1_HUMAN	R03	9313	3	1929.2	(-0.1)	3.814	0.163	0.791	2	R.IVL*FDTL*L*EEYSVL*NK#.D
SW:FAC1_HUMAN	R02	6426	2	1338.5	(+0.4)	3.244	0.310	0.970	3	R.RFEFQADAFAK#.K
SW:FAC1_HUMAN	R03	6315	2	1330.5	(+0.2)	2.622	0.357	0.957	3	R.RFEFQADAFAK.K
SW:FAC1_HUMAN	R01	6511	3	2291.5	(+0.3)	5.784	0.437	1.000	2	K.TTTHVPEL*GQIM@DSETFEK#.S
SW:FAC1_HUMAN	R01	7361	3	2275.5	(+0.0)	3.763	0.382	0.996	2	K.TTTHVPEL*GQIMDSETFEK#.S
SW:FAC1_HUMAN	R02	6266	3	2291.5	(-0.6)	4.283	0.321	0.993	2	K.TTTHVPEL*GQIM@DSETFEK#.S
SW:FAC1_HUMAN	R03	6165	3	2291.5	(+0.1)	5.097	0.472	1.000	2	K.TTTHVPEL*GQIM@DSETFEK#.S
SW:FAC1_HUMAN	R03	7059	3	2261.5	(+0.9)	3.955	0.504	0.995	2	K.TTTHVPEL*GQIMDSETFEK.S
SW:FAC1_HUMAN	R03	7057	3	2275.5	(+0.3)	3.769	0.409	0.996	2	K.TTTHVPEL*GQIMDSETFEK#.S
SW:FBRL_HUMAN	R18	1214	2	961.1	(+1.0)	2.481	0.165	0.080	6	R.GKEDALVTK.N
SW:FBRL_HUMAN	R19	7392	2	1901.2	(-0.5)	2.713	0.231	0.068	6	K.L*AAAIL*GGVDQIHK#PGAK#.V
SW:FBRL_HUMAN	R19	6062	3	2445.7	(-0.4)	4.254	0.329	0.948	5	K.M@QQENM@K#PQEQL*TL*EPYER.D
SW:FBRL_HUMAN	R18	4945	2	1519.6	(-0.1)	2.326	0.137	0.017	5	R.VSISEGDDK#IEYR.A
SW:FBRL_HUMAN	R18	4947	2	1511.6	(-0.0)	2.266	0.355	0.171	5	R.VSISEGDDKIEYR.A
SW:FBRL_HUMAN	R19	5100	2	1511.6	(-0.3)	2.393	0.284	0.108	5	R.VSISEGDDKIEYR.A
SW:FBRL_HUMAN	R19	5098	2	1519.6	(-0.2)	2.323	0.196	0.035	5	R.VSISEGDDK#IEYR.A
SW:FDFT_HUMAN	R17	1446	2	1187.2	(+0.7)	3.274	0.414	0.991	4	R.DYL*EDQQGGR.E
SW:FDFT_HUMAN	R17	1448	2	1181.2	(-0.3)	2.771	0.416	0.979	4	R.DYLEDQQGGR.E
SW:FDFT_HUMAN	R16	7314	2	2054.2	(+0.9)	4.746	0.578	0.999	4	R.L*FSASEFEDPL*VGEDTER.A
SW:FDFT_HUMAN	R16	7310	2	2042.2	(+0.6)	2.889	0.455	0.985	4	R.LFSASEFEDPLVGEDTER.A
SW:FDFT_HUMAN	R17	7788	2	2042.2	(+0.7)	4.182	0.533	1.000	4	R.LFSASEFEDPLVGEDTER.A
SW:FDFT_HUMAN	R17	7786	2	2054.2	(-0.7)	3.833	0.428	0.999	4	R.L*FSASEFEDPL*VGEDTER.A
SW:FDFT_HUMAN	R16	7192	2	1226.5	(+0.5)	2.410	0.465	0.978	4	R.MGIGMAEFL*DK#.H
SW:FDFT_HUMAN	R17	6060	2	1258.5	(-0.3)	2.852	0.286	0.924	4	R.M@GIGM@AEFL*DK#.H
SW:FDFT_HUMAN	R17	6598	2	1242.5	(-0.5)	2.345	0.187	0.624	4	R.MGIGM@AEFL*DK#.H
SW:FDFT_HUMAN	R16	8096	2	1706.9	(+0.1)	3.299	0.417	0.983	4	R.QVL*EDFPTISL*EFR.N
SW:FDFT_HUMAN	R17	8538	2	1694.9	(+0.1)	3.671	0.486	1.000	4	R.QVLEDFPTISLEFR.N
SW:FDFT_HUMAN	R17	8528	2	1706.9	(-0.1)	2.463	0.352	0.927	4	R.QVL*EDFPTISL*EFR.N
SW:FDFT_HUMAN	R16	8580	2	1514.7	(+0.7)	3.847	0.533	1.000	4	R.SFAAVIQAL*DGEMR.N
SW:FDFT_HUMAN	R16	8576	2	1508.7	(+0.6)	3.592	0.517	1.000	4	R.SFAAVIQALDGEMR.N
SW:FDFT_HUMAN	R16	7840	2	1530.7	(+0.8)	3.250	0.259	0.955	4	R.SFAAVIQAL*DGEM@R.N
SW:FDFT_HUMAN	R17	8940	2	1508.7	(+0.4)	3.298	0.348	0.980	4	R.SFAAVIQALDGEMR.N
SW:FDFT_HUMAN	R17	8938	2	1514.7	(+0.2)	3.286	0.504	1.000	4	R.SFAAVIQAL*DGEMR.N
SW:FDFT_HUMAN	R18	9067	2	1514.7	(+0.4)	2.509	0.432	0.976	4	R.SFAAVIQAL*DGEMR.N
SW:FDFT_HUMAN	R17	8322	3	2188.5	(+0.4)	3.929	0.385	0.997	4	K.VPL*L*HNFHSFL*YQPDWR.F
SW:FDFT_HUMAN	R26	9204	2	1508.7	(+0.3)	2.296	0.355	0.937	4	R.SFAAVIQALDGEMR.N
SW:FK11_HUMAN	R23	6210	2	1184.4	(-0.3)	2.303	0.211	0.671		R.AIIPSHL*AYGK#.R
SW:FK11_HUMAN	R22	6794	2	1132.3	(-0.2)	2.700	0.242	0.876	2	R.DPL*VIEL*GQK#.Q
SW:FK11_HUMAN	R23	6730	2	1112.3	(-0.7)	3.417	0.411	1.000	2	R.DPLVIELGQK.Q
SW:FK11_HUMAN	R23	6700	2	1132.3	(-0.5)	2.485	0.198	0.746	2	R.DPL*VIEL*GQK#.Q
SW:FK11_HUMAN	R23	4960	2	919.1	(+1.0)	2.236	0.163	0.747	2	R.IIDTSLTR.D
SW:FKB2_HUMAN	R25	9362	2	1586.9	(-0.3)	3.713	0.503	1.000	1	K.IPGGATLVFEVLLK.I
SW:FKB2_HUMAN	R25	7368	2	1461.7	(-0.3)	3.393	0.241	0.942	1	R.KLVIPSELGYGER.G
SW:FKB2_HUMAN	R26	9206	2	1586.9	(-0.2)	3.754	0.450	0.999	1	K.IPGGATLVFEVLLK.I
SW:FKB7_HUMAN	R21	8168	2	1246.5	(+0.5)	2.887	0.461	0.990	4	K.WFVLGVGVQVIK.G

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:FKB7_HUMAN	R21	6360	2	1120.3	(+0.1)	2.237	0.121	0.480	4	K.AEINLYLQR.E
SW:FKB8_HUMAN	R16	6624	2	1732.9	(+0.7)	4.263	0.532	1.000	2	K.TAVDGPDLMLTGQER.V
SW:FKB8_HUMAN	R16	6628	2	1744.9	(-0.2)	2.890	0.363	0.960	2	K.TAVDGPDL*EML*TGQER.V
SW:FKB8_HUMAN	R16	10546	2	3148.6	(-0.9)	2.872	0.448	0.938	2	R.EFLAAMEPEPAPAPAPEEWLDILGNLLR.K
SW:FUMH_HUMAN	R16	1420	2	1491.6	(+0.6)	4.057	0.370	0.990	1	R.AAAEVNQDYGLDPK.I
SW:FUMH_HUMAN	R16	634	2	897.9	(+0.8)	2.664	0.484	0.988	1	K.AADEVAEGK#.L
SW:FUMH_HUMAN	R16	6158	2	1205.4	(+1.0)	3.069	0.507	1.000	1	R.AIEMLGELGSK.I
SW:FUMH_HUMAN	R16	7792	3	3272.6	(+0.2)	6.060	0.630	0.994	1	K.LNDHFPLVWQGTGSGTQTNMNVNEVISNR.A
SW:FUMH_HUMAN	R16	7204	2	1519.8	(-0.1)	3.125	0.414	0.972	1	K.VAAL*TGL*PFVTAPNK#.F
SW:FUMH_HUMAN	R16	7370	2	2126.4	(-0.3)	2.280	0.194	0.581	1	R.SGLGELILPENEPGSSIMPGK.V
SW:G19P_HUMAN	R11	5482	2	1449.6	(-0.3)	3.840	0.556	1.000	2	K.AQQEQELAADAFK.E
SW:G19P_HUMAN	R11	5502	2	1463.6	(-0.1)	2.764	0.369	0.950	2	K.AQQEQEL*AADAFK#.E
SW:G19P_HUMAN	R12	5232	2	1463.6	(-0.8)	4.239	0.544	0.999	2	K.AQQEQEL*AADAFK#.E
SW:G19P_HUMAN	R12	5226	2	1449.6	(-0.1)	3.349	0.552	1.000	2	K.AQQEQELAADAFK.E
SW:G19P_HUMAN	R13	5661	2	1463.6	(-0.8)	4.253	0.538	0.999	2	K.AQQEQEL*AADAFK#.E
SW:G19P_HUMAN	R13	5653	2	1449.6	(-0.7)	4.063	0.539	1.000	2	K.AQQEQELAADAFK.E
SW:G19P_HUMAN	R14	5649	2	1449.6	(-0.6)	3.696	0.541	1.000	2	K.AQQEQELAADAFK.E
SW:G19P_HUMAN	R20	5738	2	1463.6	(-0.2)	2.885	0.424	0.971	2	K.AQQEQEL*AADAFK#.E
SW:G19P_HUMAN	R12	5362	2	1583.8	(+0.7)	3.453	0.385	0.609	1	K.ERESL*QQMAEVTR.E
SW:G19P_HUMAN	R11	5786	2	1292.4	(+0.2)	2.579	0.303	0.927	1	R.ESLQQMAEVTR.E
SW:G19P_HUMAN	R11	5792	2	1298.4	(+0.2)	2.375	0.296	0.892	1	R.ESL*QQMAEVTR.E
SW:G19P_HUMAN	R12	5494	2	1292.4	(+0.7)	3.066	0.346	0.980	1	R.ESLQQMAEVTR.E
SW:G19P_HUMAN	R14	5929	2	1292.4	(+0.8)	2.505	0.315	0.948	1	R.ESLQQMAEVTR.E
SW:G19P_HUMAN	R12	2306	2	1028.2	(+0.5)	2.350	0.178	0.746	2	K.K#L*IEL*QAGK#.K
SW:G19P_HUMAN	R12	7554	3	2169.4	(+0.6)	4.353	0.497	0.942	3	K.LGGSPTSLSGTWGSWIGPDHDK.F
SW:G19P_HUMAN	R12	7558	3	2189.4	(+0.2)	4.333	0.521	0.998	3	K.L*GGSPTSLS*GTWGSWIGPDHDK#.F
SW:G19P_HUMAN	R12	7582	2	2189.4	(+0.4)	3.313	0.382	0.979	3	K.L*GGSPTSLS*GTWGSWIGPDHDK#.F
SW:G19P_HUMAN	R12	7572	2	2169.4	(-0.8)	2.989	0.441	0.942	3	K.LGGSPTSLSGTWGSWIGPDHDK.F
SW:G19P_HUMAN	R11	5906	2	1159.3	(+0.8)	2.903	0.466	0.991	2	K.LWEEQLAAAK.A
SW:G19P_HUMAN	R12	5756	2	1159.3	(+0.5)	3.315	0.478	0.998	2	K.LWEEQLAAAK.A
SW:G19P_HUMAN	R12	5736	2	1179.3	(+0.1)	2.739	0.428	0.974	2	K.L*WEEQL*AAAK#.A
SW:G19P_HUMAN	R12	5656	2	1179.3	(-0.1)	2.464	0.429	0.965	2	K.L*WEEQL*AAAK#.A
SW:G19P_HUMAN	R13	6097	2	1179.3	(-0.0)	2.320	0.338	0.908	2	K.L*WEEQL*AAAK#.A
SW:G19P_HUMAN	R14	6067	2	1159.3	(+0.9)	2.912	0.451	0.990	2	K.LWEEQLAAAK.A
SW:G19P_HUMAN	R12	878	2	1031.1	(+0.8)	2.292	0.238	0.140	3	R.NK#FEEAER.S
SW:G19P_HUMAN	R11	6394	2	1220.4	(+0.7)	4.152	0.471	1.000	2	K.SLEDQVEMLR.T
SW:G19P_HUMAN	R11	6392	2	1232.4	(-0.4)	2.508	0.222	0.843	2	K.SL*EDQVEMLR.T
SW:G19P_HUMAN	R12	6262	2	1220.4	(+0.8)	3.186	0.443	1.000	2	K.SLEDQVEMLR.T
SW:G19P_HUMAN	R12	5900	2	1248.4	(-0.3)	2.790	0.347	0.966	2	K.SL*EDQVEM@L*R.T
SW:G19P_HUMAN	R12	6244	2	1232.4	(+0.2)	2.349	0.326	0.924	2	K.SL*EDQVEMLR.T
SW:G19P_HUMAN	R13	6647	2	1220.4	(-0.1)	2.930	0.339	0.969	2	K.SLEDQVEMLR.T
SW:G19P_HUMAN	R20	6556	2	1220.4	(+0.3)	2.641	0.271	0.943	2	K.SLEDQVEMLR.T
SW:G252_HUMAN	R22	8176	2	1111.3	(+0.4)	2.809	0.314	0.970	4	K.FSL*FAGGML*R.V
SW:G252_HUMAN	R23	7558	2	1127.3	(+0.9)	2.552	0.397	0.977	4	K.FSL*FAGGM@L*R.V
SW:G252_HUMAN	R22	5738	2	859.0	(-0.4)	2.581	0.272*	0.367	4	K.LSELQLR.V
SW:G252_HUMAN	R22	5938	3	1342.5	(-0.5)	3.782	0.147*	0.115	4	R.QLVEQVEIQK.E
SW:G252_HUMAN	R22	5916	2	1356.5	(-0.8)	2.699	0.144	0.395	4	R.QL*VEQVEIQK#.E
SW:G252_HUMAN	R23	5828	2	1356.5	(-0.8)	2.663	0.172	0.441	4	R.QL*VEQVEIQK#.E
SW:G252_HUMAN	R23	5996	2	1102.3	(+0.8)	2.481	0.195	0.111	4	K.DKSELQLR.V
SW:G3P1_HUMAN	R18	6135	2	1202.5	(+0.9)	3.570	0.538	1.000	5	R.VVDLMAHMASK.E
SW:G3P1_HUMAN	R18	2244	2	1232.5	(+0.6)	2.921	0.412*	0.398	5	R.VVDL*MAHM@ASK#.E
SW:G3P1_HUMAN	R18	6129	2	1216.5	(-0.3)	2.878	0.346	0.955	5	R.VVDL*MAHMASK#.E
SW:G3P1_HUMAN	R18	1410	2	1248.5	(+0.4)	2.409	0.193	0.747	5	R.VVDL*M@AHM@ASK#.E
SW:G3P1_HUMAN	R18	1502	2	1377.6	(+0.3)	2.802	0.351	0.411	4	R.VVDL*M@AHM@ASK#.-
SW:G3P2_HUMAN	R19	882	2	910.0	(+0.5)	2.260	0.222*	0.178	3	K.AGAHLQGGAK.R
SW:G3P2_HUMAN	R01	6255	2	1412.6	(+0.7)	3.208	0.224	0.901	3	R.GALQNIIPASTGAAK.A
SW:G3P2_HUMAN	R18	6373	2	1426.6	(-0.6)	2.733	0.291	0.881	3	R.GAL*QNIIPASTGAAK#.A
SW:G3P2_HUMAN	R18	7453	2	1770.9	(+0.1)	2.708	0.473	0.981	3	K.L*ISWYDNEFGYSNR.V
SW:G3P2_HUMAN	R18	7437	2	1764.9	(+0.0)	2.529	0.573	1.000	3	K.LISWYDNEFGYSNR.V
SW:G3P2_HUMAN	R19	7644	2	1770.9	(+0.2)	3.829	0.621	1.000	3	K.L*ISWYDNEFGYSNR.V

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:G3P2_HUMAN	R18	8095	2	1614.9	(+0.3)	2.853	0.552	1.000	3	K.LVINGNPITIFQER.D
SW:G3P2_HUMAN	R25	8518	2	1620.9	(+0.8)	3.501	0.498	1.000	3	K.L*VINGNPITIFQER.D
SW:G3P2_HUMAN	R18	7509	3	2378.8	(+0.4)	6.445	0.534	0.986	4	K.RVIISAPSADAMPFVMGVNHEK#.Y
SW:G3P2_HUMAN	R01	9763	3	2611.0	(+0.3)	5.152	0.571	1.000	3	K.VIHDNFGIVEGL*MTTVHAITATQK#.T
SW:G3P2_HUMAN	R18	9935	3	2611.0	(+0.8)	4.794	0.566	0.997	3	K.VIHDNFGIVEGL*MTTVHAITATQK#.T
SW:G3P2_HUMAN	R18	9991	3	2597.0	(+0.4)	3.894	0.328	0.980	3	K.VIHDNFGIVEGLMTTVHAITATQK.T
SW:G3P2_HUMAN	R18	8981	3	2627.0	(+0.6)	3.856	0.492*	0.088	3	K.VIHDNFGIVEGL*M@TTVHAITATQK#.T
SW:G3P2_HUMAN	R19	9912	3	2611.0	(+0.5)	6.924	0.563	0.993	3	K.VIHDNFGIVEGL*MTTVHAITATQK#.T
SW:G3P2_HUMAN	R27	7485	2	1620.9	(+0.7)	3.880	0.542	1.000	3	K.L*VINGNPITIFQER.D
SW:GCS1_HUMAN	R10	7693	2	1542.8	(-0.2)	2.264	0.306	0.790	2	R.FTLLPPTSPGDTAPK.Y
SW:GCS1_HUMAN	R10	8907	3	3095.5	(+0.6)	4.177	0.464	1.000	3	R.GAVWLVNPNYALGALHGHYGHLEGPHQAR.A
SW:GCS1_HUMAN	R10	8587	2	1844.1	(-0.5)	3.604	0.326	0.972	3	R.GFL*WDEGFHQL*VVQR.W
SW:GCS1_HUMAN	R10	7983	2	1887.1	(-0.2)	3.937	0.524	0.998	3	R.GPSGQGGQGFLLIQVTLK.I
SW:GCS1_HUMAN	R10	7979	2	1907.1	(-0.6)	3.509	0.414	0.979	3	R.GPSGQGGQGFLL*IQVTL*K#.I
SW:GCS1_HUMAN	R10	7553	2	1392.6	(+0.7)	2.851	0.380	0.464	3	R.GRDPALPTLLNPK.T
SW:GCS1_HUMAN	R10	8467	2	1925.1	(-1.0)	3.165	0.408	0.937	3	R.L*AGSL*L*EQAL*ESHAEGFR.E
SW:GCS1_HUMAN	R10	8803	2	1307.5	(-0.4)	2.333	0.140	0.505	3	R.L*GPL*L*DIL*ADSR.H
SW:GCS1_HUMAN	R10	2458	2	1274.4	(-0.1)	2.986	0.406	0.976	3	R.SLAASSSFYQGR.N
SW:GCS1_HUMAN	R10	2474	2	1280.4	(-0.0)	2.602	0.331	0.940	3	R.SL*AASSSFYQGR.N
SW:GCS1_HUMAN	R10	2390	2	1280.4	(-0.8)	2.495	0.337	0.821	3	R.SL*AASSSFYQGR.N
SW:GCS1_HUMAN	R10	2378	2	1274.4	(-0.3)	2.489	0.315	0.917	3	R.SLAASSSFYQGR.N
SW:GCS1_HUMAN	R10	5937	2	1234.4	(+0.5)	2.425	0.460	0.983	3	K.TLPSGLDDYPR.A
SW:GCS1_HUMAN	R10	9289	2	1924.3	(+0.5)	2.887	0.407	0.980	3	K.VDPALFPPVPLFTAVPSR.S
SW:GCS1_HUMAN	R10	6301	2	1091.3	(-0.4)	2.308	0.383	0.957	3	R.VPPEFL*VQR.A
SW:GCS1_HUMAN	R11	9074	3	1979.2	(+0.6)	4.271	0.337	0.998	3	R.EALGHWLGLLNADGWIGR.E
SW:GLG1_HUMAN	R06	6114	2	1610.8	(-0.1)	2.483	0.157	0.021	1	R.FCENQAGEGRVYK#.C
SW:GLG1_HUMAN	R07	6321	2	1321.5	(+1.0)	3.623	0.395	1.000	1	R.IIIQESALDYR.L
SW:GLG1_HUMAN	R07	8159	2	1300.5	(+0.5)	3.381	0.371	0.989	1	R.L*L*EL*QYFISR.D
SW:GLG1_HUMAN	R07	5999	2	1370.5	(-0.3)	3.104	0.379	0.979	1	R.VEEL*EMTEDIR.L
SW:GLG1_HUMAN	R07	6325	2	1327.5	(+0.6)	3.024	0.407	0.984	1	R.IIIQESAL*DYR.L
SW:GLYM_HUMAN	R16	7476	2	1745.1	(-0.5)	3.531	0.454	1.000	4	K.AHL*L*ADMAHISGL*VAAK#.V
SW:GLYM_HUMAN	R16	7474	2	1719.1	(-0.0)	3.355	0.575	1.000	4	K.AHLLADMAHISGLVAAK.V
SW:GLYM_HUMAN	R15	1868	2	1018.2	(+0.5)	2.228	0.253	0.877	4	R.AM@ADAL*L*ER.G
SW:GLYM_HUMAN	R16	7874	3	2465.7	(+0.9)	5.322	0.428	1.000	5	R.GWTGQESLSDSDPEMWELLQR.E
SW:GLYM_HUMAN	R16	7882	2	2465.7	(+0.0)	4.527	0.419	1.000	5	R.GWTGQESLSDSDPEMWELLQR.E
SW:GLYM_HUMAN	R16	7884	3	2483.7	(+0.2)	4.078	0.436	0.997	5	R.GWTGQESL*SDSDPEMWEL*L*QR.E
SW:GLYM_HUMAN	R16	794	2	1224.4	(+0.9)	3.439	0.470	1.000	4	K.HADIVTTTTHK.T
SW:GLYM_HUMAN	R16	798	2	1232.4	(+0.4)	3.239	0.272	0.961	4	K.HADIVTTTTHK#.T
SW:GLYM_HUMAN	R15	1624	2	886.0	(+0.8)	2.257	0.411	0.972	4	R.LGAPALTSR.Q
SW:GLYM_HUMAN	R16	1312	2	898.0	(-0.0)	2.366	0.349	0.947	4	R.L*GAPAL*TSR.Q
SW:GLYM_HUMAN	R16	5350	2	1142.3	(+0.9)	2.505	0.425	0.980	4	R.L*IIAGTSAYAR.L
SW:GLYM_HUMAN	R15	7081	2	1567.8	(-0.5)	2.654	0.358	0.947	3	K.TGL*IDYNQL*AL*STAR.L
SW:GLYM_HUMAN	R16	6502	2	1207.4	(-0.2)	3.018	0.365	0.967	4	R.VL*EL*VSITANK#.N
SW:GLYM_HUMAN	R16	5432	2	1142.3	(+0.5)	2.273	0.222	0.806	4	R.L*IIAGTSAYAR.L
SW:GPI8_HUMAN	R17	4322	2	1160.3	(+0.2)	3.026	0.487	1.000	4	R.HVANTLSVYR.S
SW:GPI8_HUMAN	R17	4478	2	1160.3	(+0.2)	2.864	0.419	0.981	4	R.HVANTLSVYR.S
SW:GPI8_HUMAN	R17	4400	2	1160.3	(-0.4)	2.776	0.478	0.987	4	R.HVANTLSVYR.S
SW:GPI8_HUMAN	R17	4554	2	1160.3	(+0.0)	2.748	0.451	0.984	4	R.HVANTLSVYR.S
SW:GPI8_HUMAN	R17	4314	2	1166.3	(+0.3)	2.742	0.500	1.000	4	R.HVANTL*SVYR.S
SW:GPI8_HUMAN	R17	4470	2	1166.3	(+0.5)	2.727	0.514	1.000	4	R.HVANTL*SVYR.S
SW:GPI8_HUMAN	R17	4394	2	1166.3	(-0.3)	2.676	0.479	0.985	4	R.HVANTL*SVYR.S
SW:GPI8_HUMAN	R17	4636	2	1160.3	(+0.3)	2.219	0.217	0.631	4	R.HVANTLSVYR.S
SW:GPI8_HUMAN	R17	2594	2	1178.4	(-0.5)	2.724	0.446	0.977	1	R.K#VEITTETIK#.L
SW:GPI8_HUMAN	R17	2588	2	1162.4	(+0.3)	2.570	0.395	0.979	1	R.KVEITTETIK.L
SW:GPI8_HUMAN	R17	2672	2	1178.4	(-0.4)	2.413	0.322	0.902	1	R.K#VEITTETIK#.L
SW:GPI8_HUMAN	R17	8630	2	1368.6	(+0.8)	4.001	0.411	1.000	4	K.NVLITDFFGSVR.K
SW:GPI8_HUMAN	R17	8628	2	1374.6	(+0.6)	3.797	0.476	0.999	4	K.NVL*ITDFFGSVR.K
SW:GPI8_HUMAN	R18	8741	2	1368.6	(+0.9)	2.593	0.337	0.959	4	K.NVLITDFFGSVR.K
SW:GR75_HUMAN	R12	8018	2	1368.6	(+0.7)	3.801	0.420	1.000	3	R.AQFEGIVTDL*IR.R
SW:GR75_HUMAN	R12	8030	1	1362.6	(-1.0)	2.042	0.389	0.001	3	R.AQFEGIVTDLIR.R
SW:GR75_HUMAN	R13	8233	2	1368.6	(+0.9)	4.226	0.468	1.000	3	R.AQFEGIVTDL*IR.R



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta M$	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:GR75_HUMAN	R12	6152	2	1243.4	(-0.2)	2.846	0.433	0.980	3	K.DAGQISGLNVLR.V
SW:GR75_HUMAN	R13	6545	2	1243.4	(+0.6)	3.152	0.302	0.931	3	K.DAGQISGLNVLR.V
SW:GR75_HUMAN	R13	6547	2	1255.4	(+0.4)	2.530	0.447	0.983	3	K.DAGQISGL*NVL*R.V
SW:GR75_HUMAN	R12	1942	2	964.1	(+0.7)	2.655	0.298	0.968	3	K.DDIENMVK.N
SW:GR75_HUMAN	R12	2162	2	1488.7	(-0.2)	2.732	0.304	0.901	3	R.EQQIVIQSSGGL*SK#.D
SW:GR75_HUMAN	R12	2062	2	1488.7	(-0.4)	2.530	0.214	0.708	3	R.EQQIVIQSSGGL*SK#.D
SW:GR75_HUMAN	R12	1390	2	1334.4	(-0.0)	3.302	0.384	0.981	1	K.ETAENYLGHATAK.N
SW:GR75_HUMAN	R12	736	2	1149.2	(+0.9)	2.665	0.199	0.883	3	R.KDSETGENIR.Q
SW:GR75_HUMAN	R12	8418	2	1594.0	(-0.6)	2.884	0.375	0.963	3	K.LLGQFTLIGIPPAPR.G
SW:GR75_HUMAN	R12	8326	2	1594.0	(+0.3)	2.766	0.311	0.937	3	K.LLGQFTLIGIPPAPR.G
SW:GR75_HUMAN	R12	8606	2	1594.0	(+0.5)	2.755	0.203	0.813	3	K.LLGQFTLIGIPPAPR.G
SW:GR75_HUMAN	R12	8514	2	1612.0	(+0.5)	2.353	0.330	0.894	3	K.L*L*GQFTL*IGIPPAPR.G
SW:GR75_HUMAN	R13	8519	2	1594.0	(+0.6)	2.976	0.347	0.970	3	K.LLGQFTLIGIPPAPR.G
SW:GR75_HUMAN	R13	8597	2	1594.0	(+0.8)	2.374	0.372	0.949	3	K.LLGQFTLIGIPPAPR.G
SW:GR75_HUMAN	R12	7878	2	1590.9	(-0.4)	2.313	0.147	0.397	3	K.L*YSPSQIGAFVL*M@K#.M
SW:GR75_HUMAN	R12	1688	2	1577.7	(-0.4)	2.951	0.399	0.966	3	R.QAVTNPNTFYATK#.R
SW:GR75_HUMAN	R12	1680	2	1569.7	(-0.4)	2.652	0.351	0.944	3	R.QAVTNPNTFYATK#.R
SW:GR75_HUMAN	R12	880	2	1158.2	(+0.8)	3.297	0.231	0.962	3	R.RYDDPEVQK#.D
SW:GR75_HUMAN	R12	870	2	1150.2	(+0.7)	3.095	0.123	0.894	3	R.RYDDPEVQK.D
SW:GR75_HUMAN	R12	6522	2	1469.7	(+0.2)	2.993	0.324	0.953	3	K.SDIGEVIL*VGGM@TR.M
SW:GR75_HUMAN	R12	7310	2	1453.7	(+0.8)	2.297	0.453	0.974	3	K.SDIGEVIL*VGGMTR.M
SW:GR75_HUMAN	R13	7537	2	1447.7	(+0.2)	3.350	0.532	1.000	3	K.SDIGEVIL*VGGMTR.M
SW:GR75_HUMAN	R13	7533	2	1453.7	(+0.3)	2.791	0.431	0.982	3	K.SDIGEVIL*VGGMTR.M
SW:GR75_HUMAN	R12	7790	2	2057.2	(+0.8)	4.768	0.577	0.999	3	K.STNGDTFLGGEDFDQALLR.H
SW:GR75_HUMAN	R12	7882	2	2057.2	(+0.4)	4.420	0.569	1.000	3	K.STNGDTFLGGEDFDQALLR.H
SW:GR75_HUMAN	R13	8089	2	2057.2	(-0.3)	2.631	0.488	0.976	3	K.STNGDTFLGGEDFDQALLR.H
SW:GR75_HUMAN	R12	7346	2	1858.1	(-0.4)	4.455	0.496	1.000	3	R.VEAVNMAEGIIHDTETK.M
SW:GR75_HUMAN	R12	7356	2	1866.1	(-0.6)	4.149	0.505	1.000	3	R.VEAVNMAEGIIHDTETK#.M
SW:GR75_HUMAN	R12	6158	2	1882.1	(-1.0)	3.733	0.478	0.997	3	R.VEAVNM@AEGIIHDTETK#.M
SW:GR75_HUMAN	R12	12756	3	2252.6	(+0.8)	3.859	0.409	0.998	3	K.VIAVYDLGGGTFDISILEIQK.G
SW:GR75_HUMAN	R12	10990	3	2252.6	(+0.6)	3.801	0.500	0.999	3	K.VIAVYDLGGGTFDISILEIQK.G
SW:GR75_HUMAN	R12	6834	2	1666.9	(-0.4)	4.326	0.533	1.000	3	R.VINEPTAAAL*AYGL*DK#.S
SW:GR75_HUMAN	R12	6840	2	1646.9	(-0.9)	4.138	0.585	0.985	3	R.VINEPTAAALAYGLDK.S
SW:GR75_HUMAN	R12	6832	3	1666.9	(+0.7)	3.774	0.354	0.997	3	R.VINEPTAAAL*AYGL*DK#.S
SW:GR75_HUMAN	R13	7135	2	1666.9	(-0.3)	4.319	0.469	1.000	3	R.VINEPTAAAL*AYGL*DK#.S
SW:GR75_HUMAN	R12	836	2	959.0	(+1.0)	2.621	0.291	0.950	3	K.VLENAEGAR.T
SW:GR75_HUMAN	R12	838	2	965.0	(+0.9)	2.563	0.206	0.878	3	K.VL*ENAEGAR.T
SW:GR75_HUMAN	R13	1076	2	965.0	(+1.0)	2.292	0.322	0.942	3	K.VL*ENAEGAR.T
SW:GR75_HUMAN	R12	6116	2	1291.4	(+0.2)	3.553	0.440	0.998	3	K.VQQTVQDLFGR.A
SW:GR75_HUMAN	R13	6509	2	1297.4	(+0.2)	2.387	0.343	0.932	3	K.VQQTVQDL*FGR.A
SW:GR75_HUMAN	R27	1614	2	959.0	(-0.1)	2.311	0.216	0.756	3	K.VLENAEGAR.T
SW:GR78_HUMAN	R12	7570	2	1513.8	(+0.4)	2.965	0.501	1.000	2	R.AKFEELNMDLFR.S
SW:GR78_HUMAN	R12	6794	2	1549.8	(+0.1)	2.616	0.252	0.122	2	R.AK#FEEL*NM@DL*FR.S
SW:GR78_HUMAN	R12	626	2	1004.1	(+0.1)	2.535	0.367	0.959	2	R.AL*SSQHQR.I
SW:GR78_HUMAN	R12	6080	2	1218.4	(+1.0)	3.494	0.513	1.000	2	K.DAGTIAGLNVMR.I
SW:GR78_HUMAN	R12	4780	2	1240.4	(+0.7)	2.796	0.303	0.958	2	K.DAGTIAGL*NVMR@R.I
SW:GR78_HUMAN	R12	6088	2	1224.4	(+0.8)	2.630	0.359	0.968	2	K.DAGTIAGL*NVMR.I
SW:GR78_HUMAN	R12	6096	2	1218.4	(-0.7)	2.368	0.303	0.888	2	K.DAGTIAGLNVMR.I
SW:GR78_HUMAN	R12	6756	2	1412.6	(+0.3)	3.131	0.336	0.972	2	K.EL*EEIVQPIISK#.L
SW:GR78_HUMAN	R13	7057	2	1398.6	(+0.8)	3.498	0.379	0.989	2	K.ELEEIVQPIISK.L
SW:GR78_HUMAN	R13	7063	2	1412.6	(-0.1)	2.776	0.201	0.797	2	K.EL*EEIVQPIISK#.L
SW:GR78_HUMAN	R12	7798	2	1326.5	(+0.7)	2.746	0.327	0.844	2	K.FEEL*NMDL*FR.S
SW:GR78_HUMAN	R13	8051	2	1326.5	(+0.5)	2.439	0.309	0.945	2	K.FEEL*NMDL*FR.S
SW:GR78_HUMAN	R12	13472	2	2166.3	(+1.0)	4.272	0.574	1.000	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	11400	3	2166.3	(+0.9)	4.225	0.435	1.000	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	10776	2	2166.3	(+0.9)	4.204	0.625	0.999	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	10726	3	2166.3	(+0.8)	4.125	0.490	1.000	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	11336	3	2166.3	(+0.0)	4.117	0.501	1.000	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	13332	2	2172.3	(+0.5)	4.067	0.548	0.999	2	R.IEIESFYEGEDFSETL*TR.A
SW:GR78_HUMAN	R12	12486	3	2166.3	(+0.8)	4.066	0.448	1.000	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	13478	2	2172.3	(+1.0)	3.995	0.604	1.000	2	R.IEIESFYEGEDFSETL*TR.A
SW:GR78_HUMAN	R12	12624	3	2166.3	(+1.0)	3.910	0.446	0.988	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	13744	3	2166.3	(+0.5)	3.843	0.402	0.995	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	7994	2	2172.3	(+0.8)	3.842	0.517	0.999	2	R.IEIESFYEGEDFSETL*TR.A
SW:GR78_HUMAN	R12	10988	3	2166.3	(+0.7)	3.824	0.459	1.000	2	R.IEIESFYEGEDFSETLTR.A

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:GR78_HUMAN	R12	12262	3	2166.3	(+0.3)	3.798	0.440	0.999	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	11136	3	2166.3	(+0.8)	3.737	0.486	0.997	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	11914	2	2166.3	(+0.5)	3.732	0.606	1.000	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	13184	2	2166.3	(+0.1)	3.704	0.566	1.000	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	13106	2	2166.3	(-0.2)	3.658	0.482	0.999	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	11268	2	2172.3	(+0.8)	3.644	0.605	1.000	2	R.IEIESFYEGEDFSETL*TR.A
SW:GR78_HUMAN	R12	12614	2	2166.3	(+0.6)	3.612	0.572	1.000	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	12694	2	2166.3	(-0.3)	3.605	0.493	1.000	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	10226	2	2166.3	(+0.6)	3.495	0.558	1.000	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	10882	2	2166.3	(-0.1)	3.492	0.536	1.000	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	13030	2	2172.3	(+0.4)	3.454	0.576	1.000	2	R.IEIESFYEGEDFSETL*TR.A
SW:GR78_HUMAN	R12	10700	2	2166.3	(+0.5)	3.417	0.570	1.000	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	11250	2	2166.3	(+0.4)	3.391	0.570	1.000	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	12382	2	2166.3	(+0.8)	3.355	0.602	1.000	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	10790	2	2172.3	(+0.2)	3.330	0.518	1.000	2	R.IEIESFYEGEDFSETL*TR.A
SW:GR78_HUMAN	R12	11408	2	2166.3	(+0.1)	3.323	0.530	1.000	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	8074	2	2172.3	(+0.7)	3.294	0.480	1.000	2	R.IEIESFYEGEDFSETL*TR.A
SW:GR78_HUMAN	R12	12478	2	2172.3	(-0.0)	3.280	0.452	0.985	2	R.IEIESFYEGEDFSETL*TR.A
SW:GR78_HUMAN	R12	12154	2	2166.3	(-0.0)	3.262	0.479	0.987	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	11834	2	2166.3	(-0.6)	3.199	0.557	1.000	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	12086	2	2172.3	(+0.4)	3.179	0.427	0.840	2	R.IEIESFYEGEDFSETL*TR.A
SW:GR78_HUMAN	R12	12206	2	2172.3	(+1.0)	3.142	0.614	1.000	2	R.IEIESFYEGEDFSETL*TR.A
SW:GR78_HUMAN	R12	11698	2	2166.3	(-0.4)	3.123	0.532	1.000	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	12768	2	2166.3	(-0.9)	3.076	0.376	0.914	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	10102	2	2166.3	(-0.2)	2.988	0.507	0.987	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	12658	2	2172.3	(-0.2)	2.983	0.433	0.979	2	R.IEIESFYEGEDFSETL*TR.A
SW:GR78_HUMAN	R12	12748	2	2172.3	(+0.3)	2.980	0.506	0.991	2	R.IEIESFYEGEDFSETL*TR.A
SW:GR78_HUMAN	R12	11344	2	2166.3	(+0.2)	2.908	0.374	0.964	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	12924	2	2166.3	(+0.1)	2.864	0.515	0.986	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	13398	2	2172.3	(-0.7)	2.813	0.432	0.975	2	R.IEIESFYEGEDFSETL*TR.A
SW:GR78_HUMAN	R12	13766	2	2166.3	(-0.1)	2.810	0.478	0.982	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	13400	2	2166.3	(-0.9)	2.787	0.306	0.800	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	11190	2	2172.3	(-0.1)	2.781	0.397	0.966	2	R.IEIESFYEGEDFSETL*TR.A
SW:GR78_HUMAN	R12	11056	2	2166.3	(-0.4)	2.779	0.492	0.983	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	13020	2	2166.3	(-0.2)	2.757	0.442	0.975	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	11030	2	2172.3	(+0.3)	2.751	0.454	0.984	2	R.IEIESFYEGEDFSETL*TR.A
SW:GR78_HUMAN	R12	11556	2	2172.3	(-0.4)	2.749	0.436	0.973	2	R.IEIESFYEGEDFSETL*TR.A
SW:GR78_HUMAN	R12	13082	2	2172.3	(-0.9)	2.726	0.459	0.934	2	R.IEIESFYEGEDFSETL*TR.A
SW:GR78_HUMAN	R12	13238	2	2172.3	(+0.3)	2.725	0.396	0.974	2	R.IEIESFYEGEDFSETL*TR.A
SW:GR78_HUMAN	R12	12464	2	2166.3	(-0.6)	2.707	0.383	0.958	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	11624	2	2166.3	(-0.3)	2.704	0.426	0.970	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	10452	2	2166.3	(-0.4)	2.690	0.381	0.956	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	11944	2	2172.3	(+0.1)	2.677	0.452	0.975	2	R.IEIESFYEGEDFSETL*TR.A
SW:GR78_HUMAN	R12	12250	2	2172.3	(-0.5)	2.643	0.308	0.911	2	R.IEIESFYEGEDFSETL*TR.A
SW:GR78_HUMAN	R12	11386	2	2172.3	(+0.0)	2.584	0.456	0.973	2	R.IEIESFYEGEDFSETL*TR.A
SW:GR78_HUMAN	R12	10942	2	2172.3	(-0.8)	2.552	0.362	0.834	2	R.IEIESFYEGEDFSETL*TR.A
SW:GR78_HUMAN	R12	13548	2	2166.3	(-0.2)	2.527	0.468	0.974	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	10688	2	2172.3	(-0.4)	2.466	0.535	0.983	2	R.IEIESFYEGEDFSETL*TR.A
SW:GR78_HUMAN	R12	10618	2	2166.3	(+0.2)	2.448	0.456	0.969	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	12076	2	2166.3	(-0.7)	2.427	0.384	0.941	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	11998	2	2166.3	(-0.6)	2.414	0.452	0.966	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	13618	2	2166.3	(-0.3)	2.409	0.393	0.944	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	10372	2	2166.3	(+0.2)	2.395	0.487	0.973	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	13724	2	2172.3	(-0.7)	2.369	0.416	0.951	2	R.IEIESFYEGEDFSETL*TR.A
SW:GR78_HUMAN	R12	11802	2	2172.3	(-0.7)	2.337	0.440	0.959	2	R.IEIESFYEGEDFSETL*TR.A
SW:GR78_HUMAN	R12	11728	2	2172.3	(-0.7)	2.330	0.372	0.924	2	R.IEIESFYEGEDFSETL*TR.A
SW:GR78_HUMAN	R12	12774	2	2172.3	(-0.9)	2.244	0.239	0.428	2	R.IEIESFYEGEDFSETL*TR.A
SW:GR78_HUMAN	R13	13405	2	2166.3	(-0.0)	3.542	0.606	1.000	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R13	13579	2	2166.3	(-0.3)	3.134	0.440	0.982	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R13	13497	2	2166.3	(-0.1)	2.832	0.487	0.983	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R13	12169	2	2166.3	(-0.5)	2.631	0.458	0.974	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R13	13835	2	2166.3	(+0.2)	2.502	0.409	0.957	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R13	13951	2	2166.3	(-0.3)	2.267	0.334	0.864	2	R.IEIESFYEGEDFSETLTR.A
SW:GR78_HUMAN	R12	6978	2	1976.1	(+0.5)	5.322	0.619	0.996	2	K.IEWLESHQDADIEDFK.A
SW:GR78_HUMAN	R12	6984	2	1990.1	(-0.6)	4.618	0.397	0.999	2	K.IEWL*ESHQDADIEDFK#.A
SW:GR78_HUMAN	R12	6980	3	1976.1	(-0.8)	3.701	0.546	1.000	2	K.IEWLESHQDADIEDFK.A

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:GR78_HUMAN	R13	7269	3	1990.1	(+0.8)	4.304	0.472	1.000	2	K.IEWL*ESHQDADIEDFK#.A
SW:GR78_HUMAN	R12	6928	2	1660.9	(+1.0)	4.622	0.600	1.000	13	R.IINEPTAAAIAYGLDK.R
SW:GR78_HUMAN	R13	7241	2	1674.9	(+0.5)	4.926	0.505	1.000	13	R.IINEPTAAAIAYGL*DK#.R
SW:GR78_HUMAN	R12	6866	2	1817.1	(-0.5)	4.061	0.526	0.999	2	R.IINEPTAAAIAYGLDKR.E
SW:GR78_HUMAN	R12	6332	2	1589.8	(-0.3)	4.377	0.446	1.000	2	K.KSDIDEIVLVGGSTR.I
SW:GR78_HUMAN	R12	6336	2	1603.8	(-1.0)	3.042	0.343	0.886	2	K.K#SDIDEIVL*VGGSTR.I
SW:GR78_HUMAN	R12	5474	2	1734.0	(+0.5)	2.861	0.341	0.349	2	K.KTKPYIQVDIGGGQTK.T
SW:GR78_HUMAN	R12	1250	2	1819.9	(-0.5)	3.894	0.435	1.000	1	K.LYGSAGPPPTGEEDTAEK.D
SW:GR78_HUMAN	R12	5380	2	2177.3	(+0.4)	5.004	0.662	1.000	1	K.LYGSAGPPPTGEEDTAEKDEL.-
SW:GR78_HUMAN	R12	5424	2	2197.3	(-0.9)	2.912	0.397	0.174	1	K.L*YGSAGPPPTGEEDTAEK#DEL*.-
SW:GR78_HUMAN	R12	1394	2	1279.4	(-0.4)	3.689	0.442	1.000	2	K.M@K#ETA EAYL*GK#.K
SW:GR78_HUMAN	R12	1834	2	1241.4	(-0.0)	3.516	0.505	0.997	2	K.MKETAEAYLGK.K
SW:GR78_HUMAN	R12	1840	2	1263.4	(-0.1)	3.480	0.326	0.404	2	K.MK#ETA EAYL*GK#.K
SW:GR78_HUMAN	R12	6228	2	1337.4	(-0.5)	2.459	0.119	0.469	2	R.NEL*ESYAYSL*K#.N
SW:GR78_HUMAN	R12	6214	2	1317.4	(+0.7)	2.260	0.270	0.877	2	R.NELESYAYSLK.N
SW:GR78_HUMAN	R12	5598	2	1678.8	(+0.4)	4.140	0.412	1.000	2	K.NQLTSNPENTVFDK.R
SW:GR78_HUMAN	R12	6610	2	1467.6	(+0.9)	2.233	0.388	0.949	2	K.SDIDEIVL*VGGSTR.I
SW:GR78_HUMAN	R12	5828	2	1838.0	(+0.8)	4.495	0.602	0.994	1	K.SQIFSTASDNQPTVTIK.V
SW:GR78_HUMAN	R12	5834	2	1846.0	(+0.7)	4.262	0.490	1.000	1	K.SQIFSTASDNQPTVTIK#.V
SW:GR78_HUMAN	R12	7936	3	1551.8	(+0.6)	3.860	0.327	0.997	2	K.TFAPEEISAMVL*TK#.M
SW:GR78_HUMAN	R12	7012	2	1567.8	(-0.0)	3.192	0.423	0.971	2	K.TFAPEEISAM@VL*TK#.M
SW:GR78_HUMAN	R12	7898	2	1551.8	(+0.5)	2.776	0.390	0.969	2	K.TFAPEEISAMVL*TK#.M
SW:GR78_HUMAN	R12	7960	2	1537.8	(-0.1)	2.339	0.377	0.930	2	K.TFAPEEISAMVLTK.M
SW:GR78_HUMAN	R12	5712	3	1621.8	(+1.0)	3.794	0.412	0.991	2	K.TK#PYIQVDIGGGQTK#.T
SW:GR78_HUMAN	R12	5620	3	1621.8	(+1.0)	3.764	0.410	0.991	2	K.TK#PYIQVDIGGGQTK#.T
SW:GR78_HUMAN	R12	5532	2	1605.8	(-0.3)	3.716	0.507	1.000	2	K.TKPYIQVDIGGGQTK.T
SW:GR78_HUMAN	R12	5536	2	1621.8	(-0.9)	3.271	0.415	0.203	2	K.TK#PYIQVDIGGGQTK#.T
SW:GR78_HUMAN	R12	5618	2	1605.8	(+0.3)	2.952	0.552	0.997	2	K.TKPYIQVDIGGGQTK.T
SW:GR78_HUMAN	R11	4888	2	1439.5	(-0.3)	2.421	0.256	0.798	2	R.TWNDPSVQQDIK#.F
SW:GR78_HUMAN	R11	4896	2	1431.5	(-0.7)	2.317	0.321	0.898	2	R.TWNDPSVQQDIK.F
SW:GR78_HUMAN	R12	4800	2	1431.5	(+0.5)	3.224	0.396	0.987	2	R.TWNDPSVQQDIK.F
SW:GR78_HUMAN	R12	4820	2	1439.5	(+0.5)	3.212	0.521	1.000	2	R.TWNDPSVQQDIK#.F
SW:GR78_HUMAN	R12	4728	2	1439.5	(-0.2)	2.764	0.381	0.956	2	R.TWNDPSVQQDIK#.F
SW:GR78_HUMAN	R12	4902	2	1439.5	(-0.9)	2.488	0.259	0.602	2	R.TWNDPSVQQDIK#.F
SW:GR78_HUMAN	R12	4720	2	1431.5	(-0.7)	2.369	0.276	0.855	2	R.TWNDPSVQQDIK.F
SW:GR78_HUMAN	R13	5241	2	1431.5	(-0.8)	2.974	0.310	0.873	2	R.TWNDPSVQQDIK.F
SW:GR78_HUMAN	R12	1044	2	1047.2	(+0.9)	2.527	0.242	0.188	2	K.VLEDSDLKK.S
SW:GR78_HUMAN	R12	2386	2	904.1	(+0.8)	2.653	0.204	0.938	2	R.VMEHFIK.L
SW:GR78_HUMAN	R12	2332	2	912.1	(+0.6)	2.401	0.336	0.962	2	R.VMEHFIK#.L
SW:GRE1_HUMAN	R21	4600	3	1808.8	(+0.0)	4.442	0.511	0.994	1	K.NSGQNL*EEDMGQSEQK#.A
SW:GRE1_HUMAN	R21	2322	3	1824.8	(+0.7)	4.287	0.425	1.000	1	K.NSGQNL*EEDM@GQSEQK#.A
SW:GRE1_HUMAN	R21	4612	2	1794.8	(-0.6)	2.755	0.446	0.976	1	K.NSGQNL EEDMGQSEQK.A
SW:GRE1_HUMAN	R21	4538	2	1015.1	(+0.5)	2.292	0.167	0.746	1	R.AL*ADTENL*R.Q
SW:GRWD_HUMAN	R15	8839	3	1822.1	(+0.7)	4.538	0.537	0.961	3	R.L*L*QVVEEPQAL*AAFL*R.D
SW:GRWD_HUMAN	R15	7599	2	1788.0	(-0.1)	3.856	0.482	1.000	3	R.VSWL*GEEPVAGVWSEK#.G
SW:GSN2_HUMAN	R01	5829	2	1217.4	(+1.0)	3.477	0.329	0.983	3	K.HYEVEILDAK.T
SW:GSN2_HUMAN	R01	5827	2	1231.4	(+0.1)	3.227	0.413	0.981	3	K.HYEVEIL*DAK#.T
SW:GSN2_HUMAN	R01	5845	2	1217.4	(-0.2)	2.838	0.386	0.976	3	K.HYEVEILDAK.T
SW:GSN2_HUMAN	R02	5892	2	1217.4	(-0.0)	2.877	0.359	0.973	3	K.HYEVEILDAK.T
SW:GSN2_HUMAN	R03	5753	2	1231.4	(+0.3)	2.567	0.352	0.961	3	K.HYEVEIL*DAK#.T
SW:GSN2_HUMAN	R03	5763	2	1217.4	(-0.2)	2.305	0.335	0.925	3	K.HYEVEILDAK.T
SW:GSN2_HUMAN	R01	6947	2	1351.6	(+0.1)	3.023	0.558	1.000	2	K.L*PVGTTATL*YFR.D
SW:GSN2_HUMAN	R01	6959	2	1339.6	(-0.1)	2.858	0.481	0.986	2	K.LPVGTTATLYFR.D
SW:GSN2_HUMAN	R02	6710	2	1339.6	(+0.7)	2.470	0.396	0.971	2	K.LPVGTTATLYFR.D
SW:GSN2_HUMAN	R03	6661	2	1351.6	(+0.2)	3.060	0.442	0.985	2	K.L*PVGTTATL*YFR.D
SW:GSN2_HUMAN	R01	1404	2	1175.3	(-0.2)	2.977	0.268	0.266	3	K.SLKDEDVLQK.L
SW:GSN2_HUMAN	R02	1920	2	1175.3	(+0.6)	2.657	0.299	0.307	3	K.SLKDEDVLQK.L
SW:GSN2_HUMAN	R03	1702	2	1175.3	(-0.4)	2.431	0.244	0.086	3	K.SLKDEDVLQK.L
SW:GSN2_HUMAN	R03	4419	2	1216.4	(+0.1)	2.505	0.190	0.657	3	K.VEPHATIAEIK#.N
SW:GSN2_HUMAN	R03	5105	2	961.2	(+0.2)	2.266	0.182	0.453	3	R.VPFIYGHK.Y
SW:GTFI_HUMAN	R08	7993	3	2370.6	(+0.7)	3.748	0.337	0.995	5	K.FEAHPNDL*YVEGL*PENIPFR.S
SW:GTFI_HUMAN	R08	6671	2	1248.5	(+1.0)	2.242	0.309	0.906	5	K.FAQALGLTEAVK.V

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:GTK1_HUMAN	R22	5214	2	1469.6	(-1.0)	2.636	0.252	0.597	3	K.AGM@SAEQAQGL*L*EK#.I
SW:GTK1_HUMAN	R22	7122	2	1743.9	(-0.4)	3.641	0.327	0.965	3	R.NEDITEPQSIL*AAAEK#.A
SW:GTK1_HUMAN	R22	8354	2	1082.3	(+0.8)	2.616	0.170	0.856	3	K.DFLSVMLEK.G
SW:H105_HUMAN	R14	1838	2	1120.3	(+0.5)	2.441	0.280	0.928	2	R.FVVQNVSAQK.D
SW:H105_HUMAN	R14	7923	2	1322.5	(+0.5)	2.300	0.295	0.894	2	K.VLGTAFDPFLGGK.N
SW:H12_HUMAN	R19	6170	2	1213.4	(+0.4)	2.237	0.379	0.936	5	K.ASGPPVSEL*ITK#.A
SW:H12_HUMAN	R20	6030	2	1199.4	(+0.6)	2.749	0.408	0.979	5	K.ASGPPVSELITK.A
SW:H12_HUMAN	R20	6026	2	1213.4	(+0.4)	2.426	0.377	0.953	5	K.ASGPPVSEL*ITK#.A
SW:H12_HUMAN	R19	5990	2	1327.6	(+0.0)	4.183	0.478	0.997	5	R.KASGPPVSELITK.A
SW:H12_HUMAN	R20	5902	2	1349.6	(-0.6)	3.908	0.464	1.000	5	R.K#ASGPPVSEL*ITK#.A
SW:H12_HUMAN	R20	5910	2	1327.6	(-0.4)	3.327	0.410	0.984	5	R.KASGPPVSELITK.A
SW:H12_HUMAN	R20	1048	2	887.1	(-0.1)	2.201	0.249	0.816	1	K.KPAAATVTK.K
SW:H15_HUMAN	R19	1756	2	1094.2	(+0.9)	3.142	0.446	0.986	1	K.ALAAGGYDVEK.N
SW:H15_HUMAN	R19	1752	2	1108.2	(+0.0)	2.727	0.243	0.868	1	K.AL*AAGGYDVEK#.N
SW:H15_HUMAN	R20	1930	2	1108.2	(+0.1)	3.112	0.403	0.977	1	K.AL*AAGGYDVEK#.N
SW:H15_HUMAN	R19	6132	2	1341.6	(+0.8)	4.832	0.406	1.000	1	R.KATGPPVSELITK.A
SW:H15_HUMAN	R19	6110	2	1363.6	(+0.2)	3.646	0.473	0.999	1	R.K#ATGPPVSEL*ITK#.A
SW:H15_HUMAN	R20	1932	2	1094.2	(+0.3)	2.833	0.419	0.986	1	K.ALAAGGYDVEK.N
SW:H1X_HUMAN	R20	6500	2	1342.6	(+0.8)	3.844	0.436	1.000		K.ALVQNDTLLQVK.G
SW:H1X_HUMAN	R20	6242	2	1214.4	(+0.4)	2.866	0.342	0.977		K.YSQL*VVETIR.R
SW:H2AA_HUMAN	R20	6204	2	945.1	(+0.6)	2.510	0.319	0.961	24	R.AGLQFPVGR.V
SW:H2AA_HUMAN	R21	6276	2	945.1	(+0.5)	2.623	0.338	0.972	24	R.AGLQFPVGR.V
SW:H2AA_HUMAN	R22	6500	2	945.1	(+0.9)	2.527	0.269	0.940	24	R.AGLQFPVGR.V
SW:H2AA_HUMAN	R22	6496	2	951.1	(+0.1)	2.244	0.215	0.766	24	R.AGL*QFPVGR.V
SW:H2AA_HUMAN	R24	6448	2	945.1	(+0.3)	2.694	0.315	0.970	24	R.AGLQFPVGR.V
SW:H2AA_HUMAN	R24	6442	2	951.1	(+0.3)	2.243	0.235	0.835	24	R.AGL*QFPVGR.V
SW:H2AA_HUMAN	R25	6882	2	951.1	(+0.9)	2.894	0.401	0.988	24	R.AGL*QFPVGR.V
SW:H2AA_HUMAN	R25	6800	2	951.1	(+0.4)	2.691	0.398	0.984	24	R.AGL*QFPVGR.V
SW:H2AA_HUMAN	R27	6013	2	945.1	(-0.2)	2.658	0.278	0.936	24	R.AGLQFPVGR.V
SW:H2AA_HUMAN	R24	6152	2	851.0	(+0.9)	2.347	0.238	0.921	20	R.HLQLAIR.N
SW:H2AA_HUMAN	R25	6794	2	1719.9	(-0.2)	4.228	0.397	0.991	18	R.HL*QL*AIRNDEEL*NK#.L
SW:H2AA_HUMAN	R25	1008	2	875.9	(+0.9)	2.512	0.111	0.747	19	R.NDEEL*NK#.L
SW:H2AA_HUMAN	R24	8890	2	1932.4	(-0.5)	2.307	0.314	0.863	14	R.VTIAQGGVLPNIQAVLLPK.K
SW:H2AA_HUMAN	R25	9120	2	1932.4	(+0.3)	4.765	0.453	0.999	14	R.VTIAQGGVLPNIQAVLLPK.K
SW:H2AA_HUMAN	R25	9030	2	1932.4	(+0.5)	3.831	0.268	0.972	14	R.VTIAQGGVLPNIQAVLLPK.K
SW:H2AA_HUMAN	R25	9590	2	1958.4	(-0.2)	2.604	0.324	0.896	14	R.VTIAQGGVL*PNIQAVL*L*PK#.K
SW:H2AA_HUMAN	R26	9002	2	1932.4	(+1.0)	4.159	0.545	0.999	14	R.VTIAQGGVLPNIQAVLLPK.K
SW:H2AA_HUMAN	R27	8101	2	1932.4	(+0.5)	3.144	0.211	0.913	14	R.VTIAQGGVLPNIQAVLLPK.K
SW:H2AA_HUMAN	R27	5755	2	851.0	(+0.7)	2.210	0.245	0.901	20	R.HLQLAIR.N
SW:H2AZ_HUMAN	R25	6594	2	1371.6	(-0.6)	3.008	0.321	0.944	1	K.ATIAGGGVIPHIHK.S
SW:H2AZ_HUMAN	R25	6588	2	1379.6	(-0.9)	2.286	0.259	0.461	1	K.ATIAGGGVIPHIHK#.S
SW:H2AZ_HUMAN	R23	6538	2	1119.2	(+0.7)	2.233	0.235	0.835	1	R.GDEELDSLIIK.A
SW:H2AZ_HUMAN	R25	7024	2	1139.2	(-0.3)	3.199	0.265	0.947	1	R.GDEEL*DSL*IK#.A
SW:H2AZ_HUMAN	R25	5880	2	1119.2	(+0.7)	2.912	0.240	0.949	1	R.GDEELDSLIIK.A
SW:H2AZ_HUMAN	R26	6696	2	1119.2	(+0.1)	2.412	0.319	0.927	1	R.GDEELDSLIIK.A
SW:H2BA_HUMAN	R25	90	2	828.9	(+1.0)	2.670	0.357	0.981	28	K.HAVSEGTK.A
SW:H2BA_HUMAN	R25	2714	2	836.9	(+0.1)	2.430	0.335	0.908	28	K.HAVSEGTK#.A
SW:H2BA_HUMAN	R25	118	2	836.9	(+0.6)	2.427	0.389	0.973	28	K.HAVSEGTK#.A
SW:H2BA_HUMAN	R25	3576	2	836.9	(-0.4)	2.371	0.390	0.935	28	K.HAVSEGTK#.A
SW:H2BA_HUMAN	R25	2792	2	836.9	(+0.3)	2.364	0.362	0.962	28	K.HAVSEGTK#.A
SW:H2BA_HUMAN	R25	162	2	836.9	(-0.6)	2.302	0.410	0.953	28	K.HAVSEGTK#.A
SW:H2BA_HUMAN	R25	3300	2	836.9	(+0.1)	2.263	0.373	0.941	28	K.HAVSEGTK#.A
SW:H2BA_HUMAN	R25	3028	2	836.9	(+0.7)	2.251	0.485	0.983	28	K.HAVSEGTK#.A
SW:H2BA_HUMAN	R25	3156	2	836.9	(-0.5)	2.215	0.309	0.888	28	K.HAVSEGTK#.A
SW:H2BA_HUMAN	R24	5810	2	1282.4	(-0.8)	2.318	0.189	0.376	15	R.K#ESYSVYVYK#.V
SW:H2BA_HUMAN	R24	5814	2	1266.4	(-0.3)	2.282	0.396	0.955	15	R.KESYSVYVYK.V
SW:H2BA_HUMAN	R25	6114	2	1282.4	(-0.5)	3.100	0.423	0.979	15	R.K#ESYSVYVYK#.V
SW:H2BA_HUMAN	R25	5920	2	1266.4	(-0.4)	2.780	0.504	1.000	15	R.KESYSVYVYK.V

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:H2BA_HUMAN	R25	5838	2	1266.4	(-0.4)	2.294	0.426	0.966	15	R.KESYSVYVYK.V
SW:H31_HUMAN	R25	4388	2	1033.2	(-0.0)	2.579	0.320	0.276	8	R.YRPGTVALR.E
SW:H31_HUMAN	R25	4466	2	1033.2	(+0.5)	2.578	0.290	0.293	8	R.YRPGTVALR.E
SW:H31_HUMAN	R25	4824	2	1033.2	(-0.7)	2.453	0.310	0.219	8	R.YRPGTVALR.E
SW:H31_HUMAN	R25	4640	2	1033.2	(+0.7)	2.339	0.156	0.054	8	R.YRPGTVALR.E
SW:H31_HUMAN	R25	4802	2	1033.2	(+0.6)	2.328	0.226	0.114	8	R.YRPGTVALR.E
SW:H31_HUMAN	R25	4550	2	1033.2	(+0.6)	2.273	0.232	0.109	8	R.YRPGTVALR.E
SW:H31_HUMAN	R25	4722	2	1033.2	(-0.1)	2.251	0.248	0.088	8	R.YRPGTVALR.E
SW:H31_HUMAN	R25	5688	2	1033.2	(+0.8)	2.202	0.136	0.013	8	R.YRPGTVALR.E
SW:H31_HUMAN	R25	2144	1	858.9	(-0.4)	2.026	0.121	0.000	9	R.EIAQDFK#.T
SW:H4_HUMAN	R25	1586	2	1135.2	(+0.4)	2.778	0.334	0.973	2	R.DAVTYTEHAK.R
SW:H4_HUMAN	R26	1770	2	1135.2	(+0.8)	3.121	0.366	0.986	2	R.DAVTYTEHAK.R
SW:H4_HUMAN	R26	1854	2	1135.2	(-0.0)	2.930	0.320	0.964	2	R.DAVTYTEHAK.R
SW:H4_HUMAN	R26	1986	2	1135.2	(+1.0)	2.916	0.373	0.983	2	R.DAVTYTEHAK.R
SW:H4_HUMAN	R26	4586	2	1135.2	(+0.1)	2.821	0.399	0.978	2	R.DAVTYTEHAK.R
SW:H4_HUMAN	R26	2278	2	1143.2	(+0.3)	2.545	0.435	0.979	2	R.DAVTYTEHAK#.R
SW:H4_HUMAN	R26	1670	2	1135.2	(-0.9)	2.490	0.114	0.309	2	R.DAVTYTEHAK.R
SW:H4_HUMAN	R26	2374	2	1143.2	(+0.3)	2.456	0.368	0.957	2	R.DAVTYTEHAK#.R
SW:H4_HUMAN	R26	2574	2	1143.2	(-0.2)	2.401	0.228	0.779	2	R.DAVTYTEHAK#.R
SW:H4_HUMAN	R26	4392	2	1143.2	(+0.5)	2.327	0.335	0.933	2	R.DAVTYTEHAK#.R
SW:H4_HUMAN	R26	1818	2	1143.2	(+0.9)	2.216	0.435	0.967	2	R.DAVTYTEHAK#.R
SW:H4_HUMAN	R26	4564	2	1143.2	(+0.1)	2.205	0.427	0.949	2	R.DAVTYTEHAK#.R
SW:H4_HUMAN	R23	5596	2	1326.5	(-0.1)	2.265	0.123	0.013	2	R.DNIQGITKPAIR.R
SW:H4_HUMAN	R25	5792	2	1334.5	(-0.7)	2.304	0.258	0.063	2	R.DNIQGITK#PAIR.R
SW:H4_HUMAN	R26	5706	2	1326.5	(+0.1)	2.908	0.247	0.171	2	R.DNIQGITKPAIR.R
SW:H4_HUMAN	R26	5576	2	1326.5	(+0.1)	2.790	0.284	0.203	2	R.DNIQGITKPAIR.R
SW:H4_HUMAN	R26	5574	2	1334.5	(-0.1)	2.606	0.332	0.237	2	R.DNIQGITK#PAIR.R
SW:H4_HUMAN	R26	9238	2	1407.7	(-0.3)	2.831	0.314	0.264	2	R.GVL*K#VFL*ENVIR.D
SW:H4_HUMAN	R26	9314	2	1407.7	(+0.2)	2.815	0.432	0.485	2	R.GVL*K#VFL*ENVIR.D
SW:H4_HUMAN	R27	8329	2	1407.7	(-0.2)	2.474	0.128	0.023	2	R.GVL*K#VFL*ENVIR.D
SW:H4_HUMAN	R22	6244	2	1181.3	(+0.6)	2.413	0.285	0.914	2	R.ISGLIYEETR.G
SW:H4_HUMAN	R26	6266	2	1187.3	(+0.4)	3.096	0.443	1.000	2	R.ISGL*YEETR.G
SW:H4_HUMAN	R26	6346	2	1187.3	(+1.0)	2.453	0.344	0.962	2	R.ISGL*YEETR.G
SW:H4_HUMAN	R26	6096	2	1187.3	(+0.7)	2.436	0.435	0.982	2	R.ISGL*YEETR.G
SW:H4_HUMAN	R27	5781	2	1187.3	(+0.4)	2.751	0.420	0.986	2	R.ISGL*YEETR.G
SW:H4_HUMAN	R26	7746	2	1461.8	(+0.3)	3.439	0.460*	0.537	2	R.K#TVTAMDVVYAL*K#.R
SW:H4_HUMAN	R26	6442	2	1337.5	(-0.4)	2.944	0.234	0.916	2	K.RISGLIYEETR.G
SW:H4_HUMAN	R26	6438	2	1343.5	(-0.4)	2.514	0.128	0.591	2	K.RISGL*YEETR.G
SW:H4_HUMAN	R26	8116	3	1325.6	(+1.0)	4.309	0.258	0.995	2	K.TVTAMDVVYAL*K#.R
SW:H4_HUMAN	R26	7108	2	1341.6	(+0.2)	2.243	0.356	0.891	2	K.TVTAM@DVVYAL*K#.R
SW:H4_HUMAN	R26	8084	2	1311.6	(-0.7)	2.211	0.351	0.908	2	K.TVTAMDVVYALK.R
SW:H4_HUMAN	R26	7902	2	1467.8	(+0.6)	3.802	0.421	1.000	2	K.TVTAMDVVYALKR.Q
SW:H4_HUMAN	R26	7888	2	1481.8	(+0.1)	3.393	0.366	0.479	2	K.TVTAMDVVYAL*K#R.Q
SW:H4_HUMAN	R26	7218	2	996.2	(+0.9)	2.352	0.160	0.791	2	K.VFL*ENVIR.D
SW:H4_HUMAN	R26	7610	3	2120.4	(+0.7)	5.012	0.473	1.000	2	K.VFL*ENVIRDAVYTEHAK#.R
SW:H4_HUMAN	R27	5783	2	1181.3	(-0.2)	2.268	0.222	0.765	2	R.ISGLIYEETR.G
SW:HBA_HUMAN	R26	6418	2	1088.3	(+0.9)	2.453	0.272	0.122	11	K.LRVDPVNFK.L
SW:HBA_HUMAN	R26	7238	2	1835.0	(-0.6)	2.934	0.534	1.000	7	K.TYFPHFDLSHGSAQVK.G
SW:HBA_HUMAN	R26	5716	2	1530.6	(-0.3)	2.655	0.177	0.699	5	K.VGAHAGEYGAEALER.M
SW:HBA_HUMAN	R26	7604	2	1072.3	(+1.0)	2.304	0.240	0.831	7	R.MFLSFPTTK.T
SW:HCC1_HUMAN	R20	5330	2	1881.0	(-0.7)	4.247	0.549	0.999	1	R.FGIVTSSAGTGTTEDTEAK#.K
SW:HCC1_HUMAN	R20	5324	2	1873.0	(-0.8)	4.005	0.559	1.000	1	R.FGIVTSSAGTGTTEDTEAK.K
SW:HCC1_HUMAN	R20	5354	2	1518.7	(-0.1)	2.663	0.302	0.174	1	K.GLSSDNKPMVNLDK.L
SW:HCC1_HUMAN	R20	6448	2	1086.2	(+0.7)	2.656	0.429	0.985	1	R.FGL*NVSSISR.K
SW:HCD2_HUMAN	R21	5252	2	1332.4	(+0.0)	3.048	0.447	0.986	2	K.GQHTLTLEDFQR.V
SW:HCD2_HUMAN	R21	7980	3	2448.7	(+0.7)	4.788	0.605	1.000	2	R.GVIINTASVAAFEGQVQQAAYSASK#.G
SW:HCD2_HUMAN	R21	7978	3	2440.7	(+0.5)	3.790	0.498	1.000	2	R.GVIINTASVAAFEGQVQQAAYSASK.G
SW:HCD2_HUMAN	R21	4258	3	1786.9	(+0.7)	4.071	0.382	0.999	2	R.LVAGEMGQNEPDQGGQR.G
SW:HCD2_HUMAN	R21	4182	3	1786.9	(+0.3)	3.871	0.368	0.998	2	R.LVAGEMGQNEPDQGGQR.G
SW:HCD2_HUMAN	R21	7226	2	2196.5	(-0.0)	4.726	0.410	0.996	1	R.LVGQASAVLLDLPNSGGEAQAQ.K
SW:HCD2_HUMAN	R21	8894	2	2086.5	(+0.0)	3.755	0.512	0.998	1	R.VMTIAPGLFGTPLLTSLEK.V

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:HCD2_HUMAN	R22	6632	2	1207.5	(+0.3)	2.764	0.280	0.945	2	K.GGIVGM@TL*PIAR.D
SW:HCDH_HUMAN	R19	8536	2	1619.0	(-0.7)	3.520	0.402	0.979	3	R.FAGL*HFFNPVPMK#.L
SW:HCDH_HUMAN	R19	8532	2	1605.0	(+1.0)	3.149	0.526	1.000	3	R.FAGLHFFNPVPMK.L
SW:HCDH_HUMAN	R19	7748	3	2783.1	(-0.1)	4.916	0.462	1.000	3	K.FIVDGWHEMDAENPL*HQSPSL*NK#.L
SW:HCDH_HUMAN	R19	7746	3	2763.1	(+0.5)	4.824	0.543	1.000	3	K.FIVDGWHEMDAENPLHQSPSLNK.L
SW:HCDH_HUMAN	R19	10272	2	2390.7	(+0.1)	3.828	0.411	0.982	3	K.L*GAGYPMGPFEL*L*DYVGL*DTTK#.F
SW:HCDH_HUMAN	R19	10270	2	2358.7	(-1.0)	3.675	0.491	1.000	3	K.LGAGYPMGPFELLDYVGLDTTK.F
SW:HCDH_HUMAN	R02	10093	3	3086.5	(+0.6)	4.190	0.532	1.000	3	K.TLSTIATSTDAASVVHSTDLVVEAIVENLK.V
SW:HDA1_HUMAN	R14	7231	2	2077.3	(-0.1)	3.001	0.283	0.161	3	R.DGIDDESIEAIFK#PVM@SK#.V
SW:HDA1_HUMAN	R13	6273	3	2254.4	(-0.1)	4.173	0.269	0.776	3	K.L*HISPSNMTNQNTNEYL*EK#.I
SW:HDA1_HUMAN	R14	6287	3	2234.4	(+0.9)	5.079	0.411*	0.332	3	K.LHISPSNMTNQNTNEYLEK.I
SW:HDA1_HUMAN	R14	5523	3	2270.4	(+0.2)	3.762	0.252	0.952	3	K.L*HISPSNM@TNQNTNEYL*EK#.I
SW:HDA1_HUMAN	R14	7495	2	1608.9	(+0.5)	4.100	0.536	0.999	5	R.MTHNLLLNYGLYR.K
SW:HDA1_HUMAN	R14	9179	3	1846.2	(+0.7)	3.799	0.402*	0.121	3	K.SFNL*PML*ML*GGGGYTIR.N
SW:HDA1_HUMAN	R14	6475	2	1381.5	(+0.6)	3.374	0.439	0.999	5	K.YGEYFPGTGDL*R.D
SW:HDA1_HUMAN	R14	6479	2	1375.5	(+0.5)	3.008	0.495	1.000	5	K.YGEYFPGTGDLR.D
SW:HDA1_HUMAN	R13	6149	2	1165.3	(+0.8)	2.772	0.319	0.974	3	K.YYAVNYPL*R.D
SW:HDA1_HUMAN	R14	6149	2	1159.3	(+0.7)	2.954	0.447	1.000	3	K.YYAVNYPLR.D
SW:HDA2_HUMAN	R14	6187	3	2235.5	(+0.6)	5.469	0.327	0.998	1	K.LHISPSNMTNQNTPEYMEK.I
SW:HDA2_HUMAN	R14	6179	3	2249.5	(-0.2)	4.605	0.411*	0.133	1	K.L*HISPSNMTNQNTPEYMEK#.I
SW:HDA2_HUMAN	R14	5419	3	2265.5	(+0.4)	4.123	0.382	0.998	1	K.L*HISPSNM@TNQNTPEYMEK#.I
SW:HDA2_HUMAN	R14	9477	2	1824.2	(+0.1)	4.098	0.567	0.999	1	K.TFNLPLMLGGGGYTIR.N
SW:HE47_HUMAN	R02	8284	3	2598.8	(+0.5)	4.480	0.406	0.999	3	R.FEVNISELPDEIDISSYIEQTR.-
SW:HE47_HUMAN	R02	6412	2	1494.6	(+0.9)	2.589	0.242	0.813	6	K.GL*AITFVSDENDAK#.I
SW:HE47_HUMAN	R16	984	2	973.1	(+0.8)	2.595	0.238	0.939	5	K.ILNDVQDR.F
SW:HE47_HUMAN	R03	6901	2	1104.3	(+1.0)	3.361	0.513*	0.702	6	R.ILVATNLFGR.G
SW:HE47_HUMAN	R16	982	2	979.1	(+0.7)	2.570	0.232	0.694	5	K.IL*NDVQDR.F
SW:HEXA_HUMAN	R15	10715	3	2205.5	(+0.9)	3.722	0.357	0.997	3	K.QLESFYIQTLLDIVSSYQK.G
SW:HEXA_HUMAN	R15	7857	2	1328.5	(+0.1)	2.274	0.217	0.615	3	R.GL*ETFSQL*VWK#.S
SW:HEXB_HUMAN	R21	8738	3	3263.6	(-0.1)	5.164	1.000*	0.127	4	K.FNVLHWHIVDDQSPYQSITFPELSNK.G
SW:HEXB_HUMAN	R21	7148	2	1100.3	(+0.8)	3.259	0.202	0.952	3	K.VLDIATINK.G
SW:HEXB_HUMAN	R21	7638	2	1423.6	(+0.9)	3.043	0.454	0.985	3	K.GSIVWQEVFDDK.A
SW:HFC1_HUMAN	R08	7141	2	1365.6	(+0.2)	3.083	0.247	0.900	1	R.SPAFVQL*APL*SSK#.V
SW:HFC1_HUMAN	R09	7154	2	1343.5	(+0.1)	2.248	0.287*	0.085	3	K.ENQWFDVGVIK#.G
SW:HM13_HUMAN	R02	6114	2	1401.5	(+0.6)	2.702	0.348	0.971	7	K.EEIINYEFDTK.D
SW:HM13_HUMAN	R01	6339	2	1633.8	(-0.2)	3.217	0.303	0.943	6	R.QYQL*L*FTQGSGENK#.E
SW:HM1X_HUMAN	R20	5852	3	1543.8	(+0.4)	4.185	0.365	0.988	6	K.IK#GEHPGL*SIGDVAK#.K
SW:HM1X_HUMAN	R20	5858	2	1521.8	(+0.9)	3.736	0.548	0.999	6	K.IKGEHPGLSIGDVAK.K
SW:HM1X_HUMAN	R20	5856	2	1543.8	(-0.8)	3.669	0.415	0.253	6	K.IK#GEHPGL*SIGDVAK#.K
SW:HM1X_HUMAN	R20	5472	2	1465.6	(-0.8)	3.297	0.425	0.955	6	K.LGEMWNNTAADDK.Q
SW:HM1X_HUMAN	R20	5916	3	2111.3	(+1.0)	3.705	0.459	0.997	5	K.LGEMWNNTAADDKQPYEK.K
SW:HM1X_HUMAN	R20	5714	2	1280.4	(+0.7)	2.898	0.512	1.000	6	K.GEHPGLSIGDVAK.K
SW:HMG1_HUMAN	R20	6018	3	1593.7	(-0.4)	4.030	0.374*	0.102	6	K.KHPDASVNFSEFSK.K
SW:HMG1_HUMAN	R20	6016	2	1593.7	(-0.3)	2.980	0.433*	0.300	6	K.KHPDASVNFSEFSK.K
SW:HMG1_HUMAN	R20	6024	2	1609.7	(-1.0)	2.628	0.257*	0.050	6	K.K#HPDASVNFSEFSK#.K
SW:HMG1_HUMAN	R20	6174	2	1465.6	(+0.8)	2.409	0.291	0.908	6	K.HPDASVNFSEFSK.K
SW:HMG2_HUMAN	R21	6168	2	1473.6	(-0.1)	2.441	0.276*	0.105	3	K.HPDSSVNFAEFSK#.K
SW:HMG2_HUMAN	R20	6000	2	1609.7	(+0.2)	3.336	0.397*	0.373	3	K.K#HPDSSVNFAEFSK#.K
SW:HMG2_HUMAN	R20	5642	2	1394.6	(-0.2)	3.694	0.478	0.999	3	K.KLGEMWSEQSAK.D
SW:HMG2_HUMAN	R20	5660	2	1416.6	(-0.9)	2.767	0.254	0.694	3	K.K#L*GEMWSEQSAK#.D
SW:HMG2_HUMAN	R20	1928	2	1296.4	(-0.1)	2.702	0.252	0.740	3	K.L*GEM@WSEQSAK#.D
SW:HMG2_HUMAN	R20	5332	2	1280.4	(-0.5)	2.619	0.408	0.963	3	K.L*GEMWSEQSAK#.D
SW:HMG2_HUMAN	R20	5424	2	1266.4	(+0.2)	2.399	0.456	0.974	3	K.LGEMWSEQSAK.D
SW:HMG2_HUMAN	R21	5692	2	1280.4	(+0.2)	3.207	0.519	1.000	3	K.L*GEMWSEQSAK#.D
SW:HMG2_HUMAN	R21	4798	2	1296.4	(-0.1)	2.982	0.402	0.972	3	K.L*GEM@WSEQSAK#.D

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:HMG2_HUMAN	R20	2316	2	1326.4	(-0.6)	2.517	0.231	0.761	3	K.SEHPGL*SIGDTAK#.K
SW:HMG2_HUMAN	R20	2328	2	1312.4	(-0.5)	2.463	0.399	0.957	3	K.SEHPGLSIGDTAK.K
SW:HMG2_HUMAN	R20	1602	2	956.1	(+0.9)	2.209	0.162	0.051	3	K.SKFE DMAK.S
SW:HMG2_HUMAN	R21	5186	2	1312.4	(-0.5)	2.202	0.407	0.940	3	K.SEHPGLSIGDTAK.K
SW:HO2_HUMAN	R19	9202	2	2419.7	(+0.3)	5.382	0.544	0.999	2	K.AFEYNMQIFNELDQAGSTLAR.E
SW:HO2_HUMAN	R19	9208	2	2431.7	(+0.3)	4.620	0.419	0.996	2	K.AFEYNMQIFNEL* DQAGSTL*AR.E
SW:HO2_HUMAN	R19	5674	2	1444.5	(-0.1)	2.665	0.366	0.956	2	R.ETLEDGFVHDGK.G
SW:HO2_HUMAN	R19	5666	2	1458.5	(-0.1)	2.416	0.316	0.873	2	R.ETL*EDGFVHDGK#.G
SW:HO2_HUMAN	R19	8284	2	2634.9	(-0.4)	4.218	0.549	1.000	2	K.LPSTGEGTQFYLFENVDNAQQFK.Q
SW:HO2_HUMAN	R19	8276	3	2654.9	(+0.5)	4.138	0.363	0.998	2	K.L*PSTGEGTQFYLFENVDNAQQFK#.Q
SW:HO2_HUMAN	R19	6070	2	1268.5	(-0.3)	2.888	0.347	0.963	2	R.YMGDL SGGQVLK.K
SW:HO2_HUMAN	R19	6068	2	1288.5	(-0.6)	2.722	0.508	0.981	2	R.YMGDL*SGGQVL*K#.K
SW:HO2_HUMAN	R19	2304	2	1304.5	(-0.0)	2.291	0.316	0.858	2	R.YM@GDL*SGGQVL*K#.K
SW:HS72_HUMAN	R12	6882	2	1082.2	(+0.2)	2.613	0.278	0.932	7	K.LLQDF FNGK.E
SW:HS72_HUMAN	R12	1538	2	1692.7	(-0.3)	3.444	0.447	0.985	5	K.STAGDTHLGGEDFDNR.M
SW:HS72_HUMAN	R13	1888	2	1698.7	(+0.9)	4.310	0.386	1.000	5	K.STAGDTHL*GGEDFDNR.M
SW:HS72_HUMAN	R13	1878	2	1692.7	(+1.0)	4.023	0.457	1.000	5	K.STAGDTHLGGEDFDNR.M
SW:HS72_HUMAN	R13	7349	2	1266.4	(+0.5)	2.427	0.285	0.930	5	R.FEEL*NADL*FR.G
SW:HS7C_HUMAN	R12	6594	2	1200.4	(-0.5)	2.556	0.315	0.924	2	K.DAGTIAGLNVLR.I
SW:HS7C_HUMAN	R12	6580	2	1212.4	(+0.9)	2.361	0.187	0.743	2	K.DAGTIAGL*NVL*R.I
SW:HS7C_HUMAN	R13	6937	2	1200.4	(-0.9)	2.592	0.303	0.791	2	K.DAGTIAGLNVLR.I
SW:HS7C_HUMAN	R12	2438	2	1255.4	(-0.2)	3.791	0.498	1.000	2	R.FDDAVVQSDMK.H
SW:HS7C_HUMAN	R12	2362	2	1263.4	(-0.1)	3.435	0.435	1.000	2	R.FDDAVVQSDMK#.H
SW:HS7C_HUMAN	R12	2440	2	1263.4	(-0.2)	3.400	0.419	0.983	2	R.FDDAVVQSDMK#.H
SW:HS7C_HUMAN	R12	3760	2	1255.4	(+0.4)	3.282	0.537	1.000	2	R.FDDAVVQSDMK.H
SW:HS7C_HUMAN	R12	2516	2	1263.4	(-0.7)	3.105	0.405	0.977	2	R.FDDAVVQSDMK#.H
SW:HS7C_HUMAN	R12	2514	2	1255.4	(-0.7)	3.049	0.451	0.987	2	R.FDDAVVQSDMK.H
SW:HS7C_HUMAN	R12	3614	2	1255.4	(+0.6)	2.849	0.457	0.989	2	R.FDDAVVQSDMK.H
SW:HS7C_HUMAN	R12	2360	2	1255.4	(-0.7)	2.845	0.473	0.986	2	R.FDDAVVQSDMK.H
SW:HS7C_HUMAN	R12	3515	2	1255.4	(+0.6)	2.637	0.394	0.965	2	R.FDDAVVQSDMK.H
SW:HS7C_HUMAN	R13	4625	2	1255.4	(-0.0)	3.373	0.513	1.000	2	R.FDDAVVQSDMK.H
SW:HS7C_HUMAN	R13	4647	2	1263.4	(-0.6)	3.016	0.439	0.980	2	R.FDDAVVQSDMK#.H
SW:HS7C_HUMAN	R13	4703	2	1255.4	(-0.5)	2.447	0.420	0.968	2	R.FDDAVVQSDMK.H
SW:HS7C_HUMAN	R12	11042	3	2515.8	(+0.9)	4.878	0.443*	0.222	3	R.GVPQIEVTFDIDANGILNVSAVDK.S
SW:HS7C_HUMAN	R12	10808	3	2515.8	(+0.4)	4.363	0.451	1.000	3	R.GVPQIEVTFDIDANGILNVSAVDK.S
SW:HS7C_HUMAN	R12	10968	3	2515.8	(+1.0)	4.309	0.419	0.987	3	R.GVPQIEVTFDIDANGILNVSAVDK.S
SW:HS7C_HUMAN	R12	12386	3	2515.8	(+0.7)	4.277	0.457	1.000	3	R.GVPQIEVTFDIDANGILNVSAVDK.S
SW:HS7C_HUMAN	R12	11662	3	2515.8	(+0.9)	4.120	0.390	0.998	3	R.GVPQIEVTFDIDANGILNVSAVDK.S
SW:HS7C_HUMAN	R12	12626	3	2515.8	(+0.4)	4.050	0.428	0.999	3	R.GVPQIEVTFDIDANGILNVSAVDK.S
SW:HS7C_HUMAN	R12	13228	3	2515.8	(+0.5)	3.982	0.369	0.997	3	R.GVPQIEVTFDIDANGILNVSAVDK.S
SW:HS7C_HUMAN	R12	11126	3	2515.8	(+0.6)	3.707	0.299	0.987	3	R.GVPQIEVTFDIDANGILNVSAVDK.S
SW:HS7C_HUMAN	R13	11813	3	2515.8	(+0.2)	4.434	0.419	0.997	3	R.GVPQIEVTFDIDANGILNVSAVDK.S
SW:HS7C_HUMAN	R12	6502	2	1244.5	(+0.8)	3.430	0.469	1.000	2	R.MVNHFAIEFK#.R
SW:HS7C_HUMAN	R12	6124	2	1260.5	(+0.8)	2.676	0.383	0.974	2	R.M@VNHFAIEFK#.R
SW:HS7C_HUMAN	R13	6841	2	1236.5	(+0.9)	3.772	0.488	0.957	2	R.MVNHFAIEFK.R
SW:HS7C_HUMAN	R12	4664	2	1674.8	(+0.4)	4.438	0.518	1.000	1	K.NQVAM@NPTNTVFDK#.R
SW:HS7C_HUMAN	R12	4584	2	1674.8	(-0.6)	3.848	0.419*	0.518	1	K.NQVAM@NPTNTVFDK#.R
SW:HS7C_HUMAN	R12	5764	2	1650.8	(+0.9)	3.703	0.573	0.999	1	K.NQVAMNPTNTVFDK.R
SW:HS7C_HUMAN	R12	4768	2	1674.8	(+0.8)	2.750	0.280	0.907	1	K.NQVAM@NPTNTVFDK#.R
SW:HS7C_HUMAN	R13	6161	2	1658.8	(-0.5)	3.287	0.372	0.967	1	K.NQVAMNPTNTVFDK#.R
SW:HS7C_HUMAN	R13	5117	2	1674.8	(-0.4)	3.115	0.374*	0.267	1	K.NQVAM@NPTNTVFDK#.R
SW:HS7C_HUMAN	R13	6155	2	1650.8	(-0.3)	2.842	0.475	0.982	1	K.NQVAMNPTNTVFDK.R
SW:HS7C_HUMAN	R12	6386	2	1304.5	(+0.2)	2.457	0.448	0.975	5	K.NSLESYAFNMK.A
SW:HS7C_HUMAN	R12	5456	2	1334.5	(-0.7)	2.303	0.188	0.546	5	K.NSL*ESYAFNM@K#.A
SW:HS7C_HUMAN	R12	4600	2	1419.6	(-0.2)	3.640	0.407	0.981	2	R.RFDDAVVQSDMK#.H
SW:HS7C_HUMAN	R12	4570	2	1411.6	(-0.3)	3.130	0.480	1.000	2	R.RFDDAVVQSDMK.H
SW:HS7C_HUMAN	R12	4660	2	1411.6	(-0.1)	3.033	0.458	0.986	2	R.RFDDAVVQSDMK.H
SW:HS7C_HUMAN	R13	5119	2	1411.6	(-0.2)	2.996	0.433	0.981	2	R.RFDDAVVQSDMK.H
SW:HS7C_HUMAN	R13	5107	2	1419.6	(-0.1)	2.863	0.334	0.942	2	R.RFDDAVVQSDMK#.H
SW:HS7C_HUMAN	R12	7410	2	1617.9	(+0.4)	4.743	0.554	0.998	2	K.SFYPEEVSSMVLTK.M
SW:HS7C_HUMAN	R12	7422	3	1631.9	(+0.9)	4.262	0.490	1.000	2	K.SFYPEEVSSMVL*TK#.M
SW:HS7C_HUMAN	R12	7406	2	1631.9	(-0.7)	2.367	0.227	0.676	2	K.SFYPEEVSSMVL*TK#.M
SW:HS7C_HUMAN	R13	7637	2	1617.9	(-0.1)	4.309	0.523	1.000	2	K.SFYPEEVSSMVLTK.M

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:HS7C_HUMAN	R13	7631	2	1631.9	(-0.1)	3.252	0.379	0.969	2	K.SFYPEEVSSMVL*TK#.M
SW:HS7C_HUMAN	R12	8702	2	2261.5	(+0.2)	5.391	0.564	0.996	2	K.SINPDEAVAYGAAVQAAILSGDK.S
SW:HS7C_HUMAN	R12	8720	2	2275.5	(+0.7)	5.246	0.610	0.992	2	K.SINPDEAVAYGAAVQAAIL*SGDK#.S
SW:HS7C_HUMAN	R12	8690	3	2275.5	(+0.4)	4.413	0.500	0.984	2	K.SINPDEAVAYGAAVQAAIL*SGDK#.S
SW:HS7C_HUMAN	R13	8863	3	2261.5	(+0.8)	4.023	0.542	1.000	2	K.SINPDEAVAYGAAVQAAILSGDK.S
SW:HS7C_HUMAN	R13	8897	2	2275.5	(-0.4)	2.771	0.312	0.906	2	K.SINPDEAVAYGAAVQAAIL*SGDK#.S
SW:HS7C_HUMAN	R12	5936	2	1488.7	(+0.4)	2.742	0.263	0.480	2	K.SQIHDIVL*VGGSTR.I
SW:HS7C_HUMAN	R13	6207	2	1482.7	(-0.5)	3.323	0.428	0.970	2	K.SQIHDIVLVGGSTR.I
SW:HS7C_HUMAN	R13	5907	2	1334.5	(-0.1)	2.375	0.284	0.847	5	K.NSL*ESYAFNM@K#.A
SW:HS9A_HUMAN	R10	7705	2	1243.4	(+0.5)	2.804	0.509	0.991	15	K.ADLINNLGTLAK.S
SW:HS9A_HUMAN	R11	6620	2	1263.4	(-0.3)	2.429	0.200	0.673	15	K.ADL*INNL*GTLAK#.S
SW:HS9A_HUMAN	R11	6604	2	1526.7	(-0.7)	2.885	0.325*	0.264	13	R.GVVDESDL*PL*NISR.E
SW:HS9A_HUMAN	R10	4553	2	1225.4	(+0.1)	2.600	0.390	0.970	7	K.HIYYITGETK.D
SW:HS9A_HUMAN	R10	4475	2	1225.4	(-0.5)	2.380	0.332	0.932	7	K.HIYYITGETK.D
SW:HS9A_HUMAN	R10	4273	2	1233.4	(+0.1)	2.359	0.325	0.902	7	K.HIYYITGETK#.D
SW:HS9A_HUMAN	R10	4413	2	1233.4	(+0.1)	2.309	0.268	0.821	7	K.HIYYITGETK#.D
SW:HS9A_HUMAN	R10	6319	2	1834.9	(-0.6)	4.077	0.512	1.000	6	R.NPDDITNEEYGEFYK.S
SW:HS9A_HUMAN	R10	6329	2	1842.9	(-0.5)	4.048	0.424	1.000	6	R.NPDDITNEEYGEFYK#.S
SW:HS9A_HUMAN	R11	6544	2	1528.7	(+0.2)	3.956	0.458	1.000	13	K.SLTNDWEDHLAVK.H
SW:HS9A_HUMAN	R10	6377	2	1380.6	(-0.6)	2.384	0.236*	0.093	4	R.TL*TIVDTGIGM@TK#.A
SW:HS9A_HUMAN	R13	6883	2	1514.7	(+0.8)	3.594	0.472*	0.625	13	R.GVVDESDLPLNISR.E
SW:HS9B_HUMAN	R10	7741	3	1796.0	(+0.0)	3.834	0.382	0.997	5	K.HL*EINPDHPIVETL*R.Q
SW:HS9B_HUMAN	R11	6886	2	1237.4	(+0.9)	2.228	0.202	0.770	4	R.RAPFDLFENK.K
SW:HS9B_HUMAN	R10	7859	2	1350.6	(+0.4)	2.949	0.500*	0.400	6	R.TLTLVDTGIGMTK.A
SW:HS9B_HUMAN	R10	7289	3	2178.3	(+0.5)	4.384	0.510	1.000	5	R.YHTSQSGDEMTSLSEYVSR.M
SW:HS9B_HUMAN	R10	7213	3	2178.3	(+0.7)	3.962	0.502	1.000	5	R.YHTSQSGDEMTSLSEYVSR.M
SW:HS9B_HUMAN	R10	7139	3	2178.3	(+0.7)	3.847	0.498	0.999	5	R.YHTSQSGDEMTSLSEYVSR.M
SW:HS9B_HUMAN	R11	4646	2	1169.3	(+0.1)	2.204	0.345	0.892	5	K.SIYYITGESK#.E
SW:H XK1_HUMAN	R10	4865	2	1095.2	(+0.4)	2.786	0.331	0.972	7	K.FLSQIESDR.L
SW:H XK1_HUMAN	R10	4869	2	1101.2	(+0.0)	2.664	0.287	0.941	7	K.FL*SQIESDR.L
SW:H XK1_HUMAN	R10	6307	2	1028.2	(+0.9)	2.711	0.444	0.984	5	K.GAALITAVGVR.L
SW:H XK1_HUMAN	R10	2290	2	1228.4	(+0.8)	2.570	0.221*	0.237		R.L*VNEYSL*NAGK#.Q
SW:H XK1_HUMAN	R10	9739	3	1502.7	(+0.9)	3.751	0.298	0.947	5	R.SANL*VAATL*GAIL*NR.L
SW:H XK1_HUMAN	R10	2318	2	1208.4	(+0.9)	2.291	0.274*	0.167		R.LVNEYSLNAGK.Q
SW:ICT1_HUMAN	R23	7748	2	1640.9	(-0.2)	3.763	0.477	1.000	1	R.FHLATAEWIAEPVR.Q
SW:ICT1_HUMAN	R23	6508	2	1305.5	(-0.1)	2.468	0.340	0.932	1	R.LGELITSESSR.Y
SW:ICT1_HUMAN	R23	5700	2	1510.6	(-0.3)	2.295	0.356	0.904	1	K.LYPESQGSdTAWR.V
SW:IDHB_HUMAN	R18	5509	2	1460.6	(+0.1)	3.167	0.482	1.000	6	R.DM@GGYSTTTDFIK#.S
SW:IDHB_HUMAN	R18	7391	2	1383.7	(-0.4)	2.293	0.335	0.906	5	R.KLDLFANVVHVK.S
SW:IDHB_HUMAN	R18	5191	2	1055.2	(+0.0)	2.244	0.205	0.688	5	K.L*EQVL*SSMK#.E
SW:IDHP_HUMAN	R16	8110	2	1163.3	(+0.8)	2.461	0.254	0.899	2	K.DIFQEIFDK#.H
SW:IDHP_HUMAN	R16	5476	2	1863.9	(-0.2)	5.007	0.410	0.999	2	R.DQTDDQVTIDSAL*ATQK#.Y
SW:IDHP_HUMAN	R16	5468	2	1849.9	(-0.6)	4.251	0.465	0.999	2	R.DQTDDQVTIDSALATQK.Y
SW:IDHP_HUMAN	R16	8290	2	1446.6	(+0.5)	3.712	0.432	1.000	2	R.FK#DIFQEIFDK#.H
SW:IDHP_HUMAN	R16	8284	2	1430.6	(+0.6)	3.367	0.445	1.000	2	R.FKDIFQEIFDK.H
SW:IDHP_HUMAN	R17	8758	2	1446.6	(+0.0)	4.077	0.374	1.000	2	R.FK#DIFQEIFDK#.H
SW:IDHP_HUMAN	R16	1488	2	1229.4	(+0.9)	3.861	0.369	0.901	2	R.GKLDGNQDLIR.F
SW:IDHP_HUMAN	R16	1356	2	1056.2	(+0.3)	2.654	0.218	0.916	2	K.L*DGNQDL*IR.F
SW:IDHP_HUMAN	R16	1338	2	1044.2	(-0.0)	2.212	0.149	0.569	2	K.LDGNQDLIR.F
SW:IDHP_HUMAN	R17	2178	2	1056.2	(+0.6)	2.683	0.179	0.886	2	K.L*DGNQDL*IR.F
SW:IDHP_HUMAN	R16	4930	3	1677.9	(+1.0)	4.450	0.458	1.000	1	K.VAKPVVEMDGDDEMTR.I
SW:IDHP_HUMAN	R16	6588	2	1107.2	(+0.1)	2.243	0.242	0.819	2	K.YFDL*GL*PNR.D
SW:IDHP_HUMAN	R17	6998	2	1095.2	(+0.3)	2.596	0.271	0.947	2	K.YFDLGLPNR.D
SW:IDHP_HUMAN	R17	7000	2	1107.2	(+0.7)	2.517	0.262	0.934	2	K.YFDL*GL*PNR.D
SW:IDHP_HUMAN	R17	8564	2	1155.3	(+0.5)	2.309	0.238	0.876	2	K.DIFQEIFDK.H
SW:ILF3_HUMAN	R10	5907	2	1320.4	(+0.1)	3.171	0.395	0.982	6	K.AVSDWIDEQEK.G
SW:ILF3_HUMAN	R11	6262	2	1041.2	(+0.9)	2.341	0.393	0.703	17	K.AYAAL*AAL*EK#.L
SW:ILF3_HUMAN	R09	2194	2	1369.5	(-0.8)	2.845	0.344	0.888	14	R.EDITQSAQHALLR.L
SW:ILF3_HUMAN	R09	2116	2	1369.5	(-0.5)	2.817	0.363	0.962	14	R.EDITQSAQHALLR.L



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ILF3_HUMAN	R09	2190	2	1375.5	(-0.1)	2.764	0.315	0.944	14	R.EDITQSAQHAL*R.L
SW:ILF3_HUMAN	R09	2112	2	1375.5	(-0.8)	2.743	0.338	0.868	14	R.EDITQSAQHAL*R.L
SW:ILF3_HUMAN	R10	2388	2	1369.5	(+0.6)	3.136	0.355	0.964	14	R.EDITQSAQHALL.R
SW:ILF3_HUMAN	R10	2358	2	1375.5	(-0.2)	2.587	0.304	0.921	14	R.EDITQSAQHAL*R.L
SW:ILF3_HUMAN	R09	7388	2	1760.1	(+0.8)	3.953	0.528	0.996	10	K.EPPLSLTIHLTSPVVR.E
SW:ILF3_HUMAN	R09	2008	3	3263.2	(+0.4)	7.524	0.584	1.000	1	K.GYNHGQGSYSYSNSYNSPGGGGGSDYNYESK#.F
SW:ILF3_HUMAN	R09	2088	3	3263.2	(-0.2)	7.168	0.563	1.000	1	K.GYNHGQGSYSYSNSYNSPGGGGGSDYNYESK#.F
SW:ILF3_HUMAN	R09	2174	3	3263.2	(-0.0)	6.884	0.539	0.995	1	K.GYNHGQGSYSYSNSYNSPGGGGGSDYNYESK#.F
SW:ILF3_HUMAN	R09	2004	3	3255.2	(+0.6)	6.810	0.585	1.000	1	K.GYNHGQGSYSYSNSYNSPGGGGGSDYNYESK#.F
SW:ILF3_HUMAN	R09	2084	3	3255.2	(-0.1)	6.765	0.485	1.000	1	K.GYNHGQGSYSYSNSYNSPGGGGGSDYNYESK#.F
SW:ILF3_HUMAN	R09	2162	3	3255.2	(-0.1)	5.442	0.423	0.995	1	K.GYNHGQGSYSYSNSYNSPGGGGGSDYNYESK#.F
SW:ILF3_HUMAN	R09	7488	3	2678.9	(+0.8)	4.338	0.577	1.000	9	K.HSSVYPTQEELEAVQNMVSHTER.A
SW:ILF3_HUMAN	R09	7492	3	2672.9	(+0.6)	4.149	0.566	0.997	9	K.HSSVYPTQEELEAVQNMVSHTER.A
SW:ILF3_HUMAN	R10	8321	3	2672.9	(+0.5)	4.330	0.603	1.000	9	K.HSSVYPTQEELEAVQNMVSHTER.A
SW:ILF3_HUMAN	R09	4800	2	985.2	(+0.2)	2.349	0.260	0.875	14	R.LAAFGQLHK.V
SW:ILF3_HUMAN	R09	4836	2	1005.2	(+0.6)	2.260	0.206	0.770	14	R.L*AAFGL*HK#.V
SW:ILF3_HUMAN	R09	6828	2	1415.6	(+0.8)	2.290	0.253	0.836	17	K.LFPDTPALDANK.K
SW:ILF3_HUMAN	R10	8037	2	1415.6	(+0.9)	2.819	0.283	0.943	17	K.LFPDTPALDANK.K
SW:ILF3_HUMAN	R09	4636	2	1302.6	(-0.5)	2.685	0.155	0.055	13	R.LNQLKPLQYK.L
SW:ILF3_HUMAN	R10	5127	2	1302.6	(+0.2)	2.591	0.228	0.103	13	R.LNQLKPLQYK.L
SW:ILF3_HUMAN	R09	6968	3	3220.6	(-0.6)	5.178	0.439	0.999	13	K.L*VSQTGPVHAPIFTM@SVEVDGNSFEASGPSK#.K
SW:ILF3_HUMAN	R09	1704	2	1074.2	(+0.4)	2.766	0.404	0.986	23	K.NPVMELNEK.R
SW:ILF3_HUMAN	R09	1708	2	1088.2	(-0.3)	2.440	0.188	0.737	23	K.NPVMEL*NEK#.R
SW:ILF3_HUMAN	R10	1924	2	1074.2	(+0.6)	2.682	0.308	0.965	23	K.NPVMELNEK.R
SW:ILF3_HUMAN	R10	1908	2	1088.2	(+0.1)	2.390	0.191	0.723	23	K.NPVMEL*NEK#.R
SW:ILF3_HUMAN	R11	1764	2	1074.2	(+1.0)	2.693	0.268	0.952	23	K.NPVMELNEK.R
SW:ILF3_HUMAN	R09	4482	3	3022.0	(-0.1)	5.542	0.557	1.000	4	R.SGGNSYSGGGASYNPGSHGGYGGGGSGGGSSYQGK#.Q
SW:ILF3_HUMAN	R09	4480	3	3014.0	(+0.0)	4.411	0.535	1.000	4	R.SGGNSYSGGGASYNPGSHGGYGGGGSGGGSSYQGK#.Q
SW:ILF3_HUMAN	R09	1172	3	3014.0	(+0.3)	3.902	0.589	1.000	4	R.SGGNSYSGGGASYNPGSHGGYGGGGSGGGSSYQGK#.Q
SW:ILF3_HUMAN	R09	2318	2	1601.8	(-0.4)	2.631	0.270	0.116	12	K.SIGTANRPMGAGEALR.R
SW:ILF3_HUMAN	R09	1788	2	1093.3	(+0.0)	2.206	0.427	0.949	14	K.VL*GM@DPL*PSK#.M
SW:ILF3_HUMAN	R10	2018	2	1093.3	(-0.2)	2.251	0.281	0.825	14	K.VL*GM@DPL*PSK#.M
SW:ILF3_HUMAN	R09	1720	2	1472.6	(-0.3)	2.919	0.253	0.902	17	K.VL*QDM@GL*PTGAEGR.D
SW:ILF3_HUMAN	R09	5562	2	1444.6	(-0.1)	2.824	0.413	0.973	17	K.VLQDMGLPTGAEGR.D
SW:ILF3_HUMAN	R10	6137	2	1444.6	(+0.6)	3.450	0.377	0.986	17	K.VLQDMGLPTGAEGR.D
SW:ILF3_HUMAN	R10	1958	2	1472.6	(+0.0)	2.261	0.267	0.783	17	K.VL*QDM@GL*PTGAEGR.D
SW:ILF3_HUMAN	R11	5922	2	1456.6	(+0.2)	3.695	0.478	0.999	17	K.VL*QDMGL*PTGAEGR.D
SW:ILF3_HUMAN	R09	5922	2	932.1	(+0.7)	2.331	0.380	0.974	13	R.VPTWGPL*R.G
SW:ILF3_HUMAN	R09	1758	2	1436.5	(-0.1)	2.669	0.358	0.953	23	K.YELISETGGSHDK.R
SW:ILF3_HUMAN	R09	1746	2	1592.7	(-0.3)	3.217	0.460	0.584	23	K.YELISETGGSHDKR.F
SW:ILF3_HUMAN	R11	4950	2	985.2	(+0.4)	2.279	0.187	0.786	14	R.LAAFGQLHK.V
SW:IM44_HUMAN	R17	1576	2	1032.2	(+0.4)	2.620	0.204	0.855	2	R.AL*SQGVESVK#.K
SW:IM44_HUMAN	R17	6694	2	1478.6	(-0.0)	3.888	0.320	0.981	2	R.DQDELNPYAAGR.L
SW:IM44_HUMAN	R17	6688	2	1484.6	(+0.4)	3.721	0.408	1.000	2	R.DQDEL*NPYAAGR.L
SW:IM44_HUMAN	R17	6132	2	1550.7	(-0.8)	2.991	0.467	0.951	1	K.EIDDSVLGQTGPYR.R
SW:IM44_HUMAN	R17	6136	2	1556.7	(+0.3)	2.810	0.286	0.942	1	K.EIDDSVL*GQTGPYR.R
SW:IM44_HUMAN	R17	8448	2	1189.4	(+0.3)	2.912	0.471	0.988	2	K.GFL*SGL*L*DNVK#.Q
SW:IM44_HUMAN	R17	6860	2	1453.7	(+0.6)	4.213	0.472	1.000	2	R.IL*DIDNVDL*AM@GK#.M
SW:IM44_HUMAN	R17	7512	2	1437.7	(+0.0)	3.910	0.473	1.000	2	R.IL*DIDNVDL*AMGK#.M
SW:IM44_HUMAN	R17	2134	2	938.1	(+0.5)	2.427	0.277	0.912	2	K.L*GEL*TGTVK#.E
SW:IM44_HUMAN	R17	8984	2	1433.6	(+0.3)	3.768	0.465	1.000	2	K.TEMSEVL*TEIL*R.V
SW:IM44_HUMAN	R17	8186	2	1176.4	(-0.1)	2.380	0.315	0.886	2	K.VTDL*L*GGL*FSK#.T
SW:IM44_HUMAN	R17	7646	2	1449.6	(-0.3)	2.364	0.260	0.830	2	K.TEM@SEVL*TEIL*R.V
SW:IMA2_HUMAN	R14	5589	2	1908.0	(-0.6)	3.808	0.513	1.000	3	K.GINSSNVENQL*QATQAAR.K
SW:IMA2_HUMAN	R15	5441	2	1902.0	(-0.8)	3.252	0.442	0.953	3	K.GINSSNVENQLQATQAAR.K
SW:IMA2_HUMAN	R14	12241	3	1992.4	(+0.1)	4.175	0.440	0.999	1	K.IIL*VIL*DAISNIFQAAEK#.L
SW:IMA2_HUMAN	R14	7973	2	1550.9	(-0.0)	2.627	0.414	0.965	3	K.LLGASELPIVTPALR.A
SW:IMA2_HUMAN	R14	7971	2	1574.9	(-0.9)	2.534	0.281	0.678	3	K.L*L*GASEL*PIVTPAL*R.A
SW:IMA2_HUMAN	R15	7717	2	1574.9	(-0.3)	3.479	0.370	0.978	3	K.L*L*GASEL*PIVTPAL*R.A
SW:IMA2_HUMAN	R15	9131	2	1944.3	(+0.2)	2.640	0.402	0.961	3	K.NPAPPIDAVEQILPTLVR.L
SW:IMB1_HUMAN	R10	9177	2	1677.9	(-0.5)	2.996	0.273	0.919	1	R.AAVENL*PTFL*VEL*SR.V
SW:IMB1_HUMAN	R10	6227	2	1835.0	(-0.5)	4.264	0.451	1.000	1	K.GDQENVHPDVMLVQPR.V
SW:IMB1_HUMAN	R10	6203	3	1841.0	(+0.8)	3.864	0.366	0.915	1	K.GDQENVHPDVML*VQPR.V

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:IMB1_HUMAN	R10	6215	2	1841.0	(+0.9)	3.389	0.547	0.999	1	K.GDQENVHPDVML*VQPR.V
SW:IMB1_HUMAN	R10	5651	2	1857.0	(-0.6)	2.734	0.250	0.862	1	K.GDQENVHPDVM@L*VQPR.V
SW:IMB1_HUMAN	R10	8541	2	1606.9	(-0.0)	3.246	0.349	0.968	1	K.LAATNALLNSLEFTK.A
SW:IMB1_HUMAN	R10	8565	2	1638.9	(-0.5)	3.070	0.254	0.888	1	K.L*AATNAL*L*NSL*EFTK#.A
SW:IMB1_HUMAN	R11	7938	2	1638.9	(-0.4)	3.373	0.210	0.878	1	K.L*AATNAL*L*NSL*EFTK#.A
SW:IMB1_HUMAN	R10	6401	3	2013.2	(+0.4)	4.184	0.486	1.000	1	R.L*QQVL*QMESHQSTSDR.I
SW:IMB1_HUMAN	R10	4657	3	2029.2	(+0.8)	3.965	0.450	0.999	1	R.L*QQVL*QM@ESHIQSTSDR.I
SW:IMB1_HUMAN	R10	8483	2	1633.8	(+0.7)	4.647	0.541	1.000	1	K.SDYDMVDYLNELR.E
SW:IMB1_HUMAN	R10	8477	2	1645.8	(-0.1)	3.430	0.341	0.976	1	K.SDYDMVDYL*NEL*R.E
SW:IMB1_HUMAN	R10	9037	2	1446.7	(+0.9)	3.664	0.385	0.990	1	K.SNEILTAIQGM.R.K
SW:IMB1_HUMAN	R10	9027	2	1452.7	(+0.3)	3.319	0.366	0.984	1	K.SNEIL*TAIQGM.R.K
SW:IMB1_HUMAN	R10	8247	2	1468.7	(+0.4)	2.748	0.308	0.953	1	K.SNEIL*TAIQGM@R.K
SW:IMB1_HUMAN	R10	8367	2	1371.6	(+0.2)	3.708	0.446	1.000	1	R.SSAYESL*MEIVK#.N
SW:IMB1_HUMAN	R10	7841	2	1387.6	(-0.7)	2.761	0.289	0.908	1	R.SSAYESL*M@EIVK#.N
SW:IMB1_HUMAN	R10	5885	2	969.2	(+0.8)	2.289	0.318	0.950	1	K.TTL*VIMER.L
SW:IMB1_HUMAN	R10	5603	2	1557.7	(-0.3)	3.256	0.320	0.340	1	K.TVSPDRLELEAAQK.F
SW:IMB1_HUMAN	R10	6161	2	956.2	(+0.7)	2.231	0.183	0.756	1	R.VAALQNLVK.I
SW:IMB1_HUMAN	R10	1142	2	1226.4	(-0.5)	2.836	0.315	0.949	1	R.VLANPGNSQVAR.V
SW:IMB1_HUMAN	R10	1120	2	1232.4	(+0.4)	2.500	0.454	0.970	1	R.VL*ANPGNSQVAR.V
SW:IMB1_HUMAN	R10	8617	2	2148.4	(+0.8)	4.712	0.588	0.999	1	K.YLEVVLNLTQQASQAQV.DK.S
SW:IMB1_HUMAN	R10	8601	3	2174.4	(+0.3)	4.531	0.529	0.985	1	K.YL*EVVL*NLT*QQASQAQV.DK#.S
SW:IMB1_HUMAN	R10	8723	2	1643.0	(-0.2)	4.223	0.505	1.000	1	K.YMEAFK#PFL*GIGL*K#.N
SW:IMB1_HUMAN	R14	8997	2	1659.9	(+0.2)	3.270	0.447	0.961	1	R.AAVENLPTFLVLSR.V
SW:ITA4_HUMAN	R08	7083	2	1301.4	(-0.2)	2.576	0.411	0.970	3	R.DNQWL*GVTL*SR.Q
SW:ITA4_HUMAN	R08	2054	2	861.0	(+0.2)	2.424	0.172	0.780	2	R.SDSAVLLR.T
SW:ITA4_HUMAN	R08	8015	2	1070.3	(+0.2)	2.246	0.183	0.628	2	K.L*PVGL*YFIK#.I
SW:ITB2_HUMAN	R11	1262	2	1090.2	(+0.9)	2.665	0.335	0.970	4	R.ALNEITESGR.I
SW:ITB2_HUMAN	R11	1264	2	1096.2	(+0.5)	2.351	0.243	0.875	4	R.AL*NEITESGR.I
SW:ITB2_HUMAN	R11	4458	2	1127.3	(-0.4)	3.111	0.379	0.976	4	K.LGAILTPNDGR.C
SW:ITB2_HUMAN	R11	4448	2	1139.3	(+0.4)	2.655	0.317	0.959	4	K.L*GAIL*TPNDGR.C
SW:ITB2_HUMAN	R12	4474	2	1139.3	(-0.3)	2.398	0.141	0.577	4	K.L*GAIL*TPNDGR.C
SW:ITB2_HUMAN	R14	5121	2	1139.3	(-0.6)	2.627	0.212	0.838	4	K.L*GAIL*TPNDGR.C
SW:ITB2_HUMAN	R14	5097	2	1127.3	(+0.4)	2.407	0.186	0.614	4	K.LGAILTPNDGR.C
SW:ITB2_HUMAN	R10	4299	2	828.0	(-0.2)	2.252	0.329*	0.077	4	K.L*TEIIPK#.S
SW:ITB2_HUMAN	R11	7238	2	1905.1	(-0.9)	3.131	0.433	0.929	3	K.SAVGEL*SEDSSNVVHL*IK#.N
SW:ITB2_HUMAN	R10	6665	2	1363.5	(+0.4)	2.390	0.315	0.937	3	K.SQWNNNDNPLFK.S
SW:ITB2_HUMAN	R11	6364	2	1363.5	(-0.4)	3.114	0.330	0.950	3	K.SQWNNNDNPLFK.S
SW:ITB2_HUMAN	R11	6358	2	1377.5	(-0.9)	2.304	0.290	0.627	3	K.SQWNNNDNPL*FK#.S
SW:ITB2_HUMAN	R11	6362	2	1368.6	(+0.3)	2.345	0.277	0.892	4	K.TVLPFVNTHPDK.L
SW:ITB2_HUMAN	R11	6582	2	1483.7	(+0.8)	3.908	0.402	0.999	4	R.VFLDHNALPDTLK.V
SW:ITB2_HUMAN	R24	6738	2	1377.5	(+0.1)	2.249	0.231	0.687	3	K.SQWNNNDNPL*FK#.S
SW:IVD_HUMAN	R14	4689	2	713.9	(+1.0)	2.235	0.230*	0.231	3	R.RLVIGR.A
SW:IVD_HUMAN	R18	5327	2	1295.4	(+0.4)	3.544	0.260	0.973	3	K.LYEIGAGTSEVR.R
SW:K052_HUMAN	R08	7015	2	1569.7	(+0.4)	3.391	0.481	1.000	3	R.DVDFEGTDEPIFGK.K
SW:K052_HUMAN	R08	6757	2	1147.4	(+0.4)	2.560	0.303	0.938	6	R.GIVIL*M@VDEK#.M
SW:K052_HUMAN	R08	7029	2	1412.6	(-0.8)	3.308	0.335	0.894	6	R.L*GFATSSDVIEMK#.G
SW:K052_HUMAN	R08	5779	2	1116.3	(+0.1)	2.833	0.345	0.968	5	K.L*TEQL*AGPL*R.Q
SW:K052_HUMAN	R08	9087	3	2580.9	(-0.1)	3.921	0.316	0.985	6	K.RFPDGIPL*L*DPIDDMGIQDQGL*K#.K
SW:K052_HUMAN	R08	7037	2	1508.7	(+0.2)	3.226	0.178	0.851	6	R.VEEINPEYML*EK#.S
SW:K052_HUMAN	R08	5985	2	929.1	(+0.4)	2.315	0.112	0.707	6	R.RLEELLR.Q
SW:K103_HUMAN	R19	10072	3	3798.1	(-0.5)	4.752	0.491	1.000		R.ELNEYLEQFVGDEAWHELAELYINEHDYAK.A
SW:K103_HUMAN	R19	1436	2	1335.5	(+0.6)	3.491	0.404	0.990	1	R.IL*QEDPTNTAAR.K
SW:K103_HUMAN	R19	1432	2	1329.5	(-0.4)	2.679	0.352	0.955	1	R.ILQEDPTNTAAR.K
SW:K103_HUMAN	R19	6024	2	1272.4	(+0.2)	3.889	0.566	1.000	1	R.YDDAIQLYDR.I
SW:K103_HUMAN	R19	6018	2	1278.4	(+0.4)	3.359	0.508	1.000	1	R.YDDAIQL*YDR.I
SW:K103_HUMAN	R19	6432	2	1480.6	(+0.8)	3.969	0.336	0.988	1	K.YTQGGLENLELSR.K
SW:K103_HUMAN	R19	6414	2	1498.6	(-1.0)	2.701	0.330	0.841	1	K.YTQGG*ENL*EL*SR.K
SW:K103_HUMAN	R19	2470	2	969.2	(+0.7)	2.248	0.344	0.928	1	R.KYFAQALK.L
SW:K179_HUMAN	R10	2334	3	2219.4	(-0.4)	5.245	0.416	0.998	1	K.HHL*QPENPGPGAAPSL*EQNR.G
SW:K179_HUMAN	R10	2376	2	1114.3	(+0.4)	2.919	0.305	0.968	1	K.SILVSPTGPSR.V

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:K179_HUMAN	R10	2392	2	1120.3	(+0.4)	2.692	0.196	0.875	1	K.SIL*VSPTGPSR.V
SW:KG09_HUMAN	R01	1288	2	1098.3	(-0.3)	2.327	0.343	0.909	4	K.AIEEQMVAAK#.D
SW:KG09_HUMAN	R08	1672	2	1098.3	(+0.2)	2.720	0.318	0.939	4	K.AIEEQMVAAK#.D
SW:KG09_HUMAN	R01	8769	2	1580.8	(+0.3)	2.624	0.407	0.976	4	R.EELEALFLPYDLK.R
SW:KG09_HUMAN	R02	8010	2	1580.8	(+0.7)	3.219	0.402	0.983	4	R.EELEALFLPYDLK.R
SW:KG09_HUMAN	R01	5517	2	1424.6	(-0.2)	2.581	0.267	0.887	4	R.TL*HEVSL*QESIR.Y
SW:KG09_HUMAN	R08	2576	2	1198.2	(-0.4)	2.632	0.381	0.955	4	K.TL*SDDL*DEAAK#.E
SW:KG09_HUMAN	R08	1900	2	1021.1	(+0.2)	2.279	0.276	0.798	4	K.L*FNEVQEK#.A
SW:KU70_HUMAN	R12	6906	2	1389.5	(-0.3)	3.123	0.463	0.987	1	R.DIISIAEDEDL.R.V
SW:KU70_HUMAN	R13	7197	2	1395.5	(+0.8)	3.624	0.390	0.990	1	R.DIISIAEDEDL*R.V
SW:KU70_HUMAN	R12	8648	2	1375.6	(-0.4)	3.388	0.359	0.973	1	R.DL*L*AVVFGYTEK#.D
SW:KU70_HUMAN	R13	8805	2	1375.6	(-0.1)	3.175	0.262	0.928	1	R.DL*L*AVVFGYTEK#.D
SW:KU70_HUMAN	R12	8750	2	1403.7	(+1.0)	4.221	0.285	0.987	1	R.DTGIFLDLMLHLK.K
SW:KU70_HUMAN	R12	8744	2	1429.7	(-0.4)	2.896	0.271	0.909	1	R.DTGIFL*DL*MHL*K#.K
SW:KU70_HUMAN	R13	8905	2	1403.7	(+0.9)	4.033	0.348	0.911	1	R.DTGIFLDLMLHLK.K
SW:KU70_HUMAN	R13	8889	2	1429.7	(-0.1)	2.570	0.249	0.827	1	R.DTGIFL*DL*MHL*K#.K
SW:KU70_HUMAN	R12	8630	3	2047.3	(+0.9)	3.893	0.310	0.965	1	K.IISSDRDL*L*AVVFGYTEK#.D
SW:KU70_HUMAN	R12	8612	3	2027.3	(+0.7)	3.857	0.381	0.989	1	K.IISSDRDLLAVVFGYTEK.D
SW:KU70_HUMAN	R12	1262	2	1074.3	(+1.0)	2.213	0.241	0.839	1	K.IMATPEQVGK.M
SW:KU70_HUMAN	R12	9796	3	2153.5	(+0.6)	3.931	0.315	0.980	1	K.IQVTPPGFQL*VFL*PFADDK#.R
SW:KU70_HUMAN	R13	9977	2	2133.5	(-0.7)	2.589	0.381	0.951	1	K.IQVTPPGFQLVFLPFADDK.R
SW:KU70_HUMAN	R12	7648	2	1400.6	(+0.5)	3.765	0.531	0.999	1	K.KPGGFDISLFYR.D
SW:KU70_HUMAN	R12	7636	2	1414.6	(-0.7)	2.835	0.416	0.978	1	K.K#PGGFDISL*FYR.D
SW:KU70_HUMAN	R13	7849	2	1400.6	(+0.9)	3.888	0.500	1.000	1	K.KPGGFDISLFYR.D
SW:KU70_HUMAN	R13	7839	2	1414.6	(-0.3)	3.068	0.441	0.985	1	K.K#PGGFDISL*FYR.D
SW:KU70_HUMAN	R13	6557	2	1173.4	(+0.7)	3.182	0.305	0.979	1	K.KQELLEALTK.H
SW:KU70_HUMAN	R13	7389	2	1594.8	(-0.5)	3.381	0.281	0.941	1	K.NIYVL*QEL*DNPGAK#.R
SW:KU70_HUMAN	R13	10201	2	2424.8	(+0.7)	4.741	0.492	0.991	1	R.NLEALALDLMEPEQAVDLTLPK.V
SW:KU70_HUMAN	R12	6310	2	1710.8	(-0.4)	3.557	0.424	0.986	2	R.SDSFENPVL*QQHFR.N
SW:KU70_HUMAN	R13	6691	2	1710.8	(+0.7)	3.335	0.399	0.986	2	R.SDSFENPVL*QQHFR.N
SW:KU70_HUMAN	R12	4906	3	2516.4	(+0.0)	5.269	0.542	1.000	1	K.TEGDEEAEEEEQEENL*EASGDYK#.Y
SW:KU70_HUMAN	R12	4916	3	2502.4	(+0.2)	5.226	0.474	0.999	1	K.TEGDEEAEEEEQEENLEASGDYK.Y
SW:KU70_HUMAN	R12	1964	3	2516.4	(+0.2)	5.141	0.567	0.923	1	K.TEGDEEAEEEEQEENL*EASGDYK#.Y
SW:KU70_HUMAN	R12	1984	3	2502.4	(+0.2)	4.467	0.521	1.000	1	K.TEGDEEAEEEEQEENLEASGDYK.Y
SW:KU70_HUMAN	R12	6432	2	1652.8	(+0.7)	3.022	0.454	0.988	1	R.TFNTSTGGLLLPSDTK.R
SW:KU70_HUMAN	R13	6789	2	1652.8	(-0.2)	3.663	0.429	0.987	1	R.TFNTSTGGLLLPSDTK.R
SW:KU70_HUMAN	R12	1316	2	1126.2	(+0.6)	2.517	0.368	0.975	2	K.VEYSEELK.T
SW:KU70_HUMAN	R13	5909	2	1535.7	(+0.1)	2.359	0.339	0.867	1	K.EL*VYPPDYNPEGK#.V
SW:KU86_HUMAN	R11	6332	2	1386.6	(+0.1)	2.937	0.330	0.943	1	R.ANPQVGVAFFPHIK#.H
SW:KU86_HUMAN	R11	6338	2	1378.6	(+0.1)	2.871	0.529	1.000	1	R.ANPQVGVAFFPHIK.H
SW:KU86_HUMAN	R11	5912	2	2252.3	(+0.5)	4.885	0.562	1.000	1	K.DQVTAQEIFQDNHEDGPTAK#.K
SW:KU86_HUMAN	R11	5918	2	2244.3	(-0.5)	3.659	0.446	1.000	1	K.DQVTAQEIFQDNHEDGPTAK.K
SW:KU86_HUMAN	R11	824	2	1395.4	(+0.6)	3.793	0.525	0.999	1	K.EEASGSSVTAEAAK.K
SW:KU86_HUMAN	R11	822	2	1403.4	(+0.4)	3.675	0.446	0.997	1	K.EEASGSSVTAEAAK#.K
SW:KU86_HUMAN	R11	6722	2	1318.5	(+0.8)	3.419	0.332	0.983	1	R.HIEIFTDLSSR.F
SW:KU86_HUMAN	R11	6716	2	1324.5	(+0.3)	3.274	0.369	0.987	1	R.HIEIFTDL*SSR.F
SW:KU86_HUMAN	R01	9309	2	1916.2	(+0.3)	2.370	0.323	0.918	1	R.HLMPLPDFDLLEDIESK.I
SW:KU86_HUMAN	R11	8860	3	1964.2	(+0.5)	3.713	0.273	0.989	1	R.HL*M@L*PDFDL*L*EDIESK#.I
SW:KU86_HUMAN	R11	6258	2	1086.3	(+0.7)	2.663	0.425	0.985	1	R.L*TIGSNL*SIR.I
SW:KU86_HUMAN	R11	6278	2	1074.3	(+0.9)	2.325	0.413	0.974	1	R.LTIGSNLSIR.I
SW:KU86_HUMAN	R11	6456	2	1254.5	(+0.8)	2.334	0.289	0.898	1	R.RFFMGNQVL*K#.V
SW:KU86_HUMAN	R11	7402	2	1287.5	(+0.2)	2.981	0.300	0.942	1	K.SQL*DIIHSL*K#.K
SW:KU86_HUMAN	R11	7126	2	1401.5	(+0.1)	3.157	0.381	0.970	1	K.TDTL*EDL*FPTTK#.I
SW:KU86_HUMAN	R01	9637	3	2348.6	(-0.0)	4.746	0.267	0.984	1	K.YAPTEAQL*NAVDAL*IDSMSL*AK#.K
SW:KU86_HUMAN	R10	9701	3	2348.6	(-0.0)	4.729	0.475	1.000	1	K.YAPTEAQL*NAVDAL*IDSMSL*AK#.K
SW:KU86_HUMAN	R11	9382	3	2348.6	(+0.3)	5.299	0.440	1.000	1	K.YAPTEAQL*NAVDAL*IDSMSL*AK#.K
SW:KU86_HUMAN	R11	9108	3	2348.6	(+0.9)	3.783	0.335	0.994	1	K.YAPTEAQL*NAVDAL*IDSMSL*AK#.K
SW:KU86_HUMAN	R12	9634	3	2348.6	(-0.5)	4.050	0.338	0.992	1	K.YAPTEAQL*NAVDAL*IDSMSL*AK#.K
SW:KU86_HUMAN	R12	10668	3	2255.6	(+0.6)	3.842	0.408	0.998	1	K.QLNHFWEIVVQDGITLITK.E
SW:LAM1_HUMAN	R13	6239	2	1415.6	(-0.5)	2.866	0.395	0.974	2	K.AEHDQLLLNYAK.K
SW:LAM1_HUMAN	R13	6235	2	1441.6	(+0.2)	2.537	0.299	0.886	2	K.AEHDQL*L*L*NYAK#.K
SW:LAM1_HUMAN	R01	1194	2	1161.3	(+0.7)	2.291	0.303	0.890	2	R.AGGPTTPL*SPTR.L

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:LAM1_HUMAN	R13	1632	2	1161.3	(+0.2)	2.278	0.325	0.895	2	R.AGGPTTPL*SPTR.L
SW:LAM1_HUMAN	R13	1552	2	1155.3	(+0.3)	2.277	0.372	0.952	2	R.AGGPTTPLSPTR.L
SW:LAM1_HUMAN	R21	4544	2	1155.3	(+0.3)	2.699	0.361	0.963	2	R.AGGPTTPLSPTR.L
SW:LAM1_HUMAN	R21	4622	2	1155.3	(+0.6)	2.658	0.438	0.981	2	R.AGGPTTPLSPTR.L
SW:LAM1_HUMAN	R12	8470	3	2569.9	(+0.8)	3.948	0.449	0.975	2	K.AGQVTIWAANAGVTASPPTDLIWK.N
SW:LAM1_HUMAN	R13	8605	2	2583.9	(+0.3)	3.184	0.438	0.984	2	K.AGQVTIWAANAGVTASPPTDL*IWK#.N
SW:LAM1_HUMAN	R01	5075	2	1252.4	(+0.1)	3.036	0.350	0.973	2	K.ALYETELADAR.R
SW:LAM1_HUMAN	R01	5065	2	1264.4	(+0.7)	2.527	0.378	0.969	2	K.AL*YETEL*ADAR.R
SW:LAM1_HUMAN	R03	5287	2	1252.4	(+0.0)	2.309	0.292	0.875	2	K.ALYETELADAR.R
SW:LAM1_HUMAN	R09	5250	2	1252.4	(+0.7)	2.224	0.209	0.714	2	K.ALYETELADAR.R
SW:LAM1_HUMAN	R10	5771	2	1264.4	(-0.6)	2.341	0.382	0.949	2	K.AL*YETEL*ADAR.R
SW:LAM1_HUMAN	R11	5600	2	1264.4	(-0.0)	2.578	0.448	0.974	2	K.AL*YETEL*ADAR.R
SW:LAM1_HUMAN	R12	5294	2	1264.4	(-0.3)	2.390	0.286	0.885	2	K.AL*YETEL*ADAR.R
SW:LAM1_HUMAN	R12	5302	2	1252.4	(+0.7)	2.294	0.363	0.954	2	K.ALYETELADAR.R
SW:LAM1_HUMAN	R13	5785	2	1252.4	(+0.8)	3.450	0.428	0.948	2	K.ALYETELADAR.R
SW:LAM1_HUMAN	R13	5693	2	1264.4	(+0.2)	2.784	0.457	0.984	2	K.AL*YETEL*ADAR.R
SW:LAM1_HUMAN	R13	5865	2	1264.4	(+0.2)	2.473	0.398	0.963	2	K.AL*YETEL*ADAR.R
SW:LAM1_HUMAN	R16	5386	2	1264.4	(+0.2)	2.332	0.476	0.976	2	K.AL*YETEL*ADAR.R
SW:LAM1_HUMAN	R21	5896	2	1252.4	(+0.2)	2.374	0.368	0.945	2	K.ALYETELADAR.R
SW:LAM1_HUMAN	R12	4092	2	1046.2	(+0.9)	2.538	0.305	0.946	2	K.DAALATALGDK.K
SW:LAM1_HUMAN	R12	4046	2	1066.2	(-0.1)	2.374	0.347	0.909	2	K.DAAL*ATAL*GDK#.K
SW:LAM1_HUMAN	R12	4174	2	1046.2	(+0.7)	2.328	0.328	0.939	2	K.DAALATALGDK.K
SW:LAM1_HUMAN	R12	3944	2	1066.2	(+0.3)	2.276	0.384	0.949	2	K.DAAL*ATAL*GDK#.K
SW:LAM1_HUMAN	R13	4839	2	1046.2	(+0.9)	3.798	0.442	0.999	2	K.DAALATALGDK.K
SW:LAM1_HUMAN	R13	4895	2	1066.2	(+0.2)	3.055	0.423	0.979	2	K.DAAL*ATAL*GDK#.K
SW:LAM1_HUMAN	R13	4779	2	1066.2	(+0.1)	3.006	0.417	0.974	2	K.DAAL*ATAL*GDK#.K
SW:LAM1_HUMAN	R13	4975	2	1066.2	(+0.7)	2.777	0.434	0.982	2	K.DAAL*ATAL*GDK#.K
SW:LAM1_HUMAN	R13	4759	2	1046.2	(-0.8)	2.208	0.362	0.798	2	K.DAALATALGDK.K
SW:LAM1_HUMAN	R18	4887	2	1066.2	(+0.1)	2.440	0.324	0.904	2	K.DAAL*ATAL*GDK#.K
SW:LAM1_HUMAN	R19	5010	2	1046.2	(+0.3)	2.357	0.253	0.877	2	K.DAALATALGDK.K
SW:LAM1_HUMAN	R12	1980	2	1202.3	(-0.4)	2.235	0.181	0.020	2	K.DAAL*ATAL*GDK#K#.S
SW:LAM1_HUMAN	R13	2352	2	1174.3	(-0.1)	4.073	0.442	0.969	2	K.DAALATALGDKK.S
SW:LAM1_HUMAN	R13	2432	2	1174.3	(-0.2)	3.591	0.355	0.521	2	K.DAALATALGDKK.S
SW:LAM1_HUMAN	R13	2340	2	1202.3	(-0.1)	2.764	0.389	0.326	2	K.DAAL*ATAL*GDK#K#.S
SW:LAM1_HUMAN	R11	7888	3	2135.3	(+0.3)	4.052	0.418	1.000	2	R.DQMQQQL*NDYEQL*L*DVK#.L
SW:LAM1_HUMAN	R11	7890	3	2109.3	(+0.3)	3.722	0.346	0.929	2	R.DQMQQQLNDYEQLLDVK.L
SW:LAM1_HUMAN	R12	8008	2	2109.3	(+0.8)	4.912	0.488	0.999	2	R.DQMQQQLNDYEQLLDVK.L
SW:LAM1_HUMAN	R12	7998	3	2135.3	(+0.2)	4.660	0.351	0.997	2	R.DQMQQQL*NDYEQL*L*DVK#.L
SW:LAM1_HUMAN	R13	7517	3	2151.3	(+0.0)	4.649	0.391	0.999	2	R.DQM@QQQL*NDYEQL*L*DVK#.L
SW:LAM1_HUMAN	R13	7485	3	2135.3	(+0.9)	3.907	0.306	0.995	2	R.DQMQQQL*NDYEQL*L*DVK#.L
SW:LAM1_HUMAN	R17	8142	2	2109.3	(-0.7)	4.354	0.440	1.000	2	R.DQMQQQLNDYEQLLDVK.L
SW:LAM1_HUMAN	R20	8078	3	2109.3	(+0.4)	4.197	0.356	0.998	2	R.DQMQQQLNDYEQLLDVK.L
SW:LAM1_HUMAN	R06	6488	2	1447.6	(+0.7)	4.482	0.486	1.000	2	R.IESLSSQLSNLQK.E
SW:LAM1_HUMAN	R06	6482	2	1473.6	(-0.4)	2.560	0.336	0.914	2	R.IESL*SSQL*SNL*QK#.E
SW:LAM1_HUMAN	R11	6366	2	1447.6	(+0.1)	3.754	0.488	0.999	2	R.IESLSSQLSNLQK.E
SW:LAM1_HUMAN	R12	6206	2	1473.6	(-0.2)	2.878	0.195	0.794	2	R.IESL*SSQL*SNL*QK#.E
SW:LAM1_HUMAN	R13	6641	2	1473.6	(-0.5)	3.566	0.421	0.976	2	R.IESL*SSQL*SNL*QK#.E
SW:LAM1_HUMAN	R13	6559	2	1473.6	(-0.3)	3.222	0.391	0.973	2	R.IESL*SSQL*SNL*QK#.E
SW:LAM1_HUMAN	R13	6563	2	1447.6	(-0.5)	2.924	0.321	0.950	2	R.IESLSSQLSNLQK.E
SW:LAM1_HUMAN	R14	6609	2	1447.6	(+0.8)	3.967	0.444	1.000	2	R.IESLSSQLSNLQK.E
SW:LAM1_HUMAN	R15	6391	2	1473.6	(-0.7)	3.013	0.306	0.936	2	R.IESL*SSQL*SNL*QK#.E
SW:LAM1_HUMAN	R16	6258	2	1473.6	(-0.7)	2.904	0.288	0.915	2	R.IESL*SSQL*SNL*QK#.E
SW:LAM1_HUMAN	R17	6554	2	1447.6	(+0.4)	2.847	0.439	0.986	2	R.IESLSSQLSNLQK.E
SW:LAM1_HUMAN	R18	6551	2	1447.6	(-0.4)	2.819	0.410	0.972	2	R.IESLSSQLSNLQK.E
SW:LAM1_HUMAN	R12	1054	2	970.1	(+0.8)	2.571	0.396	0.982	2	K.IGDTSVSYK.Y
SW:LAM1_HUMAN	R13	1336	2	970.1	(+0.9)	2.608	0.432	0.986	2	K.IGDTSVSYK.Y
SW:LAM1_HUMAN	R13	4685	2	978.1	(-0.0)	2.555	0.333	0.938	2	K.IGDTSVSYK#.Y
SW:LAM1_HUMAN	R14	1304	2	978.1	(+0.8)	2.699	0.450	0.984	2	K.IGDTSVSYK#.Y
SW:LAM1_HUMAN	R06	7092	2	1172.4	(+0.9)	3.165	0.300*	0.627	2	R.IQELEDLLAK.E
SW:LAM1_HUMAN	R13	7145	2	1198.4	(-0.1)	2.427	0.109	0.457	2	R.IQEL*EDL*L*AK#.E
SW:LAM1_HUMAN	R15	6989	2	1172.4	(+0.2)	2.250	0.267*	0.127	2	R.IQELEDLLAK.E
SW:LAM1_HUMAN	R13	1258	2	1203.3	(+0.6)	3.724	0.353	0.990	2	K.KESDLNGAQIK.L
SW:LAM1_HUMAN	R13	1252	2	1225.3	(+0.6)	3.616	0.358	0.986	2	K.K#ESDL*NGAQIK#.L
SW:LAM1_HUMAN	R12	1122	2	1114.2	(+0.1)	2.846	0.439	0.979	2	R.K#IGDTSVSYK#.Y
SW:LAM1_HUMAN	R12	1128	2	1098.2	(-0.1)	2.429	0.367	0.954	2	R.KIGDTSVSYK.Y
SW:LAM1_HUMAN	R13	1424	2	1098.2	(+0.3)	3.095	0.380	0.987	2	R.KIGDTSVSYK.Y

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:LAM1_HUMAN	R13	1408	2	1114.2	(+0.6)	2.738	0.450	0.950	2	R.K#IGDTSVSYK#.Y
SW:LAM1_HUMAN	R17	1574	2	1103.2	(+0.7)	2.917	0.144	0.888	10	R.KLLEGEER.L
SW:LAM1_HUMAN	R12	4848	2	1159.4	(-0.2)	2.898	0.329	0.966	2	K.KQLADETLK.V
SW:LAM1_HUMAN	R13	5243	2	1159.4	(+0.3)	3.035	0.164	0.909	2	K.KQLADETLK.V
SW:LAM1_HUMAN	R21	5776	2	1159.4	(+0.8)	2.956	0.333	0.978	2	K.KQLADETLK.V
SW:LAM1_HUMAN	R13	1528	2	1553.7	(+0.5)	3.719	0.468	1.000	2	R.K#SM@YEEEINETR.R
SW:LAM1_HUMAN	R12	7138	2	1282.5	(+0.5)	3.373	0.469	1.000	2	K.LALDMEISAYR.K
SW:LAM1_HUMAN	R13	7371	2	1282.5	(+1.0)	3.818	0.533	0.999	2	K.LALDMEISAYR.K
SW:LAM1_HUMAN	R13	7289	2	1282.5	(+0.7)	3.664	0.543	0.998	2	K.LALDMEISAYR.K
SW:LAM1_HUMAN	R13	7365	2	1294.5	(+0.7)	3.635	0.466	0.998	2	K.L*AL*DMEISAYR.K
SW:LAM1_HUMAN	R13	7451	2	1282.5	(+0.5)	3.291	0.535	1.000	2	K.LALDMEISAYR.K
SW:LAM1_HUMAN	R13	12375	2	1282.5	(+0.6)	3.201	0.481	0.999	2	K.LALDMEISAYR.K
SW:LAM1_HUMAN	R13	7445	2	1294.5	(+0.4)	2.908	0.437	0.988	2	K.L*AL*DMEISAYR.K
SW:LAM1_HUMAN	R13	7285	2	1294.5	(+0.4)	2.833	0.444	0.988	2	K.L*AL*DMEISAYR.K
SW:LAM1_HUMAN	R13	12113	2	1294.5	(+0.4)	2.720	0.297	0.955	2	K.L*AL*DMEISAYR.K
SW:LAM1_HUMAN	R13	6565	2	1310.5	(+0.1)	2.688	0.286	0.927	2	K.L*AL*DM@EISAYR.K
SW:LAM1_HUMAN	R13	11957	2	1294.5	(-0.7)	2.655	0.358	0.959	2	K.L*AL*DMEISAYR.K
SW:LAM1_HUMAN	R13	10865	2	1294.5	(+0.3)	2.627	0.350	0.968	2	K.L*AL*DMEISAYR.K
SW:LAM1_HUMAN	R13	12475	2	1294.5	(+0.2)	2.472	0.220	0.810	2	K.L*AL*DMEISAYR.K
SW:LAM1_HUMAN	R12	1598	2	1069.3	(+0.9)	3.975	0.424	1.000	2	K.LAQALHEMR.E
SW:LAM1_HUMAN	R12	1588	2	1081.3	(-0.6)	3.108	0.325	0.976	2	K.L*AQAL*HEMR.E
SW:LAM1_HUMAN	R13	1952	2	1069.3	(+0.7)	3.121	0.390	0.989	2	K.LAQALHEMR.E
SW:LAM1_HUMAN	R13	1928	2	1081.3	(-0.0)	3.116	0.323	0.976	2	K.L*AQAL*HEMR.E
SW:LAM1_HUMAN	R17	2156	2	1069.3	(+0.8)	3.062	0.306	0.979	2	K.LAQALHEMR.E
SW:LAM1_HUMAN	R18	2010	2	1081.3	(+0.9)	2.384	0.352	0.964	2	K.L*AQAL*HEMR.E
SW:LAM1_HUMAN	R13	3342	2	836.0	(+0.6)	2.395	0.389	0.975	2	R.L*AVYIDK#.V
SW:LAM1_HUMAN	R13	4369	2	836.0	(+0.9)	2.382	0.409	0.978	2	R.L*AVYIDK#.V
SW:LAM1_HUMAN	R13	3735	2	836.0	(+0.5)	2.359	0.374	0.970	2	R.L*AVYIDK#.V
SW:LAM1_HUMAN	R13	3715	2	822.0	(+0.8)	2.281	0.274	0.935	2	R.LAVYIDK.V
SW:LAM1_HUMAN	R13	3336	2	822.0	(+1.0)	2.277	0.329	0.958	2	R.LAVYIDK.V
SW:LAM1_HUMAN	R13	3897	2	836.0	(+0.7)	2.272	0.325	0.948	2	R.L*AVYIDK#.V
SW:LAM1_HUMAN	R13	4127	1	836.0	(-0.5)	2.169	0.334	0.038	2	R.L*AVYIDK#.V
SW:LAM1_HUMAN	R13	4281	1	836.0	(-0.5)	2.129	0.341	0.043	2	R.L*AVYIDK#.V
SW:LAM1_HUMAN	R13	4447	1	836.0	(-0.6)	2.082	0.296	0.011	2	R.L*AVYIDK#.V
SW:LAM1_HUMAN	R13	4205	1	836.0	(-0.5)	1.931	0.265	0.000	2	R.L*AVYIDK#.V
SW:LAM1_HUMAN	R12	996	2	975.0	(+0.9)	2.568	0.203	0.907	10	K.LLEGEER.L
SW:LAM1_HUMAN	R13	1302	2	975.0	(+0.9)	2.480	0.296	0.956	10	K.LLEGEER.L
SW:LAM1_HUMAN	R16	884	2	975.0	(+1.0)	2.300	0.125	0.681	10	K.LLEGEER.L
SW:LAM1_HUMAN	R13	1164	2	1045.2	(+1.0)	2.581	0.255*	0.016	5	R.LQEKEELR.E
SW:LAM1_HUMAN	R13	1986	2	1294.5	(+0.7)	2.807	0.387	0.511	2	K.LREYEAALNSK.D
SW:LAM1_HUMAN	R13	1974	2	1314.5	(-0.1)	2.756	0.160	0.049	2	K.L*REYEAAL*NSK#.D
SW:LAM1_HUMAN	R12	1146	2	1503.6	(+0.2)	3.490	0.461	1.000	2	R.L*SSEMNTSTVNSAR.E
SW:LAM1_HUMAN	R12	1150	2	1497.6	(-0.3)	2.336	0.300	0.859	2	R.LSSEMNTSTVNSAR.E
SW:LAM1_HUMAN	R13	4801	2	1503.6	(+0.5)	3.565	0.563	1.000	2	R.L*SSEMNTSTVNSAR.E
SW:LAM1_HUMAN	R13	1444	2	1497.6	(+0.5)	3.482	0.504	0.997	2	R.LSSEMNTSTVNSAR.E
SW:LAM1_HUMAN	R13	4805	2	1497.6	(-0.4)	3.440	0.442	0.987	2	R.LSSEMNTSTVNSAR.E
SW:LAM1_HUMAN	R13	1070	2	1519.6	(-0.0)	3.016	0.322	0.954	2	R.L*SSEM@NTSTVNSAR.E
SW:LAM1_HUMAN	R17	1590	2	1497.6	(+0.4)	3.487	0.445	0.990	2	R.LSSEMNTSTVNSAR.E
SW:LAM1_HUMAN	R12	4520	2	1652.8	(-0.6)	3.845	0.311	0.408	2	R.LYKEELEQTYHAK.L
SW:LAM1_HUMAN	R12	4532	3	1652.8	(-0.6)	3.769	0.211	0.641	2	R.LYKEELEQTYHAK.L
SW:LAM1_HUMAN	R13	5043	2	1652.8	(-0.5)	4.214	0.328	0.558	2	R.LYKEELEQTYHAK.L
SW:LAM1_HUMAN	R13	4961	2	1652.8	(-0.5)	3.961	0.324	0.512	2	R.LYKEELEQTYHAK.L
SW:LAM1_HUMAN	R13	4979	3	1652.8	(-0.8)	3.829	0.267	0.657	2	R.LYKEELEQTYHAK.L
SW:LAM1_HUMAN	R13	5063	2	1680.8	(-0.9)	3.137	0.334	0.121	2	R.L*YK#EEL*EQTYHAK#.L
SW:LAM1_HUMAN	R17	5440	2	1652.8	(-0.5)	4.120	0.342	0.567	2	R.LYKEELEQTYHAK.L
SW:LAM1_HUMAN	R17	5438	3	1652.8	(-0.9)	3.894	0.275	0.712	2	R.LYKEELEQTYHAK.L
SW:LAM1_HUMAN	R12	1176	2	1343.4	(-0.6)	2.908	0.365	0.960	2	K.NQNSWGTGEDVK#.V
SW:LAM1_HUMAN	R13	1466	2	1343.4	(+0.6)	3.150	0.409	0.984	2	K.NQNSWGTGEDVK#.V
SW:LAM1_HUMAN	R17	1640	2	1335.4	(-0.5)	3.385	0.451	1.000	2	K.NQNSWGTGEDVK.V
SW:LAM1_HUMAN	R02	9765	3	2529.8	(+0.8)	4.203	0.477	1.000	2	K.SLEGDLEDLKDQIAQLEASLAAK.K
SW:LAM1_HUMAN	R03	10012	3	2529.8	(+0.2)	5.639	0.587	1.000	2	K.SLEGDLEDLKDQIAQLEASLAAK.K
SW:LAM1_HUMAN	R12	10584	2	2529.8	(+0.1)	4.907	0.473	0.872	2	K.SLEGDLEDLKDQIAQLEASLAAK.K
SW:LAM1_HUMAN	R12	10670	3	2529.8	(+0.3)	3.795	0.377	0.982	2	K.SLEGDLEDLKDQIAQLEASLAAK.K
SW:LAM1_HUMAN	R13	10689	2	2529.8	(+0.1)	5.336	0.536	0.999	2	K.SLEGDLEDLKDQIAQLEASLAAK.K
SW:LAM1_HUMAN	R13	8763	3	2529.8	(+0.5)	5.271	0.434	1.000	2	K.SLEGDLEDLKDQIAQLEASLAAK.K
SW:LAM1_HUMAN	R13	10791	3	2529.8	(-0.5)	4.529	0.320	0.938	2	K.SLEGDLEDLKDQIAQLEASLAAK.K

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:LAM1_HUMAN	R14	10597	2	2529.8	(-0.1)	3.706	0.292	0.360	2	K.SLEGDLEDLKDQIAQLEASLAAAK.K
SW:LAM1_HUMAN	R16	10436	2	2529.8	(-0.1)	4.662	0.373	0.999	2	K.SLEGDLEDLKDQIAQLEASLAAAK.K
SW:LAM1_HUMAN	R21	10266	2	2529.8	(+0.0)	3.908	0.402	0.564	2	K.SLEGDLEDLKDQIAQLEASLAAAK.K
SW:LAM1_HUMAN	R12	6008	3	1837.0	(+0.7)	3.879	0.301	0.994	2	R.SL*ETENSAL*QL*QVTER.E
SW:LAM1_HUMAN	R13	12045	3	1819.0	(+1.0)	4.720	0.406	1.000	2	R.SLETENSALQLQVTER.E
SW:LAM1_HUMAN	R13	12987	3	1837.0	(+0.6)	4.348	0.392	0.999	2	R.SL*ETENSAL*QL*QVTER.E
SW:LAM1_HUMAN	R13	6401	3	1819.0	(-0.6)	4.227	0.422	0.984	2	R.SLETENSALQLQVTER.E
SW:LAM1_HUMAN	R13	11215	3	1837.0	(+0.4)	4.210	0.417	0.999	2	R.SL*ETENSAL*QL*QVTER.E
SW:LAM1_HUMAN	R13	13061	3	1837.0	(+0.4)	4.194	0.377	0.998	2	R.SL*ETENSAL*QL*QVTER.E
SW:LAM1_HUMAN	R13	11645	3	1837.0	(+0.8)	4.121	0.352	0.996	2	R.SL*ETENSAL*QL*QVTER.E
SW:LAM1_HUMAN	R13	12617	3	1837.0	(+0.7)	4.077	0.330	0.995	2	R.SL*ETENSAL*QL*QVTER.E
SW:LAM1_HUMAN	R13	12141	3	1837.0	(+0.2)	3.932	0.357	0.981	2	R.SL*ETENSAL*QL*QVTER.E
SW:LAM1_HUMAN	R13	12217	3	1837.0	(+0.4)	3.872	0.349	0.989	2	R.SL*ETENSAL*QL*QVTER.E
SW:LAM1_HUMAN	R13	12913	3	1837.0	(+0.2)	3.778	0.356	0.960	2	R.SL*ETENSAL*QL*QVTER.E
SW:LAM1_HUMAN	R13	12763	3	1837.0	(+0.1)	3.762	0.397	0.996	2	R.SL*ETENSAL*QL*QVTER.E
SW:LAM1_HUMAN	R13	12451	3	1837.0	(+0.6)	3.709	0.270	0.985	2	R.SL*ETENSAL*QL*QVTER.E
SW:LAM1_HUMAN	R13	6283	2	1837.0	(-0.0)	3.448	0.299	0.960	2	R.SL*ETENSAL*QL*QVTER.E
SW:LAM1_HUMAN	R13	6381	2	1837.0	(-0.2)	3.431	0.403	0.982	2	R.SL*ETENSAL*QL*QVTER.E
SW:LAM1_HUMAN	R21	2470	2	1025.1	(+0.8)	2.275	0.365	0.955	2	R.EYEAALNSK.D
SW:LAM2_HUMAN	R13	778	2	906.0	(+0.2)	2.481	0.407	0.964	2	K.AEDGHAVAK#.K
SW:LAM2_HUMAN	R13	1568	2	1125.3	(-0.6)	2.432	0.344	0.931	2	R.AGGPATPLSPTR.L
SW:LAM2_HUMAN	R13	1548	2	1125.3	(+0.6)	2.286	0.360	0.947	2	R.AGGPATPLSPTR.L
SW:LAM2_HUMAN	R13	7683	3	2552.9	(+0.0)	4.387	0.483	1.000	2	R.AGQM@VTVWAAGAGVAHSPSTL*VWK#.G
SW:LAM2_HUMAN	R12	5128	2	1250.3	(-0.1)	2.843	0.300	0.948	1	K.AL*YESEL*ADAR.R
SW:LAM2_HUMAN	R13	5495	2	1238.3	(+0.6)	3.489	0.365	0.987	1	K.ALYESELADAR.R
SW:LAM2_HUMAN	R13	5589	2	1250.3	(+0.1)	3.417	0.472	1.000	1	K.AL*YESEL*ADAR.R
SW:LAM2_HUMAN	R13	5485	2	1250.3	(-0.4)	2.202	0.347	0.911	1	K.AL*YESEL*ADAR.R
SW:LAM2_HUMAN	R13	1032	2	1269.3	(+0.8)	2.437	0.440	0.976	2	R.ATSSSSGSLSATGR.L
SW:LAM2_HUMAN	R13	8623	3	2077.3	(-0.5)	4.303	0.335	0.996	2	R.DVMQQQL*AEYQEL*L*DVK#.L
SW:LAM2_HUMAN	R13	1380	2	1060.2	(+0.9)	2.206	0.246	0.844	2	R.EGELTVAQGR.V
SW:LAM2_HUMAN	R13	1094	2	1157.2	(+0.4)	2.699	0.191	0.883	2	R.EL*EEAM@AGER.D
SW:LAM2_HUMAN	R13	1626	2	1135.2	(+0.8)	2.337	0.264	0.899	2	R.ELEEAMAGER.D
SW:LAM2_HUMAN	R17	1776	2	1135.2	(+0.7)	2.872	0.240	0.946	2	R.ELEEAMAGER.D
SW:LAM2_HUMAN	R13	6879	3	3194.1	(-0.0)	4.202	0.495	0.992	3	R.ENENGESEEEEEAEFGEDLFHQGGDPR.T
SW:LAM2_HUMAN	R13	6205	2	1089.2	(-0.7)	3.056	0.250	0.945	2	R.GLESDVAELR.A
SW:LAM2_HUMAN	R13	6189	2	1089.2	(+0.7)	2.539	0.402	0.979	2	R.GLESDVAELR.A
SW:LAM2_HUMAN	R12	5274	2	1410.6	(+0.1)	2.717	0.357	0.314	2	R.IREL*EEAMAGER.D
SW:LAM2_HUMAN	R13	5685	2	1404.6	(+0.5)	4.941	0.465	0.999	2	R.IRELEEAMAGER.D
SW:LAM2_HUMAN	R13	5667	2	1410.6	(-0.0)	4.458	0.435	1.000	2	R.IREL*EEAMAGER.D
SW:LAM2_HUMAN	R13	1106	2	1192.3	(+0.9)	2.596	0.392	0.482	2	K.ISEKEEVTR.E
SW:LAM2_HUMAN	R13	6531	2	1337.5	(-0.7)	2.254	0.102	0.361	2	K.L*AL*DM@EINAYR.K
SW:LAM2_HUMAN	R13	2228	2	1243.4	(-0.2)	2.767	0.143	0.724	2	K.L*EL*EQTYQAK#.L
SW:LAM2_HUMAN	R13	5399	2	1223.4	(+0.9)	2.554	0.198	0.865	2	K.LELEQTYQAK.L
SW:LAM2_HUMAN	R13	2486	2	1243.4	(+0.3)	2.431	0.133	0.628	2	K.L*EL*EQTYQAK#.L
SW:LAM2_HUMAN	R17	4146	2	1223.4	(+0.6)	2.895	0.115	0.818	2	K.LELEQTYQAK.L
SW:LAM2_HUMAN	R17	4002	2	1223.4	(+0.3)	2.674	0.123	0.766	2	K.LELEQTYQAK.L
SW:LAM2_HUMAN	R17	3914	2	1223.4	(+0.5)	2.569	0.159	0.767	2	K.LELEQTYQAK.L
SW:LAM2_HUMAN	R17	4226	2	1223.4	(+0.5)	2.266	0.133	0.600	2	K.LELEQTYQAK.L
SW:LAM2_HUMAN	R13	5441	1	801.0	(-0.5)	1.947	0.160*	0.000	2	R.LQIEIGK.L
SW:LAM2_HUMAN	R13	1914	2	1187.3	(+0.9)	3.085	0.198	0.233	2	K.LRAELDEVNK.S
SW:LAM2_HUMAN	R13	1910	2	1207.3	(+0.1)	2.877	0.116	0.044	2	K.L*RAEL*DEVNK#.S
SW:LAM2_HUMAN	R12	2050	2	1089.2	(-0.4)	2.383	0.199	0.786	2	K.M@AQUAL*EEL*R.S
SW:LAM2_HUMAN	R12	5366	2	1073.2	(-0.1)	2.297	0.172	0.687	2	K.MAQUAL*EEL*R.S
SW:LAM2_HUMAN	R13	5885	2	1061.2	(+0.7)	2.399	0.237	0.896	2	K.MAQALEELR.S
SW:LAM2_HUMAN	R17	5946	2	1061.2	(+0.9)	3.334	0.245	0.975	2	K.MAQALEELR.S
SW:LAM2_HUMAN	R13	2038	2	1548.6	(+0.1)	2.772	0.233	0.115	2	K.NNSDK#DQSL*GNWR.I
SW:LAM2_HUMAN	R13	1464	2	1061.2	(+0.9)	2.899	0.306	0.972	2	R.RLVEVDSSR.Q
SW:LAM2_HUMAN	R13	6371	2	1253.4	(+0.5)	2.460	0.486	0.981	2	R.SEVEL*AAAL*SDK#.R
SW:LAM2_HUMAN	R13	6369	2	1233.4	(+0.7)	2.249	0.455	0.976	2	R.SEVELAAALSDK.R
SW:LAM2_HUMAN	R13	6237	2	1389.5	(+0.1)	4.435	0.498	1.000	2	R.SEVELAAALSDKR.G
SW:LAM2_HUMAN	R13	6231	2	1409.5	(-0.6)	2.691	0.276	0.154	2	R.SEVEL*AAAL*SDK#.R.G
SW:LAM2_HUMAN	R13	5855	2	1504.7	(+0.9)	3.575	0.435	0.991	2	R.TVLVNADGEEVAMR.T
SW:LAM2_HUMAN	R13	5851	2	1510.7	(-0.3)	2.591	0.244	0.835	2	R.TVL*VNADGEEVAMR.T
SW:LAM2_HUMAN	R13	2294	2	1526.7	(-0.4)	2.330	0.148	0.477	2	R.TVL*VNADGEEVAM@R.T
SW:LAM2_HUMAN	R13	6839	2	1264.4	(-0.5)	2.855	0.349	0.386	2	R.VK#DL*ESL*FHR.S

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:LAM2_HUMAN	R21	5778	2	1238.3	(+0.2)	2.670	0.371	0.964	1	K.ALYESELADAR.R
SW:LAMA_HUMAN	R13	1854	2	1172.2	(+0.9)	3.820	0.412	0.999	4	K.AAYEAEEL*GDAR.K
SW:LAMA_HUMAN	R13	1862	2	1166.2	(+0.6)	3.645	0.432	1.000	4	K.AAYEAEELGDAR.K
SW:LAMA_HUMAN	R13	5911	2	1498.7	(+0.0)	2.612	0.389	0.958	4	R.TAL*INSTGEEVAMR.K
SW:LAMA_HUMAN	R13	6341	2	1183.3	(+0.8)	2.675	0.353	0.972	5	R.TLEGELHDLR.G
SW:LAMA_HUMAN	R13	1366	2	1212.3	(-0.1)	3.076	0.450	0.982	5	R.VAVEEVDEEGK#.F
SW:LAMA_HUMAN	R13	2592	2	1120.2	(+0.5)	2.322	0.259	0.878	4	K.EAALSTALSEK.R
SW:LBR_HUMAN	R01	11041	2	2469.8	(-0.4)	2.996	0.391	0.971	2	K.DPSLLNFPPPLPALYELWETR.V
SW:LBR_HUMAN	R02	10113	3	2469.8	(+0.5)	4.097	0.381	0.999	2	K.DPSLLNFPPPLPALYELWETR.V
SW:LBR_HUMAN	R01	1136	2	1021.2	(+0.9)	2.950	0.371	0.985	2	R.KFADGEVVR.G
SW:LBR_HUMAN	R01	1132	2	1029.2	(+0.6)	2.460	0.350	0.968	2	R.K#FADGEVVR.G
SW:LBR_HUMAN	R01	8533	2	2037.2	(+0.8)	5.520	0.647	1.000	2	R.NDL*SPASSGNAVYDFFIGR.E
SW:LBR_HUMAN	R01	8527	2	2031.2	(+0.9)	4.613	0.629	1.000	2	R.NDLSPASSGNAVYDFFIGR.E
SW:LBR_HUMAN	R01	8827	2	2037.2	(+1.0)	3.426	0.502	1.000	2	R.NDL*SPASSGNAVYDFFIGR.E
SW:LBR_HUMAN	R01	8831	2	2031.2	(+0.8)	3.095	0.570	1.000	2	R.NDLSPASSGNAVYDFFIGR.E
SW:LBR_HUMAN	R02	7814	2	2037.2	(+0.2)	4.511	0.591	1.000	2	R.NDL*SPASSGNAVYDFFIGR.E
SW:LBR_HUMAN	R02	7810	2	2031.2	(-0.7)	4.346	0.622	0.999	2	R.NDLSPASSGNAVYDFFIGR.E
SW:LBR_HUMAN	R03	8083	2	2037.2	(+0.7)	5.320	0.584	0.991	2	R.NDL*SPASSGNAVYDFFIGR.E
SW:LBR_HUMAN	R03	8081	2	2031.2	(-0.7)	4.627	0.633	1.000	2	R.NDLSPASSGNAVYDFFIGR.E
SW:LBR_HUMAN	R04	8348	2	2031.2	(-0.6)	4.217	0.597	1.000	2	R.NDLSPASSGNAVYDFFIGR.E
SW:LBR_HUMAN	R01	9215	2	1446.7	(+0.2)	4.253	0.562	1.000	2	K.NL*L*VSGWWGFVR.H
SW:LBR_HUMAN	R02	8386	2	1434.7	(+0.9)	4.149	0.507	1.000	2	K.NLLVSGWWGFVR.H
SW:LBR_HUMAN	R02	8384	2	1446.7	(+0.3)	4.132	0.538	0.999	2	K.NL*L*VSGWWGFVR.H
SW:LBR_HUMAN	R03	8705	2	1446.7	(+0.0)	3.700	0.497	1.000	2	K.NL*L*VSGWWGFVR.H
SW:LBR_HUMAN	R01	658	2	1115.2	(+0.8)	2.746	0.351	0.973	2	R.SASASHQADIK.E
SW:LBR_HUMAN	R01	662	2	1123.2	(+0.4)	2.225	0.210	0.709	2	R.SASASHQADIK#.E
SW:LBR_HUMAN	R03	680	2	1123.2	(+0.1)	2.811	0.272	0.909	2	R.SASASHQADIK#.E
SW:LBR_HUMAN	R03	686	2	1115.2	(+0.7)	2.717	0.252	0.915	2	R.SASASHQADIK.E
SW:LBR_HUMAN	R01	2120	2	1162.3	(-0.2)	2.372	0.448	0.965	2	K.VVEGTPL*IDGR.R
SW:LBR_HUMAN	R01	2076	2	1156.3	(+0.5)	2.282	0.362	0.942	2	K.VVEGTPLIDGR.R
SW:LBR_HUMAN	R02	4956	2	1156.3	(+0.5)	2.903	0.428	0.988	2	K.VVEGTPLIDGR.R
SW:LBR_HUMAN	R02	4864	2	1162.3	(+0.1)	2.875	0.421	0.981	2	K.VVEGTPL*IDGR.R
SW:LBR_HUMAN	R02	4318	2	1162.3	(+0.4)	2.449	0.450	0.975	2	K.VVEGTPL*IDGR.R
SW:LBR_HUMAN	R03	4609	2	1162.3	(+0.1)	2.713	0.425	0.978	2	K.VVEGTPL*IDGR.R
SW:LBR_HUMAN	R03	4685	2	1162.3	(+0.6)	2.652	0.379	0.976	2	K.VVEGTPL*IDGR.R
SW:LBR_HUMAN	R01	9359	3	2904.2	(+0.9)	5.961	0.575	1.000	2	R.WPGSSLYEVEILSHDSTSQLYTVK.Y
SW:LBR_HUMAN	R01	9361	3	2930.2	(-0.4)	4.974	0.490	1.000	2	R.WPGSSL*YYEVEIL*SHDSTSQ*YTVK#.Y
SW:LBR_HUMAN	R01	9281	3	2904.2	(+0.8)	4.553	0.410	0.999	2	R.WPGSSLYEVEILSHDSTSQLYTVK.Y
SW:LBR_HUMAN	R01	9437	3	2904.2	(-0.1)	4.215	0.495	1.000	2	R.WPGSSLYEVEILSHDSTSQLYTVK.Y
SW:LBR_HUMAN	R02	8462	3	2930.2	(-0.2)	3.772	0.411	0.968	2	R.WPGSSL*YYEVEIL*SHDSTSQ*YTVK#.Y
SW:LBR_HUMAN	R02	8452	3	2904.2	(+0.3)	3.743	0.505	1.000	2	R.WPGSSLYEVEILSHDSTSQLYTVK.Y
SW:LBR_HUMAN	R03	8855	3	2904.2	(+0.6)	4.440	0.478	0.998	2	R.WPGSSLYEVEILSHDSTSQLYTVK.Y
SW:LBR_HUMAN	R03	8831	3	2930.2	(+0.0)	3.741	0.479	0.999	2	R.WPGSSL*YYEVEIL*SHDSTSQ*YTVK#.Y
SW:LBR_HUMAN	R03	4093	2	853.0	(+0.9)	2.208	0.403	0.977	2	K.YGVAWEK.Y
SW:LBR_HUMAN	R01	1584	2	1224.3	(-0.5)	2.213	0.217	0.039	2	K.YK#DGTEL*EL*K#.E
SW:LBR_HUMAN	R03	2036	2	1196.3	(+0.0)	2.757	0.396	0.448	2	K.YKDGTELELK.E
SW:LBR_HUMAN	R04	8964	2	1446.7	(+0.2)	3.635	0.599	1.000	2	K.NL*L*VSGWWGFVR.H
SW:LCB1_HUMAN	R16	7408	3	2387.7	(+0.7)	4.260	0.318	0.973	1	K.EKEELIEEWQPELVPPVPK.D
SW:LCB1_HUMAN	R16	4324	2	887.1	(+0.2)	2.863	0.376	0.976		K.ALQGISGLK.V
SW:LCFC_HUMAN	R02	5396	2	1185.3	(+0.1)	2.386	0.254	0.739	5	K.L*QAGEYVSL*GK#.V
SW:LCFC_HUMAN	R03	5185	2	1185.3	(-0.1)	2.378	0.249	0.790	5	K.L*QAGEYVSL*GK#.V
SW:LCFC_HUMAN	R03	7687	2	1989.2	(+0.6)	3.320	0.437	0.986	5	R.LSPEPWTPETGLVTDFAK.L
SW:LCFC_HUMAN	R12	8070	2	2009.2	(-0.9)	3.066	0.451	0.933	5	R.L*SPEPWTPETGL*VTDFAK#.L
SW:LCK_HUMAN	R15	7645	2	1465.6	(+0.8)	3.852	0.371	0.991	9	K.ANSLEPEPWFFK.N
SW:LCK_HUMAN	R15	8103	2	2056.3	(+0.5)	3.328	0.517	1.000	9	K.AQSLTTGQEGFIPFNFAK.A
SW:LCK_HUMAN	R15	10529	2	2031.3	(-0.7)	2.493	0.327*	0.123	10	K.SDVWSFGILLTEIVTHGR.I
SW:LDHA_HUMAN	R19	9204	2	1658.8	(+0.6)	2.227	0.302	0.872	3	K.DLADELALVDVIEDK.L
SW:LDHA_HUMAN	R19	10406	2	1945.4	(-0.3)	2.858	0.368*	0.232	3	K.LLIVSNPVDILTYVAWK.I
SW:LDHA_HUMAN	R19	1458	2	1135.2	(+0.6)	2.207	0.304	0.913	2	K.VTLTSEEEAR.L

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:LDHB_HUMAN	R19	6160	2	1292.5	(+0.3)	2.610	0.466	0.983	1	K.M@VVESAYEVIK#.L
SW:LDHB_HUMAN	R19	9226	2	1630.8	(-0.8)	2.717	0.298	0.770	1	K.SLADELALVDVLEDK.L
SW:LONM_HUMAN	R09	6518	2	1354.6	(+0.5)	4.057	0.495	1.000	3	R.FSVGGMTDVAEIK.G
SW:LONM_HUMAN	R09	5486	2	1378.6	(+0.2)	2.907	0.161	0.730	3	R.FSVGGM@TDVAEIK#.G
SW:LONM_HUMAN	R09	6164	2	1401.6	(+0.8)	4.212	0.476	1.000	3	K.HVMDVVDDEELSK.L
SW:LONM_HUMAN	R09	6170	2	1415.6	(+0.4)	4.148	0.436	1.000	3	K.HVMDVVDDEEL*SK#.L
SW:LONM_HUMAN	R09	5094	2	1431.6	(-0.8)	2.416	0.246	0.533	3	K.HVM@DVVDEEL*SK#.L
SW:LONM_HUMAN	R09	7642	2	1301.6	(+0.6)	3.384	0.270	0.974	4	R.IL*EFIAVSQL*R.G
SW:LONM_HUMAN	R09	6406	2	1702.9	(-0.2)	4.240	0.507	1.000	3	K.LGLLDNHSSEFNVTNR.N
SW:LONM_HUMAN	R09	9310	2	1613.8	(-0.0)	3.155	0.225	0.888	4	R.NYL*DWL*TSPWVK#.Y
SW:LONM_HUMAN	R09	1546	2	1641.7	(+0.9)	3.593	0.277	0.972	3	R.QLEVEPEEPEAENK.H
SW:LONM_HUMAN	R09	7724	2	1499.7	(+0.4)	3.370	0.437	0.984	4	K.TENPLILIDEVDK.I
SW:LONM_HUMAN	R09	9412	3	3671.1	(-0.1)	5.549	0.537	1.000	3	R.VVDNPIYLSDMGAALTGAESHELQDVLEETNIPK.R
SW:LONM_HUMAN	R09	1718	2	1195.3	(+0.6)	2.780	0.404	0.985	4	K.YSNENLDLAR.A
SW:LONM_HUMAN	R09	8176	2	2164.4	(-0.7)	2.220	0.262	0.743	4	R.EIFDIAFPDEQAEALAVR.-
SW:LPRC_HUMAN	R07	1342	2	811.9	(+0.0)	2.415	0.287	0.915	4	R.ADAVWVK#.I
SW:LPRC_HUMAN	R07	7363	2	1664.9	(+0.5)	4.521	0.406	1.000	3	R.AGDMENAENILTVMR.D
SW:LPRC_HUMAN	R07	7365	2	1670.9	(-0.2)	3.725	0.451	0.999	3	R.AGDMENAENIL*TVMR.D
SW:LPRC_HUMAN	R07	2554	2	1046.2	(-0.2)	2.373	0.380	0.959	4	K.ALYEHLTAK.N
SW:LPRC_HUMAN	R07	8847	2	2222.5	(+0.0)	3.546	0.483	1.000	3	R.DAGIEPGPDTYLALLNAYAEEK.G
SW:LPRC_HUMAN	R07	8851	2	2248.5	(-0.5)	2.944	0.194	0.774	3	R.DAGIEPGPDTYL*AL*L*NAYAEEK#.G
SW:LPRC_HUMAN	R07	10461	2	1311.6	(+0.6)	3.505	0.454	1.000	3	R.DLLQIIFSFSK.A
SW:LPRC_HUMAN	R07	10463	2	1331.6	(+0.9)	3.432	0.411	0.988	3	R.DL*L*QIIFSFSK#.A
SW:LPRC_HUMAN	R07	8663	2	1866.1	(+1.0)	3.848	0.436	1.000	4	K.DTTALSFFHMLNGAALR.G
SW:LPRC_HUMAN	R07	8241	2	2338.5	(+0.6)	3.111	0.457	0.982	4	R.EGNQEVFPDVPPEL*WYEDEK#.H
SW:LPRC_HUMAN	R07	8227	2	2324.5	(-0.3)	2.747	0.332	0.937	4	R.EGNQEVFPDVPPELWYEDEK.H
SW:LPRC_HUMAN	R07	6795	2	1112.3	(+0.8)	3.160	0.422	0.991	4	K.GAYDIFLNAK.E
SW:LPRC_HUMAN	R07	6797	2	1126.3	(+0.4)	2.698	0.374	0.972	4	K.GAYDIFL*NAK#.E
SW:LPRC_HUMAN	R07	2038	2	1238.4	(+0.6)	2.952	0.243	0.916	4	K.GDVENIEVVQK#.M
SW:LPRC_HUMAN	R07	3863	2	1166.2	(+0.6)	2.919	0.525	1.000	4	K.GFTLNDAANSR.L
SW:LPRC_HUMAN	R07	3847	2	1172.2	(+0.9)	2.645	0.291	0.946	4	K.GFTL*NDAANSR.L
SW:LPRC_HUMAN	R07	2644	2	1172.2	(+0.1)	2.568	0.355	0.953	4	K.GFTL*NDAANSR.L
SW:LPRC_HUMAN	R07	3931	2	1166.2	(+0.2)	2.555	0.422	0.973	4	K.GFTLNDAANSR.L
SW:LPRC_HUMAN	R07	2488	2	1166.2	(+0.0)	2.548	0.329	0.940	4	K.GFTLNDAANSR.L
SW:LPRC_HUMAN	R07	3783	2	1166.2	(+0.8)	2.478	0.539	0.991	4	K.GFTLNDAANSR.L
SW:LPRC_HUMAN	R07	2568	2	1166.2	(-0.0)	2.436	0.383	0.956	4	K.GFTLNDAANSR.L
SW:LPRC_HUMAN	R07	3666	2	1172.2	(+0.7)	2.435	0.319	0.944	4	K.GFTL*NDAANSR.L
SW:LPRC_HUMAN	R07	2490	2	1172.2	(+0.2)	2.433	0.307	0.912	4	K.GFTL*NDAANSR.L
SW:LPRC_HUMAN	R07	3779	2	1172.2	(+0.3)	2.364	0.381	0.965	4	K.GFTL*NDAANSR.L
SW:LPRC_HUMAN	R07	3797	2	1166.2	(-0.6)	2.327	0.374	0.939	4	K.GFTLNDAANSR.L
SW:LPRC_HUMAN	R07	2642	2	1166.2	(-0.6)	2.263	0.408	0.954	4	K.GFTLNDAANSR.L
SW:LPRC_HUMAN	R07	3648	2	1166.2	(+0.9)	2.236	0.471	0.980	4	K.GFTLNDAANSR.L
SW:LPRC_HUMAN	R07	4779	2	1035.3	(-0.2)	2.923	0.282	0.958	5	K.K#IETPGIR.A
SW:LPRC_HUMAN	R07	4747	2	1027.3	(+1.0)	2.725	0.249	0.945	5	K.KIETPGIR.A
SW:LPRC_HUMAN	R07	5319	2	1512.7	(-0.3)	2.855	0.392	0.971	4	R.KVIEEQLEPAVEK.I
SW:LPRC_HUMAN	R06	10408	3	2600.0	(+0.7)	4.825	0.576	0.999	4	R.LANQFAIYKPVTDFFLQLVDAGK.V
SW:LPRC_HUMAN	R07	6999	2	1689.9	(-0.8)	3.526	0.370	0.919	2	K.L*GAVYDVSHYNAL*L*K#.V
SW:LPRC_HUMAN	R07	6997	2	1663.9	(-0.2)	3.517	0.387	0.980	2	K.LGAVYDVSHYNALLK.V
SW:LPRC_HUMAN	R07	6295	2	1419.6	(-0.4)	3.306	0.446	0.981	4	K.M@L*NGL*EDSIGL*SK#.M
SW:LPRC_HUMAN	R07	7351	2	1505.8	(-0.5)	3.764	0.452	1.000	4	K.M@VFINNIAL*AQIK#.N
SW:LPRC_HUMAN	R07	9551	3	2262.4	(-0.1)	4.254	0.380	0.997	3	K.NNNIDAAIENIENML*TSSENK#.V
SW:LPRC_HUMAN	R07	7539	2	1141.4	(+0.3)	2.454	0.334	0.945	3	K.NVQGIIEIL*K#.G
SW:LPRC_HUMAN	R07	9361	2	1725.9	(+0.7)	4.981	0.482	1.000	3	R.SEAANGNLDVLSFLK.S
SW:LPRC_HUMAN	R07	9435	2	1751.9	(+0.6)	3.384	0.439	0.986	3	R.SEAANGNL*DFVL*SFL*K#.S
SW:LPRC_HUMAN	R07	6885	2	1341.5	(-0.7)	2.555	0.195	0.762	3	K.SNTL*PISL*QSIR.S
SW:LPRC_HUMAN	R07	7963	2	1384.6	(-0.2)	2.912	0.227	0.895	4	K.SVLELIPELNEK.E
SW:LPRC_HUMAN	R07	1156	2	1273.4	(+0.6)	3.640	0.349	0.989	4	K.TVLDQQQTTPSR.L
SW:LPRC_HUMAN	R07	1160	2	1279.4	(+0.2)	2.534	0.307	0.925	4	K.TVL*DQQQTTPSR.L
SW:LPRC_HUMAN	R07	7933	2	1912.1	(+0.2)	3.148	0.403	0.970	3	K.TVQL*TSSEL*ESTL*ETL*K#.A
SW:LPRC_HUMAN	R07	7923	2	1880.1	(-0.4)	2.832	0.383	0.964	3	K.TVQLTSSELESTLET.LK.A
SW:LPRC_HUMAN	R07	5043	2	1384.6	(-0.1)	2.904	0.354	0.966	4	K.VIEEQLEPAVEK.I
SW:LPRC_HUMAN	R07	5053	2	1398.6	(-0.1)	2.839	0.380	0.961	4	K.VIEEQL*EPAVEK#.I
SW:LPRC_HUMAN	R07	5133	2	1398.6	(+0.4)	2.646	0.425	0.976	4	K.VIEEQL*EPAVEK#.I
SW:LPRC_HUMAN	R07	1688	2	1057.2	(+0.3)	2.666	0.408	0.987	2	K.VYLQNEYK.F



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:LPRC_HUMAN	R07	1694	2	1071.2	(+0.1)	2.377	0.252	0.859	2	K.VYL*QNEYK#.F
SW:LPRC_HUMAN	R07	9061	3	2722.0	(+0.5)	4.083	0.474	1.000	4	K.YAGEPVPFIEPPESFEFYAQQLR.K
SW:LPRC_HUMAN	R07	9039	2	2716.0	(-0.4)	4.069	0.431	1.000	4	K.YAGEPVPFIEPPESFEFYAQQLR.K
SW:LPRC_HUMAN	R10	9591	2	1717.0	(+0.7)	2.384	0.392	0.961	4	K.VIEPQYFGLAYLFR.K
SW:LSM2_HUMAN	R26	5472	2	1232.3	(-0.8)	3.193	0.321	0.885		K.L*TDISVTDPEK#.Y
SW:LSM2_HUMAN	R27	5211	2	1232.3	(-0.1)	3.370	0.395	0.981		K.L*TDISVTDPEK#.Y
SW:LSM2_HUMAN	R26	7892	3	2164.4	(+0.3)	5.003	0.603	0.999		R.YVQL*PADEVDTQL*L*QDAAR.K
SW:LSM2_HUMAN	R27	7075	3	2146.4	(+0.8)	4.315	0.502	0.937		R.YVQLPADEVDTQLLQDAAR.K
SW:LSM2_HUMAN	R27	5217	2	1218.3	(-0.2)	2.667	0.367	0.963		K.LTDISVTDPEK#.Y
SW:M2OM_HUMAN	R03	5831	2	1636.8	(+0.4)	2.204	0.206	0.665	2	R.AVVVNAAQLASYSQSK.Q
SW:M2OM_HUMAN	R20	8314	2	1223.4	(+0.5)	2.969	0.422	0.989	2	R.L*GIYTVL*FER.L
SW:M2OM_HUMAN	R20	6898	2	1387.6	(+0.2)	3.554	0.432	0.987	2	R.LTGADGTPPGFLK.A
SW:M2OM_HUMAN	R20	8542	2	1191.3	(+0.8)	2.595	0.477	0.987	2	R.YEGFFSL*WK#.G
SW:MA32_HUMAN	R20	8018	2	1284.5	(+1.0)	4.546	0.383	0.606	1	K.AFVDFLSDEIK.E
SW:MA32_HUMAN	R20	8014	2	1298.5	(+0.3)	3.359	0.461	1.000	1	K.AFVDFL*SDEIK#.E
SW:MA32_HUMAN	R21	7894	2	1298.5	(+0.1)	2.215	0.310	0.842	1	K.AFVDFL*SDEIK#.E
SW:MA32_HUMAN	R21	7830	2	1698.9	(-0.8)	2.981	0.313	0.105	1	K.AFVDFLSDEIKEER.K
SW:MA32_HUMAN	R21	7828	2	1712.9	(-0.5)	2.290	0.128	0.012	1	K.AFVDFL*SDEIK#EER.K
SW:MA32_HUMAN	R21	5936	2	1522.6	(-0.3)	3.401	0.519	1.000	2	R.EVSFQSTGESEWK#.D
SW:MA32_HUMAN	R21	5938	2	1514.6	(-0.2)	3.043	0.382	0.974	2	R.EVSFQSTGESEWK.D
SW:MA32_HUMAN	R21	6548	2	1658.8	(-0.7)	3.630	0.415	0.980	2	K.M@SGGWEL*EL*NGTEAK#.L
SW:MA32_HUMAN	R21	7900	2	2288.6	(+0.3)	5.044	0.493	1.000	2	K.VEEQEPELTSTPNFVVEVIK.N
SW:MA32_HUMAN	R21	7904	2	2302.6	(+0.6)	4.753	0.494	1.000	2	K.VEEQEPEL*TSTPNFVVEVIK#.N
SW:MA32_HUMAN	R25	8536	2	1298.5	(+0.9)	2.645	0.448	0.982	1	K.AFVDFL*SDEIK#.E
SW:MACF_HUMAN	R04	8134	2	1428.7	(-0.5)	2.260	0.311	0.843	3	R.L*QNVQIAL*DFL*K#.Q
SW:MACF_HUMAN	R16	4082	2	1245.5	(+0.9)	2.525	0.171	0.749	5	K.ELLGWVSTLAR.N
SW:MAGM_HUMAN	R25	8702	3	2330.6	(+0.9)	4.609	0.457	1.000	1	R.SAAASNLSGLSLQEAQQILNVSK.L
SW:MAGM_HUMAN	R25	8704	3	2362.6	(-0.1)	3.909	0.489	1.000	1	R.SAAASNLS*SL*QEAQQIL*NVSK#.L
SW:MAGM_HUMAN	R26	5936	2	1173.3	(+0.4)	2.384	0.165	0.636	1	K.SVGGSFYLQSK.V
SW:MAN1_HUMAN	R09	2470	3	1889.0	(+0.7)	4.255	0.436	1.000	1	K.APPAPL*AASEVTNSNSAER.R
SW:MAN1_HUMAN	R09	2396	3	1889.0	(+0.1)	4.183	0.429	0.994	1	K.APPAPL*AASEVTNSNSAER.R
SW:MAN1_HUMAN	R09	5440	2	1436.5	(+0.0)	3.129	0.346	0.971	1	R.DPETEEPL*WASR.T
SW:MAN1_HUMAN	R09	5656	3	1772.0	(-0.2)	4.065	0.484	0.936	2	R.FPQAL*TSNTPL*K#PSNK#.H
SW:MAN1_HUMAN	R09	6690	2	1314.5	(+0.1)	3.116	0.448	0.981	1	R.TL*SVQEAAAYL*K#.D
SW:MAN1_HUMAN	R13	5833	2	1193.3	(+0.8)	3.508	0.441	1.000	2	R.AVDFLAANESR.V
SW:MAOM_HUMAN	R14	5983	2	1650.8	(-0.3)	2.967	0.168	0.775	1	K.AL*TSQL*TDEEL*AQGR.L
SW:MAOM_HUMAN	R14	6165	2	1292.5	(-0.4)	2.476	0.259	0.852	2	K.DPFYM@GL*YQK#.R
SW:MAOM_HUMAN	R14	2266	2	1075.2	(-0.4)	2.800	0.276	0.947	3	K.GM@AFTL*QER.Q
SW:MAOM_HUMAN	R14	6083	2	1053.2	(+0.6)	2.712	0.382*	0.459	3	K.GMAFTLQER.Q
SW:MAOM_HUMAN	R14	6075	2	1059.2	(+0.8)	2.437	0.121	0.697	3	K.GMAFTL*QER.Q
SW:MAOM_HUMAN	R14	6565	2	1331.5	(-0.1)	3.170	0.433	0.978	1	R.HISDSVFL*EAAK#.A
SW:MAOM_HUMAN	R14	5323	2	1193.3	(+1.0)	2.759	0.260	0.941	3	K.IETQDIQAL*R.F
SW:MAOM_HUMAN	R14	5335	2	1187.3	(-0.0)	2.546	0.248	0.885	3	K.IETQDIQALR.F
SW:MAOM_HUMAN	R14	8285	2	1660.8	(+0.2)	3.067	0.479	0.983	2	R.TQQYDDL*IDFMK#.A
SW:MAOM_HUMAN	R14	1926	2	1101.2	(+0.6)	2.409	0.376	0.972	1	K.VTEYLYANK.M
SW:MAT3_HUMAN	R09	9872	3	2372.7	(+0.6)	4.060	0.456	0.981	1	R.DLSAAGIGLLAAATQSLSPASLGR.M
SW:MAT3_HUMAN	R09	6388	3	2375.5	(+0.9)	3.712	0.148	0.293	1	R.DSFDDRGPSSL*NPVL*DYDHGSR.S
SW:MAT3_HUMAN	R09	6720	2	1780.0	(-0.4)	3.170	0.454	0.984		R.GAPPSSNIEDFHGLLPK.G
SW:MAT3_HUMAN	R08	8409	2	1805.9	(-0.6)	2.536	0.392	0.952	1	R.GDADQASNIL*ASFGL*SAR.D
SW:MAT3_HUMAN	R09	8006	2	1793.9	(+0.7)	4.298	0.622	1.000	1	R.GDADQASNILASFGLSAR.D
SW:MAT3_HUMAN	R09	8002	2	1805.9	(+0.2)	3.626	0.395	0.983	1	R.GDADQASNIL*ASFGL*SAR.D
SW:MAT3_HUMAN	R10	8687	2	1793.9	(+0.7)	2.867	0.533	1.000	1	R.GDADQASNILASFGLSAR.D
SW:MAT3_HUMAN	R08	1350	2	1325.4	(+0.9)	2.758	0.525	0.991		R.GNLGAGNGNLQGPR.H
SW:MAT3_HUMAN	R09	1200	2	1337.4	(+0.5)	2.917	0.464	0.988		R.GNL*GAGNGNL*QGPR.H
SW:MAT3_HUMAN	R09	1088	2	1325.4	(+0.7)	2.787	0.511	0.989		R.GNLGAGNGNLQGPR.H
SW:MAT3_HUMAN	R08	1870	2	1092.2	(+0.7)	2.477	0.270	0.925	1	R.GPLPLSSQHR.G
SW:MAT3_HUMAN	R09	1526	2	1092.2	(+0.2)	2.284	0.293	0.851	1	R.GPLPLSSQHR.G
SW:MAT3_HUMAN	R09	5824	2	1627.8	(-0.3)	2.694	0.442	0.974	1	R.GPSLNPVLDYDHGSR.S

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:MAT3_HUMAN	R09	5818	2	1639.8	(-0.3)	2.676	0.294	0.902	1	R.GPSL*NPVL*DYDHGSR.S
SW:MAT3_HUMAN	R08	7955	2	1978.3	(-0.6)	3.236	0.455	0.981	3	R.IGPYQPNVPVGDYVIPK#.T
SW:MAT3_HUMAN	R08	7959	2	1970.3	(-0.5)	2.890	0.479	0.983	3	R.IGPYQPNVPVGDYVIPK.T
SW:MAT3_HUMAN	R09	7500	2	1978.3	(-0.6)	3.002	0.482	0.980	3	R.IGPYQPNVPVGDYVIPK#.T
SW:MAT3_HUMAN	R12	7776	2	1978.3	(-0.3)	2.825	0.399	0.955	3	R.IGPYQPNVPVGDYVIPK#.T
SW:MAT3_HUMAN	R09	8748	3	1621.0	(-0.8)	4.092	0.415	0.996	1	K.ITPENLPQILLQLK.R
SW:MAT3_HUMAN	R10	9227	2	1621.0	(-0.3)	2.720	0.319	0.919	1	K.ITPENLPQILLQLK.R
SW:MAT3_HUMAN	R11	8882	2	1621.0	(-0.4)	2.870	0.395	0.970	1	K.ITPENLPQILLQLK.R
SW:MAT3_HUMAN	R13	9217	2	1621.0	(+0.2)	2.292	0.365	0.919	1	K.ITPENLPQILLQLK.R
SW:MAT3_HUMAN	R09	6594	3	1956.2	(-0.2)	5.114	0.504	0.993		K.RGAPSSNIEDFHGL*L*PK#.G
SW:MAT3_HUMAN	R09	6606	3	1936.2	(+0.2)	5.094	0.452	0.994		K.RGAPSSNIEDFHGLLPK.G
SW:MAT3_HUMAN	R09	1398	2	1366.5	(+0.1)	3.027	0.329	0.964	1	R.RTEEGPTLSYGR.D
SW:MAT3_HUMAN	R09	1394	2	1372.5	(-0.1)	2.915	0.295	0.945	1	R.RTEEGPTL*SYGR.D
SW:MAT3_HUMAN	R08	1278	2	1046.1	(-0.1)	2.360	0.236	0.842	1	K.SFQQSSL*SR.D
SW:MAT3_HUMAN	R09	1030	2	1046.1	(+0.8)	2.303	0.374	0.967	1	K.SFQQSSL*SR.D
SW:MAT3_HUMAN	R08	1750	2	1210.3	(+0.2)	2.394	0.480	0.976	1	R.TEEGPTLSYGR.D
SW:MAT3_HUMAN	R09	6378	3	2258.4	(+0.7)	4.565	0.468	0.999	3	K.VDKIEELDQENEALENGIK.N
SW:MAT3_HUMAN	R09	9502	2	2439.9	(-0.1)	4.535	0.461	1.000	1	R.YQLQLVPEFGVISNHLILNK.I
SW:MAT3_HUMAN	R18	9203	2	1621.0	(+0.5)	2.634	0.429	0.980	1	K.ITPENLPQILLQLK.R
SW:MCM2_HUMAN	R08	5217	2	1016.2	(+0.9)	2.704	0.216	0.912	10	K.AGIVTSLQAR.C
SW:MCM2_HUMAN	R08	6999	2	1479.6	(-0.3)	3.182	0.530	1.000	9	R.ESLVVNYEDLAAR.E
SW:MCM2_HUMAN	R08	6593	3	2055.2	(+0.3)	3.773	0.373	0.986	9	R.FGAQQDTIEVPEK#DL*VDK#.A
SW:MCM2_HUMAN	R08	5357	2	1275.4	(+0.6)	3.043	0.422	0.988	9	K.VAVGELTDEDVK.M
SW:MCM2_HUMAN	R10	5089	2	1275.4	(+0.4)	2.377	0.336	0.943	9	K.VAVGELTDEDVK.M
SW:MCM6_HUMAN	R10	9391	2	1257.6	(+0.5)	2.985	0.431	0.984		R.GVL*L*ML*FGGVPK#.T
SW:MCM6_HUMAN	R10	5435	2	1180.3	(+0.1)	2.329	0.449	0.963	1	K.ASSAAGL*TAAVVR.D
SW:MD29_HUMAN	R26	6496	2	1650.8	(-1.0)	4.087	0.317	0.921		K.HNEETGDNVGPL*IIK#.K
SW:MD29_HUMAN	R26	11142	3	2267.6	(+0.6)	4.150	0.440	1.000		R.VEWIAAVTIAAGTAAIGYL*AYK#.R
SW:MD29_HUMAN	R26	6904	2	1490.7	(-0.2)	3.618	0.455	1.000		K.IVHAFDMEDLGDK.A
SW:MDC2_HUMAN	R21	5066	2	1112.3	(+0.3)	2.522	0.248	0.867	1	K.RPSAPVDFSK#.I
SW:MDC2_HUMAN	R21	6152	2	1069.2	(+0.4)	2.467	0.383	0.976	1	R.DGSYAWIEK.D
SW:MDHM_HUMAN	R19	5798	2	1455.6	(-0.7)	3.615	0.526	0.994		K.AGAGSATLSMAYAGAR.F
SW:MDHM_HUMAN	R19	5788	2	1461.6	(-0.4)	3.136	0.417	0.978		K.AGAGSATL*SMAYAGAR.F
SW:MDHM_HUMAN	R19	988	2	929.0	(+0.8)	2.430	0.354	0.972		K.HGVYNPNK.I
SW:MDHM_HUMAN	R19	1000	2	937.0	(+0.9)	2.267	0.305	0.924		K.HGVYNPNK#.I
SW:MDHM_HUMAN	R24	8114	2	1234.5	(+0.1)	2.588	0.293	0.921		K.IFGVTTLDIRV.A
SW:MDHM_HUMAN	R19	1338	2	1082.2	(+0.9)	2.594	0.252	0.886		R.IQEAGTEVVK#.A
SW:MDHM_HUMAN	R19	8290	3	2392.7	(+0.1)	6.358	0.517	1.000		R.L*TL*YDIAHTPGVAADL*SHIETK#.A
SW:MDHM_HUMAN	R19	8324	2	2366.7	(+0.5)	4.748	0.556	1.000		R.LTLYDIAHTPGVAADL*SHIETK.A
SW:MDHM_HUMAN	R24	8294	3	2392.7	(-0.1)	4.069	0.437	0.984		R.L*TL*YDIAHTPGVAADL*SHIETK#.A
SW:MDHM_HUMAN	R19	6456	2	1147.3	(+0.1)	2.806	0.308	0.940		K.M@ISDAIPEL*K#.A
SW:MDHM_HUMAN	R19	9258	2	1794.2	(+0.4)	3.779	0.581	1.000		K.VAVLGASGGIGQPLSLLLK.N
SW:MDHM_HUMAN	R19	7452	2	1561.7	(+0.7)	3.672	0.484	1.000		K.VDFPQDQLTALTGR.I
SW:MDHM_HUMAN	R19	7474	2	1561.7	(-0.6)	3.587	0.436	1.000		K.VDFPQDQLTALTGR.I
SW:MDHM_HUMAN	R19	7534	2	1573.7	(-0.0)	2.666	0.282	0.896		K.VDFPQDQL*TAL*TRG.I
SW:MDHM_HUMAN	R19	7406	2	1573.7	(+0.6)	2.597	0.408	0.971		K.VDFPQDQL*TAL*TRG.I
SW:MDHM_HUMAN	R19	7448	2	1573.7	(-0.9)	2.483	0.209	0.474		K.VDFPQDQL*TAL*TRG.I
SW:MDHM_HUMAN	R19	5526	2	1148.4	(-0.3)	2.930	0.294	0.945		R.VNVPVIGGHAGK.T
SW:MDHM_HUMAN	R19	5516	2	1156.4	(-0.6)	2.305	0.349	0.897		R.VNVPVIGGHAGK#.T
SW:MDHM_HUMAN	R24	8112	2	1240.5	(-0.0)	2.493	0.222	0.819		K.IFGVTTL*DIRV.A
SW:MG15_HUMAN	R18	9355	3	2265.6	(+0.2)	4.205	0.475*	0.012	6	K.IPEEL*K#PWL*VDDWDL*ITR.Q
SW:MG15_HUMAN	R18	9373	2	2239.6	(+0.2)	3.437	0.469*	0.016	6	K.IPEELKPVLVDDWDLITR.Q
SW:MG15_HUMAN	R18	10805	2	1661.0	(+0.6)	4.345	0.509	1.000	6	K.SLALLLNLYLHDFLK.Y
SW:MG15_HUMAN	R18	6357	2	1458.7	(+0.2)	2.451	0.289	0.840	6	R.IGAM@L*AYTPL*DEK#.S
SW:MGN_HUMAN	R25	8186	2	1870.0	(-0.3)	4.373	0.534	1.000	1	K.FGHEFL*EFEFRPDGK#.L
SW:MGN_HUMAN	R25	8188	2	1856.0	(-0.5)	4.220	0.560	1.000	1	K.FGHEFLEFEFRPDGK.L
SW:MGN_HUMAN	R25	6070	2	1174.3	(-0.1)	3.187	0.321	0.970	1	K.IGSLIDVNQSK.D
SW:MGN_HUMAN	R25	6068	2	1188.3	(+0.2)	3.068	0.260	0.927	1	K.IGSL*IDVNQSK#.D
SW:MGN_HUMAN	R25	2266	2	1034.2	(+0.4)	2.489	0.159	0.807	1	R.IIDDSEITK.E

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:MGN_HUMAN	R25	8214	2	1308.5	(+0.6)	3.072	0.294	0.966	2	R.VFYLL*VQDL*K#.C
SW:MGN_HUMAN	R25	6264	2	1174.3	(+0.6)	2.261	0.284	0.894	1	K.IGSLIDVNQSK.D
SW:MLN_HUMAN	R25	7054	2	1545.6	(+0.7)	2.868	0.527	1.000	8	K.DQGTIEDYVEGLR.V
SW:MLN_HUMAN	R25	6054	2	996.2	(+0.8)	2.278	0.378	0.967	8	R.HVLVTLGEK.M
SW:MLRM_HUMAN	R24	5664	2	1229.3	(-0.0)	2.983	0.385	0.978	5	K.LNGTDPEDVIR.N
SW:MLRM_HUMAN	R24	6444	2	1416.5	(-0.1)	2.802	0.368	0.969	2	R.FTDEEVDLYR.E
SW:MTA1_HUMAN	R11	8890	3	2358.5	(+0.4)	5.330	0.486	1.000	1	R.DEMEEWSASEANLFEEALEK.Y
SW:MTA1_HUMAN	R11	8196	3	2394.5	(+0.5)	3.837	0.400	0.999	1	R.DEM@EWSASEANL*FEEAL*EK#.Y
SW:MTA1_HUMAN	R12	8608	2	1653.8	(+0.6)	2.357	0.215	0.716	1	K.DFTDIQQDFLPWK.S
SW:MTA1_HUMAN	R11	7772	2	1247.4	(+0.9)	3.443	0.375	0.988	2	R.DISSTLIALADK.H
SW:MTA1_HUMAN	R11	7768	2	1267.4	(-0.2)	2.515	0.174	0.634	2	R.DISSTL*IAL*ADK#.H
SW:MTA1_HUMAN	R11	698	2	954.0	(+0.9)	2.951	0.343	0.982	1	R.GLANHGQTR.H
SW:MTA1_HUMAN	R11	696	2	960.0	(+0.5)	2.463	0.290	0.945	1	R.GL*ANHGQTR.H
SW:MTA1_HUMAN	R11	6610	2	1802.0	(+0.1)	3.718	0.437	1.000	3	R.L*ETQVWEAHNPL*TDK#.Q
SW:MTA1_HUMAN	R11	6056	2	1308.5	(-0.3)	3.258	0.304	0.954	2	R.L*PEASQSPL*VL*K#.Q
SW:MTA1_HUMAN	R11	6060	2	1282.5	(+0.7)	3.224	0.437	0.985	2	R.LPEASQSPLVLK.Q
SW:MTA1_HUMAN	R11	2108	2	1114.4	(+0.1)	2.489	0.224	0.080	2	R.RPYKPIALR.Q
SW:MTA1_HUMAN	R11	8980	2	1728.0	(+0.1)	3.054	0.410	0.973	4	K.SL*TSIIYYM@WK#.T
SW:MTA1_HUMAN	R11	944	2	1189.3	(+0.0)	2.622	0.390	0.968	1	R.SNM@SPHGL*PAR.S
SW:MTA1_HUMAN	R11	6946	2	1296.5	(+0.2)	2.290	0.453	0.952	2	K.SVSSVL*SSL*TPAK#.V
SW:MTA1_HUMAN	R11	4492	2	1116.3	(+0.4)	2.525	0.263*	0.007	6	K.TLLADKGEIR.V
SW:MTA1_HUMAN	R11	4588	2	1116.3	(+0.7)	2.227	0.225*	0.004	6	K.TLLADKGEIR.V
SW:MTA1_HUMAN	R12	4608	2	1116.3	(+0.9)	2.271	0.221*	0.004	6	K.TLLADKGEIR.V
SW:MTA1_HUMAN	R11	6072	2	1494.7	(-0.2)	3.301	0.474	0.983	2	K.VAPVINNGSPTIL*GK#.R
SW:MTA1_HUMAN	R11	7170	3	2124.3	(+0.9)	4.180	0.547	0.998	3	R.VGDYVYFENSSSNPYLIR.R
SW:MTA1_HUMAN	R11	6898	2	1180.3	(+0.8)	3.113	0.224	0.954	3	R.YQADITDLLK.E
SW:MTA1_HUMAN	R14	5125	2	1116.3	(+0.0)	2.325	0.315*	0.004	6	K.TLLADKGEIR.V
SW:MTA2_HUMAN	R12	6076	2	1550.6	(+0.8)	4.897	0.489	1.000	2	R.DISSSLNLSLADSNAR.E
SW:MTA2_HUMAN	R12	4150	2	1180.4	(+0.2)	2.686	0.395	0.390	2	K.DLVAQAPLKP.K.T
SW:MTA2_HUMAN	R12	3752	2	1180.4	(+0.4)	2.686	0.503	0.673	2	K.DLVAQAPLKP.K.T
SW:MTA2_HUMAN	R12	3988	2	1180.4	(+0.2)	2.635	0.469	0.522	2	K.DLVAQAPLKP.K.T
SW:MTA2_HUMAN	R12	3906	2	1180.4	(+0.7)	2.430	0.419	0.456	2	K.DLVAQAPLKP.K.T
SW:MTA2_HUMAN	R12	4176	2	1208.4	(-0.2)	2.289	0.194	0.031	2	K.DL*VAQAPL*K#PK#.T
SW:MTA2_HUMAN	R12	4100	2	1208.4	(+0.1)	2.262	0.335	0.131	2	K.DL*VAQAPL*K#PK#.T
SW:MTA2_HUMAN	R12	3950	2	1208.4	(-0.3)	2.259	0.124	0.012	2	K.DL*VAQAPL*K#PK#.T
SW:MTA2_HUMAN	R11	5388	3	2185.3	(+0.5)	3.867	0.325	0.965	2	R.GHL*SRPEAQL*SPYTTSANR.A
SW:MTA2_HUMAN	R12	6914	2	1653.9	(-0.3)	3.401	0.543	1.000	1	K.LNPADAPNPVVFVATK.D
SW:MTA2_HUMAN	R12	730	2	1019.1	(+0.9)	2.845	0.403	0.987	2	R.LVEGESDNR.N
SW:MTA2_HUMAN	R12	726	2	1025.1	(+0.7)	2.786	0.348	0.976	2	R.L*VEGESDNR.N
SW:MTA2_HUMAN	R12	4454	2	1116.3	(+0.6)	3.248	0.228*	0.656	2	K.TLLADQGEIR.V
SW:MTA2_HUMAN	R12	4566	2	1128.3	(-0.5)	2.494	0.316*	0.220	2	K.TL*L*ADQGEIR.V
SW:MTA2_HUMAN	R12	6968	2	2110.3	(-0.4)	4.183	0.411	1.000	2	R.VGDYVYFENSSSNPYLVR.R
SW:MTA2_HUMAN	R12	7788	3	3256.8	(+0.1)	4.782	0.566	1.000	1	K.VKPTLIAVRPPVPLPAPSHPASTNEPIVLED.-
SW:MTA2_HUMAN	R12	5946	2	1334.4	(+0.5)	2.602	0.258	0.921	2	K.VWDPDNL*TDK.Q
SW:MTA2_HUMAN	R12	3820	2	1180.4	(+0.6)	2.221	0.356	0.213	2	K.DLVAQAPLKP.K.T
SW:MTDC_HUMAN	R19	6556	2	1212.3	(+0.8)	3.555	0.429	1.000	1	K.L*VGDVDFEGVR.Q
SW:MTDC_HUMAN	R19	5070	2	1384.5	(+0.4)	2.205	0.130	0.416	1	R.QEVEEWASGNK#.R
SW:MTX2_HUMAN	R21	5574	2	1419.5	(-0.9)	3.724	0.312	0.909	1	K.GHSL*SDGL*EEVQK#.A
SW:MTX2_HUMAN	R21	5564	2	1399.5	(-0.3)	3.055	0.503	1.000	1	K.GHSLSDGLEEVQK.A
SW:MTX2_HUMAN	R21	8944	3	2421.9	(+0.8)	4.496	0.401	0.998	1	K.VPFIHVGNQVVSSEL*GPIVQFVK#.A
SW:MUTA_HUMAN	R11	7316	2	1145.4	(+0.4)	2.696	0.342	0.972	2	K.IIFDGIPLK.M
SW:MUTA_HUMAN	R11	6040	2	1216.4	(+0.8)	2.454	0.180	0.785	2	K.LTGTIQNDILK.E
SW:MYH9_HUMAN	R05	6122	2	1224.4	(+0.6)	3.820	0.367	0.987	6	R.AGVLAHLEEEER.D
SW:MYH9_HUMAN	R05	6126	2	1236.4	(-0.4)	2.968	0.124	0.767	6	R.AGVL*AHL*EEER.D
SW:MYH9_HUMAN	R06	6134	2	1236.4	(-0.6)	2.768	0.218	0.876	6	R.AGVL*AHL*EEER.D
SW:MYH9_HUMAN	R07	6061	2	1224.4	(+0.6)	3.474	0.408	0.986	6	R.AGVLAHLEEEER.D
SW:MYH9_HUMAN	R05	6276	2	1194.3	(+0.8)	3.603	0.417	1.000	5	K.ALELDSNLYR.I
SW:MYH9_HUMAN	R05	6272	2	1212.3	(+0.4)	2.885	0.401	0.930	5	K.AL*EL*DSNL*YR.I

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:MYH9_HUMAN	R06	6286	2	1194.3	(+1.0)	2.289	0.170	0.561	5	K.ALELDNSLYR.I
SW:MYH9_HUMAN	R05	4860	2	1219.4	(-0.6)	2.942	0.161	0.814	4	R.AL*EQQVEEMK#.T
SW:MYH9_HUMAN	R05	4774	2	1205.4	(-0.1)	2.922	0.199	0.895	4	R.ALEQQVEEMK.T
SW:MYH9_HUMAN	R05	4784	2	1219.4	(-0.8)	2.792	0.124	0.414	4	R.AL*EQQVEEMK#.T
SW:MYH9_HUMAN	R05	4850	2	1205.4	(-0.6)	2.610	0.224	0.868	4	R.ALEQQVEEMK.T
SW:MYH9_HUMAN	R05	4642	2	1349.4	(+0.5)	4.201	0.538	1.000	4	R.DELADEIANSSGK.G
SW:MYH9_HUMAN	R05	4748	2	1349.4	(-0.5)	3.418	0.472	0.999	4	R.DELADEIANSSGK.G
SW:MYH9_HUMAN	R05	4668	2	1363.4	(-0.7)	3.384	0.412	0.925	4	R.DEL*ADEIANSSGK#.G
SW:MYH9_HUMAN	R05	4744	2	1363.4	(-0.7)	3.040	0.334	0.941	4	R.DEL*ADEIANSSGK#.G
SW:MYH9_HUMAN	R05	4672	2	1349.4	(-0.8)	2.924	0.396	0.925	4	R.DELADEIANSSGK.G
SW:MYH9_HUMAN	R06	4712	2	1349.4	(+1.0)	2.828	0.445	0.980	4	R.DELADEIANSSGK.G
SW:MYH9_HUMAN	R05	1362	2	1213.3	(+0.3)	2.838	0.376	0.980	4	K.DLEAHIDSANK.N
SW:MYH9_HUMAN	R05	1358	2	930.0	(+0.2)	2.389	0.223	0.856	2	K.DL*EGL*SQR.H
SW:MYH9_HUMAN	R05	7598	2	2035.1	(-0.6)	3.416	0.543	0.986	5	R.ELESQISELQEDLESER.A
SW:MYH9_HUMAN	R05	5262	2	1093.2	(+0.2)	3.083	0.306	0.969	13	K.FDQLLAEK.T
SW:MYH9_HUMAN	R05	5274	2	1113.2	(+0.6)	2.387	0.110	0.573	13	K.FDQL*L*AEEK#.T
SW:MYH9_HUMAN	R05	5306	2	1113.2	(-0.7)	2.246	0.221	0.720	13	K.FDQL*L*AEEK#.T
SW:MYH9_HUMAN	R07	5783	2	1344.5	(-0.4)	2.932	0.469	0.987	5	K.HEAMITDLEER.L
SW:MYH9_HUMAN	R06	6092	2	1654.8	(+1.0)	3.189	0.366	0.980	5	R.IAEFTTNLTETEEEEK.S
SW:MYH9_HUMAN	R05	5674	2	1531.7	(+0.8)	4.048	0.466	1.000	4	K.IAQLEEQLDNETK.E
SW:MYH9_HUMAN	R05	5092	2	1258.4	(-0.5)	2.584	0.194	0.754	11	K.KEEELQAALAR.V
SW:MYH9_HUMAN	R07	4959	2	1258.4	(+0.1)	2.591	0.193	0.795	11	K.KEEELQAALAR.V
SW:MYH9_HUMAN	R05	5870	3	1441.7	(+0.5)	3.855	0.300	0.997	4	K.K#VEAQL*QEL*QVK#.F
SW:MYH9_HUMAN	R05	8822	3	2488.7	(+1.0)	4.455	0.510	1.000	5	K.LEGDSTDLSDQIAELQAQIAELK.M
SW:MYH9_HUMAN	R05	6172	2	1046.3	(+0.7)	2.701	0.199*	0.453	4	R.LEVNLQAMK.A
SW:MYH9_HUMAN	R05	1140	2	1035.2	(+0.3)	2.537	0.180	0.806	4	K.LQEMEGTVK.S
SW:MYH9_HUMAN	R05	7500	3	2502.8	(+0.1)	4.111	0.398	0.995	9	K.L*QQL*FNHTM@FIL*EQEEYQR.E
SW:MYH9_HUMAN	R05	7360	3	2334.5	(+0.8)	4.633	0.446	0.996	6	K.MQQNIQELLEEQLLEEEESAR.Q
SW:MYH9_HUMAN	R05	7364	3	2346.5	(+0.7)	3.849	0.419	0.997	6	K.MQQNIQEL*EEQL*EEEEESAR.Q
SW:MYH9_HUMAN	R05	7492	2	1687.9	(-0.7)	4.329	0.496	1.000	4	K.NFINNPL*AQADWAAK#.K
SW:MYH9_HUMAN	R05	7490	2	1673.9	(-0.4)	3.920	0.490	0.999	4	K.NFINNPLAQADWAAK.K
SW:MYH9_HUMAN	R05	8186	2	1754.0	(-0.3)	2.765	0.392	0.953	10	R.QL*L*QANPIL*EAFGNAK#.T
SW:MYH9_HUMAN	R05	6712	2	1162.4	(+0.4)	2.593	0.245	0.921	3	R.RGDL*PFVVR.R
SW:MYH9_HUMAN	R05	6392	2	1206.4	(+0.9)	3.999	0.144	0.963	5	K.TDLLLLPYNK.Y
SW:MYH9_HUMAN	R05	7536	2	1963.1	(-0.5)	4.161	0.479	1.000	10	K.TQLEEELEDELQATEDAK.L
SW:MYH9_HUMAN	R05	7538	3	1989.1	(-0.8)	3.721	0.268	0.905	10	K.TQL*EEL*EDEL*QATEDAK#.L
SW:MYH9_HUMAN	R05	8400	2	1487.8	(+0.9)	3.208	0.516	1.000	5	R.VISGVLQLGNIVFK.K
SW:MYH9_HUMAN	R07	8673	2	1487.8	(+0.7)	4.157	0.491	1.000	5	R.VISGVLQLGNIVFK.K
SW:MYH9_HUMAN	R05	7516	2	1572.8	(-0.1)	4.710	0.446	1.000	5	K.VSHLLGINVTDFTFR.G
SW:MYH9_HUMAN	R05	7512	2	1584.8	(-0.5)	3.302	0.348	0.972	5	K.VSHL*L*GINVTDFTFR.G
SW:MYH9_HUMAN	R08	6269	2	1654.8	(+0.3)	2.525	0.446	0.980	5	R.IAEFTTNLTETEEEEK.S
SW:MYHA_HUMAN	R05	7930	3	2429.5	(+0.0)	4.484	0.338	0.994		K.DAASL*ESQL*QDTQEL*L*QEETR.Q
SW:MYHA_HUMAN	R05	7434	2	1441.6	(+0.4)	3.512	0.331	0.984		K.SDLLLEGFNNYR.F
SW:N107_HUMAN	R09	5924	2	1121.3	(+0.5)	3.041	0.366	0.983	2	R.AIYAALSGNLK.Q
SW:N107_HUMAN	R09	5646	3	2528.6	(+0.5)	5.556	0.458	0.998	1	K.DNGEFSSHDLAPALDTGTTEEDR.L
SW:N107_HUMAN	R09	5644	3	2540.6	(+0.5)	4.186	0.427	0.999	1	K.DNGEFSSHDL*APAL*DTGTTEEDR.L
SW:N107_HUMAN	R10	11055	3	2453.7	(+0.7)	3.787	0.335	0.995	1	R.EDDPGEAASMSMFSDFLQSF.K.H
SW:N107_HUMAN	R09	6348	2	1324.5	(+0.9)	2.699	0.420	0.984	2	R.EYLGANWTLEK.V
SW:N107_HUMAN	R09	9868	2	1814.1	(-0.9)	3.004	0.468	0.951	2	K.FLILGDIDGLMDEFK.W
SW:N107_HUMAN	R09	9866	2	1840.1	(-1.0)	2.649	0.397	0.857	2	K.FL*IL*GDIDGL*MDEFK#.W
SW:N107_HUMAN	R09	4990	2	1140.3	(+0.3)	2.565	0.538	1.000	2	K.GHLDALTADV.K.E
SW:N107_HUMAN	R09	6266	3	2264.6	(+1.0)	4.505	0.395	0.994	2	K.HMNSVPQKPALIPQPTFTEK.V
SW:N107_HUMAN	R09	6262	3	2286.6	(-0.1)	3.761	0.312	0.892	2	K.HMNSVPQK#PAL*IPQPTFTEK#.V
SW:N107_HUMAN	R09	9170	2	1693.9	(-0.0)	3.013	0.406	0.976	2	K.IDVIDWL*VFDPAQR.A
SW:N107_HUMAN	R09	7112	2	1333.5	(+0.4)	3.278	0.432	1.000	2	K.K#YEMDFGIWK#.G
SW:N107_HUMAN	R09	7120	2	1317.5	(-0.0)	3.003	0.312	0.966	2	K.KYEMDFGIWK.G
SW:N107_HUMAN	R09	5704	3	2471.6	(+0.8)	3.822	0.339	0.995	2	K.LYHDPNVNGGTELEPVEGNPYR.R
SW:N107_HUMAN	R09	5152	2	1125.2	(+0.6)	2.977	0.263	0.967	2	R.MAEDEL.FNR.Y
SW:N107_HUMAN	R09	5144	2	1131.2	(-0.0)	2.378	0.224	0.497	2	R.MAEDEL*FNR.Y
SW:N107_HUMAN	R09	2188	2	1147.2	(+0.2)	2.366	0.239	0.851	2	R.M@AEDEL*FNR.Y
SW:N107_HUMAN	R09	2266	2	1147.2	(+0.7)	2.363	0.353	0.964	2	R.M@AEDEL*FNR.Y
SW:N107_HUMAN	R09	4862	2	975.1	(+0.8)	2.548	0.263	0.948	2	K.MPLDDLDR.E
SW:N107_HUMAN	R09	6522	2	1491.7	(+0.0)	3.321	0.323	0.972	2	K.SVYWENTLH.LTK.Q
SW:N107_HUMAN	R09	6574	2	1069.2	(+0.9)	2.654	0.325	0.970	2	K.TVVEAL*FQR.D

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:N107_HUMAN	R09	7230	2	1032.3	(+0.5)	2.472	0.110	0.727	1	K.TYIQL*L*IR.E
SW:N107_HUMAN	R08	4401	2	1180.3	(+0.5)	2.503	0.117	0.680	2	K.VFEELQATDK.K
SW:N107_HUMAN	R09	2124	2	1180.3	(+0.6)	3.154	0.405	0.985	2	K.VFEELQATDK.K
SW:N107_HUMAN	R09	2046	2	1194.3	(+0.2)	2.478	0.328	0.922	2	K.VFEEL*QATDK#.K
SW:N107_HUMAN	R09	2044	2	1180.3	(+0.5)	2.293	0.397	0.969	2	K.VFEELQATDK.K
SW:N107_HUMAN	R09	5482	2	1903.0	(-0.6)	4.098	0.579	0.990	1	R.VL*L*QASQDENFGNTTPR.N
SW:N107_HUMAN	R09	5490	2	1891.0	(-0.6)	3.909	0.506	1.000	1	R.VLLQASQDENFGNTTPR.N
SW:N107_HUMAN	R10	2428	2	1147.2	(+0.5)	2.560	0.259	0.937	2	R.M@AEDEL*FNR.Y
SW:N153_HUMAN	R06	7612	3	2535.7	(+0.5)	3.864	0.474	1.000	1	R.ESGFSYPNFSL*PAANGL*SSVGGGGGK#.M
SW:N153_HUMAN	R06	6090	2	2091.2	(-0.7)	4.070	0.433	1.000	1	K.FGVSSSSSGPSQTL*TSTGNFK#.F
SW:N153_HUMAN	R06	8792	2	2296.6	(+0.7)	4.330	0.597	0.959	1	K.GGFSFGNVEPASLPSASVFLGR.T
SW:N153_HUMAN	R06	8796	2	2308.6	(+0.8)	3.788	0.411	0.990	1	K.GGFSFGNVEPASL*PSASVFL*GR.T
SW:N153_HUMAN	R06	6498	2	1813.0	(+1.0)	4.690	0.591	1.000	1	K.IGVSSDSGSINPMSEGFK.F
SW:N153_HUMAN	R06	6490	2	1821.0	(-0.4)	3.994	0.463	1.000	1	K.IGVSSDSGSINPMSEGFK#.F
SW:N153_HUMAN	R06	5656	2	1837.0	(-0.8)	3.121	0.484	0.945	1	K.IGVSSDSGSINPM@SEGFK#.F
SW:N153_HUMAN	R06	7180	2	1595.8	(+0.8)	4.398	0.538	1.000	1	R.IPSIVSSPLNSPLDR.S
SW:N153_HUMAN	R06	7054	2	1609.8	(-0.1)	2.763	0.427	0.949	1	K.NTSL*PPL*WSPEAER.S
SW:N153_HUMAN	R06	1580	2	1562.7	(-0.2)	3.399	0.485	0.998	1	K.QL*SAQSYGVTSTAR.R
SW:N153_HUMAN	R06	6292	2	1203.3	(+0.4)	3.501	0.294	0.974	1	R.SGIDITDFQAK#.R
SW:N153_HUMAN	R06	6154	2	1211.3	(+0.6)	2.546	0.328	0.944	1	K.SSFNL*GTIETK#.S
SW:N153_HUMAN	R06	5888	2	1397.5	(-0.5)	3.177	0.427	0.984	1	K.TSQLGDSPPFYPGK.T
SW:N153_HUMAN	R06	5880	2	1411.5	(+0.1)	2.956	0.467	0.980	1	K.TSQL*GDSPPFYPGK#.T
SW:N153_HUMAN	R07	6221	2	1203.3	(+0.3)	2.613	0.227	0.868	1	R.SGIDITDFQAK#.R
SW:N155_HUMAN	R03	6223	2	978.1	(+0.3)	2.279	0.320	0.951	1	K.GLQEFLLDR.N
SW:N155_HUMAN	R07	6499	3	1830.0	(+0.7)	4.277	0.541	1.000	1	K.GVIQVYDL*GQDQGMSR.V
SW:N155_HUMAN	R07	6197	2	1846.0	(+0.7)	4.052	0.545	1.000	1	K.GVIQVYDL*GQDQGGM@SR.V
SW:N155_HUMAN	R07	6899	2	1961.1	(-0.5)	4.382	0.522	0.999	2	K.HGEPEEDIVGL*QAFQER.L
SW:N155_HUMAN	R07	5885	2	1724.9	(-0.3)	4.864	0.517	1.000	1	R.HLLVSNVGGDGEEIER.F
SW:N155_HUMAN	R07	7415	2	1625.9	(-0.3)	4.303	0.406	0.998	1	R.IM@GNIWDASL*VVER.I
SW:N155_HUMAN	R07	6383	2	1370.6	(-0.8)	3.149	0.278	0.877	2	R.IQLQIQETLQR.Q
SW:N155_HUMAN	R07	6385	2	1382.6	(+0.7)	3.098	0.428	0.988	2	R.IQL*QIQETL*QR.Q
SW:N155_HUMAN	R08	6681	2	1370.6	(-0.7)	2.897	0.276	0.939	2	R.IQLQIQETLQR.Q
SW:N155_HUMAN	R01	7935	2	1281.5	(+0.2)	2.527	0.365	0.955	2	K.ISL*QAIQQL*VR.K
SW:N155_HUMAN	R02	7348	2	1269.5	(+0.2)	2.623	0.227	0.855	2	K.ISLQAIQQLVR.K
SW:N155_HUMAN	R03	7515	2	1269.5	(+0.5)	2.399	0.362	0.961	2	K.ISLQAIQQLVR.K
SW:N155_HUMAN	R06	7924	2	1281.5	(-0.0)	2.612	0.306	0.919	2	K.ISL*QAIQQL*VR.K
SW:N155_HUMAN	R07	7827	2	1281.5	(+0.1)	3.089	0.329	0.969	2	K.ISL*QAIQQL*VR.K
SW:N155_HUMAN	R08	8073	2	1281.5	(-0.1)	2.800	0.290	0.940	2	K.ISL*QAIQQL*VR.K
SW:N155_HUMAN	R08	8077	2	1269.5	(-0.5)	2.555	0.208	0.813	2	K.ISLQAIQQLVR.K
SW:N155_HUMAN	R07	2144	3	1657.8	(+0.5)	4.173	0.408	1.000	2	R.L*ADM@HSTEISL*QQR.L
SW:N155_HUMAN	R07	5943	3	2559.9	(+0.3)	5.156	0.372	0.963	2	R.L*IGFM@RPENGNPQQM@QQEL*QR.K
SW:N155_HUMAN	R01	7943	2	1294.5	(+0.3)	2.317	0.339	0.935	2	R.L*L*EVYDQL*FK#.S
SW:N155_HUMAN	R02	7354	2	1294.5	(+0.2)	3.130	0.398	0.979	2	R.L*L*EVYDQL*FK#.S
SW:N155_HUMAN	R07	7847	2	1294.5	(-0.5)	2.580	0.336	0.937	2	R.L*L*EVYDQL*FK#.S
SW:N155_HUMAN	R08	8089	2	1294.5	(-0.6)	2.931	0.433	0.980	2	R.L*L*EVYDQL*FK#.S
SW:N155_HUMAN	R07	7059	2	1201.3	(+0.5)	3.194	0.391	0.985	2	K.L*YGEFADPFK#.L
SW:N155_HUMAN	R08	7367	2	1187.3	(+0.3)	2.658	0.347	0.972	2	K.LYGEFADPFK.L
SW:N155_HUMAN	R07	4357	2	1674.8	(+0.4)	4.726	0.545	1.000	1	R.NSQFAGGPLGNPNTTAK.V
SW:N155_HUMAN	R07	4275	2	1674.8	(-0.5)	4.252	0.625	1.000	1	R.NSQFAGGPLGNPNTTAK.V
SW:N155_HUMAN	R07	4413	2	1688.8	(-0.5)	4.200	0.449	1.000	1	R.NSQFAGGPL*GNPNTTAK#.V
SW:N155_HUMAN	R07	4259	2	1688.8	(-0.5)	3.849	0.445	1.000	1	R.NSQFAGGPL*GNPNTTAK#.V
SW:N155_HUMAN	R07	8741	3	2719.9	(+0.7)	4.005	0.279	0.986	2	R.QYSHHSSVQDAVSQDSELMITK.L
SW:N155_HUMAN	R07	8525	3	2755.9	(-0.0)	3.831	0.335	0.982	2	R.QYSHHSSVQDAVSQDSEL*M@DITK#.L
SW:N155_HUMAN	R07	6967	2	1080.3	(+0.8)	2.661	0.405	0.985	2	K.SYQALALWK.L
SW:N155_HUMAN	R08	6691	2	1382.6	(+0.4)	2.497	0.283	0.924	2	R.IQL*QIQETL*QR.Q
SW:N160_HUMAN	R01	11133	2	2104.4	(+0.8)	4.660	0.588	0.999	1	R.FVSSPQTIVEL*FFQEVAR.K
SW:N160_HUMAN	R01	11109	2	2098.4	(+0.8)	3.570	0.487	1.000	1	R.FVSSPQTIVELFFQEVAR.K
SW:N160_HUMAN	R02	10101	3	2098.4	(+1.0)	3.937	0.330	0.996	1	R.FVSSPQTIVELFFQEVAR.K
SW:N160_HUMAN	R03	10356	3	2104.4	(+0.9)	3.959	0.342	0.977	1	R.FVSSPQTIVEL*FFQEVAR.K
SW:N160_HUMAN	R04	10560	3	2104.4	(+0.8)	5.040	0.388	0.978	1	R.FVSSPQTIVEL*FFQEVAR.K
SW:N160_HUMAN	R04	10562	3	2098.4	(+0.9)	4.718	0.371	0.997	1	R.FVSSPQTIVELFFQEVAR.K
SW:N160_HUMAN	R02	6246	2	1233.4	(+0.2)	2.441	0.309	0.897	1	K.GFNPAQPL*NIR.M
SW:N160_HUMAN	R01	7931	2	1472.7	(+0.2)	3.233	0.216	0.922	1	R.QIEILELEDLEK.E

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:N160_HUMAN	R01	3763	2	1101.2	(+0.2)	2.378	0.456	0.974	3	R.SFVEL*SGAER.E
SW:N160_HUMAN	R03	5061	2	1095.2	(+0.6)	2.916	0.273	0.962	3	R.SFVELSGAER.E
SW:N160_HUMAN	R02	9120	3	2918.3	(-0.0)	4.018	0.433	0.950	1	R.SQL*QDL*VEFPYVNL*HNEVVGIIESR.A
SW:N160_HUMAN	R03	9389	3	2900.3	(+0.5)	3.844	0.395	0.998	1	R.SQLQDLVEFPYVNLHNEVVGIIESR.A
SW:N160_HUMAN	R01	9757	3	2562.9	(+0.7)	3.826	0.454	0.711	3	K.TSGDTLELMEESLDINLNNAIR.L
SW:N160_HUMAN	R07	10855	3	2098.4	(-0.1)	3.999	0.293	0.982	1	R.FVSSPQTIVELFFQEVAR.K
SW:N214_HUMAN	R01	8479	3	2542.8	(+0.9)	4.567	0.408	0.999	3	K.FAVQDVNDVLDLEWDQHLEQK.K
SW:N214_HUMAN	R05	9114	2	2252.6	(+0.5)	3.951	0.585	1.000	3	K.LGELLFPSSLAGETLGSFSGLR.V
SW:N214_HUMAN	R05	5428	3	2112.3	(-0.4)	3.963	0.413	0.998	2	K.SHL*VHGSSPGVMGTSVATSASK#.I
SW:N214_HUMAN	R05	7496	2	1791.0	(-0.3)	2.692	0.456	0.969	3	K.TSGVPSGFNFTAPPVL*GK#.H
SW:N214_HUMAN	R01	7399	2	1493.7	(+0.7)	2.383	0.173	0.671	3	K.TTLLEGFAGVEEAR.E
SW:N214_HUMAN	R03	8031	2	1827.1	(+0.0)	2.275	0.294	0.825	2	K.YGLVFAGGASGLQIFPTK.N
SW:N214_HUMAN	R05	7422	2	1505.7	(-0.3)	2.405	0.211	0.708	3	K.TTL*L*EGFAGVEEAR.E
SW:N4BM_HUMAN	R26	6002	2	1185.3	(-0.1)	3.039	0.285	0.963	1	K.REDYLYAVR.D
SW:N4BM_HUMAN	R26	5242	2	1484.6	(-0.4)	2.678	0.294	0.192	1	K.LHPEDFPEEDKK.T
SW:NB2M_HUMAN	R26	8064	2	1171.3	(+0.9)	2.429	0.476	0.982	1	K.SVSFSDVFFK#.G
SW:NB2M_HUMAN	R26	5950	2	1229.4	(-0.3)	2.382	0.129	0.529	1	K.IEGTPLETIQK.K
SW:NB4M_HUMAN	R25	5310	2	1359.5	(-0.6)	2.454	0.437	0.410	1	R.FFHETEAPRPK.D
SW:NB4M_HUMAN	R25	7844	2	919.2	(+0.3)	2.213	0.256	0.865	1	R.VVDL*L*VIK#.G
SW:NB4M_HUMAN	R26	7500	2	919.2	(+0.4)	2.379	0.228	0.871	1	R.VVDL*L*VIK#.G
SW:NB5M_HUMAN	R25	7354	2	1096.3	(+0.2)	2.858	0.220	0.825	2	R.GLIENPALLR.W
SW:NB5M_HUMAN	R26	6972	2	1096.3	(+0.9)	3.070	0.169	0.917	2	R.GLIENPALLR.W
SW:NB5M_HUMAN	R25	7628	2	2047.2	(-0.3)	2.881	0.528	1.000	2	R.TLPETLDPAEYNISPETR.R
SW:NB5M_HUMAN	R26	6974	2	1114.3	(+0.0)	2.553	0.136	0.676	2	R.GL*IENPAL*L*R.W
SW:NB6M_HUMAN	R25	8982	2	1477.7	(+0.2)	2.808	0.229	0.870	4	R.IAL*L*PL*L*QAETDR.R
SW:NB6M_HUMAN	R25	6948	2	1127.2	(+0.7)	2.616	0.230	0.924	4	R.L*QIEDFEAR.I
SW:NC5R_HUMAN	R19	7722	2	1496.7	(+0.7)	3.531	0.307	0.511	11	K.DILLRPELEELR.N
SW:NC5R_HUMAN	R20	7468	2	1496.7	(-0.4)	2.519	0.220	0.075	11	K.DILLRPELEELR.N
SW:NC5R_HUMAN	R20	7464	2	1520.7	(-0.6)	2.456	0.149	0.029	11	K.DIL*L*RPEL*EEL*R.N
SW:NC5R_HUMAN	R20	8534	3	2540.0	(-0.1)	4.820	0.449	1.000	3	R.FAL*PSPQHIL*GL*PVGQHIYL*SAR.I
SW:NC5R_HUMAN	R19	5878	2	1119.3	(+0.4)	2.999	0.497	1.000	10	R.GPSGLLVYQKG.G
SW:NC5R_HUMAN	R19	5810	2	1139.3	(-0.1)	2.607	0.233	0.828	10	R.GPSGL*L*VYQKG#.G
SW:NC5R_HUMAN	R20	8196	3	2977.4	(+0.6)	6.439	0.552	1.000	9	R.IDGNLVRPYTPISSDDDKGFVDLVK.V
SW:NC5R_HUMAN	R19	6502	2	1372.6	(-0.3)	2.535	0.270	0.871	3	R.STPAITLESPIK.Y
SW:NC5R_HUMAN	R20	6292	2	1372.6	(-0.5)	2.609	0.210	0.795	3	R.STPAITLESPIK.Y
SW:NC5R_HUMAN	R20	5844	2	1119.3	(-0.3)	2.393	0.404	0.961	10	R.GPSGLLVYQKG.G
SW:NCPR_HUMAN	R12	1456	2	1005.2	(+0.8)	2.345	0.371	0.968	4	K.IQTLTSSVR.E
SW:NCPR_HUMAN	R12	6276	2	1204.4	(+0.4)	2.684	0.474	0.989	4	K.NPFLAAVTTNR.K
SW:NCPR_HUMAN	R12	6270	2	1210.4	(+1.0)	2.236	0.457	0.978	4	K.NPFL*AAVTTNR.K
SW:NCPR_HUMAN	R12	1630	2	1067.1	(+0.4)	2.291	0.173	0.792	4	R.SDEDYL*YR.E
SW:NCPR_HUMAN	R11	9006	3	2454.7	(+0.7)	4.141	0.405	0.999	4	R.TNVLYELAQYASEPSEQELLR.K
SW:NCPR_HUMAN	R12	9202	2	2454.7	(+0.2)	2.789	0.426	0.973	4	R.TNVLYELAQYASEPSEQELLR.K
SW:NCPR_HUMAN	R14	9149	3	2454.7	(+1.0)	3.797	0.408	0.994	4	R.TNVLYELAQYASEPSEQELLR.K
SW:NISM_HUMAN	R25	7764	2	1607.7	(+0.9)	3.424	0.328	0.981		R.GDGPWYYYETIDK.E
SW:NISM_HUMAN	R25	7082	2	1233.5	(+0.6)	3.421	0.369	0.988		R.TMAVLQIEAEK.A
SW:NISM_HUMAN	R25	7090	2	1247.5	(+0.1)	3.139	0.410	0.979		R.TMAVL*QIEAEK#.A
SW:NLTP_HUMAN	R26	5542	2	1336.5	(-0.2)	3.480	0.355	0.977	5	K.KLEEEGEQFVK.K
SW:NLTP_HUMAN	R26	5460	2	1324.5	(-0.2)	3.249	0.267	0.951	5	K.LQNLQLQPGNAK.L
SW:NLTP_HUMAN	R26	5466	2	1350.5	(-0.3)	2.639	0.295	0.893	5	K.L*QNL*QL*QPGNAK#.L
SW:NLTP_HUMAN	R26	6514	2	1055.2	(+0.6)	2.355	0.295	0.918	3	K.EATWVVDVK#.N
SW:NNTM_HUMAN	R01	4291	2	1161.3	(+0.0)	2.366	0.314	0.908	1	K.AVVL*AAHFGR.F
SW:NNTM_HUMAN	R01	5727	2	1430.6	(+0.0)	3.470	0.482	1.000	2	K.GITHIGYTDLPSR.M
SW:NNTM_HUMAN	R01	6545	2	1271.5	(+0.4)	3.469	0.434	1.000	2	K.SLGAEPLEVDLK.E
SW:NNTM_HUMAN	R01	6547	2	1297.5	(+0.0)	2.573	0.318	0.901	2	K.SL*GAEPLEVDL*K#.E
SW:NNTM_HUMAN	R02	6384	2	1271.5	(+0.9)	2.994	0.392	0.984	2	K.SLGAEPLEVDLK.E

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:NNTM_HUMAN	R02	7716	3	2207.5	(+0.6)	4.330	0.501	0.997	2	K.TSGTLISFIYPAQNPPELLNK.L
SW:NNTM_HUMAN	R01	6635	2	1316.6	(-0.1)	3.067	0.501	0.999	2	R.VAL*SPAGVQNL*VK#.Q
SW:NNTM_HUMAN	R01	6629	2	1296.6	(+0.8)	2.245	0.205	0.719	2	R.VALSPAGVQNLVK.Q
SW:NNTM_HUMAN	R03	7945	3	2207.5	(+1.0)	3.911	0.550	0.977	2	K.TSGTLISFIYPAQNPPELLNK.L
SW:NO56_HUMAN	R13	8923	2	2354.7	(+0.5)	3.490	0.379	0.986	2	K.EVEEISLLQPQVEESVLNLGK.F
SW:NO56_HUMAN	R13	2476	2	925.1	(+0.7)	2.304	0.349	0.964	5	R.L*AQFIGNR.R
SW:NO56_HUMAN	R13	2478	2	919.1	(+1.0)	2.286	0.185	0.813	5	R.LAQFIGNR.R
SW:NO56_HUMAN	R13	2556	2	925.1	(+0.4)	2.226	0.321	0.946	5	R.L*AQFIGNR.R
SW:NO56_HUMAN	R13	2572	2	1127.3	(-0.3)	2.738	0.154	0.739	2	K.L*EEL*TMDGAK#.A
SW:NO56_HUMAN	R13	2210	2	1127.3	(+0.9)	2.250	0.317	0.909	2	K.L*EEL*TMDGAK#.A
SW:NO56_HUMAN	R13	6109	2	1309.6	(+0.5)	3.460	0.475	1.000	4	R.LIAHAGSLTNLAK.Y
SW:NO56_HUMAN	R13	6105	2	1335.6	(+0.0)	2.944	0.312*	0.257	4	R.L*IAHAGSL*TNL*AK#.Y
SW:NO56_HUMAN	R13	6701	2	1312.5	(+0.6)	3.631	0.503	0.998	4	R.LSFYETGEIPR.K
SW:NO56_HUMAN	R13	6695	2	1318.5	(+0.6)	3.045	0.483	1.000	4	R.L*SFYETGEIPR.K
SW:NO56_HUMAN	R13	8925	2	1886.2	(-0.0)	4.617	0.523	1.000	4	K.M@SQVAPSL*SAL*IGEAVGAR.L
SW:NO56_HUMAN	R13	9157	2	1858.2	(-0.4)	3.289	0.325	0.962	4	K.MSQVAPSLSALIGEAVGAR.L
SW:NO56_HUMAN	R12	4510	2	918.1	(+0.1)	2.699	0.276	0.914	5	K.VL*L*GVGDPK#.I
SW:NO56_HUMAN	R13	5019	2	898.1	(+1.0)	2.378	0.373	0.970	5	K.VLLGVGDPK.I
SW:NO56_HUMAN	R13	2498	2	953.1	(+0.5)	2.349	0.468	0.987	5	R.VVSLSEYR.Q
SW:NO56_HUMAN	R12	5818	2	1391.6	(-0.8)	2.965	0.224	0.664	5	K.YPASTVQIL*GAEK#.A
SW:NO56_HUMAN	R13	6193	2	1391.6	(+0.1)	3.640	0.472	0.994	5	K.YPASTVQIL*GAEK#.A
SW:NO56_HUMAN	R13	6197	2	1377.6	(-0.6)	3.477	0.396	0.984	5	K.YPASTVQILGAEK.A
SW:NO56_HUMAN	R13	5039	2	918.1	(-0.1)	2.216	0.345	0.908	5	K.VL*L*GVGDPK#.I
SW:NOC4_HUMAN	R23	5806	2	962.1	(+0.7)	3.001	0.381	0.978	1	R.ISASLLDSR.S
SW:NOC4_HUMAN	R23	5826	2	962.1	(-0.6)	2.417	0.337	0.946	1	R.ISASLLDSR.S
SW:NOC4_HUMAN	R22	5220	2	1239.3	(+0.2)	2.498	0.198	0.751	1	R.NDWTNPEINK#.A
SW:NOC4_HUMAN	R22	5208	2	1231.3	(+0.7)	2.350	0.343	0.954	1	R.NDWTNPEINK.A
SW:NOC4_HUMAN	R23	7768	2	1953.1	(+0.8)	4.648	0.442	1.000	1	R.SYETLVDFDNHLDDIR.N
SW:NOC4_HUMAN	R23	5814	2	974.1	(+0.8)	2.352	0.295	0.936	1	R.ISASL*L*DSR.S
SW:NOP5_HUMAN	R14	9669	2	1915.2	(+0.2)	4.112	0.532	0.993	2	K.FQDTAEALAAFTALMEGK.I
SW:NOP5_HUMAN	R14	4941	2	1339.5	(-0.0)	3.186	0.495	1.000	3	K.HAASTVQIL*GAEK#.A
SW:NOP5_HUMAN	R14	5019	2	1339.5	(-0.0)	3.178	0.443	0.980	3	K.HAASTVQIL*GAEK#.A
SW:NOP5_HUMAN	R14	4907	2	1325.5	(+0.2)	2.595	0.561	1.000	3	K.HAASTVQILGAEK.A
SW:NOP5_HUMAN	R14	7077	2	1353.6	(-0.2)	2.954	0.245	0.882	3	R.L*IAHAGSL*L*NL*AK#.H
SW:NOP5_HUMAN	R14	6751	2	1399.6	(+0.9)	2.836	0.470	0.988	2	R.SQMDGLIPGVEPR.E
SW:NOP5_HUMAN	R14	5953	2	1421.6	(+0.3)	2.621	0.297	0.937	2	R.SQM@DGL*IPGVEPR.E
SW:NOP5_HUMAN	R14	6463	2	1328.5	(+0.8)	3.239	0.463	1.000	3	R.TQLYEYLQNR.M
SW:NOP5_HUMAN	R14	6461	2	1340.5	(-0.1)	2.410	0.156	0.664	3	R.TQL*YEYL*QNR.M
SW:NPM_HUMAN	R18	1216	2	1024.1	(+0.7)	2.385	0.220	0.141	12	K.ADKDYHFK.V
SW:NPM_HUMAN	R18	7741	3	2160.4	(+0.4)	4.475	0.531	1.000	12	K.DEL*HIVEAEAMNYEGSPIK#.V
SW:NPM_HUMAN	R19	7852	3	2160.4	(-0.3)	4.194	0.388	0.996	12	K.DEL*HIVEAEAMNYEGSPIK#.V
SW:NPM_HUMAN	R25	8124	3	2160.4	(+0.9)	5.003	0.453	0.972	12	K.DEL*HIVEAEAMNYEGSPIK#.V
SW:NPM_HUMAN	R18	8793	2	2256.7	(+0.9)	6.039	0.609	1.000	13	K.M@SVQPTVSL*GGFEITPPVVL*R.L
SW:NPM_HUMAN	R18	8963	2	2240.7	(-0.0)	4.005	0.517	0.989	13	K.MSVQPTVSL*GGFEITPPVVL*R.L
SW:NPM_HUMAN	R18	8957	2	2228.7	(-0.7)	2.368	0.269	0.808	13	K.MSVQPTVSLGGFEITPPVVL.R.L
SW:NPM_HUMAN	R19	8924	2	2256.7	(+0.6)	5.851	0.598	1.000	13	K.M@SVQPTVSL*GGFEITPPVVL*R.L
SW:NPM_HUMAN	R18	8219	2	1843.0	(-0.0)	2.313	0.219	0.690	9	R.M@TDQEAIQDL*WQWR.K
SW:NPM_HUMAN	R18	8327	3	2959.3	(-0.2)	5.089	0.534	1.000	12	R.TVSL*GAGAK#DEL*HIVEAEAMNYEGSPIK#.V
SW:NPM_HUMAN	R18	1812	2	1569.6	(+0.5)	3.571	0.393	0.989	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	R18	1810	2	1581.6	(+0.5)	3.000	0.465	0.989	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	R19	1780	2	1581.6	(-0.8)	2.282	0.143	0.216	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	R25	8122	3	2146.4	(+0.9)	3.747	0.414	0.996	12	K.DELHIVEAEAMNYEGSPIK.V
SW:NPS1_HUMAN	R21	7540	2	1711.9	(+0.9)	3.304	0.480	1.000	1	R.GWDENVYYTVPLVR.H
SW:NPS1_HUMAN	R21	8076	3	2791.2	(+0.4)	4.651	0.520	1.000	1	K.IQFHNVKPEYLDAYNSLTEAVLPK.L
SW:NPS1_HUMAN	R21	8078	3	2825.2	(-0.4)	3.725	0.505	1.000	1	K.IQFHNVK#PEYL*DAYNSL*TEAVL*PK#.L
SW:NPS1_HUMAN	R21	6392	2	1093.3	(+0.9)	3.602	0.352	0.988	1	R.MGPNIYELR.T
SW:NPS1_HUMAN	R21	4438	2	1100.3	(-0.3)	2.397	0.258	0.865	1	R.KDAHSTLLSK.K
SW:NPS2_HUMAN	R21	8014	3	2229.5	(+0.8)	4.006	0.511	1.000	2	R.SYQLRPGTMIEWGNYWAR.A
SW:NPS2_HUMAN	R21	8622	3	2144.4	(+0.5)	3.773	0.299	0.992	2	R.K#NQL*L*L*EFSFWNEPVR.S

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:NR54_HUMAN	R14	6069	2	1087.3	(+0.9)	2.455	0.341	0.962	4	K.VELDNMPLR.G
SW:NR54_HUMAN	R15	1454	2	901.1	(+0.9)	2.692	0.119	0.755	4	K.AGEVFIHK.D
SW:NSDL_HUMAN	R18	9527	2	2192.5	(-0.4)	5.092	0.527	1.000		K.AFHITNDEPIPFWTFLSR.I
SW:NSDL_HUMAN	R18	9509	2	2192.5	(+1.0)	3.940	0.402	0.991		K.AFHITNDEPIPFWTFLSR.I
SW:NSDL_HUMAN	R18	9505	3	2192.5	(+0.8)	3.781	0.358	0.997		K.AFHITNDEPIPFWTFLSR.I
SW:NSDL_HUMAN	R18	5981	2	1239.4	(+0.7)	2.564	0.400	0.971		R.IL*TGL*NYEAPK#.Y
SW:NSF_HUMAN	R11	11530	2	1572.0	(+0.7)	4.622	0.460	1.000	5	R.FSNLVLQALLVLLK.K
SW:NSF_HUMAN	R11	6026	2	1296.5	(+0.9)	2.950	0.532	1.000	3	R.GHQLLSADVDIK.E
SW:NU43_HUMAN	R17	7614	3	2552.8	(+0.7)	5.716	0.594	0.998	1	R.HPNQQHVAVTGGQDGMPL*SIWDVR.Q
SW:NU43_HUMAN	R18	8039	3	3230.5	(+0.2)	5.124	0.470	1.000	2	R.SSTFLSHSISNQANVHQSVISSWLSTDKPAK.D
SW:NU43_HUMAN	R18	7079	2	1862.0	(+0.5)	3.816	0.605	1.000		R.TIDNADSSSTLHAVTFLLR.T
SW:NU43_HUMAN	R18	7253	2	1533.8	(+0.0)	2.920	0.200	0.796		R.TPEIL*TVNSIGQL*K#.I
SW:NU43_HUMAN	R18	7069	2	1874.0	(-0.3)	2.598	0.322	0.917		R.TIDNADSSSTL*HAVTFLLR.T
SW:NU50_HUMAN	R14	7513	3	3067.3	(-0.4)	6.257	0.525	1.000	5	R.FSGFGSGAGGK#PL*EGL*SNGNNITSAPPFASAK#.A
SW:NU50_HUMAN	R15	7255	3	3067.3	(+0.4)	6.048	0.529	0.995	5	R.FSGFGSGAGGK#PL*EGL*SNGNNITSAPPFASAK#.A
SW:NU50_HUMAN	R14	9159	3	3003.4	(+0.2)	3.839	0.450	0.998	2	K.KVDSSVLGSLSSVPLTGFSPGNSLFGK.D
SW:NU50_HUMAN	R15	8977	3	3003.4	(+0.6)	4.273	0.469	1.000	2	K.KVDSSVLGSLSSVPLTGFSPGNSLFGK.D
SW:NU50_HUMAN	R14	5563	2	1337.4	(-0.5)	3.514	0.521	1.000	5	R.NVGFESDTGGAFK#.G
SW:NU50_HUMAN	R14	5577	2	1329.4	(+0.1)	3.480	0.464	1.000	5	R.NVGFESDTGGAFK#.G
SW:NU50_HUMAN	R15	5343	2	1337.4	(+0.8)	3.268	0.416	0.984	5	R.NVGFESDTGGAFK#.G
SW:NU50_HUMAN	R14	5511	2	1523.7	(-0.3)	2.512	0.311	0.896	2	K.VAAETQSPSLFGSTK.L
SW:NU50_HUMAN	R14	5507	2	1537.7	(-1.0)	2.268	0.185	0.229	2	K.VAAETQSPSL*FGSTK#.L
SW:NU50_HUMAN	R15	5281	2	1523.7	(-0.5)	3.201	0.510	0.999	2	K.VAAETQSPSLFGSTK.L
SW:NU50_HUMAN	R15	5277	2	1537.7	(-0.3)	3.173	0.298	0.925	2	K.VAAETQSPSL*FGSTK#.L
SW:NU50_HUMAN	R14	7099	2	1661.9	(-0.3)	3.078	0.236	0.897	5	K.VAFGSLAANGPTTLVDK.V
SW:NU50_HUMAN	R15	6883	2	1681.9	(+0.3)	2.882	0.133	0.591	5	K.VAFGSL*AANGPTTL*VDK#.V
SW:NU50_HUMAN	R15	1438	2	905.0	(+0.3)	2.286	0.352	0.937	5	K.GL*VVPSSGGGR.F
SW:NU62_HUMAN	R13	9833	2	1627.9	(-0.5)	2.953	0.265	0.889	2	K.ELEDLLSPLEELVK.E
SW:NU62_HUMAN	R14	9601	2	1627.9	(+0.8)	4.473	0.360	0.989	2	K.ELEDLLSPLEELVK.E
SW:NU62_HUMAN	R14	4823	2	1115.3	(+0.1)	2.516	0.108	0.573	2	K.LAENIDAQLK.R
SW:NU88_HUMAN	R11	2476	2	1244.3	(+0.4)	2.937	0.314	0.971		R.EDVEVAESPLR.V
SW:NU88_HUMAN	R11	2494	2	1250.3	(-0.1)	2.738	0.328	0.953		R.EDVEVAESPLR.V
SW:NU88_HUMAN	R11	2388	2	1244.3	(+0.1)	2.353	0.196	0.714		R.EDVEVAESPLR.V
SW:NU88_HUMAN	R11	8628	3	2765.1	(-0.3)	4.628	0.470	0.999	1	K.HAAWYPSEIL*DPHVVL*L*TSNDVIR.I
SW:NU88_HUMAN	R11	2332	2	1236.4	(+0.7)	2.616	0.415	0.981	1	R.VLAETPDSFEK.H
SW:NU88_HUMAN	R11	2410	2	1236.4	(-0.1)	2.483	0.270	0.884	1	R.VLAETPDSFEK.H
SW:NU88_HUMAN	R11	7326	2	1026.3	(+0.3)	2.227	0.356	0.942	1	K.GL*MVL*EL*PK#.R
SW:NU98_HUMAN	R09	6916	3	1956.1	(+0.7)	3.787	0.443	1.000	3	K.ASL*L*TDEEDVDM@AL*DQR.F
SW:NU98_HUMAN	R10	7189	3	2242.5	(+0.4)	4.384	0.547	1.000	6	K.EVVVYLDDNQKPPVGEGLNR.K
SW:NU98_HUMAN	R10	7265	3	2242.5	(+0.8)	4.302	0.533	0.996	6	K.EVVVYLDDNQKPPVGEGLNR.K
SW:NU98_HUMAN	R10	6817	3	2242.5	(+0.9)	4.124	0.508	0.983	6	K.EVVVYLDDNQKPPVGEGLNR.K
SW:NU98_HUMAN	R10	6893	3	2242.5	(+0.7)	4.082	0.504	1.000	6	K.EVVVYLDDNQKPPVGEGLNR.K
SW:NU98_HUMAN	R10	7041	3	2242.5	(+0.6)	3.989	0.517	1.000	6	K.EVVVYLDDNQKPPVGEGLNR.K
SW:NU98_HUMAN	R10	6967	3	2242.5	(+0.7)	3.963	0.529	1.000	6	K.EVVVYLDDNQKPPVGEGLNR.K
SW:NU98_HUMAN	R09	6676	2	1398.6	(+0.9)	3.978	0.452	1.000	5	R.HYDLNQLLEPR.S
SW:NU98_HUMAN	R09	6672	2	1416.6	(+0.2)	2.935	0.330	0.964	5	R.HYDL*NQL*L*EPR.S
SW:NU98_HUMAN	R10	7649	2	1581.8	(-0.1)	3.923	0.498	1.000	6	R.K#AEVTL*DGWVPTDK#.T
SW:NU98_HUMAN	R10	1678	2	1057.1	(+1.0)	2.518	0.406	0.981	6	R.L*ADINYEGR.L
SW:NU98_HUMAN	R10	1684	2	1051.1	(+0.8)	2.376	0.307	0.945	6	R.LADINYEGR.L
SW:NU98_HUMAN	R08	8547	3	1642.9	(+0.8)	4.075	0.447	0.999	6	R.L*AL*L*L*SQFVGSQSVR.E
SW:NU98_HUMAN	R09	8160	2	1618.9	(+0.8)	2.972	0.354	0.972	6	R.LALLLSQFVGSQSVR.E
SW:NU98_HUMAN	R10	946	2	1015.1	(+0.7)	2.695	0.267	0.960	7	R.L*EDYQANR.K
SW:NU98_HUMAN	R09	8216	2	1339.6	(+0.9)	2.298	0.197	0.787	6	R.LSWHLWEVLR.A
SW:NU98_HUMAN	R09	9124	2	1526.7	(+0.2)	2.292	0.332	0.859	6	K.NSPVEAVFSYL*TKG#.R
SW:NU98_HUMAN	R10	9577	2	1512.7	(+0.2)	3.021	0.567	1.000	6	K.NSPVEAVFSYLTGK.R
SW:NU98_HUMAN	R08	6239	2	1157.3	(+0.0)	2.644	0.424	0.978	5	R.SITADPL*DYR.L
SW:NU98_HUMAN	R09	5624	2	1157.3	(+0.7)	2.638	0.360	0.974	5	R.SITADPL*DYR.L
SW:NU98_HUMAN	R09	5632	2	1151.3	(+0.8)	2.599	0.475	0.638	5	R.SITADPLDYR.L
SW:NU98_HUMAN	R08	6857	2	1028.2	(+0.8)	2.473	0.452	0.715	3	R.SL*VGGL*L*QSK#.F



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:NU98_HUMAN	R08	10065	2	2277.5	(-0.8)	3.154	0.425	0.943	6	R.SSL*IQDWETSGL*VYL*DIYR.V
SW:NU98_HUMAN	R10	1024	2	986.1	(+0.1)	2.204	0.330	0.879	7	K.AGVSTNISTK#.H
SW:NUAM_HUMAN	R12	8098	2	1612.8	(+0.9)	4.429	0.597	0.999	2	K.GLLTYTSWEDALSR.V
SW:NUAM_HUMAN	R12	8092	2	1630.8	(-0.3)	3.488	0.456	1.000	2	K.GL*L*TYTSWEDAL*SR.V
SW:NUAM_HUMAN	R11	7994	2	1543.7	(+0.1)	2.435	0.319	0.863	3	R.NDGAAIL*AAVSSIAQK#.I
SW:NUAM_HUMAN	R12	8128	2	1543.7	(+0.4)	3.125	0.340	0.965	3	R.NDGAAIL*AAVSSIAQK#.I
SW:NUAM_HUMAN	R12	4978	2	1355.5	(+0.5)	2.780	0.442	0.986	2	R.GNDMQVGTIEK.M
SW:NUCL_HUMAN	R09	6930	2	1649.8	(+0.5)	4.949	0.576	1.000	3	K.FGYVDFESAEDLEK.A
SW:NUCL_HUMAN	R10	8021	2	1570.6	(+0.3)	4.745	0.518	0.999	5	K.GFGFVDFNSEEDAK#.E
SW:NUCL_HUMAN	R10	7321	2	949.1	(+0.6)	2.430	0.195	0.839	4	K.GIAYIEFK#.T
SW:NUCL_HUMAN	R09	4756	2	1007.1	(+0.5)	3.295	0.322	0.986	3	K.NDL*AVVDVR.I
SW:NUCL_HUMAN	R09	4744	2	1001.1	(+0.5)	3.035	0.356	0.986	3	K.NDLAVVDVR.I
SW:NUCL_HUMAN	R09	4802	2	1001.1	(-0.7)	2.544	0.391	0.971	3	K.NDLAVVDVR.I
SW:NUCL_HUMAN	R09	5364	2	1161.3	(+0.4)	2.380	0.467	0.984	4	R.SISLYYTGEK.G
SW:NUCL_HUMAN	R10	9485	3	2534.8	(-0.0)	4.858	0.533	1.000	4	K.TL*VL*SNL*SYSATEETL*QEVFEK#.A
SW:NUCL_HUMAN	R10	9483	3	2502.8	(+1.0)	4.832	0.593	1.000	4	K.TLVLSNLSYSATEETLQEVFEK.A
SW:NUCL_HUMAN	R21	9086	3	2502.8	(+0.8)	4.492	0.507	0.998	4	K.TLVLSNLSYSATEETLQEVFEK.A
SW:NUCL_HUMAN	R14	8969	3	2313.6	(+0.9)	3.845	0.370	0.992	3	K.VEGTEPTTAFNLFVGNLNFNK.S
SW:NUCL_HUMAN	R24	4832	2	1323.4	(+0.4)	2.959	0.379	0.982	4	K.GLSEDTTEETLK.E
SW:NUCM_HUMAN	R16	7312	2	1459.6	(+0.2)	2.872	0.363	0.967	1	R.LDELEELLTNNR.I
SW:NUCM_HUMAN	R16	7206	2	1387.6	(+1.0)	2.662	0.381	0.977	1	K.TYLQALPYFDR.L
SW:NUEM_HUMAN	R19	6162	2	1069.3	(+0.8)	2.311	0.387	0.963	2	K.IPQAIQLSK.E
SW:NUEM_HUMAN	R19	10958	2	1595.0	(+0.3)	2.264	0.322	0.914	2	R.LFLPFPLPLFAYR.W
SW:NUGM_HUMAN	R21	8744	2	1385.6	(+1.0)	2.745	0.337	0.970	2	R.FEIVYNL*L*SL*R.F
SW:NUGM_HUMAN	R21	8134	2	1870.1	(+0.3)	2.884	0.443	0.985	2	R.KFDLNSPWEAFVYR.Q
SW:NUGM_HUMAN	R21	8440	2	1901.1	(+0.9)	3.892	0.542	1.000	2	K.TYTDELTPIESAVSVFK.A
SW:NUGM_HUMAN	R21	8434	2	1915.1	(-0.1)	2.608	0.281	0.846	2	K.TYTDEL*TPIESAVSVFK#.A
SW:NUGM_HUMAN	R21	8816	2	1685.9	(-0.6)	2.551	0.306	0.868	1	K.QL*SAFGEYVAEIL*PK#.Y
SW:NUHM_HUMAN	R22	8670	2	1231.4	(+0.2)	3.622	0.319	0.517	2	K.DIEEIIDEL*K#.A
SW:NUHM_HUMAN	R22	6772	2	1232.3	(+0.1)	3.190	0.336	0.966	2	R.NSDSIL*EAIQK#.K
SW:NUP1_HUMAN	R13	8471	2	1500.7	(+0.2)	4.146	0.553	1.000	1	K.MFLGDAVDVFETR.R
SW:NUP1_HUMAN	R13	6795	3	1940.1	(+0.7)	4.197	0.461	1.000	1	K.TPPGL*QHEYAAPADYFR.I
SW:NUP1_HUMAN	R13	8463	2	1506.7	(-0.2)	3.422	0.492	1.000	1	K.MFL*GDAVDVFETR.R
SW:NUPM_HUMAN	R23	8240	2	1464.7	(+0.3)	2.671	0.106	0.562		-.PGIVEL*PTL*EEL*K#.V
SW:NUPM_HUMAN	R24	8378	3	2043.3	(-0.3)	4.229	0.388	0.986		-.PGIVEL*PTL*EEL*K#VDEVK#.I
SW:NUPM_HUMAN	R24	8260	2	1438.7	(+0.8)	3.585	0.302	0.969		-.PGIVELPTLEELK.V
SW:OAT_HUMAN	R17	8514	2	1954.1	(+0.4)	3.983	0.460	1.000		R.AFYNNVLGEYEEYITK.L
SW:OAT_HUMAN	R16	4946	2	1057.2	(+0.5)	2.875	0.284	0.963		K.LPSDVVTAVR.G
SW:OAT_HUMAN	R16	4998	2	1063.2	(+0.6)	2.854	0.315	0.972		K.L*PSDVVTAVR.G
SW:OAT_HUMAN	R17	5670	2	1057.2	(+1.0)	3.189	0.270	0.968		K.LPSDVVTAVR.G
SW:ODO1_HUMAN	R09	9580	2	1661.0	(-0.2)	3.349	0.354	0.974	2	R.IEQLSPFPDLLLLK.E
SW:ODO1_HUMAN	R09	9504	2	1661.0	(+0.2)	3.234	0.261	0.936	2	R.IEQLSPFPDLLLLK.E
SW:ODO1_HUMAN	R09	6776	2	1024.2	(+0.6)	2.706	0.291	0.963	7	R.L*NVL*ANVIR.K
SW:ODP2_HUMAN	R12	8132	2	1517.7	(+0.8)	4.627	0.439	1.000	3	K.GVETIANDVVSLATK.A
SW:ODP2_HUMAN	R12	8012	2	1221.5	(+0.6)	2.341	0.326	0.219	3	K.YLEKPITMLL.-
SW:ODP2_HUMAN	R13	8323	2	1531.7	(-0.1)	2.958	0.314	0.923	3	K.GVETIANDVVSL*ATK#.A
SW:ODPA_HUMAN	R17	9012	3	3835.1	(-0.2)	4.778	0.471	0.996	1	K.EIEDAAQFATADPEPPLEELGYHIYSSDPPFEVR.G
SW:ODPA_HUMAN	R17	9016	3	3847.1	(-0.1)	4.542	0.342	0.993	1	K.EIEDAAQFATADPEPPL*EEL*GYHIYSSDPPFEVR.G
SW:ODPA_HUMAN	R17	6102	2	1470.6	(-0.3)	3.688	0.379	0.980	11	R.M@VNSNL*ASVEEL*K#.E
SW:ODPA_HUMAN	R17	6350	2	1454.6	(+0.2)	2.782	0.290	0.902	11	R.MVNSNL*ASVEEL*K#.E
SW:ODPA_HUMAN	R17	6458	2	1424.6	(+0.8)	2.528	0.351	0.957	2	R.L*EEGPPVTVL*TR.E
SW:ODPB_HUMAN	R19	5532	2	1520.6	(-0.4)	2.691	0.294	0.917	4	R.DAINQGMDEELER.D
SW:ODPB_HUMAN	R19	5692	2	1256.4	(+0.4)	2.707	0.293	0.953	4	K.ILEDNSIPQVK.D

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ODPB_HUMAN	R19	5696	2	1270.4	(+0.3)	2.582	0.358	0.933	4	K.IL*EDNSIPQVK#D
SW:ODPB_HUMAN	R19	8494	2	1755.0	(-0.1)	2.388	0.203	0.661	4	R.IMEGPAFNFL*DAPAVR.V
SW:OM22_HUMAN	R03	6309	3	2922.9	(+0.5)	5.311	0.519	1.000		K.GDAEKPEEELEEDDDEELDETLSER.L
SW:OM22_HUMAN	R24	6508	3	2922.9	(+0.2)	7.268	0.506	0.981		K.GDAEKPEEELEEDDDEELDETLSER.L
SW:OM22_HUMAN	R24	6646	3	2922.9	(+0.3)	7.238	0.568	0.999		K.GDAEKPEEELEEDDDEELDETLSER.L
SW:OM22_HUMAN	R24	6650	3	2948.9	(-0.8)	5.572	0.460	1.000		K.GDAEK#PEEEL*EEDDDEEL*DETL*SER.L
SW:OM22_HUMAN	R24	6838	3	2922.9	(+0.0)	5.450	0.511	0.972		K.GDAEKPEEELEEDDDEELDETLSER.L
SW:OM22_HUMAN	R24	6840	3	2948.9	(-0.1)	4.884	0.444	0.999		K.GDAEK#PEEEL*EEDDDEEL*DETL*SER.L
SW:OM22_HUMAN	R24	4132	2	1558.8	(-0.4)	4.499	0.370	1.000		K.LQMEQQQQQLQQR.Q
SW:OM22_HUMAN	R24	4208	2	1558.8	(-0.4)	3.947	0.370	0.987		K.LQMEQQQQQLQQR.Q
SW:OM22_HUMAN	R25	8906	2	1379.6	(+1.0)	3.441	0.503	1.000		R.LWGLTEMFPER.V
SW:OM22_HUMAN	R27	6309	3	2922.9	(+0.1)	4.594	0.478	1.000		K.GDAEKPEEELEEDDDEELDETLSER.L
SW:OM40_HUMAN	R18	10043	2	1972.4	(+0.2)	2.476	0.489	0.977	3	K.KLPPLPLTLALGAFLNHR.K
SW:OM40_HUMAN	R18	10565	2	1844.3	(+0.1)	2.222	0.445	0.953	3	K.KLPPLPLTLALGAFLNHR.K
SW:OM40_HUMAN	R18	5401	2	1432.6	(-0.0)	4.392	0.341	0.986	5	R.RPGEEGTVMFLAGK.Y
SW:OM40_HUMAN	R18	5413	2	1446.6	(-0.1)	3.686	0.415	0.981	5	R.RPGEEGTVMSL*AGK#.Y
SW:OM70_HUMAN	R13	2034	2	1006.1	(+0.8)	2.848	0.263	0.960		R.AAAFEQLQK.W
SW:OM70_HUMAN	R13	6553	2	1357.5	(+0.8)	3.165	0.422	0.989		K.NVDLSTFYQNR.A
SW:OM70_HUMAN	R13	6549	2	1363.5	(+0.4)	2.335	0.490	0.985		K.NVDL*STFYQNR.A
SW:ORP8_HUMAN	R09	7302	3	2254.5	(+0.5)	5.193	0.440	1.000	3	K.FADTRPWDPL*NDM@IQFEK#D
SW:ORP8_HUMAN	R09	7484	2	1589.8	(-0.0)	4.645	0.566	1.000	3	K.GIELGDIQSSIESIK.Q
SW:ORP8_HUMAN	R09	7474	2	1603.8	(-0.4)	3.460	0.380	0.973	3	K.GIEL*GDIQSSIESIK#.Q
SW:ORP8_HUMAN	R09	7530	2	1627.8	(-0.5)	3.231	0.434	0.983	4	K.FYGNLSAILEGEAR.L
SW:OST4_HUMAN	R01	6615	2	842.0	(+0.6)	2.367	0.202	0.831	5	R.GFELTFK.T
SW:OST4_HUMAN	R17	8210	2	1327.5	(+0.6)	3.812	0.440	1.000	5	K.L*PDVYGVFQFK#.V
SW:OST4_HUMAN	R17	8150	2	1313.5	(+0.9)	3.708	0.392	1.000	5	K.LPDVYGVFQFK.V
SW:OST4_HUMAN	R17	8180	2	1313.5	(-0.7)	2.845	0.409	0.978	5	K.LPDVYGVFQFK.V
SW:OST4_HUMAN	R17	6980	2	1188.4	(-0.1)	2.522	0.246	0.861	5	K.NTL*L*IAGL*QAR.N
SW:OST4_HUMAN	R02	5774	2	1180.3	(+0.9)	2.306	0.182	0.618	5	K.TADDPSSL*SL*IK#.Y
SW:OST4_HUMAN	R17	6154	2	1160.3	(+0.8)	3.031	0.299	0.965	5	K.TADDPSSLIK.Y
SW:OST4_HUMAN	R17	6182	2	1180.3	(+0.2)	2.344	0.310	0.873	5	K.TADDPSSL*SL*IK#.Y
SW:OST4_HUMAN	R17	6168	2	1160.3	(-0.7)	2.307	0.349	0.913	5	K.TADDPSSLIK.Y
SW:OST4_HUMAN	R27	5935	2	1160.3	(+0.9)	2.938	0.342	0.973	5	K.TADDPSSLIK.Y
SW:OST4_HUMAN	R01	8177	3	3247.6	(+0.4)	6.795	0.582	0.994	5	K.TAVIDHHNYDISDLGQHTLIVADTENLLK.A
SW:OST4_HUMAN	R17	8214	3	3247.6	(+0.4)	7.598	0.611	0.994	5	K.TAVIDHHNYDISDLGQHTLIVADTENLLK.A
SW:OST4_HUMAN	R17	8294	3	3247.6	(-0.5)	4.497	0.489	1.000	5	K.TAVIDHHNYDISDLGQHTLIVADTENLLK.A
SW:OST4_HUMAN	R01	7633	2	1270.5	(+0.2)	2.556	0.293	0.917	5	R.TLVLLDNLNVR.E
SW:OST4_HUMAN	R02	7142	2	1270.5	(+0.9)	3.117	0.307	0.975	5	R.TLVLLDNLNVR.E
SW:OST4_HUMAN	R17	7382	2	1270.5	(+0.8)	2.936	0.307	0.969	5	R.TLVLLDNLNVR.E
SW:OST4_HUMAN	R17	7774	2	1294.5	(+0.0)	2.220	0.203	0.669	5	R.TL*VL*L*DNL*NVR.E
SW:OST4_HUMAN	R17	10826	3	2357.6	(+0.9)	4.808	0.497	0.999	5	R.VIFSGSL*DFFSDFSFFNSAVQK#.A
SW:OST4_HUMAN	R17	11114	3	2343.6	(+0.9)	4.547	0.543	1.000	5	R.VIFSGSLDFFSDFSFFNSAVQK.A
SW:OST4_HUMAN	R17	11210	3	2343.6	(+0.4)	4.310	0.485	1.000	5	R.VIFSGSLDFFSDFSFFNSAVQK.A
SW:OST4_HUMAN	R17	12246	3	2343.6	(+0.3)	4.296	0.404	0.999	5	R.VIFSGSLDFFSDFSFFNSAVQK.A
SW:OST4_HUMAN	R17	11504	3	2357.6	(+0.9)	4.261	0.507	0.798	5	R.VIFSGSL*DFFSDFSFFNSAVQK#.A
SW:OST4_HUMAN	R17	11364	3	2343.6	(+0.8)	4.180	0.443	0.999	5	R.VIFSGSLDFFSDFSFFNSAVQK.A
SW:OST4_HUMAN	R17	12014	3	2343.6	(+0.3)	4.177	0.449	1.000	5	R.VIFSGSLDFFSDFSFFNSAVQK.A
SW:OST4_HUMAN	R17	11462	3	2343.6	(+0.6)	4.152	0.448	0.993	5	R.VIFSGSLDFFSDFSFFNSAVQK.A
SW:OST4_HUMAN	R17	11654	3	2343.6	(+0.8)	4.146	0.437	0.998	5	R.VIFSGSLDFFSDFSFFNSAVQK.A
SW:OST4_HUMAN	R17	11186	3	2357.6	(+0.2)	4.137	0.476	0.932	5	R.VIFSGSL*DFFSDFSFFNSAVQK#.A
SW:OST4_HUMAN	R17	11398	3	2357.6	(+0.1)	4.085	0.418	0.985	5	R.VIFSGSL*DFFSDFSFFNSAVQK#.A
SW:OST4_HUMAN	R17	11798	3	2343.6	(+0.5)	4.055	0.528	1.000	5	R.VIFSGSLDFFSDFSFFNSAVQK.A
SW:OST4_HUMAN	R17	10752	3	2357.6	(+0.6)	3.896	0.312	0.994	5	R.VIFSGSL*DFFSDFSFFNSAVQK#.A
SW:OST4_HUMAN	R17	11938	3	2343.6	(+0.8)	3.837	0.516	1.000	5	R.VIFSGSLDFFSDFSFFNSAVQK.A
SW:OST4_HUMAN	R17	11028	3	2343.6	(+0.8)	3.794	0.453	0.999	5	R.VIFSGSLDFFSDFSFFNSAVQK.A
SW:OST4_HUMAN	R17	12158	3	2343.6	(-0.2)	3.757	0.341	0.967	5	R.VIFSGSLDFFSDFSFFNSAVQK.A
SW:OST4_HUMAN	R17	11582	3	2357.6	(+0.1)	3.718	0.423	0.995	5	R.VIFSGSL*DFFSDFSFFNSAVQK#.A
SW:OST4_HUMAN	R17	8658	2	1837.0	(+0.8)	3.670	0.505	1.000	5	K.WVPFDGDDIQLFV.R.I
SW:OST4_HUMAN	R17	8666	2	1843.0	(+0.2)	3.106	0.484	0.986	5	K.WVPFDGDDIQL*EFV.R.I
SW:OST4_HUMAN	R17	6836	2	1672.8	(-0.5)	3.931	0.564	0.996	5	R.YSQTGNYELAVALS.R.W
SW:OST4_HUMAN	R17	6830	2	1684.8	(-0.4)	2.418	0.283	0.844	5	R.YSQTGNYEL*AVAL*SR.W

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:OST4_HUMAN	R17	11202	2	1672.8	(+0.8)	2.261	0.151	0.350	5	R.YSQTGNYELAVALSR.W
SW:OST4_HUMAN	R27	5927	2	1180.3	(-0.1)	2.329	0.226	0.722	5	K.TADDPSSL*SL*IK#.Y
SW:OXRP_HUMAN	R07	7911	2	1684.8	(-0.0)	4.639	0.353	1.000		K.AANSLEAFIFETQDK.L
SW:OXRP_HUMAN	R07	7921	3	1684.8	(-1.0)	4.114	0.336	0.984		K.AANSLEAFIFETQDK.L
SW:OXRP_HUMAN	R07	7069	2	1673.8	(+1.0)	5.558	0.506	1.000		K.AHFNLDESGVLSLDR.V
SW:OXRP_HUMAN	R07	12706	2	1673.8	(+0.4)	2.936	0.430	0.984		K.AHFNLDESGVLSLDR.V
SW:OXRP_HUMAN	R07	8813	3	1522.8	(-0.8)	3.874	0.421	0.996		R.DAVVYPILVEFTR.E
SW:OXRP_HUMAN	R07	8785	2	1528.8	(+0.3)	2.823	0.242	0.919		R.DAVVYPIL*VEFTR.E
SW:OXRP_HUMAN	R07	8863	2	1528.8	(-0.8)	2.779	0.343	0.868		R.DAVVYPIL*VEFTR.E
SW:OXRP_HUMAN	R07	4973	2	1007.2	(+0.9)	2.313	0.123	0.626		R.EVQYLLNK.A
SW:OXRP_HUMAN	R07	6467	2	1253.4	(+0.8)	3.120	0.491	1.000	1	R.FFGDSAASMAIK#.N
SW:OXRP_HUMAN	R07	5805	2	1269.4	(-0.2)	2.299	0.185	0.564	1	R.FFGDSAASM@AIK#.N
SW:OXRP_HUMAN	R07	6259	2	1516.7	(-0.1)	2.461	0.351	0.936	1	R.FPEHELTFDPQR.Q
SW:OXRP_HUMAN	R07	1070	2	1030.1	(+0.9)	2.504	0.269	0.931		K.KYPDYESK.G
SW:OXRP_HUMAN	R07	5867	2	1048.2	(-0.5)	3.070	0.324	0.975		R.LAGLFNEQR.K
SW:OXRP_HUMAN	R07	5875	2	1060.2	(+0.2)	2.704	0.277	0.940		R.L*AGL*FNEQR.K
SW:OXRP_HUMAN	R08	6127	2	1060.2	(+0.3)	2.827	0.266	0.961		R.L*AGL*FNEQR.K
SW:OXRP_HUMAN	R07	9765	2	2268.6	(-1.0)	2.240	0.322	0.666		R.LIPEMDQIFTEVEMTTLEK.V
SW:OXRP_HUMAN	R07	5709	2	1330.6	(-0.4)	3.175	0.324	0.309		K.L*PATEK#PVL*SK#.D
SW:OXRP_HUMAN	R07	5711	2	1296.6	(-0.3)	2.539	0.416	0.376		K.LPATEKPVLLSK.D
SW:OXRP_HUMAN	R07	8183	2	2180.5	(-0.4)	3.854	0.489	1.000		K.LSAASTWLEDEGVTMLK.E
SW:OXRP_HUMAN	R07	5091	2	1900.0	(+0.1)	3.991	0.514	1.000		K.LYQPEYQEVSTEEQR.E
SW:OXRP_HUMAN	R07	5113	2	1906.0	(-0.7)	3.726	0.464	1.000		K.L*YQPEYQEVSTEEQR.E
SW:OXRP_HUMAN	R07	7891	2	2080.3	(+0.6)	5.939	0.633	1.000		K.NINADEAAAAMGAVYQAAALSK.A
SW:OXRP_HUMAN	R07	7881	3	2094.3	(+0.9)	4.357	0.494	1.000		K.NINADEAAAAMGAVYQAAAL*SK#.A
SW:OXRP_HUMAN	R07	6315	2	1362.5	(-0.0)	3.925	0.473	1.000		R.SL*AEDFAEQPIK#.D
SW:OXRP_HUMAN	R07	6313	2	1348.5	(+0.7)	2.793	0.408	0.983		R.SLAEDFAEQPIK.D
SW:OXRP_HUMAN	R07	6699	2	1137.3	(+0.2)	2.474	0.495	0.983		R.TL*GGL*EMEL*R.L
SW:OXRP_HUMAN	R08	7001	2	1119.3	(+1.0)	2.959	0.354	0.982		R.TLGGLEMLR.L
SW:OXRP_HUMAN	R07	5797	2	885.1	(+0.2)	2.202	0.291	0.864	1	K.TPVIVTL*K#.E
SW:OXRP_HUMAN	R07	6829	3	2573.8	(-0.1)	3.953	0.336	0.991		K.TVL*SANADHM@AQIEGL*M@DDVDFK#.A
SW:OXRP_HUMAN	R07	7727	3	2557.8	(+0.5)	3.886	0.402*	0.097		K.TVL*SANADHM@AQIEGL*MDDVDFK#.A
SW:OXRP_HUMAN	R07	7321	2	1708.2	(-0.1)	4.406	0.395	1.000	1	K.VAIVKPGVPMEIVLNK.E
SW:OXRP_HUMAN	R07	7319	2	1730.2	(-0.3)	3.963	0.380	0.461	1	K.VAIVK#PGVPMEIVL*NK#.E
SW:OXRP_HUMAN	R07	9153	2	2343.5	(+0.8)	4.787	0.438	1.000		R.VESVFETLVEDSAEEEESTLTK.L
SW:OXRP_HUMAN	R07	12772	3	2343.5	(+0.8)	4.046	0.521	1.000		R.VESVFETLVEDSAEEEESTLTK.L
SW:OXRP_HUMAN	R07	9141	3	2343.5	(+0.6)	3.896	0.515	1.000		R.VESVFETLVEDSAEEEESTLTK.L
SW:OXRP_HUMAN	R07	9171	2	2343.5	(-0.8)	3.155	0.394	0.930		R.VESVFETLVEDSAEEEESTLTK.L
SW:OXRP_HUMAN	R08	9259	2	2343.5	(+0.3)	4.604	0.454	1.000		R.VESVFETLVEDSAEEEESTLTK.L
SW:OXRP_HUMAN	R07	4587	3	2008.2	(+0.8)	3.827	0.474	0.996		K.VIPPAGQTEDAEPISPEK.V
SW:OXRP_HUMAN	R07	8353	2	2114.4	(+0.9)	4.436	0.575	1.000		K.VL*QL*INDNTATAL*SYGVFR.R
SW:OXRP_HUMAN	R07	12820	3	2096.4	(+0.5)	4.366	0.420	0.998		K.VLQLINDNTATALSYGVFR.R
SW:OXRP_HUMAN	R07	8351	2	2096.4	(-0.6)	4.165	0.448	0.999		K.VLQLINDNTATALSYGVFR.R
SW:OXRP_HUMAN	R07	8383	3	2114.4	(-0.7)	3.895	0.470	0.999		K.VL*QL*INDNTATAL*SYGVFR.R
SW:OXRP_HUMAN	R08	8521	3	2114.4	(+0.8)	3.708	0.462	0.999		K.VL*QL*INDNTATAL*SYGVFR.R
SW:OXRP_HUMAN	R08	5965	2	1296.6	(+0.9)	2.616	0.352	0.355		K.LPATEKPVLLSK.D
SW:P121_HUMAN	R06	4730	3	2383.7	(-0.7)	3.725	0.457	0.966	2	K.APPTL*QAETATK#PQATSAPSPAPK#.Q
SW:P121_HUMAN	R07	4535	3	2361.7	(+0.4)	4.472	0.471	1.000	2	K.APPTLQAETATK#PQATSAPSPAPK.Q
SW:P121_HUMAN	R07	4457	3	2361.7	(+0.6)	4.396	0.500	1.000	2	K.APPTLQAETATK#PQATSAPSPAPK.Q
SW:P121_HUMAN	R07	4541	3	2383.7	(-0.3)	4.180	0.518	1.000	2	K.APPTL*QAETATK#PQATSAPSPAPK#.Q
SW:P121_HUMAN	R07	4463	3	2383.7	(+0.0)	3.973	0.505	1.000	2	K.APPTL*QAETATK#PQATSAPSPAPK#.Q
SW:P121_HUMAN	R07	7465	2	1570.7	(+0.6)	3.460	0.246	0.939	2	K.ASL*QWFNQAL*EDK#.S
SW:P121_HUMAN	R08	7729	2	1550.7	(-0.0)	3.085	0.275	0.928	2	K.ASLQWFNQALEDK.S
SW:P121_HUMAN	R24	6758	2	1006.1	(+0.5)	2.279	0.137	0.037	1	K.AVL*SPRNSR.M
SW:P24_HUMAN	R01	10265	3	3132.5	(+0.5)	4.321	0.514	1.000		K.GQDMETEAHQNKLEEMINELAVAMTAVK.H
SW:P24_HUMAN	R23	8984	3	3192.5	(-0.2)	4.616	0.504*	0.013		K.GQDM@ETEAHQNK#L*EEM@INEL*AVAMTAVK#.H
SW:P24_HUMAN	R23	7696	2	1458.7	(-0.7)	3.467	0.402	0.975		K.IVM@FTIDIGEAPK#.G
SW:P24_HUMAN	R23	7672	2	1458.7	(+0.6)	3.322	0.467	0.997		K.IVM@FTIDIGEAPK#.G
SW:P24_HUMAN	R23	5108	2	1429.6	(-0.9)	2.819	0.293	0.782		K.YTFAAHM@DGTYK#.F
SW:P24_HUMAN	R23	5990	2	1413.6	(-0.9)	2.388	0.327	0.725		K.YTFAAHMDGTYK#.F
SW:P24_HUMAN	R23	5988	2	1405.6	(-0.8)	2.201	0.365	0.786		K.YTFAAHMDGTYK.F
SW:P4H1_HUMAN	R14	8931	2	1688.9	(+1.0)	4.941	0.236	0.978	3	R.LNTEWSELENLVLK.D

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:P4H1_HUMAN	R14	5711	2	1627.7	(+0.5)	4.244	0.547	1.000	3	R.LQDTYNLDTDTISK.G
SW:P4H1_HUMAN	R14	8935	2	1720.9	(+0.8)	3.239	0.263	0.944	3	R.L*NTEWSEL*ENL*VL*K#.D
SW:P531_HUMAN	R04	918	2	947.0	(+0.7)	2.312	0.273	0.925	2	K.L*EGDHTIR.Q
SW:P531_HUMAN	R04	1412	2	1161.3	(-0.2)	2.488	0.189	0.697	1	R.L*SDVDANTAIF#.H
SW:P531_HUMAN	R04	5808	2	1542.6	(-0.6)	3.544	0.489	0.997	2	K.TSGTEPADFAL*PSSR.G
SW:P531_HUMAN	R04	4902	2	1345.5	(+0.0)	2.932	0.503	1.000	2	R.VPETVSAATQTIK.N
SW:P531_HUMAN	R04	4898	2	1353.5	(-0.7)	2.769	0.447	0.973	2	R.VPETVSAATQTIK#.N
SW:P531_HUMAN	R04	5964	2	934.1	(+0.4)	2.250	0.245	0.902	4	R.IL*DWQPR.E
SW:P5CS_HUMAN	R11	7744	3	1764.0	(+0.3)	4.049	0.474	1.000	1	R.AEIIHHL*ADL*L*TDQR.D
SW:P5CS_HUMAN	R11	1860	2	916.1	(+0.9)	2.526	0.132	0.735	1	R.DEILLANK.K
SW:P5CS_HUMAN	R11	864	2	918.9	(+0.3)	2.307	0.217	0.871	1	K.DLEEAAGR.L
SW:P5CS_HUMAN	R11	1444	2	1030.2	(+0.6)	2.486	0.321	0.957	1	K.EAVQLVNTR.E
SW:P5CS_HUMAN	R11	4834	3	1742.9	(+0.7)	4.785	0.492	0.996	1	R.GKDHVVSDVFSEHGSLK.Y
SW:P5CS_HUMAN	R11	4778	3	1764.9	(-0.2)	4.306	0.547	1.000	1	R.GK#DHVVSDVFSEHGSL*K#.Y
SW:P5CS_HUMAN	R11	4856	3	1764.9	(+0.1)	4.248	0.485	1.000	1	R.GK#DHVVSDVFSEHGSL*K#.Y
SW:P5CS_HUMAN	R11	7124	2	1211.4	(-0.6)	2.716	0.261	0.874	1	R.GPVGL*EGL*L*TTK#.W
SW:P5CS_HUMAN	R11	7142	2	1185.4	(+0.9)	2.531	0.343	0.957	1	R.GPVGLEGLLTTK.W
SW:P5CS_HUMAN	R11	5104	2	1182.4	(+0.2)	2.317	0.377	0.950	1	R.HEILLSQSVR.Q
SW:P5CS_HUMAN	R11	1010	2	808.9	(+1.0)	2.522	0.457	0.989	1	K.L*GSAVVTR.G
SW:P5CS_HUMAN	R11	1002	2	802.9	(+0.5)	2.315	0.313	0.950	1	K.LGSAVVTR.G
SW:P5CS_HUMAN	R11	7922	2	2030.3	(+0.4)	5.030	0.542	1.000	1	K.LIDIFYPGDQQSVTFGTK.S
SW:P5CS_HUMAN	R11	7920	2	2044.3	(-0.4)	3.762	0.474	0.999	1	K.L*IDIFYPGDQQSVTFGTK#.S
SW:P5CS_HUMAN	R11	4560	2	1188.4	(+0.1)	2.221	0.197	0.681	1	R.MLATLEPEQR.A
SW:P5CS_HUMAN	R11	8530	2	1623.9	(+0.9)	3.175	0.355	0.979	1	R.SWSNIPFITVPL*SR.T
SW:P5CS_HUMAN	R11	9028	2	1490.7	(-0.2)	2.873	0.371	0.969	1	R.TPL*FDQIIDM@L*R.V
SW:P5CS_HUMAN	R11	9934	2	1462.7	(+0.5)	2.470	0.521	0.989	1	R.TPLFDQIIDMLR.V
SW:P5CS_HUMAN	R11	9922	2	1474.7	(+0.3)	2.462	0.496	0.987	1	R.TPL*FDQIIDML*R.V
SW:P5CS_HUMAN	R11	6648	3	2474.8	(+0.6)	4.717	0.540	0.922	1	K.VGTFSEVFK#PAGPTVEQQGEMAR.S
SW:P5CS_HUMAN	R11	6302	2	1354.5	(+0.9)	3.454	0.300	0.975	1	K.VSGHVITDIVEGK.K
SW:P5CS_HUMAN	R12	10868	3	2504.8	(+0.6)	5.124	0.519	1.000	1	K.TDLLIVLSDVEGLFDSPPGSDDAK.L
SW:PAB1_HUMAN	R12	9826	3	2742.2	(+0.9)	4.274	0.507	1.000	3	K.ITGMLEIDNSELLHMLESPEL.R.S
SW:PAB1_HUMAN	R12	6352	2	1413.6	(+0.0)	3.523	0.380	0.983	2	R.KEFSPFGTITSAK.V
SW:PAB1_HUMAN	R12	6456	2	1930.1	(+0.8)	4.328	0.552	1.000	3	R.SLGYAYVNFQQPADAER.A
SW:PAB1_HUMAN	R12	6704	2	1285.4	(+1.0)	2.480	0.396	0.972	2	K.EFSPFGTITSAK.V
SW:PCB1_HUMAN	R18	9675	3	3380.9	(+0.4)	4.773	0.475	0.998		K.AFAMIIDKLEEDINSSMTNSTAASRPPVTLR.L
SW:PCB1_HUMAN	R18	5971	2	2097.3	(-0.9)	2.537	0.323	0.769	4	R.ESTGAQVQVAGDML*PNSTER.A
SW:PCB1_HUMAN	R18	5959	2	2091.3	(-0.8)	2.302	0.466	0.901	4	R.ESTGAQVQVAGDMLPNSTER.A
SW:PCB2_HUMAN	R18	7609	2	1359.7	(-0.5)	2.988	0.443	0.983		R.IITLAGPTNAIFK.A
SW:PCB2_HUMAN	R18	7617	2	1373.7	(+0.1)	2.969	0.315	0.937		R.IITL*AGPTNAIFK#.A
SW:PCB2_HUMAN	R18	6975	3	3404.8	(-1.0)	5.793	0.535	0.934		K.L*HQL*AMQQSHFPMTHGNTGFSGIESSSPEVK#.G
SW:PCB2_HUMAN	R18	6977	3	3384.8	(-0.6)	5.425	0.489	0.996		K.LHQLAMQQSHFPMTHGNTGFSGIESSSPEVK.G
SW:PCB2_HUMAN	R19	7816	2	1373.7	(+0.3)	2.353	0.315	0.898		R.IITL*AGPTNAIFK#.A
SW:PCD8_HUMAN	R13	1498	2	1531.6	(+0.3)	3.035	0.467	0.989	1	K.AALSASEGEEVPODK.A
SW:PCD8_HUMAN	R13	6977	2	1465.6	(-0.1)	3.174	0.443	0.982	2	K.EL*WFSDDPNVTK#.T
SW:PCD8_HUMAN	R13	5199	2	1143.3	(+0.8)	3.017	0.432	0.988	1	R.ISGLGLTPEQK.Q
SW:PCD8_HUMAN	R13	7995	2	1445.7	(+0.8)	2.447	0.276	0.900	3	R.ALGTEVIQLFPEK.G
SW:PCL1_HUMAN	R15	7349	2	1321.6	(+0.3)	3.430	0.350	0.987	3	K.FLNEMIAPVMR.V
SW:PCL1_HUMAN	R15	2128	2	1067.2	(+0.7)	3.238	0.333	0.983	3	K.IFSQETLTK.A
SW:PCL1_HUMAN	R15	7217	2	1570.8	(+0.7)	4.437	0.548	1.000	3	K.SNLISGSVMYIEEK.T
SW:PCL1_HUMAN	R15	4709	2	1569.6	(-0.4)	3.991	0.486	1.000	3	R.YQSHDYAFSSVEK#.L
SW:PCL1_HUMAN	R15	4707	2	1561.6	(-0.3)	3.929	0.554	0.999	3	R.YQSHDYAFSSVEK.L
SW:PCL1_HUMAN	R15	5121	2	871.0	(+1.0)	2.318	0.415	0.976	2	R.YGFQSLR.M
SW:PCNA_HUMAN	R19	7820	2	2096.2	(-0.7)	2.831	0.236	0.824		R.AEDNADTL*AL*VFEAPNQEK#.V
SW:PCNA_HUMAN	R20	7560	2	2096.2	(+0.9)	5.040	0.508	0.999		R.AEDNADTL*AL*VFEAPNQEK#.V
SW:PCNA_HUMAN	R20	7558	2	2076.2	(+0.2)	4.394	0.534	0.997		R.AEDNADTLALVFEAPNQEK.V
SW:PCNA_HUMAN	R19	4426	2	1294.4	(+0.5)	3.208	0.372	0.984		K.FSASGELGNQK.L
SW:PCNA_HUMAN	R19	2486	2	1308.4	(+0.2)	3.183	0.498	1.000		K.FSASGEL*GNGNIK#.L
SW:PCNA_HUMAN	R19	4264	2	1294.4	(+0.3)	3.099	0.389	0.984		K.FSASGELGNQK.L

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:PCNA_HUMAN	R19	4314	2	1308.4	(+0.4)	3.072	0.434	0.984		K.FSASGEL*GNGNIK#.L
SW:PCNA_HUMAN	R19	4452	2	1308.4	(+0.1)	2.899	0.350	0.950		K.FSASGEL*GNGNIK#.L
SW:PCNA_HUMAN	R19	4348	2	1294.4	(-0.2)	2.844	0.456	0.981		K.FSASGELGNGNIK.L
SW:PCNA_HUMAN	R19	4732	2	1308.4	(-0.1)	2.602	0.431	0.511		K.FSASGEL*GNGNIK#.L
SW:PCNA_HUMAN	R19	2572	2	1308.4	(+0.0)	2.548	0.444	0.965		K.FSASGEL*GNGNIK#.L
SW:PCNA_HUMAN	R19	4238	2	1308.4	(-0.0)	2.533	0.379	0.939		K.FSASGEL*GNGNIK#.L
SW:PCNA_HUMAN	R19	4374	2	1308.4	(-0.8)	2.489	0.365	0.805		K.FSASGEL*GNGNIK#.L
SW:PCNA_HUMAN	R19	4810	2	1308.4	(+0.2)	2.394	0.364	0.914		K.FSASGEL*GNGNIK#.L
SW:PCNA_HUMAN	R20	4982	2	1294.4	(+0.1)	3.783	0.435	1.000		K.FSASGELGNGNIK.L
SW:PCNA_HUMAN	R20	4732	2	1308.4	(+0.7)	3.697	0.536	1.000		K.FSASGEL*GNGNIK#.L
SW:PCNA_HUMAN	R20	4490	2	1308.4	(+0.2)	3.370	0.500	1.000		K.FSASGEL*GNGNIK#.L
SW:PCNA_HUMAN	R20	4644	2	1308.4	(+0.3)	3.333	0.508	1.000		K.FSASGEL*GNGNIK#.L
SW:PCNA_HUMAN	R20	4548	2	1294.4	(+0.5)	3.321	0.473	1.000		K.FSASGELGNGNIK.L
SW:PCNA_HUMAN	R20	4470	2	1294.4	(+0.3)	3.311	0.464	1.000		K.FSASGELGNGNIK.L
SW:PCNA_HUMAN	R20	4958	2	1308.4	(+0.5)	3.232	0.422	0.985		K.FSASGEL*GNGNIK#.L
SW:PCNA_HUMAN	R20	4818	2	1308.4	(+0.8)	3.219	0.474	0.997		K.FSASGEL*GNGNIK#.L
SW:PCNA_HUMAN	R20	5286	2	1308.4	(+0.2)	2.840	0.338	0.941		K.FSASGEL*GNGNIK#.L
SW:PCNA_HUMAN	R20	5294	2	1294.4	(+0.4)	2.761	0.409	0.980		K.FSASGELGNGNIK.L
SW:PCNA_HUMAN	R20	4412	2	1308.4	(-0.2)	2.727	0.494	0.979		K.FSASGEL*GNGNIK#.L
SW:PCNA_HUMAN	R20	1866	2	885.1	(+0.8)	2.445	0.215	0.878		K.IADMGLK.Y
SW:PCNA_HUMAN	R19	6338	2	1402.6	(-0.1)	2.462	0.254	0.790		R.NL*AM@GVNL*TSMSK#.I
SW:PCNA_HUMAN	R20	6760	2	1366.6	(+0.2)	3.865	0.524	1.000		R.NLAMGVNLTSMK.I
SW:PCNA_HUMAN	R20	6036	2	1402.6	(-0.2)	3.646	0.455	1.000		R.NL*AMGVNL*TSM@SK#.I
SW:PCNA_HUMAN	R20	4922	2	1418.6	(-0.6)	3.189	0.368	0.968		R.NL*AM@GVNL*TSM@SK#.I
SW:PCNA_HUMAN	R20	5038	2	1418.6	(+1.0)	3.021	0.472	0.559		R.NL*AM@GVNL*TSM@SK#.I
SW:PCNA_HUMAN	R20	6122	2	1402.6	(-0.1)	2.991	0.373*	0.274		R.NL*AM@GVNL*TSMSK#.I
SW:PCNA_HUMAN	R20	6756	2	1386.6	(-0.8)	2.727	0.183	0.450		R.NL*AMGVNL*TSMSK#.I
SW:PCNA_HUMAN	R20	5074	2	1308.4	(-0.7)	2.334	0.374	0.915		K.FSASGEL*GNGNIK#.L
SW:PDA3_HUMAN	R14	9311	2	2349.5	(+0.2)	3.971	0.437	1.000	7	K.DASIVGFFDDSFSEAHSEFLK.A
SW:PDA3_HUMAN	R15	9113	2	2349.5	(+0.6)	4.525	0.624	1.000	7	K.DASIVGFFDDSFSEAHSEFLK.A
SW:PDA3_HUMAN	R14	8139	2	1371.5	(+0.8)	3.108	0.413	0.989	7	R.ELSDFISYLQR.E
SW:PDA3_HUMAN	R15	7871	2	1383.5	(+0.3)	3.107	0.341	0.981	7	R.EL*SDFISYL*QR.E
SW:PDA3_HUMAN	R15	9055	3	2940.2	(+0.6)	7.749	0.593	1.000	7	K.FISDKDASIVGFFDDSFSEAHSEFLK.A
SW:PDA3_HUMAN	R15	9059	3	2962.2	(-0.8)	6.021	0.505	1.000	7	K.FISDK#DASIVGFFDDSFSEAHSEFL*#K#.A
SW:PDA3_HUMAN	R16	9038	3	2940.2	(+0.2)	3.766	0.469	0.990	7	K.FISDKDASIVGFFDDSFSEAHSEFLK.A
SW:PDA3_HUMAN	R14	7149	2	1380.5	(-0.3)	3.021	0.177	0.834	5	R.FL*QDYFDGNL*#K#.R
SW:PDA3_HUMAN	R15	6933	2	1360.5	(+0.6)	4.397	0.330	0.991	5	R.FLQDYFDGNL.K.R
SW:PDA3_HUMAN	R15	6931	2	1380.5	(-0.1)	3.277	0.304	0.960	5	R.FL*QDYFDGNL*#K#.R
SW:PDA3_HUMAN	R17	7318	2	1360.5	(+0.8)	3.228	0.367	0.986	5	R.FLQDYFDGNL.K.R
SW:PDA3_HUMAN	R14	1580	2	1192.3	(+0.9)	3.144	0.413	0.988	7	R.LAPEYEAATR.L
SW:PDA3_HUMAN	R15	1364	2	1192.3	(+0.6)	2.246	0.191	0.599	7	R.LAPEYEAATR.L
SW:PDA3_HUMAN	R15	4903	2	884.0	(+0.7)	2.552	0.245	0.938	7	K.L*NFAVASR.K
SW:PDA3_HUMAN	R15	4833	2	878.0	(+0.8)	2.491	0.375	0.979	7	K.LNFAVASR.K
SW:PDA3_HUMAN	R15	4825	2	884.0	(-0.8)	2.328	0.349	0.863	7	K.L*NFAVASR.K
SW:PDA3_HUMAN	R18	5039	2	878.0	(+0.7)	2.363	0.347	0.967	7	K.LNFAVASR.K
SW:PDA3_HUMAN	R14	2566	2	1055.2	(-0.0)	2.681	0.325	0.939	7	R.TADGIVSHL*#K#.K
SW:PDA3_HUMAN	R14	2710	2	1041.2	(+1.0)	2.580	0.249	0.922	7	R.TADGIVSHL.K
SW:PDA3_HUMAN	R14	2778	2	1041.2	(+0.9)	2.425	0.236	0.885	7	R.TADGIVSHL.K
SW:PDA3_HUMAN	R15	2320	2	1055.2	(-0.6)	2.432	0.348	0.929	7	R.TADGIVSHL*#K#.K
SW:PDA3_HUMAN	R15	2400	2	1055.2	(+0.6)	2.210	0.291	0.875	7	R.TADGIVSHL*#K#.K
SW:PDA3_HUMAN	R14	8439	2	2576.9	(-1.0)	4.934	0.513	1.000	7	K.TFSHELSDFGLESTAGEIPVVAIR.T
SW:PDA3_HUMAN	R15	8197	2	2576.9	(-0.3)	5.848	0.579	1.000	7	K.TFSHELSDFGLESTAGEIPVVAIR.T
SW:PDA3_HUMAN	R15	8207	2	2588.9	(-0.8)	4.602	0.565	1.000	7	K.TFSHEL*SDFGL*ESTAGEIPVVAIR.T
SW:PDA3_HUMAN	R15	8187	3	2588.9	(+0.6)	4.385	0.506	1.000	7	K.TFSHEL*SDFGL*ESTAGEIPVVAIR.T
SW:PDA3_HUMAN	R17	8432	3	2576.9	(+0.9)	3.806	0.447	0.999	7	K.TFSHELSDFGLESTAGEIPVVAIR.T
SW:PDA3_HUMAN	R15	6685	2	1842.0	(-0.6)	4.764	0.496	0.998	7	K.VVVAENFDEIVNENK#.D
SW:PDA3_HUMAN	R15	6681	2	1834.0	(+0.5)	4.494	0.481	1.000	7	K.VVVAENFDEIVNENK.D
SW:PDA3_HUMAN	R14	5549	2	1085.2	(+0.3)	2.487	0.474	0.987	7	K.YGVSGYPTL.K
SW:PDA3_HUMAN	R15	5459	2	1085.2	(+0.9)	2.912	0.532	1.000	7	K.YGVSGYPTL.K
SW:PDA3_HUMAN	R15	5357	2	1099.2	(-0.3)	2.767	0.507	1.000	7	K.YGVSGYPTL*#K#.I
SW:PDA3_HUMAN	R15	5437	2	1099.2	(+0.2)	2.649	0.518	1.000	7	K.YGVSGYPTL*#K#.I
SW:PDA3_HUMAN	R17	5806	2	1085.2	(+1.0)	2.698	0.469	0.984	7	K.YGVSGYPTL.K
SW:PDA3_HUMAN	R20	5698	2	1085.2	(+0.7)	2.210	0.332	0.933	7	K.YGVSGYPTL.K
SW:PDA4_HUMAN	R11	7942	2	2137.4	(+0.2)	2.678	0.275	0.883		R.EVSPQDWTPPEVTLVLT.K.E

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:PDA4_HUMAN	R12	8084	2	2137.4	(+0.7)	2.876	0.483	0.988		R.EVSQPDWTPPEVTLVLTKE
SW:PDA4_HUMAN	R12	8082	2	2157.4	(+0.8)	2.762	0.370	0.960		R.EVSQPDWTPPEVTL*VL*TK#.E
SW:PDA4_HUMAN	R11	6766	2	1687.8	(+1.0)	2.420	0.433	0.974		K.FAMEPEEFDSDTLR.E
SW:PDA4_HUMAN	R12	6720	2	1693.8	(+0.1)	2.809	0.269	0.865		K.FAMEPEEFDSDTL*R.E
SW:PDA4_HUMAN	R12	6714	2	1687.8	(+0.5)	2.695	0.340	0.757		K.FAMEPEEFDSDTLR.E
SW:PDA4_HUMAN	R12	5940	2	1127.3	(+0.8)	2.743	0.419*	0.422		R.FDVSGYPTLK.I
SW:PDA4_HUMAN	R11	5946	3	2041.1	(+0.7)	4.061	0.454	1.000		K.GESDPAYQQYQDAANNLR.E
SW:PDA4_HUMAN	R12	5682	2	2041.1	(-0.6)	3.482	0.547	1.000		K.GESDPAYQQYQDAANNLR.E
SW:PDA4_HUMAN	R11	2130	2	1191.3	(+0.6)	3.018	0.460	0.989		K.IDATSASVLSR.F
SW:PDA4_HUMAN	R11	2214	2	1197.3	(+0.2)	2.757	0.450	0.981		K.IDATSASVL*ASR.F
SW:PDA4_HUMAN	R12	2102	2	1191.3	(+0.0)	2.682	0.413	0.973		K.IDATSASVLSR.F
SW:PDA4_HUMAN	R12	2190	2	1197.3	(+0.5)	2.628	0.445	0.984		K.IDATSASVL*ASR.F
SW:PDA4_HUMAN	R12	2182	2	1191.3	(-0.3)	2.467	0.435	0.970		K.IDATSASVLSR.F
SW:PDA4_HUMAN	R12	2110	2	1197.3	(+0.4)	2.407	0.386	0.966		K.IDATSASVL*ASR.F
SW:PDA4_HUMAN	R12	5920	2	1297.5	(-0.4)	2.757	0.399	0.964		K.RFDVSGYPTL*K#.I
SW:PDA4_HUMAN	R11	1988	2	979.2	(-0.3)	2.201	0.199	0.709		K.RSPPIPLAK.V
SW:PDA4_HUMAN	R12	5908	2	1161.3	(+0.4)	3.126	0.438	0.988		K.TFDSIVMDPK#.K
SW:PDA4_HUMAN	R11	1146	2	1134.2	(+0.5)	3.207	0.278	0.971		K.VDATAETDLAK.R
SW:PDA4_HUMAN	R11	1148	2	1148.2	(+0.1)	2.286	0.335	0.889		K.VDATAETDL*AK#.R
SW:PDA4_HUMAN	R12	1136	2	1134.2	(-0.3)	3.021	0.304	0.959		K.VDATAETDLAK.R
SW:PDA4_HUMAN	R11	5032	2	1443.7	(-0.3)	3.046	0.313	0.955		K.VSQGQLVVMQPEK.F
SW:PDA4_HUMAN	R12	4860	2	1457.7	(-0.2)	3.353	0.199	0.878		K.VSQGQL*VVMQPEK#.F
SW:PDA4_HUMAN	R12	7388	2	1793.0	(+0.4)	4.020	0.550	1.000		K.YGIVDYMIEQSGPPSK#.E
SW:PDA4_HUMAN	R12	7890	2	1299.5	(-0.1)	2.383	0.102	0.340		K.DGDDVIIIIVFK#.G
SW:PDA6_HUMAN	R16	9812	2	2639.0	(-0.4)	3.202	0.294	0.947	2	R.ALDFSDNAPPELLEIINEDIAK.R
SW:PDA6_HUMAN	R16	7896	3	2402.5	(+1.0)	5.000	0.552	0.998	2	R.DGELPVEDDIDLSDVELDDLK.D
SW:PDA6_HUMAN	R16	7898	2	2402.5	(+0.1)	4.509	0.558	0.999	2	R.DGELPVEDDIDLSDVELDDLK.D
SW:PDA6_HUMAN	R16	8512	2	2759.9	(-0.4)	4.213	0.483	1.000	2	R.DGELPVEDDIDLSDVELDDLKDEL.-
SW:PDA6_HUMAN	R16	6890	2	1484.6	(+0.2)	3.471	0.454	1.000	2	K.GSFSEQGINEFLR.E
SW:PDA6_HUMAN	R16	6316	2	1827.1	(+0.9)	4.525	0.533	1.000	2	K.HHSLGGQYGVQGFPTIK.I
SW:PDA6_HUMAN	R16	6332	3	1827.1	(-0.8)	4.247	0.354	0.988	2	K.HHSLGGQYGVQGFPTIK.I
SW:PDA6_HUMAN	R16	6324	2	1841.1	(+0.2)	3.842	0.576	0.999	2	K.HHSL*GGQYGVQGFPTIK#.I
SW:PDA6_HUMAN	R16	6806	2	1540.7	(-0.1)	3.971	0.452	1.000	2	K.L*AAVDATVNQVL*ASR.Y
SW:PDA6_HUMAN	R16	8098	2	1387.6	(+0.9)	3.952	0.258	0.977	2	R.TGEAIVDAALSALR.Q
SW:PDA6_HUMAN	R16	6374	3	2582.9	(+0.9)	6.963	0.631	1.000	2	K.VGAVDADKHHSLLGGQYGVQGFPTIK.I
SW:PDA6_HUMAN	R16	6382	3	2604.9	(-0.2)	4.214	0.575	1.000	2	K.VGAVDADK#HHSLL*GGQYGVQGFPTIK#.I
SW:PDA6_HUMAN	R16	6516	2	1529.7	(+0.2)	3.019	0.430	0.974	2	K.NL*EPEWAAAASEVK#.E
SW:PDI_HUMAN	R14	1538	2	1047.2	(-0.1)	2.288	0.304	0.882	4	K.DHENIVIAK#.M
SW:PDI_HUMAN	R14	7111	3	3759.7	(-0.3)	3.886	0.308	0.978	3	K.FLESGGQDGAGDDDDLEDLEEAEPPDMEEDDDQK.A
SW:PDI_HUMAN	R14	7939	2	1966.2	(+0.3)	3.888	0.467	1.000	2	K.HNQLPLVIEFTEQTAPK.I
SW:PDI_HUMAN	R14	8127	2	967.2	(-0.6)	2.352	0.192	0.766	3	R.ILEFFGLK.K
SW:PDI_HUMAN	R14	5565	2	1287.5	(-0.6)	2.834	0.388	0.972	2	R.KSNFAEALAAHK.Y
SW:PDI_HUMAN	R14	5533	3	1753.0	(+0.4)	4.215	0.566	1.000	4	K.L*GETYK#DHENIVIAK#.M
SW:PDI_HUMAN	R14	5617	3	1731.0	(+0.1)	4.124	0.517	1.000	4	K.LGETYKDHENIVIAK.M
SW:PDI_HUMAN	R14	1288	2	1318.4	(+0.7)	3.397	0.540	1.000	4	K.M@DSTANEVEAVK#.V
SW:PDI_HUMAN	R14	6059	2	1222.3	(+0.8)	2.640	0.366	0.968	4	K.NFEDVAFDEK#.K
SW:PDI_HUMAN	R14	6063	2	1214.3	(+1.0)	2.326	0.185	0.728	4	K.NFEDVAFDEK.K
SW:PDI_HUMAN	R14	9139	2	2715.0	(-0.4)	3.070	0.303	0.944	2	K.QFLQAAEAIDDIPFGITSNSDVFSK.Y
SW:PDI_HUMAN	R14	10543	3	2937.3	(+0.8)	4.087	0.454	0.999	1	R.TGPAATTLDPGAAAESLVESSEVAVIGFFK.D
SW:PDI_HUMAN	R14	5975	2	1781.9	(+0.7)	5.218	0.538	0.999	2	K.VDATEESDLAQQYGV.R
SW:PDI_HUMAN	R14	5955	3	1781.9	(+0.8)	4.677	0.355	0.998	2	K.VDATEESDLAQQYGV.R
SW:PDI_HUMAN	R15	7423	2	1082.4	(+0.6)	2.802	0.294	0.969	2	K.THILLFLPK.S
SW:PDX1_HUMAN	R21	6926	2	935.1	(+0.6)	2.810	0.250	0.940	3	R.GL*FIIDDK#.G
SW:PDX1_HUMAN	R22	7150	2	935.1	(+0.9)	2.462	0.208	0.866	3	R.GL*FIIDDK#.G
SW:PDX1_HUMAN	R23	7116	2	935.1	(+0.2)	2.609	0.131	0.665	3	R.GL*FIIDDK#.G
SW:PDX1_HUMAN	R22	6746	2	1211.4	(+0.3)	3.111	0.415	0.986	2	R.L*VQAFQFTDK#.H
SW:PDX1_HUMAN	R23	7650	2	1643.9	(-0.7)	3.164	0.339	0.561	2	K.QGGL*GPMNIPL*VSDPK#.R
SW:PDX1_HUMAN	R22	6190	2	1122.3	(+0.3)	2.676	0.408	0.978	2	R.TIAQDYGVL*K#.A
SW:PDX1_HUMAN	R22	6194	2	1108.3	(+1.0)	2.577	0.461	0.987	2	R.TIAQDYGVLK.A
SW:PDX1_HUMAN	R23	6030	2	1108.3	(+0.8)	2.536	0.373	0.974	2	R.TIAQDYGVLK.A
SW:PDX2_HUMAN	R23	9298	2	1736.0	(+0.9)	2.489	0.410	0.969	1	K.EGGLGPLNIPLADVTR.R
SW:PDX2_HUMAN	R23	5676	2	1044.2	(+0.3)	2.604	0.376	0.973	2	R.L*SEDYGVK*K#.T

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:PDX2_HUMAN	R23	5680	2	1024.2	(+0.5)	2.577	0.304	0.960	2	R.LSEDYGVLK.T
SW:PDX2_HUMAN	R23	5838	2	1180.3	(+0.7)	2.515	0.383	0.975	2	R.RLSEDYGVLK.T
SW:PDX2_HUMAN	R23	5192	2	987.1	(+0.8)	2.359	0.239	0.841	2	K.ATAVVDGAFK#.E
SW:PDX3_HUMAN	R22	8228	2	1300.6	(+0.7)	3.050	0.168	0.857	1	R.GL*FIIDPNGVIK#.H
SW:PDX3_HUMAN	R22	8226	2	1286.6	(+0.7)	2.829	0.312	0.944	1	R.GLFIIDPNGVIK.H
SW:PDX3_HUMAN	R23	8210	2	1300.6	(-0.3)	3.227	0.107	0.726	1	R.GL*FIIDPNGVIK#.H
SW:PDX3_HUMAN	R24	8258	2	1286.6	(+0.7)	2.928	0.284	0.957	1	R.GLFIIDPNGVIK.H
SW:PDX3_HUMAN	R23	4946	2	1030.1	(+0.7)	2.239	0.374	0.946	1	K.GTAVVNGEFK#.D
SW:PDX3_HUMAN	R22	6362	2	1207.4	(+1.0)	2.802	0.378	0.980	1	K.HLSVNDLPVGR.S
SW:PDX3_HUMAN	R22	6360	2	1219.4	(+0.0)	2.386	0.220	0.782	1	K.HL*SVNDL*PVGR.S
SW:PDX3_HUMAN	R23	7860	2	1803.0	(+0.5)	2.392	0.256	0.805	1	K.NGGL*GHM@NIAL*L*SDL*TK#.Q
SW:PDX3_HUMAN	R24	6298	2	1207.4	(+0.7)	2.433	0.469	0.985	1	K.HLSVNDLPVGR.S
SW:PDX4_HUMAN	R21	6288	2	1637.7	(-0.1)	3.318	0.361	0.970		K.DYGVYL*EDSGHTL*R.G
SW:PDX4_HUMAN	R21	7696	2	1465.7	(+0.7)	3.427	0.416	0.990		R.IPLLSDLTHQISK.D
SW:PDX4_HUMAN	R21	5786	2	1227.4	(-0.4)	2.777	0.338	0.952	1	R.L*VQAFQYTDK#.H
SW:PDX4_HUMAN	R22	6918	2	1226.4	(+0.9)	2.781	0.236*	0.396		R.QITLNDLPVGR.S
SW:PDX4_HUMAN	R21	5550	2	1293.5	(-0.2)	3.219	0.357	0.976		R.VSVADHSLHLSK.A
SW:PDX4_HUMAN	R22	5962	2	1227.4	(+0.2)	2.493	0.385	0.953	1	R.L*VQAFQYTDK#.H
SW:PDX5_HUMAN	R25	7646	2	1560.8	(-0.3)	3.039	0.318	0.939	1	K.THL*PGFVEQAEAL*K#.A
SW:PDX5_HUMAN	R25	6734	2	1090.3	(-0.1)	2.356	0.461	0.974	1	R.LLADPTGAFGK.E
SW:PGC1_HUMAN	R22	9572	3	3625.8	(+0.0)	6.716	0.607	0.999	1	K.EALKDEYDDLSDLTAAQETLSDWESQFTFK.Y
SW:PGC1_HUMAN	R23	9524	3	3625.8	(-0.4)	4.926	0.501	1.000	1	K.EALKDEYDDLSDLTAAQETLSDWESQFTFK.Y
SW:PGC1_HUMAN	R22	5126	2	2043.1	(-0.8)	3.727	0.527	1.000	2	R.GDQPAASGSDSDDEPPPL*PR.L
SW:PGC1_HUMAN	R22	5200	2	2037.1	(-0.9)	3.484	0.578	0.999	2	R.GDQPAASGSDSDDEPPPLPR.L
SW:PGC1_HUMAN	R22	5122	2	2037.1	(-1.0)	3.338	0.563	1.000	2	R.GDQPAASGSDSDDEPPPLPR.L
SW:PGC1_HUMAN	R22	5728	2	1105.2	(-0.0)	2.839	0.207	0.897	2	R.RDFTPAELR.R
SW:PGC1_HUMAN	R23	5706	2	1105.2	(+0.9)	2.619	0.189	0.886	2	R.RDFTPAELR.R
SW:PGC1_HUMAN	R24	9532	3	3625.8	(-0.1)	5.297	0.521	1.000	1	K.EALKDEYDDLSDLTAAQETLSDWESQFTFK.Y
SW:PGC2_HUMAN	R21	7110	3	2589.7	(+0.7)	3.765	0.497	1.000		K.DAL*RDEYDDL*SDL*NAVQM@ESVR.E
SW:PGC2_HUMAN	R21	6522	3	2128.2	(+0.4)	4.160	0.307	0.991		R.DEYDDL*SDL*NAVQM@ESVR.E
SW:PGC2_HUMAN	R21	5616	2	1698.8	(-0.4)	3.455	0.396	0.981		R.GLGAGAGAGEESPATSLPR.M
SW:PGC2_HUMAN	R21	5618	2	1710.8	(-0.4)	3.211	0.468	0.986		R.GL*GAGAGAGEESPATSL*PR.M
SW:PGC2_HUMAN	R24	5792	2	1698.8	(+0.7)	4.708	0.562	0.999		R.GLGAGAGAGEESPATSLPR.M
SW:PGC2_HUMAN	R24	5824	3	1867.0	(+0.6)	4.377	0.363	0.998		R.RGL*GAGAGAGEESPATSL*PR.M
SW:PGC2_HUMAN	R24	5826	3	1855.0	(+1.0)	4.184	0.422	0.999		R.RGLGAGAGAGEESPATSLPR.M
SW:PGC2_HUMAN	R24	5790	2	1710.8	(-0.5)	3.072	0.405	0.976		R.GL*GAGAGAGEESPATSL*PR.M
SW:PHB_HUMAN	R20	8556	3	2023.3	(+0.2)	4.013	0.514	1.000		K.AAEL*IANSL*ATAGDGL*IEL*R.K
SW:PHB_HUMAN	R20	8562	2	1999.3	(-0.6)	2.468	0.296	0.872		K.AAELIANSLATAGDGLIELR.K
SW:PHB_HUMAN	R20	1550	2	1070.2	(-0.2)	2.679	0.273	0.892		K.AAIIAEGDSK#.A
SW:PHB_HUMAN	R20	1526	2	1062.2	(+0.5)	2.287	0.392	0.964		K.AAIIAEGDSK.A
SW:PHB_HUMAN	R20	9340	2	2120.5	(-0.5)	4.151	0.500	1.000		R.AATFGLILDDVSLTHLTFGK.E
SW:PHB_HUMAN	R20	6290	2	1150.3	(+0.9)	2.404	0.427	0.980	1	R.FDAGELITQR.E
SW:PHB_HUMAN	R20	6882	2	1409.7	(-0.5)	2.541	0.210	0.069		R.IL*FRPVASQL*PR.I
SW:PHB_HUMAN	R20	7044	2	1627.8	(-0.8)	4.513	0.483	0.996		R.K#L*EAAEDIAYQL*SR.S
SW:PHB_HUMAN	R21	7006	3	1607.8	(+0.7)	3.885	0.124	0.820		R.KLEAAEDIAYQLSR.S
SW:PHB_HUMAN	R22	6588	2	1156.3	(+0.8)	2.385	0.360	0.963	1	R.FDAGEL*ITQR.E
SW:PIS_HUMAN	R01	6641	2	1215.5	(+0.3)	2.638	0.431	0.984	1	K.MIDLSGNPVLRI
SW:PIS_HUMAN	R01	9031	2	1406.7	(+0.3)	3.290	0.464	0.996	1	K.SL*ISVIHL*ITAAR.N
SW:PIS_HUMAN	R03	8569	2	1406.7	(+0.1)	3.713	0.442	1.000	1	K.SL*ISVIHL*ITAAR.N
SW:PLE1_HUMAN	R03	5547	2	1300.4	(+1.0)	2.840	0.407	0.984	1	K.AQVEQEL*TTL*R.L
SW:PLE1_HUMAN	R03	4545	3	2077.2	(-0.1)	4.554	0.522	1.000	1	K.AYSDPSTGEPATYQEL*QQR.C
SW:PLE1_HUMAN	R03	4905	2	1055.2	(+0.1)	2.775	0.245	0.927	1	R.L*AAEQEL*IR.L
SW:PLE1_HUMAN	R03	5693	2	1138.3	(+0.1)	2.918	0.281	0.889	1	K.TPVEVPVGGFK#.G
SW:PLE1_HUMAN	R04	5164	2	1055.2	(+0.0)	2.225	0.145	0.564	1	R.L*AAEQEL*IR.L
SW:PLSL_HUMAN	R13	5147	2	995.1	(+0.9)	2.778	0.356	0.980	2	K.IGNFSTDIK.D
SW:PLSL_HUMAN	R13	5135	2	1003.1	(+0.5)	2.453	0.266	0.909	2	K.IGNFSTDIK#.D
SW:PLSL_HUMAN	R13	10831	2	2700.1	(-0.5)	3.118	0.407	0.977	2	K.ISTSLPVLDLIDAIQPGSINYDLLK.T

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:PLSL_HUMAN	R13	7065	3	2540.8	(+0.1)	5.742	0.459	0.995	2	R.YPALHKPENQDIDWGALEGETR.E
SW:PLSL_HUMAN	R13	7449	2	1155.3	(+0.3)	2.213	0.455	0.981	7	K.YAFVNWINK.A
SW:PM5P_HUMAN	R03	7723	2	1691.9	(+0.7)	3.089	0.356	0.976	5	R.DGENYVLLDSTLPR.S
SW:PM5P_HUMAN	R01	1544	2	1187.3	(+0.4)	2.435	0.186	0.813	4	R.EQQLAEIEAR.R
SW:PM5P_HUMAN	R02	7936	3	2537.8	(-0.1)	4.020	0.510	1.000	5	R.FEQAFYTYDTSSPSIL*TL*TAIR.H
SW:PM5P_HUMAN	R02	6472	3	2173.4	(+0.1)	3.839	0.481	0.996	4	K.GAYSVGPL*HSDL*EYTVTSQK#.E
SW:PM5P_HUMAN	R01	6167	2	1379.6	(+0.1)	3.351	0.496	1.000	5	K.GQPLGPAGVQVSLR.N
SW:PM5P_HUMAN	R01	6159	2	1391.6	(-0.2)	2.365	0.353	0.918	5	K.GQPL*GPAGVQVSL*R.N
SW:PM5P_HUMAN	R02	6002	2	1379.6	(+0.2)	2.493	0.436	0.966	5	K.GQPLGPAGVQVSLR.N
SW:PM5P_HUMAN	R03	5879	2	1379.6	(+0.5)	2.731	0.492	0.988	5	K.GQPLGPAGVQVSLR.N
SW:PM5P_HUMAN	R01	11565	3	3167.7	(-0.5)	5.244	0.551	0.998	4	K.LPEQDIAQGSYIALPLTLLVLLAGYNHDK.L
SW:PM5P_HUMAN	R01	7229	2	1526.8	(+0.7)	3.494	0.394	0.985	6	K.SSIDSEPALVGLPLK.S
SW:PM5P_HUMAN	R01	7231	2	1552.8	(-0.1)	2.983	0.292	0.912	6	K.SSIDSEPAL*VL*GPL*K#.S
SW:PM5P_HUMAN	R01	768	2	1119.3	(+0.4)	2.283	0.397	0.378	5	K.VVLSSQDKDK.S
SW:PMG1_HUMAN	R21	5580	2	1313.4	(+0.6)	2.343	0.179	0.740	1	R.HGESAWNLENR.F
SW:PMG1_HUMAN	R21	5232	2	1060.2	(+1.0)	2.341	0.269	0.728	7	R.HYGGTLGLNK.A
SW:PMG1_HUMAN	R21	5600	2	1319.4	(+0.2)	2.327	0.364	0.518	1	R.HGESAWN*ENR.F
SW:POR1_HUMAN	R19	9446	3	2419.8	(+0.6)	6.040	0.562	1.000	2	R.GALVLGYEGWLAGYQMNFFETAK.S
SW:POR1_HUMAN	R19	9366	3	2445.8	(+0.5)	5.105	0.560	1.000	2	R.GAL*VL*GYEGWL*AGYQMNFFETAK#.S
SW:POR1_HUMAN	R19	9044	3	2461.8	(+0.6)	4.255	0.494	1.000	2	R.GAL*VL*GYEGWL*AGYQM@NFETAK#.S
SW:POR1_HUMAN	R21	8570	3	2461.8	(+0.2)	4.440	0.440	0.999	2	R.GAL*VL*GYEGWL*AGYQM@NFETAK#.S
SW:POR1_HUMAN	R19	6942	2	1947.2	(+0.9)	6.049	0.655	1.000	2	K.KLETAVNLAWTAGNSNTR.F
SW:POR1_HUMAN	R20	6198	2	1401.5	(-0.7)	3.880	0.543	0.994	2	K.LTFDSSFSPTGK.K
SW:POR1_HUMAN	R20	6194	2	1415.5	(-0.1)	3.802	0.561	0.998	2	K.L*TFDSSFSPTGK#.K
SW:POR1_HUMAN	R22	6492	2	1401.5	(+1.0)	3.950	0.548	1.000	2	K.LTFDSSFSPTGK.K
SW:POR1_HUMAN	R19	2088	2	1961.0	(+0.6)	5.569	0.589	1.000	3	K.SENGLLEFTSSGSANTETTK.V
SW:POR1_HUMAN	R19	5298	2	1975.0	(-0.3)	3.015	0.418	0.969	3	K.SENGL*EFTSSGSANTETTK#.V
SW:POR1_HUMAN	R19	13300	3	2601.7	(+0.5)	4.259	0.481	1.000	2	K.TDEFQLHTNVNDGTEFGGSIYQK.V
SW:POR1_HUMAN	R20	6790	3	2601.7	(+0.4)	5.135	0.494	0.999	2	K.TDEFQLHTNVNDGTEFGGSIYQK.V
SW:POR1_HUMAN	R20	6796	3	2615.7	(+0.0)	4.741	0.377	0.998	2	K.TDEFQL*HTNVNDGTEFGGSIYQK#.V
SW:POR1_HUMAN	R21	6722	3	2601.7	(+0.3)	4.145	0.462	0.997	2	K.TDEFQLHTNVNDGTEFGGSIYQK.V
SW:POR1_HUMAN	R19	7256	2	2104.5	(+0.8)	4.333	0.570*	0.066	2	K.VNNSLIQLGYTQTLKPGIK.L
SW:POR1_HUMAN	R19	2160	2	1222.4	(+0.6)	2.363	0.387	0.957	2	R.VTQSNFAVGYK#.T
SW:POR1_HUMAN	R20	4100	2	1214.4	(-0.4)	2.937	0.454	0.985	2	R.VTQSNFAVGYK.T
SW:POR1_HUMAN	R20	4172	2	1214.4	(+0.2)	2.923	0.428	0.983	2	R.VTQSNFAVGYK.T
SW:POR1_HUMAN	R20	3890	2	1214.4	(+0.4)	2.825	0.391	0.963	2	R.VTQSNFAVGYK.T
SW:POR1_HUMAN	R20	3826	2	1214.4	(+0.2)	2.589	0.327	0.942	2	R.VTQSNFAVGYK.T
SW:POR1_HUMAN	R20	4214	2	1222.4	(+0.1)	2.428	0.396	0.948	2	R.VTQSNFAVGYK#.T
SW:POR1_HUMAN	R20	4140	2	1222.4	(-0.6)	2.203	0.245	0.712	2	R.VTQSNFAVGYK#.T
SW:POR1_HUMAN	R19	7112	2	1389.5	(-0.4)	2.440	0.133	0.505	3	R.WTEYGL*TFTEK#.W
SW:POR1_HUMAN	R21	6908	2	1375.5	(+1.0)	2.573	0.491	0.989	3	R.WTEYGLTFTEK.W
SW:POR1_HUMAN	R25	6862	2	1401.5	(-0.0)	3.057	0.476	0.987	2	K.LTFDSSFSPTGK.K
SW:POR2_HUMAN	R19	6692	2	1429.6	(+0.8)	3.419	0.604	1.000	4	K.LTFDITTFSPNTGK.K
SW:POR2_HUMAN	R19	6906	3	2529.7	(+0.7)	6.217	0.508	1.000	4	R.TGDFQLHTNVNDGTEFGGSIYQK.V
SW:POR2_HUMAN	R19	6910	3	2543.7	(-0.1)	4.989	0.489	1.000	4	R.TGDFQL*HTNVNDGTEFGGSIYQK#.V
SW:POR2_HUMAN	R19	13134	3	2529.7	(+1.0)	4.856	0.484	0.561	4	R.TGDFQLHTNVNDGTEFGGSIYQK.V
SW:POR2_HUMAN	R19	12822	3	2529.7	(+0.5)	4.778	0.436	0.870	4	R.TGDFQLHTNVNDGTEFGGSIYQK.V
SW:POR2_HUMAN	R19	13474	3	2529.7	(+0.7)	4.468	0.516	0.997	4	R.TGDFQLHTNVNDGTEFGGSIYQK.V
SW:POR2_HUMAN	R19	12664	3	2529.7	(+0.9)	4.359	0.387	0.804	4	R.TGDFQLHTNVNDGTEFGGSIYQK.V
SW:POR2_HUMAN	R19	12052	3	2529.7	(+0.2)	4.343	0.476	0.987	4	R.TGDFQLHTNVNDGTEFGGSIYQK.V
SW:POR2_HUMAN	R19	11888	3	2529.7	(+0.1)	4.271	0.385	0.983	4	R.TGDFQLHTNVNDGTEFGGSIYQK.V
SW:POR2_HUMAN	R19	13052	3	2529.7	(+0.4)	4.235	0.498	0.999	4	R.TGDFQLHTNVNDGTEFGGSIYQK.V
SW:POR2_HUMAN	R19	12806	3	2543.7	(+0.8)	4.105	0.290*	0.126	4	R.TGDFQL*HTNVNDGTEFGGSIYQK#.V
SW:POR2_HUMAN	R19	12898	3	2529.7	(+0.4)	4.089	0.373	0.883	4	R.TGDFQLHTNVNDGTEFGGSIYQK.V
SW:POR2_HUMAN	R19	11378	3	2529.7	(+0.2)	3.962	0.437	0.998	4	R.TGDFQLHTNVNDGTEFGGSIYQK.V
SW:POR2_HUMAN	R19	11532	3	2529.7	(+0.1)	3.946	0.477	0.999	4	R.TGDFQLHTNVNDGTEFGGSIYQK.V
SW:POR2_HUMAN	R19	13552	3	2529.7	(+0.7)	3.942	0.418	0.999	4	R.TGDFQLHTNVNDGTEFGGSIYQK.V
SW:POR2_HUMAN	R19	12366	3	2529.7	(+0.5)	3.931	0.380	0.997	4	R.TGDFQLHTNVNDGTEFGGSIYQK.V
SW:POR2_HUMAN	R19	12290	3	2529.7	(+0.8)	3.928	0.511	0.774	4	R.TGDFQLHTNVNDGTEFGGSIYQK.V
SW:POR2_HUMAN	R19	12590	3	2529.7	(+0.7)	3.725	0.444	0.843	4	R.TGDFQLHTNVNDGTEFGGSIYQK.V
SW:POR2_HUMAN	R20	12787	3	2529.7	(-0.2)	4.637	0.393	0.998	4	R.TGDFQLHTNVNDGTEFGGSIYQK.V
SW:POR2_HUMAN	R20	6702	3	2543.7	(+0.1)	4.125	0.408*	0.057	4	R.TGDFQL*HTNVNDGTEFGGSIYQK#.V



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:POR2_HUMAN	R21	6630	3	2529.7	(+0.4)	6.142	0.488	1.000	4	R.TGDFQLHTNVNDGTEFGGSIYQK.V
SW:POR2_HUMAN	R21	6638	3	2543.7	(-0.4)	5.379	0.514	1.000	4	R.TGDFQL*HTNVNDGTEFGGSIYQK#.V
SW:POR2_HUMAN	R19	6884	2	2104.4	(-0.6)	3.480	0.485	1.000	4	K.VNNSLIGVGYTQTLRPGVK.L
SW:POR2_HUMAN	R20	5716	2	1308.4	(+0.4)	2.272	0.305	0.870	4	K.YQL*DPTASISAK#.V
SW:POR2_HUMAN	R27	5599	2	1294.4	(+0.5)	2.819	0.414	0.981	4	K.YQLDPTASISAK.V
SW:POR3_HUMAN	R20	6622	3	2536.7	(+0.7)	6.542	0.565	0.557	1	K.AADFQLHHTVNDGTEFGGSIYQK.V
SW:POR3_HUMAN	R20	6628	3	2550.7	(-0.1)	6.218	0.572	1.000	1	K.AADFQL*HTHVNDGTEFGGSIYQK#.V
SW:POR3_HUMAN	R20	5898	2	1275.4	(+0.1)	2.768	0.339	0.946	1	K.L*SQNNFAL*GYK#.A
SW:POR3_HUMAN	R20	5900	2	1255.4	(-0.4)	2.347	0.315	0.906	1	K.LSQNNFALGYK.A
SW:POR3_HUMAN	R01	7509	2	1419.7	(+0.9)	4.024	0.591	1.000	1	K.LTLDTIFVPNTGK.K
SW:POR3_HUMAN	R01	7529	2	1419.7	(-0.7)	2.314	0.175	0.582	1	K.LTLDTIFVPNTGK.K
SW:POR3_HUMAN	R20	7592	2	1439.7	(-0.3)	2.543	0.358	0.928	1	K.L*TL*DTIFVPNTGK#.K
SW:POR3_HUMAN	R20	7122	2	2102.4	(-0.9)	3.493	0.353	0.203		K.VNNASLIGLGYTQTLRPGVK.L
SW:POR3_HUMAN	R20	5746	2	1275.4	(+0.8)	2.217	0.123	0.430	1	K.L*SQNNFAL*GYK#.A
SW:PP1A_HUMAN	R19	9910	2	1954.4	(-0.3)	4.158	0.489	1.000	8	R.EIFLSQPILLELEAPL.K.I
SW:PP1A_HUMAN	R18	2338	2	1222.3	(+0.5)	2.450	0.261	0.912	2	K.NVQL*TENEIR.G
SW:PP1A_HUMAN	R19	8138	2	1211.4	(+0.4)	2.312	0.194	0.811	8	K.YPENFFL*L*R.G
SW:PPIA_HUMAN	R25	9354	2	1953.2	(+0.8)	3.632	0.350	0.983		-.VNPTVFFDIAVDGEPL*GR.V
SW:PPIA_HUMAN	R25	9340	2	1947.2	(-0.5)	2.727	0.481	0.981		-.VNPTVFFDIAVDGEPLGR.V
SW:PPIA_HUMAN	R25	7324	2	1169.3	(+0.0)	2.474	0.256	0.866	2	K.FEDENFIL*K#.H
SW:PPIB_HUMAN	R23	6418	2	1245.5	(+0.2)	3.368	0.151	0.139	2	K.IEVEKPFIAK.E
SW:PPIB_HUMAN	R23	7248	2	1379.5	(+0.3)	2.421	0.415	0.963	2	K.TVDNFVAL*ATGEK#.G
SW:PPIB_HUMAN	R23	7242	2	1365.5	(+0.9)	2.392	0.294	0.893	2	K.TVDNFVALATGEK.G
SW:PPIB_HUMAN	R23	6040	2	1032.2	(+0.1)	2.842	0.481	1.000	2	K.VLEGMEVVR.K
SW:PPIB_HUMAN	R23	2528	2	1054.2	(+0.5)	2.485	0.366	0.935	2	K.VL*EGM@EVVR.K
SW:PPIB_HUMAN	R23	6402	2	1261.5	(-0.7)	2.305	0.160	0.021	2	K.IEVEK#PFIAK#.E
SW:PPIE_HUMAN	R19	8052	2	1682.9	(+0.5)	3.568	0.488	0.500	3	K.HVVFGEVTEGL*DVL*R.Q
SW:PPIE_HUMAN	R19	7102	2	1507.7	(+0.3)	4.110	0.464	1.000	2	R.VLYVGGLAEEVDDK.V
SW:PPIE_HUMAN	R19	7088	2	1527.7	(+0.1)	2.908	0.314	0.927	2	R.VL*YVGGGL*AEEVDDK#.V
SW:PPIF_HUMAN	R24	7628	3	2835.0	(+0.6)	4.899	0.531	1.000		K.GSGDPSSSSSSGNPLVYLDVDANGKPLGR.V
SW:PPIF_HUMAN	R24	7634	3	2861.0	(-0.6)	4.746	0.519	1.000		K.GSGDPSSSSSSGNPL*VYL*DVDANGK#PL*GR.V
SW:PPIF_HUMAN	R24	6716	2	1111.2	(+0.3)	2.624	0.287	0.956		R.FPDENFTLK.H
SW:PPOL_HUMAN	R08	8165	3	2217.4	(+0.8)	4.014	0.436	1.000	5	K.NTHATTHNAYDL*EVIDIFK#.I
SW:PPOL_HUMAN	R08	6475	2	1200.3	(-0.5)	2.461	0.465	0.971	5	K.TL*GDFAAEYAK#.S
SW:PPOL_HUMAN	R08	7807	2	1390.6	(+0.0)	2.703	0.386	0.964	5	R.TTNFAGIL*SQGL*R.I
SW:PPOL_HUMAN	R10	8297	2	1378.6	(+0.8)	3.932	0.523	0.992	5	R.TTNFAGILSQGLR.I
SW:PPOL_HUMAN	R10	7911	2	1625.8	(+0.9)	5.048	0.580	0.999	5	R.VVSEDFLQDVSASTK.S
SW:PRKD_HUMAN	R04	8208	2	1150.4	(+1.0)	2.666	0.471	0.988	3	K.AALSALESFLK.Q
SW:PRKD_HUMAN	R04	8764	3	3144.6	(+0.4)	5.666	0.537	1.000	3	R.AGLLHNILPSQSTDLHHSVGTTELLSLVYK.G
SW:PRKD_HUMAN	R05	8550	3	3144.6	(+0.1)	4.806	0.496	1.000	3	R.AGLLHNILPSQSTDLHHSVGTTELLSLVYK.G
SW:PRKD_HUMAN	R04	9472	3	2091.4	(+0.8)	4.009	0.482	1.000	3	K.AVAFFL*ESIAMHDIIAAEK#.C
SW:PRKD_HUMAN	R04	4628	2	1762.8	(-0.5)	3.069	0.349	0.950	2	R.DPESETDNDSQEIFK#.L
SW:PRKD_HUMAN	R04	10296	2	1697.0	(+0.5)	2.643	0.375	0.966	3	R.EFFSTIVDAIDVLK.S
SW:PRKD_HUMAN	R05	10168	2	1711.0	(-0.1)	3.551	0.458	1.000	3	R.EFFSTIVDAIDVL*K#.S
SW:PRKD_HUMAN	R04	10006	2	1606.9	(+0.0)	2.734	0.147	0.644	3	K.EVYAAAAEVL*GL*IL*R.Y
SW:PRKD_HUMAN	R04	9164	2	1347.7	(-0.0)	2.777	0.228	0.858	2	R.FMNAVFFL*L*PK#.F
SW:PRKD_HUMAN	R04	7090	2	1642.8	(+0.4)	2.918	0.293	0.246	3	K.FYQGFL*FSEK#PEK#.N
SW:PRKD_HUMAN	R04	6024	2	1061.2	(+0.7)	3.191	0.331	0.978	2	R.GIFTSEIGTK#.Q
SW:PRKD_HUMAN	R05	9652	3	2337.7	(+0.7)	4.354	0.497	0.998	2	K.GQAVTLLPFFTSLTGGSLEELR.R
SW:PRKD_HUMAN	R03	5717	2	1150.3	(+0.1)	2.580	0.166	0.708	2	R.HGDL*PDIQIK#.H
SW:PRKD_HUMAN	R04	6044	2	1150.3	(-0.6)	3.373	0.367	0.979	2	R.HGDL*PDIQIK#.H
SW:PRKD_HUMAN	R04	6058	2	1136.3	(+0.6)	3.306	0.577	1.000	2	R.HGDL*PDIQIK.H
SW:PRKD_HUMAN	R04	2012	2	1501.6	(-0.2)	3.626	0.483	1.000	4	R.IL*EL*SGSSSEDSEK#.V
SW:PRKD_HUMAN	R03	9861	2	1661.9	(+0.3)	3.321	0.416	0.984	3	R.L*GL*IEWL*ENTVTL*K#.D
SW:PRKD_HUMAN	R04	10098	2	1661.9	(+0.5)	3.665	0.376	0.984	3	R.L*GL*IEWL*ENTVTL*K#.D
SW:PRKD_HUMAN	R04	10104	2	1629.9	(+0.4)	2.278	0.182	0.650	3	R.LGLIEWLENTVTLK.D
SW:PRKD_HUMAN	R06	10274	2	1661.9	(+0.3)	3.674	0.379	0.982	3	R.L*GL*IEWL*ENTVTL*K#.D
SW:PRKD_HUMAN	R04	4508	2	1157.3	(+0.2)	2.901	0.424	0.981	2	R.LGLPGDEVDNK.V

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:PRKD_HUMAN	R04	4584	2	1177.3	(+0.4)	2.258	0.301	0.885	2	R.L*GL*PGDEVDNK#.V
SW:PRKD_HUMAN	R04	6986	2	1251.5	(-0.1)	2.537	0.400	0.957	2	R.L*L*AL*NSL*YSPK#.I
SW:PRKD_HUMAN	R03	5819	2	897.1	(+0.6)	2.257	0.156	0.782	4	R.L*L*QIIER.Y
SW:PRKD_HUMAN	R04	6146	2	897.1	(+0.2)	2.488	0.214	0.894	4	R.L*L*QIIER.Y
SW:PRKD_HUMAN	R03	5087	2	1411.5	(-0.8)	3.232	0.313	0.878	3	K.L*NESTFDTQITK#.K
SW:PRKD_HUMAN	R04	5344	2	1411.5	(+0.3)	4.153	0.562	0.998	3	K.L*NESTFDTQITK#.K
SW:PRKD_HUMAN	R04	5366	2	1397.5	(-0.5)	3.039	0.434	0.983	3	K.LNESTFDTQITK.K
SW:PRKD_HUMAN	R05	5534	2	1411.5	(+0.1)	3.020	0.387	0.970	3	K.L*NESTFDTQITK#.K
SW:PRKD_HUMAN	R05	5518	2	1397.5	(+0.5)	2.725	0.519	0.991	3	K.LNESTFDTQITK.K
SW:PRKD_HUMAN	R03	1098	2	928.0	(+0.4)	2.436	0.264	0.924	2	R.L*PSNTL*DR.L
SW:PRKD_HUMAN	R05	1170	2	928.0	(-0.4)	2.433	0.299	0.935	2	R.L*PSNTL*DR.L
SW:PRKD_HUMAN	R04	1290	2	1116.2	(-0.5)	2.560	0.249	0.888	4	R.L*QETL*SAADR.C
SW:PRKD_HUMAN	R01	11271	3	2202.5	(+0.2)	3.954	0.370	0.996	2	K.L*QSVQAL*TEIQEFISFISK#.Q
SW:PRKD_HUMAN	R03	10476	3	2202.5	(-0.4)	4.006	0.340	0.994	2	K.L*QSVQAL*TEIQEFISFISK#.Q
SW:PRKD_HUMAN	R05	10584	3	2202.5	(+0.7)	4.568	0.445	1.000	2	K.L*QSVQAL*TEIQEFISFISK#.Q
SW:PRKD_HUMAN	R05	10576	2	2202.5	(+0.7)	3.614	0.383	0.983	2	K.L*QSVQAL*TEIQEFISFISK#.Q
SW:PRKD_HUMAN	R06	10878	3	2202.5	(+0.3)	4.152	0.390	0.999	2	K.L*QSVQAL*TEIQEFISFISK#.Q
SW:PRKD_HUMAN	R07	10973	2	2182.5	(-0.6)	2.372	0.398	0.943	2	K.LQSVQALTEIQEFISFISK.Q
SW:PRKD_HUMAN	R04	7974	2	1685.9	(-0.8)	2.205	0.103	0.082	3	K.L*SDFNITNM@L*L*K#.M
SW:PRKD_HUMAN	R04	5646	3	2328.4	(+0.7)	4.435	0.497	1.000	2	K.L*TPL*PEDNSMNVDDQDGDPSDR.M
SW:PRKD_HUMAN	R04	1948	3	2344.4	(+0.2)	3.726	0.417	0.997	2	K.L*TPL*PEDNSM@NVDQDGDPSDR.M
SW:PRKD_HUMAN	R04	2264	3	2344.4	(+0.1)	3.712	0.445	0.998	2	K.L*TPL*PEDNSM@NVDQDGDPSDR.M
SW:PRKD_HUMAN	R04	1292	2	996.1	(+0.8)	2.367	0.273	0.901	4	R.M@YAAL*GDPK#.A
SW:PRKD_HUMAN	R05	6652	2	1575.7	(+0.6)	2.468	0.264	0.881	3	K.NLSSNEAISLEEIR.I
SW:PRKD_HUMAN	R04	9022	2	1340.6	(+0.9)	2.931	0.379	0.981	2	K.QLFSSLSFGILK.E
SW:PRKD_HUMAN	R04	7920	2	1657.9	(-0.2)	3.264	0.294	0.936	4	R.SDPGL*L*TNTMDVFK#.E
SW:PRKD_HUMAN	R03	5615	2	1058.2	(+0.6)	2.308	0.252	0.894	2	R.SIGEYDVL*R.G
SW:PRKD_HUMAN	R04	1832	2	1474.6	(-0.2)	2.437	0.213	0.726	3	R.SL*GPPQGEEDSVPR.D
SW:PRKD_HUMAN	R03	7949	3	3268.5	(-0.7)	5.211	0.497	0.999	2	R.SSFDWL*TGSSTDP*VDHTSPSSDSL*L*FAHK#.R
SW:PRKD_HUMAN	R04	8180	3	3268.5	(-0.5)	6.394	0.490	1.000	2	R.SSFDWL*TGSSTDP*VDHTSPSSDSL*L*FAHK#.R
SW:PRKD_HUMAN	R03	7623	2	1848.1	(-0.5)	2.552	0.301	0.862	3	R.TVGAL*QVL*GTEAQSSL*L*K#.A
SW:PRKD_HUMAN	R05	7862	2	1848.1	(-0.2)	3.091	0.313	0.935	3	R.TVGAL*QVL*GTEAQSSL*L*K#.A
SW:PRKD_HUMAN	R03	4501	2	1188.3	(-0.5)	2.309	0.212	0.734	3	R.VTEL*AL*TASDR.Q
SW:PRKD_HUMAN	R04	4772	2	1176.3	(+0.4)	3.384	0.516	1.000	3	R.VTELALTASDR.Q
SW:PRKD_HUMAN	R04	4756	2	1188.3	(-0.4)	2.256	0.227	0.747	3	R.VTEL*AL*TASDR.Q
SW:PRKD_HUMAN	R05	4880	2	1176.3	(+0.2)	3.193	0.494	0.999	3	R.VTELALTASDR.Q
SW:PRKD_HUMAN	R05	4840	2	1188.3	(+0.2)	2.541	0.424	0.973	3	R.VTEL*AL*TASDR.Q
SW:PRKD_HUMAN	R04	5532	2	1480.7	(+0.2)	3.262	0.291	0.939	3	R.VVQM@L*GSL*GGQINK#.N
SW:PRKD_HUMAN	R08	10977	3	2202.5	(+0.0)	4.279	0.359	0.997	2	K.L*QSVQAL*TEIQEFISFISK#.Q
SW:PRO1_HUMAN	R25	7472	2	1491.7	(+0.8)	2.963	0.328	0.957	2	R.SSFYVNGL*TL*GGQK#.C
SW:PRO1_HUMAN	R26	7052	2	1471.7	(-0.2)	3.729	0.464	1.000	2	R.SSFYVNGLTLGGQK.C
SW:PRO1_HUMAN	R25	8644	2	1659.0	(-0.1)	2.354	0.285	0.789	2	K.TFVNITPAEVGL*VGK#.D
SW:PRO1_HUMAN	R26	8448	3	1645.0	(+0.9)	4.225	0.422	0.999	2	K.TFVNITPAEVGLVVGK.D
SW:PRO1_HUMAN	R26	8452	2	1659.0	(+0.3)	3.266	0.470	0.988	2	K.TFVNITPAEVGL*VGK#.D
SW:PRO1_HUMAN	R26	8476	2	1645.0	(-0.7)	3.029	0.241	0.895	2	K.TFVNITPAEVGLVVGK.D
SW:PTB_HUMAN	R15	6073	2	1440.6	(+0.3)	3.254	0.424	0.986	3	R.GQPIYQFSNHK#.E
SW:PTB_HUMAN	R14	1542	2	998.1	(+0.4)	2.416	0.249	0.924	3	K.HQNVQL*PR.E
SW:PTB_HUMAN	R15	1304	2	998.1	(+0.0)	2.535	0.268	0.928	3	K.HQNVQL*PR.E
SW:PTB_HUMAN	R15	8431	2	2300.6	(+0.4)	4.550	0.520	1.000	3	R.IAIPGL*AGAGNSVL*L*VSNL*NPER.V
SW:PTB_HUMAN	R15	10927	2	2516.0	(-0.8)	2.280	0.263	0.451	3	R.IIVENL*FYPVTL*DVL*HQIFSK#.F
SW:PTB_HUMAN	R14	9069	2	2011.3	(-0.9)	2.650	0.363	0.815	3	K.L*PIDVTEGEVISL*GL*PFGK#.V
SW:PTB_HUMAN	R15	8871	2	1985.3	(-0.4)	5.017	0.629	1.000	3	K.LPIDVTEGEVISLGLPFGK.V
SW:PTB_HUMAN	R15	8863	2	2011.3	(-0.6)	3.906	0.561	1.000	3	K.L*PIDVTEGEVISL*GL*PFGK#.V
SW:PTB_HUMAN	R15	7795	3	2264.5	(-0.5)	4.223	0.515	1.000	3	K.NNQFQAL*L*QYADPVSAQHAH#.L
SW:PTB_HUMAN	R15	7813	3	2244.5	(-0.7)	4.141	0.540	1.000	3	K.NNQFQALLQYADPVSAQHAH.L
SW:PTB_HUMAN	R17	8070	3	2244.5	(+0.9)	4.851	0.507	0.999	3	K.NNQFQALLQYADPVSAQHAH.L
SW:PTB_HUMAN	R15	5467	2	1107.3	(+0.8)	3.207	0.288	0.974	3	K.VLFSSNGGVVK.G
SW:PTB_HUMAN	R15	5501	2	1121.3	(+0.2)	2.289	0.397	0.937	3	K.VL*FSSNGGVVK#.G
SW:PTB_HUMAN	R14	9705	3	2052.4	(+1.0)	4.624	0.454	0.930	3	R.VTPQSL*FIL*FGVYGDVQR.V
SW:PTB_HUMAN	R17	8084	3	2264.5	(-0.7)	4.152	0.450	0.999	3	K.NNQFQAL*L*QYADPVSAQHAH#.L
SW:PTCA_HUMAN	R20	6178	2	856.0	(+1.0)	2.518	0.356	0.976		R.L*GAAL*WGR.T
SW:PTCA_HUMAN	R20	5952	2	1095.2	(+0.7)	2.470	0.295	0.801		R.AAGGQGLHVTAL.-

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:PTN1_HUMAN	R16	6320	2	1541.7	(+0.6)	4.266	0.479	0.997	4	K.FIMGDSVVDQWQW.E
SW:PTN1_HUMAN	R16	5360	2	1565.7	(-0.2)	3.650	0.443	0.998	4	K.FIM@GDSVVDQWQW#.E
SW:PTN1_HUMAN	R16	7260	2	1212.4	(+0.2)	3.017	0.430	0.979	4	R.FSYL*AVIEGAK#.F
SW:PTN1_HUMAN	R16	6328	2	1258.5	(+0.2)	2.766	0.463	0.984	4	R.MGL*IQTADQL*.R.F
SW:R11A_HUMAN	R22	6978	2	1208.3	(+0.9)	2.859	0.271	0.964	3	R.DDEYDYLK.V
SW:R11A_HUMAN	R22	6970	2	1222.3	(+0.3)	2.767	0.465	0.988	3	R.DDEYDYL*FK#.V
SW:R11A_HUMAN	R22	7178	2	1656.9	(+0.1)	4.672	0.492	0.999	3	R.DHADSNIWIM@L*VGNK#.S
SW:R11A_HUMAN	R22	7820	3	1640.9	(+1.0)	4.477	0.423	0.999	3	R.DHADSNIWIML*VGNK#.S
SW:R11A_HUMAN	R22	8082	2	1290.5	(+0.5)	4.017	0.431	1.000	3	R.GAVGALLVYDIK.H
SW:R11A_HUMAN	R22	8006	2	1310.5	(-0.0)	3.409	0.353	0.970	3	R.GAVGAL*L*VYDIK#.H
SW:R11A_HUMAN	R22	10760	2	1290.5	(+0.7)	2.455	0.349	0.942	3	R.GAVGALLVYDIK.H
SW:R11A_HUMAN	R22	11547	2	1290.5	(-0.4)	2.231	0.450	0.961	3	R.GAVGALLVYDIK.H
SW:R11A_HUMAN	R22	4476	2	1161.3	(+0.3)	2.563	0.458	0.988	3	K.HLTYENVER.W
SW:R11A_HUMAN	R22	4884	2	981.1	(+0.3)	2.326	0.198	0.850	3	R.NEFNLESK.S
SW:R11A_HUMAN	R21	5746	2	1044.2	(+0.8)	2.609	0.387*	0.252	3	K.VVLIGDSGVGK.S
SW:R11A_HUMAN	R21	5750	2	1058.2	(+0.0)	2.245	0.303*	0.065	3	K.VVL*IGDSGVGK#.S
SW:R11A_HUMAN	R22	5846	2	1058.2	(-0.9)	3.250	0.315*	0.215	3	K.VVL*IGDSGVGK#.S
SW:R11A_HUMAN	R22	6014	2	1058.2	(+0.9)	2.403	0.283*	0.103	3	K.VVL*IGDSGVGK#.S
SW:R11A_HUMAN	R22	5582	2	1044.2	(+0.4)	2.380	0.348*	0.160	3	K.VVLIGDSGVGK.S
SW:R11A_HUMAN	R22	4270	2	1167.3	(+0.0)	2.218	0.384	0.948	3	K.HL*TYENVER.W
SW:R18B_HUMAN	R20	6994	3	2484.7	(+0.2)	5.088	0.561	0.999	1	K.APSEEDSL*SSVPISPYK#DEPWK#.Y
SW:R18B_HUMAN	R20	6988	3	2462.7	(+0.7)	4.742	0.515	0.996	1	K.APSEEDSLSSVPISPYKDEPWK.Y
SW:R18B_HUMAN	R20	9024	3	3665.0	(-0.1)	4.660	0.487	1.000	1	R.DLDFSTSHGAVSATPPAPTLVSGDPWYPWYNWK.Q
SW:R18B_HUMAN	R20	9026	3	3685.0	(-0.2)	4.277	0.508	1.000	1	R.DL*DFSTSHGAVSATPPAPTL*VSGDPWYPWYNWK#.Q
SW:R18B_HUMAN	R20	2186	3	2161.4	(+0.6)	3.810	0.317	0.991	2	R.L*YQGH*QEESGPPPEM@PK#.M
SW:RA21_HUMAN	R09	6482	2	1328.4	(+0.0)	2.581	0.246	0.825		K.GGEADNL*DEFL*K#.E
SW:RA21_HUMAN	R09	6234	3	3115.2	(-0.1)	5.440	0.527	1.000		K.INHLEYEDQYKDDNFGEGNDGGILDDK.L
SW:RA21_HUMAN	R09	6226	3	3143.2	(-0.6)	4.573	0.414	0.990		K.INHL*EYEDQYK#DDNFGEGNDGGIL*DDK#.L
SW:RA21_HUMAN	R10	7565	3	3115.2	(+0.2)	6.850	0.584	1.000		K.INHLEYEDQYKDDNFGEGNDGGILDDK.L
SW:RA21_HUMAN	R10	7563	3	3143.2	(-0.7)	5.032	0.385	0.988		K.INHL*EYEDQYK#DDNFGEGNDGGIL*DDK#.L
SW:RA21_HUMAN	R10	7513	2	1436.6	(+0.5)	3.126	0.338	0.977		R.KGGEADNLDEFK.E
SW:RA21_HUMAN	R10	8451	2	1574.8	(+0.2)	3.369	0.354	0.977		K.L*FSL*PAQPL*WNNR.L
SW:RA21_HUMAN	R10	1400	2	1156.3	(+0.4)	2.400	0.302	0.938		R.L*QESVMEASR.T
SW:RA21_HUMAN	R10	7187	2	1152.4	(+0.5)	3.206	0.460	0.999	1	R.TSGHLLLVVR.I
SW:RA21_HUMAN	R10	7151	2	1170.4	(-0.6)	2.303	0.127	0.475	1	R.TSGHL*L*L*GVVR.I
SW:RA21_HUMAN	R10	7225	2	1170.4	(+0.1)	2.233	0.145	0.493	1	R.TSGHL*L*L*GVVR.I
SW:RAB7_HUMAN	R22	6394	2	1182.3	(+0.9)	2.439	0.246	0.891	1	R.DEFL*IQASPR.D
SW:RAB7_HUMAN	R23	6250	2	1176.3	(+0.7)	3.264	0.340	0.985	1	R.DEFLIQASPR.D
SW:RAB7_HUMAN	R23	6290	2	1182.3	(+0.9)	2.867	0.335	0.977	1	R.DEFL*IQASPR.D
SW:RAB7_HUMAN	R01	7863	2	1476.7	(-0.4)	2.580	0.323	0.927	2	R.DPENFPFVVLGNK.I
SW:RAB7_HUMAN	R02	7296	2	1476.7	(+0.3)	2.227	0.390	0.937	2	R.DPENFPFVVLGNK.I
SW:RAB7_HUMAN	R22	8108	2	1476.7	(-0.3)	4.140	0.530	1.000	2	R.DPENFPFVVLGNK.I
SW:RAB7_HUMAN	R22	8030	2	1476.7	(-0.4)	4.033	0.498	1.000	2	R.DPENFPFVVLGNK.I
SW:RAB7_HUMAN	R22	8026	2	1490.7	(-0.7)	3.087	0.370*	0.311	2	R.DPENFPFVVL*GNK#.I
SW:RAB7_HUMAN	R23	8022	2	1476.7	(+1.0)	4.137	0.509	1.000	2	R.DPENFPFVVLGNK.I
SW:RAB7_HUMAN	R23	8016	2	1490.7	(+0.2)	3.413	0.373	0.974	2	R.DPENFPFVVL*GNK#.I
SW:RAB7_HUMAN	R23	8098	2	1490.7	(+0.1)	2.934	0.308	0.922	2	R.DPENFPFVVL*GNK#.I
SW:RAB7_HUMAN	R23	8040	2	1476.7	(-0.3)	2.872	0.404	0.973	2	R.DPENFPFVVLGNK.I
SW:RAB7_HUMAN	R22	8618	2	1901.2	(-1.0)	2.437	0.209	0.431	2	R.GADCCVLVFDVTAPNTFK.T
SW:RAB7_HUMAN	R23	8582	2	1901.2	(-0.8)	2.716	0.310	0.791	2	R.GADCCVLVFDVTAPNTFK.T
SW:RAB7_HUMAN	R23	7450	2	1648.9	(-0.4)	2.735	0.449*	0.210	2	R.LVTMQIWDTAGQER.F
SW:RAB7_HUMAN	R22	7492	2	1980.2	(-0.7)	3.062	0.404	0.968	1	K.QETEVELYNEFPEPIK#.L
SW:RAB7_HUMAN	R22	7490	2	1966.2	(-0.7)	2.758	0.365	0.954	1	K.QETEVELYNEFPEPIK.L
SW:RAB7_HUMAN	R23	7538	2	1966.2	(+0.5)	4.369	0.510	0.993	1	K.QETEVELYNEFPEPIK.L
SW:RAB7_HUMAN	R22	5652	2	1212.4	(+0.5)	2.403	0.432	0.974	2	K.TSL*MNQYVNK#.K
SW:RAB7_HUMAN	R22	6218	2	1072.3	(+0.1)	2.477	0.158	0.605	2	K.VIIL*GDSGVGK#.T
SW:RAB7_HUMAN	R23	6092	2	1058.3	(+0.9)	2.622	0.200	0.866	2	K.VIILGDSGVGK.T
SW:RAB7_HUMAN	R27	5805	2	1058.3	(+0.9)	2.829	0.229	0.926	2	K.VIILGDSGVGK.T
SW:RAB7_HUMAN	R27	5413	2	1212.4	(-0.0)	2.445	0.348	0.922	2	K.TSL*MNQYVNK#.K
SW:RAB8_HUMAN	R22	8524	2	1586.8	(+0.9)	2.248	0.439	0.969	2	K.ANINVENAFFTL*AR.D
SW:RAB8_HUMAN	R23	6864	2	1072.3	(-0.6)	3.499	1.000*	0.622	15	K.LLLIGDSGVGK.T

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:RALY_HUMAN	R18	5569	2	1170.3	(-0.0)	3.806	0.292	0.974	3	K.K#SDVETIFSK#.Y
SW:RALY_HUMAN	R18	5663	2	1170.3	(+0.4)	3.102	0.417	0.987	3	K.K#SDVETIFSK#.Y
SW:RALY_HUMAN	R18	5671	2	1154.3	(-0.0)	2.692	0.352	0.964	3	K.KSDVETIFSK.Y
SW:RALY_HUMAN	R18	5587	2	1154.3	(-0.1)	2.434	0.328	0.935	3	K.KSDVETIFSK.Y
SW:RALY_HUMAN	R19	5740	2	1170.3	(-0.4)	3.702	0.443	1.000	3	K.K#SDVETIFSK#.Y
SW:RALY_HUMAN	R19	5774	2	1154.3	(+0.8)	3.396	0.456	1.000	3	K.KSDVETIFSK.Y
SW:RALY_HUMAN	R18	1326	2	1044.2	(+0.5)	3.022	0.277	0.964	2	R.L*EQIAAEQK#.A
SW:RALY_HUMAN	R18	1328	2	1030.2	(+0.6)	2.644	0.353	0.976	2	R.LEQIAAEQK.A
SW:RALY_HUMAN	R18	1352	2	1044.2	(-0.8)	2.448	0.338	0.821	2	R.L*EQIAAEQK#.A
SW:RALY_HUMAN	R19	1306	2	1030.2	(+0.8)	2.978	0.313	0.979	2	R.LEQIAAEQK.A
SW:RALY_HUMAN	R18	1124	2	989.1	(-0.2)	2.545	0.390	0.963	3	K.L*QASNVTNK#.N
SW:RALY_HUMAN	R18	6941	3	3553.5	(+0.4)	5.570	0.549	1.000	2	R.TRDDGDEEGL*L*THSEEL*EHSQDTDADDGAL*Q.-
SW:RALY_HUMAN	R18	6943	3	3529.5	(+0.3)	4.563	0.523	1.000	2	R.TRDDGDEEGLLTHSEEELEHSQDTDADDGALQ.-
SW:RALY_HUMAN	R18	6433	3	2251.6	(+0.9)	3.765	0.478	0.997	3	R.VLAGQTLDINMAGEPKPDRPK.G
SW:RALY_HUMAN	R19	6636	3	2279.6	(+0.1)	3.933	0.327*	0.008	3	R.VL*AGQTL*DIMMAGEPK#PDRPK#.G
SW:RALY_HUMAN	R19	1304	2	1044.2	(+0.1)	2.879	0.272	0.936	2	R.L*EQIAAEQK#.A
SW:RAN_HUMAN	R01	5767	2	1303.4	(-0.5)	2.663	0.334*	0.210	4	K.FNVWDTAGQEK#.F
SW:RAN_HUMAN	R02	5850	2	1295.4	(+0.3)	2.800	0.319*	0.390	4	K.FNVWDTAGQEK.F
SW:RAN_HUMAN	R01	8349	2	1786.0	(+0.1)	3.374	0.454	0.602	5	K.SNYNFEKPFLLWLAR.K
SW:RAN_HUMAN	R20	8382	2	1786.0	(-0.0)	3.474	0.429	0.580	5	K.SNYNFEKPFLLWLAR.K
SW:RAN_HUMAN	R21	8214	2	1786.0	(-0.1)	2.713	0.297	0.150	5	K.SNYNFEKPFLLWLAR.K
SW:RAN_HUMAN	R21	6256	2	1295.4	(-0.3)	2.242	0.310*	0.108	4	K.FNVWDTAGQEK.F
SW:RAPA_HUMAN	R22	9474	2	1495.7	(+0.9)	4.248	0.526	1.000	2	K.INVNEIFYDLVR.Q
SW:RAPA_HUMAN	R22	9476	2	1501.7	(+0.8)	3.770	0.482	1.000	2	K.INVNEIFYDL*VR.Q
SW:RAPA_HUMAN	R23	9384	2	1495.7	(+0.7)	4.352	0.519	0.997	2	K.INVNEIFYDLVR.Q
SW:RAPA_HUMAN	R23	9380	2	1501.7	(+0.8)	3.060	0.429	0.988	2	K.INVNEIFYDL*VR.Q
SW:RAPA_HUMAN	R24	9400	2	1501.7	(+0.9)	3.920	0.530	0.999	2	K.INVNEIFYDL*VR.Q
SW:RAPA_HUMAN	R23	5824	2	1006.2	(+0.1)	2.313	0.273	0.812	3	K.L*VVL*GSGGVGK#.S
SW:RAPA_HUMAN	R24	5922	2	1006.2	(+0.2)	2.751	0.268	0.898	3	K.L*VVL*GSGGVGK#.S
SW:RB10_HUMAN	R01	9057	2	1280.5	(+0.2)	2.482	0.422	0.970	1	K.AFL*TL*AEDIL*R.K
SW:RB10_HUMAN	R02	8252	2	1262.5	(+0.9)	3.797	0.432	1.000	1	K.AFLTLAEDILR.K
SW:RB10_HUMAN	R02	8250	2	1280.5	(+0.1)	2.741	0.390	0.971	1	K.AFL*TL*AEDIL*R.K
SW:RB10_HUMAN	R03	8557	2	1262.5	(+0.8)	3.604	0.485	1.000	1	K.AFLTLAEDILR.K
SW:RB10_HUMAN	R01	5967	3	2375.6	(-0.1)	3.878	0.325	0.916	1	K.TPVK#EPNSENVDISSGGVGTGWK#.S
SW:RB10_HUMAN	R03	8553	2	1280.5	(+0.0)	2.573	0.352	0.953	1	K.AFL*TL*AEDIL*R.K
SW:RB14_HUMAN	R22	6592	3	3152.4	(+0.1)	3.748	0.483	0.978	1	K.IYQNIQDGLDLNAAESGVQHKPSAPQGGR.L
SW:RB14_HUMAN	R01	7511	2	1644.9	(-0.3)	2.490	0.303	0.853	1	R.NL*TNPNTVIL*IGNK#.A
SW:RB14_HUMAN	R22	7764	2	1624.9	(+0.4)	3.146	0.465	0.969	1	R.NLTNPNTVILIGNK.A
SW:RB14_HUMAN	R22	7772	2	1644.9	(-0.9)	2.293	0.344	0.679	1	R.NL*TNPNTVIL*IGNK#.A
SW:RB14_HUMAN	R23	7826	2	1624.9	(+0.2)	3.728	0.436	1.000	1	R.NLTNPNTVILIGNK.A
SW:RB14_HUMAN	R22	7252	2	1663.8	(+0.1)	2.738	0.245	0.867	1	R.STYNHL*SSWL*TDAR.N
SW:RB14_HUMAN	R22	7192	2	1494.6	(+0.2)	3.833	0.472	1.000	1	K.TGENVEDAFLEAAK.K
SW:RB14_HUMAN	R22	7184	2	1508.6	(-0.3)	3.645	0.424	0.982	1	K.TGENVEDAFL*EAAK#.K
SW:RB14_HUMAN	R22	6416	2	1190.4	(+0.4)	2.509	0.271	0.898	1	K.YIIIGDM@GVGK#.S
SW:RB14_HUMAN	R23	6282	2	1190.4	(+0.1)	2.309	0.175	0.568	1	K.YIIIGDM@GVGK#.S
SW:RB18_HUMAN	R23	7240	2	1391.6	(+0.8)	3.187	0.374	0.984		R.GAQQVILVYDVTR.R
SW:RB18_HUMAN	R23	7268	2	1391.6	(-0.7)	2.314	0.299	0.863		R.GAQQVILVYDVTR.R
SW:RB18_HUMAN	R23	6562	2	1757.9	(-0.4)	3.620	0.542	1.000		K.IIQTPLWESENQNK.G
SW:RB18_HUMAN	R23	6564	2	1771.9	(-0.4)	3.494	0.475	1.000		K.IIQTPL*WESENQNK#.G
SW:RB18_HUMAN	R22	6626	2	1100.3	(+0.1)	2.538	0.157	0.631	1	K.IL*IIGESGVGK#.S
SW:RB18_HUMAN	R23	6496	2	1100.3	(+0.5)	3.387	0.451*	0.601	1	K.IL*IIGESGVGK#.S
SW:RB18_HUMAN	R22	6628	2	1260.4	(+0.7)	3.120	0.532	0.999		K.LAIWDTAGQER.F
SW:RB18_HUMAN	R23	6506	2	1266.4	(+0.5)	2.728	0.313	0.676		K.L*AIWDTAGQER.F
SW:RB18_HUMAN	R23	7622	2	1231.4	(+0.4)	3.515	0.196	0.942		R.NDIVNML*VGNK#.I
SW:RB18_HUMAN	R23	6608	2	1247.4	(-0.8)	2.657	0.149	0.391		R.NDIVNM@L*VGNK#.I
SW:RB18_HUMAN	R23	6502	2	1260.4	(+0.7)	2.276	0.444	0.977		K.LAIWDTAGQER.F
SW:RB21_HUMAN	R22	7218	2	1473.6	(+0.1)	4.226	0.298*	0.748	2	R.VNLAIWDTAGQER.F
SW:RB21_HUMAN	R22	6938	2	1360.6	(+0.3)	3.334	0.386	0.988		K.HITTLQASFLTK.K

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:RB2A_HUMAN	R23	8176	2	1731.9	(-0.5)	3.551	0.374*	0.519	1	R.DTFNHL*TTWL*EDAR.Q
SW:RB2A_HUMAN	R23	6810	2	1363.6	(+0.1)	2.497	0.266	0.869	4	R.EHGLIFMETSAK.T
SW:RB2A_HUMAN	R22	7722	2	1320.5	(+1.0)	2.517	0.214	0.832	4	R.GAAGALLVYDITR.R
SW:RB2A_HUMAN	R23	7760	2	1320.5	(-0.1)	2.869	0.326	0.946	4	R.GAAGALLVYDITR.R
SW:RB2A_HUMAN	R23	6824	2	1769.9	(-0.4)	3.840	0.398	0.979	2	K.IQEGVFDINNEANGIK#.I
SW:RB2A_HUMAN	R23	6774	2	1761.9	(+0.5)	3.301	0.457	0.977	2	K.IQEGVFDINNEANGIK.I
SW:RB2A_HUMAN	R23	1862	2	1045.1	(+0.2)	2.439	0.163	0.731	2	K.K#EEGEAFAR.E
SW:RB2A_HUMAN	R22	7134	2	1551.7	(-0.1)	4.707	0.488	1.000	3	K.LQIWDTAGQESFR.S
SW:RB2A_HUMAN	R23	7114	2	1551.7	(+0.3)	3.626	0.506	0.999	3	K.LQIWDTAGQESFR.S
SW:RB2A_HUMAN	R23	6592	2	1503.6	(-0.2)	3.039	0.394	0.967	1	K.TASNVEEAFINTAK#.E
SW:RB2A_HUMAN	R23	6590	2	1495.6	(-0.1)	2.916	0.422	0.977	1	K.TASNVEEAFINTAK.E
SW:RB2A_HUMAN	R23	7778	2	1332.5	(+0.3)	2.323	0.322	0.922	4	R.GAAGAL*L*VYDITR.R
SW:RB5A_HUMAN	R21	4908	2	1314.4	(-0.0)	2.934	0.270	0.919		R.GVDLTEPTQPTR.N
SW:RB5A_HUMAN	R22	4782	2	1320.4	(-0.1)	2.759	0.318	0.945		R.GVDL*TEPTQPTR.N
SW:RB5A_HUMAN	R22	4786	2	1314.4	(-0.2)	2.730	0.208	0.839		R.GVDLTEPTQPTR.N
SW:RB5A_HUMAN	R21	6504	2	1112.3	(+0.4)	2.436	0.307	0.919	7	K.L*VL*L*GESAVGK#.S
SW:RB5A_HUMAN	R22	6762	2	1086.3	(-0.9)	2.505	0.354*	0.073	7	K.LVLLGESAVGK.S
SW:RB5C_HUMAN	R21	4154	2	1300.4	(-0.1)	3.406	0.393	0.984	1	R.GVDLQENNPASR.S
SW:RB5C_HUMAN	R21	4076	2	1300.4	(-0.1)	3.303	0.403	0.984	1	R.GVDLQENNPASR.S
SW:RB5C_HUMAN	R21	4072	2	1306.4	(+0.6)	3.174	0.478	1.000	1	R.GVDL*QENNPASR.S
SW:RB5C_HUMAN	R21	4120	2	1306.4	(-0.8)	2.501	0.253	0.656	1	R.GVDL*QENNPASR.S
SW:RB5C_HUMAN	R22	8180	2	1577.9	(+0.4)	2.781	0.375*	0.242	1	K.TAM@NVNEIFMAIAK#.K
SW:RB5C_HUMAN	R22	2204	2	1306.4	(+0.8)	2.495	0.417	0.977	1	R.GVDL*QENNPASR.S
SW:RB6A_HUMAN	R22	7458	2	1396.6	(-0.3)	2.871	0.108	0.601	1	K.EL*NVMFIETSAK#.A
SW:RB6A_HUMAN	R22	7156	2	1276.5	(-0.1)	2.965	0.422	0.971	2	R.GSDVIIM@L*VGNK#.T
SW:RB6A_HUMAN	R22	5748	2	1446.6	(-0.4)	2.881	0.377	0.966	1	R.VAAALPGMESTQDR.S
SW:RB6A_HUMAN	R22	6920	2	1412.6	(-0.9)	2.503	0.317	0.740	1	K.EL*NVM@FIETSAK#.A
SW:RB8A_HUMAN	R23	5278	2	965.1	(+1.0)	3.038	0.371	0.985	1	K.FAEYGEIK#.N
SW:RB8A_HUMAN	R23	5282	2	957.1	(-0.5)	2.460	0.231	0.884	1	K.FAEYGEIK.N
SW:RB8A_HUMAN	R23	6426	2	1380.5	(+0.6)	2.822	0.411	0.980	1	K.GYTL*VEYETYK#.E
SW:RB8A_HUMAN	R24	6506	2	1366.5	(+0.9)	3.098	0.601	1.000	1	K.GYTLVEYETYK.E
SW:RB8A_HUMAN	R24	6500	2	1380.5	(+0.0)	2.477	0.312	0.899	1	K.GYTL*VEYETYK#.E
SW:RB8B_HUMAN	R01	8027	2	1542.7	(+0.1)	3.311	0.323	0.966		K.SSANVEEAFFTLAR.D
SW:RB8B_HUMAN	R23	8270	2	1548.7	(+0.6)	2.817	0.370	0.973		K.SSANVEEAFFTL*AR.D
SW:RB8B_HUMAN	R23	8276	2	1542.7	(+1.0)	2.311	0.114	0.441		K.SSANVEEAFFTLAR.D
SW:RB8B_HUMAN	R23	6186	2	907.1	(+0.9)	2.274	0.172*	0.207		K.L*AIDYGIK#.F
SW:RBB4_HUMAN	R15	5481	2	1137.2	(-0.2)	2.617	0.373	0.946	1	K.GEFGGFGSVSGK#.I
SW:RBB4_HUMAN	R16	5270	2	1137.2	(+0.9)	3.629	0.605	0.999	1	K.GEFGGFGSVSGK#.I
SW:RBB4_HUMAN	R16	5276	2	1129.2	(+0.7)	3.412	0.527	1.000	1	K.GEFGGFGSVSGK.I
SW:RBB4_HUMAN	R16	5162	2	1137.2	(+0.2)	2.938	0.595	1.000	1	K.GEFGGFGSVSGK#.I
SW:RBB4_HUMAN	R16	5196	2	1129.2	(-0.9)	2.744	0.451	0.943	1	K.GEFGGFGSVSGK.I
SW:RBB4_HUMAN	R16	6814	3	2875.1	(+0.8)	5.016	0.463	1.000	1	K.IGEEQSPEDAEDGPPPELLFIHGGHTAK.I
SW:RBB4_HUMAN	R16	6812	3	2895.1	(+0.3)	4.505	0.505	1.000	1	K.IGEEQSPEDAEDGPPEL*L*FIHGGHTAK#.I
SW:RBB4_HUMAN	R16	7072	3	3617.9	(-0.5)	7.002	0.618	1.000	1	K.L*HSFESHK#DEIFQVQWSPHNETIL*ASSGTDR.R
SW:RBB4_HUMAN	R16	6384	2	941.1	(+0.9)	2.418	0.339	0.973	3	K.L*MIWDTR.S
SW:RBB4_HUMAN	R16	10500	3	3828.4	(-0.2)	4.855	0.556	0.962		K.NTPFLYDLVMTHALEWPSLTAQWLDPVTRPEGK.D
SW:RBB4_HUMAN	R16	9220	3	3440.8	(-0.0)	6.506	0.637	1.000	1	K.TIFTGHTAVVEDVSVHLLHESLFGSVADDQK.L
SW:RBB4_HUMAN	R16	9210	3	3466.8	(-0.9)	5.193	0.473	1.000	1	K.TIFTGHTAVVEDVSVHLL*HESL*FGSVADDQK#.L
SW:RBB4_HUMAN	R15	6815	2	1486.6	(-0.0)	2.567	0.305	0.887	2	K.TPSSDVL*VFDYTK#.H
SW:RBB4_HUMAN	R16	6554	2	1486.6	(-0.2)	3.479	0.234	0.925	2	K.TPSSDVL*VFDYTK#.H
SW:RBB4_HUMAN	R17	7030	2	1472.6	(-0.1)	3.827	0.490	1.000	2	K.TPSSDVLVFDYTK.H
SW:RBB4_HUMAN	R17	7026	2	1486.6	(-0.8)	2.979	0.372	0.891	2	K.TPSSDVL*VFDYTK#.H
SW:RBB4_HUMAN	R20	6948	2	1486.6	(-0.1)	2.753	0.327	0.928	2	K.TPSSDVL*VFDYTK#.H
SW:RBB4_HUMAN	R23	7102	2	1486.6	(+0.4)	2.730	0.373	0.962	2	K.TPSSDVL*VFDYTK#.H
SW:RBMA_HUMAN	R08	7905	2	1731.9	(+0.5)	3.575	0.404	0.987	5	R.GFAFVEFSHL*QDATR.W
SW:RBMA_HUMAN	R08	5205	2	1198.4	(+0.2)	2.271	0.151	0.536	5	R.LDQQTLPLGGR.E
SW:RBMA_HUMAN	R08	5073	2	1366.5	(-0.6)	2.415	0.312	0.905	5	R.ML*PQAATEDDIR.G
SW:RBMA_HUMAN	R09	4244	2	1216.4	(-0.4)	2.207	0.192	0.629	5	R.L*DQQTL*PL*GGR.E

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta M$	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:RBP2_HUMAN	R06	7104	2	1730.8	(+0.1)	3.232	0.399	0.978	1	K.DTSFL*GSDDIGNIDVR.E
SW:RBP2_HUMAN	R04	6184	3	2426.5	(+0.3)	4.455	0.507	0.999	4	R.EDAL*DDSVSSSSVHASPL*ASSPVR.K
SW:RBP2_HUMAN	R04	7812	2	1591.8	(-0.4)	2.571	0.272	0.836	1	R.EL*L*QSFDSAL*QSVK#.S
SW:RBP2_HUMAN	R05	7822	2	1591.8	(-0.2)	2.844	0.312	0.920	1	R.EL*L*QSFDSAL*QSVK#.S
SW:RBP2_HUMAN	R04	7550	2	1618.9	(-0.4)	2.931	0.402	0.963	1	K.EL*VGPPL*AETVFTPK#.T
SW:RBP2_HUMAN	R04	7560	2	1598.9	(+0.8)	2.731	0.382	0.971	1	K.ELVGPPLAETVFTPK.T
SW:RBP2_HUMAN	R05	7634	2	1618.9	(-0.0)	3.852	0.517	1.000	1	K.EL*VGPPL*AETVFTPK#.T
SW:RBP2_HUMAN	R06	7704	2	1618.9	(-0.3)	3.104	0.478	0.981	1	K.EL*VGPPL*AETVFTPK#.T
SW:RBP2_HUMAN	R03	5321	2	1110.2	(-0.3)	2.420	0.133	0.642	2	R.FDAEVSQWK.E
SW:RBP2_HUMAN	R04	5610	2	1110.2	(+0.3)	2.512	0.248	0.924	2	R.FDAEVSQWK.E
SW:RBP2_HUMAN	R04	5614	2	1118.2	(+1.0)	2.325	0.342	0.944	2	R.FDAEVSQWK#.E
SW:RBP2_HUMAN	R05	5718	2	1118.2	(+0.6)	2.349	0.330	0.929	2	R.FDAEVSQWK#.E
SW:RBP2_HUMAN	R06	5716	2	1118.2	(+0.0)	2.307	0.268	0.840	2	R.FDAEVSQWK#.E
SW:RBP2_HUMAN	R06	5612	2	1079.2	(+0.7)	2.231	0.280	0.881	2	K.FEEAQSIL*K#.A
SW:RBP2_HUMAN	R04	7292	2	1469.6	(+1.0)	3.148	0.567	0.990	2	R.FGESTTGFNFSEFK.S
SW:RBP2_HUMAN	R04	7286	2	1477.6	(+0.2)	2.804	0.310	0.918	2	R.FGESTTGFNFSEFK#.S
SW:RBP2_HUMAN	R05	7410	2	1477.6	(+0.2)	4.198	0.435	0.995	2	R.FGESTTGFNFSEFK#.S
SW:RBP2_HUMAN	R05	7414	2	1469.6	(+1.0)	2.648	0.337	0.949	2	R.FGESTTGFNFSEFK.S
SW:RBP2_HUMAN	R03	6191	3	2645.8	(+0.5)	4.633	0.487	0.990	1	K.FGHVDQENSPSFM@FQGSSNTEFK#.S
SW:RBP2_HUMAN	R04	6460	3	2645.8	(+0.6)	5.465	0.513	1.000	1	K.FGHVDQENSPSFM@FQGSSNTEFK#.S
SW:RBP2_HUMAN	R05	6568	3	2645.8	(+0.9)	4.384	0.510	1.000	1	K.FGHVDQENSPSFM@FQGSSNTEFK#.S
SW:RBP2_HUMAN	R05	7026	3	2629.8	(+0.5)	3.907	0.421	0.999	1	K.FGHVDQENSPSFM@FQGSSNTEFK#.S
SW:RBP2_HUMAN	R04	1772	2	1214.3	(+0.0)	2.919	0.185	0.825	3	K.FGISEPGNQEK#.K
SW:RBP2_HUMAN	R05	1742	2	1206.3	(+0.8)	2.849	0.417	0.985	3	K.FGISEPGNQEK.K
SW:RBP2_HUMAN	R05	1734	2	1214.3	(+0.1)	2.391	0.140	0.500	3	K.FGISEPGNQEK#.K
SW:RBP2_HUMAN	R06	1696	2	1214.3	(+0.3)	2.296	0.158	0.596	3	K.FGISEPGNQEK#.K
SW:RBP2_HUMAN	R04	8626	2	1684.9	(+0.4)	4.612	0.518	1.000	1	R.FLGLLYELEENTDK.A
SW:RBP2_HUMAN	R05	8494	2	1684.9	(+0.3)	3.114	0.484	0.991	1	R.FLGLLYELEENTDK.A
SW:RBP2_HUMAN	R06	8746	2	1716.9	(+0.2)	3.982	0.420	1.000	1	R.FL*GL*L*YEL*EENTDK#.A
SW:RBP2_HUMAN	R03	5289	2	1112.3	(+1.0)	2.237	0.226	0.762	1	K.GHVSLAAELSK.E
SW:RBP2_HUMAN	R04	5592	2	1112.3	(+0.5)	3.033	0.406	0.987	1	K.GHVSLAAELSK.E
SW:RBP2_HUMAN	R04	5580	2	1132.3	(-0.3)	2.229	0.363	0.906	1	K.GHVSL*AAEL*SK#.E
SW:RBP2_HUMAN	R05	5714	2	1112.3	(+0.7)	2.745	0.386	0.980	1	K.GHVSLAAELSK.E
SW:RBP2_HUMAN	R04	6920	3	3427.6	(-0.6)	5.052	0.473	1.000	2	K.GSGTGAAGASDTTIK#PNPENTGPTL*EWDNYDL*R.E
SW:RBP2_HUMAN	R03	5965	3	2475.5	(-0.1)	4.752	0.419	0.993	1	K.HDGTGGQSIYGDK#FEDENFDVK#.H
SW:RBP2_HUMAN	R04	6282	3	2459.5	(+1.0)	5.234	0.622	1.000	1	K.HDGTGGQSIYGDK#FEDENFDVK.H
SW:RBP2_HUMAN	R04	6276	3	2475.5	(+0.5)	4.997	0.547	1.000	1	K.HDGTGGQSIYGDK#FEDENFDVK#.H
SW:RBP2_HUMAN	R06	6610	2	941.1	(+0.9)	2.458	0.424	0.980	1	K.HVVFQVVK#.D
SW:RBP2_HUMAN	R04	6252	2	1208.4	(+0.8)	3.332	0.482	1.000	2	K.IAVAVL*EETTR.E
SW:RBP2_HUMAN	R04	5094	2	1405.5	(-0.1)	3.897	0.314	0.979	1	K.IIDSDSNLSVVK.K
SW:RBP2_HUMAN	R04	5084	2	1419.5	(-0.7)	3.352	0.280	0.944	1	K.IIDSDSNL*SVVK#.K
SW:RBP2_HUMAN	R06	5294	2	1405.5	(-0.1)	2.960	0.340	0.961	1	K.IIDSDSNLSVVK.K
SW:RBP2_HUMAN	R04	1048	2	1008.1	(+0.6)	2.735	0.178	0.911	5	K.ILQNYDNK.Q
SW:RBP2_HUMAN	R04	5278	3	2293.5	(+0.4)	5.396	0.480	1.000	1	K.K#SEK#PL*ENGTGFQAQDISGQK#.N
SW:RBP2_HUMAN	R04	5434	3	2293.5	(-0.3)	4.505	0.480	0.999	1	K.K#SEK#PL*ENGTGFQAQDISGQK#.N
SW:RBP2_HUMAN	R05	5484	3	2293.5	(-0.5)	4.986	0.399	0.992	1	K.K#SEK#PL*ENGTGFQAQDISGQK#.N
SW:RBP2_HUMAN	R02	6062	2	1354.6	(+0.4)	2.997	0.373	0.976	3	R.L*L*VQHEINTL*R.A
SW:RBP2_HUMAN	R03	5949	2	1354.6	(+0.1)	2.373	0.383	0.952	3	R.L*L*VQHEINTL*R.A
SW:RBP2_HUMAN	R06	6338	2	1336.6	(+0.7)	3.001	0.275	0.955	3	R.LLVQHEINTLR.A
SW:RBP2_HUMAN	R06	6326	2	1354.6	(-0.3)	2.336	0.333	0.916	3	R.L*L*VQHEINTL*R.A
SW:RBP2_HUMAN	R04	1534	3	2417.4	(+0.5)	5.297	0.556	1.000	3	K.L*NQSGTSSVGTDEESDVTQEEER.D
SW:RBP2_HUMAN	R04	7954	2	2110.3	(+1.0)	5.681	0.609	0.998	1	K.NL*FASFPTEESSINYTFK#.T
SW:RBP2_HUMAN	R03	5799	3	2525.5	(+0.4)	5.311	0.560	1.000	1	K.NRPDYVSEEEEEDEDFETAVK#.K
SW:RBP2_HUMAN	R04	6124	3	2525.5	(+0.0)	4.957	0.521	0.932	1	K.NRPDYVSEEEEEDEDFETAVK#.K
SW:RBP2_HUMAN	R04	6126	3	2517.5	(+0.8)	4.883	0.539	1.000	1	K.NRPDYVSEEEEEDEDFETAVK.K
SW:RBP2_HUMAN	R06	6172	3	2525.5	(+0.8)	3.872	0.493	1.000	1	K.NRPDYVSEEEEEDEDFETAVK#.K
SW:RBP2_HUMAN	R06	7362	2	1370.6	(+0.4)	2.276	0.208	0.757	3	K.NSIPEPIDPLFK.H
SW:RBP2_HUMAN	R04	4872	3	1839.0	(+0.9)	3.821	0.535	1.000	1	K.NVSGISFTENM@GSSQQK#.N
SW:RBP2_HUMAN	R04	4838	2	1839.0	(-0.7)	3.419	0.523	1.000	1	K.NVSGISFTENM@GSSQQK#.N
SW:RBP2_HUMAN	R06	6796	2	1554.7	(+0.2)	2.696	0.457	0.971	2	K.SDAGNL*NFFEQVAK#.K
SW:RBP2_HUMAN	R04	5350	3	2157.3	(-0.5)	4.270	0.429	0.991	1	K.SEK#PL*ENGTGFQAQDISGQK#.N
SW:RBP2_HUMAN	R04	8330	3	2599.9	(+0.2)	4.883	0.466	1.000	2	R.SFVWHALDYADELPKPEQLAIR.F
SW:RBP2_HUMAN	R05	6162	2	1310.4	(+0.6)	2.879	0.239	0.920	1	K.SGEEDEEIL*FK#.E
SW:RBP2_HUMAN	R06	6162	2	1296.4	(+0.0)	2.329	0.216	0.752	1	K.SGEEDEEILFK.E
SW:RBP2_HUMAN	R04	6354	2	1012.1	(+0.4)	2.510	0.429	0.979	5	K.SGFEGMFTK#.K
SW:RBP2_HUMAN	R05	6434	2	1004.1	(+0.2)	3.194	0.381	0.985	5	K.SGFEGMFTK.K

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:RBP2_HUMAN	R05	6424	2	1012.1	(+0.6)	2.651	0.405	0.980	5	K.SGFEGMFTK#.K
SW:RBP2_HUMAN	R04	4728	2	1282.4	(+0.1)	3.187	0.525	1.000	1	K.SGSSFVHQASFK.F
SW:RBP2_HUMAN	R04	8698	3	2580.9	(+0.2)	3.738	0.509	1.000	2	K.SKPFAPGNSSATGSLFGFSFNAPLK.S
SW:RBP2_HUMAN	R04	4106	2	1153.2	(-0.0)	2.542	0.448	0.970	3	K.STSGEGFQFGK#.K
SW:RBP2_HUMAN	R04	4250	2	1153.2	(-0.2)	2.530	0.430	0.965	3	K.STSGEGFQFGK#.K
SW:RBP2_HUMAN	R04	4226	2	1145.2	(+0.1)	2.489	0.454	0.973	3	K.STSGEGFQFGK#.K
SW:RBP2_HUMAN	R04	4152	2	1145.2	(-0.3)	2.488	0.444	0.975	3	K.STSGEGFQFGK#.K
SW:RBP2_HUMAN	R04	4298	2	1145.2	(+0.1)	2.450	0.356	0.945	3	K.STSGEGFQFGK#.K
SW:RBP2_HUMAN	R04	4322	2	1153.2	(-0.4)	2.290	0.412	0.944	3	K.STSGEGFQFGK#.K
SW:RBP2_HUMAN	R04	4178	2	1153.2	(-0.7)	2.265	0.465	0.963	3	K.STSGEGFQFGK#.K
SW:RBP2_HUMAN	R05	2518	2	1153.2	(-0.2)	2.597	0.514	0.982	3	K.STSGEGFQFGK#.K
SW:RBP2_HUMAN	R06	2454	2	1153.2	(+0.6)	2.338	0.430	0.969	3	K.STSGEGFQFGK#.K
SW:RBP2_HUMAN	R04	1190	2	1030.1	(-0.4)	2.210	0.196	0.611	4	R.SVEL*NPTQK#.D
SW:RBP2_HUMAN	R04	5326	2	1345.4	(+0.1)	2.793	0.160	0.768	1	K.TGSGLSNFYDQR.E
SW:RBP2_HUMAN	R03	5397	2	1064.2	(-0.1)	2.699	0.242	0.917	4	K.TPELAEFEK.Q
SW:RBP2_HUMAN	R04	5704	2	1064.2	(+0.5)	2.999	0.215	0.951	4	K.TPELAEFEK.Q
SW:RBP2_HUMAN	R04	5696	2	1078.2	(+0.5)	2.859	0.264	0.950	4	K.TPEL*AEFEK#.Q
SW:RBP2_HUMAN	R06	5790	2	1078.2	(+0.5)	2.243	0.169	0.670	4	K.TPEL*AEFEK#.Q
SW:RBP2_HUMAN	R04	1450	2	1248.3	(+0.9)	3.183	0.521	1.000	1	K.VELVTGEEDEK.V
SW:RBP2_HUMAN	R04	1440	2	1262.3	(-0.6)	2.630	0.235	0.836	1	K.VEL*VTGEEDEK#.V
SW:RBP2_HUMAN	R07	7353	2	1469.6	(+0.1)	2.880	0.431	0.979	2	R.FGESTTGFNFSFK.S
SW:RCC1_HUMAN	R17	7756	2	1420.6	(+0.7)	3.005	0.377	0.975	1	R.DNNGVIGL*L*EPMK#.K
SW:RCC1_HUMAN	R17	1710	2	1003.1	(+0.5)	2.502	0.256	0.918	1	R.LGLGEGAEK.S
SW:RCC1_HUMAN	R17	1706	2	1023.1	(+0.3)	2.422	0.324	0.935	1	R.L*GL*GEGAEK#.S
SW:RCC1_HUMAN	R17	8240	3	2995.3	(+0.4)	5.732	0.609	1.000	1	R.SHSTEPGLVLTGQGDVGLGLGENVMER.K
SW:RCC1_HUMAN	R17	6110	2	946.1	(+0.6)	2.402	0.364	0.973	1	R.VPELFANR.G
SW:RCN1_HUMAN	R17	6524	3	1951.1	(+0.9)	4.500	0.471	1.000		R.HWILPQDYDHAQAEAR.H
SW:RCN1_HUMAN	R17	2394	2	1281.4	(+0.4)	2.291	0.346	0.945		K.TFDQLTPDESK.E
SW:RCN2_HUMAN	R17	7840	2	1943.1	(+0.2)	4.730	0.439	0.999		R.WDPTANEDPEWILVEK.D
SW:RCN2_HUMAN	R17	7412	2	1727.9	(-0.6)	3.021	0.356	0.951		R.EAL*L*GVQEDVDEYVK#.L
SW:RED_HUMAN	R12	790	2	967.0	(+0.8)	2.223	0.375	0.931	4	R.AVGPTAEADK#.S
SW:RED_HUMAN	R11	6346	3	2891.0	(-0.5)	4.889	0.448	0.998	5	R.DSEPFSNPL*APDGHVDVDDPHSFHQSK#.L
SW:RED_HUMAN	R12	6200	3	2891.0	(+0.5)	4.557	0.511	0.998	5	R.DSEPFSNPL*APDGHVDVDDPHSFHQSK#.L
SW:RED_HUMAN	R11	7840	3	2500.7	(+0.5)	4.125	0.472	1.000	2	K.K#PPEADM@NIFEDIGDYVPSTTK#.T
SW:RED_HUMAN	R12	7340	2	1125.3	(+0.0)	2.216	0.288	0.877	2	K.L*TQIL*SYL*R.Q
SW:REQU_HUMAN	R16	5816	2	1549.7	(-0.3)	3.758	0.446	1.000	1	R.GPGL*ASGQL*YSYPAR.R
SW:REQU_HUMAN	R16	4708	2	1014.2	(+0.6)	2.965	0.311	0.981	1	K.LLGEQYYK.D
SW:RFA1_HUMAN	R13	7673	3	2095.2	(+0.7)	4.026	0.404	0.994		K.DK#NEQAFEEVFQANFR.S
SW:RFA1_HUMAN	R13	8153	2	1625.8	(-0.3)	3.373	0.227	0.926		K.L*FSL*EL*VDESGEIR.A
SW:RFA1_HUMAN	R13	1712	2	1212.3	(+0.3)	3.267	0.404	0.988		K.VIDQQNGL*YR.C
SW:RFA3_HUMAN	R26	8658	2	2046.3	(-0.2)	3.583	0.402	0.984		K.IIHDFPQFYPL*GIVQHD.-
SW:RFA3_HUMAN	R26	10938	3	2512.8	(+0.9)	3.819	0.460	0.998		K.NGTIEL*MEPL*DEEISGIVEVVGR.V
SW:RFA3_HUMAN	R26	5882	2	1127.3	(-0.2)	2.490	0.298	0.899		K.M@FIL*SDGEGK#.N
SW:RFC1_HUMAN	R07	8575	2	1161.4	(+0.5)	2.560	0.299	0.928	4	R.GGIQEL*IGL*IK#.H
SW:RFC1_HUMAN	R07	5495	2	1087.3	(-0.6)	2.216	0.104	0.261	4	K.AAL*L*SGPPGVGK#.T
SW:RFC4_HUMAN	R18	9061	3	3088.4	(+0.6)	7.875	0.584	0.999	2	K.DLIDEGHAATQLVNQLHDVVVNNLSDK.Q
SW:RFC4_HUMAN	R18	9055	3	3120.4	(-0.7)	7.339	0.504	1.000	2	K.DL*IDEGHAATQL*VNQL*HDVVVNNL*SDK#.Q
SW:RFC4_HUMAN	R18	5405	2	1186.3	(+0.2)	2.398	0.219	0.784	2	K.NFAQL*TVSGSR.S
SW:RGP1_HUMAN	R13	7319	2	1437.5	(+0.3)	3.274	0.183	0.927	1	K.EIEDFDSLEALR.L
SW:RGP1_HUMAN	R13	5067	2	991.2	(+0.9)	2.725	0.365	0.978	1	K.GAVAMAETLK.T
SW:RGP1_HUMAN	R13	1492	2	1222.3	(+0.7)	3.266	0.505	0.995	1	R.L*EGNTVGVEAAR.V
SW:RGP1_HUMAN	R13	1496	2	1216.3	(+0.7)	3.223	0.473	1.000	1	R.LEGNTVGVEAAR.V
SW:RGP1_HUMAN	R13	7123	2	1478.6	(+0.5)	4.309	0.556	1.000	1	R.LENDGATALAEAFR.V
SW:RGP1_HUMAN	R13	7113	2	1490.6	(-0.0)	3.507	0.491	0.997	1	R.L*ENDGATAL*AEAFR.V
SW:RGP1_HUMAN	R13	2010	2	1733.8	(+0.2)	4.899	0.572	0.918	2	K.SSVL*IAQQTDTSDPEK#.V
SW:RGP1_HUMAN	R11	4378	2	1150.3	(+0.4)	2.373	0.431	0.970	1	K.TQVAGGQL*SFK#.G

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:RGP1_HUMAN	R13	4915	2	1136.3	(+0.5)	3.016	0.360	0.978	1	K.TQVAGGQLSFK.G
SW:RGP1_HUMAN	R13	4835	2	1136.3	(-0.5)	2.264	0.352	0.921	1	K.TQVAGGQLSFK.G
SW:RGP1_HUMAN	R11	5952	2	1408.6	(+1.0)	2.740	0.370	0.963	1	R.VINLNDNTFTEK.G
SW:RGP1_HUMAN	R13	6129	2	1422.6	(+0.1)	2.726	0.331	0.918	1	R.VINL*NDNTFTEK#.G
SW:RGP1_HUMAN	R14	5009	2	1136.3	(-0.1)	2.675	0.351	0.958	1	K.TQVAGGQLSFK.G
SW:RIB1_HUMAN	R13	7211	2	1320.5	(-0.4)	2.213	0.188	0.586	1	K.AL*TSEIAL*L*QSR.L
SW:RIB1_HUMAN	R01	7715	3	2589.9	(+0.5)	4.933	0.475	1.000	1	R.APDEL*HYTYL*DTFGRPVIVAYK#.K
SW:RIB1_HUMAN	R12	7692	3	2569.9	(+0.2)	4.865	0.549	1.000	1	R.APDELHYTYLDTFGRPVIVAYK.K
SW:RIB1_HUMAN	R12	7696	3	2589.9	(-0.1)	4.418	0.386	0.983	1	R.APDEL*HYTYL*DTFGRPVIVAYK#.K
SW:RIB1_HUMAN	R13	7891	3	2569.9	(+0.8)	5.520	0.577	0.999	1	R.APDELHYTYLDTFGRPVIVAYK.K
SW:RIB1_HUMAN	R01	8673	2	1660.9	(-0.9)	2.597	0.160	0.296	2	R.ATSFLLALEPELEAR.L
SW:RIB1_HUMAN	R01	8659	2	1684.9	(-0.6)	2.309	0.164	0.498	2	R.ATSFL*L*AL*EPEL*EAR.L
SW:RIB1_HUMAN	R02	7918	2	1684.9	(+0.1)	2.364	0.111	0.349	2	R.ATSFL*L*AL*EPEL*EAR.L
SW:RIB1_HUMAN	R03	8205	2	1660.9	(+0.3)	3.712	0.326	0.982	2	R.ATSFLLALEPELEAR.L
SW:RIB1_HUMAN	R13	8779	2	1684.9	(-0.5)	2.537	0.166	0.619	2	R.ATSFL*L*AL*EPEL*EAR.L
SW:RIB1_HUMAN	R13	8167	2	1992.2	(-0.5)	4.655	0.556	1.000	1	R.FVDHVFDEQVIDSLTVK.I
SW:RIB1_HUMAN	R13	13381	3	2006.2	(+0.7)	4.200	0.330	0.998	1	R.FVDHVFDEQVIDSL*TVK#.I
SW:RIB1_HUMAN	R13	13457	3	1992.2	(+1.0)	4.061	0.328	0.996	1	R.FVDHVFDEQVIDSLTVK.I
SW:RIB1_HUMAN	R14	8115	3	2006.2	(+0.7)	3.851	0.327	0.997	1	R.FVDHVFDEQVIDSL*TVK#.I
SW:RIB1_HUMAN	R01	1088	2	1433.4	(+0.4)	3.679	0.407	0.983	1	K.GEDEEENLEVR.E
SW:RIB1_HUMAN	R13	1452	2	1433.4	(+0.6)	3.424	0.389	0.986	1	K.GEDEEENLEVR.E
SW:RIB1_HUMAN	R01	8583	3	2884.3	(+0.7)	4.352	0.504	0.999	1	K.ISVIVETVYTHVHPYPTQITQSEK.Q
SW:RIB1_HUMAN	R01	8585	3	2898.3	(+0.1)	4.048	0.462	0.999	1	K.ISVIVETVYTHV*HPYPTQITQSEK#.Q
SW:RIB1_HUMAN	R02	7848	3	2884.3	(+0.9)	6.071	0.498	1.000	1	K.ISVIVETVYTHVHPYPTQITQSEK.Q
SW:RIB1_HUMAN	R02	7836	3	2898.3	(+1.0)	4.244	0.315	0.994	1	K.ISVIVETVYTHV*HPYPTQITQSEK#.Q
SW:RIB1_HUMAN	R03	8131	3	2884.3	(+0.6)	6.025	0.453	0.987	1	K.ISVIVETVYTHVHPYPTQITQSEK.Q
SW:RIB1_HUMAN	R03	8127	3	2898.3	(+0.7)	4.938	0.437	0.999	1	K.ISVIVETVYTHV*HPYPTQITQSEK#.Q
SW:RIB1_HUMAN	R12	8558	3	2884.3	(+0.4)	5.414	0.449	1.000	1	K.ISVIVETVYTHVHPYPTQITQSEK.Q
SW:RIB1_HUMAN	R12	8554	3	2898.3	(-0.2)	5.110	0.511	1.000	1	K.ISVIVETVYTHV*HPYPTQITQSEK#.Q
SW:RIB1_HUMAN	R13	8757	3	2884.3	(+1.0)	6.334	0.508	1.000	1	K.ISVIVETVYTHVHPYPTQITQSEK.Q
SW:RIB1_HUMAN	R13	8767	3	2898.3	(+0.3)	6.021	0.501	1.000	1	K.ISVIVETVYTHV*HPYPTQITQSEK#.Q
SW:RIB1_HUMAN	R13	8669	3	2898.3	(+0.5)	4.871	0.486	0.998	1	K.ISVIVETVYTHV*HPYPTQITQSEK#.Q
SW:RIB1_HUMAN	R13	8847	3	2884.3	(-0.7)	3.864	0.423	0.997	1	K.ISVIVETVYTHVHPYPTQITQSEK.Q
SW:RIB1_HUMAN	R01	1892	2	965.2	(+1.0)	2.646	0.241	0.935	1	R.LAHLGVQVK.G
SW:RIB1_HUMAN	R01	4257	2	1001.2	(-0.0)	2.398	0.325	0.854	1	K.L*PVAL*DPGAK#.I
SW:RIB1_HUMAN	R01	4337	2	1001.2	(+0.3)	2.223	0.118	0.453	1	K.L*PVAL*DPGAK#.I
SW:RIB1_HUMAN	R13	5543	2	1001.2	(+0.7)	2.227	0.359	0.936	1	K.L*PVAL*DPGAK#.I
SW:RIB1_HUMAN	R01	8303	3	2212.5	(+0.8)	5.400	0.504	0.999	1	K.NL*VEQHIQDIVVHYTFNK#.V
SW:RIB1_HUMAN	R12	8290	3	2198.5	(+0.8)	5.758	0.578	1.000	1	K.NLVEQHIQDIVVHYTFNK.V
SW:RIB1_HUMAN	R13	8449	3	2198.5	(+0.1)	5.211	0.578	1.000	1	K.NLVEQHIQDIVVHYTFNK.V
SW:RIB1_HUMAN	R01	7385	2	1312.4	(+0.7)	3.935	0.490	1.000	1	R.SEDLLDYGPF.R
SW:RIB1_HUMAN	R02	6998	2	1324.4	(+0.6)	2.336	0.440	0.977	1	R.SEDL*L*DYGPFR.D
SW:RIB1_HUMAN	R03	7039	2	1324.4	(+0.7)	2.414	0.434	0.979	1	R.SEDL*L*DYGPFR.D
SW:RIB1_HUMAN	R13	7577	2	1312.4	(+0.9)	2.528	0.461	0.985	1	R.SEDLLDYGPF.R
SW:RIB1_HUMAN	R13	7567	2	1324.4	(+0.3)	2.506	0.402	0.972	1	R.SEDL*L*DYGPFR.D
SW:RIB1_HUMAN	R13	7593	2	1312.4	(-0.9)	2.267	0.124	0.206	1	R.SEDLLDYGPF.R
SW:RIB1_HUMAN	R02	7952	3	2999.3	(-0.1)	4.921	0.445	1.000	1	K.THYIVGYNLPSYEYLYNLGDQYALK.M
SW:RIB1_HUMAN	R03	8253	3	2999.3	(+0.6)	4.727	0.443	0.999	1	K.THYIVGYNLPSYEYLYNLGDQYALK.M
SW:RIB1_HUMAN	R13	8855	3	2999.3	(+0.7)	5.384	0.562	0.998	1	K.THYIVGYNLPSYEYLYNLGDQYALK.M
SW:RIB1_HUMAN	R01	6565	2	1481.7	(+0.6)	3.330	0.391	0.985	1	K.TILPAAAQDVYYR.D
SW:RIB1_HUMAN	R02	6342	2	1487.7	(+0.8)	3.873	0.500	1.000	1	K.TIL*PAAAQDVYYR.D
SW:RIB1_HUMAN	R02	6332	2	1481.7	(+0.2)	3.430	0.422	0.986	1	K.TILPAAAQDVYYR.D
SW:RIB1_HUMAN	R03	6229	2	1481.7	(+0.3)	2.767	0.472	0.987	1	K.TILPAAAQDVYYR.D
SW:RIB1_HUMAN	R03	6233	2	1487.7	(+0.3)	2.446	0.327	0.937	1	K.TIL*PAAAQDVYYR.D
SW:RIB1_HUMAN	R12	6398	2	1487.7	(-0.1)	3.380	0.472	1.000	1	K.TIL*PAAAQDVYYR.D
SW:RIB1_HUMAN	R13	6735	2	1487.7	(+0.2)	3.034	0.379	0.972	1	K.TIL*PAAAQDVYYR.D
SW:RIB1_HUMAN	R13	2138	2	1071.2	(+0.8)	2.693	0.271	0.948		R.TVDLSSLAK.V
SW:RIB1_HUMAN	R13	12695	3	2152.4	(+0.8)	4.540	0.363	0.999	1	R.VIEVSHWGNIAVEENVDLK.H
SW:RIB1_HUMAN	R13	11483	3	2166.4	(+0.8)	4.327	0.345	0.998	1	R.VIEVSHWGNIAVEENVDL*K#.H
SW:RIB1_HUMAN	R13	13959	3	2152.4	(+0.8)	4.298	0.278	0.971	1	R.VIEVSHWGNIAVEENVDLK.H
SW:RIB1_HUMAN	R13	13453	3	2152.4	(+0.9)	4.232	0.307	0.995	1	R.VIEVSHWGNIAVEENVDLK.H
SW:RIB1_HUMAN	R13	13527	3	2152.4	(+0.6)	4.152	0.291	0.985	1	R.VIEVSHWGNIAVEENVDLK.H
SW:RIB1_HUMAN	R13	12623	3	2152.4	(+0.4)	4.128	0.333	0.997	1	R.VIEVSHWGNIAVEENVDLK.H
SW:RIB1_HUMAN	R13	11997	3	2166.4	(+0.5)	4.082	0.282	0.992	1	R.VIEVSHWGNIAVEENVDL*K#.H
SW:RIB1_HUMAN	R13	11901	3	2152.4	(+0.6)	4.020	0.270	0.982	1	R.VIEVSHWGNIAVEENVDLK.H



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta M$	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:RIB1_HUMAN	R13	12091	3	2166.4	(-0.1)	3.995	0.352	0.994	1	R.VIEVSHWGNIAVEENVDL*K#.H
SW:RIB1_HUMAN	R13	11975	3	2152.4	(+0.3)	3.947	0.323	0.985	1	R.VIEVSHWGNIAVEENVDLK.H
SW:RIB1_HUMAN	R13	13377	3	2152.4	(+0.8)	3.916	0.331	0.995	1	R.VIEVSHWGNIAVEENVDLK.H
SW:RIB1_HUMAN	R13	12477	3	2152.4	(-0.7)	3.890	0.220	0.899	1	R.VIEVSHWGNIAVEENVDLK.H
SW:RIB1_HUMAN	R13	12833	3	2166.4	(+0.4)	3.888	0.240	0.977	1	R.VIEVSHWGNIAVEENVDL*K#.H
SW:RIB1_HUMAN	R13	11665	3	2152.4	(+0.8)	3.883	0.275	0.987	1	R.VIEVSHWGNIAVEENVDLK.H
SW:RIB1_HUMAN	R13	12919	3	2152.4	(+0.7)	3.829	0.247	0.926	1	R.VIEVSHWGNIAVEENVDLK.H
SW:RIB1_HUMAN	R13	13817	3	2152.4	(+0.8)	3.762	0.153	0.818	1	R.VIEVSHWGNIAVEENVDLK.H
SW:RIB1_HUMAN	R13	13935	3	2166.4	(+0.8)	3.706	0.240	0.963	1	R.VIEVSHWGNIAVEENVDL*K#.H
SW:RIB1_HUMAN	R01	6805	2	1654.9	(+0.1)	5.021	0.607	0.999	1	K.VTAEVVLAHLGGGSTR.A
SW:RIB1_HUMAN	R01	6809	2	1666.9	(-0.4)	2.442	0.145	0.504	1	K.VTAEVVL*AHL*GGGSTR.A
SW:RIB1_HUMAN	R13	7009	2	1654.9	(-0.2)	4.858	0.581	0.997	1	K.VTAEVVLAHLGGGSTR.A
SW:RIB1_HUMAN	R13	6997	2	1666.9	(-0.4)	4.158	0.522	1.000	1	K.VTAEVVL*AHL*GGGSTR.A
SW:RIB1_HUMAN	R26	8960	2	1660.9	(+0.8)	2.325	0.288	0.875	2	R.ATSFLLALEPELEAR.L
SW:RIB2_HUMAN	R01	9653	2	1636.9	(-0.0)	4.523	0.492	0.997	4	K.EDQVIQLMNAIFSK.K
SW:RIB2_HUMAN	R01	9649	2	1650.9	(-0.9)	3.692	0.351	0.924	4	K.EDQVIQL*MNAIFSK#.K
SW:RIB2_HUMAN	R02	8820	2	1650.9	(+0.8)	2.788	0.283	0.904	4	K.EDQVIQL*MNAIFSK#.K
SW:RIB2_HUMAN	R01	8421	2	2610.9	(-0.8)	3.868	0.476	1.000	3	K.EETVLATVQALQTASHLSQQADLR.S
SW:RIB2_HUMAN	R01	8501	2	2610.9	(-0.9)	2.689	0.362	0.858	3	K.EETVLATVQALQTASHLSQQADLR.S
SW:RIB2_HUMAN	R01	7773	2	2135.4	(+0.5)	4.629	0.575	1.000	5	K.FPEEEAPSTVLSQNLFTPK.Q
SW:RIB2_HUMAN	R01	8391	3	2436.7	(+0.8)	4.483	0.525	1.000	3	K.KNFESLSEAFSVASAAVLSHNR.Y
SW:RIB2_HUMAN	R02	7728	3	2456.7	(+0.3)	5.521	0.610	1.000	3	K.K#NFESL*SEAFSVASAAVLSHNR.Y
SW:RIB2_HUMAN	R01	1918	2	1341.5	(-0.1)	2.915	0.306	0.934	4	K.L*MDHVGTEPSIK#.E
SW:RIB2_HUMAN	R01	9549	3	2945.4	(+0.2)	5.173	0.471	1.000	4	K.LMDHVGTEPSIKEDQVIQLMNAIFSK.K
SW:RIB2_HUMAN	R01	9547	3	2973.4	(-1.0)	3.926	0.274	0.527	4	K.L*MDHVGTEPSIK#EDQVIQL*MNAIFSK#.K
SW:RIB2_HUMAN	R02	6804	2	1867.2	(-0.8)	3.083	0.385	0.897	3	R.L*QVTNVL*SQPL*QTATVK#.L
SW:RIB2_HUMAN	R01	8965	2	2320.5	(-0.3)	3.664	0.476	1.000	3	K.NFESL*SEAFSVASAAVLSHNR.Y
SW:RIB2_HUMAN	R02	8148	3	2320.5	(-0.2)	3.876	0.388	0.996	3	K.NFESL*SEAFSVASAAVLSHNR.Y
SW:RIB2_HUMAN	R01	8617	2	1495.8	(+0.2)	3.496	0.425	0.983	4	K.NPIL*WNVADVVIK#.F
SW:RIB2_HUMAN	R01	8615	2	1481.8	(+0.4)	3.276	0.510	1.000	4	K.NPILWNVADVVIK.F
SW:RIB2_HUMAN	R02	7884	2	1495.8	(+0.3)	3.152	0.440	0.986	4	K.NPIL*WNVADVVIK#.F
SW:RIB2_HUMAN	R03	8157	2	1481.8	(+0.9)	3.582	0.540	1.000	4	K.NPILWNVADVVIK.F
SW:RIB2_HUMAN	R01	9427	2	1379.5	(+0.2)	3.727	0.463	1.000	4	R.SIVEEIEDL*VAR.L
SW:RIB2_HUMAN	R01	9429	2	1373.5	(+0.9)	2.496	0.505	0.988	4	R.SIVEEIEDLVAR.L
SW:RIB2_HUMAN	R02	8574	2	1373.5	(+0.9)	4.342	0.491	1.000	4	R.SIVEEIEDLVAR.L
SW:RIB2_HUMAN	R02	8572	2	1379.5	(+0.7)	3.662	0.444	1.000	4	R.SIVEEIEDL*VAR.L
SW:RIB2_HUMAN	R03	8891	2	1373.5	(+0.8)	3.785	0.498	1.000	4	R.SIVEEIEDLVAR.L
SW:RIB2_HUMAN	R03	8889	2	1379.5	(+0.6)	3.398	0.485	1.000	4	R.SIVEEIEDL*VAR.L
SW:RIB2_HUMAN	R04	9154	2	1373.5	(+0.8)	3.554	0.502	1.000	4	R.SIVEEIEDLVAR.L
SW:RIB2_HUMAN	R01	4319	2	1533.7	(+0.9)	3.743	0.450	0.996	4	K.TGQEVVFAEPDNK.N
SW:RIB2_HUMAN	R01	4399	2	1533.7	(+0.9)	3.740	0.416	0.991	4	K.TGQEVVFAEPDNK.N
SW:RIB2_HUMAN	R01	4149	2	1533.7	(+0.5)	3.716	0.256	0.966	4	K.TGQEVVFAEPDNK.N
SW:RIB2_HUMAN	R01	4269	2	1541.7	(-1.0)	3.701	0.432	1.000	4	K.TGQEVVFAEPDNK#.N
SW:RIB2_HUMAN	R01	4511	2	1541.7	(-0.2)	3.641	0.368	0.976	4	K.TGQEVVFAEPDNK#.N
SW:RIB2_HUMAN	R01	4481	2	1533.7	(+0.6)	3.560	0.461	1.000	4	K.TGQEVVFAEPDNK.N
SW:RIB2_HUMAN	R01	4241	2	1533.7	(-1.0)	2.937	0.324	0.861	4	K.TGQEVVFAEPDNK.N
SW:RIB2_HUMAN	R02	5332	2	1541.7	(+1.0)	4.312	0.404	1.000	4	K.TGQEVVFAEPDNK#.N
SW:RIB2_HUMAN	R04	5418	2	1541.7	(-0.1)	3.831	0.419	1.000	4	K.TGQEVVFAEPDNK#.N
SW:RIB2_HUMAN	R01	9211	3	2060.3	(+1.0)	4.580	0.538	0.998	3	K.TSFTPVGDVFEL*NFMNVK#.F
SW:RIB2_HUMAN	R01	6795	3	2510.8	(+0.6)	4.087	0.305	0.991	4	R.YHVPVVVVPEGSASDTHEQAIL*R.L
SW:RIB2_HUMAN	R01	6807	2	2510.8	(-0.5)	3.855	0.458	1.000	4	R.YHVPVVVVPEGSASDTHEQAIL*R.L
SW:RIB2_HUMAN	R01	6797	3	2504.8	(+0.8)	3.732	0.436	0.996	4	R.YHVPVVVVPEGSASDTHEQAILR.L
SW:RIB2_HUMAN	R02	6582	3	2504.8	(+0.3)	4.121	0.500	1.000	4	R.YHVPVVVVPEGSASDTHEQAILR.L
SW:RIB2_HUMAN	R03	6513	3	2504.8	(+0.3)	4.371	0.474	1.000	4	R.YHVPVVVVPEGSASDTHEQAILR.L
SW:RIB2_HUMAN	R01	2212	2	1079.2	(+0.6)	2.710	0.285	0.961	4	R.YIANTVELR.V
SW:RIB2_HUMAN	R04	9150	2	1379.5	(+0.3)	2.726	0.281	0.943	4	R.SIVEEIEDL*VAR.L
SW:RL18_HUMAN	R22	7836	2	1461.7	(+0.4)	3.725	0.543	1.000	2	K.ILTFDQLALDSPK.G
SW:RL18_HUMAN	R22	7832	2	1487.7	(+0.3)	2.959	0.513	1.000	2	K.IL*TFDQL*AL*DSPK#.G
SW:RL18_HUMAN	R23	7868	2	1487.7	(-0.5)	3.612	0.457	1.000	2	K.IL*TFDQL*AL*DSPK#.G
SW:RL18_HUMAN	R22	6126	2	1251.4	(+1.0)	2.355	0.177	0.740	2	R.TNSTFNQVVLK.R
SW:RL1X_HUMAN	R23	8308	2	1232.4	(+0.4)	3.118	0.475	1.000		R.FWYFVSQL*K#.K
SW:RL1X_HUMAN	R23	7736	2	912.1	(+1.0)	2.418	0.125	0.788		K.NFGIWL*R.Y

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:RL22_HUMAN	R25	6172	2	1243.4	(-0.1)	3.020	0.469	0.986	2	K.AGNLGGGVVTIER.S
SW:RL22_HUMAN	R25	6174	2	1249.4	(+0.1)	2.328	0.350	0.885	2	K.AGNL*GGGVVTIER.S
SW:RL22_HUMAN	R25	6810	2	1208.4	(+0.2)	3.022	0.467	0.987	2	K.ITVTSEVPFSK.R
SW:RL22_HUMAN	R25	6816	2	1216.4	(-0.0)	2.321	0.142	0.467	2	K.ITVTSEVPFSK#.R
SW:RL24_HUMAN	R23	7342	2	1262.5	(+1.0)	3.377	0.539	1.000		R.AITGASLADIMAK.R
SW:RL24_HUMAN	R23	7632	2	1193.4	(+0.7)	2.320	0.226	0.831		R.QINWTVLYR.R
SW:RL24_HUMAN	R23	6228	2	1292.5	(-0.7)	2.226	0.169	0.444		R.AITGASL*ADIM@AK#.R
SW:RL2B_HUMAN	R23	4894	2	1242.4	(-0.2)	2.894	0.449	0.553	3	K.VNTLIRPDGEK.K
SW:RL2B_HUMAN	R23	6246	2	1405.5	(+0.9)	2.317	0.372	0.952	4	R.LAPDYDALDVANK.I
SW:RL7_HUMAN	R20	6522	2	1183.4	(+0.8)	2.972	0.480	0.983	1	R.IAL*TDNAL*IAR.S
SW:RL7_HUMAN	R20	5288	2	980.1	(+0.1)	2.227	0.251	0.813	2	K.SVNEL*IYK#.R
SW:RL9_HUMAN	R22	6826	2	1185.3	(+0.1)	2.871	0.376	0.968	2	K.FL*DGIVYSEK#.G
SW:RL9_HUMAN	R22	7756	2	2114.4	(-0.9)	2.542	0.190	0.421		K.TILSNQTVDIPENV DITLK.G
SW:RLA2_HUMAN	R25	6216	2	1418.5	(-0.1)	2.687	0.379	0.961		K.ILDSVGI EADDDR.L
SW:RLA2_HUMAN	R25	6218	2	1424.5	(-0.0)	2.268	0.417	0.951		K.IL*DSVGI EADDDR.L
SW:RLA2_HUMAN	R25	7800	2	1265.4	(+0.4)	3.207	0.372	0.980		K.NIEDVIAQ GIGK#.L
SW:RLA2_HUMAN	R26	7526	2	1257.4	(+0.4)	3.459	0.498	1.000		K.NIEDVIAQ GIGK.L
SW:RM12_HUMAN	R23	6754	2	1375.6	(-0.6)	2.708	0.304	0.901	2	K.NYIQGINL*VQAK#.K
SW:RM12_HUMAN	R24	6294	2	1284.5	(+0.6)	2.367	0.299	0.875	2	K.KLVESLPQEIK.A
SW:RNP2_HUMAN	R13	8147	2	1286.4	(+0.3)	3.485	0.371	0.985	3	R.DL*EEFFSTVGK#.V
SW:RNP2_HUMAN	R13	9585	3	2392.8	(-0.4)	3.803	0.416	0.997	3	K.GIAYVEFVDVSSVPLAIGLTGQR.V
SW:RNP2_HUMAN	R13	6655	2	1830.9	(-0.4)	2.809	0.423	0.973	2	R.TDASSASSFLDSDELER.T
SW:RNP2_HUMAN	R13	7473	2	1566.9	(-0.1)	3.807	0.546	1.000	2	R.VL*GVPIIVQASQA EK#.N
SW:RNP2_HUMAN	R13	1922	2	997.1	(+0.6)	2.469	0.328	0.957	3	R.TGIDL*GTTGR.L
SW:ROA0_HUMAN	R19	8018	2	2179.3	(+0.7)	4.908	0.618	1.000	1	K.GDVAEGDLIEHFSQFGTVEK.A
SW:ROA0_HUMAN	R19	8000	3	2193.3	(+0.6)	4.688	0.527	0.999	1	K.GDVAEGDL*IEHFSQFGTVEK#.A
SW:ROA0_HUMAN	R19	8034	2	2179.3	(-0.8)	4.238	0.503	1.000	1	K.GDVAEGDLIEHFSQFGTVEK.A
SW:ROA0_HUMAN	R20	7808	2	2193.3	(+0.6)	4.178	0.513	0.999	1	K.GDVAEGDL*IEHFSQFGTVEK#.A
SW:ROA0_HUMAN	R19	7652	2	1691.9	(+0.6)	4.450	0.447	0.999	2	K.LFIGGLNVQTSSEGLR.G
SW:ROA0_HUMAN	R19	7648	2	1709.9	(-0.8)	3.090	0.321	0.870	2	K.L*FIGGL*NVQTSSEGL*R.G
SW:ROA0_HUMAN	R19	7760	2	1709.9	(+0.7)	2.572	0.385	0.957	2	K.L*FIGGL*NVQTSSEGL*R.G
SW:ROA0_HUMAN	R19	11182	2	1691.9	(+0.5)	2.475	0.340	0.940	2	K.LFIGGLNVQTSSEGLR.G
SW:ROA0_HUMAN	R20	7424	2	1709.9	(-0.4)	4.147	0.411	1.000	2	K.L*FIGGL*NVQTSSEGL*R.G
SW:ROA0_HUMAN	R26	7738	2	1691.9	(-0.2)	3.732	0.437	1.000	2	K.LFIGGLNVQTSSEGLR.G
SW:ROA1_HUMAN	R18	4737	2	1058.1	(+0.9)	2.240	0.290*	0.191	1	R.DYFEQY GK#.I
SW:ROA1_HUMAN	R19	2496	2	1058.1	(+0.9)	2.804	0.416*	0.506	1	R.DYFEQY GK#.I
SW:ROA1_HUMAN	R19	2414	2	1058.1	(+0.9)	2.725	0.322*	0.462	1	R.DYFEQY GK#.I
SW:ROA1_HUMAN	R19	2334	2	1058.1	(-1.0)	2.496	0.397	0.904	1	R.DYFEQY GK#.I
SW:ROA1_HUMAN	R19	2474	2	1050.1	(+1.0)	2.493	0.474*	0.390	1	R.DYFEQY GK.I
SW:ROA1_HUMAN	R19	4894	2	1058.1	(-0.3)	2.394	0.393*	0.204	1	R.DYFEQY GK#.I
SW:ROA1_HUMAN	R19	2310	2	1050.1	(-0.6)	2.314	0.442*	0.212	1	R.DYFEQY GK.I
SW:ROA1_HUMAN	R19	2580	2	1058.1	(+0.8)	2.312	0.420*	0.226	1	R.DYFEQY GK#.I
SW:ROA1_HUMAN	R19	4896	2	1050.1	(-0.1)	2.240	0.442*	0.176	1	R.DYFEQY GK.I
SW:ROA1_HUMAN	R19	4324	1	1058.1	(+0.2)	1.964	0.410*	0.000	1	R.DYFEQY GK#.I
SW:ROA1_HUMAN	R19	4402	1	1058.1	(+0.2)	1.907	0.290*	0.000	1	R.DYFEQY GK#.I
SW:ROA1_HUMAN	R21	5348	2	1050.1	(-0.5)	2.329	0.426*	0.219	1	R.DYFEQY GK.I
SW:ROA1_HUMAN	R23	5378	2	1050.1	(+0.1)	2.379	0.419*	0.245	1	R.DYFEQY GK.I
SW:ROA1_HUMAN	R18	1516	2	1438.6	(+0.5)	3.336	0.297	0.415	2	R.EDSQRPGAHLTVK.K
SW:ROA1_HUMAN	R21	4530	2	1438.6	(-0.3)	2.771	0.204	0.086	2	R.EDSQRPGAHLTVK.K
SW:ROA1_HUMAN	R18	988	2	1166.2	(+0.9)	2.510	0.261	0.885	5	K.EDTEEHHLR.D
SW:ROA1_HUMAN	R19	912	2	1172.2	(+0.9)	2.572	0.210	0.864	5	K.EDTEEHHL*R.D
SW:ROA1_HUMAN	R19	910	2	1166.2	(+1.0)	2.318	0.218	0.808	5	K.EDTEEHHLR.D
SW:ROA1_HUMAN	R20	1104	2	1166.2	(+0.9)	2.332	0.252	0.899	5	K.EDTEEHHLR.D
SW:ROA1_HUMAN	R19	7374	2	1708.8	(-0.5)	4.194	0.501	0.820	3	R.GFAFVTFDDHDSVDK#.I
SW:ROA1_HUMAN	R19	7786	2	1708.8	(+0.5)	2.496	0.372	0.945	3	R.GFAFVTFDDHDSVDK#.I
SW:ROA1_HUMAN	R23	7470	2	1708.8	(-0.3)	5.003	0.534	0.995	3	R.GFAFVTFDDHDSVDK#.I
SW:ROA1_HUMAN	R19	6272	3	1895.1	(+0.7)	4.303	0.490*	0.041	2	K.IFVGGIK#EDTEEHHL*R.D

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ROA1_HUMAN	R19	8102	2	1940.2	(-0.9)	3.271	0.371	0.925	1	R.K#L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	8070	2	1914.2	(-0.5)	2.851	0.422	0.974	1	R.KLFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R21	7760	2	1914.2	(+0.6)	3.620	0.431	0.990	1	R.KLFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R18	8279	2	1804.0	(-0.5)	3.324	0.346	0.969	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R18	8295	2	1786.0	(-0.4)	2.435	0.122	0.423	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	8488	2	1786.0	(-0.9)	4.818	0.424	0.996	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	8472	2	1804.0	(-0.3)	4.780	0.437	0.951	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	13274	2	1804.0	(+0.2)	4.644	0.468	1.000	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	9432	2	1804.0	(-0.1)	4.599	0.471	1.000	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	13198	2	1786.0	(+0.2)	4.571	0.436	0.999	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	12670	2	1786.0	(+0.6)	4.417	0.473	1.000	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	12316	2	1786.0	(+0.9)	4.359	0.451	0.996	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	12142	2	1804.0	(+0.4)	4.298	0.510	1.000	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	13718	2	1804.0	(+0.9)	4.149	0.494	0.999	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	13308	2	1786.0	(-0.6)	4.129	0.436	1.000	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	11980	2	1786.0	(+0.2)	4.110	0.367	0.985	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	9448	2	1786.0	(+0.3)	4.085	0.410	1.000	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	9122	2	1786.0	(+0.9)	4.070	0.317	0.985	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	13700	2	1786.0	(+1.0)	4.021	0.276	0.979	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	13122	2	1786.0	(+0.5)	4.019	0.484	1.000	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	10386	2	1804.0	(+0.3)	4.007	0.458	1.000	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	13836	2	1786.0	(+0.4)	3.992	0.404	0.991	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	10658	2	1804.0	(+0.3)	3.953	0.454	0.999	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	8672	2	1804.0	(+0.4)	3.909	0.365	0.987	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	12298	2	1804.0	(+0.3)	3.905	0.487	1.000	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	9674	2	1786.0	(+0.2)	3.904	0.450	0.825	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	9646	2	1804.0	(+0.2)	3.883	0.401	0.986	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	10294	2	1804.0	(+0.7)	3.856	0.376	0.984	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	13040	2	1786.0	(+0.7)	3.855	0.329	0.984	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	12862	2	1786.0	(+0.8)	3.846	0.437	1.000	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	10042	2	1804.0	(-0.5)	3.841	0.438	1.000	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	12406	2	1786.0	(+0.9)	3.837	0.398	0.990	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	12490	2	1786.0	(+0.5)	3.799	0.405	0.990	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	14140	2	1786.0	(+0.6)	3.767	0.438	1.000	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	12242	2	1786.0	(+0.6)	3.762	0.413	0.991	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	10208	2	1804.0	(+0.7)	3.737	0.412	0.990	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	13634	2	1804.0	(+0.3)	3.688	0.383	0.988	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	12684	2	1804.0	(+0.2)	3.677	0.350	0.978	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	13908	2	1786.0	(+0.5)	3.666	0.375	0.987	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	12222	2	1804.0	(+0.3)	3.645	0.506	1.000	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	11658	2	1786.0	(+0.1)	3.630	0.408	0.985	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	11242	2	1804.0	(+0.3)	3.592	0.484	0.999	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	11558	2	1804.0	(+0.4)	3.552	0.393	0.987	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	10526	2	1786.0	(+0.2)	3.500	0.367	0.978	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	11460	2	1786.0	(+0.4)	3.497	0.432	0.990	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	12608	2	1804.0	(-0.1)	3.466	0.332	0.969	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	8578	2	1804.0	(+0.6)	3.456	0.447	0.990	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	13026	2	1804.0	(+0.6)	3.432	0.423	0.989	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	9342	2	1804.0	(-1.0)	3.407	0.386	0.939	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	12066	2	1804.0	(+0.2)	3.391	0.365	0.975	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	12848	2	1804.0	(-0.4)	3.374	0.354	0.971	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	13882	2	1804.0	(-0.8)	3.364	0.448	0.958	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	12166	2	1786.0	(+0.4)	3.310	0.418	0.988	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	11890	2	1804.0	(+0.1)	3.194	0.453	0.984	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	10980	2	1804.0	(+0.7)	3.183	0.428	0.987	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	11082	2	1804.0	(+0.3)	3.179	0.415	0.986	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	12596	2	1786.0	(-0.7)	3.144	0.396	0.976	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	14106	2	1804.0	(-0.0)	3.141	0.346	0.964	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	12760	2	1804.0	(+0.1)	3.138	0.420	0.980	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	13958	2	1804.0	(+0.2)	3.137	0.418	0.979	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	11352	2	1804.0	(-0.1)	3.109	0.421	0.979	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	11158	2	1804.0	(+0.7)	3.100	0.432	0.987	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	13760	2	1786.0	(-0.4)	3.085	0.314	0.949	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	11348	2	1786.0	(+0.8)	3.029	0.360	0.975	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	11582	2	1786.0	(+0.1)	2.960	0.271	0.913	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	12786	2	1786.0	(-0.3)	2.940	0.443	0.979	1	K.LFIGGLSFETTDESLR.S

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ROA1_HUMAN	R19	12932	2	1804.0	(+0.8)	2.938	0.444	0.966	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	13392	2	1786.0	(+0.6)	2.777	0.459	0.985	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	11718	2	1804.0	(+0.2)	2.747	0.357	0.950	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	10468	2	1804.0	(-0.3)	2.652	0.365	0.925	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	13546	2	1786.0	(+0.4)	2.645	0.466	0.984	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	12090	2	1786.0	(-0.6)	2.641	0.368	0.948	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	11904	2	1786.0	(+0.1)	2.641	0.292	0.895	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	11272	2	1786.0	(-0.1)	2.626	0.233	0.813	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	13528	2	1804.0	(+0.5)	2.613	0.403	0.972	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	9232	2	1786.0	(+0.1)	2.525	0.118	0.454	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	12506	2	1786.0	(-0.8)	2.515	0.344	0.799	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	9516	2	1804.0	(-0.3)	2.494	0.284	0.862	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	10968	2	1786.0	(+0.8)	2.448	0.421	0.971	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	11384	2	1786.0	(-0.9)	2.423	0.283	0.641	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	11004	2	1804.0	(-0.8)	2.415	0.305	0.693	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	10796	2	1786.0	(+0.3)	2.369	0.364	0.945	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	11112	2	1786.0	(+0.7)	2.353	0.410	0.963	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	8866	2	1804.0	(+0.1)	2.299	0.353	0.904	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R19	13448	2	1804.0	(+0.2)	2.213	0.354	0.892	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R20	11876	2	1786.0	(+0.9)	2.533	0.290	0.911	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R20	8126	2	1804.0	(-0.8)	2.514	0.260	0.616	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R20	12473	2	1786.0	(+0.5)	2.239	0.205	0.679	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R24	8374	2	1786.0	(+0.4)	2.513	0.221	0.817	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R26	8460	2	1804.0	(-0.2)	4.000	0.490	0.998	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	R26	8462	2	1786.0	(+0.4)	3.339	0.404	0.987	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	R19	1296	2	1300.4	(-0.3)	2.734	0.236	0.132	1	K.SESPKEPEQLR.K
SW:ROA1_HUMAN	R19	2612	2	1629.8	(-0.3)	3.478	0.468	1.000	3	R.SSGPYGGGQYFAKPR.N
SW:ROA1_HUMAN	R27	7599	2	1804.0	(-0.4)	3.894	0.446	1.000	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA2_HUMAN	R18	4333	2	1059.1	(+0.7)	2.798	0.251	0.949	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R18	4493	2	1059.1	(+0.7)	2.651	0.231	0.920	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R18	4655	2	1059.1	(+0.9)	2.599	0.255	0.933	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R18	4413	2	1059.1	(+0.9)	2.479	0.248	0.912	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R18	4573	2	1059.1	(+0.7)	2.472	0.246	0.909	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R18	4585	2	1051.1	(+0.9)	2.462	0.266	0.941	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R18	4251	2	1059.1	(+0.7)	2.417	0.262	0.914	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R18	4503	2	1051.1	(+1.0)	2.415	0.469	0.987	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R18	4901	2	1059.1	(+0.3)	2.358	0.277	0.871	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R19	4122	2	1059.1	(+0.9)	2.749	0.270	0.954	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R19	4840	2	1059.1	(+0.7)	2.735	0.227	0.926	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R19	4758	2	1059.1	(+0.9)	2.672	0.243	0.933	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R19	4276	2	1059.1	(+0.9)	2.607	0.269	0.940	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R19	4048	2	1059.1	(+0.9)	2.588	0.275	0.943	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R19	2704	2	1059.1	(+0.8)	2.554	0.322	0.960	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R19	4434	2	1059.1	(+0.7)	2.553	0.257	0.929	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R19	4198	2	1059.1	(+0.8)	2.494	0.272	0.932	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R19	4596	2	1059.1	(+0.7)	2.427	0.229	0.884	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R19	4354	2	1059.1	(+0.5)	2.427	0.258	0.912	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R19	4846	2	1051.1	(+0.5)	2.396	0.286	0.944	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R19	2778	2	1059.1	(+0.7)	2.344	0.324	0.945	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R19	4514	2	1059.1	(+0.8)	2.314	0.243	0.874	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R19	4510	2	1051.1	(+0.9)	2.292	0.275	0.926	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R19	4976	2	1059.1	(+0.2)	2.286	0.231	0.799	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R19	4676	2	1051.1	(+0.8)	2.252	0.274	0.919	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R19	4678	2	1059.1	(+0.7)	2.238	0.239	0.849	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R23	5538	2	1059.1	(+0.3)	2.452	0.240	0.900	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R23	5542	2	1051.1	(+0.4)	2.204	0.247	0.882	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	R18	1142	2	1339.5	(+0.6)	2.285	0.317	0.171	2	R.EESGKPGAHVTVK.K
SW:ROA2_HUMAN	R19	1066	2	1355.5	(+0.4)	2.295	0.295	0.111	2	R.EESGK#PGAHVTVK#.K
SW:ROA2_HUMAN	R18	7273	2	1696.8	(-0.0)	4.562	0.504	0.844	2	R.GFGVTFDDHDPVDK.I
SW:ROA2_HUMAN	R18	7307	2	1704.8	(-0.6)	3.929	0.506	0.992	2	R.GFGVTFDDHDPVDK#.I
SW:ROA2_HUMAN	R19	7492	2	1696.8	(+0.6)	4.176	0.481	1.000	2	R.GFGVTFDDHDPVDK.I
SW:ROA2_HUMAN	R19	7408	2	1696.8	(+0.9)	4.033	0.522	1.000	2	R.GFGVTFDDHDPVDK.I
SW:ROA2_HUMAN	R19	7286	2	1704.8	(-0.0)	3.828	0.504	1.000	2	R.GFGVTFDDHDPVDK#.I
SW:ROA2_HUMAN	R20	7302	2	1696.8	(-0.3)	3.369	0.481	0.994	2	R.GFGVTFDDHDPVDK.I
SW:ROA2_HUMAN	R21	7244	2	1696.8	(-0.5)	3.855	0.494	0.997	2	R.GFGVTFDDHDPVDK.I

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ROA2_HUMAN	R21	7248	2	1704.8	(-0.4)	3.386	0.513	1.000	2	R.GFGFVTFDDHDPVDK#.I
SW:ROA2_HUMAN	R18	8055	2	1928.2	(-0.3)	3.245	0.344	0.967	2	R.KLFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	8192	2	1928.2	(+0.8)	4.162	0.328	0.987	2	R.KLFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	9251	2	1800.0	(+0.4)	4.303	0.399	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	11983	2	1800.0	(+0.5)	4.121	0.425	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	11149	2	1800.0	(+0.5)	4.120	0.451	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	12455	2	1818.0	(+0.4)	4.019	0.506	1.000	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	12541	2	1818.0	(+0.1)	3.837	0.466	0.997	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	11383	2	1800.0	(+0.5)	3.714	0.376	0.988	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	13505	2	1800.0	(+0.1)	3.705	0.420	0.986	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	12601	2	1800.0	(+0.5)	3.665	0.460	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	12681	2	1818.0	(-0.1)	3.656	0.446	1.000	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	12367	2	1818.0	(+0.3)	3.624	0.462	0.996	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	12953	2	1800.0	(+0.9)	3.607	0.411	0.989	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	11029	2	1818.0	(-0.4)	3.606	0.477	1.000	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	12679	2	1800.0	(-0.1)	3.589	0.405	0.984	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	9111	2	1818.0	(-0.2)	3.574	0.495	1.000	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	12055	2	1800.0	(+0.6)	3.547	0.406	0.989	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	11105	2	1818.0	(-0.1)	3.530	0.409	0.984	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	11537	2	1800.0	(-0.2)	3.525	0.359	0.977	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	9125	2	1800.0	(-0.0)	3.488	0.421	0.984	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	11977	2	1818.0	(+0.5)	3.479	0.467	1.000	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	11905	2	1800.0	(+0.9)	3.475	0.458	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	12205	2	1800.0	(+0.0)	3.469	0.404	0.982	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	13807	2	1800.0	(+0.2)	3.451	0.432	0.985	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	13703	2	1818.0	(-0.7)	3.451	0.484	1.000	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	13031	2	1800.0	(+0.2)	3.444	0.382	0.979	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	12527	2	1800.0	(+0.7)	3.407	0.319	0.976	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	13665	2	1800.0	(+0.3)	3.406	0.429	0.989	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	12427	2	1800.0	(+0.4)	3.393	0.333	0.978	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	11225	2	1800.0	(+0.0)	3.337	0.412	0.982	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	11831	2	1800.0	(-0.2)	3.329	0.447	0.985	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	12127	2	1800.0	(+0.3)	3.326	0.368	0.982	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	11309	2	1800.0	(+0.0)	3.324	0.464	0.986	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	12223	2	1818.0	(-0.7)	3.289	0.499	1.000	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	9337	2	1800.0	(-0.4)	3.287	0.382	0.976	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	8643	2	1800.0	(+0.4)	3.249	0.352	0.978	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	12069	2	1818.0	(-0.6)	3.230	0.449	0.968	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	11739	2	1800.0	(-0.3)	3.188	0.393	0.976	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	12825	2	1818.0	(+0.5)	3.153	0.462	0.989	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	11065	2	1800.0	(-0.2)	3.151	0.349	0.965	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	13141	2	1818.0	(-0.1)	3.141	0.440	0.982	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	11271	2	1818.0	(-0.3)	3.140	0.359	0.968	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	13625	2	1818.0	(-0.8)	3.133	0.438	0.947	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	12915	2	1818.0	(-0.4)	3.101	0.394	0.975	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	11459	2	1800.0	(+0.4)	3.087	0.391	0.982	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	12277	2	1800.0	(+0.3)	3.046	0.450	0.987	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	10647	2	1800.0	(+0.8)	2.993	0.452	0.980	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	13429	2	1800.0	(+0.8)	2.966	0.382	0.978	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	10983	2	1800.0	(+0.8)	2.946	0.347	0.970	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	13467	2	1818.0	(-0.6)	2.929	0.436	0.978	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	13973	2	1800.0	(+0.1)	2.921	0.367	0.962	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	12141	2	1818.0	(+0.2)	2.913	0.409	0.973	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	13737	2	1800.0	(+0.2)	2.890	0.408	0.972	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	11797	2	1818.0	(-0.5)	2.879	0.390	0.967	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	12991	2	1818.0	(-0.2)	2.876	0.395	0.969	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	11407	2	1818.0	(-0.6)	2.867	0.341	0.728	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	12771	2	1800.0	(-0.1)	2.829	0.399	0.968	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	13221	2	1818.0	(+0.2)	2.775	0.378	0.960	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	11723	2	1818.0	(-0.6)	2.750	0.348	0.944	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	13187	2	1800.0	(-0.6)	2.736	0.379	0.957	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	12875	2	1800.0	(+0.3)	2.727	0.416	0.978	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	11903	2	1818.0	(-1.0)	2.726	0.428	0.918	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	13893	2	1800.0	(-0.0)	2.714	0.358	0.948	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	9431	2	1800.0	(-0.6)	2.698	0.414	0.967	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	12753	2	1818.0	(-0.8)	2.696	0.404	0.899	2	K.L*FIGGL*SFETTEESL*R.N

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ROA2_HUMAN	R18	9195	2	1818.0	(-0.2)	2.669	0.376	0.942	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	8937	2	1818.0	(+0.4)	2.658	0.407	0.975	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	13065	2	1818.0	(-0.3)	2.633	0.459	0.975	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	13391	2	1818.0	(-0.4)	2.609	0.412	0.963	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	8551	2	1818.0	(-0.8)	2.608	0.240	0.599	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	8857	2	1818.0	(-0.4)	2.560	0.356	0.935	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	13349	2	1800.0	(+0.5)	2.545	0.428	0.975	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	13915	2	1818.0	(+0.1)	2.532	0.368	0.941	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	9783	2	1818.0	(+0.6)	2.503	0.363	0.563	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	13985	2	1818.0	(-0.4)	2.477	0.310	0.889	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	13845	2	1818.0	(-0.3)	2.465	0.352	0.925	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	10363	2	1800.0	(-0.2)	2.374	0.384	0.936	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	11481	2	1818.0	(-0.6)	2.370	0.367	0.925	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	10951	2	1818.0	(-0.0)	2.366	0.416	0.952	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	11179	2	1818.0	(-0.7)	2.345	0.363	0.919	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R18	10827	2	1800.0	(+0.3)	2.329	0.327	0.916	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R18	13265	2	1800.0	(+0.6)	2.313	0.355	0.935	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	8592	2	1800.0	(+0.8)	5.378	0.433	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	8674	2	1800.0	(+1.0)	5.107	0.431	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	10532	2	1800.0	(+0.5)	4.621	0.446	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	10598	2	1818.0	(+0.8)	4.613	0.508	1.000	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	13290	2	1818.0	(-0.0)	4.377	0.523	1.000	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	9264	2	1800.0	(+0.9)	4.355	0.391	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	12068	2	1800.0	(+1.0)	4.247	0.412	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	9948	2	1800.0	(+0.3)	4.243	0.357	0.985	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	9438	2	1800.0	(+0.1)	4.188	0.353	0.985	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	12686	2	1800.0	(+0.0)	4.078	0.362	0.984	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	10138	2	1818.0	(-0.4)	4.034	0.409	1.000	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	12384	2	1818.0	(+0.0)	3.988	0.406	1.000	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	10108	2	1800.0	(-0.2)	3.909	0.377	0.984	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	9782	2	1800.0	(+0.6)	3.901	0.444	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	12852	2	1800.0	(+0.0)	3.816	0.419	0.987	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	13810	2	1800.0	(+0.5)	3.815	0.303	0.980	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	12610	2	1800.0	(+0.3)	3.757	0.409	0.989	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	13284	2	1800.0	(-0.1)	3.737	0.406	0.983	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	12386	2	1800.0	(+0.0)	3.707	0.403	0.985	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	13680	2	1818.0	(-0.2)	3.695	0.456	1.000	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	13720	2	1800.0	(+0.7)	3.675	0.450	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	12626	2	1818.0	(-0.1)	3.668	0.440	0.998	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	14092	2	1818.0	(-0.1)	3.628	0.484	1.000	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	10052	2	1818.0	(-0.4)	3.617	0.412	0.984	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	9302	2	1818.0	(-0.3)	3.561	0.477	0.984	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	12720	2	1818.0	(+0.5)	3.560	0.462	1.000	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	13018	2	1818.0	(-0.1)	3.544	0.456	1.000	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	12302	2	1800.0	(+0.9)	3.540	0.327	0.980	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	11970	2	1800.0	(+0.6)	3.539	0.439	0.989	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	13764	2	1818.0	(-0.2)	3.488	0.526	1.000	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	13102	2	1800.0	(+0.0)	3.472	0.384	0.960	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	8602	2	1818.0	(-0.8)	3.458	0.391	0.943	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	10708	2	1818.0	(-0.6)	3.398	0.466	1.000	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	12534	2	1800.0	(+0.1)	3.391	0.452	0.986	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	8760	2	1800.0	(-0.2)	3.391	0.433	0.985	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	12952	2	1800.0	(+0.3)	3.390	0.310	0.973	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	12798	2	1818.0	(-0.7)	3.377	0.418	0.982	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	10666	2	1800.0	(-0.6)	3.366	0.425	0.984	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	11468	2	1800.0	(+0.8)	3.354	0.438	0.989	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	12772	2	1800.0	(-0.0)	3.336	0.376	0.976	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	10218	2	1800.0	(+0.2)	3.330	0.449	0.985	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	13884	2	1800.0	(+0.3)	3.322	0.482	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	14034	2	1800.0	(+0.1)	3.317	0.387	0.978	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	13934	2	1818.0	(-0.0)	3.299	0.440	0.984	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	11640	2	1800.0	(+0.2)	3.286	0.450	0.985	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	9800	2	1818.0	(-0.4)	3.268	0.465	0.986	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	12082	2	1818.0	(+0.2)	3.268	0.466	0.985	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	9552	2	1800.0	(-0.1)	3.262	0.390	0.977	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	13368	2	1818.0	(-0.7)	3.257	0.393	0.958	2	K.L*FIGGL*SFETTEESL*R.N

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ROA2_HUMAN	R19	10308	2	1800.0	(-0.2)	3.251	0.437	0.984	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	8680	2	1818.0	(-0.7)	3.236	0.353	0.969	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	13734	2	1800.0	(-0.7)	3.220	0.371	0.973	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	14178	2	1800.0	(+0.2)	3.168	0.456	0.984	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	9224	2	1818.0	(+0.3)	3.166	0.397	0.984	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	13598	2	1818.0	(+0.0)	3.162	0.487	0.987	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	9090	2	1818.0	(-0.1)	3.158	0.415	0.979	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	11354	2	1800.0	(+0.5)	3.154	0.410	0.985	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	14020	2	1818.0	(-0.4)	3.123	0.403	0.976	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	9350	2	1800.0	(-0.5)	3.113	0.376	0.971	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	10522	2	1818.0	(-0.9)	3.079	0.438	0.945	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	12460	2	1800.0	(+0.1)	3.055	0.318	0.950	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	14108	2	1800.0	(+0.3)	3.025	0.390	0.980	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	10582	2	1800.0	(-0.8)	3.018	0.484	0.957	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	11492	2	1818.0	(-0.3)	2.985	0.448	0.981	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	12224	2	1800.0	(-0.6)	2.981	0.292	0.932	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	11340	2	1818.0	(-0.6)	2.968	0.352	0.957	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	11612	2	1818.0	(-0.5)	2.939	0.438	0.979	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	13028	2	1800.0	(+0.0)	2.893	0.419	0.974	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	13962	2	1800.0	(-0.1)	2.869	0.311	0.935	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	11012	2	1818.0	(-0.5)	2.861	0.406	0.971	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	11202	2	1818.0	(-0.1)	2.825	0.443	0.977	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	12552	2	1818.0	(-0.9)	2.822	0.440	0.930	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	10296	2	1818.0	(-0.8)	2.813	0.439	0.931	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	8758	2	1818.0	(-0.8)	2.751	0.379	0.884	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	13178	2	1800.0	(+0.2)	2.746	0.303	0.918	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	10784	2	1818.0	(+0.0)	2.722	0.402	0.965	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	12146	2	1800.0	(-0.8)	2.721	0.323	0.813	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	12236	2	1818.0	(-1.0)	2.715	0.433	0.920	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	13530	2	1800.0	(+0.4)	2.659	0.357	0.961	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	13094	2	1818.0	(-0.9)	2.564	0.307	0.746	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	11766	2	1818.0	(-0.1)	2.560	0.305	0.897	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	11276	2	1800.0	(-0.2)	2.468	0.336	0.913	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	11930	2	1818.0	(-0.6)	2.372	0.272	0.814	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R19	9160	2	1800.0	(-0.7)	2.370	0.287	0.839	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	11482	2	1800.0	(-0.5)	2.345	0.373	0.926	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R20	8246	2	1800.0	(+1.0)	5.119	0.419	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R20	13403	2	1800.0	(+0.3)	3.036	0.345	0.972	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R20	11870	2	1818.0	(+0.1)	2.930	0.401	0.971	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R20	11720	2	1818.0	(+0.7)	2.724	0.365	0.966	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R20	12971	2	1800.0	(+0.4)	2.635	0.465	0.984	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R20	13233	2	1800.0	(-0.4)	2.499	0.366	0.937	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R20	11944	2	1800.0	(+0.3)	2.491	0.462	0.980	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R20	11028	2	1818.0	(-0.5)	2.372	0.430	0.957	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R20	12257	2	1800.0	(-0.6)	2.253	0.353	0.897	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R20	13353	2	1818.0	(-0.5)	2.248	0.218	0.639	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R20	13179	2	1818.0	(-0.4)	2.247	0.325	0.864	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R20	11644	2	1818.0	(-0.6)	2.216	0.298	0.815	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R22	8458	2	1800.0	(+0.9)	4.310	0.399	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R22	8452	2	1818.0	(-0.1)	3.725	0.548	1.000	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	R25	8724	2	1800.0	(-0.3)	4.338	0.448	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	R19	6422	3	1901.1	(+0.2)	4.733	0.500	1.000	2	K.L*FVGGIK#EDTEEHL*R.D
SW:ROA2_HUMAN	R19	6274	3	1881.1	(+1.0)	4.551	0.583*	0.056	2	K.LFVGGIKEDTEEHLR.D
SW:ROA2_HUMAN	R20	6222	3	1901.1	(+0.8)	4.106	0.443	0.994	2	K.L*FVGGIK#EDTEEHL*R.D
SW:ROA2_HUMAN	R18	2588	2	1096.2	(+0.7)	3.000	0.407	0.988	2	R.NYYEQWVK.L
SW:ROA2_HUMAN	R18	4847	2	1088.2	(+0.4)	2.553	0.261	0.947	2	R.NYYEQWVK.L
SW:ROA2_HUMAN	R18	4747	2	1088.2	(+0.4)	2.533	0.356	0.977	2	R.NYYEQWVK.L
SW:ROA2_HUMAN	R18	2670	2	1096.2	(+0.7)	2.277	0.326	0.939	2	R.NYYEQWVK.L
SW:ROA2_HUMAN	R18	4607	2	1096.2	(+0.3)	2.275	0.419	0.922	2	R.NYYEQWVK.L
SW:ROA2_HUMAN	R18	2496	2	1096.2	(+0.5)	2.246	0.346	0.946	2	R.NYYEQWVK.L
SW:ROA2_HUMAN	R18	2518	2	1088.2	(-0.8)	2.240	0.397	0.875	2	R.NYYEQWVK.L
SW:ROA2_HUMAN	R18	2876	2	1088.2	(+1.0)	2.228	0.323	0.947	2	R.NYYEQWVK.L
SW:ROA2_HUMAN	R18	3909	2	1096.2	(+0.7)	2.206	0.334	0.935	2	R.NYYEQWVK.L
SW:ROA2_HUMAN	R19	2610	2	1088.2	(+0.4)	2.948	0.380	0.988	2	R.NYYEQWVK.L
SW:ROA2_HUMAN	R19	2604	2	1096.2	(+0.7)	2.912	0.429	0.988	2	R.NYYEQWVK.L
SW:ROA2_HUMAN	R19	2524	2	1088.2	(+0.6)	2.786	0.438	0.988	2	R.NYYEQWVK.L

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ROA2_HUMAN	R19	2434	2	1096.2	(+0.7)	2.774	0.425	0.986	2	R.NYYEQWVGK#.L
SW:ROA2_HUMAN	R19	2516	2	1096.2	(+0.6)	2.723	0.425	0.959	2	R.NYYEQWVGK#.L
SW:ROA2_HUMAN	R19	2442	2	1088.2	(+0.6)	2.654	0.459	0.989	2	R.NYYEQWVGK.L
SW:ROA2_HUMAN	R19	4780	2	1088.2	(+0.9)	2.575	0.326	0.972	2	R.NYYEQWVGK.L
SW:ROA2_HUMAN	R19	4990	2	1088.2	(+0.3)	2.503	0.360	0.976	2	R.NYYEQWVGK.L
SW:ROA2_HUMAN	R19	4622	2	1088.2	(+0.3)	2.491	0.313	0.904	2	R.NYYEQWVGK.L
SW:ROA2_HUMAN	R19	4710	2	1096.2	(+0.3)	2.350	0.424	0.977	2	R.NYYEQWVGK#.L
SW:ROA2_HUMAN	R19	4956	2	1096.2	(+0.5)	2.343	0.420	0.975	2	R.NYYEQWVGK#.L
SW:ROA2_HUMAN	R20	4828	2	1096.2	(+0.7)	2.397	0.385	0.970	2	R.NYYEQWVGK#.L
SW:ROA2_HUMAN	R24	5528	2	1088.2	(-0.2)	2.224	0.192	0.740	2	R.NYYEQWVGK.L
SW:ROA2_HUMAN	R25	5564	2	1096.2	(+0.8)	2.381	0.417	0.976	2	R.NYYEQWVGK#.L
SW:ROA2_HUMAN	R25	5574	2	1088.2	(+0.0)	2.379	0.372	0.963	2	R.NYYEQWVGK.L
SW:ROA2_HUMAN	R18	5185	2	1058.2	(+0.9)	2.645	0.297	0.962		K.TLETVPLER.K
SW:ROA2_HUMAN	R18	5187	2	1070.2	(+0.4)	2.493	0.421	0.983		K.TL*ETVPL*ER.K
SW:ROA2_HUMAN	R24	5844	2	1058.2	(+0.1)	2.440	0.314	0.936		K.TLETVPLER.K
SW:ROA2_HUMAN	R25	5666	2	1051.1	(+0.7)	2.229	0.307	0.938	2	R.DYFEEYGK.I
SW:ROA3_HUMAN	R19	2564	2	1050.2	(+0.9)	2.347	0.420*	0.008	2	R.DYFEKYGK.I
SW:ROA3_HUMAN	R19	5258	2	1050.2	(+0.8)	2.232	0.292*	0.006	2	R.DYFEKYGK.I
SW:ROA3_HUMAN	R18	7975	2	1900.1	(-0.2)	4.611	0.487	1.000	2	R.KLFIGGLSFETDDSLR.E
SW:ROA3_HUMAN	R20	7870	2	1900.1	(-0.5)	2.413	0.119	0.338	2	R.KLFIGGLSFETDDSLR.E
SW:ROA3_HUMAN	R18	8261	2	1790.0	(+0.3)	3.360	0.337	0.978	2	K.L*FIGGL*SFETDDSL*R.E
SW:ROA3_HUMAN	R18	8375	2	1790.0	(-0.2)	3.116	0.298	0.944	2	K.L*FIGGL*SFETDDSL*R.E
SW:ROA3_HUMAN	R18	12375	2	1790.0	(+0.3)	2.668	0.360	0.962	2	K.L*FIGGL*SFETDDSL*R.E
SW:ROA3_HUMAN	R18	12079	2	1790.0	(-0.2)	2.652	0.302	0.904	2	K.L*FIGGL*SFETDDSL*R.E
SW:ROA3_HUMAN	R18	11431	2	1772.0	(-0.7)	2.563	0.325	0.915	2	K.LFIGGLSFETDDSLR.E
SW:ROA3_HUMAN	R18	12117	2	1772.0	(+0.4)	2.470	0.212	0.786	2	K.LFIGGLSFETDDSLR.E
SW:ROA3_HUMAN	R18	12303	2	1772.0	(-0.5)	2.411	0.284	0.844	2	K.LFIGGLSFETDDSLR.E
SW:ROA3_HUMAN	R18	11451	2	1790.0	(-0.4)	2.342	0.385	0.933	2	K.L*FIGGL*SFETDDSL*R.E
SW:ROA3_HUMAN	R20	8154	2	1772.0	(+0.8)	3.315	0.424	0.985	2	K.LFIGGLSFETDDSLR.E
SW:ROA3_HUMAN	R18	8289	3	2468.7	(-0.1)	3.747	0.296	0.853	2	K.L*FIGGL*SFETDDSL*REHFKE#.W
SW:ROA3_HUMAN	R22	5360	2	1050.2	(+0.1)	2.267	0.445*	0.005	2	R.DYFEKYGK.I
SW:ROCL_HUMAN	R18	7119	2	1332.5	(+0.1)	2.688	0.190	0.081	1	K.GFAFVQYDKEK.N
SW:ROCL_HUMAN	R17	6066	2	1140.3	(+0.0)	2.274	0.252	0.781	8	K.K#SDVEAIFSK#.Y
SW:ROCL_HUMAN	R18	5823	2	1140.3	(+0.6)	3.206	0.384	0.985	8	K.K#SDVEAIFSK#.Y
SW:ROCL_HUMAN	R18	5735	2	1140.3	(-0.9)	2.718	0.293	0.799	8	K.K#SDVEAIFSK#.Y
SW:ROCL_HUMAN	R18	5925	2	1140.3	(+0.0)	2.403	0.343	0.923	8	K.K#SDVEAIFSK#.Y
SW:ROCL_HUMAN	R18	5751	1	1140.3	(-0.7)	2.250	0.234	0.000	8	K.K#SDVEAIFSK#.Y
SW:ROCL_HUMAN	R19	6028	2	1140.3	(+0.3)	2.357	0.318	0.926	8	K.K#SDVEAIFSK#.Y
SW:ROCL_HUMAN	R20	5960	2	1124.3	(+0.9)	3.001	0.265	0.960	8	K.KSDVEAIFSK.Y
SW:ROCL_HUMAN	R20	5946	2	1140.3	(+0.7)	2.615	0.326	0.954	8	K.K#SDVEAIFSK#.Y
SW:ROCL_HUMAN	R21	6092	2	1140.3	(+0.5)	3.028	0.389	0.982	8	K.K#SDVEAIFSK#.Y
SW:ROCL_HUMAN	R23	6182	2	1124.3	(+0.9)	3.065	0.264	0.966	8	K.KSDVEAIFSK.Y
SW:ROCL_HUMAN	R23	6180	2	1140.3	(+0.0)	2.598	0.237	0.850	8	K.K#SDVEAIFSK#.Y
SW:ROCL_HUMAN	R01	1514	2	1101.3	(+0.9)	3.217	0.390	0.641	9	K.LKGDDLQAIK.Q
SW:ROCL_HUMAN	R03	1884	2	1129.3	(-0.3)	2.319	0.253	0.072	9	K.L*K#GDDL*QAIK#.Q
SW:ROCL_HUMAN	R18	2092	2	1101.3	(-0.6)	3.333	0.414	1.000	9	K.LKGDDLQAIK.Q
SW:ROCL_HUMAN	R18	2174	2	1101.3	(+1.0)	3.170	0.401	0.648	9	K.LKGDDLQAIK.Q
SW:ROCL_HUMAN	R18	2178	2	1129.3	(-0.5)	2.658	0.328	0.234	9	K.L*K#GDDL*QAIK#.Q
SW:ROCL_HUMAN	R18	2072	2	1129.3	(-0.3)	2.586	0.224	0.086	9	K.L*K#GDDL*QAIK#.Q
SW:ROCL_HUMAN	R19	2078	2	1101.3	(+0.9)	2.716	0.356	0.447	9	K.LKGDDLQAIK.Q
SW:ROCL_HUMAN	R20	2392	2	1101.3	(+0.4)	3.353	0.403	0.684	9	K.LKGDDLQAIK.Q
SW:ROCL_HUMAN	R22	5180	2	1101.3	(+0.8)	3.108	0.385	0.610	9	K.LKGDDLQAIK.Q
SW:ROCL_HUMAN	R23	5240	2	1101.3	(+0.9)	2.669	0.301	0.315	9	K.LKGDDLQAIK.Q
SW:ROCL_HUMAN	R01	6741	2	1416.6	(+0.2)	2.282	0.278	0.045	9	K.QKVDLSLENLEK.I
SW:ROCL_HUMAN	R19	7080	2	1416.6	(+0.8)	2.296	0.331	0.162	9	K.QKVDLSLENLEK.I
SW:ROCL_HUMAN	R18	5897	2	996.1	(-0.7)	2.226	0.326	0.916	8	K.SDVEAIFSK.Y
SW:ROCL_HUMAN	R21	6154	2	996.1	(+0.6)	2.522	0.200	0.879	8	K.SDVEAIFSK.Y
SW:ROCL_HUMAN	R24	6336	2	1004.1	(+0.8)	2.685	0.122	0.752	8	K.SDVEAIFSK#.Y
SW:ROCL_HUMAN	R01	6705	2	1160.3	(+0.6)	2.258	0.303	0.921	9	K.VDSLENLEK.I
SW:ROCL_HUMAN	R17	7656	2	1337.6	(-0.1)	2.987	0.383	0.968	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	7343	2	1317.6	(+0.8)	3.258	0.363	0.983	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	R18	13313	2	1317.6	(+1.0)	3.072	0.478	1.000	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	R18	7875	2	1317.6	(+0.9)	3.050	0.408	0.972	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	R18	13947	2	1317.6	(+0.7)	2.950	0.354	0.977	9	R.VFIGNLNTLVVK.K



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ROCL_HUMAN	R18	13629	2	1317.6	(+0.8)	2.731	0.336	0.966	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	R18	13485	2	1337.6	(+0.4)	2.726	0.408	0.973	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	7939	2	1337.6	(-0.3)	2.718	0.342	0.938	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	12101	2	1337.6	(+0.2)	2.686	0.403	0.962	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	12029	2	1337.6	(+0.2)	2.609	0.353	0.936	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	11391	2	1337.6	(+0.2)	2.608	0.373	0.946	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	11499	2	1337.6	(+0.3)	2.596	0.407	0.971	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	12369	2	1337.6	(+0.0)	2.575	0.359	0.935	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	13863	2	1317.6	(+0.7)	2.569	0.370	0.967	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	R18	7631	2	1317.6	(-0.7)	2.562	0.294	0.909	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	R18	12191	2	1337.6	(-0.0)	2.560	0.367	0.939	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	7589	2	1337.6	(+0.2)	2.554	0.352	0.518	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	13793	2	1317.6	(+0.7)	2.537	0.418	0.978	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	R18	13561	2	1337.6	(+0.4)	2.533	0.391	0.964	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	12993	2	1337.6	(-0.0)	2.514	0.334	0.914	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	13389	2	1317.6	(+0.2)	2.503	0.384	0.956	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	R18	11021	2	1337.6	(+0.2)	2.500	0.346	0.921	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	11955	2	1337.6	(-0.3)	2.495	0.341	0.917	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	12829	2	1337.6	(-0.3)	2.492	0.287	0.863	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	7759	2	1337.6	(-0.3)	2.467	0.293	0.858	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	11709	2	1337.6	(+0.2)	2.446	0.445	0.963	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	7679	2	1337.6	(-0.2)	2.438	0.282	0.845	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	8697	2	1337.6	(+0.2)	2.438	0.224	0.737	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	11297	2	1337.6	(+0.1)	2.437	0.371	0.929	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	12547	2	1337.6	(+0.2)	2.415	0.345	0.910	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	7859	2	1337.6	(-0.8)	2.405	0.296	0.662	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	12283	2	1337.6	(+0.7)	2.353	0.434	0.968	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	13925	2	1337.6	(+0.5)	2.321	0.363	0.937	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	11867	2	1337.6	(-0.0)	2.312	0.216	0.663	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	13075	2	1337.6	(-0.1)	2.312	0.319	0.866	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	11137	2	1337.6	(-0.4)	2.282	0.357	0.901	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	13101	2	1317.6	(+0.6)	2.279	0.498	0.984	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	R18	12911	2	1337.6	(+0.4)	2.246	0.280	0.841	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R18	13649	2	1337.6	(+0.6)	2.236	0.271	0.824	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R20	7564	2	1337.6	(+0.3)	2.961	0.444	0.985	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R21	7492	2	1317.6	(+1.0)	2.226	0.461	0.976	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	R23	7784	2	1317.6	(+0.5)	2.694	0.337	0.964	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	R23	7772	2	1337.6	(+0.5)	2.564	0.374	0.959	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R24	7810	2	1317.6	(-0.2)	3.291	0.444	0.987	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	R25	8116	2	1337.6	(-0.3)	2.503	0.326	0.906	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R26	7900	2	1317.6	(+0.9)	3.651	0.412	0.999	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	R26	7898	2	1337.6	(-0.1)	2.930	0.392	0.968	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	R27	5857	2	1140.3	(+0.0)	2.899	0.319	0.952	8	K.K#SDVEAIFSK#.Y
SW:ROC_HUMAN	R18	5631	2	1051.2	(-0.3)	2.389	0.256*	0.166	7	R.GDDQL*EL*IK#.D
SW:ROC_HUMAN	R18	5639	2	1031.2	(+0.6)	2.316	0.300	0.935	7	R.GDDQLELIK.D
SW:ROC_HUMAN	R18	5517	2	1518.6	(-0.5)	3.304	0.389	0.501	7	R.GDDQLELIKDDEK.E
SW:ROC_HUMAN	R18	5425	2	1546.6	(-0.3)	2.855	0.212	0.081	7	R.GDDQL*EL*IK#DDEK#.E
SW:ROC_HUMAN	R01	7519	2	1684.0	(+0.4)	4.628	0.518	1.000	6	R.MIAGQVLDINLAAEPK.V
SW:ROC_HUMAN	R01	7091	2	1720.0	(+0.5)	3.708	0.452	1.000	6	R.M@IAGQVL*DINL*AAEPK#.V
SW:ROC_HUMAN	R03	6757	2	1720.0	(+0.3)	3.539	0.461	1.000	6	R.M@IAGQVL*DINL*AAEPK#.V
SW:ROC_HUMAN	R04	7014	2	1720.0	(+0.4)	2.611	0.418	0.968	6	R.M@IAGQVL*DINL*AAEPK#.V
SW:ROC_HUMAN	R18	7853	2	1684.0	(-0.1)	4.630	0.546	0.999	6	R.MIAGQVLDINLAAEPK.V
SW:ROC_HUMAN	R18	13109	3	1704.0	(+0.4)	4.612	0.499	0.999	6	R.MIAGQVL*DINL*AAEPK#.V
SW:ROC_HUMAN	R18	7217	2	1720.0	(+0.0)	4.486	0.573	1.000	6	R.M@IAGQVL*DINL*AAEPK#.V
SW:ROC_HUMAN	R18	7737	2	1684.0	(+0.4)	4.450	0.470	1.000	6	R.MIAGQVLDINLAAEPK.V
SW:ROC_HUMAN	R18	11957	2	1684.0	(+0.1)	4.350	0.541	1.000	6	R.MIAGQVLDINLAAEPK.V
SW:ROC_HUMAN	R18	11211	2	1684.0	(+0.4)	4.334	0.505	1.000	6	R.MIAGQVLDINLAAEPK.V
SW:ROC_HUMAN	R18	10451	3	1684.0	(-0.0)	4.325	0.273	0.984	6	R.MIAGQVLDINLAAEPK.V
SW:ROC_HUMAN	R18	12179	2	1684.0	(+0.4)	4.270	0.466	1.000	6	R.MIAGQVLDINLAAEPK.V
SW:ROC_HUMAN	R18	13057	2	1684.0	(+0.9)	4.201	0.518	1.000	6	R.MIAGQVLDINLAAEPK.V
SW:ROC_HUMAN	R18	7941	2	1684.0	(-0.4)	4.201	0.447	1.000	6	R.MIAGQVLDINLAAEPK.V
SW:ROC_HUMAN	R18	7765	3	1704.0	(-0.4)	4.173	0.478	1.000	6	R.MIAGQVL*DINL*AAEPK#.V
SW:ROC_HUMAN	R18	10679	3	1704.0	(+0.3)	4.147	0.457	1.000	6	R.MIAGQVL*DINL*AAEPK#.V
SW:ROC_HUMAN	R18	7773	2	1684.0	(-0.8)	4.121	0.512	1.000	6	R.MIAGQVLDINLAAEPK.V
SW:ROC_HUMAN	R18	12309	2	1684.0	(+0.1)	4.040	0.567	1.000	6	R.MIAGQVLDINLAAEPK.V

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta M$	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ROC_HUMAN	R18	11317	2	1684.0	(+0.7)	3.973	0.485	0.998	6	R.MIAGQVLDINLAAEPK.V
SW:ROC_HUMAN	R18	12237	2	1704.0	(+0.6)	3.849	0.511	1.000	6	R.MIAGQVL*DINL*AAEPK#.V
SW:ROC_HUMAN	R18	12073	2	1684.0	(+0.4)	3.776	0.463	0.999	6	R.MIAGQVLDINLAAEPK.V
SW:ROC_HUMAN	R18	13269	3	1704.0	(+0.1)	3.770	0.384	0.997	6	R.MIAGQVL*DINL*AAEPK#.V
SW:ROC_HUMAN	R18	12699	2	1684.0	(-0.0)	3.733	0.464	0.995	6	R.MIAGQVLDINLAAEPK.V
SW:ROC_HUMAN	R18	12159	2	1704.0	(+0.3)	3.663	0.486	1.000	6	R.MIAGQVL*DINL*AAEPK#.V
SW:ROC_HUMAN	R18	13555	2	1704.0	(-0.1)	3.592	0.292	0.952	6	R.MIAGQVL*DINL*AAEPK#.V
SW:ROC_HUMAN	R18	11437	2	1684.0	(-0.2)	3.583	0.484	1.000	6	R.MIAGQVLDINLAAEPK.V
SW:ROC_HUMAN	R18	12323	2	1704.0	(-0.6)	3.516	0.382	0.974	6	R.MIAGQVL*DINL*AAEPK#.V
SW:ROC_HUMAN	R18	11345	2	1684.0	(-0.7)	3.450	0.444	0.985	6	R.MIAGQVLDINLAAEPK.V
SW:ROC_HUMAN	R18	11865	2	1704.0	(+0.3)	3.437	0.527	0.999	6	R.MIAGQVL*DINL*AAEPK#.V
SW:ROC_HUMAN	R18	11545	2	1704.0	(-0.6)	3.278	0.284	0.930	6	R.MIAGQVL*DINL*AAEPK#.V
SW:ROC_HUMAN	R18	12595	2	1704.0	(-0.7)	3.260	0.220	0.875	6	R.MIAGQVL*DINL*AAEPK#.V
SW:ROC_HUMAN	R18	13163	2	1704.0	(-0.7)	3.224	0.300	0.937	6	R.MIAGQVL*DINL*AAEPK#.V
SW:ROC_HUMAN	R18	8871	2	1684.0	(-0.2)	3.219	0.373	0.972	6	R.MIAGQVLDINLAAEPK.V
SW:ROC_HUMAN	R18	10871	2	1684.0	(-0.2)	3.206	0.397	0.976	6	R.MIAGQVLDINLAAEPK.V
SW:ROC_HUMAN	R18	11961	2	1704.0	(+0.2)	3.155	0.375	0.963	6	R.MIAGQVL*DINL*AAEPK#.V
SW:ROC_HUMAN	R18	13661	2	1704.0	(+0.5)	2.995	0.414	0.978	6	R.MIAGQVL*DINL*AAEPK#.V
SW:ROC_HUMAN	R18	11405	2	1704.0	(-0.5)	2.930	0.111	0.545	6	R.MIAGQVL*DINL*AAEPK#.V
SW:ROC_HUMAN	R18	13105	2	1684.0	(-0.3)	2.884	0.379	0.961	6	R.MIAGQVLDINLAAEPK.V
SW:ROC_HUMAN	R18	11763	2	1704.0	(-0.3)	2.719	0.319	0.906	6	R.MIAGQVL*DINL*AAEPK#.V
SW:ROC_HUMAN	R18	9095	2	1704.0	(+0.2)	2.624	0.165	0.588	6	R.MIAGQVL*DINL*AAEPK#.V
SW:ROC_HUMAN	R18	10283	2	1684.0	(-0.6)	2.570	0.312	0.905	6	R.MIAGQVLDINLAAEPK.V
SW:ROC_HUMAN	R18	9193	2	1684.0	(+0.4)	2.435	0.342	0.938	6	R.MIAGQVLDINLAAEPK.V
SW:ROC_HUMAN	R19	7394	2	1720.0	(-0.8)	2.952	0.306	0.790	6	R.M@IAGQVL*DINL*AAEPK#.V
SW:ROC_HUMAN	R18	880	2	1570.6	(+0.2)	3.576	0.258	0.236	7	K.NDK#SEEEQSSSSVK#.K
SW:ROC_HUMAN	R18	8533	3	3435.7	(-0.4)	6.616	0.633	0.999	2	R.SAAEMYGSVTEHPSPLSSSFDDLDYDFQR.D
SW:ROC_HUMAN	R18	8587	3	3453.7	(-0.9)	5.527	0.529	1.000	2	R.SAAEMYGSVTEHPSPL*L*SSSFDL*DYDFQR.D
SW:ROC_HUMAN	R18	8247	3	3469.7	(-0.2)	5.208	0.552	0.998	2	R.SAAEM@YGSVTEHPSPL*L*SSSFDL*DYDFQR.D
SW:ROC_HUMAN	R18	8763	3	3435.7	(+0.7)	5.083	0.580	1.000	2	R.SAAEMYGSVTEHPSPLSSSFDDLDYDFQR.D
SW:ROC_HUMAN	R18	11377	3	3453.7	(-1.0)	5.072	0.504	1.000	2	R.SAAEMYGSVTEHPSPL*L*SSSFDL*DYDFQR.D
SW:ROC_HUMAN	R18	12081	3	3453.7	(-0.3)	5.032	0.578	0.989	2	R.SAAEMYGSVTEHPSPL*L*SSSFDL*DYDFQR.D
SW:ROC_HUMAN	R18	8727	3	3453.7	(-0.5)	4.836	0.574	0.977	2	R.SAAEMYGSVTEHPSPL*L*SSSFDL*DYDFQR.D
SW:ROC_HUMAN	R18	8889	3	3453.7	(-0.8)	4.590	0.432	0.996	2	R.SAAEMYGSVTEHPSPL*L*SSSFDL*DYDFQR.D
SW:ROC_HUMAN	R18	13335	3	3435.7	(+0.4)	4.392	0.485	1.000	2	R.SAAEMYGSVTEHPSPLSSSFDDLDYDFQR.D
SW:ROC_HUMAN	R18	11135	3	3435.7	(-0.7)	4.344	0.516	1.000	2	R.SAAEMYGSVTEHPSPLSSSFDDLDYDFQR.D
SW:ROC_HUMAN	R18	11121	3	3453.7	(-0.1)	4.261	0.471	0.998	2	R.SAAEMYGSVTEHPSPL*L*SSSFDL*DYDFQR.D
SW:ROC_HUMAN	R18	8865	3	3435.7	(-0.4)	4.228	0.477	0.999	2	R.SAAEMYGSVTEHPSPLSSSFDDLDYDFQR.D
SW:ROC_HUMAN	R18	11213	3	3453.7	(+0.0)	4.166	0.479	1.000	2	R.SAAEMYGSVTEHPSPL*L*SSSFDL*DYDFQR.D
SW:ROC_HUMAN	R18	11819	3	3453.7	(-0.4)	4.143	0.382	0.996	2	R.SAAEMYGSVTEHPSPL*L*SSSFDL*DYDFQR.D
SW:ROC_HUMAN	R18	12713	3	3435.7	(+0.7)	4.133	0.471	1.000	2	R.SAAEMYGSVTEHPSPLSSSFDDLDYDFQR.D
SW:ROC_HUMAN	R18	11877	3	3435.7	(+0.6)	4.035	0.499	1.000	2	R.SAAEMYGSVTEHPSPLSSSFDDLDYDFQR.D
SW:ROC_HUMAN	R21	8020	3	3469.7	(-0.9)	5.379	0.543	0.993	2	R.SAAEM@YGSVTEHPSPL*L*SSSFDL*DYDFQR.D
SW:ROC_HUMAN	R18	856	2	1197.2	(+0.8)	3.187	0.355	0.984	7	K.SEEEQSSSSVK.K
SW:ROC_HUMAN	R18	852	2	1205.2	(+0.5)	2.765	0.390	0.975	7	K.SEEEQSSSSVK#.K
SW:ROD_HUMAN	R17	8382	3	2176.4	(+0.6)	4.453	0.457	1.000	10	R.EYFGGFGEVESIEL*PMDNK#.T
SW:ROD_HUMAN	R17	7868	3	2192.4	(+0.8)	3.854	0.336	0.991	10	R.EYFGGFGEVESIEL*PM@DNK#.T
SW:ROD_HUMAN	R17	8312	2	2176.4	(+0.8)	3.656	0.320	0.973	10	R.EYFGGFGEVESIEL*PMDNK#.T
SW:ROD_HUMAN	R17	7884	2	2192.4	(+0.5)	3.654	0.488	1.000	10	R.EYFGGFGEVESIEL*PM@DNK#.T
SW:ROD_HUMAN	R17	8316	2	2162.4	(-0.0)	3.411	0.364	0.976	10	R.EYFGGFGEVESIELPMDNK.T
SW:ROD_HUMAN	R18	8405	2	2176.4	(+0.5)	3.735	0.344	0.979	10	R.EYFGGFGEVESIEL*PMDNK#.T
SW:ROD_HUMAN	R18	7919	2	2192.4	(-0.8)	2.430	0.213	0.373	10	R.EYFGGFGEVESIEL*PM@DNK#.T
SW:ROD_HUMAN	R16	5978	2	1489.7	(+0.4)	4.719	0.404	0.866	10	K.IFVGGLSPDTPEEK.I
SW:ROD_HUMAN	R16	5974	2	1503.7	(-0.5)	3.706	0.474	1.000	10	K.IFVGGL*SPDTPEEK#.I
SW:ROD_HUMAN	R17	6248	2	1503.7	(-0.0)	3.786	0.517	0.614	10	K.IFVGGL*SPDTPEEK#.I
SW:ROD_HUMAN	R18	6189	2	1503.7	(+0.5)	4.540	0.426	1.000	10	K.IFVGGL*SPDTPEEK#.I
SW:ROD_HUMAN	R19	6460	2	1503.7	(+1.0)	4.586	0.509	0.999	10	K.IFVGGL*SPDTPEEK#.I
SW:ROD_HUMAN	R20	6256	2	1503.7	(-0.9)	3.320	0.465	1.000	10	K.IFVGGL*SPDTPEEK#.I
SW:ROD_HUMAN	R21	6274	2	1503.7	(-0.2)	3.573	0.436	0.983	10	K.IFVGGL*SPDTPEEK#.I
SW:ROD_HUMAN	R17	1436	2	1068.2	(-0.1)	2.356	0.160	0.622	9	K.K#YHNVGL*SK#.C
SW:ROD_HUMAN	R18	1236	2	1068.2	(+0.2)	2.371	0.343	0.928	9	K.K#YHNVGL*SK#.C
SW:ROD_HUMAN	R16	7212	2	1370.6	(+0.3)	2.855	0.454	0.984	9	K.MFIGGL*SWDTTK#.K
SW:ROD_HUMAN	R17	7776	2	1370.6	(+0.2)	2.681	0.397	0.960	9	K.MFIGGL*SWDTTK#.K
SW:ROD_HUMAN	R18	7125	2	1386.6	(-0.2)	2.698	0.304	0.913	9	K.M@FIGGL*SWDTTK#.K
SW:ROD_HUMAN	R22	6520	2	1489.7	(-0.0)	2.722	0.306	0.924	10	K.IFVGGLSPDTPEEK.I

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ROF_HUMAN	R15	8455	2	1998.2	(+0.0)	3.147	0.365	0.964	2	K.ATENDIYNFFSPLNPVR.V
SW:ROF_HUMAN	R16	8326	2	2004.2	(+0.0)	3.847	0.441	1.000	2	K.ATENDIYNFFSPL*NPVR.V
SW:ROF_HUMAN	R16	8264	2	1998.2	(-0.2)	2.874	0.395	0.969	2	K.ATENDIYNFFSPLNPVR.V
SW:ROF_HUMAN	R17	8718	2	2004.2	(+0.4)	3.821	0.533	1.000	2	K.ATENDIYNFFSPL*NPVR.V
SW:ROF_HUMAN	R18	8791	2	1998.2	(+0.4)	3.180	0.429	0.972	2	K.ATENDIYNFFSPLNPVR.V
SW:ROF_HUMAN	R20	8664	2	1998.2	(+0.4)	3.455	0.435	0.990	2	K.ATENDIYNFFSPLNPVR.V
SW:ROF_HUMAN	R20	8676	2	2004.2	(-0.4)	3.262	0.373	0.974	2	K.ATENDIYNFFSPL*NPVR.V
SW:ROF_HUMAN	R21	8484	2	2004.2	(-0.6)	3.066	0.398	0.972	2	K.ATENDIYNFFSPL*NPVR.V
SW:ROF_HUMAN	R17	8468	3	1869.1	(+0.7)	4.519	0.459	0.999	1	K.ITGEAFVQFASQELAEK.A
SW:ROF_HUMAN	R22	8862	2	2004.2	(-0.7)	2.208	0.303	0.822	2	K.ATENDIYNFFSPL*NPVR.V
SW:ROG_HUMAN	R17	5896	2	835.0	(+0.2)	2.296	0.240	0.855	2	K.ALEAVFGK.Y
SW:ROG_HUMAN	R20	5814	2	835.0	(+0.7)	2.382	0.225	0.897	2	K.ALEAVFGK.Y
SW:ROG_HUMAN	R17	7620	2	1487.7	(+0.5)	4.098	0.402	0.998	5	R.GFAFVTFESPADAK.D
SW:ROG_HUMAN	R17	7640	2	1495.7	(-0.3)	3.836	0.478	1.000	5	R.GFAFVTFESPADAK#.D
SW:ROG_HUMAN	R17	7704	2	1487.7	(+0.7)	3.046	0.428	0.986	5	R.GFAFVTFESPADAK.D
SW:ROG_HUMAN	R19	7828	2	1487.7	(+0.5)	2.549	0.390	0.969	5	R.GFAFVTFESPADAK.D
SW:ROG_HUMAN	R16	6206	2	1456.6	(+0.2)	3.004	0.235	0.878	3	K.L*FIGGL*NTETNEK#.A
SW:ROG_HUMAN	R17	6542	2	1436.6	(+0.3)	3.468	0.367	0.986	3	K.LFIGGLNTETNEK.A
SW:ROG_HUMAN	R17	6540	2	1456.6	(+0.1)	3.113	0.296	0.938	3	K.L*FIGGL*NTETNEK#.A
SW:ROG_HUMAN	R17	6572	2	1436.6	(-1.0)	2.964	0.339	0.819	3	K.LFIGGLNTETNEK.A
SW:ROG_HUMAN	R19	6728	2	1436.6	(+0.8)	3.629	0.234	0.965	3	K.LFIGGLNTETNEK.A
SW:ROG_HUMAN	R19	6726	2	1456.6	(-0.1)	2.836	0.249	0.868	3	K.L*FIGGL*NTETNEK#.A
SW:ROG_HUMAN	R20	6528	2	1436.6	(+0.6)	4.036	0.337	0.988	3	K.LFIGGLNTETNEK.A
SW:ROG_HUMAN	R21	6526	2	1436.6	(+0.1)	3.234	0.297	0.958	3	K.LFIGGLNTETNEK.A
SW:ROG_HUMAN	R17	1530	2	1444.6	(+0.0)	2.808	0.237	0.125	2	K.VEQATK#PSFESGR.R
SW:ROG_HUMAN	R21	7526	2	1495.7	(-0.0)	2.903	0.343	0.943	5	R.GFAFVTFESPADAK#.D
SW:ROH1_HUMAN	R16	6074	2	1365.5	(+0.2)	2.777	0.396	0.908		K.SNNVEM@DWVL*K#.H
SW:ROH1_HUMAN	R16	6732	2	1349.5	(+0.5)	2.312	0.354	0.937		K.SNNVEMDWVL*K#.H
SW:ROH1_HUMAN	R22	7322	2	1335.5	(-0.1)	2.932	0.177	0.852		K.SNNVEMDWVLK.H
SW:ROH1_HUMAN	R15	7521	2	1851.0	(-0.5)	3.116	0.390	0.966	1	R.STGEAFVQFASQEIAEK#.A
SW:ROH1_HUMAN	R16	7300	2	1851.0	(+0.9)	4.954	0.549	0.999	1	R.STGEAFVQFASQEIAEK#.A
SW:ROH1_HUMAN	R16	7298	2	1843.0	(+0.7)	2.749	0.358	0.965	1	R.STGEAFVQFASQEIAEK.A
SW:ROH1_HUMAN	R18	7797	2	1843.0	(+0.5)	2.240	0.333	0.909	1	R.STGEAFVQFASQEIAEK.A
SW:ROH1_HUMAN	R22	7870	2	1851.0	(-0.6)	4.559	0.536	1.000	1	R.STGEAFVQFASQEIAEK#.A
SW:ROH1_HUMAN	R22	7864	2	1843.0	(+0.8)	3.905	0.458	1.000	1	R.STGEAFVQFASQEIAEK.A
SW:ROH3_HUMAN	R19	8990	2	1926.1	(+0.7)	3.203	0.412	0.986	6	R.ATENDIANFFSPL*NPVR.V
SW:ROH3_HUMAN	R20	8706	2	1920.1	(-0.4)	3.699	0.458	1.000	6	R.ATENDIANFFSPLNPVR.V
SW:ROH3_HUMAN	R19	7116	2	2187.4	(+0.7)	2.289	0.362*	0.085	6	R.ATGEADVFEVTHEDAVAAMSK#.D
SW:ROH3_HUMAN	R20	6784	3	2187.4	(+0.7)	4.122	0.535	1.000	6	R.ATGEADVFEVTHEDAVAAMSK#.D
SW:ROH3_HUMAN	R19	6496	2	2182.3	(+0.3)	4.665	0.584	0.999	4	R.MGMGNNSYGGYGTDPDGLGGYGR.G
SW:ROH3_HUMAN	R19	6494	2	2188.3	(-0.9)	3.670	0.422	0.959	4	R.MGMGNNSYGGYGTDPDGL*GGYGR.G
SW:ROH3_HUMAN	R18	6173	2	1280.4	(+0.7)	4.392	0.441	0.999	2	R.STGEAFVQFASK#.E
SW:ROH3_HUMAN	R19	6382	2	1280.4	(+0.9)	3.844	0.455	0.999	2	R.STGEAFVQFASK#.E
SW:ROH3_HUMAN	R19	6476	2	1272.4	(+0.9)	2.349	0.493	0.985	2	R.STGEAFVQFASK.E
SW:ROH3_HUMAN	R19	8052	3	2523.8	(+0.9)	4.281	0.430	0.500	4	R.YIELFLNSTPGGGSGMGGSGMGYGR.D
SW:ROH3_HUMAN	R26	6556	2	1280.4	(+0.9)	2.392	0.251	0.803	2	R.STGEAFVQFASK#.E
SW:ROK_HUMAN	R14	1318	2	1020.1	(+0.6)	2.346	0.291	0.933	1	R.GGDL*M@AYDR.R
SW:ROK_HUMAN	R15	1746	2	1004.1	(+0.1)	2.484	0.333	0.949	1	R.GGDL*MAYDR.R
SW:ROK_HUMAN	R15	1136	2	1020.1	(+0.4)	2.434	0.346	0.964	1	R.GGDL*M@AYDR.R
SW:ROK_HUMAN	R14	7411	2	1918.2	(+0.8)	4.637	0.573	0.999	1	R.GSYGDLGGPIITQVTIPK.D
SW:ROK_HUMAN	R14	7405	2	1932.2	(+0.9)	4.613	0.525	0.938	1	R.GSYGDL*GGPIITQVTIPK#.D
SW:ROK_HUMAN	R15	7183	3	1932.2	(+0.6)	3.917	0.459	0.899	1	R.GSYGDL*GGPIITQVTIPK#.D
SW:ROK_HUMAN	R14	1556	2	1266.3	(+0.1)	3.156	0.255	0.947	1	K.IDEPL*EGSEDR.I
SW:ROK_HUMAN	R14	1560	2	1260.3	(+0.6)	2.711	0.359	0.974	1	K.IDEPL*EGSEDR.I
SW:ROK_HUMAN	R15	1354	2	1266.3	(-0.3)	2.216	0.219	0.710	1	K.IDEPL*EGSEDR.I
SW:ROK_HUMAN	R14	8245	2	1361.6	(-0.2)	2.909	0.248	0.889	1	K.IIL*DL*ISESPIK#.G
SW:ROK_HUMAN	R17	8300	2	1341.6	(-0.1)	3.535	0.365	0.983	1	K.IILDISESPIK.G
SW:ROK_HUMAN	R17	8288	2	1361.6	(-0.0)	2.938	0.291	0.889	1	K.IIL*DL*ISESPIK#.G
SW:ROK_HUMAN	R20	8214	2	1341.6	(+0.9)	3.473	0.376	0.988	1	K.IILDISESPIK.G
SW:ROK_HUMAN	R14	8255	3	2590.9	(+0.7)	5.550	0.636	1.000	1	R.IITITGTQDQIQNAQYLLQNSVK.Q
SW:ROK_HUMAN	R14	7885	3	2590.9	(+0.8)	5.179	0.580	0.998	1	R.IITITGTQDQIQNAQYLLQNSVK.Q

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ROK_HUMAN	R14	8279	2	2590.9	(-0.9)	3.675	0.475	1.000	1	R.IITITGTQDQIQNAQYLLQNSVK.Q
SW:ROK_HUMAN	R14	8273	2	2610.9	(+0.0)	3.155	0.352	0.956	1	R.IITITGTQDQIQNAQYL*L*QNSVK#.Q
SW:ROK_HUMAN	R20	8198	3	2590.9	(+0.8)	5.471	0.615	1.000	1	R.IITITGTQDQIQNAQYLLQNSVK.Q
SW:ROK_HUMAN	R14	10013	2	1716.0	(+0.8)	4.900	0.498	1.000	1	R.ILSISADIETIGEILK.K
SW:ROK_HUMAN	R14	9927	2	1716.0	(+0.6)	4.758	0.587	0.999	1	R.ILSISADIETIGEILK.K
SW:ROK_HUMAN	R14	9923	2	1736.0	(+0.5)	3.955	0.450	1.000	1	R.IL*SISADIETIGEIL*K#.K
SW:ROK_HUMAN	R14	10043	2	1716.0	(-0.6)	3.820	0.566	1.000	1	R.ILSISADIETIGEILK.K
SW:ROK_HUMAN	R14	10405	2	1716.0	(-0.1)	3.179	0.455	0.984	1	R.ILSISADIETIGEILK.K
SW:ROK_HUMAN	R14	10011	2	1736.0	(-0.4)	3.116	0.280	0.911	1	R.IL*SISADIETIGEIL*K#.K
SW:ROK_HUMAN	R15	9675	2	1716.0	(+0.9)	5.094	0.628	0.999	1	R.ILSISADIETIGEILK.K
SW:ROK_HUMAN	R15	9649	2	1736.0	(-0.0)	2.297	0.363	0.888	1	R.IL*SISADIETIGEIL*K#.K
SW:ROK_HUMAN	R14	7391	2	1519.9	(+0.2)	4.369	0.397	0.999	1	R.LLIHQSLAGGIIGVK.G
SW:ROK_HUMAN	R14	7387	2	1545.9	(-0.9)	2.627	0.199	0.418	1	R.L*L*IHQSL*AGGIIGVK#.G
SW:ROK_HUMAN	R15	7163	2	1545.9	(-0.7)	3.387	0.386	0.972	1	R.L*L*IHQSL*AGGIIGVK#.G
SW:ROK_HUMAN	R14	2368	2	1107.2	(+0.1)	2.672	0.278	0.938	1	R.NTDEMVELR.I
SW:ROK_HUMAN	R14	2518	2	1107.2	(+0.5)	2.631	0.178	0.723	1	R.NTDEMVELR.I
SW:ROK_HUMAN	R14	2452	2	1113.2	(+0.8)	2.365	0.270	0.904	1	R.NTDEMVEL*R.I
SW:ROK_HUMAN	R14	2360	2	1113.2	(+0.9)	2.289	0.308	0.937	1	R.NTDEMVEL*R.I
SW:ROK_HUMAN	R15	2140	2	1113.2	(+0.3)	2.516	0.100	0.678	1	R.NTDEMVEL*R.I
SW:ROK_HUMAN	R15	1212	2	1129.2	(+0.4)	2.444	0.155	0.777	1	R.NTDEM@VEL*R.I
SW:ROK_HUMAN	R15	2220	2	1113.2	(+0.7)	2.360	0.204	0.844	1	R.NTDEMVEL*R.I
SW:ROK_HUMAN	R14	1994	2	1588.7	(+0.5)	3.926	0.530	1.000	1	K.RPAEDMEEEEQAFK#.R
SW:ROK_HUMAN	R14	1428	2	1604.7	(-0.3)	2.872	0.447	0.975	1	K.RPAEDM@EEEQAFK#.R
SW:ROK_HUMAN	R14	1968	3	1736.9	(+1.0)	5.178	0.474	1.000	1	K.RPAEDMEEEEQAFKR.S
SW:ROK_HUMAN	R14	2016	2	1054.3	(-0.7)	2.487	0.242	0.113	1	R.VVLIGGKPD.R.V
SW:ROK_HUMAN	R14	2020	2	1068.3	(+0.9)	2.483	0.322	0.295	1	R.VVL*IGGK#PDR.V
SW:ROK_HUMAN	R17	2328	2	1054.3	(+0.8)	2.722	0.316	0.325	1	R.VVLIGGKPD.R.V
SW:ROL_HUMAN	R13	6373	2	1665.9	(-0.1)	3.501	0.209	0.851	1	R.AITHL*NNNFM@FGQK#.L
SW:ROL_HUMAN	R14	5791	2	2735.8	(-0.9)	3.561	0.468	1.000	1	K.NDQDTWDYTNPNLSGQGDPGSNPNK.R
SW:ROL_HUMAN	R13	5777	3	2905.9	(-0.0)	4.755	0.428	0.992	1	K.NDQDTWDYTNPNL*SGQGDPGSNPNK#.R.Q
SW:ROL_HUMAN	R13	5781	3	2891.9	(+0.5)	4.214	0.577	1.000	1	K.NDQDTWDYTNPNLSGQGDPGSNPNK.R.Q
SW:ROL_HUMAN	R14	5723	3	2905.9	(+0.2)	5.430	0.515	1.000	1	K.NDQDTWDYTNPNL*SGQGDPGSNPNK#.R.Q
SW:ROL_HUMAN	R14	5727	3	2891.9	(+0.5)	4.717	0.570	1.000	1	K.NDQDTWDYTNPNLSGQGDPGSNPNK.R.Q
SW:ROL_HUMAN	R14	5757	2	2905.9	(-0.2)	3.491	0.423	0.560	1	K.NDQDTWDYTNPNL*SGQGDPGSNPNK#.R.Q
SW:ROL_HUMAN	R15	5675	3	2905.9	(-0.2)	4.453	0.422	0.989	1	K.NDQDTWDYTNPNL*SGQGDPGSNPNK#.R.Q
SW:ROL_HUMAN	R16	5450	3	2891.9	(+0.3)	4.550	0.559	1.000	1	K.NDQDTWDYTNPNLSGQGDPGSNPNK.R.Q
SW:ROL_HUMAN	R16	5446	3	2905.9	(-0.1)	4.465	0.464	1.000	1	K.NDQDTWDYTNPNL*SGQGDPGSNPNK#.R.Q
SW:ROL_HUMAN	R17	5902	3	2905.9	(+0.1)	4.530	0.462	1.000	1	K.NDQDTWDYTNPNL*SGQGDPGSNPNK#.R.Q
SW:ROL_HUMAN	R14	7689	2	1910.1	(+0.9)	3.440	0.446	0.987	1	K.SDAL*ETL*GFL*NHYQM@K#.N
SW:ROL_HUMAN	R14	8027	2	1868.1	(+0.8)	3.291	0.519	1.000	1	K.SDALETGLFLNHYQMK.N
SW:ROL_HUMAN	R14	8019	2	1894.1	(-0.5)	2.863	0.350	0.939	1	K.SDAL*ETL*GFL*NHYQMK#.N
SW:ROL_HUMAN	R13	6699	3	1877.1	(+1.0)	3.750	0.494	1.000	1	K.SK#PGAAMVEMADGYAVDR.A
SW:ROL_HUMAN	R14	6707	2	1869.1	(+0.9)	4.948	0.640	1.000	1	K.SK#PGAAMVEMADGYAVDR.A
SW:ROL_HUMAN	R14	6701	2	1877.1	(-0.6)	4.419	0.579	1.000	1	K.SK#PGAAMVEMADGYAVDR.A
SW:ROL_HUMAN	R14	5439	3	1893.1	(+0.6)	4.169	0.458*	0.028	1	K.SK#PGAAM@VEMADGYAVDR.A
SW:ROL_HUMAN	R14	6451	2	1223.3	(-0.0)	3.082	0.361	0.974	1	R.SSSGLEWESK.S
SW:ROL_HUMAN	R13	4323	3	2990.9	(-0.2)	5.584	0.536	1.000	1	K.TDNAGDQHGGGGGGGGGAGAAGGGGGGENYDDPHK#.T
SW:ROL_HUMAN	R13	4325	3	2982.9	(-0.1)	5.302	0.578	0.998	1	K.TDNAGDQHGGGGGGGGGAGAAGGGGGGENYDDPHK.T
SW:ROL_HUMAN	R14	4241	3	2982.9	(-0.0)	4.879	0.459	1.000	1	K.TDNAGDQHGGGGGGGGGAGAAGGGGGGENYDDPHK.T
SW:ROL_HUMAN	R14	4233	3	2990.9	(+0.4)	4.012	0.530	0.999	1	K.TDNAGDQHGGGGGGGGGAGAAGGGGGGENYDDPHK#.T
SW:ROL_HUMAN	R14	7721	3	3787.2	(-0.3)	7.403	0.609	0.994	1	R.YGPQYGHPPPPPPPEYGPHADSPVLMVYGLDQSK.M
SW:ROL_HUMAN	R18	5651	3	2905.9	(-0.2)	5.667	0.522	1.000	1	K.NDQDTWDYTNPNL*SGQGDPGSNPNK#.R.Q
SW:ROM_HUMAN	R12	1112	2	1104.2	(+0.3)	2.244	0.222	0.077	7	R.ADILEDKDKGK.S
SW:ROM_HUMAN	R11	7512	2	1273.5	(+0.4)	3.458	0.428	0.995	6	R.AFITNIPFDVK#.W
SW:ROM_HUMAN	R12	7612	2	1265.5	(+1.0)	3.237	0.413	0.990	6	R.AFITNIPFDVK.W
SW:ROM_HUMAN	R12	7608	2	1273.5	(+0.3)	2.795	0.381	0.641	6	R.AFITNIPFDVK#.W
SW:ROM_HUMAN	R13	7847	2	1273.5	(+0.5)	3.369	0.443	1.000	6	R.AFITNIPFDVK#.W
SW:ROM_HUMAN	R13	7845	2	1265.5	(+0.1)	2.915	0.356	0.970	6	R.AFITNIPFDVK.W
SW:ROM_HUMAN	R12	8146	3	2179.6	(+1.0)	4.529	0.488*	0.172	7	K.GIGMGNIGPAGMGMEGIGFGINK.M
SW:ROM_HUMAN	R12	7546	3	2203.6	(+0.8)	4.020	1.000*	0.113	7	K.GIGMGNIGPAGMGMEGIGFGINK#.M
SW:ROM_HUMAN	R12	6416	2	2235.6	(+0.3)	3.906	0.583*	0.625	7	K.GIGM@GNIGPAGM@GM@EGIGFGINK#.M
SW:ROM_HUMAN	R11	6796	2	1447.6	(+0.0)	2.852	0.123	0.608	7	R.L*GSTVFNANL*DYK#.V
SW:ROM_HUMAN	R12	6768	2	1427.6	(+0.1)	3.329	0.443	0.987	7	R.LGSTVFNANLDYK.V
SW:ROM_HUMAN	R12	1294	2	1877.0	(+0.3)	3.274	0.432	0.985	2	K.MEEESGAPGVPSGNGAPGPK#.G

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ROM_HUMAN	R12	1296	2	1869.0	(+0.4)	2.732	0.408	0.977	2	K.MEEESGAPGVPSGNGAPGPK.G
SW:ROM_HUMAN	R11	1880	2	1164.3	(+0.9)	2.505	0.384	0.972	9	R.M@GAGM@GFGL*ER.M
SW:ROM_HUMAN	R12	5034	2	1148.3	(+0.3)	3.126	0.443	0.991	9	R.MGAGM@GFGL*ER.M
SW:ROM_HUMAN	R12	5500	2	1148.3	(-0.2)	2.887	0.238	0.910	9	R.M@GAGMGFGL*ER.M
SW:ROM_HUMAN	R12	958	2	905.0	(+0.9)	2.424	0.286	0.900	8	R.MGANNLER.M
SW:ROM_HUMAN	R11	4890	2	1406.6	(-0.2)	2.566	0.208	0.741	6	R.M@GL*AMGGGGGASFDRA
SW:ROM_HUMAN	R12	1348	2	1422.6	(-0.1)	2.733	0.335	0.938	6	R.M@GL*AM@GGGGGASFDRA
SW:ROM_HUMAN	R12	2224	2	1406.6	(-0.3)	2.660	0.408*	0.168	6	R.MGL*AM@GGGGGASFDRA
SW:ROM_HUMAN	R11	2342	2	1466.7	(-0.4)	3.207	0.280	0.940	8	R.M@GPAM@GPAL*GAGIER.M
SW:ROM_HUMAN	R11	2264	2	1466.7	(-0.4)	3.166	0.255	0.922	8	R.M@GPAM@GPAL*GAGIER.M
SW:ROM_HUMAN	R12	6074	2	1434.7	(+0.0)	2.791	0.329	0.939	8	R.MGPAMGPAL*GAGIER.M
SW:ROM_HUMAN	R12	6082	2	1428.7	(-0.6)	2.741	0.354	0.948	8	R.MGPAMGPALGAGIER.M
SW:ROM_HUMAN	R12	2210	2	1466.7	(-0.4)	2.598	0.204	0.745	8	R.M@GPAM@GPAL*GAGIER.M
SW:ROM_HUMAN	R12	6790	2	1614.9	(+0.7)	5.044	0.604	1.000	9	R.MGPLGLDHMASSIER.M
SW:ROM_HUMAN	R12	6368	2	1642.9	(-0.4)	3.601	0.385	0.982	9	R.M@GPL*GL*DHEMASSIER.M
SW:ROM_HUMAN	R11	7736	2	1790.0	(-0.3)	3.054	0.503	0.983	6	K.VGEVTVVEL*L*M@DAEGK#.S
SW:ROM_HUMAN	R12	8454	3	1774.0	(+0.9)	4.397	0.455	1.000	6	K.VGEVTVVEL*L*MDAEGK#.S
SW:ROM_HUMAN	R15	7561	2	1273.5	(+0.7)	2.324	0.332	0.923	6	R.AFITNIPFDVK#.W
SW:ROR_HUMAN	R11	8170	2	1610.8	(+0.8)	2.957	0.482	0.990	2	R.DLYEDELVPLFEK.A
SW:ROR_HUMAN	R11	8162	2	1636.8	(-0.2)	2.558	0.293	0.872	2	R.DL*YEDEL*VPL*FEK#.A
SW:ROR_HUMAN	R12	8300	2	1610.8	(+0.6)	3.325	0.394	0.986	2	R.DLYEDELVPLFEK.A
SW:ROR_HUMAN	R13	8483	2	1610.8	(+0.3)	3.721	0.425	1.000	2	R.DLYEDELVPLFEK.A
SW:ROR_HUMAN	R12	8298	2	1739.9	(+0.4)	4.260	0.460	1.000	2	R.EFNEEGALSVLQQFK.E
SW:ROR_HUMAN	R11	818	2	1157.2	(+0.8)	2.536	0.311	0.944	2	K.ESDLSHVQNK.S
SW:ROR_HUMAN	R13	880	2	1239.3	(+0.8)	3.153	0.440	0.988	5	R.K#ADGYNQPDSK#.R
SW:ROR_HUMAN	R13	7219	3	2637.0	(+0.6)	3.721	0.416	0.999	2	R.KYGGPPPDSVYSGVQPGIGTEVFVGK.I
SW:ROR_HUMAN	R11	6104	2	1274.5	(-0.1)	3.069	0.448*	0.445	2	R.L*MMDPL*SGQNR.G
SW:ROR_HUMAN	R12	5934	2	1274.5	(+0.6)	2.842	0.432	0.987	2	R.L*MMDPL*SGQNR.G
SW:ROR_HUMAN	R13	6321	2	1274.5	(-0.6)	2.714	0.267*	0.282	2	R.L*MMDPL*SGQNR.G
SW:ROR_HUMAN	R14	4809	2	1290.5	(+0.7)	2.282	0.248*	0.164	2	R.L*MM@DPL*SGQNR.G
SW:ROR_HUMAN	R11	8020	2	1481.7	(+0.5)	3.329	0.465	1.000	2	R.NL*ATTVTEEIL*EK#.S
SW:ROR_HUMAN	R12	8156	2	1481.7	(+0.3)	3.598	0.441	1.000	2	R.NL*ATTVTEEIL*EK#.S
SW:ROR_HUMAN	R13	8369	2	1461.7	(+0.8)	4.021	0.398	1.000	2	R.NLATTVTEEILEK.S
SW:ROR_HUMAN	R13	8399	2	1481.7	(-0.3)	3.284	0.296	0.947	2	R.NL*ATTVTEEIL*EK#.S
SW:ROR_HUMAN	R14	8275	2	1481.7	(-0.5)	3.087	0.266	0.915	2	R.NL*ATTVTEEIL*EK#.S
SW:ROR_HUMAN	R17	8306	2	1481.7	(+0.1)	3.369	0.327	0.962	2	R.NL*ATTVTEEIL*EK#.S
SW:ROR_HUMAN	R18	8343	2	1481.7	(-0.4)	3.445	0.378	0.975	2	R.NL*ATTVTEEIL*EK#.S
SW:ROR_HUMAN	R11	4270	2	1312.4	(+0.1)	2.868	0.423	0.979	8	R.TGYTLDVTTGQR.K
SW:ROR_HUMAN	R11	4190	2	1312.4	(+0.0)	2.844	0.390	0.973	8	R.TGYTLDVTTGQR.K
SW:ROR_HUMAN	R11	3886	2	1318.4	(-0.0)	2.749	0.422	0.976	8	R.TGYTL*DVTTGQR.K
SW:ROR_HUMAN	R11	3960	2	1312.4	(+0.0)	2.714	0.336	0.950	8	R.TGYTLDVTTGQR.K
SW:ROR_HUMAN	R11	4038	2	1312.4	(-0.6)	2.692	0.379	0.965	8	R.TGYTLDVTTGQR.K
SW:ROR_HUMAN	R11	4046	2	1318.4	(-0.5)	2.681	0.404	0.971	8	R.TGYTL*DVTTGQR.K
SW:ROR_HUMAN	R11	4114	2	1312.4	(-0.1)	2.629	0.414	0.971	8	R.TGYTLDVTTGQR.K
SW:ROR_HUMAN	R11	4276	2	1318.4	(-0.1)	2.547	0.267	0.881	8	R.TGYTL*DVTTGQR.K
SW:ROR_HUMAN	R11	4122	2	1318.4	(-0.4)	2.499	0.272	0.878	8	R.TGYTL*DVTTGQR.K
SW:ROR_HUMAN	R11	3972	2	1318.4	(-0.1)	2.498	0.354	0.943	8	R.TGYTL*DVTTGQR.K
SW:ROR_HUMAN	R11	4198	2	1318.4	(-0.7)	2.296	0.332	0.894	8	R.TGYTL*DVTTGQR.K
SW:ROR_HUMAN	R12	4192	2	1312.4	(+0.5)	3.119	0.458	0.991	8	R.TGYTLDVTTGQR.K
SW:ROR_HUMAN	R12	4326	2	1312.4	(-0.5)	2.945	0.370	0.972	8	R.TGYTLDVTTGQR.K
SW:ROR_HUMAN	R12	4116	2	1312.4	(-0.4)	2.814	0.392	0.972	8	R.TGYTLDVTTGQR.K
SW:ROR_HUMAN	R12	3890	2	1312.4	(-0.5)	2.770	0.255	0.903	8	R.TGYTLDVTTGQR.K
SW:ROR_HUMAN	R12	4040	2	1312.4	(-0.6)	2.752	0.398	0.972	8	R.TGYTLDVTTGQR.K
SW:ROR_HUMAN	R12	3952	2	1318.4	(-0.6)	2.645	0.324	0.939	8	R.TGYTL*DVTTGQR.K
SW:ROR_HUMAN	R12	4266	2	1318.4	(+0.3)	2.574	0.422	0.980	8	R.TGYTL*DVTTGQR.K
SW:ROR_HUMAN	R12	3880	2	1318.4	(-0.7)	2.422	0.333	0.917	8	R.TGYTL*DVTTGQR.K
SW:ROR_HUMAN	R12	3742	2	1318.4	(+0.1)	2.394	0.336	0.922	8	R.TGYTL*DVTTGQR.K
SW:ROR_HUMAN	R12	3816	2	1312.4	(-0.1)	2.393	0.249	0.820	8	R.TGYTLDVTTGQR.K
SW:ROR_HUMAN	R12	4250	2	1312.4	(-0.8)	2.366	0.327	0.770	8	R.TGYTLDVTTGQR.K
SW:ROR_HUMAN	R12	4190	2	1318.4	(-0.1)	2.348	0.350	0.926	8	R.TGYTL*DVTTGQR.K
SW:ROR_HUMAN	R12	4114	2	1318.4	(-0.4)	2.252	0.329	0.894	8	R.TGYTL*DVTTGQR.K
SW:ROR_HUMAN	R12	3810	2	1318.4	(+0.3)	2.237	0.334	0.926	8	R.TGYTL*DVTTGQR.K
SW:ROR_HUMAN	R13	4785	2	1312.4	(+0.0)	2.563	0.390	0.962	8	R.TGYTLDVTTGQR.K
SW:ROR_HUMAN	R13	4687	2	1318.4	(+0.5)	2.349	0.330	0.937	8	R.TGYTL*DVTTGQR.K
SW:ROR_HUMAN	R14	4905	2	1312.4	(-0.1)	2.598	0.398	0.966	8	R.TGYTLDVTTGQR.K

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ROR_HUMAN	R14	4767	2	1318.4	(-0.1)	2.582	0.295	0.913	8	R.TGYTL*DVTTGQR.K
SW:ROR_HUMAN	R15	4553	2	1312.4	(-0.3)	2.489	0.262	0.863	8	R.TGYTLDVTTGQR.K
SW:ROR_HUMAN	R11	6566	2	1360.5	(-0.4)	3.739	0.439	0.983	2	K.TK#ENIL*EEFSK#.V
SW:ROR_HUMAN	R11	6554	2	1338.5	(+0.1)	3.249	0.323	0.413	2	K.TKENILEEFSK.V
SW:ROR_HUMAN	R12	6484	2	1338.5	(+1.0)	4.237	0.329	1.000	2	K.TKENILEEFSK.V
SW:ROR_HUMAN	R12	6464	2	1360.5	(-0.6)	2.704	0.234	0.101	2	K.TK#ENIL*EEFSK#.V
SW:ROR_HUMAN	R14	6809	2	1338.5	(+0.6)	3.353	0.326	0.535	2	K.TKENILEEFSK.V
SW:ROR_HUMAN	R14	6805	2	1360.5	(-0.8)	2.471	0.138	0.008	2	K.TK#ENIL*EEFSK#.V
SW:ROR_HUMAN	R11	5452	2	1090.3	(+0.2)	2.752	0.450	0.978	1	K.TL*IEAGL*PQK#.V
SW:ROR_HUMAN	R12	5192	2	1090.3	(+0.1)	2.436	0.368	0.940	1	K.TL*IEAGL*PQK#.V
SW:ROR_HUMAN	R13	7933	2	1942.2	(-0.5)	3.548	0.418	0.980		K.VTEGLVDVILYHQPDDK.K
SW:ROR_HUMAN	R14	7889	2	1942.2	(+0.5)	3.913	0.555	1.000		K.VTEGLVDVILYHQPDDK.K
SW:ROR_HUMAN	R11	7068	3	2516.8	(+0.3)	3.735	0.263	0.968	2	K.YGGPPDPSVYSGVQPGIGTEVFVGK#.I
SW:ROR_HUMAN	R12	7150	3	2516.8	(+0.4)	3.765	0.445	0.998	2	K.YGGPPDPSVYSGVQPGIGTEVFVGK#.I
SW:ROR_HUMAN	R13	7369	3	2516.8	(+0.7)	4.700	0.453	0.999	2	K.YGGPPDPSVYSGVQPGIGTEVFVGK#.I
SW:ROR_HUMAN	R13	7377	2	2508.8	(-0.4)	2.584	0.319	0.912	2	K.YGGPPDPSVYSGVQPGIGTEVFVGK.I
SW:ROR_HUMAN	R21	8198	2	1610.8	(-0.1)	2.394	0.254	0.814	2	R.DLYEDELVPLFEK.A
SW:ROU_HUMAN	R09	1764	2	1022.2	(+0.9)	2.357	0.304	0.910	7	K.DLPEHAVLK.M
SW:ROU_HUMAN	R04	8290	3	2740.1	(-0.2)	3.723	0.401	0.972	6	K.EK#PYFFPIPEEYTFIQNVPL*EDR.V
SW:ROU_HUMAN	R05	8152	3	2740.1	(+0.4)	5.306	0.465	1.000	6	K.EK#PYFFPIPEEYTFIQNVPL*EDR.V
SW:ROU_HUMAN	R07	8401	3	2740.1	(+0.2)	4.635	0.331	0.959	6	K.EK#PYFFPIPEEYTFIQNVPL*EDR.V
SW:ROU_HUMAN	R08	8539	3	2740.1	(+0.7)	5.170	0.468	1.000	6	K.EK#PYFFPIPEEYTFIQNVPL*EDR.V
SW:ROU_HUMAN	R08	8541	3	2726.1	(-0.0)	4.457	0.442	0.993	6	K.EKPYFFPIPEEYTFIQNVPLEDR.V
SW:ROU_HUMAN	R08	8555	2	2740.1	(-0.8)	3.162	0.344	0.148	6	K.EK#PYFFPIPEEYTFIQNVPL*EDR.V
SW:ROU_HUMAN	R09	8228	3	2726.1	(-0.1)	4.894	0.473	1.000	6	K.EKPYFFPIPEEYTFIQNVPLEDR.V
SW:ROU_HUMAN	R09	8218	3	2740.1	(+0.2)	4.034	0.371	0.966	6	K.EK#PYFFPIPEEYTFIQNVPL*EDR.V
SW:ROU_HUMAN	R10	8725	3	2726.1	(+0.7)	3.966	0.434	0.994	6	K.EKPYFFPIPEEYTFIQNVPLEDR.V
SW:ROU_HUMAN	R11	8328	3	2726.1	(+0.1)	5.775	0.473	1.000	6	K.EKPYFFPIPEEYTFIQNVPLEDR.V
SW:ROU_HUMAN	R11	8324	3	2740.1	(+0.3)	4.765	0.504	1.000	6	K.EK#PYFFPIPEEYTFIQNVPL*EDR.V
SW:ROU_HUMAN	R12	8474	3	2740.1	(-0.3)	4.587	0.429	0.991	6	K.EK#PYFFPIPEEYTFIQNVPL*EDR.V
SW:ROU_HUMAN	R01	6393	2	1292.4	(+0.7)	3.087	0.238	0.958	5	R.GYFEYIEENK.Y
SW:ROU_HUMAN	R01	6391	2	1300.4	(-0.3)	3.081	0.301	0.955	5	R.GYFEYIEENK#.Y
SW:ROU_HUMAN	R02	6216	2	1292.4	(+0.2)	2.953	0.380	0.979	5	R.GYFEYIEENK.Y
SW:ROU_HUMAN	R03	6097	2	1300.4	(-0.1)	2.433	0.139	0.498	5	R.GYFEYIEENK#.Y
SW:ROU_HUMAN	R06	6492	2	1292.4	(+0.6)	3.484	0.282	0.981	5	R.GYFEYIEENK.Y
SW:ROU_HUMAN	R07	6399	2	1300.4	(+0.6)	3.673	0.329	0.985	5	R.GYFEYIEENK#.Y
SW:ROU_HUMAN	R07	6397	2	1292.4	(+0.1)	3.219	0.357	0.981	5	R.GYFEYIEENK.Y
SW:ROU_HUMAN	R08	6667	2	1300.4	(-0.2)	3.008	0.253	0.926	5	R.GYFEYIEENK#.Y
SW:ROU_HUMAN	R09	6090	2	1300.4	(+0.2)	3.603	0.307	0.974	5	R.GYFEYIEENK#.Y
SW:ROU_HUMAN	R09	6174	2	1300.4	(+0.1)	3.023	0.292	0.948	5	R.GYFEYIEENK#.Y
SW:ROU_HUMAN	R09	6120	2	1292.4	(-0.1)	2.432	0.248	0.861	5	R.GYFEYIEENK.Y
SW:ROU_HUMAN	R10	6775	2	1300.4	(-0.5)	2.576	0.220	0.819	5	R.GYFEYIEENK#.Y
SW:ROU_HUMAN	R11	6372	2	1292.4	(+0.8)	3.595	0.396	1.000	5	R.GYFEYIEENK.Y
SW:ROU_HUMAN	R14	6631	2	1292.4	(+0.6)	2.465	0.357	0.967	5	R.GYFEYIEENK.Y
SW:ROU_HUMAN	R15	6403	2	1292.4	(+0.8)	3.504	0.331	0.987	5	R.GYFEYIEENK.Y
SW:ROU_HUMAN	R15	6401	2	1300.4	(-0.1)	3.246	0.288	0.958	5	R.GYFEYIEENK#.Y
SW:ROU_HUMAN	R08	1494	2	1295.4	(+0.0)	2.531	0.257	0.109	6	K.L*L*EQYK#EESK#.K
SW:ROU_HUMAN	R09	1190	2	1295.4	(-0.6)	3.261	0.362	0.444	6	K.L*L*EQYK#EESK#.K
SW:ROU_HUMAN	R01	6381	3	3152.3	(+0.5)	6.195	0.631	1.000	3	R.L*QAAL*DDEEAGGRPAMEPGNGSL*DL*GGDSAGR.S
SW:ROU_HUMAN	R01	5973	3	3168.3	(+0.2)	4.678	0.504	1.000	3	R.L*QAAL*DDEEAGGRPAM@EPGNGSL*DL*GGDSAGR.S
SW:ROU_HUMAN	R02	5752	3	3168.3	(+0.2)	5.173	0.520	1.000	3	R.L*QAAL*DDEEAGGRPAM@EPGNGSL*DL*GGDSAGR.S
SW:ROU_HUMAN	R03	5641	3	3168.3	(+0.2)	5.439	0.581	1.000	3	R.L*QAAL*DDEEAGGRPAM@EPGNGSL*DL*GGDSAGR.S
SW:ROU_HUMAN	R04	5996	3	3168.3	(+0.3)	5.305	0.518	0.997	3	R.L*QAAL*DDEEAGGRPAM@EPGNGSL*DL*GGDSAGR.S
SW:ROU_HUMAN	R08	6695	3	3152.3	(+1.0)	6.299	0.621	1.000	3	R.L*QAAL*DDEEAGGRPAMEPGNGSL*DL*GGDSAGR.S
SW:ROU_HUMAN	R08	6197	3	3168.3	(-0.0)	5.269	0.539	1.000	3	R.L*QAAL*DDEEAGGRPAM@EPGNGSL*DL*GGDSAGR.S
SW:ROU_HUMAN	R08	6347	3	3168.3	(+0.5)	5.196	0.548	0.999	3	R.L*QAAL*DDEEAGGRPAM@EPGNGSL*DL*GGDSAGR.S
SW:ROU_HUMAN	R08	6585	3	3152.3	(+0.5)	4.988	0.517	0.995	3	R.L*QAAL*DDEEAGGRPAMEPGNGSL*DL*GGDSAGR.S
SW:ROU_HUMAN	R09	6144	3	3128.3	(+0.8)	5.772	0.564	1.000	3	R.LQAALDDEEAGGRPAMEPGNGSLDLGGDSAGR.S
SW:ROU_HUMAN	R09	5796	3	3168.3	(-0.0)	5.495	0.532	1.000	3	R.L*QAAL*DDEEAGGRPAM@EPGNGSL*DL*GGDSAGR.S
SW:ROU_HUMAN	R09	5634	3	3168.3	(-0.2)	5.467	0.605	1.000	3	R.L*QAAL*DDEEAGGRPAM@EPGNGSL*DL*GGDSAGR.S
SW:ROU_HUMAN	R09	6020	3	3152.3	(+0.2)	5.446	0.576	1.000	3	R.L*QAAL*DDEEAGGRPAMEPGNGSL*DL*GGDSAGR.S
SW:ROU_HUMAN	R09	5716	3	3168.3	(-0.2)	5.135	0.469	1.000	3	R.L*QAAL*DDEEAGGRPAM@EPGNGSL*DL*GGDSAGR.S
SW:ROU_HUMAN	R10	6209	3	3168.3	(+0.7)	4.849	0.498	0.996	3	R.L*QAAL*DDEEAGGRPAM@EPGNGSL*DL*GGDSAGR.S
SW:ROU_HUMAN	R10	6595	3	3152.3	(-0.2)	4.663	0.450	0.994	3	R.L*QAAL*DDEEAGGRPAMEPGNGSL*DL*GGDSAGR.S
SW:ROU_HUMAN	R15	6353	3	3152.3	(-0.1)	4.324	0.519	1.000	3	R.L*QAAL*DDEEAGGRPAMEPGNGSL*DL*GGDSAGR.S

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ROU_HUMAN	R01	6325	2	1648.8	(+0.9)	4.899	0.429	1.000	6	R.NFILDQTNVSAQAQR.R
SW:ROU_HUMAN	R03	6015	2	1648.8	(+0.2)	4.441	0.497	1.000	6	R.NFILDQTNVSAQAQR.R
SW:ROU_HUMAN	R08	6577	3	1648.8	(+0.7)	4.443	0.407	0.998	6	R.NFILDQTNVSAQAQR.R
SW:ROU_HUMAN	R08	6581	2	1654.8	(-0.3)	4.125	0.402	1.000	6	R.NFIL*DQTNVSAQAQR.R
SW:ROU_HUMAN	R08	6583	2	1648.8	(-0.3)	3.135	0.385	0.974	6	R.NFILDQTNVSAQAQR.R
SW:ROU_HUMAN	R09	6000	2	1648.8	(+0.5)	3.965	0.495	1.000	6	R.NFILDQTNVSAQAQR.R
SW:ROU_HUMAN	R09	5996	2	1654.8	(-0.3)	3.849	0.413	0.987	6	R.NFIL*DQTNVSAQAQR.R
SW:ROU_HUMAN	R10	6565	2	1648.8	(+0.9)	4.256	0.482	1.000	6	R.NFILDQTNVSAQAQR.R
SW:ROU_HUMAN	R10	6637	3	1648.8	(+0.7)	3.851	0.265	0.985	6	R.NFILDQTNVSAQAQR.R
SW:ROU_HUMAN	R10	6569	2	1654.8	(+0.4)	3.164	0.357	0.978	6	R.NFIL*DQTNVSAQAQR.R
SW:ROU_HUMAN	R08	5285	2	1049.2	(+0.8)	3.070	0.378	0.986	7	K.NGQDLGVAFK.I
SW:ROU_HUMAN	R09	4352	2	1063.2	(+0.8)	2.552	0.108	0.614	7	K.NGQDL*GVAFK#.I
SW:ROU_HUMAN	R09	4626	2	1063.2	(-0.0)	2.287	0.224	0.725	7	K.NGQDL*GVAFK#.I
SW:ROU_HUMAN	R10	4873	2	1049.2	(+0.2)	2.510	0.387	0.964	7	K.NGQDLGVAFK.I
SW:ROU_HUMAN	R10	5031	2	1049.2	(+0.8)	2.434	0.382	0.971	7	K.NGQDLGVAFK.I
SW:ROU_HUMAN	R12	4488	2	1049.2	(+0.6)	2.877	0.391	0.978	7	K.NGQDLGVAFK.I
SW:ROU_HUMAN	R12	4502	2	1063.2	(-0.4)	2.419	0.135	0.532	7	K.NGQDL*GVAFK#.I
SW:ROU_HUMAN	R14	5091	2	1063.2	(+0.9)	2.312	0.147	0.605	7	K.NGQDL*GVAFK#.I
SW:ROU_HUMAN	R08	7541	3	3668.9	(-0.5)	4.813	0.531	1.000	6	K.NQSQGYNQWQQGQFWGQK#PWSQHYHQGY.-
SW:ROU_HUMAN	R09	7078	3	3668.9	(-0.7)	4.880	0.416	0.991	6	K.NQSQGYNQWQQGQFWGQK#PWSQHYHQGY.-
SW:ROU_HUMAN	R09	7082	3	3660.9	(-0.3)	4.344	0.504	1.000	6	K.NQSQGYNQWQQGQFWGQK#PWSQHYHQGY.-
SW:ROU_HUMAN	R09	1430	2	1075.2	(+0.7)	3.175	0.372*	0.041	4	K.VSELKEELK.K
SW:ROU_HUMAN	R01	5879	2	1413.6	(+0.0)	2.560	0.139	0.549	6	K.YNIL*GTNTIM@DK#.M
SW:ROU_HUMAN	R02	5860	2	1413.6	(+0.5)	2.804	0.404	0.977	6	K.YNIL*GTNTIM@DK#.M
SW:ROU_HUMAN	R04	6080	2	1413.6	(-0.0)	2.452	0.252	0.792	6	K.YNIL*GTNTIM@DK#.M
SW:ROU_HUMAN	R08	6969	2	1383.6	(+0.0)	3.875	0.336	0.983	6	K.YNILGTNTIMDK.M
SW:ROU_HUMAN	R08	6967	2	1397.6	(-0.6)	2.876	0.374	0.961	6	K.YNIL*GTNTIMDK#.M
SW:ROU_HUMAN	R08	6301	2	1413.6	(-0.2)	2.588	0.319	0.911	6	K.YNIL*GTNTIM@DK#.M
SW:ROU_HUMAN	R09	6412	2	1397.6	(-0.2)	3.234	0.424	0.980	6	K.YNIL*GTNTIMDK#.M
SW:ROU_HUMAN	R09	5742	2	1413.6	(-0.9)	2.379	0.268	0.577	6	K.YNIL*GTNTIM@DK#.M
SW:ROU_HUMAN	R10	7717	2	1383.6	(+0.2)	2.919	0.326	0.956	6	K.YNILGTNTIMDK.M
SW:ROU_HUMAN	R10	6269	2	1413.6	(+0.5)	2.908	0.416	0.981	6	K.YNIL*GTNTIM@DK#.M
SW:ROU_HUMAN	R10	7745	2	1397.6	(-0.1)	2.262	0.244	0.714	6	K.YNIL*GTNTIMDK#.M
SW:ROU_HUMAN	R11	6630	2	1397.6	(+0.2)	2.635	0.372	0.948	6	K.YNIL*GTNTIMDK#.M
SW:ROU_HUMAN	R12	6576	2	1397.6	(+0.1)	2.729	0.404	0.964	6	K.YNIL*GTNTIMDK#.M
SW:RPB1_HUMAN	R05	6660	2	1257.5	(+0.2)	2.486	0.334	0.937	1	R.AEIQELAMVPR.M
SW:RPB1_HUMAN	R05	6134	2	1279.5	(-0.5)	2.422	0.148	0.610	1	R.AEIQEL*AM@VPR.M
SW:RPB1_HUMAN	R05	6220	2	1638.8	(+1.0)	4.021	0.522	1.000	1	K.DVLSNAHIQNELER.E
SW:RPB1_HUMAN	R05	6212	2	1650.8	(-0.1)	3.299	0.337	0.969	1	K.DVL*SNAHIQNEL*ER.E
SW:RPB1_HUMAN	R05	5248	2	1564.6	(-0.3)	3.030	0.338	0.959	1	K.FGVEQPEGDEDLTK.E
SW:RPB1_HUMAN	R05	5246	2	1578.6	(-0.2)	2.767	0.219	0.793	1	K.FGVEQPEGDEDL*TK#.E
SW:RPB1_HUMAN	R06	5292	2	1578.6	(-0.9)	2.644	0.259	0.617	1	K.FGVEQPEGDEDL*TK#.E
SW:RPB1_HUMAN	R05	9386	2	1900.2	(-0.2)	2.230	0.130	0.281	1	R.GEVM@NL*L*M@FL*STWDGK#.V
SW:RPB1_HUMAN	R05	5996	2	1173.3	(+0.5)	2.296	0.129	0.473	1	K.IIITEDGEFK#.A
SW:RPB1_HUMAN	R05	7926	3	1905.2	(+1.0)	5.263	0.501	0.988	1	K.INISQVIAVVGQQNVEGK#.R
SW:RPB1_HUMAN	R06	8128	3	1897.2	(+0.8)	4.994	0.475	1.000	1	K.INISQVIAVVGQQNVEGK.R
SW:RPB1_HUMAN	R05	5192	2	1213.4	(+0.3)	2.473	0.204	0.816	1	R.K#L*TMEQIAEK#.I
SW:RPB1_HUMAN	R05	10496	3	3433.9	(-0.0)	4.034	0.480	0.993	1	R.LFYNSIQTVINWLLIEGHTIGIGDSIADSK.T
SW:RPB1_HUMAN	R05	1214	2	1000.1	(+0.7)	2.408	0.193	0.841	1	K.LLVDSNPK.I
SW:RPB1_HUMAN	R05	9096	2	1795.0	(+0.8)	3.972	0.472	0.998		R.LSGEAFDWLLGEIESK.F
SW:RPB1_HUMAN	R06	9398	2	1795.0	(+0.8)	4.000	0.489	1.000		R.LSGEAFDWLLGEIESK.F
SW:RPB1_HUMAN	R05	6372	2	1298.5	(+0.9)	3.329	0.341	0.983	1	K.LVIVNGDDPLSR.Q
SW:RPB1_HUMAN	R05	6368	2	1310.5	(-0.1)	2.584	0.280	0.900	1	K.L*VIVNGDDPL*SR.Q
SW:RPB1_HUMAN	R05	7872	3	2550.0	(+0.7)	6.057	0.511*	0.115	1	R.M@IVTPQSNRPMGIVQDTL*TAVR.K
SW:RPB1_HUMAN	R05	7528	3	2550.0	(+0.8)	5.174	0.401	0.996	1	R.MIVTPQSNRPM@GIVQDTL*TAVR.K
SW:RPB1_HUMAN	R05	5862	2	1171.3	(+0.0)	3.186	0.361	0.980	1	R.NSINQVQLR.Y
SW:RPB1_HUMAN	R06	5836	2	1171.3	(+0.4)	2.418	0.321	0.950	1	R.NSINQVQLR.Y
SW:RPB1_HUMAN	R06	5834	2	1177.3	(+0.5)	2.340	0.272	0.907	1	R.NSINQVQL*R.Y
SW:RPB1_HUMAN	R05	6046	2	1073.2	(+0.8)	2.380	0.176	0.698	1	K.QDVIEVIEK.A
SW:RPB1_HUMAN	R05	7110	2	1216.3	(-0.6)	2.350	0.332	0.904	2	R.SGL*EL*YAEWK#.H
SW:RPB1_HUMAN	R05	7994	2	1508.7	(-0.4)	3.101	0.347	0.957	1	K.TPSL*TVFL*L*GQSAR.D
SW:RPB1_HUMAN	R05	9974	3	2078.4	(+1.0)	4.040	0.403	0.996	1	R.TTSNDIVEIFTVLGIEAVR.K
SW:RPB1_HUMAN	R05	9986	2	2078.4	(-0.1)	3.145	0.294	0.944	1	R.TTSNDIVEIFTVLGIEAVR.K
SW:RPB1_HUMAN	R05	7034	2	1928.2	(+0.4)	4.076	0.461	1.000	1	R.TVITPDPNL*SIDQVGVPR.S
SW:RPB1_HUMAN	R05	7036	2	1922.2	(-0.5)	3.587	0.449	1.000	1	R.TVITPDPNLSIDQVGVPR.S

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:RPB1_HUMAN	R05	1982	2	1232.4	(+0.1)	2.622	0.434	0.973	1	K.TYQDIQNTIK#.K
SW:RPB1_HUMAN	R05	1984	2	1224.4	(+0.7)	2.272	0.306	0.925	1	K.TYQDIQNTIK.K
SW:RPB1_HUMAN	R05	7118	2	1332.5	(+0.7)	3.697	0.353	0.987	1	R.VQFGVLSPELDELK.R
SW:RPB1_HUMAN	R05	7114	2	1352.5	(+0.8)	2.238	0.332	0.903	1	R.VQFGVL*SPDEL*K#.R
SW:RPB1_HUMAN	R05	7348	3	2568.8	(-0.8)	4.953	0.545	1.000	1	R.YGEDGLAGESVEFQNLATLKPSNK.A
SW:RPB1_HUMAN	R06	7396	3	2602.8	(+0.1)	3.715	0.488	0.979	1	R.YGEDGL*AGESVEFQNL*ATL*K#PSNK#.A
SW:RPB1_HUMAN	R05	1368	2	1513.6	(-0.2)	2.925	0.452	0.982	3	K.YSPTSPTYSPK.Y
SW:RPB1_HUMAN	R05	1374	2	1521.6	(-0.2)	2.479	0.170	0.559	3	K.YSPTSPTYSPK#.Y
SW:RPB1_HUMAN	R06	1974	2	1232.4	(-0.2)	2.259	0.279	0.778	1	K.TYQDIQNTIK#.K
SW:RPB2_HUMAN	R07	6125	2	1783.9	(+0.9)	4.524	0.467	1.000	2	K.GEIGDATPFNDVAVNVQK#.I
SW:RPB2_HUMAN	R07	5923	2	1333.4	(+0.7)	2.978	0.436	0.988	2	R.GNEVL*YNGFTGR.K
SW:RPB2_HUMAN	R07	6637	3	1969.2	(-0.7)	4.273	0.393	0.985	2	R.HAIYDKLDDGLIAPGVR.V
SW:RPB2_HUMAN	R07	5921	2	1241.4	(+1.0)	3.305	0.341	0.983	2	K.LDDDGLIAPGVR.V
SW:RPB2_HUMAN	R07	10873	2	1446.8	(+0.8)	3.641	0.411	0.990	1	R.LDLAGPLLAFLFR.G
SW:RPB2_HUMAN	R07	6983	2	1264.5	(-0.2)	2.286	0.327	0.907	1	R.L*TFASTL*SHL*R.R
SW:RPB2_HUMAN	R07	7181	2	1618.8	(-0.6)	3.404	0.391	0.975	1	R.NL*TYSAPL*YVDITK#.T
SW:RPB2_HUMAN	R08	7463	2	1618.8	(-0.2)	3.191	0.539	0.998	1	R.NL*TYSAPL*YVDITK#.T
SW:RPB2_HUMAN	R07	8395	3	2227.5	(+0.3)	4.222	0.463	1.000	2	R.TSETGIVDQVMVTL*NQEGYK#.F
SW:RPB2_HUMAN	R07	5631	2	1859.9	(-0.6)	2.468	0.351	0.922	2	K.TVTL*PENEDEL*ESTNR.R
SW:RPB2_HUMAN	R07	5639	2	1847.9	(-0.7)	2.387	0.331	0.570	2	K.TVTL*PENEDEL*ESTNR.R
SW:RPB2_HUMAN	R07	1890	2	1003.1	(+0.7)	2.892	0.276	0.962	2	R.VSGDDVIIGK.T
SW:RPB2_HUMAN	R08	1934	2	1003.1	(+0.3)	2.601	0.368	0.968	2	R.VSGDDVIIGK.T
SW:RPB2_HUMAN	R07	5697	2	1354.4	(-0.6)	2.628	0.319	0.916	1	K.YSL*ATGNWGDQK#.K
SW:RPB2_HUMAN	R08	6075	2	911.1	(+0.8)	2.600	0.199	0.910	2	R.GPIQILNR.Q
SW:RPB3_HUMAN	R19	1748	2	1162.3	(+0.8)	2.698	0.377	0.872	1	R.ITELTDENVK.F
SW:RPB3_HUMAN	R19	1738	2	1176.3	(+0.3)	2.656	0.361	0.966	1	R.ITEL*TDENVK#.F
SW:RPB3_HUMAN	R19	7744	2	1676.9	(-0.8)	2.362	0.171	0.285	1	K.FIIENTDLAVANSIR.R
SW:RPB4_HUMAN	R25	9248	2	1965.1	(+0.7)	5.151	0.459	1.000		R.FEDELQILDDIQT.K.R
SW:RPB4_HUMAN	R25	7912	2	1633.8	(-0.1)	3.775	0.420	0.982		R.AGDVEEDASQL*IFPK#.E
SW:RPB5_HUMAN	R22	8662	2	2029.2	(+0.8)	4.866	0.573	1.000	3	R.GYLVTDQDELDTLEEFK.A
SW:RPB5_HUMAN	R22	8664	2	2055.2	(-1.0)	4.047	0.357	0.937	3	R.GYL*VTQDEL*DTLEEFK#.A
SW:RPB5_HUMAN	R22	8310	3	3199.5	(-0.5)	4.506	0.464	1.000	3	R.RTDL*TVL*VAHNDPTDQDM@FVFFPEEPK#.V
SW:RPB5_HUMAN	R22	6372	2	1457.7	(-0.5)	3.243	0.485	1.000	3	R.AL*IVVQGMTPSAK#.Q
SW:RPB7_HUMAN	R23	6110	2	1358.5	(+0.1)	2.334	0.303	0.872		K.GEVVDAVVTQVNVK.V
SW:RPB7_HUMAN	R23	10618	2	2286.6	(+0.4)	3.116	0.382	0.502		R.VDKNDIFAIGSLMDDYLGLVS.-
SW:RPB7_HUMAN	R23	10604	2	2312.6	(-0.2)	2.252	0.166	0.017		R.VDK#NDIFAIGSL*MDDYL*GL*VS.-
SW:RRB1_HUMAN	R06	5398	2	1777.9	(+0.7)	3.040	0.437	0.986	5	R.TAGPLESSETEEASQLK.E
SW:RRB1_HUMAN	R06	6400	2	965.1	(+0.2)	2.230	0.234	0.697	5	R.L*IEIL*SEK#.A
SW:RS10_HUMAN	R23	9028	2	1130.4	(+0.7)	2.830	0.348	0.974	1	R.IAIYEL*L*FK#.E
SW:RS10_HUMAN	R24	6110	2	1570.7	(-0.4)	4.721	0.508	0.999	1	K.KAEAGAGSATEFQFR.G
SW:RS13_HUMAN	R24	8782	2	1695.0	(-0.2)	2.253	0.387	0.925	1	K.GLAPDLPEDLYHLIK.K
SW:RS13_HUMAN	R24	7542	2	1266.5	(-0.0)	2.244	0.328	0.892	2	K.GL*TPSQIGVIL*R.D
SW:RS16_HUMAN	R02	6382	2	1188.4	(+0.5)	2.599	0.385	0.965	1	K.GPLQSVQVFGR.K
SW:RS16_HUMAN	R25	7316	2	1194.4	(-0.1)	3.046	0.349	0.972	1	K.GPL*QSVQVFGR.K
SW:RS16_HUMAN	R25	7318	2	1188.4	(-0.1)	2.963	0.272	0.942	1	K.GPLQSVQVFGR.K
SW:RS16_HUMAN	R25	8624	2	1095.4	(-0.6)	2.578	0.154	0.680	1	K.LLEPVLLLK.E
SW:RS18_HUMAN	R24	2396	2	1248.3	(+0.6)	2.579	0.434	0.976		R.AGELTEDEVER.V
SW:RS18_HUMAN	R24	7288	2	948.2	(+0.9)	3.190	0.375	0.989		K.IAFAITAIK.G
SW:RS18_HUMAN	R24	7290	2	956.2	(+0.9)	2.881	0.462	0.995		K.IAFAITAIK#.G
SW:RS18_HUMAN	R25	1986	2	904.1	(+1.0)	2.685	0.322	0.975		R.KADIDLTK.R
SW:RS18_HUMAN	R25	1984	2	926.1	(+0.3)	2.337	0.152	0.715		R.K#ADIDL*TK#.R
SW:RS18_HUMAN	R24	2324	2	1008.1	(+0.3)	2.362	0.116	0.494		R.VL*NTNIDGR.R
SW:RS18_HUMAN	R25	2110	2	1002.1	(+0.7)	2.975	0.276	0.971		R.VLNTNIDGR.R
SW:RS18_HUMAN	R25	1970	2	1002.1	(-0.4)	2.584	0.296	0.939		R.VLNTNIDGR.R
SW:RS18_HUMAN	R25	1980	2	1008.1	(+0.1)	2.358	0.382	0.959		R.VL*NTNIDGR.R
SW:RS18_HUMAN	R24	5310	2	1342.5	(+0.6)	3.396	0.273	0.964		K.YSQVL*ANGL*DNK#.L



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:RS18_HUMAN	R24	5646	2	1322.5	(-0.1)	3.142	0.411	0.964		K.YSQVLANGLDNK.L
SW:RS18_HUMAN	R25	5786	2	1322.5	(-0.1)	3.035	0.390	0.977		K.YSQVLANGLDNK.L
SW:RS18_HUMAN	R25	5434	2	1322.5	(+0.2)	2.932	0.376	0.968		K.YSQVLANGLDNK.L
SW:RS18_HUMAN	R25	5400	2	1342.5	(+1.0)	2.240	0.156	0.526		K.YSQVL*ANGL*DNK#.L
SW:RS18_HUMAN	R26	7830	2	1061.2	(+0.6)	2.751	0.330	0.979		K.IPDWFLNR.Q
SW:RS19_HUMAN	R25	8066	2	1710.8	(-0.3)	3.617	0.457	0.999	2	K.EL*APYDENWFYTR.A
SW:RS19_HUMAN	R25	1288	2	951.1	(+0.5)	2.994	0.347	0.976	2	R.IAGQVAAANK#.K
SW:RS19_HUMAN	R25	6770	2	1081.2	(+0.3)	2.495	0.422	0.924	2	K.VPEWVDTVK#.L
SW:RS19_HUMAN	R25	6762	2	1073.2	(+0.2)	2.392	0.440	0.976	2	K.VPEWVDTVK.L
SW:RS25_HUMAN	R25	7604	2	1319.5	(+0.9)	2.971	0.263	0.300		R.DKLNLLVLFDK.A
SW:RS25_HUMAN	R25	7614	2	1353.5	(-0.8)	2.582	0.132	0.009		R.DK#L*NNL*VL*FDK#.A
SW:RS25_HUMAN	R25	7600	2	1102.3	(-0.4)	2.301	0.117	0.451		K.L*NNL*VL*FDK#.A
SW:RS2_HUMAN	R20	2584	2	1034.2	(+0.4)	2.632	0.465	0.980	5	R.GTGIVSAPVPK#.K
SW:RS2_HUMAN	R20	2500	2	1026.2	(+0.7)	2.571	0.339	0.929	5	R.GTGIVSAPVPK.K
SW:RS2_HUMAN	R20	6788	2	1464.6	(+0.2)	3.604	0.381	0.985	6	K.SPYQEFTDHLVK.T
SW:RS2_HUMAN	R22	9248	2	1552.9	(+0.5)	2.335	0.295	0.890	6	K.SLEEIYLFSLPIK.E
SW:RS3_HUMAN	R03	6069	2	1093.2	(+0.5)	2.988	0.365	0.986	4	K.AELNEFLTR.E
SW:RS3_HUMAN	R02	5696	2	1485.6	(+0.1)	2.329	0.235	0.699	5	K.DEIL*PTTPISEQ#.G
SW:RS3_HUMAN	R20	6028	2	1485.6	(+0.8)	2.287	0.309	0.880	5	K.DEIL*PTTPISEQ#.G
SW:RS3_HUMAN	R20	5150	2	1424.5	(-0.2)	2.269	0.268	0.801	4	R.ELAEDGYSGVEVR.V
SW:RS3_HUMAN	R20	7316	2	1587.7	(-0.8)	3.719	0.506	1.000	4	R.FGFPEGSVEL*YAEK#.V
SW:RS3_HUMAN	R20	7540	3	2491.8	(+0.6)	4.520	0.546	1.000	5	K.FVDGL*M@IHSGBPNNYYVDTAVR.H
SW:RS3_HUMAN	R20	7864	3	2469.8	(-0.5)	4.134	0.359	0.992	5	K.FVDGLMIHSGBPNNYYVDTAVR.H
SW:RS3_HUMAN	R20	6710	2	1030.3	(+0.6)	2.399	0.325	0.955	4	R.TEIIILATR.T
SW:RS3_HUMAN	R20	6496	2	1105.2	(+0.2)	2.234	0.265	0.849	4	K.AEL*NEFL*TR.E
SW:RS4_HUMAN	R20	7028	2	991.2	(-0.5)	3.259	0.331	0.980	2	R.LSNIFVIGK.G
SW:RS4_HUMAN	R20	7016	2	1005.2	(+0.9)	2.674	0.487	0.988	2	R.L*SNIFVIGK#.G
SW:RS4_HUMAN	R20	8478	2	1887.2	(+1.0)	4.222	0.544	1.000	2	R.TDITYPAGFMDVISIDK.T
SW:RS4_HUMAN	R20	8486	3	1887.2	(+0.7)	3.861	0.486	0.999	2	R.TDITYPAGFMDVISIDK.T
SW:RS4_HUMAN	R20	6298	2	1460.6	(+0.2)	4.162	0.408	0.999	2	K.VNDTIQIDL*ETGK#.I
SW:RS4_HUMAN	R20	6310	2	1446.6	(-0.0)	4.082	0.494	0.999	2	K.VNDTIQIDLETGK.I
SW:RS4_HUMAN	R21	7004	2	1005.2	(+0.4)	3.349	0.473	0.998	2	R.L*SNIFVIGK#.G
SW:RS5_HUMAN	R23	1774	2	927.0	(+0.7)	2.231	0.158	0.526	2	K.GSSNSYAIK.K
SW:RS5_HUMAN	R23	5332	2	1147.3	(+0.4)	2.354	0.186	0.786	1	R.RQAVDVSP*LR.R
SW:RS5_HUMAN	R25	5326	2	985.1	(-0.4)	2.242	0.201	0.686	1	R.QAVDVSP*LR.R
SW:RS7_HUMAN	R23	8840	2	1352.7	(-0.8)	2.816	0.393*	0.093	1	K.AIIIFVVPVQL*K#.S
SW:RS7_HUMAN	R23	9230	3	3332.7	(-0.5)	3.845	0.338	0.914	1	K.IVKPNGEKPDFEFESGISQALLELEMNSDLK.A
SW:RS7_HUMAN	R23	5514	2	1030.2	(+0.7)	2.489	0.287	0.946	2	K.VETFSGVYK.K
SW:RS9_HUMAN	R22	6858	2	1051.2	(+0.3)	2.267	0.269	0.902	3	R.L*FEGNAL*L*R.R
SW:RS9_HUMAN	R23	6034	2	933.1	(+0.4)	2.822	0.365	0.985	4	K.L*IGEYGL*R.N
SW:RS9_HUMAN	R23	6050	2	921.1	(+0.0)	2.797	0.362	0.978	4	K.LIGEYGLR.N
SW:RS9_HUMAN	R22	5326	2	1020.2	(-0.5)	2.260	0.243	0.850	3	R.RLQTQVFK.L
SW:RS9_HUMAN	R22	5306	2	1020.2	(+0.8)	2.250	0.292	0.931	3	R.RLQTQVFK.L
SW:RS9_HUMAN	R23	6782	2	1051.2	(+0.4)	2.343	0.267	0.915	3	R.L*FEGNAL*L*R.R
SW:RSMB_HUMAN	R20	5458	2	1585.8	(-0.9)	2.693	0.351	0.806	8	R.GENL*VSM@TVEGPPPK#.D
SW:RSMB_HUMAN	R21	6318	2	1569.8	(-0.4)	4.013	0.409	0.999	8	R.GENL*VSM@TVEGPPPK#.D
SW:RSMB_HUMAN	R21	6356	2	1555.8	(-0.3)	3.613	0.505	1.000	8	R.GENLVSM@TVEGPPPK#.D
SW:RSMB_HUMAN	R20	1846	2	1098.3	(+0.7)	2.394	0.254	0.908	8	K.M@L*QHIDYR.M
SW:RSMB_HUMAN	R20	5090	2	1199.4	(-0.2)	3.077	0.363	0.969	4	R.VPL*AGAAGGPGIGR.A
SW:RSMB_HUMAN	R21	7772	2	883.2	(-0.4)	2.518	0.479	0.986	8	R.VLGLVLLR.G
SW:RT02_HUMAN	R20	5546	2	956.1	(+0.6)	2.404	0.352	0.970	1	R.L*FQTAITR.A
SW:RT02_HUMAN	R20	5842	2	994.1	(+0.5)	2.388	0.372	0.693		K.HSDFFNVK.E
SW:RT10_HUMAN	R24	8118	3	2679.0	(+0.5)	4.837	0.526	1.000	1	K.TQLEQLPEHIKEPIWETLSEEK.E
SW:RT10_HUMAN	R24	5974	2	1318.5	(-0.1)	2.334	0.302	0.849	1	R.NL*PEGVAM@EVTK#.T

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta M$	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:RT22_HUMAN	R18	9273	3	2920.2	(+0.8)	4.807	0.466	1.000		R.DLIDDATNLVQLYHVLHPDGGQSAQGAK.D
SW:RT22_HUMAN	R18	5491	2	1391.6	(+0.6)	3.429	0.436	1.000	1	K.LMTQAQLEEATR.Q
SW:RT22_HUMAN	R18	5487	2	1403.6	(-0.1)	3.061	0.358	0.972	1	K.L*MTQAQL*EEATR.Q
SW:RT23_HUMAN	R22	7314	2	1073.3	(+0.4)	2.960	0.303	0.973	2	K.AL*L*AEGVIL*R.R
SW:RT23_HUMAN	R22	5804	3	2325.5	(+0.2)	4.098	0.387	0.978		R.KSEHLSVRPQTALEENETQK.E
SW:RT23_HUMAN	R22	7000	2	1115.3	(+0.4)	2.603	0.415	0.983		R.L*ETVGSIFSR.T
SW:RT23_HUMAN	R22	5892	3	2197.4	(+0.9)	4.200	0.566	1.000		K.SEHLSVRPQTALEENETQK.E
SW:RT23_HUMAN	R22	5900	3	2217.4	(-0.5)	3.943	0.434	0.991		K.SEHL*SVRPQTAL*EENETQK#.E
SW:RT23_HUMAN	R22	9390	2	1994.3	(-0.1)	2.202	0.316	0.094	2	K.EKPLWFDVYDAFPPLR.E
SW:RT26_HUMAN	R22	5146	2	1316.5	(+0.6)	3.444	0.358	0.984		R.KAEVQAWAQR.K
SW:RT26_HUMAN	R22	1744	2	860.9	(+0.7)	2.631	0.253	0.950	1	R.VEAALDSR.K
SW:RT27_HUMAN	R17	10832	3	2510.9	(+0.8)	3.920	0.424	0.999	1	K.VQYGIFPDNFTFNLLMDSFIK.K
SW:RT27_HUMAN	R17	8162	2	1230.5	(+0.8)	3.155	0.358	0.982	1	R.NFGASLLLPLGK.Q
SW:RT31_HUMAN	R18	9541	3	2587.9	(+0.9)	4.755	0.536	1.000		K.QLATVNEQPLQNGFEELIQWTK.E
SW:RT31_HUMAN	R18	10377	2	2341.7	(-0.6)	2.290	0.323	0.871		R.IEPLSPELVAAASAVADSLPFDK.Q
SW:RTN4_HUMAN	R01	4551	2	1272.5	(+0.4)	2.266	0.371	0.947	4	R.GPLPAAPPVAPER.Q
SW:RTN4_HUMAN	R02	5328	2	1278.5	(-0.0)	2.490	0.224	0.786	4	R.GPL*PAAPPVAPER.Q
SW:RTN4_HUMAN	R02	5304	2	1272.5	(+0.2)	2.249	0.342	0.899	4	R.GPLPAAPPVAPER.Q
SW:RTN4_HUMAN	R16	5104	2	1272.5	(+0.5)	2.796	0.350	0.957	4	R.GPLPAAPPVAPER.Q
SW:RTN4_HUMAN	R01	6059	2	1608.8	(+0.8)	4.854	0.559	1.000	10	R.HQAQIDHYLGLANK.N
SW:RTN4_HUMAN	R16	5112	2	1278.5	(+0.6)	2.597	0.130	0.668	4	R.GPL*PAAPPVAPER.Q
SW:RU17_HUMAN	R14	1256	2	799.9	(+0.2)	2.768	0.429	0.983	6	R.L*GGGL*GGTR.R
SW:RU17_HUMAN	R14	6175	2	1238.4	(+0.7)	3.468	0.527	1.000	4	R.REFEVYGIPIK.R
SW:RU17_HUMAN	R14	1350	2	1274.4	(-0.4)	2.321	0.257	0.806	4	R.RQQEVETEL*K#.M
SW:RU17_HUMAN	R17	7394	2	1282.5	(+0.7)	2.244	0.253	0.850	3	R.DPIPYLPPLEK.L
SW:RU2A_HUMAN	R20	2164	2	1127.2	(-0.0)	2.646	0.317	0.935	1	K.GGPPSPGDVEAIK.N
SW:RU2A_HUMAN	R20	2172	2	1135.2	(-0.5)	2.517	0.368	0.936	1	K.GGPPSPGDVEAIK#.N
SW:RU2A_HUMAN	R20	5668	2	1138.3	(+0.4)	2.980	0.373	0.917	2	K.GL*L*QSGQIPGR.E
SW:RU2A_HUMAN	R20	5676	2	1126.3	(-0.3)	2.802	0.331	0.958	2	K.GLLQSGQIPGR.E
SW:RU2A_HUMAN	R21	5812	2	1126.3	(+0.7)	3.663	0.330	0.987	2	K.GLLQSGQIPGR.E
SW:RU2A_HUMAN	R21	5810	2	1138.3	(+0.8)	2.444	0.308	0.932	2	K.GL*L*QSGQIPGR.E
SW:RU2A_HUMAN	R20	7254	2	1059.3	(+0.9)	2.328	0.397	0.974	2	R.KLDGFPLLR.R
SW:RU2A_HUMAN	R20	6080	2	1465.6	(-0.5)	3.051	0.462	0.984	2	K.NAIANASTL*AEVER.L
SW:RU2A_HUMAN	R21	6108	2	1459.6	(+0.5)	3.628	0.559	0.999	2	K.NAIANASTLAEVER.L
SW:RU2A_HUMAN	R21	6112	2	1465.6	(+0.4)	3.347	0.431	0.990	2	K.NAIANASTL*AEVER.L
SW:RU2A_HUMAN	R20	7662	2	1066.3	(+1.0)	2.888	0.363	0.984	2	K.SLTYLSILR.N
SW:RU2A_HUMAN	R20	5536	2	1232.4	(-0.2)	2.386	0.251	0.775	2	K.TFNPGAGL*PTDK#.K
SW:RU2A_HUMAN	R21	7196	2	1085.3	(-0.1)	2.244	0.238	0.776	2	R.K#L*DGFPPL*L*R.R
SW:RUN1_HUMAN	R15	4967	3	2365.5	(+0.6)	4.432	0.446	0.999	4	R.ASL*NHSTAFNPQPQSQMQDTR.Q
SW:RUN1_HUMAN	R15	4969	3	2359.5	(+0.2)	3.858	0.320	0.985	4	R.ASLNHSTAFNPQPQSQMQDTR.Q
SW:RUN1_HUMAN	R15	5165	3	1700.8	(+0.5)	4.138	0.535	1.000	7	K.L*DDQTK#PGSL*SFSER.L
SW:RUN1_HUMAN	R15	6409	2	1163.3	(+0.2)	2.380	0.488	0.526	3	R.LEEAVWRPY.-
SW:RUN1_HUMAN	R15	6405	2	1169.3	(+0.6)	2.232	0.179	0.055	3	R.L*EEAVWRPY.-
SW:RUN1_HUMAN	R15	5133	2	988.1	(+0.8)	2.874	0.106*	0.612	7	R.LSELEQLR.R
SW:RUN1_HUMAN	R15	5127	2	1006.1	(+0.5)	2.266	0.414	0.974	7	R.L*SEL*EQL*R.R
SW:RUN1_HUMAN	R15	6491	2	1503.6	(-0.7)	2.840	0.342	0.952	3	R.L*STAPDL*TAFSDPR.Q
SW:RUN1_HUMAN	R15	6495	2	1491.6	(-0.8)	2.423	0.225	0.494	3	R.LSTAPDLTAFSDPR.Q
SW:RUN1_HUMAN	R15	6515	2	1783.0	(-0.5)	2.835	0.275	0.878	13	K.M@SEAL*PL*GAPDAGAAL*AGK#.L
SW:RUN1_HUMAN	R16	4860	2	988.1	(+0.6)	2.789	0.108*	0.568	7	R.LSELEQLR.R
SW:RUV1_HUMAN	R16	7962	2	1689.0	(+0.6)	2.417	0.436	0.973	1	R.ALESSIAPIVIFASNR.G
SW:RUV1_HUMAN	R15	4907	2	1081.3	(+0.1)	2.649	0.278	0.907	1	R.AVLLAGPPGTGK.T
SW:RUV1_HUMAN	R16	4490	2	1081.3	(+0.8)	3.541	0.440	1.000	1	R.AVLLAGPPGTGK.T
SW:RUV1_HUMAN	R16	4322	2	1081.3	(+0.4)	3.244	0.300	0.973	1	R.AVLLAGPPGTGK.T
SW:RUV1_HUMAN	R16	4402	2	1081.3	(+0.4)	3.085	0.464	0.991	1	R.AVLLAGPPGTGK.T
SW:RUV1_HUMAN	R16	4382	2	1101.3	(+0.0)	2.558	0.286	0.874	1	R.AVL*L*AGPPGTGK#.T
SW:RUV1_HUMAN	R16	728	2	931.0	(+0.4)	2.250	0.230	0.828	1	K.ILADQQDK.Y
SW:RUV1_HUMAN	R16	7742	2	1531.8	(+0.5)	3.185	0.453	0.990	1	R.YSVQLLTPANLLAK.I

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:RUV1_HUMAN	R16	554	2	879.0	(+0.8)	2.210	0.252	0.883	1	R.IASHSHVK.G
SW:RUV2_HUMAN	R16	1288	2	1126.3	(-0.3)	3.224	0.375	0.973	2	R.AVL*IAGQPPTGK#.T
SW:RUV2_HUMAN	R16	4494	2	1402.6	(+0.7)	3.550	0.464	0.998	1	K.DKVQAGDVITDK.A
SW:RUV2_HUMAN	R16	7394	2	1517.7	(+0.5)	3.329	0.258	0.966		K.EYQDAFLFNLK.G
SW:RUV2_HUMAN	R16	7392	2	1537.7	(-0.2)	3.066	0.263	0.920		K.EYQDAFL*FNEL*K#.G
SW:RUV2_HUMAN	R16	6142	2	1371.6	(-0.3)	2.686	0.365	0.948	1	R.L*L*IVSTTPYSEK#.D
SW:RUV2_HUMAN	R16	6162	2	1351.6	(-0.4)	2.478	0.345	0.930	1	R.LLIVSTTPYSEK.D
SW:RUV2_HUMAN	R16	6176	2	1174.3	(+0.1)	2.307	0.250	0.813	2	R.GL*GL*DDAL*EPR.Q
SW:S3A1_HUMAN	R08	7161	2	1111.3	(+1.0)	2.350	0.325	0.952	3	K.LQYEGIFIK.D
SW:S3A1_HUMAN	R09	6630	2	1125.3	(+0.5)	2.272	0.401	0.964	3	K.L*QYEGIFIK#.D
SW:S3A1_HUMAN	R08	2332	2	912.1	(+0.3)	2.367	0.330	0.944	4	K.L*TAQFVAR.N
SW:S3A1_HUMAN	R08	6991	2	1536.7	(+0.3)	4.050	0.341	0.988	3	R.RTDIFGVEETAIGK.K
SW:S3A1_HUMAN	R08	6983	2	1544.7	(+0.0)	3.834	0.353	0.977	3	R.RTDIFGVEETAIGK#.K
SW:S3A1_HUMAN	R09	6444	2	1544.7	(-0.4)	4.224	0.420	1.000	3	R.RTDIFGVEETAIGK#.K
SW:S3A1_HUMAN	R08	7209	2	1380.5	(+1.0)	4.632	0.524	0.999	3	R.TDIFGVEETAIGK.K
SW:S3A1_HUMAN	R08	7207	2	1388.5	(+0.8)	4.262	0.574	0.999	3	R.TDIFGVEETAIGK#.K
SW:S3A1_HUMAN	R09	6694	2	1388.5	(+0.7)	3.979	0.526	1.000	3	R.TDIFGVEETAIGK#.K
SW:S3A1_HUMAN	R09	6698	2	1380.5	(+0.9)	3.963	0.583	1.000	3	R.TDIFGVEETAIGK.K
SW:S3A1_HUMAN	R09	6468	2	1624.7	(+0.7)	2.876	0.225	0.708	3	K.TEDSL*M@PEEEFL*R.R
SW:S3A1_HUMAN	R09	5736	2	1461.7	(+0.7)	2.445	0.421	0.966	4	K.VQAQVIQETIVPK#.E
SW:S3A1_HUMAN	R09	1356	2	1059.2	(+0.5)	2.205	0.306	0.924	2	K.VQVPNMQDK.T
SW:S3A3_HUMAN	R14	7415	3	2243.4	(+1.0)	5.950	0.484	0.542		R.K#EEL*NAISGPNFEAFYNR.L
SW:S3A3_HUMAN	R14	6079	2	1516.7	(+0.6)	3.580	0.419	0.684		R.VKPLQDQNELFGK.I
SW:S3A3_HUMAN	R14	2142	2	1069.2	(+0.8)	3.171	0.372	0.988		R.YMEVSGNLR.D
SW:S3A3_HUMAN	R14	7417	2	1337.5	(+0.2)	2.985	0.406	0.973		K.SL*ESL*DTSL*FAK#.N
SW:S3B1_HUMAN	R07	7495	3	2593.9	(+0.8)	4.212	0.432*	0.019	1	K.AAGL*ATMISTM@RPDIDNMDEYVR.N
SW:S3B1_HUMAN	R07	9407	3	1690.0	(-0.9)	4.683	0.362	0.990	1	K.AIGPHDVLATLLNLLK.V
SW:S3B1_HUMAN	R07	9383	2	1690.0	(+0.6)	3.519	0.482	1.000	1	K.AIGPHDVLATLLNLLK.V
SW:S3B1_HUMAN	R07	9033	2	2250.6	(-1.0)	3.664	0.487	1.000	1	K.AIGYL*IPL*MDAEYANYYTR.E
SW:S3B1_HUMAN	R07	9029	2	2238.6	(+0.1)	3.478	0.585	1.000	1	K.AIGYLIPLMDAEYANYYTR.E
SW:S3B1_HUMAN	R07	5217	2	1106.3	(+0.3)	2.912	0.226	0.924		K.AIVNVIGM@HK#.M
SW:S3B1_HUMAN	R07	5893	2	1193.4	(+0.9)	2.566	0.385	0.967	1	R.ATVNTFGYIAK#.A
SW:S3B1_HUMAN	R07	9405	2	1999.3	(-0.6)	3.236	0.390	0.974	2	K.DYIYAVTPLLEDALMDR.D
SW:S3B1_HUMAN	R07	1178	2	1374.4	(+0.7)	3.452	0.431	0.989	1	R.GGDSIGETPTPGASK.R
SW:S3B1_HUMAN	R07	1182	2	1382.4	(-0.0)	2.507	0.310	0.865	1	R.GGDSIGETPTPGASK#.R
SW:S3B1_HUMAN	R07	5503	2	1355.6	(-0.1)	3.689	0.399	0.985		K.IMGNLGAADIDHK.L
SW:S3B1_HUMAN	R07	5505	2	1369.6	(-0.8)	2.453	0.223	0.457		K.IMGNL*GAADIDHK#.L
SW:S3B1_HUMAN	R07	5663	2	1608.7	(-0.9)	2.425	0.154	0.009		R.IVDDL*K#DEAEQYR.K
SW:S3B1_HUMAN	R07	5665	2	1594.7	(-0.2)	2.370	0.410	0.295		R.IVDDLKDEAEQYR.K
SW:S3B1_HUMAN	R07	6919	3	2410.7	(+0.3)	4.277	0.392	0.999	1	R.K#L*TATPTPL*GGMTGFHMQTEDR.T
SW:S3B1_HUMAN	R07	6421	2	1829.0	(-0.5)	2.847	0.303	0.907	1	K.L*L*VDVDESTL*SPEEQK#.E
SW:S3B1_HUMAN	R07	5907	2	1895.0	(-0.6)	3.130	0.423	0.980	1	K.L*SSWDQAETPGHTPSL*R.W
SW:S3B1_HUMAN	R07	5909	2	1883.0	(-0.5)	2.951	0.395	0.971	1	K.LSSWDQAETPGHTPSLR.W
SW:S3B1_HUMAN	R07	7179	3	2132.3	(+0.4)	4.866	0.371	0.993	1	R.NRPL*SDEEL*DAMFPEGYK#.V
SW:S3B1_HUMAN	R07	8429	2	1838.1	(+0.7)	4.466	0.440	0.999	1	R.SLVEIIEHGLVDEQK#.V
SW:S3B1_HUMAN	R08	8609	3	1858.1	(+0.7)	4.103	0.438	1.000	1	R.SL*VEIIEHGL*VDEQK#.V
SW:S3B1_HUMAN	R07	6227	2	1310.5	(+0.7)	3.719	0.393	0.990	1	R.VPELVQNGVLK.S
SW:S3B1_HUMAN	R07	6145	2	1330.5	(+0.9)	3.448	0.438	1.000	1	R.VPEL*NVQNGVL*K#.S
SW:S3B1_HUMAN	R07	6225	2	1330.5	(-0.5)	2.353	0.207	0.658	1	R.VPEL*NVQNGVL*K#.S
SW:S3B1_HUMAN	R07	1268	2	1516.6	(+0.2)	2.487	0.381	0.947	1	R.WDQTADQTPGATPK.K
SW:S3B2_HUMAN	R07	2154	2	1029.2	(+0.5)	2.676	0.212	0.918	4	R.AAVLLEQER.Q
SW:S3B2_HUMAN	R08	2212	2	1029.2	(+0.8)	3.340	0.205	0.965	4	R.AAVLLEQER.Q
SW:S3B2_HUMAN	R08	2226	2	1041.2	(+1.0)	2.917	0.183	0.924	4	R.AAVL*L*EQER.Q
SW:S3B2_HUMAN	R08	5561	3	2423.6	(-0.0)	4.534	0.431	0.993	8	R.EQQAQVEK#EDFSDM@VAEHAAK#.Q
SW:S3B2_HUMAN	R08	6407	3	2407.6	(-0.0)	4.165	0.430	0.990	8	R.EQQAQVEK#EDFSDMVAEHAAK#.Q
SW:S3B2_HUMAN	R08	8323	2	1652.9	(-0.1)	3.835	0.399	0.525	6	R.GIEK#PPFEL*PDFIK#.R
SW:S3B2_HUMAN	R07	4981	2	1245.4	(+0.8)	3.085	0.399	0.985	4	K.L*AEIGAPIQGNR.E
SW:S3B2_HUMAN	R07	4915	2	1239.4	(+0.0)	2.489	0.424	0.968	4	K.LAEIGAPIQGNR.E
SW:S3B2_HUMAN	R07	4901	2	1245.4	(-0.8)	2.427	0.257	0.636	4	K.L*AEIGAPIQGNR.E
SW:S3B2_HUMAN	R08	5165	2	1239.4	(+0.0)	2.762	0.366	0.964	4	K.LAEIGAPIQGNR.E
SW:S3B2_HUMAN	R08	5163	2	1245.4	(-0.5)	2.532	0.204	0.778	4	K.L*AEIGAPIQGNR.E

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:S3B2_HUMAN	R08	5245	2	1239.4	(-0.3)	2.351	0.346	0.924	4	K.LAEIGAPIQGNR.E
SW:S3B2_HUMAN	R08	6271	2	1776.0	(-0.6)	3.713	0.481	0.998	5	K.L*AQQQAAL*L*MQQEER.A
SW:S3B2_HUMAN	R07	7895	3	1809.1	(+0.3)	4.490	0.487	1.000	6	K.RGIEK#PPFEL*PDFIK#.R
SW:S3B2_HUMAN	R08	8117	3	1809.1	(+1.0)	4.331	0.514	0.999	6	K.RGIEK#PPFEL*PDFIK#.R
SW:S3B2_HUMAN	R08	2484	2	1956.0	(-0.8)	4.054	0.588	1.000	5	R.SSL*GQSASETEEDTVSVSK#.K
SW:S3B2_HUMAN	R08	2490	2	1942.0	(-0.8)	3.954	0.612	1.000	5	R.SSLGQSASETEEDTVSVSK.K
SW:S3B2_HUMAN	R07	2162	2	1315.4	(-0.5)	2.287	0.423	0.958	5	R.VGEPValseeER.L
SW:S3B2_HUMAN	R07	2152	2	1321.4	(-0.0)	2.279	0.362	0.926	5	R.VGEPVAL*seeER.L
SW:S3B2_HUMAN	R08	2196	2	1321.4	(-0.1)	2.752	0.466	0.983	5	R.VGEPVAL*seeER.L
SW:S3B2_HUMAN	R08	8013	2	1314.6	(+0.4)	2.392	0.436	0.972	7	K.VPPPWL*IAMQR.Y
SW:S3B2_HUMAN	R10	4801	2	1245.4	(-0.4)	2.542	0.302	0.914	4	K.L*AEIGAPIQGNR.E
SW:S3B3_HUMAN	R01	4565	2	962.2	(+0.4)	2.321	0.322	0.948	2	R.AVMISAIEK.Q
SW:S3B3_HUMAN	R01	10375	2	2534.9	(-0.7)	3.804	0.362	0.981	3	R.ELAAEMAAAFLENLNPESIFGAPK.A
SW:S3B3_HUMAN	R03	9675	3	2534.9	(+1.0)	5.040	0.551	0.993	3	R.ELAAEMAAAFLENLNPESIFGAPK.A
SW:S3B3_HUMAN	R04	9910	3	2534.9	(+0.8)	4.772	0.496	0.995	3	R.ELAAEMAAAFLENLNPESIFGAPK.A
SW:S3B3_HUMAN	R01	7143	2	1304.5	(+0.5)	3.830	0.324	0.987	1	R.FLAVGLVDNTR.V
SW:S3B3_HUMAN	R01	7137	2	1316.5	(+0.5)	3.345	0.483	1.000	1	R.FL*AVGL*VDNTR.V
SW:S3B3_HUMAN	R02	6824	2	1304.5	(-0.0)	2.520	0.312	0.919	1	R.FLAVGLVDNTR.V
SW:S3B3_HUMAN	R03	6807	2	1304.5	(+0.6)	2.365	0.307	0.919	1	R.FLAVGLVDNTR.V
SW:S3B3_HUMAN	R03	6799	2	1316.5	(+0.3)	2.327	0.380	0.959	1	R.FL*AVGL*VDNTR.V
SW:S3B3_HUMAN	R01	8037	2	1786.0	(+0.3)	2.713	0.485	0.987	2	R.FSNTGEDWYVLVGVAK.D
SW:S3B3_HUMAN	R03	6285	2	1492.7	(+0.8)	2.495	0.199	0.056	2	K.IL*EL*L*RPDPNTGK#.V
SW:S3B3_HUMAN	R01	6163	2	1204.4	(-0.1)	2.404	0.359	0.933	2	R.IVIL*EYQPSK#.N
SW:S3B3_HUMAN	R01	6165	2	1190.4	(+0.7)	2.359	0.456	0.983	2	R.IVILEYQPSK.N
SW:S3B3_HUMAN	R02	6038	2	1204.4	(-0.2)	2.353	0.269	0.834	2	R.IVIL*EYQPSK#.N
SW:S3B3_HUMAN	R01	8243	2	1934.2	(+0.2)	3.857	0.469	0.945	1	K.L*GAVFNQVAFPL*QYTPR.K
SW:S3B3_HUMAN	R03	1068	2	968.0	(+0.4)	2.299	0.221	0.760	4	K.NVSEEL*DR.T
SW:S3B3_HUMAN	R01	5725	2	1200.4	(+0.2)	3.168	0.546	1.000	3	R.SVAGGFVYTYK#.L
SW:S3B3_HUMAN	R01	5733	2	1192.4	(+0.6)	2.745	0.449	0.987	3	R.SVAGGFVYTYK.L
SW:S3B3_HUMAN	R02	5790	2	1200.4	(+0.1)	2.859	0.553	1.000	3	R.SVAGGFVYTYK#.L
SW:S3B3_HUMAN	R03	5655	2	1200.4	(+0.2)	2.281	0.556	0.980	3	R.SVAGGFVYTYK#.L
SW:S3B3_HUMAN	R01	6065	2	1501.6	(-0.1)	3.654	0.429	0.990	1	R.TVL*DPVTGDL*SDTR.T
SW:S3B3_HUMAN	R01	6073	2	1489.6	(-0.2)	3.584	0.496	1.000	1	R.TVLDPVTGDLSDTR.T
SW:S3B3_HUMAN	R02	5924	2	1489.6	(+0.6)	3.809	0.506	1.000	1	R.TVLDPVTGDLSDTR.T
SW:S3B3_HUMAN	R02	5910	2	1501.6	(-0.1)	3.609	0.504	1.000	1	R.TVL*DPVTGDL*SDTR.T
SW:S3B3_HUMAN	R03	5789	2	1501.6	(-0.2)	2.960	0.499	0.986	1	R.TVL*DPVTGDL*SDTR.T
SW:S3B3_HUMAN	R03	5775	2	1489.6	(+0.9)	2.749	0.418	0.513	1	R.TVLDPVTGDLSDTR.T
SW:S3B3_HUMAN	R03	5801	2	1489.6	(-0.9)	2.415	0.385	0.846	1	R.TVLDPVTGDLSDTR.T
SW:S3B3_HUMAN	R04	6136	2	1501.6	(-0.5)	2.217	0.345	0.889	1	R.TVL*DPVTGDL*SDTR.T
SW:S3B3_HUMAN	R05	9774	3	2534.9	(+0.8)	4.839	0.458	1.000	3	R.ELAAEMAAAFLENLNPESIFGAPK.A
SW:S611_HUMAN	R01	1326	2	1216.4	(+0.9)	2.522	0.364	0.916	6	R.ETSMVHELNR.Y
SW:S611_HUMAN	R01	10089	2	2323.6	(+0.8)	4.273	0.549	0.996	4	R.FSGNLLVSLGLTWSDTSSGGPAR.A
SW:S611_HUMAN	R01	10091	2	2347.6	(-0.2)	3.356	0.508	0.999	4	R.FSGNL*L*VSL*L*GTWSDTSSGGPAR.A
SW:S611_HUMAN	R02	9152	3	2347.6	(-0.3)	3.806	0.461	0.999	4	R.FSGNL*L*VSL*L*GTWSDTSSGGPAR.A
SW:S611_HUMAN	R03	9439	3	2347.6	(+0.7)	4.667	0.491	1.000	4	R.FSGNL*L*VSL*L*GTWSDTSSGGPAR.A
SW:S611_HUMAN	R03	9449	2	2323.6	(+0.7)	3.975	0.500	0.999	4	R.FSGNLLVSLGLTWSDTSSGGPAR.A
SW:S611_HUMAN	R01	1340	2	980.1	(+0.7)	2.394	0.205	0.818	5	K.IIEVGDTPK#.D
SW:S611_HUMAN	R04	9688	3	2347.6	(-0.1)	4.127	0.437	0.995	4	R.FSGNL*L*VSL*L*GTWSDTSSGGPAR.A
SW:SARA_HUMAN	R23	6712	2	1328.5	(-0.4)	2.566	0.443	0.877		R.EIFGL*YGQTTGK#.G
SW:SARA_HUMAN	R23	7460	2	1173.4	(-0.3)	2.322	0.330	0.886	2	K.L*VFL*GL*DNAGK#.T
SW:SARA_HUMAN	R23	7436	2	1147.4	(+0.8)	2.209	0.193	0.714	2	K.LVFLGLDNAGK.T
SW:SC63_HUMAN	R10	6171	2	1514.7	(-0.3)	2.944	0.298	0.907	4	K.L*SQM@AVQGL*QQFK#.S
SW:SC63_HUMAN	R10	7571	2	1498.7	(-0.7)	2.747	0.285	0.894	4	K.L*SQMAVQGL*QQFK#.S
SW:SC63_HUMAN	R11	6614	3	2246.4	(+0.6)	4.195	0.465	1.000	3	K.QNKDDEAEWQELQQSIQR.K
SW:SC63_HUMAN	R10	5519	2	1065.2	(+0.9)	2.973	0.263	0.967	4	R.YSGDQILIR.T
SW:SC63_HUMAN	R11	5306	2	1065.2	(+0.7)	3.112	0.248	0.967	4	R.YSGDQILIR.T
SW:SC63_HUMAN	R11	7354	2	1799.0	(+0.1)	2.579	0.295	0.890	4	K.SPL*L*QL*PHIEEDNL*R.R
SW:SCB1_HUMAN	R17	7862	3	2644.9	(+0.6)	5.826	0.579	1.000	8	K.L*HGGTPANFL*DVGGGATVHQVTEAFK#.L
SW:SCB1_HUMAN	R17	8332	3	3037.4	(+0.5)	4.181	0.513	1.000	3	R.SFQGPVLIGSSHGGVNIEDVAAETPEAIK.E
SW:SCB1_HUMAN	R17	1812	2	1065.2	(+0.9)	3.400	0.431	1.000	6	K.SPDEAYIAK.K
SW:SCB1_HUMAN	R17	1820	2	1073.2	(+0.9)	3.309	0.481	1.000	6	K.SPDEAYIAK#.K

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:SCD1_HUMAN	R14	2306	3	2254.5	(+0.6)	5.797	0.553	1.000	4	R.K#RPAPQQIQVQQQAVQNR.N
SW:SCD1_HUMAN	R14	2296	3	2246.5	(+0.6)	5.568	0.525	1.000	4	R.KRPAPQQIQVQQQAVQNR.N
SW:SCD1_HUMAN	R14	9309	3	2519.0	(+0.2)	4.928	0.540	0.851	4	R.L*L*GIHTQTRPVIIQAL*WQYIK#.T
SW:SCD1_HUMAN	R14	6337	2	1325.5	(-0.0)	2.932	0.322	0.908	4	R.RQEL*EQAL*GIR.N
SW:SCD1_HUMAN	R14	1772	2	1434.5	(+0.5)	3.158	0.526	1.000	4	R.TATTQETDGFQVK#.R
SW:SCD1_HUMAN	R14	6677	2	1312.5	(+0.3)	3.359	0.368	0.988	3	K.YLQQIFESQR.M
SW:SCD1_HUMAN	R14	1778	2	1426.5	(+0.4)	2.533	0.259	0.896	4	R.TATTQETDGFQVK.R
SW:SCOT_HUMAN	R15	7413	3	2596.9	(+0.7)	4.723	0.552	1.000	1	R.AGGAGVPAFYTPTGYGTLVQEGGSPK.Y
SW:SCOT_HUMAN	R15	7431	2	2596.9	(-0.2)	4.327	0.583	1.000	1	R.AGGAGVPAFYTPTGYGTLVQEGGSPK.Y
SW:SCOT_HUMAN	R15	8765	2	2102.4	(-0.6)	3.898	0.456	1.000	1	K.GLTAVSNNAGVDNFGLLGLLR.S
SW:SCOT_HUMAN	R15	7365	2	1379.6	(+0.2)	3.010	0.344	0.863	5	K.YGDL*ANWMPGK#.M
SW:SDFL_HUMAN	R22	7066	3	2158.4	(+0.4)	3.903	0.412	0.993	2	K.AM@EGIFIK#PSVEPSAGHDEL*.-
SW:SDFL_HUMAN	R22	7478	3	2142.4	(+0.7)	3.790	0.380	0.986	2	K.AMEGIFIK#PSVEPSAGHDEL*.-
SW:SDFL_HUMAN	R22	5492	3	2040.2	(+0.4)	4.279	0.467	0.999	3	R.GQHEVHGMPSANTHNTWK#.A
SW:SDFL_HUMAN	R22	5484	3	2032.2	(+0.5)	4.138	0.436	1.000	3	R.GQHEVHGMPSANTHNTWK.A
SW:SDFL_HUMAN	R23	7064	3	2158.4	(+0.4)	4.296	0.429	0.987	2	K.AM@EGIFIK#PSVEPSAGHDEL*.-
SW:SERA_HUMAN	R15	1630	2	1131.3	(+0.5)	3.216	0.381	0.987	1	K.VTADVINAEEK.L
SW:SERA_HUMAN	R15	4899	2	1489.6	(-0.8)	3.133	0.559	0.998	1	R.AGTGVDNVDLEAATR.K
SW:SFPQ_HUMAN	R10	5989	3	2471.6	(-0.8)	4.607	0.425	0.976	3	K.DK#L*ESEM@EDAYHEHQANL*L*R.Q
SW:SFPQ_HUMAN	R10	7903	3	2455.6	(-0.1)	4.303	0.379	0.976	3	K.DK#L*ESEMEDAYHEHQANL*L*R.Q
SW:SFPQ_HUMAN	R10	4705	2	1144.3	(+0.8)	3.032	0.439	0.990	4	R.FATHAAALSVR.N
SW:SFPQ_HUMAN	R10	4723	2	1150.3	(+0.5)	2.793	0.482	0.990	4	R.FATHAAAL*SVR.N
SW:SFPQ_HUMAN	R10	4805	2	1150.3	(+0.2)	2.682	0.382	0.968	4	R.FATHAAAL*SVR.N
SW:SFPQ_HUMAN	R10	4783	2	1144.3	(+0.5)	2.598	0.314	0.955	4	R.FATHAAALSVR.N
SW:SFPQ_HUMAN	R10	8487	3	1829.0	(+0.5)	3.750	0.476	1.000	3	R.L*FVGNL*PADITEDEFK#.R
SW:SFPQ_HUMAN	R10	8485	2	1829.0	(-0.9)	2.949	0.239	0.652	3	R.L*FVGNL*PADITEDEFK#.R
SW:SFPQ_HUMAN	R10	9753	2	2658.9	(+0.7)	2.463	0.351	0.942	4	R.NL*SPYVSNEL*L*EEAFSQFGPIER.A
SW:SFPQ_HUMAN	R10	5879	2	1253.4	(+0.9)	3.683	0.485	0.997	4	K.YGEPGEVFINCK.G
SW:SFPQ_HUMAN	R10	5875	2	1261.4	(-0.5)	2.715	0.208	0.814	4	K.YGEPGEVFINCK#.G
SW:SFR1_HUMAN	R20	6474	2	1257.5	(+0.4)	3.103	0.440	0.990	4	R.IYVGNLPPDIR.T
SW:SFR1_HUMAN	R20	6600	2	1263.5	(+0.7)	3.102	0.428	0.990	4	R.IYVGNL*PPDIR.T
SW:SFR1_HUMAN	R20	6558	2	1257.5	(+0.4)	2.845	0.365	0.976	4	R.IYVGNLPPDIR.T
SW:SFR1_HUMAN	R20	6504	2	1263.5	(+0.3)	2.699	0.377	0.977	4	R.IYVGNL*PPDIR.T
SW:SFR1_HUMAN	R20	6654	2	1257.5	(+0.3)	2.566	0.402	0.925	4	R.IYVGNLPPDIR.T
SW:SFR1_HUMAN	R19	1548	2	1121.3	(+0.1)	2.377	0.325	0.935	3	R.K#EDMTYAVR.K
SW:SFR1_HUMAN	R20	1698	2	1121.3	(+0.8)	2.443	0.358	0.970	3	R.K#EDMTYAVR.K
SW:SFR1_HUMAN	R20	6258	2	1274.4	(+0.5)	4.007	0.473	1.000	4	R.TK#DIEDVIFYK#.Y
SW:SFR1_HUMAN	R20	6274	2	1274.4	(-0.9)	3.361	0.261	0.118	4	R.TK#DIEDVIFYK#.Y
SW:SFR1_HUMAN	R19	7178	2	1669.9	(-0.3)	2.279	0.162	0.474	4	R.VVVSGLPPSGSWQDLK.D
SW:SFR1_HUMAN	R20	6950	2	1669.9	(-0.7)	2.363	0.310	0.843	4	R.VVVSGLPPSGSWQDLK.D
SW:SFR3_HUMAN	R23	6578	2	1044.2	(+0.5)	2.390	0.458	0.974	1	R.AFGYYGPLR.S
SW:SFR3_HUMAN	R22	2456	2	1263.4	(+0.7)	2.453	0.356	0.890	1	K.VYVGNL*GNNGNK#.T
SW:SFR3_HUMAN	R23	4262	2	1249.4	(+0.3)	3.060	0.397	0.986	1	K.VYVGNLGNNGNK.T
SW:SFR3_HUMAN	R23	4336	2	1249.4	(+1.0)	2.936	0.365	0.978	1	K.VYVGNLGNNGNK.T
SW:SFR3_HUMAN	R23	2576	2	1263.4	(+1.0)	2.893	0.487	0.987	1	K.VYVGNL*GNNGNK#.T
SW:SFR3_HUMAN	R23	4260	2	1263.4	(+0.9)	2.773	0.365	0.955	1	K.VYVGNL*GNNGNK#.T
SW:SFR3_HUMAN	R23	4410	2	1249.4	(+0.8)	2.751	0.385	0.978	1	K.VYVGNLGNNGNK.T
SW:SFR3_HUMAN	R23	2734	2	1249.4	(+0.9)	2.746	0.413	0.982	1	K.VYVGNLGNNGNK.T
SW:SFR3_HUMAN	R23	4346	2	1263.4	(+0.3)	2.680	0.362	0.962	1	K.VYVGNL*GNNGNK#.T
SW:SFR3_HUMAN	R23	4420	2	1263.4	(+1.0)	2.676	0.342	0.955	1	K.VYVGNL*GNNGNK#.T
SW:SFR3_HUMAN	R23	4484	2	1249.4	(+0.4)	2.634	0.376	0.973	1	K.VYVGNLGNNGNK.T
SW:SFR3_HUMAN	R23	4456	2	1263.4	(-0.8)	2.622	0.355	0.833	1	K.VYVGNL*GNNGNK#.T
SW:SFR3_HUMAN	R23	2496	2	1263.4	(-1.0)	2.333	0.197	0.347	1	K.VYVGNL*GNNGNK#.T
SW:SFR3_HUMAN	R23	2548	2	1249.4	(-0.5)	2.293	0.266	0.820	1	K.VYVGNLGNNGNK.T
SW:SFR3_HUMAN	R23	3940	2	1263.4	(-0.0)	2.272	0.358	0.885	1	K.VYVGNL*GNNGNK#.T
SW:SFR9_HUMAN	R21	6954	2	1300.5	(+1.0)	2.291	0.340	0.263		R.EKDLEDLFYK.Y
SW:SFR9_HUMAN	R21	6264	2	1247.4	(+0.9)	3.248	0.499	1.000		R.IYVGNLPTDVR.E
SW:SFR9_HUMAN	R21	5324	2	1155.3	(+0.5)	2.247	0.328	0.944		R.KEDMEYALR.K

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:SFR9_HUMAN	R22	6524	2	1247.4	(+0.8)	2.356	0.278	0.885		R.IYVGNLPTDVR.E
SW:SFX1_HUMAN	R19	1358	2	1109.2	(+0.8)	2.866	0.269	0.964	1	K.IQESHPELR.R
SW:SFX1_HUMAN	R01	6215	2	1519.7	(+1.0)	2.557	0.312	0.941		R.NIL*L*TNEQL*ESAR.K
SW:SFX1_HUMAN	R19	6574	2	1501.7	(-0.1)	4.701	0.494	1.000		R.NILLTNEQLESAR.K
SW:SFX1_HUMAN	R19	6182	2	1651.7	(-0.9)	4.063	0.524	0.998	1	K.YIYDSAFHPDTEGK#.M
SW:SFX1_HUMAN	R19	6164	2	1643.7	(-0.2)	3.079	0.483	0.987	1	K.YIYDSAFHPDTEGK.M
SW:SJ2B_HUMAN	R25	7974	2	1441.6	(-0.2)	3.016	0.344	0.968	1	K.NLLHQDAVDLFR.N
SW:SJ2B_HUMAN	R25	5868	2	1087.3	(+0.3)	2.444	0.383	0.972		K.ILSVNGQDLK.N
SW:SKD3_HUMAN	R14	6161	2	1283.4	(+0.8)	3.353	0.426	0.990		K.ELLDGGANPLQR.N
SW:SKD3_HUMAN	R14	6147	2	1301.4	(-0.1)	2.882	0.238	0.902		K.EL*L*DGGANPL*QR.N
SW:SKD3_HUMAN	R14	2282	2	930.0	(+0.6)	2.708	0.275	0.957		K.DAALLEAAR.A
SW:SMD1_HUMAN	R01	6571	2	1285.5	(+0.8)	2.439	0.329	0.935	1	R.EPVQLETLSIR.G
SW:SMD1_HUMAN	R25	6932	3	2224.5	(+0.2)	3.863	0.315	0.986	1	K.NGTQVHGTITGVDSMNTHL*K#.A
SW:SMD1_HUMAN	R01	6467	2	1555.8	(+0.5)	3.691	0.459	0.999	1	K.NREPVQLETLSIR.G
SW:SMD1_HUMAN	R01	6459	2	1567.8	(-0.6)	3.170	0.381	0.457	1	K.NREPVQL*ETL*SIR.G
SW:SMD1_HUMAN	R25	7218	2	1567.8	(-0.8)	3.613	0.384	0.287	1	K.NREPVQL*ETL*SIR.G
SW:SMD1_HUMAN	R01	10577	2	2288.7	(+0.3)	4.812	0.563	0.999	1	R.YFILPDSLPLDTLLVDVEPK.V
SW:SMD1_HUMAN	R01	10583	3	2288.7	(+0.9)	4.390	0.422	0.999	1	R.YFILPDSLPLDTLLVDVEPK.V
SW:SMD1_HUMAN	R02	9672	3	2288.7	(-0.7)	3.833	0.403	0.997	1	R.YFILPDSLPLDTLLVDVEPK.V
SW:SMD1_HUMAN	R02	9628	2	2288.7	(+0.2)	2.537	0.412	0.960	1	R.YFILPDSLPLDTLLVDVEPK.V
SW:SMD1_HUMAN	R04	10146	2	2288.7	(+0.1)	2.789	0.482	0.982	1	R.YFILPDSLPLDTLLVDVEPK.V
SW:SMD1_HUMAN	R25	6552	2	1290.5	(+0.2)	2.579	0.246	0.841		K.L*SHETVTIEL*K#.N
SW:SMD2_HUMAN	R25	8690	2	2008.2	(-0.4)	3.828	0.600	1.000		R.EEEEEFNTGPLSVLTQSVK.N
SW:SMD2_HUMAN	R25	8616	2	2028.2	(-0.5)	2.289	0.293	0.784		R.EEEEEFNTGPL*SVL*TQSVK#.N
SW:SMD2_HUMAN	R25	8308	3	2184.4	(+0.6)	5.202	0.545	1.000		K.REEEEEFNTGPL*SVL*TQSVK#.N
SW:SMD2_HUMAN	R25	8306	3	2164.4	(+0.7)	4.621	0.555	0.996		K.REEEEEFNTGPLSVLTQSVK.N
SW:SMD2_HUMAN	R25	8440	3	2184.4	(+0.7)	4.383	0.469	0.996		K.REEEEEFNTGPL*SVL*TQSVK#.N
SW:SMD2_HUMAN	R25	8356	2	2164.4	(-0.8)	4.265	0.564	0.997		K.REEEEEFNTGPLSVLTQSVK.N
SW:SMD2_HUMAN	R25	6880	2	958.1	(+0.6)	2.251	0.296	0.924		R.GDSVIVVLR.N
SW:SMD3_HUMAN	R25	8932	2	1090.4	(-0.6)	2.558	0.114	0.657		R.FLILPDMLK.N
SW:SMD3_HUMAN	R25	6714	2	1219.4	(+0.8)	2.474	0.238	0.897		R.VAQLQVYIR.G
SW:SMD3_HUMAN	R25	6736	2	1219.4	(-0.4)	2.286	0.249	0.823		R.VAQLQVYIR.G
SW:SMD3_HUMAN	R26	6424	2	1219.4	(+0.3)	3.706	0.361	0.991		R.VAQLQVYIR.G
SW:SMD3_HUMAN	R27	5929	2	1219.4	(+0.7)	3.156	0.306	0.979		R.VAQLQVYIR.G
SW:SMD3_HUMAN	R27	5925	2	1225.4	(+0.0)	2.787	0.240	0.913		R.VAQL*EQVYIR.G
SW:SMF1_HUMAN	R04	5342	2	1274.5	(+0.2)	2.390	0.401	0.950	9	R.AAGPGL*GNVAMGPR.Q
SW:SMF1_HUMAN	R04	1472	2	1256.5	(+0.5)	2.567	0.337	0.958	9	K.AM@GM@TNL*PAVGR.K
SW:SMF1_HUMAN	R05	1428	2	1256.5	(+0.5)	2.883	0.436	0.987	9	K.AM@GM@TNL*PAVGR.K
SW:SMF1_HUMAN	R06	5952	2	1877.0	(-0.9)	2.217	0.258	0.394	14	R.EL*ATNL*NVGTSSSAASSL*K#.K
SW:SMF1_HUMAN	R04	4852	3	2538.7	(+0.4)	5.423	0.548	1.000	9	R.K#APGSDPFM@SSGQGPNGGM@GDPYSR.A
SW:SMF1_HUMAN	R05	5648	3	2522.7	(+0.4)	6.006	0.544*	0.433	9	R.K#APGSDPFMSSGQGPNGGM@GDPYSR.A
SW:SMF1_HUMAN	R05	4986	3	2538.7	(+0.4)	4.945	0.508	0.999	9	R.K#APGSDPFM@SSGQGPNGGM@GDPYSR.A
SW:SMF1_HUMAN	R04	8244	2	2132.4	(-0.4)	2.794	0.374	0.959	15	K.L*SIQDNNVDL*IL*ATPPFSR.L
SW:SMF1_HUMAN	R04	4540	2	1163.3	(-0.0)	2.425	0.235	0.789	6	K.LYELGGEPER.K
SW:SMF1_HUMAN	R05	4250	2	1163.3	(+0.6)	2.708	0.257	0.941	6	K.LYELGGEPER.K
SW:SMF1_HUMAN	R05	4414	2	1163.3	(-0.3)	2.500	0.169	0.738	6	K.LYELGGEPER.K
SW:SMF1_HUMAN	R05	4620	2	1175.3	(+0.4)	2.468	0.313	0.950	6	K.L*YEL*GGEPER.K
SW:SMF1_HUMAN	R05	4342	2	1163.3	(+0.1)	2.413	0.162	0.682	6	K.LYELGGEPER.K
SW:SMF1_HUMAN	R06	4372	2	1163.3	(+0.7)	2.333	0.220	0.841	6	K.LYELGGEPER.K
SW:SMF1_HUMAN	R05	2264	3	2065.3	(-0.0)	3.840	0.281	0.972	6	R.NPQM@PQYSSPQPGSAL*SPR.Q
SW:SMF1_HUMAN	R05	6340	2	2126.2	(-0.7)	3.604	0.468	1.000	9	R.SNSVGIQDAFNDGSDSTFQK#.R
SW:SN21_HUMAN	R08	2172	2	1048.1	(+0.7)	2.412	0.297	0.936	1	K.DIDVLNSSGK.M
SW:SN21_HUMAN	R08	7697	2	1776.9	(+0.0)	3.272	0.435	0.984	1	K.ESEL*TDEDITIL*ER.G
SW:SN21_HUMAN	R08	5593	2	1056.2	(+0.8)	2.746	0.236	0.942	1	R.FEVSPSYVK.G
SW:SN21_HUMAN	R08	5613	2	1064.2	(+0.2)	2.461	0.142	0.533	1	R.FEVSPSYVK#.G
SW:SN21_HUMAN	R08	1220	2	1063.2	(+0.3)	3.357	0.529	1.000	2	R.HGATHVFASK#.E
SW:SN21_HUMAN	R08	1224	2	1055.2	(-0.3)	2.837	0.477	0.987	2	R.HGATHVFASK.E
SW:SN21_HUMAN	R08	4695	2	1135.3	(+0.7)	3.550	0.152	0.947	2	R.L*DSIVIQGR.L

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:SN21_HUMAN	R08	4773	2	1135.3	(+0.6)	3.062	0.167	0.888	2	R.L*DSIVIQQGR.L
SW:SN21_HUMAN	R08	4723	2	1129.3	(-0.3)	2.261	0.239	0.797	2	R.LDSIVIQQGR.L
SW:SN21_HUMAN	R08	8483	2	1114.4	(+0.8)	3.524	0.261	0.982	2	R.LLNILMQLR.K
SW:SN21_HUMAN	R08	8477	2	1138.4	(+0.6)	2.933	0.364	0.985	2	R.L*L*NIL*MQL*R.K
SW:SN21_HUMAN	R08	8491	2	1138.4	(-0.8)	2.355	0.292	0.765	2	R.L*L*NIL*MQL*R.K
SW:SN21_HUMAN	R08	8599	2	1334.6	(+0.1)	3.261	0.431	0.986	1	K.TLQTIALLGYLK.H
SW:SN21_HUMAN	R08	7139	2	1101.3	(+0.5)	2.551	0.402	0.982	2	R.VL*IFSQMTR.L
SW:SN21_HUMAN	R08	7143	2	1095.3	(+0.7)	2.449	0.434	0.984	2	R.VLIFSQMTR.L
SW:SN21_HUMAN	R08	5341	2	1116.3	(+0.6)	2.866	0.237	0.952	2	R.YLVIDEAHR.I
SW:SN21_HUMAN	R08	5317	2	1122.3	(+0.4)	2.851	0.181	0.914	2	R.YL*VIDEAHR.I
SW:SN21_HUMAN	R08	5399	2	1122.3	(+0.1)	2.849	0.296	0.959	2	R.YL*VIDEAHR.I
SW:SN22_HUMAN	R06	2224	2	1256.3	(+0.4)	2.747	0.424	0.985	1	R.DVDYSDALTEK.Q
SW:SN22_HUMAN	R05	8998	2	1637.9	(-0.3)	3.072	0.356	0.960	7	K.FNVL*L*TTYEYIIK#.D
SW:SN22_HUMAN	R06	6594	3	1601.8	(+0.6)	3.910	0.236	0.987	5	K.HQEYL*NSIL*QHAK#.D
SW:SN22_HUMAN	R01	8087	2	1603.9	(+1.0)	3.534	0.263	0.971	7	R.LMEEDELPSWIK.D
SW:SN22_HUMAN	R06	8060	2	1623.9	(+0.1)	3.958	0.293	0.969	7	R.L*MEEDEL*PSWIK#.D
SW:SN22_HUMAN	R06	7858	3	2418.7	(+0.5)	4.507	0.407	0.995	7	R.LMEEDELPSWIKDDAEVER.L
SW:SN22_HUMAN	R06	5866	2	1524.8	(+0.1)	3.368	0.390	0.982	6	K.L*TQVL*NTHYVAPR.R
SW:SN22_HUMAN	R06	7366	2	1429.6	(-0.2)	2.511	0.233	0.826	8	R.QL*SEVFIQL*PSR.K
SW:SN22_HUMAN	R06	7880	2	1233.5	(+0.2)	2.510	0.383	0.964	7	K.TL*MNTIMQL*R.K
SW:SN22_HUMAN	R06	7620	2	1569.8	(+0.4)	3.415	0.370	0.959	7	R.VDL*NEEETIL*IIR.R
SW:SN22_HUMAN	R01	2478	2	1137.3	(+0.0)	2.903	0.332	0.961	7	K.VIQAGMFDQK.S
SW:SN22_HUMAN	R06	6484	2	1198.4	(-0.1)	2.280	0.157*	0.119	1	R.ILLTGTPQLNK.L
SW:SN24_HUMAN	R06	8682	3	3520.8	(-0.5)	3.956	0.461	0.999	5	R.AGGL*GL*NL*QSADTVIIFDSDWNPHQDL*QAQDR.A
SW:SN24_HUMAN	R06	8064	3	2144.4	(+0.6)	4.325	0.435	0.975	3	K.AGQL*EAWL*EMNPGYEVAPR.S
SW:SN24_HUMAN	R06	7634	3	2160.4	(-0.1)	3.891	0.425*	0.050	3	K.AGQL*EAWL*EM@NPGYEVAPR.S
SW:SN24_HUMAN	R06	7528	2	1746.9	(-0.2)	4.629	0.354	1.000	5	K.AIEEGTLEEIEIEEVR.Q
SW:SN24_HUMAN	R06	7518	2	1752.9	(-0.2)	3.056	0.332	0.956	5	K.AIEEGTLEEIEIEEVR.Q
SW:SN24_HUMAN	R06	5754	2	1147.3	(+0.8)	2.992	0.372	0.965	2	R.DTALETALNAK.A
SW:SN24_HUMAN	R06	1606	2	1019.1	(+0.8)	2.670	0.177	0.862	5	K.GVLLTDGSEK.D
SW:SN24_HUMAN	R06	6838	2	1375.5	(+0.2)	3.205	0.319	0.974	5	R.HEEFDL*FM@R.M
SW:SN24_HUMAN	R06	11278	2	2665.1	(+0.3)	2.864	0.211	0.843	3	R.INGPFL*IIVPL*STL*SNWAYEFDK#.W
SW:SN24_HUMAN	R06	7570	2	1725.9	(+0.9)	5.263	0.530	1.000	2	R.IQELENLPGSLAGDLR.T
SW:SN24_HUMAN	R06	6206	3	3270.5	(-0.9)	4.418	0.333	0.976	3	K.K#AENAEGQTPAIGPDGEPL*DETSQM@SDL*PVK#.V
SW:SN24_HUMAN	R06	6734	3	3226.5	(+0.2)	4.379	0.367	0.996	3	K.KAENAEGQTPAIGPDGEPLDETSQMSDLPVK.V
SW:SN24_HUMAN	R06	6712	3	3254.5	(-0.9)	4.251	0.330	0.884	3	K.K#AENAEGQTPAIGPDGEPL*DETSQMSDL*PVK#.V
SW:SN24_HUMAN	R06	2472	3	1766.8	(+0.8)	3.887	0.417	0.998	3	K.K#IPDPDSDDVSEVDAR.H
SW:SN24_HUMAN	R06	4262	3	1758.8	(+0.5)	3.773	0.380	0.999	3	K.KIPDPDSDDVSEVDAR.H
SW:SN24_HUMAN	R06	5760	2	1672.7	(-0.3)	3.379	0.436	0.985	3	K.QDVDDEYGVSQL*AR.G
SW:SN24_HUMAN	R06	5770	2	1666.7	(-0.2)	2.749	0.279	0.898	3	K.QDVDDEYGVSQLAR.G
SW:SN24_HUMAN	R06	886	2	877.0	(+0.7)	2.449	0.409	0.977	3	K.VIHVESGK#.I
SW:SNAA_HUMAN	R20	8748	2	1390.7	(+0.4)	3.294	0.393	0.989	6	R.LDQWLTTMLLR.I
SW:SNAA_HUMAN	R20	8066	2	1564.7	(-0.5)	3.973	0.514	1.000	2	K.NSQSFFSGL*FGSSK#.I
SW:SNAA_HUMAN	R20	7080	2	1454.7	(+0.8)	4.639	0.548	1.000	2	K.VAGYAALLEQYQK.A
SW:SNAA_HUMAN	R20	7398	2	1461.6	(+0.8)	3.740	0.514	0.584	3	K.YEELFPAFSDSR.E
SW:SNAA_HUMAN	R20	7418	2	1467.6	(+0.5)	3.223	0.386	0.987	3	K.YEEL*FPAFSDSR.E
SW:SNAA_HUMAN	R20	7076	2	1474.7	(+0.6)	2.326	0.230	0.547	2	K.VAGYAAL*L*EQYQK#.A
SW:SNF5_HUMAN	R17	6594	2	1548.6	(-0.3)	3.951	0.481	1.000	5	K.ASEVEEILDGNDEK.Y
SW:SNF5_HUMAN	R17	6592	2	1562.6	(-0.3)	3.259	0.349	0.962	5	K.ASEVEEILDGNDEK#.Y
SW:SNF5_HUMAN	R16	6026	2	1434.6	(+0.9)	2.351	0.222	0.798	5	K.AVSISTEPPTYLR.E
SW:SNF5_HUMAN	R17	6450	2	1256.4	(+0.8)	2.786	0.348	0.977	3	R.DAFTWNNMNEK.L
SW:SNF5_HUMAN	R17	6446	2	1264.4	(-0.1)	2.648	0.370	0.956	3	R.DAFTWNNMNEK#.L
SW:SNF5_HUMAN	R17	2542	2	1063.2	(+0.2)	2.833	0.406	0.976	3	R.L*DMEIDGQK#.L
SW:SNF5_HUMAN	R17	8168	2	1922.2	(-0.1)	4.373	0.474	1.000	3	K.TYAFSENPLPTVEIAIR.N
SW:SNF5_HUMAN	R17	1800	2	984.1	(+0.5)	2.303	0.243	0.898	3	R.GQLSWHQK.T
SW:SON_HUMAN	R03	6143	2	1355.5	(+0.3)	3.432	0.457	1.000	9	R.AGIEGPLLASDVGR.D
SW:SON_HUMAN	R04	6440	2	1367.5	(-0.6)	2.862	0.435	0.978	9	R.AGIEGPL*L*ASDVGR.D
SW:SON_HUMAN	R04	6444	2	1355.5	(+0.5)	2.783	0.361	0.964	9	R.AGIEGPLLASDVGR.D
SW:SON_HUMAN	R05	6552	2	1367.5	(-0.1)	3.447	0.468	1.000	9	R.AGIEGPL*L*ASDVGR.D
SW:SON_HUMAN	R06	6542	2	1367.5	(-0.1)	3.758	0.455	1.000	9	R.AGIEGPL*L*ASDVGR.D
SW:SON_HUMAN	R03	6333	2	1705.9	(-0.3)	2.572	0.119	0.413	8	K.DIHL*DL*PSNNNL*VSK#.D

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:SON_HUMAN	R04	6594	2	1705.9	(+0.4)	2.655	0.200	0.771	8	K.DIHL*DL*PSNNNL*VSK#.D
SW:SON_HUMAN	R08	1688	2	1028.1	(+0.6)	2.255	0.225	0.846	8	K.DTEELPVK.E
SW:SON_HUMAN	R03	6369	2	1616.7	(+0.5)	4.261	0.370	0.998	8	K.EADSVYGEWVPEK#.N
SW:SON_HUMAN	R04	6638	2	1616.7	(-0.2)	2.671	0.249	0.822	8	K.EADSVYGEWVPEK#.N
SW:SON_HUMAN	R03	6903	2	1373.5	(+0.8)	2.523	0.315	0.939	8	K.ESDQTLAALLSPK.E
SW:SON_HUMAN	R03	6467	2	1632.8	(+1.0)	4.132	0.474	1.000	7	K.FDSEPSAVAL*EL*PTR.A
SW:SON_HUMAN	R03	6469	3	1644.8	(+0.1)	3.809	0.263	0.970	7	K.FDSEPSAVAL*EL*PTR.A
SW:SON_HUMAN	R03	6461	2	1644.8	(-0.2)	3.464	0.369	0.978	7	K.FDSEPSAVAL*EL*PTR.A
SW:SON_HUMAN	R04	6720	2	1632.8	(+1.0)	3.211	0.483	0.991	7	K.FDSEPSAVAL*EL*PTR.A
SW:SON_HUMAN	R04	6714	2	1644.8	(+0.2)	2.707	0.308	0.754	7	K.FDSEPSAVAL*EL*PTR.A
SW:SON_HUMAN	R06	6874	2	1644.8	(-0.7)	3.204	0.348	0.967	7	K.FDSEPSAVAL*EL*PTR.A
SW:SON_HUMAN	R03	1456	2	800.9	(+1.0)	2.325	0.233	0.894	4	K.GLVAVGER.A
SW:SON_HUMAN	R03	7371	2	1573.8	(+0.5)	3.122	0.393	0.983	11	K.IEEVLSGVLDTEL.R.Y
SW:SON_HUMAN	R03	7363	2	1591.8	(-0.5)	2.344	0.215	0.693	11	K.IEEVL*SGVL*DTEL*R.Y
SW:SON_HUMAN	R04	7618	2	1573.8	(+0.1)	3.122	0.359	0.969	11	K.IEEVLSGVLDTEL.R.Y
SW:SON_HUMAN	R03	7503	2	1858.2	(+0.7)	3.699	0.476	1.000	7	K.ILDSFAAAPVPTTTLVLK.S
SW:SON_HUMAN	R04	7752	2	1858.2	(+0.8)	2.877	0.520	0.991	7	K.ILDSFAAAPVPTTTLVLK.S
SW:SON_HUMAN	R06	7906	2	1858.2	(+0.8)	2.904	0.434	0.984	7	K.ILDSFAAAPVPTTTLVLK.S
SW:SON_HUMAN	R04	5890	2	1127.4	(+0.4)	2.465	0.210	0.686	7	K.IM@L*VEPPVAK#.V
SW:SON_HUMAN	R04	6338	2	1111.4	(+0.2)	2.356	0.388	0.944	7	K.IML*VEPPVAK#.V
SW:SON_HUMAN	R03	7279	3	3104.5	(+0.4)	4.163	0.432	0.994	7	R.LPEQPVDVPSEIADSSMTRPQELPEL.PK.T
SW:SON_HUMAN	R04	7528	3	3104.5	(+0.6)	4.669	0.360	0.988	7	R.LPEQPVDVPSEIADSSMTRPQELPEL.PK.T
SW:SON_HUMAN	R04	7182	3	3146.5	(-0.4)	4.414	0.373	0.976	7	R.L*PEQPVDVPSEIADSSM@TRPQEL*PEL*PK#.T
SW:SON_HUMAN	R05	7570	3	3104.5	(+0.6)	4.736	0.365	0.990	7	R.LPEQPVDVPSEIADSSMTRPQELPEL.PK.T
SW:SON_HUMAN	R05	7572	3	3130.5	(-0.9)	3.993	0.350	0.848	7	R.L*PEQPVDVPSEIADSSMTRPQEL*PEL*PK#.T
SW:SON_HUMAN	R06	7376	3	3146.5	(-0.7)	4.912	0.421	0.969	7	R.L*PEQPVDVPSEIADSSM@TRPQEL*PEL*PK#.T
SW:SON_HUMAN	R06	7680	3	3104.5	(+0.8)	4.673	0.452	0.997	7	R.LPEQPVDVPSEIADSSMTRPQELPEL.PK.T
SW:SON_HUMAN	R06	7682	3	3130.5	(-0.1)	4.214	0.381	0.976	7	R.L*PEQPVDVPSEIADSSMTRPQEL*PEL*PK#.T
SW:SON_HUMAN	R03	1732	3	2586.6	(+0.3)	5.772	0.554	1.000	11	R.NEGQLNGETNTPIEGNQAGDAAASAR.S
SW:SON_HUMAN	R03	1708	3	2592.6	(+0.9)	5.758	0.652	1.000	11	R.NEGQL*NGETNTPIEGNQAGDAAASAR.S
SW:SON_HUMAN	R03	6435	3	3328.4	(+0.2)	5.522	0.531	0.998	6	K.NGEENK#DDDNVFSNL*PSEPVDISTAM@SER.A
SW:SON_HUMAN	R04	6678	3	3328.4	(+0.2)	4.557	0.440	0.992	6	K.NGEENK#DDDNVFSNL*PSEPVDISTAM@SER.A
SW:SON_HUMAN	R03	4891	2	1249.3	(-0.4)	2.645	0.334	0.928	9	K.SGGATIEEL*TEK#.C
SW:SON_HUMAN	R05	5324	2	1235.3	(+0.6)	2.555	0.415	0.978	9	K.SGGATIEELTEK.C
SW:SON_HUMAN	R05	5312	2	1249.3	(+0.2)	2.420	0.330	0.897	9	K.SGGATIEEL*TEK#.C
SW:SON_HUMAN	R04	6542	2	1792.9	(-0.1)	3.762	0.219	0.936	7	K.SHDDGNIDLESDFLK.F
SW:SON_HUMAN	R04	6426	2	1716.0	(+0.7)	2.448	0.384	0.959	7	K.SSEPVVTMSVEYQMK.S
SW:SON_HUMAN	R10	6917	2	1355.5	(+0.0)	3.810	0.540	0.999	9	R.AGIEGPLLASDVGR.D
SW:SP22_HUMAN	R22	7294	2	1414.6	(+0.7)	2.560	0.474	0.986		K.NNALNQVVLWDK.I
SW:SP22_HUMAN	R23	7292	2	1434.6	(-0.2)	2.714	0.354	0.944		K.NNAL*NQVVL*WDK#.I
SW:SP22_HUMAN	R23	7434	2	1434.6	(+0.0)	2.383	0.357	0.915		K.NNAL*NQVVL*WDK#.I
SW:SP22_HUMAN	R23	7856	2	1337.4	(+0.2)	3.007	0.305	0.947		K.YFFFDDGNGL*K#.G
SW:SP22_HUMAN	R23	7940	2	1337.4	(+0.6)	2.435	0.316	0.912		K.YFFFDDGNGL*K#.G
SW:SP22_HUMAN	R24	7282	2	1434.6	(-0.5)	2.963	0.466	0.981		K.NNAL*NQVVL*WDK#.I
SW:SP25_HUMAN	R01	7359	3	2215.4	(+1.0)	3.963	0.340	0.982	2	K.FFDHSGTLVMDAYEPEISR.L
SW:SP25_HUMAN	R23	7136	3	2237.4	(+0.5)	4.363	0.454	0.995	2	K.FFDHSGTL*VM@DAYEPEISR.L
SW:SP25_HUMAN	R23	7656	3	2215.4	(+0.6)	3.820	0.330	0.995	2	K.FFDHSGTLVMDAYEPEISR.L
SW:SP25_HUMAN	R23	7608	3	2178.4	(-0.1)	4.586	0.372	0.995	2	R.K#DPTGM@DPDDIWQL*SSSL*K#.R
SW:SP25_HUMAN	R23	5418	2	1066.2	(-0.4)	2.591	0.196	0.844	2	R.L*HDSL*AIER.K
SW:SP25_HUMAN	R23	5458	2	1054.2	(+0.8)	2.475	0.365	0.973	2	R.LHDSLAIER.K
SW:SP25_HUMAN	R23	6852	2	1283.4	(+0.8)	3.090	0.519	1.000	1	K.YVENFGLIDGR.L
SW:SP25_HUMAN	R23	5270	2	1030.2	(+0.8)	2.292	0.149	0.053	2	R.FDDKYTLK.L
SW:SPC4_HUMAN	R25	7794	2	1067.2	(+0.8)	2.256	0.198	0.798	3	R.GDL*L*FL*TNR.V
SW:SPC4_HUMAN	R24	8448	2	1358.5	(-0.4)	2.271	0.208	0.707	1	-.M@L*SL*DFL*DDVR.R
SW:SPC4_HUMAN	R25	8720	2	1358.5	(+0.2)	2.789	0.306	0.947	1	-.M@L*SL*DFL*DDVR.R
SW:SPCN_HUMAN	R07	8019	2	1708.9	(+0.6)	3.353	0.404	0.988	2	R.AQLADSFHLQQFFR.D
SW:SPCN_HUMAN	R04	1730	2	1193.3	(-0.7)	2.341	0.254	0.808	3	K.DL*TNVQNL*QK#.K
SW:SPCN_HUMAN	R05	5686	3	1646.7	(+0.5)	3.881	0.406	0.999	3	K.HQL*L*EADISAHEDR.L
SW:SPCN_HUMAN	R07	4885	2	1074.2	(+0.1)	2.487	0.235	0.849	6	R.SLQQLAEER.S
SW:SPCN_HUMAN	R08	8021	2	1588.8	(-0.1)	2.551	0.284	0.868	3	R.ELPTAFDYVEFTR.S
SW:SPCO_HUMAN	R05	10364	2	1969.1	(-0.2)	2.626	0.204	0.754	1	K.DGL*NEAWADL*L*EL*IDTR.T



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:SPCO_HUMAN	R05	7792	2	1394.5	(+0.7)	2.811	0.488	0.991	2	R.DL*DDFQSWL*SR.T
SW:SPCO_HUMAN	R05	6230	2	1110.3	(+0.6)	2.775	0.380	0.983	1	R.ITDLYTDLR.D
SW:SPCO_HUMAN	R05	6224	2	1122.3	(+0.1)	2.500	0.383	0.967	1	R.ITDL*YTDL*R.D
SW:SPCO_HUMAN	R05	7558	2	1464.6	(-0.1)	3.037	0.297	0.939	2	R.L*AEISDVWEEMK#.T
SW:SPCO_HUMAN	R05	6612	2	1525.7	(-0.5)	2.762	0.297	0.925	2	R.LQALDTGWNELHK.M
SW:SPCO_HUMAN	R05	8046	3	2828.0	(-0.1)	5.622	0.510	0.778	1	R.VDTVNHL*ADEL*INSGHSDAATIAEWK#.D
SW:SPCO_HUMAN	R05	8048	3	2808.0	(+0.6)	4.120	0.450	0.999	1	R.VDTVNHLADELINSGHSDAATIAEWK.D
SW:SPCO_HUMAN	R06	5548	2	1122.3	(-0.3)	2.806	0.240	0.916	2	K.VLVLSQDYGK.H
SW:SR68_HUMAN	R12	8198	2	1526.7	(+0.3)	3.163	0.294	0.967	4	K.DLPDVQELITQVR.S
SW:SR68_HUMAN	R12	8196	2	1538.7	(-0.2)	2.336	0.201	0.672	4	K.DL*PDVQEL*ITQVR.S
SW:SR68_HUMAN	R12	4470	2	1057.2	(-0.5)	2.260	0.301*	0.154	2	K.L*EAL*ITQTR.A
SW:SRPB_HUMAN	R21	5630	2	1347.4	(+0.4)	3.390	0.466	1.000	1	R.GDVGSADIQDLEK.W
SW:SRPB_HUMAN	R21	5632	2	1361.4	(-0.6)	2.912	0.237	0.866	1	R.GDVGSADIQDL*EK#.W
SW:SRPB_HUMAN	R20	7070	2	1423.7	(+0.2)	3.867	0.484	0.993	1	K.GKEFEFSQLPLK.V
SW:SRPB_HUMAN	R20	7256	2	1746.9	(-0.1)	2.666	0.265	0.869	1	R.GNSL*TL*IDL*PGHESL*R.L
SW:SRPB_HUMAN	R20	1748	2	1000.2	(+1.0)	2.291	0.193	0.830	1	K.LIQQQLEK.E
SW:SRPB_HUMAN	R20	2446	2	1789.9	(-0.7)	2.885	0.404	0.971		R.SAAPSTLDSSTAPAQLGK.K
SW:SRPB_HUMAN	R21	5106	2	1789.9	(-0.6)	3.308	0.446	0.985		R.SAAPSTLDSSTAPAQLGK.K
SW:SRPB_HUMAN	R20	7174	2	1908.1	(-0.5)	3.660	0.354	0.978		R.VADGGGAGGTFQPYL*DTL*R.Q
SW:SRPB_HUMAN	R20	7168	2	1896.1	(-0.6)	3.048	0.360	0.965		R.VADGGGAGGTFQPYLDTLR.Q
SW:SRPB_HUMAN	R21	7120	2	1896.1	(-0.6)	2.781	0.382	0.954		R.VADGGGAGGTFQPYLDTLR.Q
SW:SSB_HUMAN	R25	9556	2	1780.1	(+0.3)	2.968	0.544	1.000		K.NPVTIFSLATNEMWR.S
SW:SSB_HUMAN	R25	6024	2	1612.7	(-0.4)	4.987	0.430	0.996		R.SGDSEVYQLGDVSQK.T
SW:SSB_HUMAN	R25	6032	2	1626.7	(-0.3)	3.289	0.283	0.927		R.SGDSEVYQL*GDVSQK#.T
SW:SSB_HUMAN	R25	1982	2	884.0	(+0.8)	2.605	0.252	0.947		R.VGQDPVLR.Q
SW:SSB_HUMAN	R25	5902	2	1134.2	(-0.0)	2.298	0.197	0.744		K.IDYGEYMDK.N
SW:SSRA_HUMAN	R19	5636	2	1212.3	(+0.9)	3.091	0.444	0.988	3	K.GEDFPANNIVK#.F
SW:SSRA_HUMAN	R19	5554	2	1212.3	(-0.4)	2.508	0.333	0.920	3	K.GEDFPANNIVK#.F
SW:SSRA_HUMAN	R19	8972	2	1686.8	(+0.4)	2.936	0.489	0.990	4	K.GTEDFIVESLDASFR.Y
SW:SSRA_HUMAN	R20	8592	2	1686.8	(-0.6)	2.794	0.421	0.971	4	K.GTEDFIVESLDASFR.Y
SW:SSRD_HUMAN	R25	7928	2	1406.5	(+0.3)	2.736	0.483	0.990	1	R.FFDEESYSLLR.K
SW:SSRD_HUMAN	R25	9018	2	2173.4	(+0.7)	4.072	0.398	0.998	1	R.NNEDISIIPPL*FTVSVDR.H
SW:SSRD_HUMAN	R25	9014	2	2167.4	(-0.2)	3.646	0.457	1.000	1	R.NNEDISIIPPLFTVSVDR.G
SW:SSRD_HUMAN	R25	6512	2	1366.6	(+0.2)	4.299	0.518	1.000	2	R.VQNMALYADVGGK.Q
SW:SSRD_HUMAN	R25	6530	2	1380.6	(-0.2)	4.066	0.413	1.000	2	R.VQNMAL*YADVGGK#.Q
SW:SSRD_HUMAN	R25	5328	2	1396.6	(-0.3)	3.331	0.394	0.976	2	R.VQNM@AL*YADVGGK#.Q
SW:SSRD_HUMAN	R25	6836	2	1277.4	(+0.5)	2.289	0.271	0.868	2	R.YQVSWSL*DHK#.S
SW:SSRD_HUMAN	R25	6748	2	1263.4	(-0.6)	2.238	0.266	0.836	2	R.YQVSWSLDHK.S
SW:SSRP_HUMAN	R11	6568	2	1206.4	(+0.7)	3.185	0.276	0.970		K.ASSGLLYPLER.G
SW:SSRP_HUMAN	R11	5960	2	1384.5	(+0.7)	3.087	0.295	0.954		K.SDHPGISITDL*SK#.K
SW:SSRP_HUMAN	R11	6444	2	1124.2	(+0.4)	2.256	0.400	0.962		R.SFDFEIETK#.Q
SW:SSRP_HUMAN	R11	7122	2	1707.9	(+0.2)	3.472	0.466	1.000		K.VDNIQAGEL*TEGIWR.R
SW:SSRP_HUMAN	R11	6446	2	1116.2	(+1.0)	2.230	0.304	0.927		R.SFDFEIETK.Q
SW:STB1_HUMAN	R13	8217	2	1733.0	(+0.7)	2.793	0.514	0.990		R.AIVPILLDANVSTYDK.I
SW:STB1_HUMAN	R24	6508	2	1948.2	(+0.8)	2.315	0.167	0.019		R.WTPIIKDIMEDTIEDK.L
SW:STM1_HUMAN	R11	6296	3	2331.6	(+0.8)	4.992	0.516	0.997	1	K.AHSLMELSPSAPPGGSPHLDSSR.S
SW:STM1_HUMAN	R11	8400	2	1513.8	(+0.7)	2.933	0.427	0.985	1	K.ALDTVLFPGPLLTR.H
SW:STM1_HUMAN	R11	5948	2	1398.6	(-0.0)	3.656	0.329	0.971	1	R.L*IEGVHPGSL*VEK#.L
SW:STM1_HUMAN	R11	1556	2	912.1	(+0.7)	2.539	0.235	0.900	1	K.LPDPSPALAK.K
SW:STM1_HUMAN	R11	2186	2	1072.2	(-0.6)	2.284	0.138	0.026	1	K.LRDEINLAK.Q
SW:STM1_HUMAN	R11	2048	2	1266.4	(-0.1)	2.561	0.249	0.889	1	K.YAEEEELEQVR.E
SW:STM1_HUMAN	R11	2042	2	1272.4	(+0.2)	2.495	0.207	0.815	1	K.YAEEEL*EQVR.E
SW:STM1_HUMAN	R11	6312	2	1159.3	(+0.3)	2.283	0.298	0.911	1	K.QALSEVTAALR.E
SW:STT3_HUMAN	R01	1260	2	1051.2	(+0.6)	2.552	0.410	0.978	4	R.FGQVYTEAK#.R
SW:STT3_HUMAN	R01	6085	2	1118.2	(+0.6)	2.752	0.342	0.952	3	R.FL*AEEGFYK#.F
SW:STT3_HUMAN	R01	6091	2	1104.2	(+0.8)	2.573	0.306	0.961	3	R.FLAEEGFYK.F
SW:STT3_HUMAN	R02	6014	2	1104.2	(+0.1)	2.343	0.151	0.653	3	R.FLAEEGFYK.F

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:STT3_HUMAN	R03	5873	2	1118.2	(-0.5)	2.956	0.327	0.963	3	R.FL*AEEGFYK#.F
SW:STXH_HUMAN	R17	8648	3	2555.9	(+0.3)	4.604	0.520	0.999	1	K.VL*QQEAEIDSIHQL*VVGATENIK#.E
SW:STXH_HUMAN	R17	4732	2	1215.4	(+0.5)	2.283	0.399	0.958	1	K.ALGVAVGGGVDGSR.D
SW:SUR1_HUMAN	R20	7866	2	1158.3	(+0.9)	3.576	0.432	1.000		K.LNLIAELESR.V
SW:SUR1_HUMAN	R20	7752	2	1720.1	(+0.2)	2.445	0.362	0.929		R.VLAEPVPLPADPMEK.N
SW:SYG_HUMAN	R11	9244	3	2248.5	(+0.9)	3.839	0.460	1.000	4	R.L*GDAVEQGVINNTVL*GYFIGR.I
SW:SYG_HUMAN	R11	8800	2	1458.7	(+0.8)	3.590	0.445	0.999	4	R.TFFSFPVAVVAPFK.C
SW:SYG_HUMAN	R11	8810	2	1466.7	(+0.4)	3.462	0.513	0.995	4	R.TFFSFPVAVVAPFK#.C
SW:SYLM_HUMAN	R10	8863	2	1536.8	(+0.4)	3.093	0.506	1.000		K.FYVLSMFPYPSGK.L
SW:SYLM_HUMAN	R10	1882	2	1062.2	(+0.6)	2.763	0.344	0.978		R.LPSGQYLQR.E
SW:SYI_HUMAN	R14	6559	2	1412.6	(+0.7)	2.875	0.410	0.978	3	K.DFAAEVHPGDL*K#.N
SW:SYI_HUMAN	R14	8201	2	1127.3	(+0.7)	2.511	0.374	0.976	3	K.APWELLELR.V
SW:T150_HUMAN	R07	4919	3	2064.2	(+0.2)	4.466	0.485	0.997	3	K.ASESSK#PWPDATYGTGSASR.A
SW:T150_HUMAN	R07	4835	3	2064.2	(+0.5)	4.335	0.485	0.997	3	K.ASESSK#PWPDATYGTGSASR.A
SW:T150_HUMAN	R07	4839	3	2056.2	(+0.8)	4.167	0.442	0.997	3	K.ASESSK#PWPDATYGTGSASR.A
SW:T150_HUMAN	R07	5321	2	991.2	(+0.1)	2.502	0.126	0.608	5	K.SPL*QSVVVR.R
SW:T150_HUMAN	R07	6369	2	1231.4	(+0.3)	3.211	0.455	0.999	1	K.WEGL*VYAPPGK#.E
SW:T150_HUMAN	R08	5569	2	985.2	(+0.8)	2.283	0.229	0.860	5	K.SPLQSVVVR.R
SW:T172_HUMAN	R06	6872	2	1501.6	(-0.7)	3.462	0.421	0.986		R.IIEGLQDLDDVVR.A
SW:T172_HUMAN	R06	6866	2	1513.6	(-0.6)	2.896	0.303	0.942		R.IIEGL*QDL*DDVVR.A
SW:T172_HUMAN	R06	6230	2	1302.5	(+0.5)	3.217	0.399	0.990		K.LLTQEQWEVR.H
SW:T172_HUMAN	R06	6232	2	1314.5	(+0.7)	2.676	0.424	0.985		K.L*L*TQEQWEVR.H
SW:T172_HUMAN	R06	9240	3	2578.0	(+0.1)	4.356	0.414	0.987	2	K.SMLDIVEHDLLKPHLPSVTYLR.L
SW:T172_HUMAN	R20	6438	2	1170.4	(+0.9)	3.937	0.490	1.000		R.IAAGQAVEAIVK.N
SW:TBA1_HUMAN	R15	7841	2	1708.9	(+0.6)	3.880	0.453	1.000	5	R.AVFVDL*EPTVIDEVR.T
SW:TBA1_HUMAN	R15	5119	2	1024.2	(+0.1)	2.271	0.224	0.717	13	K.DVNAAIATIK#.T
SW:TBA1_HUMAN	R16	4870	2	1016.2	(+0.7)	3.035	0.327	0.979	13	K.DVNAAIATIK.T
SW:TBA1_HUMAN	R16	4874	2	1024.2	(-0.1)	2.603	0.165	0.714	13	K.DVNAAIATIK#.T
SW:TBA1_HUMAN	R20	5506	2	1024.2	(+0.3)	2.719	0.234	0.907	13	K.DVNAAIATIK#.T
SW:TBA1_HUMAN	R16	8448	2	2428.7	(+0.4)	3.636	0.464	1.000	16	R.FDGAL*NVDL*TEFQTNL*VPYPR.I
SW:TBA1_HUMAN	R16	8442	2	2410.7	(-1.0)	2.908	0.403	0.918	16	R.FDGALNVDLTEFQTNLVPYPR.I
SW:TBA1_HUMAN	R16	7398	2	1758.1	(-0.2)	2.933	0.466	0.982	15	R.IHFPLATYAPVISAER.A
SW:TBA1_HUMAN	R16	7390	2	1772.1	(-0.6)	2.925	0.417	0.967	15	R.IHFPL*ATYAPVISAER#.A
SW:TBA1_HUMAN	R16	9138	2	1488.8	(-0.1)	3.905	0.567	1.000	9	R.LISQIVSSITASLR.F
SW:TBA1_HUMAN	R16	9128	2	1500.8	(-0.1)	2.872	0.406	0.973	9	R.L*ISQIVSSITASLR.F
SW:TBA1_HUMAN	R19	9654	2	1488.8	(+0.6)	2.973	0.508	1.000	9	R.LISQIVSSITASLR.F
SW:TBA1_HUMAN	R16	5870	2	1731.9	(+0.5)	2.691	0.242	0.142	16	R.NL*DIERPTYTNL*NR.L
SW:TBA1_HUMAN	R16	7054	2	2017.1	(-0.5)	4.176	0.403	0.997	10	K.TIGGGDDSFNTFFSETGAGK#.H
SW:TBA1_HUMAN	R15	6633	2	1826.1	(-0.6)	3.095	0.433	0.981	19	K.VGINYPPTVPPGGDLAK.V
SW:TBA1_HUMAN	R16	6426	2	1840.1	(+1.0)	4.161	0.511	0.999	19	K.VGINYPPTVPPGGDL*AK#.V
SW:TBA1_HUMAN	R21	9154	2	1488.8	(+0.7)	3.456	0.502	0.976	9	R.LISQIVSSITASLR.F
SW:TBB1_HUMAN	R16	6990	2	1628.9	(+0.6)	4.160	0.457*	0.746	13	R.AIL*VDL*EPGTMDSVR.S
SW:TBB1_HUMAN	R16	6984	2	1616.9	(+0.4)	3.781	0.425	0.991	13	R.AILVDLEPGTMDSVR.S
SW:TBB1_HUMAN	R16	6508	2	1644.9	(-0.1)	2.788	0.317	0.932	13	R.AIL*VDL*EPGTM@DSVR.S
SW:TBB1_HUMAN	R16	7000	2	1616.9	(-0.8)	2.727	0.306	0.787	13	R.AILVDLEPGTMDSVR.S
SW:TBB1_HUMAN	R16	1650	2	1447.6	(+0.6)	3.514	0.260	0.966	16	K.EVDEQMLNVQNK.N
SW:TBB1_HUMAN	R16	1006	2	1477.6	(-0.1)	2.810	0.188	0.782	16	K.EVDEQM@L*NVQNK#.N
SW:TBB1_HUMAN	R16	5784	2	1131.3	(+0.0)	2.403	0.141	0.616	32	R.FPGQLNADLR.K
SW:TBB1_HUMAN	R16	7190	3	3116.3	(+0.4)	5.125	0.552*	0.255	4	K.FWEVISDEHGIDPTGTGHDSDL*QL*DR.I
SW:TBB1_HUMAN	R16	7188	3	3104.3	(+0.3)	4.669	0.502*	0.175	4	K.FWEVISDEHGIDPTGTGHDSDLQLDR.I
SW:TBB1_HUMAN	R15	8521	3	1972.2	(+0.9)	3.959	0.527	1.000	19	K.GHYTEGAEL*VDSVL*DVVR.K
SW:TBB1_HUMAN	R16	8368	2	1972.2	(-0.2)	4.072	0.445	1.000	19	K.GHYTEGAEL*VDSVL*DVVR.K
SW:TBB1_HUMAN	R16	8380	2	1960.2	(-0.9)	3.599	0.480	1.000	19	K.GHYTEGAELVDSVLDVVR.K
SW:TBB1_HUMAN	R16	6300	2	1328.6	(+0.4)	3.791	0.505	1.000	17	R.IMNTFSVVPSPK#.V
SW:TBB1_HUMAN	R16	5812	2	1344.6	(+0.6)	3.166	0.373	0.977	17	R.IM@NTFSVVPSPK#.V
SW:TBB1_HUMAN	R16	1502	2	1302.4	(+0.9)	2.436	0.415	0.974	4	R.ISVYYNEATGGK.Y
SW:TBB1_HUMAN	R16	1536	2	1310.4	(-0.6)	2.298	0.375	0.918	4	R.ISVYYNEATGGK#.Y

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:TBB1_HUMAN	R16	6828	2	1150.4	(+0.8)	2.531	0.451	0.986	31	K.L*AVNMVFPFR.L
SW:TBB1_HUMAN	R16	8082	2	1633.9	(+0.3)	3.702	0.444	1.000	20	R.L*HFFMPGFAPL*TSR.G
SW:TBB1_HUMAN	R16	7410	2	1649.9	(-0.5)	3.454	0.311	0.967	20	R.L*HFFM@PGFAPL*TSR.G
SW:TBB1_HUMAN	R16	8672	2	1871.2	(+0.7)	3.362	0.458	0.991	7	K.MAVTFIGNSTAIQELFK.R
SW:TBB1_HUMAN	R16	7376	2	1705.9	(+0.6)	3.390	0.476	1.000	26	K.NSSYFVEWIPNNVK#.T
SW:TBB1_HUMAN	R16	8136	3	2808.1	(+0.9)	5.153	0.594	1.000	13	R.SGPFQIFRPDNFVFGQSGAGNNWAK#.G
SW:TBB1_HUMAN	R26	5366	2	1302.4	(-0.1)	2.482	0.345	0.930	4	R.ISVYYNEATGGK.Y
SW:TBL2_HUMAN	R17	8416	2	1488.7	(+0.8)	3.171	0.473	1.000	3	R.AFIVWL*ANGDTL*R.V
SW:TBL2_HUMAN	R17	5406	2	1555.7	(-0.8)	2.977	0.156	0.482	2	R.L*QQQL*TQAQETL*K#.S
SW:TCOF_HUMAN	R05	1100	2	907.0	(+0.7)	2.463	0.398	0.964	3	R.GPASVPSVGK#.A
SW:TCOF_HUMAN	R05	1156	2	1028.2	(+0.5)	2.909	0.401	0.981	2	K.L*PEVQQATK#.A
SW:TCOF_HUMAN	R05	1270	2	877.1	(+0.9)	2.218	0.203	0.503	3	K.AGPVAVQVK#.A
SW:TCP4_HUMAN	R25	2574	2	1092.2	(+0.5)	2.736	0.212	0.884	2	R.DDNM@FQIGK#.M
SW:TCP4_HUMAN	R25	8078	2	1520.7	(+0.2)	3.123	0.198	0.849	2	K.GISL*NPEQWSQL*K#.E
SW:TCP4_HUMAN	R25	6480	2	1076.2	(+0.6)	2.667	0.347	0.968	2	R.DDNMFQIGK#.M
SW:TDBP_HUMAN	R17	8638	2	1342.6	(+0.6)	3.314	0.318	0.979	3	K.TSDLIVLGLPWK.T
SW:TDBP_HUMAN	R17	5290	2	1260.4	(-0.4)	2.488	0.234	0.776	2	K.GISVHISNAEPK#.H
SW:TEBP_HUMAN	R25	8990	2	1536.7	(+0.8)	4.338	0.457	1.000		K.LNWLSVDFNNWK.D
SW:TEBP_HUMAN	R25	2614	2	965.1	(+0.2)	2.436	0.314	0.934		K.DVNVNFEK.S
SW:TEM2_HUMAN	R25	5470	2	957.2	(+0.4)	2.860	0.404	0.985		K.ITLVSAAPGK.V
SW:TEM2_HUMAN	R25	7376	2	1310.5	(-0.1)	3.515	0.491	0.998		K.TLAFTSVDLTNK.A
SW:TEM2_HUMAN	R25	7366	2	1330.5	(-0.9)	2.566	0.267	0.654		K.TL*AFTSVDL*TNK#.A
SW:TEM2_HUMAN	R25	5448	2	971.2	(+0.5)	2.441	0.364	0.957		K.ITL*VSAAPGK#.V
SW:TERA_HUMAN	R10	9317	2	1463.8	(-0.3)	3.407	0.396	0.976	2	R.IVSQL*L*TL*MDGL*K#.Q
SW:TERA_HUMAN	R10	6289	2	962.2	(+0.5)	2.584	0.322	0.971	1	R.K#GDIFL*VR.G
SW:TERA_HUMAN	R10	5569	3	1660.9	(+0.7)	3.787	0.395	0.999	2	R.K#YEM@FAQTL*QQSR.G
SW:TERA_HUMAN	R10	1074	2	1088.2	(+0.1)	2.841	0.135	0.782	2	K.L*AGESESNL*R.K
SW:TERA_HUMAN	R10	1068	2	1076.2	(+0.1)	2.687	0.368	0.965	2	K.LAGESESNL.R.K
SW:TERA_HUMAN	R10	8511	3	2520.0	(+0.4)	3.896	0.446	0.990	2	K.NVFIIGATNRPDIIDPAILRPGR.L
SW:TERA_HUMAN	R10	6247	2	1330.5	(+0.5)	4.035	0.391	1.000	3	R.WALSQSNPSALR.E
SW:TERA_HUMAN	R10	6251	2	1342.5	(-0.0)	2.694	0.309	0.934	3	R.WAL*SQSNPSAL*R.E
SW:TERA_HUMAN	R10	7415	2	1080.2	(-0.8)	2.332	0.185	0.526		K.M@DEL*QL*FR.G
SW:TF1B_HUMAN	R10	6619	2	1200.4	(+0.4)	3.302	0.240	0.946	5	K.ADVQSIIGLQR.F
SW:TF1B_HUMAN	R10	7545	2	1521.6	(+0.3)	4.338	0.569	1.000	2	K.DHQYQFLEDAVR.N
SW:TF1B_HUMAN	R10	7543	2	1527.6	(-0.0)	3.421	0.443	0.831	2	K.DHQYQFL*EDAVR.N
SW:TF1B_HUMAN	R09	7600	2	1309.5	(+0.7)	3.481	0.362	0.989	2	K.FQWDLNAWTK.S
SW:TF1B_HUMAN	R09	6380	2	1218.5	(-0.1)	2.380	0.113	0.557	2	K.KLIYFQLHR.A
SW:TF1B_HUMAN	R09	7088	2	1685.9	(-0.5)	2.570	0.192	0.645	5	R.L*DL*DL*TADSQPPVFK#.V
SW:TF1B_HUMAN	R09	6402	2	1885.0	(-0.7)	2.820	0.479	0.982	5	K.L*SPPYSSPQEFAQDVGR.M
SW:TF1B_HUMAN	R09	6404	2	1879.0	(-0.7)	2.540	0.402	0.956	5	K.LSPPYSSPQEFAQDVGR.M
SW:TF1B_HUMAN	R09	6196	3	3567.7	(-0.2)	5.715	0.512	1.000	2	K.QGSGSSQPMEVQEGYGFSGDDPYSSAEPHVSGVK#.R
SW:TF1B_HUMAN	R09	6202	3	3559.7	(-0.5)	5.007	0.563	1.000	2	K.QGSGSSQPMEVQEGYGFSGDDPYSSAEPHVSGVK.R
SW:TF1B_HUMAN	R10	7535	3	3567.7	(-0.3)	6.147	0.478	1.000	2	K.QGSGSSQPMEVQEGYGFSGDDPYSSAEPHVSGVK#.R
SW:TF1B_HUMAN	R10	7519	3	3559.7	(-0.2)	4.985	0.568	1.000	2	K.QGSGSSQPMEVQEGYGFSGDDPYSSAEPHVSGVK.R
SW:TF1B_HUMAN	R09	2034	2	1122.2	(+0.1)	2.411	0.217	0.784	4	R.SGEGEVSGLMR.K
SW:TF1B_HUMAN	R10	2302	2	1122.2	(+0.0)	3.018	0.368	0.976	4	R.SGEGEVSGLMR.K
SW:TF1B_HUMAN	R10	2280	2	1128.2	(-0.4)	2.409	0.243	0.798	4	R.SGEGEVSGL*MR.K
SW:TF1B_HUMAN	R10	972	2	887.0	(+0.7)	2.262	0.287	0.930	2	R.VLVNDAQK.V
SW:TFR1_HUMAN	R10	7579	3	1993.2	(+0.4)	4.129	0.404	0.994	1	K.HPVTGQFL*YQDSNWASK#.V
SW:TFR1_HUMAN	R10	8675	3	2139.4	(+0.1)	3.793	0.457	0.999	1	R.HVFWGSGSHTL*PAL*L*ENL*K#.L
SW:TFR1_HUMAN	R10	8741	2	1031.3	(+0.5)	2.482	0.200	0.836	1	K.IL*NIFGVK#.G
SW:TFR1_HUMAN	R10	5845	2	1228.3	(+0.7)	2.937	0.455	0.990		K.LDSTDFTSTIK.L
SW:TFR1_HUMAN	R10	5847	2	1242.3	(+0.1)	2.470	0.439	0.965		K.L*DSTDFTSTIK#.L
SW:TFR1_HUMAN	R10	7083	2	1475.7	(-0.2)	3.060	0.406	0.974	1	R.SSGL*PNIPVQTISR.A
SW:TFR1_HUMAN	R10	7085	2	1469.7	(-0.1)	3.045	0.381	0.962	1	R.SSGLPNIPVQTISR.A
SW:TFR1_HUMAN	R10	6933	2	1469.7	(-0.2)	2.892	0.419	0.975	1	R.SSGLPNIPVQTISR.A
SW:TFR1_HUMAN	R10	7157	2	1475.7	(-0.9)	2.883	0.349	0.879	1	R.SSGL*PNIPVQTISR.A

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:TFR1_HUMAN	R10	6973	2	1475.7	(-0.2)	2.874	0.310	0.939	1	R.SSSL*PNIPVQTISR.A
SW:TFR1_HUMAN	R10	7233	2	1469.7	(-0.1)	2.809	0.393	0.968	1	R.SSGLPNIPVQTISR.A
SW:TFR1_HUMAN	R10	7159	2	1469.7	(-0.2)	2.741	0.460	0.979	1	R.SSGLPNIPVQTISR.A
SW:TFR1_HUMAN	R10	7333	2	1469.7	(+0.6)	2.600	0.348	0.956	1	R.SSGLPNIPVQTISR.A
SW:TFR1_HUMAN	R10	8577	2	1434.7	(+0.8)	4.126	0.564	1.000	1	K.VSASPLLYTLIEK.T
SW:TFR1_HUMAN	R10	8063	2	1227.4	(+0.8)	2.251	0.315	0.928	1	R.YNSQLLSFVR.D
SW:TFR1_HUMAN	R11	8236	3	2107.4	(+0.2)	3.917	0.397	0.997	1	R.HVFWGSGSHTLPALLENLK.L
SW:THIK_HUMAN	R17	8642	2	1595.9	(-0.1)	3.478	0.369	0.464		R.SKAEELGLPILGVL.R.S
SW:THIK_HUMAN	R17	9040	2	1404.7	(-0.3)	2.570	0.231	0.822		K.AEEL*GL*PIL*GVL*R.S
SW:THIL_HUMAN	R17	2072	2	1025.1	(+1.0)	2.991	0.356	0.984	2	K.DGLTDVYNK.I
SW:THIL_HUMAN	R17	1944	2	1025.1	(+0.2)	2.477	0.232	0.869	2	K.DGLTDVYNK.I
SW:THIL_HUMAN	R17	5984	2	1879.1	(-0.7)	3.252	0.440	0.984	3	K.EAYMGNVLQGGEGQAPTR.Q
SW:THIL_HUMAN	R17	5990	2	1885.1	(-0.8)	2.746	0.407	0.906	3	K.EAYMGNVL*QGEGQAPTR.Q
SW:THIL_HUMAN	R17	6944	2	1411.7	(-1.0)	2.411	0.301	0.655	2	K.FGNEVIPVTVTVK#.G
SW:THIL_HUMAN	R17	6912	2	1411.7	(+0.4)	2.354	0.290	0.870	2	K.FGNEVIPVTVTVK#.G
SW:THIL_HUMAN	R17	6224	2	1214.4	(+0.2)	3.460	0.440	0.851	3	K.L*GSIAIQGAIEK#.A
SW:THIO_HUMAN	R26	6672	2	1337.4	(-0.5)	3.711	0.248	0.959	5	K.TAFQEALDAAGDK.L
SW:THIO_HUMAN	R26	7540	2	1279.4	(-0.4)	2.223	0.320	0.135	3	K.EK#L*EATINEL*V.-
SW:THO1_HUMAN	R11	5938	3	1691.9	(+0.3)	4.112	0.352	0.982	1	R.DK#PVTGEQIEVFANK#.L
SW:THO1_HUMAN	R11	10354	3	3414.7	(+0.5)	4.260	0.422	0.994		R.EHMPTL*EEFFEEAIEQADPENMVENEYK#.A
SW:THO1_HUMAN	R11	9992	3	3430.7	(+0.1)	3.936	0.289	0.965		R.EHM@PTL*EEFFEEAIEQADPENMVENEYK#.A
SW:THO1_HUMAN	R11	8002	2	1456.7	(+0.6)	2.728	0.281	0.901		K.SL*PEYL*ENMVIK#.L
SW:THO1_HUMAN	R11	6856	2	1457.6	(+0.4)	2.333	0.241	0.842	1	K.L*MDL*QL*SDSNFR.R
SW:THO2_HUMAN	R06	5644	2	1277.3	(-0.4)	2.516	0.386	0.965	1	K.ADQL*DYENFR.H
SW:THO2_HUMAN	R06	5748	2	1794.9	(+0.6)	3.700	0.404	0.989		K.FYQEPNGETPSSL*YR.V
SW:THO2_HUMAN	R06	7900	2	1428.7	(+0.4)	3.822	0.518	1.000		R.LDPETLESGLIK.Q
SW:THO2_HUMAN	R06	6614	2	1131.3	(+0.4)	2.649	0.349	0.973	1	K.VL*NL*GQAL*ER.R
SW:THO2_HUMAN	R18	12015	3	2119.2	(+0.9)	4.033	0.327	0.973	1	R.ATGFDGGNKADQLDYENFR.H
SW:THO4_HUMAN	R20	7476	2	1195.4	(+0.3)	2.559	0.239	0.886		K.MDMSL*DDIHK#.L
SW:THO4_HUMAN	R20	6844	2	2036.2	(+0.7)	4.137	0.489	1.000	1	K.QQLSAEELDAQLDAYNAR.M
SW:THO4_HUMAN	R20	6840	3	2054.2	(+0.5)	3.850	0.459	0.999	1	K.QQL*SAEEL*DAQL*DAYNAR.M
SW:THO4_HUMAN	R20	6834	2	2054.2	(+0.9)	3.579	0.453	1.000	1	K.QQL*SAEEL*DAQL*DAYNAR.M
SW:THO4_HUMAN	R20	5566	2	1238.3	(+0.0)	3.762	0.475	1.000		R.SL*GTADVHFER.K
SW:THO4_HUMAN	R20	6536	2	1211.4	(+0.2)	2.239	0.269*	0.096		K.MDM@SL*DDIHK#.L
SW:THPA_HUMAN	R15	8643	2	2189.4	(-0.9)	3.096	0.350	0.897	7	K.DDLDVTELTNEDLLDQLVK.Y
SW:THPA_HUMAN	R11	8874	3	2320.6	(+0.9)	3.914	0.369	0.996	3	R.DSGSFVAFQNIPIGSELMSSFAK.T
SW:THPA_HUMAN	R11	8856	2	2334.6	(+0.5)	3.343	0.380	0.979	3	R.DSGSFVAFQNIPIGSEL*MSSFAK#.T
SW:THPA_HUMAN	R15	7735	2	1738.0	(-0.2)	2.350	0.226	0.724	7	K.DVYVQL*YL*QHL*TAR.N
SW:THPA_HUMAN	R16	1364	2	1360.5	(+0.5)	2.520	0.361	0.954	7	R.EPTPVL*GSGAAAAGR.S
SW:THPA_HUMAN	R14	6243	3	2571.7	(+0.3)	5.886	0.541	0.999	7	K.GPPDFSSDEEREPTVLGSGAAAAGR.S
SW:THPA_HUMAN	R14	6241	3	2577.7	(+0.6)	5.125	0.473	1.000	7	K.GPPDFSSDEEREPTVL*GSGAAAAGR.S
SW:THPA_HUMAN	R15	6101	3	2571.7	(+0.1)	6.166	0.615	1.000	7	K.GPPDFSSDEEREPTVLGSGAAAAGR.S
SW:THPA_HUMAN	R15	6099	3	2577.7	(+0.3)	5.626	0.517	0.998	7	K.GPPDFSSDEEREPTVL*GSGAAAAGR.S
SW:THPA_HUMAN	R15	6017	3	2571.7	(+0.3)	5.210	0.557	1.000	7	K.GPPDFSSDEEREPTVLGSGAAAAGR.S
SW:THPA_HUMAN	R16	5944	3	2571.7	(+0.6)	5.081	0.536	1.000	7	K.GPPDFSSDEEREPTVLGSGAAAAGR.S
SW:THPA_HUMAN	R17	6204	3	2571.7	(-0.2)	4.613	0.431	0.988	7	K.GPPDFSSDEEREPTVLGSGAAAAGR.S
SW:THPA_HUMAN	R15	7339	3	1874.2	(+0.4)	3.727	0.318	0.995	7	R.K#DVYVQL*YL*QHL*TAR.N
SW:THPA_HUMAN	R15	1058	2	1266.4	(-0.4)	2.275	0.257	0.056	7	R.NRPPL*PAGTNSK#.G
SW:THPA_HUMAN	R08	7051	2	1395.6	(-0.8)	3.281	0.370	0.922	1	-.PEFL*EDPSVL*TK#.D
SW:THPA_HUMAN	R11	6696	2	1375.6	(-0.1)	3.942	0.402	1.000	1	-.PEFLEDPSVLTK.D
SW:THPA_HUMAN	R11	6690	2	1395.6	(-0.7)	3.047	0.271	0.924	1	-.PEFL*EDPSVL*TK#.D
SW:THPA_HUMAN	R14	6959	2	1375.6	(+0.7)	4.844	0.411	1.000	1	-.PEFLEDPSVLTK.D
SW:THPA_HUMAN	R14	6953	2	1395.6	(+0.4)	3.132	0.388	0.981	1	-.PEFL*EDPSVL*TK#.D
SW:THPA_HUMAN	R14	6975	2	1375.6	(-0.9)	2.369	0.375	0.831	1	-.PEFLEDPSVLTK.D
SW:THPA_HUMAN	R15	6729	2	1375.6	(+0.6)	3.404	0.365	0.987	1	-.PEFLEDPSVLTK.D
SW:THPA_HUMAN	R16	6546	2	1375.6	(+0.9)	4.807	0.395	0.990	1	-.PEFLEDPSVLTK.D
SW:THPA_HUMAN	R16	6544	2	1395.6	(+0.2)	3.845	0.500	1.000	1	-.PEFL*EDPSVL*TK#.D
SW:THPA_HUMAN	R17	6956	2	1395.6	(-0.2)	3.405	0.283	0.953	1	-.PEFL*EDPSVL*TK#.D
SW:THPA_HUMAN	R19	7104	2	1375.6	(+0.4)	3.698	0.412	1.000	1	-.PEFLEDPSVLTK.D

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:THPA_HUMAN	R19	7106	2	1395.6	(+0.8)	2.573	0.407	0.970	1	-.PEFL*EDPSVL*TK#.D
SW:THPA_HUMAN	R20	6920	2	1375.6	(+0.7)	4.048	0.416	1.000	1	-.PEFLEDPSVLTK.D
SW:THPA_HUMAN	R15	8293	2	2689.9	(+0.1)	2.760	0.331	0.229	7	R.QEDKDDLDVTELTNEDLLDQLVK.Y
SW:THPA_HUMAN	R18	8647	2	2689.9	(-0.4)	2.382	0.174	0.025	7	R.QEDKDDLDVTELTNEDLLDQLVK.Y
SW:THPA_HUMAN	R11	5728	2	1698.9	(+0.2)	4.525	0.512	1.000	7	K.SELVANNVTLPAGEQR.K
SW:THPA_HUMAN	R11	5704	2	1710.9	(-0.4)	2.840	0.398	0.968	7	K.SEL*VANNVTL*PAGEQR.K
SW:THPA_HUMAN	R14	5803	2	1698.9	(+0.9)	4.204	0.496	1.000	7	K.SELVANNVTLPAGEQR.K
SW:THPA_HUMAN	R15	5729	2	1698.9	(+0.6)	4.325	0.598	1.000	7	K.SELVANNVTLPAGEQR.K
SW:THPA_HUMAN	R15	5647	2	1698.9	(+0.8)	4.083	0.546	1.000	7	K.SELVANNVTLPAGEQR.K
SW:THPA_HUMAN	R15	5741	2	1710.9	(-0.9)	3.546	0.475	1.000	7	K.SEL*VANNVTL*PAGEQR.K
SW:THPA_HUMAN	R15	5645	2	1710.9	(-0.4)	3.342	0.463	0.987	7	K.SEL*VANNVTL*PAGEQR.K
SW:THPA_HUMAN	R16	5522	2	1710.9	(-0.4)	4.361	0.523	1.000	7	K.SEL*VANNVTL*PAGEQR.K
SW:THPA_HUMAN	R18	5719	2	1698.9	(+0.9)	4.012	0.483	1.000	7	K.SELVANNVTLPAGEQR.K
SW:THPA_HUMAN	R11	5020	2	1648.8	(-0.6)	2.999	0.446	0.981	7	R.SSTPLPTISSSAENTR.Q
SW:THPA_HUMAN	R11	4996	2	1654.8	(-0.8)	2.800	0.235	0.657	7	R.SSTPL*PTISSSAENTR.Q
SW:THPA_HUMAN	R11	4932	2	1648.8	(-0.5)	2.701	0.261	0.870	7	R.SSTPLPTISSSAENTR.Q
SW:THPA_HUMAN	R11	4910	2	1654.8	(+0.1)	2.646	0.239	0.828	7	R.SSTPL*PTISSSAENTR.Q
SW:THPA_HUMAN	R14	5287	2	1654.8	(-0.5)	2.622	0.254	0.844	7	R.SSTPL*PTISSSAENTR.Q
SW:THPA_HUMAN	R14	5367	2	1654.8	(-0.7)	2.349	0.172	0.546	7	R.SSTPL*PTISSSAENTR.Q
SW:THPA_HUMAN	R15	4819	2	1648.8	(-0.1)	3.257	0.434	0.983	7	R.SSTPLPTISSSAENTR.Q
SW:THPA_HUMAN	R15	5083	2	1654.8	(+0.1)	3.249	0.395	0.978	7	R.SSTPL*PTISSSAENTR.Q
SW:THPA_HUMAN	R15	5089	2	1648.8	(+0.3)	3.164	0.449	0.987	7	R.SSTPLPTISSSAENTR.Q
SW:THPA_HUMAN	R15	4807	2	1654.8	(-0.1)	3.100	0.387	0.973	7	R.SSTPL*PTISSSAENTR.Q
SW:THPA_HUMAN	R15	4729	2	1654.8	(+0.6)	2.962	0.353	0.972	7	R.SSTPL*PTISSSAENTR.Q
SW:THPA_HUMAN	R15	4727	2	1648.8	(+0.4)	2.893	0.306	0.953	7	R.SSTPLPTISSSAENTR.Q
SW:THPA_HUMAN	R15	5005	2	1654.8	(-0.5)	2.885	0.356	0.957	7	R.SSTPL*PTISSSAENTR.Q
SW:THPA_HUMAN	R15	5009	2	1648.8	(-0.5)	2.883	0.366	0.960	7	R.SSTPLPTISSSAENTR.Q
SW:THPA_HUMAN	R15	5173	2	1648.8	(-0.7)	2.787	0.339	0.944	7	R.SSTPLPTISSSAENTR.Q
SW:THPA_HUMAN	R16	4600	2	1648.8	(-0.5)	2.595	0.462	0.975	7	R.SSTPLPTISSSAENTR.Q
SW:THPA_HUMAN	R16	4680	2	1648.8	(-0.5)	2.555	0.318	0.908	7	R.SSTPLPTISSSAENTR.Q
SW:THPA_HUMAN	R17	5540	2	1654.8	(-0.4)	2.665	0.259	0.862	7	R.SSTPL*PTISSSAENTR.Q
SW:THPA_HUMAN	R17	5550	2	1648.8	(+0.7)	2.583	0.313	0.934	7	R.SSTPLPTISSSAENTR.Q
SW:THPA_HUMAN	R18	5281	2	1648.8	(+0.8)	3.185	0.361	0.979	7	R.SSTPLPTISSSAENTR.Q
SW:THPA_HUMAN	R18	5201	2	1648.8	(-0.3)	2.802	0.419	0.971	7	R.SSTPLPTISSSAENTR.Q
SW:THPA_HUMAN	R18	5209	2	1654.8	(-0.7)	2.648	0.302	0.905	7	R.SSTPL*PTISSSAENTR.Q
SW:THPA_HUMAN	R20	5484	2	1654.8	(-0.4)	2.670	0.298	0.905	7	R.SSTPL*PTISSSAENTR.Q
SW:THPA_HUMAN	R20	5482	2	1648.8	(-0.4)	2.440	0.297	0.868	7	R.SSTPLPTISSSAENTR.Q
SW:THPA_HUMAN	R11	5134	2	1068.3	(+0.2)	2.480	0.394	0.966	2	R.THQALGILSK.T
SW:THPB_HUMAN	R14	7975	2	1800.1	(-0.4)	2.237	0.339	0.880	1	K.HASPIL*PITEFSDIPR.R
SW:THPB_HUMAN	R15	7697	2	1794.1	(-0.3)	3.081	0.428	0.980	1	K.HASPILPITEFSDIPR.R
SW:THPB_HUMAN	R15	7695	2	1800.1	(-0.3)	2.865	0.456	0.980	1	K.HASPIL*PITEFSDIPR.R
SW:THPB_HUMAN	R15	7763	3	2953.3	(+0.2)	4.091	0.513	0.999	1	R.IDGPVISESTPIAETIM@ASSNESL*VVNR.V
SW:THPB_HUMAN	R15	8385	3	2937.3	(+0.6)	3.736	0.342	0.994	1	R.IDGPVISESTPIAETIMASSNESL*VVNR.V
SW:THPB_HUMAN	R14	5721	3	2691.8	(+0.4)	5.217	0.564	0.989	1	R.RVEHNQSYSQAGITETEWTSGSSK#.G
SW:THPB_HUMAN	R14	5719	3	2683.8	(+0.3)	4.777	0.573	0.999	1	R.RVEHNQSYSQAGITETEWTSGSSK#.G
SW:THPB_HUMAN	R15	5625	3	2691.8	(+0.3)	6.860	0.667	1.000	1	R.RVEHNQSYSQAGITETEWTSGSSK#.G
SW:THPB_HUMAN	R15	5627	3	2683.8	(+0.2)	6.739	0.589	0.991	1	R.RVEHNQSYSQAGITETEWTSGSSK#.G
SW:THPB_HUMAN	R15	5707	3	2691.8	(+0.7)	6.178	0.673	0.992	1	R.RVEHNQSYSQAGITETEWTSGSSK#.G
SW:THPB_HUMAN	R15	5787	3	2691.8	(+0.3)	6.032	0.632	1.000	1	R.RVEHNQSYSQAGITETEWTSGSSK#.G
SW:THPB_HUMAN	R15	5543	3	2691.8	(+0.9)	4.975	0.554	1.000	1	R.RVEHNQSYSQAGITETEWTSGSSK#.G
SW:THPB_HUMAN	R15	5709	3	2683.8	(+0.1)	4.862	0.601	1.000	1	R.RVEHNQSYSQAGITETEWTSGSSK#.G
SW:THPB_HUMAN	R15	5585	2	2683.8	(-0.4)	4.758	0.505	1.000	1	R.RVEHNQSYSQAGITETEWTSGSSK#.G
SW:THPB_HUMAN	R15	5579	2	2691.8	(-0.4)	4.470	0.496	1.000	1	R.RVEHNQSYSQAGITETEWTSGSSK#.G
SW:THPB_HUMAN	R16	5400	3	2683.8	(+0.4)	5.780	0.543	1.000	1	R.RVEHNQSYSQAGITETEWTSGSSK#.G
SW:THPB_HUMAN	R16	5384	3	2691.8	(+0.9)	5.071	0.631	0.995	1	R.RVEHNQSYSQAGITETEWTSGSSK#.G
SW:THPB_HUMAN	R18	5619	3	2683.8	(+0.4)	6.068	0.607	1.000	1	R.RVEHNQSYSQAGITETEWTSGSSK#.G
SW:THPB_HUMAN	R18	5617	3	2691.8	(+0.1)	5.248	0.483	1.000	1	R.RVEHNQSYSQAGITETEWTSGSSK#.G
SW:THPB_HUMAN	R14	5701	3	2535.6	(+0.7)	4.326	0.373	0.773	1	R.VEHNQSYSQAGITETEWTSGSSK#.G
SW:THPB_HUMAN	R15	5567	2	2527.6	(-0.3)	5.904	0.666	1.000	1	R.VEHNQSYSQAGITETEWTSGSSK#.G
SW:THPB_HUMAN	R15	5553	3	2527.6	(+0.3)	5.688	0.574	1.000	1	R.VEHNQSYSQAGITETEWTSGSSK#.G
SW:THPB_HUMAN	R15	5551	3	2535.6	(+0.7)	5.670	0.479	0.999	1	R.VEHNQSYSQAGITETEWTSGSSK#.G
SW:THPB_HUMAN	R15	5753	3	2527.6	(+0.4)	4.210	0.417	0.999	1	R.VEHNQSYSQAGITETEWTSGSSK#.G
SW:THPB_HUMAN	R15	5631	3	2535.6	(+0.6)	4.108	0.421	0.999	1	R.VEHNQSYSQAGITETEWTSGSSK#.G
SW:THPB_HUMAN	R15	1632	2	1592.7	(-0.1)	2.816	0.234	0.096	3	R.YSDNEEDSK#IEL*K#.L
SW:THPB_HUMAN	R23	8160	2	1794.1	(-0.4)	2.696	0.422	0.969	1	K.HASPILPITEFSDIPR.R

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:TIAR_HUMAN	R17	7796	3	2602.8	(+0.8)	5.118	0.450	1.000	1	K.DTSNHFHVFVGDLSPEITTEDIK.S
SW:TIAR_HUMAN	R17	1826	2	1258.4	(+0.6)	2.539	0.305	0.929	1	R.FEDVVNQSSPK#.N
SW:TIAR_HUMAN	R17	6610	3	2600.9	(+0.1)	5.664	0.547	1.000	1	R.FSTHESAAHAIVSVNGTTIEGHVVK#.C
SW:TIAR_HUMAN	R17	7628	3	2731.0	(+1.0)	5.569	0.538	0.988	1	K.KDTSNHFHVFVGDLSPEITTEDIK.S
SW:TIAR_HUMAN	R17	1844	2	1250.4	(+0.9)	2.487	0.448	0.983	1	R.FEDVVNQSSPK.N
SW:TM21_HUMAN	R01	7611	2	1285.6	(+0.9)	3.245	0.482	1.000	2	R.IPDQLVILDMK.H
SW:TM21_HUMAN	R23	7100	2	1321.6	(-0.1)	2.402	0.241	0.782	2	R.IPDQL*VIL*DM@K#.H
SW:TM21_HUMAN	R23	7896	2	1305.6	(+0.1)	2.390	0.336	0.907	2	R.IPDQL*VIL*DMK#.H
SW:TM21_HUMAN	R24	7930	2	1305.6	(+0.4)	2.713	0.246	0.828	2	R.IPDQL*VIL*DMK#.H
SW:TM21_HUMAN	R23	5494	2	1305.5	(-0.6)	2.978	0.467	0.986	3	K.ITDSAGHILYSK.E
SW:TM21_HUMAN	R23	5496	2	1319.5	(-0.8)	2.401	0.225	0.337	3	K.ITDSAGHIL*YSK#.E
SW:TM21_HUMAN	R24	5534	2	1305.5	(-0.1)	3.569	0.519	0.998	3	K.ITDSAGHILYSK.E
SW:TM21_HUMAN	R24	5526	2	1319.5	(+0.4)	3.383	0.444	0.999	3	K.ITDSAGHIL*YSK#.E
SW:TM21_HUMAN	R23	8052	3	1911.1	(+0.9)	5.282	0.467	0.989	2	R.L*EDL*SESIVNDFAYM@K#.K
SW:TM21_HUMAN	R23	8154	3	2067.3	(+0.9)	3.955	0.327	0.997	2	R.RL*EDL*SESIVNDFAYM@K#.K
SW:TM21_HUMAN	R24	5550	2	1319.5	(-0.9)	2.450	0.216	0.331	3	K.ITDSAGHIL*YSK#.E
SW:TO1A_HUMAN	R19	10082	3	2973.4	(+0.6)	4.418	0.505	1.000	2	K.MHAGLIDAIKPFDDYDLVDGVSYQK.A
SW:TO1A_HUMAN	R19	10662	2	1898.2	(+0.8)	3.255	0.436	0.985	2	R.NL*IDYFVPFL*PL*EYK#.H
SW:TOP1_HUMAN	R10	6647	2	1121.3	(+0.3)	2.548	0.390	0.971	4	K.AEEVATFFAK#.M
SW:TOP1_HUMAN	R10	6669	2	1113.3	(-0.2)	2.502	0.412	0.971	4	K.AEEVATFFAK.M
SW:TOP1_HUMAN	R10	1042	2	938.0	(+0.6)	2.585	0.163	0.822	7	K.L*EVQATDR.E
SW:TOP1_HUMAN	R10	8771	3	2855.1	(-0.2)	5.183	0.552	1.000	4	R.VEHINL*HPEL*DGQEYVVEFDL*GK#.D
SW:TOP1_HUMAN	R10	7597	2	1157.3	(+0.5)	2.462	0.270*	0.258	8	K.NL*QL*FMENK#.Q
SW:TP2A_HUMAN	R06	6804	2	1449.5	(-0.0)	2.752	0.215	0.849	7	K.EL*IL*FSNSDNER.S
SW:TP2A_HUMAN	R06	8140	2	1350.6	(+0.1)	2.691	0.329	0.933	3	R.FL*EEFITPIVK#.V
SW:TP2A_HUMAN	R11	8016	2	1350.6	(+0.4)	2.536	0.262	0.868	3	R.FL*EEFITPIVK#.V
SW:TPR_HUMAN	R04	6030	2	1530.7	(+0.1)	3.628	0.333	0.971	2	K.AIQDHL*L*EVEQSK#.D
SW:TPR_HUMAN	R04	6900	2	1301.4	(+0.6)	2.419	0.348	0.956	2	K.EDVDDL*VSQL*R.Q
SW:TPR_HUMAN	R06	6238	2	1643.8	(+0.7)	2.646	0.533	0.990	2	K.EGVQGPLNVSLSEEGK.S
SW:TPR_HUMAN	R04	5972	2	1546.6	(+0.1)	2.351	0.318	0.890	1	R.ELQELEDLSNAER.E
SW:TPR_HUMAN	R04	2020	2	1310.4	(+0.4)	2.450	0.185	0.795	2	K.ESAETFQTLQEK.K
SW:TPR_HUMAN	R05	1942	2	1310.4	(+0.5)	2.405	0.282	0.916	2	K.ESAETFQTLQEK.K
SW:TPR_HUMAN	R04	6296	2	1178.3	(+0.9)	2.226	0.189	0.739	3	R.FEVAQVESL.R.Y
SW:TPR_HUMAN	R05	6364	2	1178.3	(+0.6)	3.102	0.304	0.977	3	R.FEVAQVESL.R.Y
SW:TPR_HUMAN	R06	6358	2	1184.3	(+0.6)	3.412	0.364	0.989	3	R.FEVAQVESL*R.Y
SW:TPR_HUMAN	R05	6632	3	1821.0	(+0.6)	3.964	0.306	0.976	5	K.FK#VESEQQYFEIEK#.R
SW:TPR_HUMAN	R06	6630	3	1821.0	(+0.7)	4.996	0.367	0.997	5	K.FK#VESEQQYFEIEK#.R
SW:TPR_HUMAN	R04	6066	2	1484.6	(-0.7)	3.117	0.162	0.790	3	K.FL*ADQQSEIDGL*K#.G
SW:TPR_HUMAN	R05	6118	2	1464.6	(-0.0)	3.516	0.444	0.993	3	K.FLADQQSEIDGLK.G
SW:TPR_HUMAN	R06	6106	2	1484.6	(-0.7)	3.918	0.406	1.000	3	K.FL*ADQQSEIDGL*K#.G
SW:TPR_HUMAN	R06	6112	2	1464.6	(+0.3)	3.807	0.372	0.988	3	K.FLADQQSEIDGLK.G
SW:TPR_HUMAN	R06	7474	3	2051.3	(+0.4)	4.952	0.499	0.997	2	K.GAIL*SEEL*AAMSPTAAAVAK#.I
SW:TPR_HUMAN	R05	9582	2	2025.4	(+1.0)	5.026	0.575	1.000	2	R.GQNLLLTNLQTIQGILER.S
SW:TPR_HUMAN	R06	9902	2	2025.4	(+1.0)	5.353	0.637	1.000	2	R.GQNLLLTNLQTIQGILER.S
SW:TPR_HUMAN	R06	6742	2	1901.0	(+0.8)	3.591	0.476	1.000	2	K.GQPSNKEDVDDLVSQLR.Q
SW:TPR_HUMAN	R05	2242	2	955.1	(+0.4)	2.205	0.293	0.905	2	K.HVEDLLTK.L
SW:TPR_HUMAN	R05	7774	3	2836.3	(+0.7)	5.003	0.587	0.997	2	R.ILLSQTGVAIPLHASSLDDVSLASTPK.R
SW:TPR_HUMAN	R03	4699	2	1193.3	(+0.3)	2.315	0.241	0.867	2	R.IQQL*TEEIGR.L
SW:TPR_HUMAN	R05	5074	2	1187.3	(+0.6)	3.317	0.361	0.988	2	R.IQQLTEEIGR.L
SW:TPR_HUMAN	R05	5108	2	1193.3	(+0.7)	2.407	0.283	0.926	2	R.IQQL*TEEIGR.L
SW:TPR_HUMAN	R06	5094	2	1187.3	(+0.2)	2.631	0.364	0.965	2	R.IQQLTEEIGR.L
SW:TPR_HUMAN	R06	5084	2	1193.3	(+0.5)	2.552	0.287	0.944	2	R.IQQL*TEEIGR.L
SW:TPR_HUMAN	R04	5492	2	1110.3	(-0.2)	2.497	0.306	0.928	2	K.ISTQLDFASK.R
SW:TPR_HUMAN	R05	5634	2	1110.3	(+0.9)	2.623	0.240	0.921	2	K.ISTQLDFASK.R
SW:TPR_HUMAN	R04	4940	2	1324.4	(-0.4)	3.687	0.322	0.972	3	K.L*DEL*QASDVSVK#.Y
SW:TPR_HUMAN	R04	4954	2	1304.4	(-0.6)	3.269	0.208	0.919	3	K.LDELQASDVSVK.Y
SW:TPR_HUMAN	R05	5124	2	1324.4	(+0.1)	3.857	0.397	1.000	3	K.L*DEL*QASDVSVK#.Y
SW:TPR_HUMAN	R05	5122	2	1304.4	(+0.0)	3.616	0.441	1.000	3	K.LDELQASDVSVK.Y
SW:TPR_HUMAN	R06	5152	2	1324.4	(-0.6)	2.436	0.169	0.587	3	K.L*DEL*QASDVSVK#.Y
SW:TPR_HUMAN	R05	7646	2	1426.6	(-0.6)	2.687	0.133	0.661	2	K.L*ESAL*TEL*EQL*R.K

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:TPR_HUMAN	R04	1804	2	1114.2	(+0.6)	2.242	0.186	0.723	2	K.L*QEQTDL*R.S
SW:TPR_HUMAN	R06	1736	2	1102.2	(-0.1)	2.853	0.248	0.937	2	K.LQEQTDLR.S
SW:TPR_HUMAN	R06	1726	2	1114.2	(-0.2)	2.495	0.328	0.947	2	K.L*QEQTDL*R.S
SW:TPR_HUMAN	R06	6576	2	1185.3	(-0.1)	2.750	0.312	0.939	2	R.NL*DVQL*L*DTK#.R
SW:TPR_HUMAN	R06	6574	2	1159.3	(+0.6)	2.656	0.419	0.984	2	R.NLDVQLLDTK.R
SW:TPR_HUMAN	R05	6670	2	1773.9	(+0.3)	2.948	0.219	0.897	2	R.NLQEQTQVLQSELSR.L
SW:TPR_HUMAN	R05	6918	3	2705.0	(+0.3)	5.344	0.516	1.000	2	K.RPSTSQTVSTPAPVPVIESTEAEIAK#.A
SW:TPR_HUMAN	R05	6916	3	2697.0	(+0.2)	5.077	0.526	0.997	2	K.RPSTSQTVSTPAPVPVIESTEAEIAK#.A
SW:TPR_HUMAN	R06	6914	3	2705.0	(+0.2)	5.252	0.489	1.000	2	K.RPSTSQTVSTPAPVPVIESTEAEIAK#.A
SW:TPR_HUMAN	R06	6910	3	2697.0	(+0.2)	3.930	0.418	0.997	2	K.RPSTSQTVSTPAPVPVIESTEAEIAK#.A
SW:TPR_HUMAN	R05	5942	2	1275.4	(-0.6)	2.561	0.146	0.673	2	K.SLESQVENLQK.T
SW:TPR_HUMAN	R04	6416	2	1771.9	(-0.9)	3.187	0.292	0.812	2	R.SNASL*TNNQNL*IQSL*K#.E
SW:TPR_HUMAN	R05	6506	2	1771.9	(-0.4)	2.730	0.345	0.927	2	R.SNASL*TNNQNL*IQSL*K#.E
SW:TPR_HUMAN	R04	7206	2	1241.4	(+0.3)	2.891	0.497	1.000	3	K.SQEQL*EIL*R.F
SW:TPR_HUMAN	R05	7352	2	1229.4	(+0.9)	3.788	0.199	0.973	3	K.SQEQL*EIL.R.F
SW:TPR_HUMAN	R05	7342	2	1241.4	(+0.3)	2.837	0.455	0.990	3	K.SQEQL*EIL*R.F
SW:TPR_HUMAN	R04	6186	2	1006.1	(+0.6)	2.524	0.256	0.931	2	K.TDEL*L*AL*GR.E
SW:TPR_HUMAN	R05	6258	2	988.1	(+0.8)	2.857	0.230	0.948	2	K.TDELLALGR.E
SW:TPR_HUMAN	R05	6264	2	1006.1	(-0.2)	2.406	0.307	0.927	2	K.TDEL*L*AL*GR.E
SW:TPR_HUMAN	R06	6256	2	1006.1	(+0.4)	2.385	0.348	0.963	2	K.TDEL*L*AL*GR.E
SW:TPR_HUMAN	R04	5854	3	3082.2	(-0.3)	4.799	0.408	0.990	2	R.TREEEDSTIEASDQVSDDTVEM@PL*PK#.K
SW:TPR_HUMAN	R05	5918	3	3082.2	(-0.5)	3.866	0.361	0.929	2	R.TREEEDSTIEASDQVSDDTVEM@PL*PK#.K
SW:TPR_HUMAN	R05	8174	3	2480.7	(+0.1)	3.744	0.333	0.988	2	K.TSTSNVEQYQAMVTSL*EESL*NK#.E
SW:TPR_HUMAN	R06	8454	3	2480.7	(+0.1)	5.327	0.482	1.000	2	K.TSTSNVEQYQAMVTSL*EESL*NK#.E
SW:TPR_HUMAN	R04	900	2	942.1	(-0.6)	3.100	0.474	1.000	3	K.VTAAAMAGNK#.S
SW:TPR_HUMAN	R05	888	2	942.1	(+0.0)	2.388	0.408	0.955	3	K.VTAAAMAGNK#.S
SW:TPR_HUMAN	R04	4922	2	1539.7	(-0.4)	2.854	0.107	0.656	2	R.YEM@L*QDNVEGYR.R
SW:TPR_HUMAN	R08	5279	2	1324.4	(+0.6)	2.202	0.141	0.452	3	K.L*DEL*QASDVSVK#.Y
SW:TRAL_HUMAN	R12	6612	2	1511.7	(-0.2)	2.453	0.274	0.715	5	R.AQL*L*QPTL*EINPR.H
SW:TRAL_HUMAN	R12	11966	3	3111.5	(-0.1)	4.147	0.509	1.000	2	R.ASEPGL*AQL*L*VDQIENAM@IAAGL*VDDPR.A
SW:TRAL_HUMAN	R12	7434	2	1347.5	(+0.1)	2.228	0.309	0.890	7	K.FFEDYGL*FM@R.E
SW:TRAL_HUMAN	R11	6600	2	1514.7	(+0.7)	3.210	0.467*	0.480	8	R.GVVDESDIPLNLSR.E
SW:TRAL_HUMAN	R12	6536	2	1526.7	(+0.1)	2.566	0.292	0.871	8	R.GVVDESDIPL*NL*SR.E
SW:TRAL_HUMAN	R12	822	2	998.1	(+0.5)	2.526	0.207	0.879	9	K.HEFQAETK#.K
SW:TRAL_HUMAN	R12	8346	2	1579.9	(+0.2)	3.616	0.401	0.838	9	R.MNTLQAIWMMDPK.D
SW:TRAL_HUMAN	R12	6844	2	2147.3	(-0.9)	4.077	0.558	1.000	6	R.YESSALPSGQLTSLSEYASR.M
SW:TRAL_HUMAN	R13	5383	2	1304.4	(+0.5)	2.579	0.417	0.979	7	R.EGIVTATEQEVK.E
SW:TRIB_HUMAN	R05	7402	3	2139.3	(-0.4)	3.765	0.262	0.963		R.L*VDNFQHEENL*L*QQVASK#.D
SW:TRIB_HUMAN	R09	8722	2	1338.6	(+0.8)	2.229	0.334	0.925		K.IDPLALVQAIER.Y
SW:TXTP_HUMAN	R20	7724	2	1261.5	(-0.2)	2.957	0.403	0.971	1	R.GL*SSL*L*YGSIPK#.A
SW:TXTP_HUMAN	R20	6368	2	1252.5	(+0.3)	2.732	0.370	0.960	1	K.GTYQGLTATVLK.Q
SW:TXTP_HUMAN	R20	1870	2	1015.1	(+0.4)	2.359	0.178	0.827	1	K.TQL*QL*DER.S
SW:TXTP_HUMAN	R20	6370	2	1272.5	(-0.1)	2.203	0.254	0.712	1	K.GTYQGL*TATVL*K#.Q
SW:U2AF_HUMAN	R14	7117	3	2160.4	(+0.0)	4.632	0.389	0.995	1	R.L*GGL*QAPGNPVL*AVQINQDK#.N
SW:U2AF_HUMAN	R14	8061	2	1807.1	(-0.3)	2.460	0.131	0.466	1	K.LFIGGLPNYLNDQVK.E
SW:U520_HUMAN	R01	7389	2	1769.0	(+0.2)	2.697	0.409	0.956	7	R.EEEVTGPVIAPL*FPQK#.R
SW:U520_HUMAN	R03	7041	2	1755.0	(+0.6)	3.087	0.471	0.738	7	R.EEEVTGPVIAPLFPQK.R
SW:U520_HUMAN	R01	7121	2	1422.7	(+1.0)	2.615	0.323	0.946	3	R.FQIMNEIVYEK#.I
SW:U520_HUMAN	R02	8064	3	2842.2	(-0.4)	4.062	0.347	0.951	2	K.GL*FYFDNSFRPVPL*EQTYVGITEK#.K
SW:U520_HUMAN	R02	8068	3	2822.2	(+0.5)	4.041	0.462	0.997	2	K.GLFYFDNSFRPVPLEQTYVGITEK.K
SW:U520_HUMAN	R03	8379	3	2822.2	(+0.2)	4.879	0.466	1.000	2	K.GLFYFDNSFRPVPLEQTYVGITEK.K
SW:U520_HUMAN	R03	8375	3	2842.2	(+0.7)	4.339	0.430	0.996	2	K.GL*FYFDNSFRPVPL*EQTYVGITEK#.K
SW:U520_HUMAN	R04	8640	3	2822.2	(+0.7)	4.144	0.471	0.997	2	K.GLFYFDNSFRPVPLEQTYVGITEK.K
SW:U520_HUMAN	R04	8638	3	2842.2	(-0.2)	3.976	0.375	0.968	2	K.GL*FYFDNSFRPVPL*EQTYVGITEK#.K
SW:U520_HUMAN	R02	8274	3	2022.3	(+0.7)	4.218	0.574	0.998	7	R.GL*IEIISNAEYENIPIR.H
SW:U520_HUMAN	R01	9329	3	3573.0	(-0.4)	6.038	1.000*	0.032	3	R.IASHYYITNDTVQTYNQLLKPTLSEIELFR.V
SW:U520_HUMAN	R01	4305	2	1210.4	(+0.1)	2.815	0.467	0.979	3	R.IVAL*SSSL*SNAK#.D
SW:U520_HUMAN	R01	4225	2	1210.4	(+0.2)	2.703	0.390	0.958	3	R.IVAL*SSSL*SNAK#.D
SW:U520_HUMAN	R01	4383	2	1210.4	(+0.1)	2.481	0.367	0.933	3	R.IVAL*SSSL*SNAK#.D
SW:U520_HUMAN	R01	4333	2	1190.4	(-0.0)	2.436	0.314	0.910	3	R.IVALSSSLSNAK.D
SW:U520_HUMAN	R03	5113	2	1210.4	(-0.1)	2.463	0.194	0.672	3	R.IVAL*SSSL*SNAK#.D

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:U520_HUMAN	R02	6118	2	1142.4	(+0.6)	2.585	0.466	0.988	4	K.KPVIVFVPSR.K
SW:U520_HUMAN	R01	9341	2	2094.4	(+0.4)	2.302	0.299	0.884	3	R.LIGLSATLPNYEDVATFLR.V
SW:U520_HUMAN	R03	8803	2	2118.4	(-0.3)	2.314	0.162	0.430	3	R.L*IGL*SATL*PNYEDVATFL*R.V
SW:U520_HUMAN	R01	5681	2	1302.4	(+0.2)	3.330	0.493	0.998	2	R.NSAFESLYQDK.F
SW:U520_HUMAN	R01	5659	2	1316.4	(+0.0)	2.519	0.224	0.787	2	R.NSAFESL*YQDK#.F
SW:U520_HUMAN	R02	5760	2	1316.4	(-0.6)	2.536	0.268	0.862	2	R.NSAFESL*YQDK#.F
SW:U520_HUMAN	R03	5619	2	1316.4	(+0.2)	2.583	0.318	0.918	2	R.NSAFESL*YQDK#.F
SW:U520_HUMAN	R01	8115	2	1596.9	(+0.9)	3.839	0.466	0.999	4	R.RLDLVHTAALMLDK.N
SW:U520_HUMAN	R03	7135	2	1365.6	(+1.0)	2.349	0.450	0.977	6	R.SGGPVVVL*VQL*ER.E
SW:U520_HUMAN	R01	7899	2	1296.5	(+0.7)	3.621	0.476	1.000	4	R.SL*VQEMVGSFGK#.R
SW:U520_HUMAN	R01	7895	2	1282.5	(+0.5)	2.965	0.451	0.989	4	R.SLVQEMVGSFGK.R
SW:U520_HUMAN	R01	5113	2	1228.3	(+0.1)	3.137	0.463	1.000	4	K.TGNFQVTEL*GR.I
SW:U520_HUMAN	R01	5109	2	1222.3	(+0.2)	2.993	0.338	0.968	4	K.TGNFQVTELGR.I
SW:U520_HUMAN	R02	5514	2	1228.3	(+0.4)	2.622	0.407	0.980	4	K.TGNFQVTEL*GR.I
SW:U520_HUMAN	R03	5349	2	1222.3	(+0.7)	3.001	0.350	0.980	4	K.TGNFQVTELGR.I
SW:U520_HUMAN	R01	10109	2	1717.0	(+0.2)	4.772	0.511	1.000	3	R.WTELGALDILQMLGR.A
SW:U520_HUMAN	R01	4861	2	1118.2	(+0.8)	2.658	0.306	0.960	5	K.YAQAGFEGFK.T
SW:U520_HUMAN	R01	4933	2	1126.2	(+0.3)	2.481	0.434	0.977	5	K.YAQAGFEGFK#.T
SW:U520_HUMAN	R01	4851	2	1126.2	(-0.9)	2.209	0.372	0.785	5	K.YAQAGFEGFK#.T
SW:U520_HUMAN	R03	5315	2	1126.2	(+0.7)	2.548	0.255	0.901	5	K.YAQAGFEGFK#.T
SW:U520_HUMAN	R05	7562	2	1728.9	(-0.2)	2.517	0.407	0.489	7	R.NALLQLTDSQIADVAR.F
SW:U5S1_HUMAN	R08	8787	2	1800.0	(+0.3)	4.846	0.621	1.000	2	K.AFIPAIDSFGFETDLR.T
SW:U5S1_HUMAN	R08	8813	2	1806.0	(-0.3)	3.613	0.509	1.000	2	K.AFIPAIDSFGFETDL*R.T
SW:U5S1_HUMAN	R08	8627	2	1465.7	(-0.2)	3.494	0.385	0.978	2	K.FFDDPML*L*EL*AK#.Q
SW:U5S1_HUMAN	R08	8043	2	1481.7	(-0.7)	2.860	0.237	0.870	2	K.FFDDPM@L*L*EL*AK#.Q
SW:U5S1_HUMAN	R08	6845	2	1895.2	(+1.0)	4.410	0.452	1.000	2	R.GHVTQDAPIPGSPLYTIK.A
SW:U5S1_HUMAN	R08	6861	2	1909.2	(-0.6)	3.726	0.534	1.000	2	R.GHVTQDAPIPGSPL*YTIK#.A
SW:U5S1_HUMAN	R08	2066	2	1049.1	(+0.2)	2.588	0.394	0.961	2	K.GL*SEDVSISK#.F
SW:U5S1_HUMAN	R08	6467	2	1416.6	(-0.6)	3.277	0.279	0.252	2	R.GNEEAQIFRPL*K#.F
SW:U5S1_HUMAN	R08	6483	2	1402.6	(+0.2)	2.764	0.253	0.127	2	R.GNEEAQIFRPLK.F
SW:U5S1_HUMAN	R09	5926	2	1407.6	(-0.1)	3.056	0.407	0.972	2	K.IAVEPVNPSEL*PK#.M
SW:U5S1_HUMAN	R08	7505	2	1595.8	(+0.1)	4.079	0.490	1.000	2	K.IL*AQVVGDVDTSL*PR.T
SW:U5S1_HUMAN	R08	6435	2	1461.7	(+0.7)	3.347	0.486	1.000	1	K.ILDAVVAQEPLHR.G
SW:U5S1_HUMAN	R08	10583	3	2250.6	(+0.6)	3.979	0.446	0.999	2	R.ISDGVVLFIDAAEGVMLNTER.L
SW:U5S1_HUMAN	R08	6421	2	1159.4	(+0.2)	2.322	0.275	0.836	2	K.ITMIAEPL*EK#.G
SW:U5S1_HUMAN	R08	7617	2	1896.1	(+0.8)	5.691	0.599	0.965	2	K.IYADTFGDINYQEFAK.R
SW:U5S1_HUMAN	R08	7613	2	1904.1	(-0.5)	5.369	0.582	1.000	2	K.IYADTFGDINYQEFAK#.R
SW:U5S1_HUMAN	R08	6251	2	984.1	(-0.1)	2.866	0.436	0.983	2	K.L*GEFFQTK#.Y
SW:U5S1_HUMAN	R08	6253	2	970.1	(+1.0)	2.723	0.385	0.986	2	K.LGEFFQTK.Y
SW:U5S1_HUMAN	R08	7691	2	1267.4	(-0.4)	3.333	0.487	1.000	2	R.L*WGDIYFNPK#.T
SW:U5S1_HUMAN	R08	5553	2	1007.2	(+0.9)	2.387	0.263	0.910	2	K.MYSEIDIK#.V
SW:U5S1_HUMAN	R08	7485	2	1409.6	(+0.6)	3.143	0.192	0.931	2	K.RLWGDYFNPK.T
SW:U5S1_HUMAN	R08	9499	2	1505.8	(-0.0)	2.406	0.242	0.766	2	R.SFVEFIL*EPL*YK#.I
SW:U5S1_HUMAN	R08	8929	2	2779.0	(-0.1)	3.461	0.390	0.975	2	R.SIWAFGPDATGPNIL*VDDTL*PSEVDK#.A
SW:U5S1_HUMAN	R08	8721	3	2685.0	(+0.4)	3.968	0.522	1.000	2	K.SYLFNIMDTPGHVNFSDVETAGLR.I
SW:U5S1_HUMAN	R08	6901	2	1240.4	(+0.9)	3.995	0.395	0.981	2	R.TLDELGIHLTK.E
SW:U5S1_HUMAN	R08	6913	2	1266.4	(-0.0)	2.844	0.397	0.969	2	R.TL*DEL*GIHL*TK#.E
SW:U5S1_HUMAN	R08	8121	2	1935.3	(+0.8)	5.253	0.560	1.000	2	R.VPAGNWWLIEGVDQPIVK.T
SW:U5S1_HUMAN	R08	8133	2	1949.3	(-0.5)	4.587	0.365	1.000	2	R.VPAGNWWL*IEGVDQPIVK#.T
SW:U5S1_HUMAN	R08	8137	2	1935.3	(-0.5)	4.583	0.502	0.989	2	R.VPAGNWWLIEGVDQPIVK.T
SW:U5S1_HUMAN	R09	7058	2	1595.8	(+0.7)	2.907	0.426	0.973	2	K.IL*AQVVGDVDTSL*PR.T
SW:U84B_HUMAN	R11	1818	2	1461.5	(-0.3)	2.765	0.151	0.681	3	R.AEHQQDSEDL*FK#.K
SW:U84B_HUMAN	R11	9726	2	2016.2	(-0.1)	3.859	0.505	0.999	3	R.DDVESQFPWISQFL*AR.G
SW:U84B_HUMAN	R11	9718	2	2010.2	(+0.0)	3.698	0.512	1.000	3	R.DDVESQFPWISQFLAR.G
SW:U84B_HUMAN	R11	5094	2	1059.2	(+0.6)	3.397	0.148	0.945	3	R.IQEELSALR.A
SW:U84B_HUMAN	R11	5064	2	1071.2	(+0.0)	2.480	0.266	0.874	3	R.IQEEL*SAL*R.A
SW:U84B_HUMAN	R11	9158	2	1925.2	(+0.1)	4.679	0.574	0.999	3	R.LEDQLAGLQQELAALALK.Q
SW:U84B_HUMAN	R11	9460	2	1644.9	(-0.1)	3.015	0.342	0.919	3	R.L*TTAASL*L*DVFL*TR.R
SW:U84B_HUMAN	R12	8672	3	2577.8	(+0.5)	4.116	0.477	1.000	3	R.QGAPGQGGGGGLSHEDTLALLEGLVSR.R
SW:U84B_HUMAN	R11	9252	2	2081.4	(-0.0)	4.749	0.542	1.000	3	R.RLEDQLAGLQQELAALALK.Q
SW:U84B_HUMAN	R11	4768	3	2512.5	(+0.1)	4.082	0.479	0.999	2	R.YSQGDDDDGSSSSGSSVAGSQSTLTK.D
SW:U84B_HUMAN	R12	9456	3	2081.4	(-0.1)	3.770	0.439	0.996	3	R.RLEDQLAGLQQELAALALK.Q
SW:UBCE_HUMAN	R21	5080	3	2456.6	(-0.2)	4.152	0.445	0.999	2	R.AL*ASGTEASSTDPGAPGGPGAEGPMAK#.K



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:UBCE_HUMAN	R21	6916	2	1484.6	(+0.7)	3.006	0.471	0.991	3	R.LLLENYEEYAAR.A
SW:UBCE_HUMAN	R21	6910	2	1502.6	(-1.0)	2.423	0.384	0.865	3	R.L*L*L*ENYEEYAAR.A
SW:UBCI_HUMAN	R24	6864	2	1323.5	(-0.1)	3.079	0.331	0.956	4	K.DHPFGFVAVPTK#.N
SW:UBCI_HUMAN	R24	6736	3	1459.7	(+0.8)	4.099	0.384	0.999	4	R.K#DHPFGFVAVPTK#.N
SW:UBCI_HUMAN	R24	6750	2	1459.7	(-0.8)	3.089	0.336	0.869	4	R.K#DHPFGFVAVPTK#.N
SW:UBCI_HUMAN	R24	6862	2	1315.5	(+0.7)	2.350	0.316	0.928	4	K.DHPFGFVAVPTK.N
SW:UCR1_HUMAN	R16	6418	2	1441.6	(+0.3)	3.386	0.463	1.000	1	R.ADLTEYLSTHYK.A
SW:UCR1_HUMAN	R16	6214	2	1257.4	(+0.8)	2.395	0.468	0.985	1	R.RIPLAEWESR.I
SW:UCR2_HUMAN	R16	6558	3	2357.6	(+0.8)	5.988	0.604	0.995		K.AVAFQNPQTHVIENL*HAAAYR.N
SW:UCR2_HUMAN	R16	11168	3	4087.5	(-0.5)	4.926	0.561	0.999	1	R.EQNGDSLVAHFAVAESAVAGSAEANAFSVLQHVLGAGPHVK.R
SW:UCR2_HUMAN	R16	6980	2	1435.8	(+0.6)	4.083	0.483	0.998	1	R.MALIGLGVSHPLK.Q
SW:UCR2_HUMAN	R16	1232	2	1631.8	(+1.0)	3.250	0.545	1.000		K.TIAQGNLSNTDVQAAK.N
SW:UCR2_HUMAN	R16	6818	3	2166.4	(+0.7)	4.163	0.483	1.000	1	K.VTSEELHYFVQNHFTSAR.M
SW:UCR2_HUMAN	R16	6590	2	1666.8	(+0.5)	5.108	0.539	0.997	1	R.YEDFSNLGTTLLR.L
SW:UCR2_HUMAN	R16	6594	2	1684.8	(-0.2)	3.326	0.289	0.955	1	R.YEDFSNL*GTTHL*L*R.L
SW:UCR2_HUMAN	R16	5820	2	1911.1	(+0.7)	3.208	0.522	1.000	1	K.ATAAPAGAPPQPQDLEFTK.L
SW:UCR6_HUMAN	R26	5436	2	1134.2	(-0.1)	2.906	0.244	0.939	3	R.LPENLYNDR.M
SW:UCR6_HUMAN	R26	6594	2	1242.4	(+0.8)	2.323	0.411	0.965	6	K.WYNAAGFNK#.L
SW:UCR6_HUMAN	R26	7854	2	1757.9	(-0.6)	2.576	0.170*	0.139	3	K.YEEENFYL*EPYL*K#.E
SW:UCR6_HUMAN	R26	2578	2	1350.4	(-0.2)	2.204	0.350	0.889	3	R.DDTIYEDEDVK#.E
SW:UCRI_HUMAN	R22	8320	3	2147.4	(+0.3)	4.129	0.476	1.000	2	K.NAVTQFVSSM@SASADVL*AL*AK#.I
SW:UCRI_HUMAN	R21	5426	2	1061.2	(+0.3)	2.321	0.292	0.931	2	R.RLEVLDSTK.S
SW:UCRI_HUMAN	R22	5350	2	1061.2	(+0.1)	3.057	0.373	0.982	2	R.RLEVLDSTK.S
SW:UCRI_HUMAN	R22	5352	2	1081.2	(-0.4)	2.423	0.217	0.792	2	R.RL*EVL*DSTK#.S
SW:UCRY_HUMAN	R09	6508	2	1707.1	(+0.3)	2.407	0.117	0.009	1	R.LILDWVPYINGKFK.K
SW:UCRY_HUMAN	R27	8093	2	1431.7	(+0.3)	3.435	0.392	0.989	1	R.LILDWVPYINGK.F
SW:VAPA_HUMAN	R20	7152	2	1567.8	(+0.4)	4.696	0.507	1.000	2	K.FKGPFTDVVTTNLK.L
SW:VAPA_HUMAN	R20	7154	2	1589.8	(-0.5)	4.587	0.398	1.000	2	K.FK#GPFTDVVTTNL*K#.L
SW:VAPA_HUMAN	R20	6742	2	1292.5	(+0.9)	3.983	0.407	1.000	5	K.GPFTDVVTTNLK.L
SW:VAPA_HUMAN	R20	6824	2	1292.5	(+1.0)	2.960	0.378	0.981	5	K.GPFTDVVTTNLK.L
SW:VAPA_HUMAN	R20	6724	2	1306.5	(-0.1)	2.411	0.204	0.676	5	K.GPFTDVVTTNL*K#.L
SW:VAPA_HUMAN	R21	6704	2	1292.5	(+0.9)	3.125	0.392	0.986	5	K.GPFTDVVTTNLK.L
SW:VAPA_HUMAN	R20	1458	2	996.1	(+0.8)	2.724	0.327	0.453	2	R.HLRDEGLR.L
SW:VAPA_HUMAN	R20	1454	2	1008.1	(+0.1)	2.450	0.166	0.065	2	R.HL*RDEGL*R.L
SW:VAPA_HUMAN	R20	1478	2	1648.8	(-0.3)	3.062	0.511	1.000	2	K.VAHSKPGSTSTASFR.D
SW:VAPA_HUMAN	R20	1484	2	1656.8	(-0.8)	2.694	0.391	0.135	2	K.VAHSK#PGSTSTASFR.D
SW:VAPA_HUMAN	R21	6692	2	1306.5	(+0.1)	2.649	0.316	0.916	5	K.GPFTDVVTTNL*K#.L
SW:VAPB_HUMAN	R21	6090	2	1571.8	(+0.9)	3.362	0.526	1.000	3	K.TVQSNPISALAPTQK.E
SW:VAPB_HUMAN	R21	6412	2	1649.9	(-0.4)	4.258	0.469	0.999	2	K.VEQVLSLEPQHELF.F
SW:VAPB_HUMAN	R21	5410	2	1301.4	(-0.7)	2.563	0.277	0.865	3	K.SL*SSSL*DDTEVK#.K
SW:VATF_HUMAN	R26	7188	3	2055.3	(+0.4)	4.038	0.495	0.999		R.HALDAHQQSIPAVLEIPSK.E
SW:VATF_HUMAN	R26	5520	2	1062.2	(+0.1)	2.437	0.273	0.905		R.GM@FTAEDL*R.-
SW:VIME_HUMAN	R15	1424	2	1843.9	(+1.0)	4.312	0.415	0.990	5	R.DGQVINETSQHDDDL*E.-
SW:VIME_HUMAN	R15	1428	2	1837.9	(+0.1)	2.854	0.331	0.927	5	R.DGQVINETSQHDDLE.-
SW:VIME_HUMAN	R15	4809	2	1324.4	(+0.3)	2.570	0.399	0.978	6	R.EEAENTLQSFR.Q
SW:VIME_HUMAN	R15	4805	2	1330.4	(+0.0)	2.483	0.386	0.960	6	R.EEAENTL*QSFR.Q
SW:VIME_HUMAN	R15	4883	2	1330.4	(+0.7)	2.357	0.430	0.977	6	R.EEAENTL*QSFR.Q
SW:VIME_HUMAN	R15	6433	2	1669.8	(+0.8)	3.125	0.492	0.991	5	R.ETNLDLPLVDTHSK.R
SW:VIME_HUMAN	R15	1720	2	1094.2	(+0.5)	3.301	0.404	0.988	7	K.FADLSEAANR.N
SW:VIME_HUMAN	R15	1710	2	1100.2	(+0.6)	2.686	0.391	0.981	7	K.FADL*SEAANR.N
SW:VIME_HUMAN	R15	1696	2	871.0	(+1.0)	2.497	0.309	0.969	5	R.FANYIDK.V
SW:VIME_HUMAN	R15	1724	2	879.0	(+0.9)	2.382	0.378	0.973	5	R.FANYIDK#.V
SW:VIME_HUMAN	R15	7631	2	1202.4	(+0.0)	2.371	0.175	0.635	5	K.IL*L*AEL*EQL*K#.G
SW:VIME_HUMAN	R15	8525	2	1571.9	(+0.6)	3.086	0.396	0.983	6	R.ISLPLPNFSSLNLR.E
SW:VIME_HUMAN	R15	7329	2	1562.8	(+0.4)	4.003	0.519	1.000	7	R.K#VESL*QEEIAFL*K#.K
SW:VIME_HUMAN	R15	7327	3	1562.8	(+0.8)	3.931	0.215	0.980	7	R.K#VESL*QEEIAFL*K#.K

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:VIME_HUMAN	R15	5633	2	1255.4	(-0.4)	2.341	0.364	0.945	5	R.LGDLYEEEMR.E
SW:VIME_HUMAN	R15	8697	2	2153.4	(+0.6)	2.736	0.355	0.952	5	R.L*L*QDSVDFSL*ADAINTEFK#.N
SW:VIME_HUMAN	R15	1574	2	1133.3	(-0.3)	2.615	0.235	0.870	7	R.L*QDEIQNMK#.E
SW:VIME_HUMAN	R15	1592	2	1059.2	(+0.5)	2.699	0.153	0.856	7	K.L*QEEML*QR.E
SW:VIME_HUMAN	R15	1594	2	1047.2	(+0.9)	2.597	0.181	0.892	7	K.LQEEMLQR.E
SW:VIME_HUMAN	R15	4697	2	1429.6	(-0.2)	3.650	0.448	0.999	3	R.SLYASSPPGGVYATR.S
SW:VIME_HUMAN	R15	4691	2	1435.6	(-0.2)	3.509	0.493	1.000	3	R.SL*YASSPPGGVYATR.S
SW:VIME_HUMAN	R15	4769	2	1435.6	(-0.7)	2.858	0.526	1.000	3	R.SL*YASSPPGGVYATR.S
SW:VIME_HUMAN	R15	7577	2	1406.6	(+0.7)	3.537	0.537*	0.676	7	K.VESLQEEIAFLK.K
SW:VIME_HUMAN	R15	7575	2	1426.6	(+0.5)	3.311	0.411	0.986	7	K.VESL*QEEIAFL*K#.K
SW:VIME_HUMAN	R16	4282	2	1324.4	(+0.6)	2.419	0.360	0.961	6	R.EEAENTLQSF.R.Q
SW:VP36_HUMAN	R19	8152	3	2339.6	(+0.5)	5.515	0.484	0.963		K.L*FQL*MVEHTPDEESIDWTK#.I
SW:VP36_HUMAN	R19	7750	3	2752.0	(+0.1)	4.762	0.515	1.000		R.L*PTGYFYGASAGTGDL*SDNHDHISMK#.L
SW:VP36_HUMAN	R19	7736	3	2355.6	(-0.5)	4.225	0.390	0.998		K.L*FQL*M@VEHTPDEESIDWTK#.I
SW:VP45_HUMAN	R14	6329	2	1243.4	(+0.6)	2.577	0.385	0.978	2	K.AFVENYPQFK.K
SW:VP45_HUMAN	R14	5219	2	1097.3	(-0.1)	2.295	0.249	0.826	2	K.HVTVVGELSR.L
SW:VRK1_HUMAN	R16	5994	3	3137.3	(+0.2)	5.580	0.447	1.000	1	K.EIEESKEPGVEDTEWSNTQTEEAQTR.S
SW:VRK1_HUMAN	R16	5988	3	3145.3	(+0.3)	5.088	0.514	1.000	1	K.EIEESK#EPGVEDTEWSNTQTEEAQTR.S
SW:VRK1_HUMAN	R16	7050	2	1799.0	(+0.8)	3.872	0.576	1.000	1	K.NPDQVYL*VDYGL*AYR.Y
SW:VRK1_HUMAN	R16	896	2	808.9	(+0.5)	2.477	0.256	0.862	1	R.FGSDL*QK#.I
SW:WNT3_HUMAN	R03	6715	2	2239.5	(+0.1)	2.272	0.103	0.002	1	R.DRTCNTVSHGIDGCDLLCCGR.G
SW:WNT3_HUMAN	R07	7029	2	1558.8	(+0.6)	2.786	0.200	0.821	1	R.NYIEIMPSVAEGVK#.L
SW:WNT3_HUMAN	R11	6924	2	2239.5	(+0.3)	2.493	0.134	0.004	1	R.DRTCNTVSHGIDGCDLLCCGR.G
SW:XAB2_HUMAN	R10	1204	2	1023.1	(+0.9)	2.453	0.389	0.976	3	R.L*ATVVNDER.F
SW:XAB2_HUMAN	R10	8339	2	1691.8	(-0.6)	2.456	0.247	0.758	3	K.L*SPESAEEYIEYL*K#.S
SW:XAB2_HUMAN	R10	8383	3	3011.3	(+0.2)	4.649	0.505	1.000	2	R.L*SRPERPDL*VFEEEDL*PYEEIIMR.N
SW:XAB2_HUMAN	R10	7819	2	1234.4	(+0.9)	2.819	0.329	0.971	5	K.VQSL*NVDAIR.G
SW:XAB2_HUMAN	R10	9141	2	1724.9	(+0.5)	3.466	0.409	0.985	4	K.WPNVSDIWSTYL*TK#.F
SW:XAB2_HUMAN	R10	9185	2	1724.9	(-1.0)	2.497	0.197	0.377	4	K.WPNVSDIWSTYL*TK#.F
SW:XAB2_HUMAN	R10	1214	2	1017.1	(+0.7)	2.400	0.431	0.982	3	R.LATVVNDER.F
SW:Y152_HUMAN	R20	6038	2	1446.6	(-0.8)	3.108	0.405	0.945		K.FAEVYFAQSQK.V
SW:Y152_HUMAN	R20	6630	2	1367.5	(-0.7)	3.422	0.469	0.999		K.L*SVQGEVSTFTGK#.L
SW:Y152_HUMAN	R01	5379	2	1593.7	(+0.3)	4.323	0.471	0.987		R.SNPEDQILYQTER.Y
SW:Y152_HUMAN	R01	5377	2	1599.7	(-0.2)	3.193	0.347	0.971		R.SNPEDQIL*YQTER.Y
SW:Y152_HUMAN	R03	5431	2	1599.7	(-0.4)	2.978	0.356	0.965		R.SNPEDQIL*YQTER.Y
SW:Y152_HUMAN	R20	5884	2	1599.7	(+1.0)	3.256	0.439	0.990		R.SNPEDQIL*YQTER.Y
SW:Y152_HUMAN	R20	5888	2	1593.7	(-0.4)	2.801	0.442	0.979		R.SNPEDQILYQTER.Y
SW:Y152_HUMAN	R20	8050	3	2736.0	(+0.6)	4.741	0.535	1.000		R.YNEETFGYEVPIKEEGDYVLVK.F
SW:Y152_HUMAN	R20	6632	2	1353.5	(+0.8)	2.609	0.476	0.986		K.LSVQGEVSTFTGK.L
SW:Y539_HUMAN	R05	7824	2	1429.6	(+0.7)	3.556	0.538	0.947		R.EDVYDVVEGYIK.I
SW:Y539_HUMAN	R05	8830	2	1852.1	(+0.1)	2.832	0.315	0.934	2	R.FQEQSLLYLLDVVR.N
SW:Y539_HUMAN	R05	6080	2	1253.4	(-0.6)	2.376	0.137	0.473	2	R.FTVNETVL*STK#.D
SW:Y539_HUMAN	R05	9454	3	2597.0	(+0.2)	4.194	0.534	1.000	2	K.HLRPTLAPVQLTNFFGLDSVLR.Y
SW:Y539_HUMAN	R05	7804	2	1712.0	(+0.3)	4.660	0.588	0.999	1	R.ILLTLVANPYSYTDK.A
SW:Y539_HUMAN	R05	7814	2	1738.0	(-0.8)	2.592	0.391	0.841	1	R.IL*L*TL*VANPYSYTDK#.A
SW:Y539_HUMAN	R05	9912	2	1938.3	(-0.2)	3.470	0.331	0.960	1	K.IL*PDL*NTVVVVWQSL*K#.K
SW:Y539_HUMAN	R05	9920	2	1912.3	(+0.7)	2.473	0.383	0.960	1	K.ILPDLNTVVVVWQSLK.K
SW:Y539_HUMAN	R05	7576	2	1511.7	(-0.2)	3.101	0.388	0.977	2	R.SL*WQQQSVGDIL*R.L
SW:Y539_HUMAN	R05	9954	2	1812.0	(+0.9)	4.318	0.529	0.999	1	K.TAADDDL*VADL*VVNIL*K#.V
SW:Y539_HUMAN	R05	7782	3	2422.8	(+0.5)	3.845	0.395	0.999	1	K.TPPQLEALQELHPYMEGAQLR.E
SW:Y539_HUMAN	R05	988	2	1002.1	(+0.6)	2.243	0.153	0.627	2	R.SVAEHPL*SR.A
SW:YU20_HUMAN	R10	5417	2	1302.4	(+0.1)	3.462	0.288	0.331	5	R.DREIQL*EISGK#.E
SW:YU20_HUMAN	R01	6735	2	1252.5	(+0.4)	2.849	0.412	0.987	1	K.L*FHEVVQAFR.A
SW:YU20_HUMAN	R10	7791	2	1246.5	(+0.8)	2.416	0.363	0.963	1	K.LFHEVVQAFR.A
SW:YU20_HUMAN	R10	1286	2	1045.2	(+0.4)	2.406	0.357	0.967	3	K.LSNVNLQEK.A
SW:YU20_HUMAN	R10	6819	2	1351.6	(-0.3)	2.981	0.461	0.981	3	R.ML*QPSSSPL*WGK#.L
SW:YU20_HUMAN	R10	6179	2	1367.6	(-0.4)	2.928	0.275	0.915	3	R.M@L*QPSSSPL*WGK#.L
SW:YU20_HUMAN	R10	6741	2	1351.6	(-0.2)	2.367	0.343	0.883	3	R.ML*QPSSSPL*WGK#.L

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:YU20_HUMAN	R10	7875	2	1499.7	(+0.2)	3.612	0.519	0.998	3	R.MVVVWSTGEESL*R.V
SW:YU20_HUMAN	R10	6605	2	1515.7	(+0.0)	2.356	0.197	0.668	3	R.M@VVVWSTGEESL*R.V
SW:YU20_HUMAN	R10	1284	2	1065.2	(-0.2)	2.285	0.211	0.675	3	K.L*SNVNL*QEK#.A
SW:YV03_HUMAN	R18	2276	2	1276.4	(+0.6)	3.184	0.469	1.000		R.TVTQLVAEDGSR.V
SW:YV03_HUMAN	R18	4363	2	965.1	(+0.0)	2.411	0.194	0.819	3	K.MDESTLLR.E
SW:Z148_HUMAN	R09	7624	2	1767.1	(-0.8)	2.669	0.253	0.591	5	R.L*PQGL*QYAL*NVPISVK#.Q
SW:Z148_HUMAN	R10	5205	2	1003.1	(+0.2)	2.274	0.179	0.733	4	K.FL*QQAL*DR.T
SW:ZAP3_HUMAN	R04	4890	2	1163.2	(-0.3)	2.823	0.137	0.781	1	R.GHEEFPL*DGR.N
SW:ZAP3_HUMAN	R04	4896	2	1157.2	(+0.3)	2.782	0.401	0.984	1	R.GHEEFPLDGR.N
SW:ZAP3_HUMAN	R04	1756	3	2358.5	(-0.3)	5.322	0.506	0.885	3	K.SQAEPL*SGNK#EPL*ADTSSNQK#.N
SW:ZAP3_HUMAN	R04	1760	3	2330.5	(+0.8)	4.942	0.562	0.999	3	K.SQAEPLSGNKEPLADTSSNQK#.N
SW:ZAP3_HUMAN	R04	10412	3	2095.3	(+0.7)	3.791	0.221	0.956	2	K.TL*DDGFFPFIL*DAINDR.V
SW:ZAP3_HUMAN	R04	1124	2	1402.5	(-0.0)	2.559	0.400	0.951	1	K.TTVQQEPL*ESGAK#.N
SW:ZAP3_HUMAN	R04	10424	2	2083.3	(+0.1)	2.332	0.417	0.950	2	K.TLDDGFFPFILDAINDR.V
SW:ZW10_HUMAN	R10	9365	2	1618.9	(+0.5)	3.609	0.499	0.996	1	K.AMGTLNNTAISEVIGK.I
SW:ZW10_HUMAN	R10	9145	3	2333.5	(-0.4)	4.070	0.219	0.933	1	K.L*QQYEEIIQSTEEFENAL*K#.E
SW:ZW10_HUMAN	R10	10743	3	2324.8	(+0.3)	3.764	0.352	0.996	1	K.TPMPPISSVLLAFSVLGLHLSK.L
SW:ZW10_HUMAN	R10	6749	2	1046.2	(+0.0)	2.464	0.275	0.911	1	K.LSEDIDLLK.S
SWN:1B73_HUMAN	R17	5668	3	2652.7	(+0.3)	4.243	0.510	1.000	214	R.DGEDQTQDTEL*VETRPAGDGTGFK#.W
SWN:1B73_HUMAN	R17	6396	2	1222.3	(+0.7)	2.863	0.440*	0.485	572	K.DYIALNEDLR.S
SWN:1B73_HUMAN	R17	6386	2	1234.3	(+0.1)	2.357	0.305*	0.164	572	K.DYIAL*NEDL*R.S
SWN:1B73_HUMAN	R18	5381	3	2652.7	(+0.3)	3.882	0.339	0.970	214	R.DGEDQTQDTEL*VETRPAGDGTGFK#.W
SWN:ACD9_HUMAN	R14	8313	2	1587.8	(+0.5)	4.418	0.547	0.995	2	K.IPVENILGEVGDGFK.V
SWN:ACD9_HUMAN	R14	8311	2	1601.8	(+0.9)	4.171	0.471	1.000	2	K.IPVENIL*GEVGDGFK#.V
SWN:ACD9_HUMAN	R14	6629	3	2329.5	(-0.5)	3.769	0.395	0.996	3	R.TVDL*GL*TGNGHVHPSL*ADSANK#.F
SWN:ACD9_HUMAN	R14	6675	2	1184.3	(-0.1)	2.261	0.156	0.513	2	R.L*SEFGL*IQEK#.F
SWN:ASH2_HUMAN	R11	9016	3	1777.0	(-0.2)	3.835	0.425	0.999	2	K.DIFEGVYFPAISL*YK#.S
SWN:ASH2_HUMAN	R11	5378	2	937.1	(+0.7)	2.335	0.324	0.957	3	R.VLLALHDR.A
SWN:ASH2_HUMAN	R11	2162	2	1027.1	(+0.0)	2.218	0.213	0.751	3	R.SDPL*FSAQR.L
SWN:C5P3_HUMAN	R14	9419	2	1622.9	(+0.3)	3.793	0.317	0.983	1	K.DNTYLVELSSLLVR.N
SWN:C5P3_HUMAN	R14	8221	2	1690.0	(-0.4)	2.733	0.381	0.286	1	R.MK#DWQEIAL*YEK#.D
SWN:C5P3_HUMAN	R14	6425	2	1177.3	(+0.8)	2.420	0.421	0.979	2	R.NVNYEIPSLK.K
SWN:C5P3_HUMAN	R14	2070	2	993.1	(+0.6)	2.317	0.274	0.864	2	R.VTEFLQK.L
SWN:C5P3_HUMAN	R20	6352	2	1177.3	(+0.9)	2.667	0.419	0.984	2	R.NVNYEIPSLK.K
SWN:CF66_HUMAN	R23	4996	2	987.1	(+0.2)	2.727	0.193	0.838		K.DPVSSL*QVK#.A
SWN:CF66_HUMAN	R23	8952	2	1565.9	(+0.6)	2.593	0.392*	0.221		K.ISIVEALTLLNHHK.L
SWN:CF66_HUMAN	R23	5016	2	973.1	(+0.1)	2.517	0.324	0.947		K.DPVSSLQVK.A
SWN:CG21_HUMAN	R21	4846	2	1185.3	(+0.4)	3.488	0.418	0.999		K.FL*NDSEQVAR.A
SWN:CG21_HUMAN	R21	4866	2	1179.3	(+0.8)	3.333	0.240	0.969		K.FLNDSEQVAR.A
SWN:CG21_HUMAN	R23	4744	2	1185.3	(+0.2)	3.385	0.440	0.995		K.FL*NDSEQVAR.A
SWN:CG21_HUMAN	R23	4682	2	1179.3	(+0.6)	3.190	0.268	0.972		K.FLNDSEQVAR.A
SWN:CG21_HUMAN	R20	1722	2	1191.3	(-0.1)	2.407	0.343	0.928		R.GEAPGAETPSL*R.H
SWN:CG21_HUMAN	R21	4474	2	1191.3	(+0.2)	2.398	0.492	0.979		R.GEAPGAETPSL*R.H
SWN:CG21_HUMAN	R23	4668	2	1185.3	(-0.3)	3.086	0.403	0.984		K.FL*NDSEQVAR.A
SWN:CTB6_HUMAN	R17	10284	2	1968.3	(-0.2)	2.876	0.432	0.975	2	K.FIYITPEELAAVANFIR.Q
SWN:CTB6_HUMAN	R17	2262	2	1425.6	(+0.5)	2.604	0.355	0.962	2	R.VAQPGPL*EPEEPR.A
SWN:CTB6_HUMAN	R17	2274	2	1419.6	(-0.3)	2.273	0.469	0.968	2	R.VAQPGPLEPEEPR.A
SWN:CTB6_HUMAN	R18	8923	2	1512.8	(+1.0)	2.538	0.367	0.961	2	K.VVLLLEDLASQVGLR.T
SWN:DOC2_HUMAN	R06	9670	2	1592.8	(+0.7)	2.690	0.486	0.988	1	K.ETLYETIIGYFDK.G
SWN:DOC2_HUMAN	R06	6100	2	1134.4	(+0.2)	2.550	0.183	0.814	1	K.KFENEILK.L
SWN:DOC2_HUMAN	R06	8584	2	1676.0	(+0.5)	2.359	0.163	0.389	1	R.RPFGVAVMDITDIK.G
SWN:FUB1_HUMAN	R12	1488	2	657.8	(+1.0)	2.296	0.141	0.769	7	K.AGLVIGK.G
SWN:FUB1_HUMAN	R12	5198	2	1353.5	(+0.4)	3.287	0.343	0.981	3	K.IQIAPDSGGLPER.S

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SWN:FUB1_HUMAN	R12	5194	2	1359.5	(+0.1)	2.947	0.265	0.922	3	K.IQIAPDSGGL*PER.S
SWN:FUB1_HUMAN	R11	5300	2	958.1	(+0.7)	2.835	0.129	0.855	3	R.LLDQIVEK.G
SWN:FUB1_HUMAN	R13	5577	2	958.1	(+0.8)	2.535	0.196	0.897	3	R.LLDQIVEK.G
SWN:FUB2_HUMAN	R10	6563	3	2801.0	(+0.5)	4.550	0.445	1.000	2	R.GGPPGQFHDNANGGQNGTVQEIMIPAGK#.A
SWN:FUB2_HUMAN	R10	7569	2	1080.3	(+0.9)	2.781	0.295	0.967	2	K.MMLDDIVSR.G
SWN:FUB2_HUMAN	R10	7547	2	1086.3	(+0.2)	2.565	0.290	0.934	2	K.MML*DDIVSR.G
SWN:FUB2_HUMAN	R10	2304	2	1118.3	(-0.3)	2.363	0.153	0.669	2	K.M@M@L*DDIVSR.G
SWN:FUB2_HUMAN	R11	1688	2	1317.5	(+0.7)	2.609	0.269	0.892	2	R.SVSL*TGAPESVQK#.A
SWN:FUB2_HUMAN	R10	8363	2	1227.5	(+0.8)	2.955	0.524	1.000	3	R.VPDGMVGLIIGR.G
SWN:FUB2_HUMAN	R10	8357	2	1233.5	(+0.6)	2.932	0.531	0.997	3	R.VPDGMVGL*IIGR.G
SWN:FUB2_HUMAN	R10	6765	2	1249.5	(+0.7)	2.304	0.280	0.871	3	R.VPDGM@VGL*IIGR.G
SWN:FUB2_HUMAN	R10	2356	2	1355.5	(+0.6)	3.383	0.314	0.978	2	K.VQISPDSSGGLPER.S
SWN:FUB2_HUMAN	R11	2194	2	1355.5	(+0.8)	3.424	0.289	0.973	2	K.VQISPDSSGGLPER.S
SWN:FUB2_HUMAN	R11	2208	2	1355.5	(-0.7)	2.490	0.188	0.704	2	K.VQISPDSSGGLPER.S
SWN:FUB2_HUMAN	R11	2184	2	1361.5	(-0.7)	2.467	0.260	0.842	2	K.VQISPDSSGGL*PER.S
SWN:FUB3_HUMAN	R13	5735	2	1121.2	(+0.3)	2.351	0.327	0.947		K.AEGFVDAL*HR.V
SWN:FUB3_HUMAN	R13	4681	2	935.0	(+0.5)	2.317	0.213	0.825	2	R.DGFGGLAAAR.G
SWN:FUB3_HUMAN	R14	4589	2	935.0	(-0.5)	2.350	0.283	0.886	2	R.DGFGGLAAAR.G
SWN:FUB3_HUMAN	R13	7549	3	2735.0	(-0.4)	4.498	0.406	0.998	1	K.IDSIPHL*NNSTPL*VDPVSVYGYGVQK#.R
SWN:FUB3_HUMAN	R13	7543	3	2715.0	(+0.6)	4.266	0.473	0.998	1	K.IDSIPHLNNSTPLVDPSVYGYGVQK.R
SWN:FUB3_HUMAN	R14	7549	3	2715.0	(+0.7)	3.787	0.285	0.983	1	K.IDSIPHLNNSTPLVDPSVYGYGVQK.R
SWN:FUB3_HUMAN	R13	5683	2	1510.7	(-0.1)	3.721	0.426	0.998	2	R.IQFK#PDDGISPER.A
SWN:FUB3_HUMAN	R13	5649	2	926.1	(+0.4)	2.444	0.436	0.986	2	R.L*L*GQIVDR.C
SWN:FUB3_HUMAN	R13	6913	3	1964.2	(+0.9)	4.158	0.462	1.000		K.RPL*DDGVGNQL*GAL*VHQR.T
SWN:FUB3_HUMAN	R14	4587	2	941.0	(+0.6)	2.246	0.224	0.821	2	R.DGFGGL*AAAR.G
SWN:IMMT_HUMAN	R11	7294	2	1395.6	(+0.6)	3.535	0.445	0.991	6	K.AHQLWLSVEALK.Y
SWN:IMMT_HUMAN	R10	5997	2	1136.3	(+0.1)	2.536	0.266	0.859	4	K.AVDEAADAL*L*K#.A
SWN:IMMT_HUMAN	R10	5999	2	1116.3	(+0.2)	2.263	0.387	0.945	4	K.AVDEAADALLK.A
SWN:IMMT_HUMAN	R11	5790	2	1136.3	(+0.5)	2.828	0.328	0.962	4	K.AVDEAADAL*L*K#.A
SWN:IMMT_HUMAN	R10	8303	2	1604.8	(-0.5)	3.031	0.307	0.923	4	R.EL*DSITPEVL*PGWK#.G
SWN:IMMT_HUMAN	R10	2258	2	1023.1	(+0.6)	3.037	0.397	0.985	3	K.GMSVSDLADK.L
SWN:IMMT_HUMAN	R10	1542	2	1054.1	(+0.8)	2.475	0.442	0.985	5	R.GVYSEETLR.A
SWN:IMMT_HUMAN	R10	6055	2	1244.4	(-0.8)	3.599	0.320	0.934	4	R.KAVDEAADALLK.A
SWN:IMMT_HUMAN	R10	8179	2	1510.8	(+0.1)	4.385	0.533	1.000	4	K.LHNMIVDLDNVVK.K
SWN:IMMT_HUMAN	R10	8169	2	1530.8	(+0.4)	4.192	0.364	1.000	4	K.L*HNMIVDL*DNVVK#.K
SWN:IMMT_HUMAN	R01	5235	2	1150.3	(+0.5)	2.748	0.271	0.958	6	K.LSEQELQFR.R
SWN:IMMT_HUMAN	R10	5851	2	1150.3	(+0.9)	3.151	0.314	0.983	6	K.LSEQELQFR.R
SWN:IMMT_HUMAN	R10	5853	2	1162.3	(+0.6)	2.920	0.181	0.918	6	K.L*SEQEL*QFR.R
SWN:IMMT_HUMAN	R11	5666	2	1150.3	(+0.4)	3.709	0.329	0.989	6	K.LSEQELQFR.R
SWN:IMMT_HUMAN	R11	5664	2	1162.3	(-0.5)	2.430	0.172	0.747	6	K.L*SEQEL*QFR.R
SWN:IMMT_HUMAN	R10	1466	2	1225.3	(+0.8)	2.253	0.364	0.942	6	K.SEFEQNL*SEK#.L
SWN:IMMT_HUMAN	R10	5867	3	2596.8	(+0.5)	5.435	0.571	1.000	3	K.TDHPEIGEGKPTPALSEEASSSSIR.E
SWN:IMMT_HUMAN	R10	5869	3	2610.8	(+0.1)	4.885	0.424	0.992	3	K.TDHPEIGEGK#PTPAL*SEEASSSSIR.E
SWN:IMMT_HUMAN	R11	5700	3	2610.8	(+0.7)	5.322	0.403	0.997	3	K.TDHPEIGEGK#PTPAL*SEEASSSSIR.E
SWN:IMMT_HUMAN	R10	8053	2	1873.1	(+0.5)	2.633	0.389	0.969	6	K.TSSAETPTIPLGSAVEAIK.A
SWN:IMMT_HUMAN	R10	5677	2	1528.8	(-0.3)	3.311	0.450	0.987	4	K.VVSQYHELVVQAR.D
SWN:IMMT_HUMAN	R11	5522	2	1528.8	(+0.4)	2.598	0.436	0.981	4	K.VVSQYHELVVQAR.D
SWN:IMMT_HUMAN	R10	1010	2	1260.3	(-0.2)	2.607	0.410	0.950	3	R.YSTSGSSGL*TTGK#.I
SWN:IMMT_HUMAN	R13	7361	2	1873.1	(+0.1)	2.448	0.430	0.961	6	K.TSSAETPTIPLGSAVEAIK.A
SWN:KG62_HUMAN	R16	8748	2	1737.0	(+0.8)	3.323	0.465	0.991	2	R.GPGIFEDLQNYILEK.K
SWN:KG62_HUMAN	R16	4962	2	1276.4	(+0.2)	3.281	0.292	0.962	2	K.VDVIQEPGL*SGR.F
SWN:KG62_HUMAN	R16	4994	2	1270.4	(-0.6)	2.537	0.460	0.976	2	K.VDVIQEPGLSGR.F
SWN:KG62_HUMAN	R17	9088	2	1737.0	(+0.6)	4.753	0.464	0.987	2	R.GPGIFEDLQNYILEK.K
SWN:KTN1_HUMAN	R06	1806	3	2267.3	(+0.9)	3.899	0.379	0.998	3	K.AAGDTTVIENS DVSPETESSEK.E
SWN:KTN1_HUMAN	R06	5900	2	1499.7	(-0.7)	2.819	0.231	0.094	4	K.AL*K#EEIGNVQL*EK#.A
SWN:KTN1_HUMAN	R06	7248	3	2757.0	(-0.5)	6.718	0.535	0.990	4	K.AQIQFHSQIAAQTASVLA*EEL*HK#.V
SWN:KTN1_HUMAN	R06	7234	3	2737.0	(+0.3)	4.000	0.403	0.998	4	K.AQIQFHSQIAAQTASVLA*EEL*HK#.V
SWN:KTN1_HUMAN	R06	1274	2	1018.2	(+0.5)	2.456	0.162	0.802	3	K.AQLNETLTK.L
SWN:KTN1_HUMAN	R06	1344	2	1421.5	(+0.4)	3.133	0.293	0.956	4	R.DAVSNNTNQL*ESK#.Q
SWN:KTN1_HUMAN	R06	1348	2	1407.5	(-0.1)	2.685	0.271	0.897	4	R.DAVSNNTNQL*ESK#.Q
SWN:KTN1_HUMAN	R06	7434	2	1236.5	(+1.0)	3.369	0.342	0.721	4	K.DIQNMNFKK.A

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SWN:KTN1_HUMAN	R06	7432	2	1256.5	(+0.4)	2.505	0.182	0.784	4	K.DIQNMNFL*L*K#.A
SWN:KTN1_HUMAN	R06	7978	2	1801.0	(+0.9)	2.407	0.212	0.713	3	K.EASSASQFEEL*EIVL*K#.E
SWN:KTN1_HUMAN	R06	8374	3	2272.5	(+0.3)	4.927	0.360	0.999	4	K.EESL*QMQVQDIL*EQNEAL*K#.A
SWN:KTN1_HUMAN	R06	8380	3	2246.5	(+0.6)	4.663	0.357	0.999	4	K.EESLQMQVQDILEQNEALK.A
SWN:KTN1_HUMAN	R06	7670	2	1111.4	(+0.8)	3.230	0.316	0.550	4	K.FKDFLLSLK.T
SWN:KTN1_HUMAN	R06	7666	2	1145.4	(-0.8)	2.373	0.156	0.010	4	K.FK#DFL*L*SL*K#.T
SWN:KTN1_HUMAN	R06	7838	2	1510.7	(+0.7)	4.914	0.434	0.964	4	K.GELTTLIHQLQE.K
SWN:KTN1_HUMAN	R06	1076	2	997.2	(+0.4)	2.227	0.279	0.882	4	K.KVEPVPVTK.Q
SWN:KTN1_HUMAN	R06	1026	2	1074.2	(+0.5)	2.900	0.149	0.860	4	K.NAEQAATQLK.V
SWN:KTN1_HUMAN	R06	5088	2	931.1	(+0.0)	3.202	0.171	0.920	4	K.SGVIQDALK.K
SWN:KTN1_HUMAN	R06	8462	2	1373.6	(+0.9)	4.872	0.365	1.000	4	K.SVEELLEAELLK.V
SWN:KTN1_HUMAN	R07	8441	2	1373.6	(+0.6)	3.522	0.382	0.989	4	K.SVEELLEAELLK.V
SWN:KTN1_HUMAN	R06	6916	2	1288.5	(+1.0)	3.927	0.430	1.000	3	K.SVLAETEGILQK.L
SWN:KTN1_HUMAN	R06	6912	2	1308.5	(-0.8)	2.342	0.242	0.485	3	K.SVL*AETEGIL*QK#.L
SWN:KTN1_HUMAN	R06	5134	2	1431.5	(-0.2)	3.457	0.413	0.986	3	K.TQLLQDVQDENK.L
SWN:KTN1_HUMAN	R07	5057	2	1451.5	(-0.4)	2.789	0.253	0.877	3	K.TQL*L*QDVQDENK#.L
SWN:KTN1_HUMAN	R06	8122	3	2621.9	(-0.6)	4.757	0.408	0.991	4	R.VNK#EESL*QMQVQDIL*EQNEAL*K#.A
SWN:KTN1_HUMAN	R06	990	2	973.1	(+0.7)	2.472	0.152	0.819	4	K.VQLQEAER.R
SWN:KTN1_HUMAN	R06	978	2	979.1	(+0.4)	2.383	0.237	0.909	4	K.VQL*QEAER.R
SWN:KTN1_HUMAN	R06	6508	2	1658.8	(+0.3)	3.413	0.358	0.926	3	K.WL*QDL*QEENESL*K#.A
SWN:KTN1_HUMAN	R06	6518	2	1632.8	(+0.6)	3.203	0.432	0.989	3	K.WLQDLQEENESLK.A
SWN:KTN1_HUMAN	R08	6763	2	1085.3	(+0.4)	2.569	0.256	0.936	4	K.VQELQNLK.G
SWN:N133_HUMAN	R08	6639	2	1532.7	(-0.0)	2.891	0.458	0.982	3	K.AHATL*L*GL*ANM@ETR.Y
SWN:N133_HUMAN	R08	1442	2	886.9	(+0.7)	2.470	0.371	0.979	3	R.ANEYDFK.K
SWN:N133_HUMAN	R07	7591	2	1491.7	(+0.4)	2.631	0.153	0.743	3	K.DGIQLSEYLPEVK.D
SWN:N133_HUMAN	R08	7831	2	1491.7	(+0.4)	3.383	0.269	0.962	3	K.DGIQLSEYLPEVK.D
SWN:N133_HUMAN	R08	7821	2	1511.7	(+0.3)	2.804	0.339	0.957	3	K.DGIQL*SEYL*PEVK#.D
SWN:N133_HUMAN	R08	8481	3	3059.2	(-0.6)	4.757	0.451	1.000	2	K.DL*GHAQM@VVDEL*FSSHSDL*DSDSEL*DR.A
SWN:N133_HUMAN	R08	6907	2	1333.5	(-0.6)	2.479	0.188	0.663	3	K.DL*L*QADQL*GSL*K#.S
SWN:N133_HUMAN	R08	8589	2	1899.1	(+0.9)	4.406	0.491	0.999	3	R.EYEIPSNLTPADVFR.E
SWN:N133_HUMAN	R08	7877	2	1910.2	(-0.4)	4.552	0.542	1.000	3	R.FLLHQETLPEQLLAEK.Q
SWN:N133_HUMAN	R08	8185	2	1841.2	(+0.7)	5.352	0.596	0.996	1	K.GLPLGSAVSSPVLFPVGR.R
SWN:N133_HUMAN	R02	5902	3	1971.3	(+0.0)	5.119	0.416	0.998	1	K.IHQHIL*PQGQGM@L*SGIGR.K
SWN:N133_HUMAN	R07	6085	3	1971.3	(+0.5)	5.397	0.516	1.000	1	K.IHQHIL*PQGQGM@L*SGIGR.K
SWN:N133_HUMAN	R08	6985	3	1955.3	(+0.4)	5.108	0.460	0.999	1	K.IHQHIL*PQGQGM*SGIGR.K
SWN:N133_HUMAN	R08	6819	3	1811.0	(+0.3)	4.573	0.440	1.000	3	K.L*AAL*ASDFSEDML*QEK#.I
SWN:N133_HUMAN	R08	7695	2	1795.0	(-1.0)	2.897	0.331	0.816	3	K.L*AAL*ASDFSEDML*QEK#.I
SWN:N133_HUMAN	R08	5855	2	1348.5	(-0.6)	3.575	0.403	0.984	1	R.RGPL*AGL*GPGSTPR.T
SWN:N133_HUMAN	R08	5831	2	1348.5	(+0.7)	2.603	0.428	0.978	1	R.RGPL*AGL*GPGSTPR.T
SWN:N133_HUMAN	R08	5845	2	1336.5	(+0.5)	2.546	0.523	0.989	1	R.RGPLAGLPGSTPR.T
SWN:N133_HUMAN	R08	10991	3	2532.9	(+0.1)	4.494	0.536	1.000	3	K.RSDLLSPLLSLGQYLWAASLAEK.Y
SWN:N133_HUMAN	R04	11185	3	2376.8	(+0.9)	3.866	0.442	0.999	3	R.SDLLSPLLSLGQYLWAASLAEK.Y
SWN:N133_HUMAN	R06	11442	3	2376.8	(+0.8)	4.435	0.528	1.000	3	R.SDLLSPLLSLGQYLWAASLAEK.Y
SWN:N133_HUMAN	R07	11529	3	2376.8	(+0.4)	4.155	0.373	0.998	3	R.SDLLSPLLSLGQYLWAASLAEK.Y
SWN:N133_HUMAN	R08	11512	2	2376.8	(+0.1)	3.158	0.467	0.963	3	R.SDLLSPLLSLGQYLWAASLAEK.Y
SWN:N133_HUMAN	R08	7937	2	1244.4	(+0.8)	3.283	0.459	0.999	3	K.SNPYFEFVLK.A
SWN:N133_HUMAN	R08	7935	2	1258.4	(+0.3)	2.591	0.431	0.980	3	K.SNPYFEFVL*K#.A
SWN:N133_HUMAN	R08	6351	2	1421.5	(-0.5)	3.582	0.466	0.999	1	R.SSFYSLTSSNISK.W
SWN:N133_HUMAN	R08	5557	2	950.1	(+0.4)	2.318	0.402	0.960	1	K.TFGSSL*PVK#.V
SWN:N133_HUMAN	R08	10193	2	2480.8	(-0.1)	2.657	0.381	0.955	1	K.VSSLFGILSPSSDLTSSVLWDR.E
SWN:N133_HUMAN	R08	2160	2	1109.1	(+0.2)	2.327	0.254	0.834	1	K.WELDDSEK.H
SWN:N133_HUMAN	R08	6543	2	1466.6	(-0.7)	2.822	0.323	0.942	3	R.YDNL*EMEYL*QK#.R
SWN:N133_HUMAN	R08	6009	2	1482.6	(-0.5)	2.452	0.214	0.743	3	R.YDNL*EM@EYL*QK#.R
SWN:N133_HUMAN	R08	8915	2	2037.2	(+0.5)	2.958	0.454	0.987	3	R.YMTQFADQNFSDFL*FR.W
SWN:N133_HUMAN	R08	7985	3	2409.5	(+1.0)	3.864	0.478	0.998	1	R.YWPSLAGEDTYTEAFVDSGGDK.T
SWN:N133_HUMAN	R10	11673	3	2376.8	(-0.8)	4.367	0.491	1.000	3	R.SDLLSPLLSLGQYLWAASLAEK.Y
SWN:PPIH_HUMAN	R24	7732	2	1131.4	(+0.9)	3.267	0.388	0.989		K.IELFADVVPK.T
SWN:PPIH_HUMAN	R24	5762	2	1033.1	(+0.6)	2.517	0.171	0.796		R.GPFADENFK#.L
SWN:RDHB_HUMAN	R20	2384	2	1587.8	(-0.4)	3.164	0.259	0.931	3	K.EIQTTTGNQQVLVR.K
SWN:RDHB_HUMAN	R20	6626	2	1415.6	(-0.1)	3.839	0.381	0.986	2	R.IVNVSSL*AHHL*GR.I
SWN:RDHB_HUMAN	R20	7654	2	1407.6	(-0.8)	2.741	0.393*	0.104	3	K.L*ANIL*FTQEL*AR.R
SWN:RDHB_HUMAN	R20	2578	2	1223.4	(+0.8)	2.867	0.277	0.930	2	K.VVVVTGANTGIGK#.E
SWN:RDHB_HUMAN	R20	2688	2	1223.4	(+0.8)	2.376	0.165	0.603	2	K.VVVVTGANTGIGK#.E

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SWN:RDHB_HUMAN	R20	4462	2	1223.4	(-0.1)	2.315	0.153	0.604	3	R.IHFHNLQGEK.F
SWN:RDHE_HUMAN	R19	11278	3	2521.1	(+1.0)	3.862	0.518	1.000		R.HIHIPLLVKPLFNLVSWAFFK.T
SWN:RDHE_HUMAN	R19	10286	2	1503.8	(+0.4)	3.033	0.369	0.978		K.LWDISEVMVGLLK.-
SWN:ROAA_HUMAN	R18	8469	2	2245.5	(+0.9)	4.606	0.411	1.000	3	R.EYFGEFGEIEAIEL*PM@DPK#.L
SWN:ROAA_HUMAN	R18	8461	3	2245.5	(+0.4)	4.350	0.377	0.999	3	R.EYFGEFGEIEAIEL*PM@DPK#.L
SWN:ROAA_HUMAN	R18	1080	2	991.1	(+1.0)	2.291	0.290	0.924	3	K.KFHTVSGSK.C
SWN:ROAA_HUMAN	R17	6752	2	1358.5	(-0.8)	2.436	0.286	0.650	3	K.M@FVGGL*SWDTSK#.K
SWN:ROAA_HUMAN	R18	7177	2	1342.5	(+0.4)	3.197	0.449	0.988	3	K.MFVGGL*SWDTSK#.K
SWN:ROAA_HUMAN	R18	6997	2	1456.7	(+0.4)	3.369	0.400	0.623	3	K.MFVGGLSWDTSK.D
SWN:ROAA_HUMAN	R18	6991	2	1478.7	(-0.4)	2.353	0.237	0.047	3	K.MFVGGL*SWDTSK#K#.D
SWN:SA1_HUMAN	R07	2258	2	1066.2	(+0.4)	2.840	0.200	0.928		K.ALQSLYTNR.E
SWN:SA1_HUMAN	R07	2244	2	1078.2	(+0.0)	2.439	0.338	0.903		K.AL*QSL*YTNR.E
SWN:SA1_HUMAN	R07	6623	2	935.0	(+0.9)	2.230	0.429	0.972	7	K.DGIEFAFK#.Y
SWN:SA1_HUMAN	R07	8465	2	1403.6	(+0.0)	2.247	0.253	0.798	1	R.EDVWL*PL*ISYR.N
SWN:SA1_HUMAN	R07	7985	2	1273.5	(+0.1)	2.602	0.334*	0.188	1	R.FAL*TFGL*DQIK#.T
SWN:SA1_HUMAN	R08	9513	3	3210.4	(+0.1)	3.961	0.529	0.998		R.FNHSVEDLLQEGEEADDDDIYNVLSTLK.R
SWN:SA1_HUMAN	R08	6679	2	857.1	(+0.6)	2.317	0.197	0.803	6	R.LELLLQK.R
SWN:SA1_HUMAN	R07	7145	2	1567.8	(+0.9)	4.818	0.554	1.000	5	K.MYSDAFLNDSYLK.Y
SWN:SA1_HUMAN	R07	7135	2	1587.8	(-0.4)	2.457	0.209	0.685	5	K.MYSDAFL*NDSYL*K#.Y
SWN:SA1_HUMAN	R07	8097	2	1559.8	(+0.1)	3.944	0.400	1.000	1	R.REDVWL*PL*ISYR.N
SWN:SA1_HUMAN	R07	8555	2	1758.9	(+0.6)	3.128	0.541	1.000	6	K.SAMQSVVDDWIESYK.Q
SWN:SA1_HUMAN	R07	6833	2	1228.3	(+0.8)	3.116	0.408	0.989		R.SQL*IDFVDR.F
SWN:SA1_HUMAN	R07	6837	2	1222.3	(+0.8)	2.814	0.294	0.964		R.SQLIDFVDR.F
SWN:SA1_HUMAN	R07	5941	2	1272.4	(+0.3)	2.640	0.347	0.956	7	K.YYNDYGDIIK#.E
SWN:SA1_HUMAN	R08	7419	2	1587.8	(-0.3)	2.268	0.263	0.740	5	K.MYSDAFL*NDSYL*K#.Y
SWN:SA2_HUMAN	R07	5327	2	1136.3	(+0.7)	2.586	0.384	0.977	5	K.EYDVAVQAIK.L
SWN:SA2_HUMAN	R07	8103	2	1279.5	(-1.0)	2.632	0.226	0.603	5	R.FAL*TFGL*DQL*K#.T
SWN:SA2_HUMAN	R07	2018	2	1368.5	(-0.2)	2.359	0.180	0.577	5	R.ITAFHNAHDL*SK#.W
SWN:SA2_HUMAN	R07	7095	3	2062.4	(+0.3)	3.994	0.391	0.992	5	R.IVSM@TL*DK#EYDVAVQAIK#.L
SWN:SA2_HUMAN	R07	6153	2	1132.3	(+0.2)	2.352	0.302	0.905	5	R.SQLIDELADK.F
SWN:SDR4_HUMAN	R19	8094	3	2367.7	(+0.9)	4.707	0.456	0.999	1	K.EKDILVPLDLTDTGSHEAATK.A
SWN:SDR4_HUMAN	R19	8140	2	1275.6	(+0.8)	2.250	0.343	0.907	1	R.L*ML*ISMANDL*K#.E
SWN:SDR4_HUMAN	R19	11560	3	3353.8	(+0.3)	4.092	0.390	0.993		R.RPEWELTDMVVVWTGASSGIGEELAYQLSK.L
SWN:SM1A_HUMAN	R06	5582	2	1074.2	(+0.2)	2.315	0.333	0.924	3	R.AATLAQELEK.F
SWN:SM1A_HUMAN	R07	6715	2	1075.3	(+0.9)	2.677	0.360	0.972	3	R.AQVQLQLFK.L
SWN:SM1A_HUMAN	R07	5249	3	1681.7	(+0.8)	4.984	0.417	0.996	1	R.DK#FQETSDEFEAAR.K
SWN:SM1A_HUMAN	R07	5263	2	1681.7	(-0.4)	3.870	0.437	0.991	1	R.DK#FQETSDEFEAAR.K
SWN:SM1A_HUMAN	R07	5261	2	1673.7	(-0.5)	3.567	0.387	0.530	1	R.DKFQETSDEFEAAR.K
SWN:SM1A_HUMAN	R07	6543	2	1515.7	(-0.2)	3.569	0.356	0.789	3	K.EL*NQVMEQL*GDAR.I
SWN:SM1A_HUMAN	R07	4953	2	1351.5	(-0.0)	3.095	0.304	0.312	1	R.FRPMDNLSGGEK.T
SWN:SM1A_HUMAN	R06	5600	2	1066.2	(+0.9)	2.285	0.212	0.834	2	R.HLALNLQEK.S
SWN:SM1A_HUMAN	R07	5541	2	1066.2	(-0.0)	2.616	0.325	0.955	2	R.HLALNLQEK.S
SWN:SM1A_HUMAN	R06	6890	2	1538.8	(+0.2)	3.241	0.270	0.908	1	K.IIDETMAQL*QDL*K#.N
SWN:SM1A_HUMAN	R07	6767	2	1538.8	(+0.2)	4.084	0.354	0.981	1	K.IIDETMAQL*QDL*K#.N
SWN:SM1A_HUMAN	R07	1552	2	967.2	(+0.7)	2.383	0.313*	0.264	3	K.K#YQIAVTK#.V
SWN:SM1A_HUMAN	R06	1564	2	1084.2	(+0.7)	2.555	0.206	0.893	3	K.LEEYITTSK.Q
SWN:SM1A_HUMAN	R07	1750	2	1098.2	(+0.1)	2.838	0.277	0.936	3	K.L*EEYITTSK#.Q
SWN:SM1A_HUMAN	R07	1752	2	1084.2	(+0.6)	2.642	0.246	0.938	3	K.LEEYITTSK.Q
SWN:SM1A_HUMAN	R07	6181	2	1233.4	(+0.1)	2.567	0.196	0.794	2	K.LESELANFGPR.I
SWN:SM1A_HUMAN	R07	6195	2	1245.4	(+0.5)	2.422	0.435	0.980	2	K.L*ESEL*ANFGPR.I
SWN:SM1A_HUMAN	R06	6556	2	1020.2	(+0.5)	2.428	0.102	0.564	2	K.L*IEIENFK#.S
SWN:SM1A_HUMAN	R07	6433	2	1020.2	(+0.6)	2.624	0.163	0.844	2	K.L*IEIENFK#.S
SWN:SM1A_HUMAN	R07	1506	2	1215.4	(+0.2)	2.447	0.223	0.828	1	K.LNEQQSVLQR.I
SWN:SM1A_HUMAN	R07	1502	2	1227.4	(+0.4)	2.221	0.207	0.778	1	K.L*NEQQSVL*QR.I
SWN:SM1A_HUMAN	R07	8155	2	1685.0	(-0.9)	4.140	0.477	0.998	3	R.NFL*VFQGAVESIAM@K#.N
SWN:SM1A_HUMAN	R07	1838	2	1259.4	(+0.6)	2.551	0.358	0.957	3	K.NM@DAIIVDSEK#.T
SWN:SM1A_HUMAN	R07	1626	2	1064.2	(+0.1)	2.607	0.105	0.705	2	K.RLEFENQK.T
SWN:SM1A_HUMAN	R07	1346	2	1296.4	(+0.0)	3.037	0.422	0.542	3	R.SGELAQEYDKR.K
SWN:SM1A_HUMAN	R06	1512	2	1091.2	(+0.5)	2.903	0.358	0.977	2	K.SGVISGGASDLK.A
SWN:SM1A_HUMAN	R07	1702	2	1091.2	(+0.6)	3.028	0.401	0.986	2	K.SGVISGGASDLK.A

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SWN:SM1A_HUMAN	R07	1698	2	1105.2	(+0.3)	2.900	0.427	0.982	2	K.SGVISGGASDL*K#.A
SWN:SM1A_HUMAN	R07	6683	2	1468.6	(-0.6)	3.567	0.480	1.000	2	K.SK#L*ESEL*ANFGPR.I
SWN:SM1A_HUMAN	R07	8731	2	1560.8	(-0.1)	2.655	0.111	0.451	4	K.SNL*M@DAISFVL*GEK#.T
SWN:SM1A_HUMAN	R07	9733	2	1544.8	(+0.2)	2.402	0.389	0.928	4	K.SNL*MDAISFVL*GEK#.T
SWN:SM1A_HUMAN	R06	6500	2	1072.2	(+0.4)	2.545	0.425	0.956	3	R.TAL*FEEISR.S
SWN:SM1A_HUMAN	R07	6391	2	1066.2	(+0.9)	2.860	0.330	0.979	3	R.TALFEEISR.S
SWN:SM1A_HUMAN	R07	6555	2	1193.4	(+0.7)	2.379	0.482	0.985	3	K.TVALDGTFLFQK.S
SWN:SM1A_HUMAN	R07	6557	2	1213.4	(-0.0)	2.300	0.244	0.751	3	K.TVAL*DGTL*FQK#.S
SWN:SM1A_HUMAN	R07	5869	2	1623.8	(-0.8)	2.732	0.187	0.475	4	K.VVQL*HEYSEEL*EK#.L
SWN:SM1A_HUMAN	R07	1116	2	1213.3	(-0.3)	2.769	0.381	0.966	3	K.YSQSDL*EQTK#.T
SWN:SM1A_HUMAN	R08	6863	2	1193.4	(+0.3)	2.756	0.217	0.889	3	K.TVALDGTFLFQK.S
SWN:SMC2_HUMAN	R07	5933	2	1215.3	(-0.0)	3.061	0.282	0.953	1	R.SL*EDAL*AEAQR.V
SWN:SMC2_HUMAN	R07	6457	2	1529.7	(-0.1)	2.760	0.324	0.926	3	K.TIL*EEEITPTIQK#.L
SWN:SMC2_HUMAN	R07	6305	2	1099.2	(+0.2)	2.286	0.328	0.893		R.AL*EEEL*AGL*K#.N
SWN:SMC3_HUMAN	R07	7957	2	1861.1	(+0.8)	2.303	0.454	0.973	1	K.AELGTDLLSQLSLEDQK.R
SWN:SMC3_HUMAN	R07	6091	2	1158.3	(+0.9)	2.706	0.330	0.966	1	K.AILNGIDSINK.V
SWN:SMC3_HUMAN	R07	6657	2	1440.6	(-0.3)	3.420	0.491	1.000	2	K.AL*DQFVNFSEQK#.E
SWN:SMC3_HUMAN	R07	6429	2	1870.0	(+0.8)	4.568	0.483	0.996	1	R.AL*EYTIYNQEL*NETR.A
SWN:SMC3_HUMAN	R07	6417	3	1870.0	(+0.5)	4.503	0.375	0.999	1	R.AL*EYTIYNQEL*NETR.A
SWN:SMC3_HUMAN	R07	6427	2	1858.0	(-0.6)	2.483	0.373	0.935	1	R.ALEYTIYNQELNETR.A
SWN:SMC3_HUMAN	R07	950	2	1049.1	(+0.2)	2.453	0.397	0.959	1	K.DL*EDTEANK#.E
SWN:SMC3_HUMAN	R07	2560	2	1475.5	(+0.5)	3.673	0.511	1.000	1	K.DLQDELAGNSEQR.K
SWN:SMC3_HUMAN	R07	2552	2	1487.5	(-0.2)	3.428	0.322	0.972	1	K.DL*QDEL*AGNSEQR.K
SWN:SMC3_HUMAN	R07	2480	2	1475.5	(-0.4)	3.365	0.216	0.925	1	K.DLQDELAGNSEQR.K
SWN:SMC3_HUMAN	R07	3835	2	1475.5	(+0.3)	3.073	0.434	0.988	1	K.DLQDELAGNSEQR.K
SWN:SMC3_HUMAN	R07	3913	2	1487.5	(-0.1)	2.750	0.442	0.978	1	K.DL*QDEL*AGNSEQR.K
SWN:SMC3_HUMAN	R07	3749	2	1487.5	(+0.1)	2.713	0.423	0.974	1	K.DL*QDEL*AGNSEQR.K
SWN:SMC3_HUMAN	R07	3686	2	1487.5	(-0.2)	2.601	0.328	0.932	1	K.DL*QDEL*AGNSEQR.K
SWN:SMC3_HUMAN	R07	3823	2	1487.5	(-0.2)	2.520	0.451	0.974	1	K.DL*QDEL*AGNSEQR.K
SWN:SMC3_HUMAN	R07	6215	2	1348.5	(+0.9)	2.672	0.391	0.977	2	R.ELGSLPQEAFAE.Y
SWN:SMC3_HUMAN	R07	7501	2	2065.2	(+0.9)	3.896	0.547	1.000	2	R.ETEGGTVLTATTSELEAINK.R
SWN:SMC3_HUMAN	R07	4557	2	1346.5	(-0.0)	3.871	0.432	1.000	1	R.KAEEELGELEAK.L
SWN:SMC3_HUMAN	R07	4581	2	1374.5	(-0.0)	3.483	0.283	0.956	1	R.K#AEEEL*GEL*EAK#.L
SWN:SMC3_HUMAN	R07	4461	2	1374.5	(-0.9)	2.947	0.243	0.725	1	R.K#AEEEL*GEL*EAK#.L
SWN:SMC3_HUMAN	R07	4453	2	1346.5	(-0.2)	2.743	0.325	0.947	1	R.KAEEELGELEAK.L
SWN:SMC3_HUMAN	R07	4635	2	1346.5	(-0.1)	2.523	0.202	0.770	1	R.KAEEELGELEAK.L
SWN:SMC3_HUMAN	R07	2288	2	1057.2	(+0.5)	2.880	0.284	0.971	1	K.KDQYFLDK.K
SWN:SMC3_HUMAN	R07	6505	2	1241.5	(+0.7)	3.544	0.378	0.991	2	R.KYEAQLTFK.Q
SWN:SMC3_HUMAN	R07	6483	2	1263.5	(-0.0)	3.369	0.412	0.999	2	R.K#YEAIQL*TFK#.Q
SWN:SMC3_HUMAN	R07	5621	2	1164.3	(+0.9)	3.218	0.397	0.987	1	R.LALLHEGTGPR.V
SWN:SMC3_HUMAN	R07	1408	2	1094.2	(-0.1)	2.322	0.249	0.815	1	K.L*DQDL*NEVK#.A
SWN:SMC3_HUMAN	R07	6371	2	1667.8	(-0.2)	4.477	0.442	0.997	1	R.L*FYHIVDSDEVSTK#.I
SWN:SMC3_HUMAN	R07	6355	3	1667.8	(+0.8)	3.800	0.494	0.998	1	R.L*FYHIVDSDEVSTK#.I
SWN:SMC3_HUMAN	R07	5827	2	1299.5	(+0.9)	3.450	0.403	0.593	1	R.LPIDKEEVSLR.R
SWN:SMC3_HUMAN	R07	7883	2	1573.9	(+0.9)	4.511	0.416	1.000	1	K.MNLPGEVTFPLPLNK.L
SWN:SMC3_HUMAN	R07	7565	2	1581.7	(+0.3)	3.514	0.413	0.989	1	K.NDVM@NL*L*ESAGFSR.S
SWN:SMC3_HUMAN	R07	8257	2	1565.7	(+0.2)	3.416	0.360	0.977	1	K.NDVMNL*L*ESAGFSR.S
SWN:SMC3_HUMAN	R07	7021	2	1642.8	(+0.0)	4.548	0.401	1.000	2	K.RLDQVEQELNELR.E
SWN:SMC3_HUMAN	R07	2256	2	1201.3	(-0.4)	2.664	0.278	0.928	1	K.RVDALNDEIR.Q
SWN:SMC3_HUMAN	R07	5487	2	1735.8	(-0.6)	3.386	0.362	0.432	2	R.SEDLDNSIDKTEAGIK.E
SWN:SMC3_HUMAN	R07	1362	2	1004.1	(+0.6)	2.523	0.344	0.970	1	K.SLDQAINDK.K
SWN:SMC3_HUMAN	R07	7685	2	1761.0	(-0.2)	4.457	0.596	1.000	1	R.SLQSLEASLHAMESTR.E
SWN:SMC3_HUMAN	R07	2118	2	1122.3	(+0.7)	3.516	0.428	1.000	1	R.SMEVSTQLAR.A
SWN:SMC3_HUMAN	R07	2130	2	1128.3	(+0.7)	3.499	0.306	0.985	1	R.SMEVSTQL*AR.A
SWN:SMC3_HUMAN	R07	2048	2	1045.1	(+0.8)	3.422	0.301	0.979	1	R.VDALNDEIR.Q
SWN:SMC3_HUMAN	R07	2044	2	1051.1	(+0.6)	2.820	0.140	0.864	1	R.VDAL*NDEIR.Q
SWN:SMC3_HUMAN	R07	6265	2	1422.7	(+0.3)	3.782	0.431	1.000	2	K.VSHIDVITAEMAK#.D
SWN:SMC3_HUMAN	R07	5233	2	1438.7	(-0.3)	3.361	0.376	0.973	2	K.VSHIDVITAEM@AK#.D
SWN:SMC3_HUMAN	R07	5863	2	1172.3	(+0.8)	2.224	0.353	0.925	1	K.AIL*NGIDSINK#.V
SWN:SMC4_HUMAN	R06	6898	2	1475.6	(+0.4)	3.567	0.407	0.988	2	K.FTQL*DL*EDVQVR.E
SWN:SMC4_HUMAN	R06	1138	2	1099.2	(+0.3)	2.882	0.445	0.989	3	R.HNTAVSQLTK.A
SWN:SMC4_HUMAN	R06	5148	2	1031.2	(+0.5)	3.133	0.397	0.988	3	R.LGDLGAIDEK.Y
SWN:SMC4_HUMAN	R06	10420	2	1823.1	(+0.8)	2.873	0.442	0.985	3	K.NIAIEFLTLENEIFR.K

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SWN:SNE1_HUMAN	R04	5216	2	1551.7	(+0.9)	2.717	0.255	0.918	8	K.DYQEEIAIAQENK.I
SWN:SNE1_HUMAN	R04	8254	3	2092.3	(+0.4)	3.751	0.240	0.975	5	R.IDSQWTDL*L*TNIPAVQEK#.L
SWN:SNE1_HUMAN	R04	6166	3	2448.6	(+0.3)	3.792	0.369	0.997	4	K.IHPSTSASQEFYEPGLEPSATAK.L
SWN:SNE1_HUMAN	R04	6580	2	1495.7	(-0.4)	2.222	0.198	0.600	6	K.K#EDVSSIVM@STL*R.E
SWN:SNE1_HUMAN	R04	7060	2	1474.7	(+0.9)	2.622	0.243	0.903	4	R.LQQILNFQNDLK.V
SWN:SNE1_HUMAN	R04	7064	2	1500.7	(+0.8)	2.619	0.233	0.860	4	R.L*QQIL*NFQNDL*K#.V
SWN:SNE1_HUMAN	R04	7596	2	1546.8	(+0.4)	2.237	0.229	0.763	6	K.L*TL*L*SNQWQGVIR.R
SWN:SNE1_HUMAN	R04	9846	3	2522.7	(+0.3)	6.301	0.615	0.999	4	K.SAVTSL*L*DGL*NQAFEEVSSQSGGAK#.R
SWN:SNE1_HUMAN	R04	9850	3	2496.7	(+0.8)	5.598	0.563	0.980	4	K.SAVTSLLDGLNQAFEEVSSQSGGAK.R
SWN:SNE1_HUMAN	R05	9710	3	2496.7	(+0.9)	4.902	0.574	0.998	4	K.SAVTSLLDGLNQAFEEVSSQSGGAK.R
SWN:SNE1_HUMAN	R05	9698	3	2522.7	(+0.5)	4.764	0.495	0.996	4	K.SAVTSL*L*DGL*NQAFEEVSSQSGGAK#.R
SWN:SNE1_HUMAN	R06	10018	3	2496.7	(+0.6)	5.246	0.561	0.999	4	K.SAVTSLLDGLNQAFEEVSSQSGGAK.R
SWN:SNE1_HUMAN	R06	10006	3	2522.7	(-0.1)	4.914	0.473	1.000	4	K.SAVTSL*L*DGL*NQAFEEVSSQSGGAK#.R
SWN:SNE1_HUMAN	R04	7890	2	1422.6	(+0.1)	2.561	0.274	0.861	6	K.SWQIL*QGL*VTEK#.I
SWN:SNE1_HUMAN	R04	6302	2	1128.3	(+0.1)	2.929	0.390	0.973	4	K.VL*FTSL*ADNK#.Y
SWN:SNE1_HUMAN	R04	1958	2	1284.4	(-0.3)	2.582	0.305	0.908	4	K.YQDSL*QSISTK#.M
SWN:SNE2_HUMAN	R03	5895	2	1066.3	(-0.2)	2.928	0.314	0.504	2	K.AL*VSNL*ISTK#.E
SWN:SNE2_HUMAN	R04	6226	2	1066.3	(-0.4)	2.320	0.330	0.859	2	K.AL*VSNL*ISTK#.E
SWN:SNE2_HUMAN	R03	8337	2	1473.6	(+0.1)	2.739	0.331	0.935	4	K.ANEFEFVL*SQFK#.D
SWN:SNE2_HUMAN	R03	1942	2	1251.4	(-0.1)	2.293	0.238	0.806	2	K.EL*VQTEIQER.H
SWN:SNE2_HUMAN	R04	2076	2	1251.4	(+0.5)	2.523	0.268	0.929	2	K.EL*VQTEIQER.H
SWN:SNE2_HUMAN	R03	6087	2	1630.7	(+0.1)	2.578	0.367	0.947	3	K.EQSL*NVSQDL*DTIR.S
SWN:SNE2_HUMAN	R03	7533	2	1339.6	(+0.7)	2.277	0.215	0.794	5	R.INIEHAL*TFL*R.N
SWN:SNE2_HUMAN	R04	5380	2	1190.3	(+0.4)	2.709	0.355	0.972	2	K.L*EEDWEINK#.D
SWN:SNE2_HUMAN	R03	5663	2	1518.7	(-0.4)	3.473	0.218	0.923	2	K.L*EEIQQIL*QK#.H
SWN:SNE2_HUMAN	R03	6249	2	1703.9	(-0.1)	3.569	0.410	0.981	4	K.L*L*ENVTQEQL*L*K#.V
SWN:SNE2_HUMAN	R04	6984	2	1264.4	(-0.2)	2.288	0.266	0.811	7	R.L*NTWVVFNEK#.N
SWN:SNE2_HUMAN	R03	5275	3	2112.2	(+0.1)	4.719	0.391	0.999	2	K.L*SETHGYGVQEEFTEENK#.L
SWN:SNE2_HUMAN	R04	5574	3	2112.2	(+0.0)	5.700	0.450	1.000	2	K.L*SETHGYGVQEEFTEENK#.L
SWN:SNE2_HUMAN	R05	5690	3	2112.2	(+0.4)	4.066	0.347	0.989	2	K.L*SETHGYGVQEEFTEENK#.L
SWN:SNE2_HUMAN	R03	5687	2	1098.3	(-0.1)	2.462	0.356	0.944	10	R.L*TQL*EL*INK#.Q
SWN:SNE2_HUMAN	R04	6040	2	1098.3	(-0.1)	2.724	0.165	0.790	10	R.L*TQL*EL*INK#.Q
SWN:SNE2_HUMAN	R03	5137	2	1340.5	(+0.2)	2.928	0.336	0.955	2	R.NEL*L*L*NQEVNK#.G
SWN:SNE2_HUMAN	R04	5412	2	1340.5	(-0.1)	2.759	0.271	0.902	2	R.NEL*L*L*NQEVNK#.G
SWN:SNE2_HUMAN	R04	1660	2	1268.4	(+0.1)	2.971	0.157	0.789	2	K.NIQDVQSQISK#.I
SWN:SNE2_HUMAN	R03	9539	3	2431.8	(+0.8)	4.138	0.345	0.996	2	K.NLLGELNPSIPLLPDDILSQIR.K
SWN:SNE2_HUMAN	R05	9628	3	2431.8	(+0.2)	3.909	0.393	0.996	2	K.NLLGELNPSIPLLPDDILSQIR.K
SWN:SNE2_HUMAN	R03	7237	2	1471.6	(-0.2)	2.884	0.124	0.653	3	K.SEQFEEL*QSIL*K#.K
SWN:SNE2_HUMAN	R04	7508	2	1471.6	(+0.5)	2.464	0.125	0.551	3	K.SEQFEEL*QSIL*K#.K
SWN:SNE2_HUMAN	R03	7531	2	1670.0	(+0.0)	2.369	0.115	0.323	2	K.SQL*QQPL*L*INL*EIK#.H
SWN:SNE2_HUMAN	R03	8293	3	3456.7	(-0.8)	3.773	0.382	0.876	3	K.SSEPEHQEAL*QPVNL*SEL*ESIVTERPQFSR.Q
SWN:SNE2_HUMAN	R04	8542	3	3456.7	(-0.2)	3.872	0.387	0.966	3	K.SSEPEHQEAL*QPVNL*SEL*ESIVTERPQFSR.Q
SWN:SNE2_HUMAN	R04	4142	2	1266.3	(-0.1)	2.739	0.400	0.977	2	K.TEDYYENL*GR.A
SWN:SNE2_HUMAN	R04	4236	2	1266.3	(+0.0)	2.724	0.425	0.980	2	K.TEDYYENL*GR.A
SWN:SNE2_HUMAN	R03	5503	3	2149.3	(+0.0)	4.839	0.395	0.999	3	R.TL*SHHASTVQM@AL*EDSEQK#.H
SWN:SNE2_HUMAN	R03	5649	3	2133.3	(+0.3)	3.918	0.365	0.998	3	R.TL*SHHASTVQMAL*EDSEQK#.H
SWN:SNE2_HUMAN	R03	8591	3	2949.2	(-0.9)	3.819	0.447	0.995	2	K.TL*TDISNQWDNTL*HL*ASTYL*SHQEK#.L
SWN:SUM2_HUMAN	R19	2450	2	1225.4	(+0.4)	2.456	0.307	0.940	3	R.FLMGTNSPDSR.D
SWN:SUM2_HUMAN	R19	7020	2	1478.6	(+0.8)	3.427	0.505	1.000	3	R.LPTEEEWEFAAR.G
SWN:SUM2_HUMAN	R19	5436	2	1582.7	(-0.4)	3.877	0.451	1.000	2	R.MGNTPDSASDNLGFR.C
SWN:SUM2_HUMAN	R20	8756	2	1257.5	(+0.9)	2.870	0.418	0.980	3	K.SVLWWLPVEK.A
SWN:SUM2_HUMAN	R20	4712	2	1225.4	(+0.6)	2.550	0.320	0.935	3	R.FLMGTNSPDSR.D
SWN:TXN5_HUMAN	R16	8200	2	2194.5	(-0.6)	2.457	0.384	0.505	5	K.ALAPTWEQLALGLEHSETVK.I
SWN:TXN5_HUMAN	R16	1136	2	1152.2	(+0.7)	2.230	0.208	0.809	5	R.EYVESQLQR.T
SWN:UXD2_HUMAN	R14	8743	2	1704.1	(-0.0)	3.910	0.552	1.000		-.ML*WFQGAIPAAIATAK#.R
SWN:UXD2_HUMAN	R14	7161	3	2279.4	(+0.7)	3.860	0.354	0.997	1	R.LPDGSSFTNQFPSDAPLEEAR.Q
SWN:XRN2_HUMAN	R09	6902	2	1309.5	(+0.6)	2.561	0.380	0.971	2	R.GVGAPELLPWNR.M
SWN:XRN2_HUMAN	R09	1280	2	958.1	(+0.6)	2.275	0.168	0.062	3	R.VREEILAK.G
SWN:XRN2_HUMAN	R09	5880	2	994.2	(+0.5)	2.248	0.226	0.114	3	R.L*FSIVRPR.R



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GP:AB043584_1	S05	6988	2	1145.3	(+0.9)	2.530	0.405	0.968	1	K.DPFL*GFTDAR.Q
GP:AB043584_1	S05	6970	2	1139.3	(+0.5)	2.338	0.346	0.937	1	K.DPFLGFTDAR.Q
GP:AB043584_1	S05	8204	2	1704.9	(+0.5)	2.201	0.320	0.856	1	R.GGGFAPGTEPFPGLFPR.K
GP:AB088099_1	S04	6033	3	2356.6	(+0.7)	6.146	0.515	1.000	2	R.AHEVGAQGGPPVAQVEQDLPISE
GP:AB088099_1	S04	6017	3	2362.6	(+0.6)	5.551	0.547	1.000	2	R.AHEVGAQGGPPVAQVEQDL*PISE
GP:AB088099_1	S05	6996	3	2356.6	(+0.2)	5.080	0.560	1.000	2	R.AHEVGAQGGPPVAQVEQDLPISE
GP:AB088099_1	S04	4211	2	2249.4	(-0.7)	2.562	0.363	0.652	2	K.L*EPSTSTDQPVTPPTSQATR.G
GP:AB088099_1	S04	4199	2	2243.4	(-0.5)	2.387	0.407	0.894	2	K.LEPSTSTDQPVTPPTSQATR.G
GP:AB088099_1	S04	5183	3	2632.9	(+0.5)	4.135	0.487	0.998	2	K.TPEPVPTAPEPHPTTSTDQPVTPK#.L
GP:AB088099_1	S05	5744	3	2632.9	(+0.6)	3.775	0.451	0.996	2	K.TPEPVPTAPEPHPTTSTDQPVTPK#.L
GP:AB088099_1	S06	5718	3	2624.9	(+0.4)	3.715	0.461	0.998	2	K.TPEPVPTAPEPHPTTSTDQPVTPK#.L
GP:AB088099_1	S03	5079	2	1168.3	(-0.2)	2.265	0.383	0.792	2	K.TPETL*VPTAPK#.L
GP:AB088099_1	S04	4891	2	1154.3	(+1.0)	2.998	0.400	0.976	2	K.TPETLVPTAPK.L
GP:AB088099_1	S04	4879	2	1168.3	(+0.3)	2.271	0.405	0.822	2	K.TPETL*VPTAPK#.L
GP:AB088099_1	S06	5332	2	1154.3	(+0.9)	2.750	0.373	0.966	2	K.TPETLVPTAPK.L
GP:AB088099_1	S04	5629	3	3370.6	(-0.5)	3.731	0.414	0.988	2	K.TPETVVPTAPEL*QPSTSTDQPVTPPTSQATR.G
GP:AB088099_1	S07	5384	2	1154.3	(+0.6)	2.574	0.346	0.950	2	K.TPETLVPTAPK.L
GP:AF112222_1	S05	1776	2	1304.4	(+0.6)	2.775	0.384	0.422	2	K.FK#QESTVATER.Q
GP:AF112222_1	S05	1774	2	1296.4	(+0.8)	2.483	0.266	0.152	2	K.FKQESTVATER.Q
GP:AF112222_1	S05	5608	2	1100.2	(+0.6)	2.743	0.340	0.932	2	R.IEFAEQINK#.M
GP:AF112222_1	S05	5674	2	1016.2	(-0.3)	2.672	0.325	0.892	2	R.L*L*AL*SGPGGGR.G
GP:AF112222_1	S10	5926	2	998.2	(+0.5)	2.405	0.258	0.862	2	R.LLALSGPGGGR.G
GP:AF112222_1	S14	5726	2	1016.2	(+0.2)	2.358	0.334	0.850	2	R.L*L*AL*SGPGGGR.G
GP:AF112222_1	S05	6840	2	1875.2	(+0.8)	3.901	0.575	1.000	1	K.LTEVPVEPVLTVHPESK.S
GP:AF112222_1	S05	5888	2	1256.4	(-0.1)	2.375	0.234	0.523	2	R.RIEFAEQINK#.M
GP:AF112222_1	S15	5724	2	998.2	(+0.7)	2.540	0.156	0.710	2	R.LLALSGPGGGR.G
GP:AF113534_1	S07	4392	2	1176.4	(+0.5)	2.531	0.333	0.952	1	R.KYVSQYYPK.L
GP:AF113534_1	S07	4470	2	1176.4	(+0.2)	2.399	0.225	0.721	1	R.KYVSQYYPK.L
GP:AF113534_1	S07	4362	2	1192.4	(+0.4)	2.360	0.345	0.895	1	R.K#YVSQYYPK#.L
GP:AF113534_1	S06	4878	2	1174.3	(-0.1)	2.444	0.353	0.809	1	K.NGWME@EQISGK#.G
GP:AF113534_1	S07	4816	2	1174.3	(+0.4)	2.635	0.263	0.846	1	K.NGWME@EQISGK#.G
GP:AF113534_1	S06	7562	2	1614.8	(-0.1)	2.510	0.202	0.549		K.TIPSWATL*SASQL*AR.A
GP:AF113534_1	S07	7638	2	1602.8	(+0.8)	2.438	0.349	0.922		K.TIPSWATLSASQLAR.A
GP:AF113534_1	S12	7460	2	1602.8	(+0.4)	2.981	0.366	0.963		K.TIPSWATLSASQLAR.A
GP:AF113534_1	S11	6196	2	1007.1	(+0.5)	2.248	0.126	0.361	1	K.YPSLELER.R
GP:AF113534_1	S13	7806	2	1602.8	(+0.5)	2.732	0.495	0.979		K.TIPSWATLSASQLAR.A
GP:AF152961_1	S04	4437	2	1270.4	(+0.9)	3.050	0.414	0.981		R.DDLYAEQMER.E
GP:AF152961_1	S04	4421	2	1276.4	(+0.7)	2.667	0.382	0.968		R.DDL*YAEQMER.E
GP:AF152961_1	S05	4792	2	1276.4	(+0.7)	2.215	0.376	0.940		R.DDL*YAEQMER.E
GP:AF152961_1	S08	5068	2	1270.4	(+0.4)	2.920	0.398	0.977		R.DDLYAEQMER.E
GP:AF152961_1	S05	5826	2	1116.2	(+0.5)	2.405	0.276	0.875	1	R.DL*GFNGAPYR.S
GP:AF152961_1	S07	5878	2	1116.2	(+0.9)	2.249	0.166	0.627	1	R.DL*GFNGAPYR.S
GP:AF152961_1	S08	6034	2	1116.2	(+0.6)	2.467	0.196	0.799	1	R.DL*GFNGAPYR.S
GP:AF152961_1	S09	6140	2	1116.2	(+0.5)	2.350	0.286	0.894	1	R.DL*GFNGAPYR.S
GP:AF152961_1	S10	6044	2	1110.2	(+0.5)	2.290	0.205	0.752	1	R.DLGFNGAPYR.S
GP:AF152961_1	S11	5964	2	1116.2	(+0.8)	2.560	0.262	0.905	1	R.DL*GFNGAPYR.S
GP:AF152961_1	S11	5954	2	1110.2	(+0.4)	2.321	0.231	0.815	1	R.DLGFNGAPYR.S
GP:AF152961_1	S14	7948	2	1295.4	(+0.7)	2.218	0.111	0.207		K.EEELFEVFPFR.D
GP:AF152961_1	S04	5547	2	1414.6	(+0.6)	3.397	0.310	0.262		R.GDK#VDIL*YNNIK#.H
GP:AF152961_1	S04	5645	2	1414.6	(+0.1)	2.988	0.244	0.059		R.GDK#VDIL*YNNIK#.H
GP:AF152961_1	S05	6344	2	1392.6	(+0.9)	2.362	0.280	0.132		R.GDKVDILYNNIK.H
GP:AF152961_1	S09	6646	2	1392.6	(+1.0)	2.782	0.301	0.230		R.GDKVDILYNNIK.H
GP:AF152961_1	S03	5689	2	1172.3	(+0.9)	2.604	0.269	0.917		K.QDSLVINLNR.S
GP:AF152961_1	S04	5573	2	1092.3	(+0.9)	3.099	0.221	0.943		K.VDILYNNIK.H
GP:AF152961_1	S04	5579	2	1106.3	(+0.4)	2.373	0.298	0.851		K.VDIL*YNNIK#.H
GP:AF152961_1	S05	6226	2	1092.3	(+0.8)	2.916	0.276	0.954		K.VDILYNNIK.H
GP:AF152961_1	S06	6174	2	1092.3	(+0.9)	2.207	0.365	0.940		K.VDILYNNIK.H
GP:AF152961_1	S08	6404	2	1092.3	(+0.9)	2.888	0.248	0.941		K.VDILYNNIK.H
GP:AF152961_1	S09	6530	2	1092.3	(+0.6)	2.697	0.326	0.959		K.VDILYNNIK.H
GP:AF152961_1	S10	6434	2	1092.3	(+0.4)	2.394	0.335	0.943		K.VDILYNNIK.H
GP:AF152961_1	S11	6330	2	1092.3	(+0.5)	2.542	0.265	0.917		K.VDILYNNIK.H

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GP:AF152961_1	S16	6186	2	1092.3	(+0.3)	2.530	0.412	0.942		K.VDILYNNIK.H
GP:AF152961_1	S01	6100	2	1440.6	(-0.1)	3.263	0.369	0.902	1	K.YTEGVQSL*NWTK#.I
GP:AF152961_1	S03	5621	2	1426.6	(+0.1)	3.799	0.467	1.000	1	K.YTEGVQSLNWT.K.I
GP:AF152961_1	S04	5565	2	1426.6	(+0.1)	3.352	0.430	0.963	1	K.YTEGVQSLNWT.K.I
GP:AF152961_1	S04	5517	2	1440.6	(+1.0)	3.021	0.388	0.949	1	K.YTEGVQSL*NWTK#.I
GP:AF152961_1	S04	5569	2	1440.6	(-0.3)	2.620	0.342	0.803	1	K.YTEGVQSL*NWTK#.I
GP:AF152961_1	S05	6242	2	1440.6	(-0.1)	3.193	0.445	0.928	1	K.YTEGVQSL*NWTK#.I
GP:AF152961_1	S06	6178	2	1426.6	(-0.1)	2.620	0.377	0.915	1	K.YTEGVQSLNWT.K.I
GP:AF152961_1	S06	6194	2	1440.6	(-0.8)	2.226	0.267	0.205	1	K.YTEGVQSL*NWTK#.I
GP:AF152961_1	S07	6268	2	1426.6	(-0.6)	2.205	0.279	0.687	1	K.YTEGVQSLNWT.K.I
GP:AF152961_1	S08	6406	2	1426.6	(-0.1)	2.910	0.398	0.943	1	K.YTEGVQSLNWT.K.I
GP:AF152961_1	S08	6410	2	1440.6	(-0.7)	2.267	0.325	0.344	1	K.YTEGVQSL*NWTK#.I
GP:AF152961_1	S10	6442	2	1440.6	(+0.4)	2.252	0.348	0.843	1	K.YTEGVQSL*NWTK#.I
GP:AF152961_1	S11	6328	2	1426.6	(-0.1)	2.350	0.283	0.752	1	K.YTEGVQSLNWT.K.I
GP:AF152961_1	S12	6102	2	1426.6	(+0.0)	2.762	0.406	0.939	1	K.YTEGVQSLNWT.K.I
GP:AF152961_1	S17	6468	2	1092.3	(-0.4)	2.456	0.305	0.865		K.VDILYNNIK.H
GP:AF385437_1	S05	7984	2	1125.4	(+0.8)	2.262	0.119	0.521	1	K.LLYTFPGWK.V
GP:AF385437_1	S06	7802	2	1125.4	(+1.0)	2.535	0.164	0.787	1	K.LLYTFPGWK.V
GP:AF385437_1	S08	8050	2	1125.4	(+0.9)	2.290	0.291	0.901	1	K.LLYTFPGWK.V
GP:AF385437_1	S04	7483	2	1613.0	(+0.8)	2.970	0.466	0.979	1	K.SAPFFIPTIPGLVPR.Y
GP:AF385437_1	S05	9132	2	1613.0	(-0.6)	2.291	0.400	0.874	1	K.SAPFFIPTIPGLVPR.Y
GP:AF385437_1	S07	9142	2	1613.0	(+0.1)	2.630	0.370	0.893	1	K.SAPFFIPTIPGLVPR.Y
GP:AF385437_1	S07	9144	2	1619.0	(-0.4)	2.427	0.256	0.667	1	K.SAPFFIPTIPGL*VPR.Y
GP:AF385437_1	S08	9350	2	1613.0	(+0.3)	2.569	0.407	0.913	1	K.SAPFFIPTIPGLVPR.Y
GP:AF385437_1	S08	9360	2	1619.0	(+0.7)	2.366	0.314	0.882	1	K.SAPFFIPTIPGL*VPR.Y
GP:AF385437_1	S09	9318	2	1613.0	(-0.2)	2.348	0.410	0.892	1	K.SAPFFIPTIPGLVPR.Y
GP:AF385437_1	S10	9382	2	1613.0	(+0.5)	2.662	0.421	0.966	1	K.SAPFFIPTIPGLVPR.Y
GP:AF385437_1	S11	9226	2	1613.0	(+0.5)	2.365	0.351	0.915	1	K.SAPFFIPTIPGLVPR.Y
GP:AF385437_1	S14	9470	2	1613.0	(+0.7)	2.920	0.483	0.981	1	K.SAPFFIPTIPGLVPR.Y
GP:AF385437_1	S06	7100	2	1047.2	(+0.7)	2.265	0.330	0.918	1	R.TASAL*FAGFR.A
GP:AF385437_1	S07	6950	2	1051.2	(+0.7)	2.806	0.404	0.977	1	K.YDTALNLLK.E
GP:AF385437_1	S16	9064	2	1613.0	(+0.4)	2.304	0.315	0.872	1	K.SAPFFIPTIPGLVPR.Y
GP:AK023702_1	S07	6918	2	1283.5	(+0.7)	3.165	0.300	0.956		R.GLEALLADPQQK.I
GP:AK023702_1	S06	8118	2	1544.9	(+0.7)	3.421	0.508	1.000		R.ILSVQGTEPLVLFK.E
GP:AK023702_1	S06	8112	2	1570.9	(-0.1)	2.868	0.278	0.727		R.IL*SVQGTEPL*VL*FK#.E
GP:AK023702_1	S07	8164	2	1544.9	(+0.8)	3.104	0.439	0.979		R.ILSVQGTEPLVLFK.E
GP:AK023702_1	S07	8160	2	1570.9	(-0.0)	2.913	0.332	0.819		R.IL*SVQGTEPL*VL*FK#.E
GP:AK023702_1	S12	8012	2	1544.9	(+1.0)	3.430	0.423	0.981		R.ILSVQGTEPLVLFK.E
GP:AK023702_1	S12	8008	2	1570.9	(-0.4)	2.906	0.298	0.770		R.IL*SVQGTEPL*VL*FK#.E
GP:AK023702_1	S13	8344	2	1544.9	(+0.7)	3.332	0.437	0.982		R.ILSVQGTEPLVLFK.E
GP:AK023702_1	S15	8092	2	1544.9	(+0.6)	3.308	0.485	1.000		R.ILSVQGTEPLVLFK.E
GP:AK023702_1	S15	8088	2	1570.9	(-0.4)	2.539	0.188	0.372		R.IL*SVQGTEPL*VL*FK#.E
GP:AK023702_1	S16	8068	2	1544.9	(-0.4)	2.977	0.289	0.870		R.ILSVQGTEPLVLFK.E
GP:AK023702_1	S16	8074	2	1570.9	(-0.1)	2.900	0.210	0.581		R.IL*SVQGTEPL*VL*FK#.E
GP:AK023702_1	S17	8274	2	1570.9	(+0.4)	3.079	0.419	0.954		R.IL*SVQGTEPL*VL*FK#.E
GP:AK023702_1	S06	5680	2	1360.5	(+0.2)	3.011	0.364	0.941		R.IWNNEDVNLDK.V
GP:AK023702_1	S07	5738	2	1360.5	(+0.1)	2.270	0.323	0.814		R.IWNNEDVNLDK.V
GP:AK023702_1	S12	5566	2	1374.5	(+0.3)	2.580	0.314	0.768		R.IWNNEDVNL*DK#.V
GP:AK023702_1	S12	5576	2	1360.5	(+0.2)	2.345	0.296	0.792		R.IWNNEDVNLDK.V
GP:AK023702_1	S15	5754	2	1374.5	(+0.1)	2.267	0.197	0.344		R.IWNNEDVNL*DK#.V
GP:AK023702_1	S07	5332	2	1245.3	(+0.3)	2.752	0.401	0.941		K.TDQFL*VTDSGR.T
GP:AK023702_1	S07	5334	2	1239.3	(+0.8)	2.516	0.391	0.962		K.TDQFLVTDGR.T
GP:AK023702_1	S11	5388	2	1239.3	(+0.9)	2.325	0.232	0.798		K.TDQFLVTDGR.T
GP:AK023702_1	S07	7292	2	1593.8	(-0.6)	2.679	0.284	0.813		K.YTLLLGQDENSVIK.S
GP:AK023702_1	S17	8270	2	1544.9	(+0.2)	2.999	0.461	0.958		R.ILSVQGTEPLVLFK.E
GP:AK093060_1	S02	6076	2	1359.5	(+0.4)	2.712	0.268	0.911	3	R.DLDLDSIIAEVR.A
GP:AK093060_1	S03	5741	2	1359.5	(+0.6)	3.175	0.196	0.885	3	R.DLDLDSIIAEVR.A
GP:AK093060_1	S05	6466	2	1359.5	(+0.7)	2.702	0.233	0.804	3	R.DLDLDSIIAEVR.A
GP:AK093060_1	S06	6412	2	1359.5	(+0.5)	2.241	0.213	0.614	3	R.DLDLDSIIAEVR.A
GP:AK093060_1	S13	6770	2	1359.5	(+0.7)	2.574	0.133	0.533	3	R.DLDLDSIIAEVR.A
GP:AK093060_1	S03	5175	2	1477.7	(+0.2)	3.068	0.168*	0.247	5	R.FLEQQNQVLETK.W
GP:AK093060_1	S15	5538	2	1477.7	(+0.3)	2.971	0.195*	0.214	5	R.FLEQQNQVLETK.W

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GP:AL833978_1	S07	4906	2	1087.2	(+0.5)	3.174	0.362	0.946		K.GASGSFVVVQK#.S
GP:AL833978_1	S10	5166	2	1079.2	(+0.5)	2.603	0.177	0.782		K.GASGSFVVVQK.S
GP:AL833978_1	S06	7958	2	1292.5	(+0.4)	2.204	0.441	0.960		K.L*EDVL*PL*AFTR.L
GP:AL833978_1	S10	8074	2	1274.5	(+0.4)	3.022	0.412	0.979		K.LEDVLPLAFTR.L
GP:AL833978_1	S10	8082	2	1292.5	(-0.3)	2.652	0.323	0.887		K.L*EDVL*PL*AFTR.L
GP:AL833978_1	S11	8030	2	1292.5	(+0.0)	2.315	0.300	0.790		K.L*EDVL*PL*AFTR.L
GP:AL833978_1	S11	8024	2	1274.5	(+0.6)	2.251	0.386	0.927		K.LEDVLPLAFTR.L
GP:AL833978_1	S19	5020	2	1079.2	(-0.6)	2.324	0.187	0.511		K.GASGSFVVVQK.S
GP:AL834470_1	S05	7220	2	1035.2	(-0.5)	2.235	0.135	0.366		K.FPTLWSGAR.S
GP:AL834470_1	S05	7150	2	1041.2	(+1.0)	2.227	0.195	0.730		K.FPTL*WSGAR.S
GP:AL834470_1	S07	7188	2	1035.2	(+0.1)	2.690	0.365	0.934		K.FPTLWSGAR.S
GP:AL834470_1	S05	5626	2	1126.3	(+0.7)	2.702	0.361	0.965		R.YGGQPLFSEK.F
GP:AL834470_1	S08	5864	2	1126.3	(-0.1)	2.831	0.449	0.948		R.YGGQPLFSEK.F
GP:AL834470_1	S09	5932	2	1126.3	(+0.2)	2.919	0.447	0.962		R.YGGQPLFSEK.F
GP:AL834470_1	S05	6766	2	1636.9	(+0.6)	3.040	0.359	0.964		R.YNVL*GAETVL*NQM@R.M
GP:AL834470_1	S12	7498	2	1608.9	(-0.2)	2.655	0.305	0.838		R.YNVLGAETVLNQM.R
GP:D87716_1	S06	7108	2	1028.2	(+0.3)	2.852	0.198	0.831	1	R.LLNVWQVR.S
GP:D87716_1	S10	7300	2	1028.2	(+0.3)	2.221	0.105	0.257	1	R.LLNVWQVR.S
GP:D87716_1	S12	7020	2	1028.2	(-0.2)	2.996	0.269	0.920	1	R.LLNVWQVR.S
GP:D87716_1	S13	7410	2	1028.2	(+0.6)	2.783	0.327	0.968	1	R.LLNVWQVR.S
GP:D87716_1	S14	7360	2	1028.2	(+0.1)	2.416	0.114	0.401	1	R.LLNVWQVR.S
GP:D87716_1	S07	6874	2	909.1	(+0.3)	2.296	0.223	0.600	1	K.L*WVL*ETK#.E
GP:D87716_1	S16	7106	2	1028.2	(+0.4)	3.129	0.254	0.963	1	R.LLNVWQVR.S
GP:Y19208_1	S01	5900	2	1193.3	(-0.3)	2.712	0.296*	0.157	2	R.ATAENEFVALK.K
GP:Y19208_1	S02	5850	2	1193.3	(+0.9)	2.998	0.318*	0.429	2	R.ATAENEFVALK.K
GP:Y19208_1	S03	5515	2	1193.3	(+0.8)	2.743	0.375*	0.304	2	R.ATAENEFVALK.K
GP:Y19208_1	S01	5624	2	1321.5	(+0.8)	2.331	0.218*	0.003	2	R.ATAENEFVALKK.D
GP:Y19208_1	S02	5650	2	1321.5	(+0.3)	2.617	0.336*	0.003	2	R.ATAENEFVALKK.D
GP:Y19208_1	S03	5319	2	1321.5	(+1.0)	2.603	0.296*	0.006	2	R.ATAENEFVALKK.D
GPN:AF227948_1	S04	7201	3	2015.1	(+0.9)	3.789	0.321	0.985	2	R.FDEFDEAIDEAIEDDIK.E
GPN:AF227948_1	S06	7138	2	1514.7	(+0.1)	3.862	0.359	0.959	3	K.LEEQLQDLVDALK.K
GPN:AK010310_1	S10	6310	2	1175.3	(+0.4)	2.846	0.432	0.955	3	R.DIIGL*AETGSGK#.T
GPN:AK010310_1	S10	6542	2	1158.3	(-0.1)	2.480	0.265	0.778	5	R.SIL*L*ATDVASR.G
GPN:AK010310_1	S10	10768	2	1926.3	(+0.0)	3.559	0.428	0.961	3	K.TGAFALPILNALLETPQR.L
GPN:AK010310_1	S10	5616	2	1118.2	(-0.1)	2.494	0.342	0.903	5	K.YL*VMDEADR.I
GPN:AK010310_1	S10	2344	2	1083.2	(-0.2)	2.411	0.295	0.844	5	R.LIDHLENTK.G
GPN:AK014456_1	S09	7758	2	1707.0	(+0.5)	3.191	0.524	1.000	3	K.DLVLGSPGVLQGIKPGK.C
GPN:AK014456_1	S08	8606	2	1552.7	(+0.4)	3.182	0.508	1.000	3	R.FQQAQVDAVEEFLR.R
GPN:AK014456_1	S09	8548	2	1552.7	(-0.8)	2.484	0.342	0.616	3	R.FQQAQVDAVEEFLR.R
GPN:AK014456_1	S10	8534	2	1552.7	(+0.6)	2.326	0.273	0.838	3	R.FQQAQVDAVEEFLR.R
GPN:AK074420_1	S14	5852	2	2238.3	(-1.0)	3.751	0.522	1.000		R.AVYDEQGTVDSPVLTQDR.D
GPN:AK074420_1	S14	8214	3	3245.4	(+0.1)	4.395	0.562	1.000		R.AVYDEQGTVDSPVLTQDRDWEAYWR.L
GPN:AK074420_1	S14	7618	2	1441.6	(-0.4)	2.928	0.346	0.856	1	K.EMDNFL*AQMEAK#.Y
GPN:AK074420_1	S14	7600	2	1427.6	(-0.2)	2.465	0.341	0.867	1	K.EMDNFLAQMEAK.Y
GPN:AK074420_1	S13	5232	2	1091.2	(+0.6)	2.908	0.204	0.903		K.GSEELADIK.Q
GPN:AK074420_1	S14	4892	2	1091.2	(+0.6)	2.562	0.270	0.913		K.GSEELADIK.Q
GPN:AK074420_1	S14	4956	2	1105.2	(+0.1)	2.548	0.203	0.537		K.GSEEL*ADIK#.Q
GPN:AK074420_1	S14	5080	2	1091.2	(+0.6)	2.538	0.295	0.927		K.GSEELADIK.Q
GPN:AK074420_1	S14	7588	2	1307.5	(+0.3)	4.005	0.392	1.000		K.ISL*EDIQAFEK#.T
GPN:AK074420_1	S14	6212	2	1403.6	(-0.1)	4.029	0.506	1.000	1	R.KELGLDEGVDSLK.A
GPN:AK074420_1	S14	7368	2	1443.6	(-0.0)	3.559	0.524	1.000		K.K#ISL*EDIQAFEK#.T
GPN:AK074420_1	S14	8680	2	2186.4	(+0.6)	4.136	0.514	1.000	1	R.NIIQQAIDAGEVPSYNAFVK#.E
GPN:AK074420_1	S14	8676	2	2178.4	(+0.8)	3.919	0.482	1.000	1	R.NIIQQAIDAGEVPSYNAFVK.E
GPN:AK074420_1	S14	8704	2	2178.4	(-0.7)	2.609	0.340	0.619	1	R.NIIQQAIDAGEVPSYNAFVK.E
GPN:AK074420_1	S14	8434	2	2178.4	(+0.4)	2.590	0.406	0.959	1	R.NIIQQAIDAGEVPSYNAFVK.E
GPN:AK074420_1	S14	2360	2	1057.2	(+0.7)	2.433	0.121	0.632		K.VSL*QVHPDR.V
GPN:AY363225_1	S12	7198	2	1714.8	(-0.3)	3.650	0.410	0.960		R.GFAFVTFDDHDTVDK.I
GPN:AY363225_1	S13	7626	2	1722.8	(+0.8)	3.454	0.450	0.966		R.GFAFVTFDDHDTVDK#.I

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GPN:AY363225_1	S13	7704	2	1722.8	(+0.2)	2.769	0.380	0.842		R.GFAFVTFDDHDTVDK#.I
GPN:AY363225_1	S12	6566	2	1898.1	(+0.8)	4.328	0.493	1.000		K.IFVGGIK#EDTEEYNL*R.D
GPN:AY363225_1	S12	6562	2	1884.1	(-0.5)	4.093	0.455	1.000		K.IFVGGIKEDTEEYNL.R.D
GPN:AY363225_1	S14	7652	2	1714.8	(+0.9)	2.719	0.203	0.680		R.GFAFVTFDDHDTVDK.I
GPN:BC000131_1	S05	5822	2	1100.2	(+0.5)	2.662	0.286	0.942	4	R.DL*IDNSFN.R.Y
GPN:BC000131_1	S05	5800	2	1094.2	(+0.6)	2.654	0.358	0.966	4	R.DLIDNSFN.R.Y
GPN:BC000131_1	S10	6028	2	1094.2	(+0.7)	2.400	0.289	0.901	4	R.DLIDNSFN.R.Y
GPN:BC000131_1	S10	8658	2	1654.9	(+0.8)	4.484	0.620	1.000	4	R.ILDPEGLALGAVIASSK.K
GPN:BC000131_1	S10	7332	2	1747.9	(-0.4)	2.407	0.368	0.861	4	K.SDDDGFIVPIEDPAK.H
GPN:BC000131_1	S04	6779	3	2390.5	(+0.4)	3.996	0.375	0.995	4	R.YTFNEDEGELPEWVFVQEEK.Q
GPN:BC000131_1	S11	8514	2	1654.9	(+0.7)	3.554	0.533	1.000	4	R.ILDPEGLALGAVIASSK.K
GPN:BC000488_1	S06	5790	2	1067.2	(+0.4)	2.469	0.248	0.892	1	R.LSESQLSFR.R
GPN:BC000488_1	S07	5854	2	1067.2	(+0.4)	2.624	0.337	0.959	1	R.LSESQLSFR.R
GPN:BC000488_1	S08	6028	2	1067.2	(+0.8)	2.832	0.302	0.958	1	R.LSESQLSFR.R
GPN:BC000488_1	S10	6052	2	1067.2	(+0.7)	2.846	0.340	0.969	1	R.LSESQLSFR.R
GPN:BC000488_1	S12	5678	2	1067.2	(+0.8)	3.305	0.381	0.982	1	R.LSESQLSFR.R
GPN:BC000488_1	S15	5880	2	1067.2	(+0.8)	3.600	0.362	0.984	1	R.LSESQLSFR.R
GPN:BC000488_1	S13	6034	3	2466.6	(+0.8)	3.855	0.511	1.000	1	R.TQSSASLAASYAAQQHPQAAAASYR.G
GPN:BC000488_1	S16	5584	3	2466.6	(+0.5)	4.789	0.541	1.000	1	R.TQSSASLAASYAAQQHPQAAAASYR.G
GPN:BC000488_1	S15	5550	2	1238.3	(+0.6)	2.273	0.429	0.963	1	R.YGGSYNDYLR.A
GPN:BC000488_1	S16	5736	2	1067.2	(+0.9)	2.412	0.293	0.921	1	R.LSESQLSFR.R
GPN:BC000591_1	S06	8840	2	2043.4	(-0.8)	3.358	0.505	1.000		K.ALLTTNQLPQPDVFPLFK.D
GPN:BC000591_1	S06	8844	2	2075.4	(-0.1)	2.976	0.265	0.712		K.AL*L*TTNQL*PQPDVFPL*FK#.D
GPN:BC000591_1	S07	8918	2	2043.4	(+0.7)	2.641	0.388	0.956		K.ALLTTNQLPQPDVFPLFK.D
GPN:BC000591_1	S07	8610	2	1574.8	(-0.6)	2.504	0.130	0.364	1	K.NQIAL*WDQL*L*EGR.I
GPN:BC000591_1	S06	7192	2	1550.7	(+0.6)	3.208	0.466	0.966	1	K.TPGFSVQSISDFEK#.F
GPN:BC000591_1	S12	8430	2	1574.8	(+0.0)	3.273	0.307	0.919	1	K.NQIAL*WDQL*L*EGR.I
GPN:BC001024_1	S07	8938	3	2530.9	(+0.7)	4.564	0.324	0.987	3	K.QITIIDSPSFIVSPLNSSALALR.S
GPN:BC001024_1	S08	9182	3	2530.9	(+0.8)	3.948	0.307	0.978	3	K.QITIIDSPSFIVSPLNSSALALR.S
GPN:BC001024_1	S08	7060	2	1186.3	(-0.3)	2.225	0.242	0.484	3	K.SGFNL*EEL*EK#.N
GPN:BC001024_1	S07	6910	2	1087.3	(+0.6)	2.883	0.374	0.970	3	R.VGVIGFPNVGK.S
GPN:BC001024_1	S08	6994	2	1087.3	(+0.8)	3.926	0.480	1.000	3	R.VGVIGFPNVGK.S
GPN:BC001024_1	S12	8768	3	2530.9	(+0.5)	4.212	0.353	0.986	3	K.QITIIDSPSFIVSPLNSSALALR.S
GPN:BC001041_1	S05	9300	2	2245.5	(+0.1)	2.399	0.305	0.766	3	K.EDPFVFIPEDDPLFPPIEK.F
GPN:BC001041_1	S06	7924	2	1378.6	(+0.6)	2.973	0.397	0.976	3	K.ILLTQENPFFR.K
GPN:BC001041_1	S14	8206	2	1378.6	(+0.6)	3.917	0.457	1.000	3	K.ILLTQENPFFR.K
GPN:BC001107_1	S12	5416	2	1281.3	(+0.4)	2.611	0.346	0.952	2	R.DAEDAL*HNL*DR.K
GPN:BC001107_1	S16	5450	2	1281.3	(+0.4)	2.364	0.125	0.525	2	R.DAEDAL*HNL*DR.K
GPN:BC001107_1	S12	8728	2	1918.2	(+0.1)	3.571	0.573	1.000	2	R.YGPIVDVYVPLDFYTR.R
GPN:BC001107_1	S15	8860	2	1918.2	(-0.6)	2.204	0.268	0.601	2	R.YGPIVDVYVPLDFYTR.R
GPN:BC001107_1	S17	8960	2	1924.2	(+0.8)	3.636	0.503	1.000	2	R.YGPIVDVYVPL*DFYTR.R
GPN:BC001107_1	S13	7134	2	1463.7	(+1.0)	2.612	0.318	0.216	2	R.YLRPPNTSLFVR.N
GPN:BC001107_1	S16	6844	2	1463.7	(+0.2)	2.617	0.395	0.221	2	R.YLRPPNTSLFVR.N
GPN:BC001107_1	S16	6840	2	1475.7	(+0.2)	2.523	0.255	0.066	2	R.YL*RPPNTSL*FVR.N
GPN:BC001107_1	S17	8948	2	1918.2	(+0.8)	3.321	0.487	1.000	2	R.YGPIVDVYVPLDFYTR.R
GPN:BC001378_1	S09	6568	3	2556.7	(+0.4)	4.377	0.559	1.000		R.ALVEFESNPEETREPGSPPSVQR.A
GPN:BC001378_1	S10	6462	3	2556.7	(+0.4)	4.963	0.544	1.000		R.ALVEFESNPEETREPGSPPSVQR.A
GPN:BC001378_1	S08	6284	2	902.1	(+1.0)	2.367	0.214	0.799		R.DTLALLQK.Q
GPN:BC001378_1	S08	5574	3	2166.4	(+0.6)	4.272	0.478	1.000		R.GQHEPSK#PPPAGETVTGGFGAK#.K
GPN:BC001378_1	S09	5622	3	2166.4	(+0.5)	4.844	0.566	1.000		R.GQHEPSK#PPPAGETVTGGFGAK#.K
GPN:BC001378_1	S09	5542	3	2166.4	(-0.1)	4.236	0.529	0.992		R.GQHEPSK#PPPAGETVTGGFGAK#.K
GPN:BC001378_1	S09	5600	3	2150.4	(+0.7)	4.198	0.341	0.931		R.GQHEPSKPPPAGETVTGGFGAK.K
GPN:BC001378_1	S09	5678	3	2150.4	(+0.9)	3.947	0.359	0.950		R.GQHEPSKPPPAGETVTGGFGAK.K
GPN:BC001378_1	S10	5530	3	2166.4	(+0.2)	4.139	0.553	1.000		R.GQHEPSK#PPPAGETVTGGFGAK#.K
GPN:BC001378_1	S09	5258	2	1042.3	(+0.1)	3.266	0.155	0.835		R.KAEVVQVIR.N
GPN:BC001378_1	S09	5314	2	1050.3	(+0.6)	2.707	0.423	0.978		R.K#AEVVQVIR.N
GPN:BC001378_1	S09	5232	2	1050.3	(+0.4)	2.561	0.434	0.976		R.K#AEVVQVIR.N
GPN:BC001378_1	S09	5346	2	1042.3	(+0.9)	2.358	0.326	0.924		R.KAEVVQVIR.N
GPN:BC001378_1	S10	4688	3	2304.5	(+0.8)	4.606	0.533	1.000	1	R.LQQGAGLESPQQPEPGAASPQR.Q

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GPN:BC001378_1	S10	4610	3	2304.5	(+0.7)	4.264	0.516	1.000	1	R.LQQGAGLESPPQQPEPGAASPR.Q
GPN:BC001378_1	S10	5194	2	1042.3	(+0.3)	2.498	0.148	0.564		R.KAEVVQVIR.N
GPN:BC001568_1	S05	6408	2	965.1	(+0.9)	2.969	0.301	0.969	2	R.YADLLEK.E
GPN:BC001568_1	S05	7518	2	1011.3	(+0.3)	2.408	0.501	0.917	2	R.L*GL*L*GL*PAPK#.N
GPN:BC003413_1	S15	6706	2	1077.2	(+0.9)	3.262	0.194	0.940		K.VDEIFGQLR.D
GPN:BC003413_1	S15	7216	2	1554.8	(+0.4)	2.397	0.308	0.895		K.VPYFNPVYLENK.E
GPN:BC003413_1	S16	7172	2	1568.8	(-0.5)	2.635	0.352	0.806		K.VPYFNPVYLL*ENK#.E
GPN:BC003413_1	S16	6622	2	1077.2	(-0.7)	2.614	0.183	0.389		K.VDEIFGQLR.D
GPN:BC005102_1	S17	7076	2	1225.5	(+0.7)	2.487	0.587	1.000		K.GKPLALVEEIR.N
GPN:BC005102_1	S17	8486	2	1837.2	(+0.5)	2.272	0.300	0.845		R.QLTSTPGTIIIGTIPVK.G
GPN:BC005102_1	S17	6386	2	1209.4	(+0.7)	2.212	0.431	0.955		R.HVFLTGPPGVGK.T
GPN:BC005125_1	S06	6772	3	2108.4	(+0.7)	4.151	0.203	0.592	2	R.LKEDQQTVLKPFYIEK.A
GPN:BC005125_1	S06	6952	2	1103.2	(+1.0)	3.040	0.483	1.000	1	K.SLPEWLSDR.K
GPN:BC006224_1	S15	6498	3	2311.5	(+0.5)	4.394	0.473	1.000		K.GEAVL*RPGL*DAEPEL*SPEEQR.V
GPN:BC006224_1	S16	5466	2	1954.1	(-0.8)	3.206	0.549	1.000		K.ASAEGLLPPEAAPSPEGAGSK.G
GPN:BC006487_1	S17	7386	2	1103.3	(+0.5)	3.330	0.439	1.000		K.LYALGLVPTR.G
GPN:BC006487_1	S17	7398	2	1555.7	(-0.1)	5.188	0.526	1.000		R.SM@EDFVTWVDSSK#.I
GPN:BC006487_1	S17	8214	2	1531.7	(+0.2)	3.548	0.549	1.000		R.SMEDFVTWVDSSK.I
GPN:BC006487_1	S17	8202	2	1539.7	(+0.2)	3.545	0.470	1.000		R.SMEDFVTWVDSSK#.I
GPN:BC006487_1	S17	7662	2	1586.8	(-0.0)	3.212	0.495	0.966		R.VGPDVWTDPAFLVTR.S
GPN:BC006487_1	S17	7666	2	1592.8	(-0.0)	2.985	0.197	0.711		R.VGPDVWTDPAFL*VTR.S
GPN:BC006504_1	S15	6904	2	1118.3	(+0.7)	2.995	0.274	0.951	3	R.GEVGL*L*FTNR.T
GPN:BC006504_1	S15	6396	2	1427.6	(-0.6)	3.012	0.259	0.076	3	R.TK#EEVNEWFTK#.Y
GPN:BC006504_1	S15	6390	2	1411.6	(+0.2)	2.691	0.426	0.287	3	R.TKEEVNEWFTK.Y
GPN:BC006504_1	S15	2214	2	1747.9	(+0.7)	2.291	0.392	0.247	3	R.SPSDEYKDNLHQVSK.R
GPN:BC012583_1	S12	5796	3	1825.9	(-0.1)	3.782	0.432	0.953		K.HNNQQAL*SHSIEEL*K#.I
GPN:BC012583_1	S12	7808	2	1438.6	(-0.1)	2.408	0.145	0.423		K.TWELSLYELQR.T
GPN:BC013889_1	S05	5412	2	1328.4	(+0.6)	3.060	0.261	0.883	1	K.AEVEQVEL*PDGK#.K
GPN:BC013889_1	S05	5400	2	1314.4	(+0.5)	3.031	0.378	0.973	1	K.AEVEQVELPDGK.K
GPN:BC013889_1	S07	5468	2	1314.4	(+0.2)	2.353	0.113	0.266	1	K.AEVEQVELPDGK.K
GPN:BC013889_1	S11	5564	2	1314.4	(+0.5)	2.820	0.329	0.953	1	K.AEVEQVELPDGK.K
GPN:BC013889_1	S05	5676	2	1271.4	(+0.5)	2.361	0.491	0.975	1	K.AGSTSWTGFQTK.A
GPN:BC013889_1	S13	8704	2	930.1	(+0.7)	2.310	0.270*	0.093	1	R.GFGFVQFK.N
GPN:BC013889_1	S09	10360	3	2555.8	(+0.9)	4.109	0.437	0.998	1	R.NLSFDSEEEELGELLQQFGELK.Y
GPN:BC013889_1	S07	7944	2	1690.9	(+0.5)	3.093	0.417	0.975	1	R.SEQLEELFSQVGPVK.Q
GPN:BC013889_1	S15	5512	2	1169.3	(+0.4)	2.315	0.297	0.910	1	R.FNQLVEQYK.Q
GPN:BC014046_1	S01	5866	2	1167.3	(+0.5)	2.555	0.364	0.955	1	K.AASITSEVFNK.F
GPN:BC014046_1	S03	5475	2	1175.3	(+0.8)	3.103	0.467	0.969	1	K.AASITSEVFNK#.F
GPN:BC014046_1	S03	5479	2	1167.3	(+0.7)	2.452	0.378	0.954	1	K.AASITSEVFNK.F
GPN:BC014046_1	S10	6208	2	1167.3	(-0.2)	2.875	0.431	0.954	1	K.AASITSEVFNK.F
GPN:BC014046_1	S10	6204	2	1175.3	(+0.4)	2.254	0.292	0.771	1	K.AASITSEVFNK#.F
GPN:BC014046_1	S13	6316	2	1167.3	(+0.8)	2.928	0.492	1.000	1	K.AASITSEVFNK.F
GPN:BC014046_1	S05	7646	2	1827.1	(-0.5)	2.549	0.352	0.866	1	K.APGEQTVPALNLQNAFR.I
GPN:BC014046_1	S07	7560	2	1827.1	(+0.5)	2.746	0.472	0.977	1	K.APGEQTVPALNLQNAFR.I
GPN:BC014046_1	S08	7678	2	1827.1	(+0.5)	3.103	0.508	0.984	1	K.APGEQTVPALNLQNAFR.I
GPN:BC014046_1	S11	7576	2	1827.1	(-0.6)	3.201	0.520	1.000	1	K.APGEQTVPALNLQNAFR.I
GPN:BC014046_1	S12	7366	2	1827.1	(-0.1)	2.650	0.412	0.923	1	K.APGEQTVPALNLQNAFR.I
GPN:BC014046_1	S15	7462	2	1827.1	(+0.8)	2.736	0.410	0.966	1	K.APGEQTVPALNLQNAFR.I
GPN:BC014046_1	S16	7456	2	1827.1	(+0.9)	3.516	0.496	1.000	1	K.APGEQTVPALNLQNAFR.I
GPN:BC014046_1	S04	4401	2	1216.3	(+0.2)	2.506	0.309	0.850	1	K.ELAAQLNEEAK.R
GPN:BC014046_1	S04	4323	2	1236.3	(+0.3)	2.392	0.310	0.701	1	K.EL*AAQL*NEEAK#.R
GPN:BC014046_1	S06	4110	2	1216.3	(+0.9)	2.726	0.395	0.970	1	K.ELAAQLNEEAK.R
GPN:BC014046_1	S06	4202	2	1216.3	(+0.8)	2.422	0.365	0.947	1	K.ELAAQLNEEAK.R
GPN:BC014046_1	S06	4034	2	1216.3	(+0.9)	2.297	0.377	0.943	1	K.ELAAQLNEEAK.R
GPN:BC014046_1	S07	3904	2	1216.3	(+1.0)	2.593	0.344	0.950	1	K.ELAAQLNEEAK.R
GPN:BC014046_1	S07	3978	2	1216.3	(+0.8)	2.588	0.362	0.956	1	K.ELAAQLNEEAK.R

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GPN:BC014046_1	S07	3832	2	1216.3	(+0.6)	2.547	0.308	0.929	1	K.ELAAQLNEEAK.R
GPN:BC014046_1	S07	4052	2	1216.3	(+0.6)	2.322	0.368	0.941	1	K.ELAAQLNEEAK.R
GPN:BC014046_1	S08	4912	2	1236.3	(-0.1)	2.339	0.274	0.600	1	K.EL*AAQL*NEEAK#.R
GPN:BC014046_1	S08	4832	2	1216.3	(+0.2)	2.293	0.384	0.889	1	K.ELAAQLNEEAK.R
GPN:BC014046_1	S09	4330	2	1216.3	(+0.4)	2.543	0.331	0.941	1	K.ELAAQLNEEAK.R
GPN:BC014046_1	S09	4112	2	1216.3	(+0.6)	2.425	0.314	0.919	1	K.ELAAQLNEEAK.R
GPN:BC014046_1	S09	4258	2	1216.3	(+0.5)	2.370	0.418	0.962	1	K.ELAAQLNEEAK.R
GPN:BC014046_1	S12	4402	2	1216.3	(+0.9)	2.760	0.374	0.967	1	K.ELAAQLNEEAK.R
GPN:BC014046_1	S12	4326	2	1216.3	(+0.1)	2.422	0.405	0.919	1	K.ELAAQLNEEAK.R
GPN:BC014046_1	S13	4818	2	1216.3	(+0.7)	2.308	0.389	0.949	1	K.ELAAQLNEEAK.R
GPN:BC014046_1	S15	4434	2	1216.3	(-0.1)	2.252	0.328	0.816	1	K.ELAAQLNEEAK.R
GPN:BC014046_1	S16	4286	2	1216.3	(+0.5)	2.321	0.390	0.950	1	K.ELAAQLNEEAK.R
GPN:BC014046_1	S16	4368	2	1216.3	(+0.7)	2.285	0.363	0.935	1	K.ELAAQLNEEAK.R
GPN:BC014046_1	S17	4822	2	1216.3	(+0.7)	2.312	0.393	0.951	1	K.ELAAQLNEEAK.R
GPN:BC014046_1	S04	4557	2	1372.5	(-0.9)	2.236	0.200	0.004	1	K.ELAAQLNEEAKR.R
GPN:BC014046_1	S03	6517	2	1636.8	(+0.9)	3.442	0.347	0.970	1	K.GNENANGAPAITL*L*IR.E
GPN:BC014046_1	S04	6549	2	1624.8	(+1.0)	4.440	0.492	1.000	1	K.GNENANGAPAITLLIR.E
GPN:BC014046_1	S04	6551	2	1636.8	(+0.3)	3.813	0.435	1.000	1	K.GNENANGAPAITL*L*IR.E
GPN:BC014046_1	S08	7924	2	1636.8	(+0.9)	3.131	0.317	0.953	1	K.GNENANGAPAITL*L*IR.E
GPN:BC014046_1	S08	7834	2	1624.8	(+0.3)	3.011	0.434	0.950	1	K.GNENANGAPAITLLIR.E
GPN:BC014046_1	S15	7592	2	1624.8	(+0.3)	2.586	0.459	0.939	1	K.GNENANGAPAITLLIR.E
GPN:BC014046_1	S16	7630	2	1624.8	(+0.9)	3.616	0.431	0.983	1	K.GNENANGAPAITLLIR.E
GPN:BC014046_1	S17	7882	2	1636.8	(+0.8)	2.467	0.153	0.433	1	K.GNENANGAPAITL*L*IR.E
GPN:BC014046_1	S04	5369	2	1311.5	(+0.2)	3.670	0.490	1.000	1	K.K#AASITSEVFNK#.F
GPN:BC014046_1	S01	6314	3	2408.4	(+1.0)	4.263	0.503	0.996	1	K.NEDEEEEEEEKDEAEDLLGR.G
GPN:BC014046_1	S01	6312	3	2428.4	(+0.6)	4.047	0.317	0.916	1	K.NEDEEEEEEEK#DEAEDL*L*GR.G
GPN:BC014046_1	S02	6086	3	2428.4	(+0.1)	3.795	0.396	0.919	1	K.NEDEEEEEEEK#DEAEDL*L*GR.G
GPN:BC014046_1	S03	5747	3	2428.4	(+0.6)	4.263	0.429	0.987	1	K.NEDEEEEEEEK#DEAEDL*L*GR.G
GPN:BC014046_1	S04	5731	3	2428.4	(+0.7)	4.533	0.323	0.950	1	K.NEDEEEEEEEK#DEAEDL*L*GR.G
GPN:BC014046_1	S04	5745	2	2408.4	(-1.0)	4.169	0.325	0.108	1	K.NEDEEEEEEEKDEAEDLLGR.G
GPN:BC014046_1	S04	5747	2	2428.4	(-1.0)	3.495	0.257	0.045	1	K.NEDEEEEEEEK#DEAEDL*L*GR.G
GPN:BC014046_1	S05	6510	3	2408.4	(+0.9)	4.532	0.538	1.000	1	K.NEDEEEEEEEKDEAEDLLGR.G
GPN:BC014046_1	S06	6454	3	2408.4	(+0.7)	4.517	0.515	0.999	1	K.NEDEEEEEEEKDEAEDLLGR.G
GPN:BC014046_1	S06	6458	3	2428.4	(+0.4)	4.040	0.385	0.973	1	K.NEDEEEEEEEK#DEAEDL*L*GR.G
GPN:BC014046_1	S08	6692	2	2408.4	(+0.3)	4.582	0.389	1.000	1	K.NEDEEEEEEEKDEAEDLLGR.G
GPN:BC014046_1	S08	6674	3	2408.4	(+0.6)	4.318	0.484	0.781	1	K.NEDEEEEEEEKDEAEDLLGR.G
GPN:BC014046_1	S08	6676	3	2428.4	(+0.5)	3.820	0.422	0.981	1	K.NEDEEEEEEEK#DEAEDL*L*GR.G
GPN:BC014046_1	S09	6782	3	2408.4	(+0.9)	4.702	0.501	0.777	1	K.NEDEEEEEEEKDEAEDLLGR.G
GPN:BC014046_1	S10	6666	3	2408.4	(+1.0)	4.204	0.462	0.992	1	K.NEDEEEEEEEKDEAEDLLGR.G
GPN:BC014046_1	S11	6586	3	2408.4	(+0.7)	3.748	0.477	0.990	1	K.NEDEEEEEEEKDEAEDLLGR.G
GPN:BC014046_1	S12	6366	3	2408.4	(+0.8)	4.867	0.529	0.870	1	K.NEDEEEEEEEKDEAEDLLGR.G
GPN:BC014046_1	S16	6468	3	2408.4	(+0.4)	4.608	0.458	0.904	1	K.NEDEEEEEEEKDEAEDLLGR.G
GPN:BC014046_1	S17	6762	3	2408.4	(+0.5)	4.131	0.529	0.999	1	K.NEDEEEEEEEKDEAEDLLGR.G
GPN:BC014046_1	S19	6600	3	2408.4	(+0.8)	3.828	0.514	0.999	1	K.NEDEEEEEEEKDEAEDLLGR.G
GPN:BC014046_1	S03	6239	2	1685.9	(-0.3)	3.613	0.318	0.875	1	R.NEGNIFPNPEATFVK#.E
GPN:BC014046_1	S04	6335	2	1685.9	(+0.7)	2.980	0.294	0.877	1	R.NEGNIFPNPEATFVK#.E
GPN:BC014046_1	S05	7384	2	1685.9	(+0.7)	3.512	0.383	0.951	1	R.NEGNIFPNPEATFVK#.E
GPN:BC014046_1	S05	7400	2	1685.9	(-0.8)	2.863	0.187	0.193	1	R.NEGNIFPNPEATFVK#.E
GPN:BC014046_1	S06	7224	2	1685.9	(+1.0)	4.156	0.312	0.953	1	R.NEGNIFPNPEATFVK#.E
GPN:BC014046_1	S07	7360	2	1677.9	(-0.8)	3.528	0.410	0.854	1	R.NEGNIFPNPEATFVK.E
GPN:BC014046_1	S07	7348	2	1685.9	(-0.3)	2.653	0.338	0.766	1	R.NEGNIFPNPEATFVK#.E
GPN:BC014046_1	S09	7506	2	1685.9	(+0.0)	2.768	0.230	0.481	1	R.NEGNIFPNPEATFVK#.E
GPN:BC014046_1	S13	7484	2	1677.9	(+1.0)	3.748	0.336	0.974	1	R.NEGNIFPNPEATFVK.E
GPN:BC014046_1	S14	7532	2	1677.9	(+0.7)	2.518	0.336	0.921	1	R.NEGNIFPNPEATFVK.E
GPN:BC014046_1	S16	7218	2	1677.9	(+1.0)	3.783	0.395	0.981	1	R.NEGNIFPNPEATFVK.E
GPN:BC014046_1	S16	7220	2	1685.9	(-0.2)	2.936	0.335	0.816	1	R.NEGNIFPNPEATFVK#.E
GPN:BC014046_1	S04	1913	2	1173.3	(+0.9)	2.677	0.283	0.876	1	R.VM@EIVDADEK#.V
GPN:BC014046_1	S04	4701	2	1149.3	(+0.7)	2.241	0.260	0.838	1	R.VMEIVDADEK.V
GPN:BC014046_1	S20	6948	2	1677.9	(+0.7)	3.564	0.390	0.979	1	R.NEGNIFPNPEATFVK.E
GPN:BC014987_1	S05	9104	2	1582.8	(+0.5)	2.467	0.367	0.943	2	R.TPLEQEIFNLLHK.N
GPN:BC014987_1	S05	4170	2	1464.5	(+0.9)	3.809	0.453	1.000	3	K.VSEFNVSSEGSGEK#.L
GPN:BC014987_1	S05	4174	2	1456.5	(+0.6)	3.597	0.430	0.982	3	K.VSEFNVSSEGSGEK.L
GPN:BC014987_1	S05	6144	2	1332.4	(+0.5)	2.397	0.419	0.961	1	K.DSGSQEVL*SEL*R.V
GPN:BC015796_1	S11	5194	3	2282.5	(-0.3)	4.176	0.369	0.860		K.EQDQRPL*HPVANPHAEISTK#.V

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GPN:BC015796_1	S11	5272	3	2282.5	(+0.1)	3.831	0.258	0.344		K.EQDQRPL*HPVANPHAEISTK#.V
GPN:BC015796_1	S11	1464	2	1346.5	(+0.2)	3.484	0.542	1.000		K.VK#DAVEQQGEVK#.K
GPN:BC015796_1	S14	7990	2	1631.8	(+0.6)	2.212	0.352	0.901		R.ELLEQISAFDNVPR.K
GPN:BC016944_1	S14	7872	2	1574.8	(-0.6)	3.083	0.357	0.923	1	K.EIFLTVPVGGGESLR.L
GPN:BC016944_1	S14	7840	2	1586.8	(-0.1)	2.534	0.387	0.896	1	K.EIFL*TVPVGGGESL*R.L
GPN:BC016944_1	S14	4960	2	934.1	(+0.7)	2.228	0.265	0.878	6	R.L*L*ASDL*QR.H
GPN:BC019069_1	S08	7214	2	1841.0	(+0.9)	2.853	0.451	0.976	4	K.ATNESEDEIPQLVPIGK.K
GPN:BC019069_1	S08	7220	2	1855.0	(+0.9)	2.252	0.311	0.748	4	K.ATNESEDEIPQL*VPIGK#.K
GPN:BC019069_1	S07	9580	2	2071.3	(-0.2)	2.917	0.429	0.945	4	K.SAALPIFSSFVSNWDEATK.R
GPN:BC019069_1	S08	9734	2	2071.3	(+0.5)	4.728	0.577	1.000	4	K.SAALPIFSSFVSNWDEATK.R
GPN:BC019069_1	S09	9784	2	2071.3	(+0.6)	4.015	0.489	0.995	4	K.SAALPIFSSFVSNWDEATK.R
GPN:BC019069_1	S12	9422	3	2071.3	(+0.5)	4.265	0.368	0.992	4	K.SAALPIFSSFVSNWDEATK.R
GPN:BC019069_1	S12	9386	2	2071.3	(+0.2)	3.369	0.492	1.000	4	K.SAALPIFSSFVSNWDEATK.R
GPN:BC019069_1	S08	6630	2	1056.3	(-0.4)	2.702	0.449	0.956	4	K.VPVSVNLLSK.N
GPN:BC019069_1	S08	6614	2	1076.3	(+0.3)	2.477	0.468	0.908	4	K.VPVSVNL*L*SK#.N
GPN:BC019069_1	S10	6648	2	1056.3	(+0.7)	2.496	0.455	0.976	4	K.VPVSVNLLSK.N
GPN:BC019069_1	S13	9778	2	2071.3	(+0.9)	4.658	0.612	1.000	4	K.SAALPIFSSFVSNWDEATK.R
GPN:BC020641_1	S12	6764	2	1251.4	(+0.6)	3.628	0.431	1.000		K.SEEGPGWTL*R.D
GPN:BC020641_1	S12	4900	2	1213.5	(+0.8)	2.429	0.400	0.356		K.TPESKPTILVK.N
GPN:BC020641_1	S12	4884	2	1235.5	(+0.3)	2.294	0.314	0.046		K.TPESK#PTIL*VK#.N
GPN:BC023144_1	S04	5379	2	1060.2	(+0.6)	2.771	0.306	0.907		K.DIDIL*NSAGK#.M
GPN:BC023144_1	S06	5916	2	1046.2	(+0.9)	3.282	0.281	0.965		K.DIDILNSAGK.M
GPN:BC023144_1	S08	6152	2	1046.2	(+0.8)	2.921	0.306	0.959		K.DIDILNSAGK.M
GPN:BC023144_1	S08	6156	2	1060.2	(+0.3)	2.321	0.324	0.729		K.DIDIL*NSAGK#.M
GPN:BC023144_1	S05	7186	2	1734.8	(-0.3)	2.496	0.436	0.923		K.ESEITDEDIDGILER.G
GPN:BC023144_1	S06	7050	2	1734.8	(-0.3)	2.552	0.329	0.840		K.ESEITDEDIDGILER.G
GPN:BC023144_1	S09	7340	2	1734.8	(-0.3)	2.540	0.336	0.847		K.ESEITDEDIDGILER.G
GPN:BC023144_1	S09	7106	2	1322.5	(+0.7)	2.961	0.339	0.965		K.LLTQGFNWNK.R
GPN:BC023144_1	S10	6996	2	1322.5	(+0.4)	3.015	0.395	0.977		K.LLTQGFNWNK.R
GPN:BC023144_1	S10	2116	2	1281.4	(+0.5)	2.203	0.244	0.759		R.NPELPNAAQAQK.E
GPN:BC023144_1	S04	4831	2	1767.8	(+0.7)	4.806	0.451	1.000		R.TEQEEDEELLTESSK.A
GPN:BC023144_1	S06	5236	2	1767.8	(+0.7)	3.360	0.483	1.000		R.TEQEEDEELLTESSK.A
GPN:BC023144_1	S07	5302	2	1767.8	(+0.6)	2.882	0.385	0.964		R.TEQEEDEELLTESSK.A
GPN:BC023144_1	S12	5280	2	1763.8	(-0.5)	3.700	0.436	0.965		K.IDEAESLNDEELEEK.E
GPN:BC023247_1	S09	5404	3	2172.4	(+0.6)	3.753	0.378	0.995	1	R.LQQQHSEQPPLQSPVTR.R
GPN:BC023247_1	S19	4800	3	2382.4	(+0.6)	4.239	0.484	1.000	2	R.DSHSSEDEASSQTDLSTISK.K
GPN:BC024238_1	S13	8428	2	1529.7	(-0.1)	3.462	0.244	0.802	2	K.GIDYDFPSL*IL*QK#.T
GPN:BC024238_1	S13	6312	2	1531.8	(+0.8)	3.713	0.451	1.000	1	K.K#QEQL*TPGVVYVR.H
GPN:BC024238_1	S13	6680	2	2081.2	(+0.8)	5.906	0.585	1.000	2	K.SQVAELNDDDKDDEIVFK.Q
GPN:BC024238_1	S13	6692	2	2103.2	(-0.9)	3.649	0.306	0.038	2	K.SQVAEL*NDDDK#DDEIVFK#.Q
GPN:BC024238_1	S13	6782	2	1679.9	(+1.0)	2.235	0.152*	0.043	2	K.IVAETM@NNYL*FGER.L
GPN:BC028396_1	S12	5630	3	2708.9	(+0.5)	5.052	0.521	1.000	4	K.LPQQDHTTTTTDSEMEEPYLQESK.E
GPN:BC028396_1	S12	5638	3	2728.9	(-0.2)	4.162	0.449	0.990	4	K.L*PQQDHTTTTTDSEMEEPYL*QESK#.E
GPN:BC028396_1	S12	5548	2	1053.2	(+0.2)	2.590	0.366	0.927	4	K.YAQGLPEK.L
GPN:BC032638_1	S11	9498	3	3722.1	(-0.5)	4.532	0.547	1.000	1	K.GLQGVGPGSNDETLLSAVASALHTSSAPITGQVSAAVEK.N
GPN:BC032638_1	S11	7174	2	1622.8	(-0.6)	3.402	0.514	1.000	1	R.L*QGL*SASDVTEQIIK#.T
GPN:BC032640_1	S06	9202	2	2068.3	(-0.8)	2.826	0.429	0.803	2	R.EPLENLTSEYDLDFR.R
GPN:BC032640_1	S07	9276	2	2068.3	(+0.0)	3.446	0.551	1.000	2	R.EPLENLTSEYDLDFR.R
GPN:BC032640_1	S07	6412	2	1138.3	(+0.8)	2.668	0.246	0.896	2	K.GSISVFEVDGK.K
GPN:BC032640_1	S06	5766	2	1700.8	(-0.5)	3.432	0.463	0.965		R.NLQSFTEEPAYSTR.R
GPN:BC032640_1	S07	5844	2	1706.8	(-0.4)	3.398	0.416	0.956		R.NL*QSFTEEPAYSTR.R
GPN:BC032640_1	S07	5840	2	1700.8	(-0.5)	3.157	0.466	0.961		R.NLQSFTEEPAYSTR.R
GPN:BC032640_1	S07	1542	2	1211.4	(+0.2)	2.292	0.287	0.759	2	R.SQQPTPTVTPK.K
GPN:BC032640_1	S13	9466	2	2068.3	(+0.6)	2.724	0.465	0.975	2	R.EPLENLTSEYDLDFR.R
GPN:BC032643_1	S06	9030	2	1594.8	(+0.4)	2.714	0.419	0.964	6	R.DLFEDELVPLFEK.A
GPN:BC032643_1	S07	9096	2	1594.8	(+0.1)	3.245	0.398	0.953	6	R.DLFEDELVPLFEK.A

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
GPN:BC032643_1	S08	9296	2	1594.8	(+0.7)	3.737	0.357	0.979	6	R.DLFEDELVPLFEK.A
GPN:BC032643_1	S09	9270	2	1594.8	(-0.3)	2.593	0.361	0.893	6	R.DLFEDELVPLFEK.A
GPN:BC032643_1	S10	9342	2	1594.8	(+0.2)	2.620	0.355	0.893	6	R.DLFEDELVPLFEK.A
GPN:BC032643_1	S11	9180	2	1594.8	(+0.8)	2.380	0.379	0.942	6	R.DLFEDELVPLFEK.A
GPN:BC032643_1	S12	8934	2	1594.8	(+0.5)	3.036	0.365	0.968	6	R.DLFEDELVPLFEK.A
GPN:BC032643_1	S07	8464	2	1729.9	(-0.5)	2.275	0.167	0.192	5	K.EFNEDGAL*AVL*QQFK#.D
GPN:BC032643_1	S13	7970	2	1494.7	(-0.5)	2.350	0.137	0.184	6	R.NL*ANTVTEEIL*EK#.A
GPN:BC032643_1	S16	9022	2	1594.8	(+0.6)	2.547	0.304	0.885	6	R.DLFEDELVPLFEK.A
GPN:BC035744_1	S09	6014	2	1359.5	(+0.1)	2.297	0.299	0.765	4	R.DIDNNLITSTPR.A
GPN:BC035744_1	S09	1466	2	1256.3	(+0.9)	2.630	0.434	0.972	2	K.LEDNPSSGSPPR.T
GPN:BC035744_1	S09	7284	2	952.1	(+0.2)	2.331	0.317	0.770	6	K.L*L*NIL*DPK#.K
GPN:BC035744_1	S09	6010	2	1984.1	(+0.2)	4.873	0.574	1.000	6	K.NGTSGSDSPGQAVEAEEIVK#.Q
GPN:BC035744_1	S09	5982	2	1976.1	(+0.2)	4.215	0.457	1.000	6	K.NGTSGSDSPGQAVEAEEIVK.Q
GPN:BC035744_1	S15	7072	2	926.1	(+0.1)	2.809	0.165	0.742	6	K.LLNILDPK.K
GPN:BC036800_1	S13	6084	2	1338.4	(+1.0)	3.414	0.363	0.979	2	R.DVDTQEFNLEK.A
GPN:BC036800_1	S06	6462	2	1130.3	(+0.3)	2.207	0.188	0.385	1	K.KSAPSILSNR.I
GPN:BC036800_1	S13	6242	2	1065.2	(+0.5)	2.959	0.271	0.955	2	R.LAQETDIFK.K
GPN:BC043619_1	S14	9556	2	1645.9	(-0.1)	2.966	0.328	0.812	1	K.L*SGL*NAFDIAEEL*VK#.T
GPN:BC043619_1	S14	7514	2	1637.8	(+0.4)	2.446	0.331	0.915	1	R.YL*GGSM@DL*STDFDR.T
GPN:BC043619_1	S15	9174	2	1619.9	(+0.6)	3.136	0.471	0.982	1	K.LSGLNAFDIAEELVK.T
GPN:BC049850_1	S05	1878	2	1170.3	(+1.0)	2.383	0.457	0.971		R.DLSSESSEPVHAK.K
GPN:BC049850_1	S06	8538	2	1308.6	(+0.6)	2.665	0.348	0.945	2	R.SPLLPAVLEGLAK.F
GPN:BC050528_1	S11	6992	2	1370.6	(+0.9)	3.738	0.384	0.982	2	K.ALIAAQLDNAIEK.E
GPN:BC050528_1	S11	6990	2	1390.6	(-0.2)	3.500	0.331	0.890	2	K.AL*IAAQL*DNAIEK#.E
GPN:BC050528_1	S11	7914	3	2308.5	(+0.9)	4.271	0.473	1.000	2	R.L*K#QDQTYGDIYNFPIHAFDK#.A
GPN:BC050528_1	S15	7734	3	2286.5	(+0.4)	4.114	0.437	0.988	2	R.LKQDQTYGDIYNFPIHAFDK.A
GPN:BC050528_1	S16	7730	3	2286.5	(+0.4)	5.637	0.492	1.000	2	R.LKQDQTYGDIYNFPIHAFDK.A
GPN:BC050528_1	S17	7956	3	2286.5	(+0.5)	4.018	0.460	0.991	2	R.LKQDQTYGDIYNFPIHAFDK.A
GPN:BC050546_1	S04	6703	2	1174.4	(+0.8)	3.182	0.536	1.000	2	K.ALVDILSEVSK.A
GPN:BC050546_1	S08	9030	3	2284.5	(+0.8)	3.714	0.479	0.999	2	R.AMFLQPDLDLSDVDFSTNNQK.K
GPN:BC050546_1	S12	8204	2	1354.6	(+0.9)	2.539	0.326	0.894	2	K.ATLQEILPEVLK.A
GPN:BC050546_1	S08	6032	2	886.1	(+0.3)	2.251	0.191	0.555	1	R.LITGLGVGR.E
GPN:BC050546_1	S09	6130	2	886.1	(+0.2)	2.377	0.370	0.908	1	R.LITGLGVGR.E
GPN:BC050546_1	S14	8670	2	1354.6	(+0.2)	2.223	0.298	0.737	2	K.ATLQEILPEVLK.A
GPN:BC052604_1	S13	5970	3	1620.8	(-0.6)	3.849	0.400	0.992	1	K.GAEHITTYTFNTHK.A
GPN:BC052604_1	S13	5960	2	1620.8	(-0.2)	3.383	0.407	0.956	1	K.GAEHITTYTFNTHK.A
GPN:BC052604_1	S13	8356	2	1571.8	(-0.8)	3.057	0.458	0.758	1	K.L*L*L*DTFEYQGL*VK#.H
GPN:BC052604_1	S13	9242	2	1539.8	(+1.0)	2.264	0.327	0.892	1	K.LLLDTFEYQGLVK.H
GPN:BC052604_1	S16	8098	2	1539.8	(+0.6)	4.426	0.557	1.000	1	K.LLLDTFEYQGLVK.H
GPN:BC056406_1	S16	7786	3	2166.4	(-0.0)	3.790	0.393	0.976	2	K.SSVTSAAAVSAL*AGVQDQL*IEK#.R
GPN:BC056406_1	S16	6898	2	1541.7	(+0.5)	2.917	0.406	0.973	2	R.K#QEL*AETL*ANL*ER.Q
GPN:BC058020_1	S15	6802	2	1100.3	(+0.1)	3.193	0.452	1.000		R.IDGVSLVQR.T
GPN:BC058020_1	S15	6780	2	1112.3	(+0.8)	2.916	0.348	0.969		R.IDGVSL*L*VQR.T
GPN:BC058020_1	S15	6948	2	1290.4	(+0.9)	2.488	0.442	0.974		R.LESFLHDSWR.Q
GPN:BX640750_1	S06	7480	3	2923.2	(+0.2)	4.634	0.503	1.000	1	R.LSGGQVLSEYTGPTSADLDHFPSVSQTK.A
GPN:BX640750_1	S06	5206	2	1393.5	(-0.3)	2.261	0.307	0.555	1	R.EQFEGE*GSTPDAK#.L
PIR1:UQHUB	S16	6428	2	1068.3	(-0.6)	2.803	0.272	0.888	65	K.ESTLHLVLR.L
PIR1:UQHUB	S17	7006	2	1803.0	(-0.6)	2.821	0.377	0.846	58	K.TITL*EVEPSDTIENVK#.A
PIR1:UQHUB	S18	6962	2	1803.0	(-0.1)	2.231	0.288*	0.011	58	K.TITL*EVEPSDTIENVK#.A
PIR1:UQHUB	S16	3844	2	1096.2	(+1.0)	2.735	0.378	0.947	67	R.TL*SDYNIQK#.E
PIR1:UQHUB	S16	3930	2	1096.2	(+0.8)	2.546	0.386	0.930	67	R.TL*SDYNIQK#.E
PIR1:UQHUB	S17	4472	2	1096.2	(+0.6)	2.461	0.331	0.899	67	R.TL*SDYNIQK#.E
PIR1:UQHUB	S17	4550	2	1096.2	(+0.9)	2.391	0.374	0.919	67	R.TL*SDYNIQK#.E
PIR1:UQHUB	S20	6230	2	1068.3	(+1.0)	2.467	0.221	0.834	65	K.ESTLHLVLR.L



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
PIR2:A42184	S05	4984	2	1019.1	(+0.6)	2.221	0.284	0.658	2	K.ATQEWL*EK#.Q
PIR2:A42184	S08	5240	2	1019.1	(+0.4)	2.392	0.390	0.891	2	K.ATQEWL*EK#.Q
PIR2:A42184	S06	8162	2	1514.8	(+0.4)	3.712	0.478	1.000		K.GEVLGDVLQLETLK.Q
PIR2:A42184	S08	8412	2	1514.8	(+0.1)	2.488	0.382	0.892		K.GEVLGDVLQLETLK.Q
PIR2:A42184	S04	5007	2	1259.4	(-0.2)	2.296	0.128	0.183	1	K.L*ADDL*STL*QEK#.M
PIR2:A42184	S06	6492	3	2234.4	(+1.0)	3.819	0.253	0.945	2	K.LSQLLEEHLSQLQDNPPQEK.G
PIR2:A42184	S04	5509	3	2145.3	(+0.1)	3.758	0.450	0.994		K.QAQL*AQTL*QQQEASQGL*R.H
PIR2:A42184	S05	9040	3	2194.4	(+1.0)	4.270	0.496	1.000	4	R.SQAPLESSLDSLGDVFLDSGR.K
PIR2:A42184	S06	8984	3	2194.4	(+0.7)	4.228	0.520	1.000	4	R.SQAPLESSLDSLGDVFLDSGR.K
PIR2:A42184	S12	8870	3	2194.4	(+0.5)	3.949	0.410	0.997	4	R.SQAPLESSLDSLGDVFLDSGR.K
PIR2:A42184	S12	8898	2	2218.4	(-0.5)	2.830	0.348	0.898	4	R.SQAPL*ESSL*DSL*GDVFL*DSGR.K
PIR2:A42184	S14	8220	2	1723.0	(+0.4)	2.637	0.287	0.796	4	K.VESLESLYFTPIPAR.S
PIR2:A42184	S11	2036	2	1563.7	(+0.1)	2.593	0.345	0.866	5	R.VSLEPHQGGPTPESK.K
PIR2:A42184	S04	4923	2	1055.2	(+0.5)	2.281	0.235	0.831	2	K.YVQEL*AAVR.A
PIR2:A42184	S05	5382	2	1055.2	(+0.4)	3.127	0.392*	0.600	2	K.YVQEL*AAVR.A
PIR2:A42184	S06	5328	2	1055.2	(+0.2)	2.564	0.302*	0.164	2	K.YVQEL*AAVR.A
PIR2:A42184	S09	5656	2	1049.2	(+0.8)	2.230	0.111*	0.140	2	K.YVQELAAVR.A
PIR2:A42184	S17	8998	3	2503.7	(+0.7)	4.098	0.470	0.999	3	K.FVLHDHEDGLNLNEDLENFLQK.A
PIR2:A54857	S11	8066	2	1436.7	(-0.4)	3.064	0.245	0.712		K.IL*PTL*EAVAAL*GNK#.V
PIR2:A54857	S11	8044	2	1410.7	(+0.6)	2.925	0.369	0.964		K.ILPTLEAVALGNK.V
PIR2:A54857	S12	7858	2	1410.7	(+1.0)	2.520	0.504	0.978		K.ILPTLEAVALGNK.V
PIR2:A54857	S11	7956	2	2100.3	(+0.7)	5.025	0.639	1.000		R.NQDLAPNSAEQASILSLVTK.I
PIR2:A54857	S11	6906	2	1733.0	(-0.5)	2.831	0.494	0.346		R.VKPAPDETSFSEALLK.R
PIR2:A54857	S11	6552	2	1054.3	(+0.6)	2.784	0.382	0.972	1	K.VL*QSAL*AAIR.H
PIR2:A54857	S11	5594	2	1434.5	(-0.7)	2.325	0.453	0.631	1	R.WFEENASQSTVK#.V
PIR2:A54857	S16	5372	2	1426.5	(+0.4)	3.018	0.444	0.981	1	R.WFEENASQSTVK.V
PIR2:A54857	S17	8152	2	1410.7	(+0.9)	2.356	0.409	0.950		K.ILPTLEAVALGNK.V
PIR2:JC4525	S10	7522	2	1449.6	(-0.4)	3.741	0.428	1.000	3	K.DHIMEIFSTYGK#.I
PIR2:JC4525	S10	7498	2	1441.6	(+0.3)	2.729	0.321	0.886	3	K.DHIMEIFSTYGK.I
PIR2:JC4525	S10	6562	2	1769.8	(-0.5)	2.588	0.347	0.766	3	K.GYAYVEFENPDEAEK#.A
PIR2:JC4525	S10	6560	2	1761.8	(-0.6)	2.224	0.326	0.752	3	K.GYAYVEFENPDEAEK.A
PIR2:JC4525	S11	6470	2	1769.8	(+0.5)	4.402	0.499	1.000	3	K.GYAYVEFENPDEAEK#.A
PIR2:JC4525	S11	7458	2	1441.6	(+0.9)	2.427	0.434	0.966	3	K.DHIMEIFSTYGK.I
PIR2:JC7168	S07	1984	1	853.0	(-0.2)	1.986	0.367	0.000	5	K.AVDITTPK#.A
PIR2:JC7168	S07	7178	2	1633.8	(-0.2)	2.654	0.441	0.939	5	K.GFNEGLWEIDNPNK.V
PIR2:JC7168	S10	7238	2	1633.8	(-0.1)	2.970	0.232	0.759	5	K.GFNEGLWEIDNPNK.V
PIR2:JC7168	S11	7182	2	1647.8	(-0.1)	2.847	0.298	0.757	5	K.GFNEGL*WEIDNPNK#.V
PIR2:JC7168	S08	2158	2	959.0	(+0.9)	2.506	0.133*	0.325	3	K.IDNLDVNR.C
PIR2:JC7168	S07	7028	2	1761.9	(-0.4)	3.585	0.481	1.000	5	R.KGFNEGLWEIDNPNK.V
PIR2:JC7168	S08	7098	2	1761.9	(-0.4)	3.809	0.428	0.965	5	R.KGFNEGLWEIDNPNK.V
PIR2:JC7168	S07	8900	2	1985.3	(-0.9)	2.729	0.416	0.632	3	K.NMFL*VGEGDSVITQVL*NK#.S
PIR2:JC7168	S08	9096	2	1965.3	(+0.8)	5.380	0.512	1.000	3	K.NMFLVGEGDSVITQVLNK.S
PIR2:JC7168	S06	2316	2	1582.8	(+0.6)	2.474	0.334	0.111	6	R.VDEVPDGAVK#PPTNK#.L
PIR2:JC7168	S07	2336	2	1582.8	(-0.1)	2.997	0.244	0.046	6	R.VDEVPDGAVK#PPTNK#.L
PIR2:JC7168	S07	2258	2	1582.8	(+0.5)	2.292	0.313	0.070	6	R.VDEVPDGAVK#PPTNK#.L
PIR2:JC7168	S07	2274	2	1566.8	(-0.0)	2.203	0.157	0.002	6	R.VDEVPDGAVKPPTNK.L
PIR2:JC7168	S08	4796	2	1566.8	(-0.2)	2.835	0.366	0.191	6	R.VDEVPDGAVKPPTNK.L
PIR2:JC7168	S11	2238	2	1566.8	(+0.7)	3.203	0.296	0.297	6	R.VDEVPDGAVKPPTNK.L
PIR2:JC7168	S11	2252	2	1582.8	(-0.7)	2.232	0.294	0.006	6	R.VDEVPDGAVK#PPTNK#.L
PIR2:JC7168	S12	6974	2	1647.8	(+0.2)	3.121	0.387	0.890	5	K.GFNEGL*WEIDNPNK#.V
PIR2:JW0079	S13	8988	2	2204.5	(-0.2)	3.051	0.452	0.955	3	K.EYFGAFGEIENIELPMDTK.T
PIR2:JW0079	S13	8516	2	2234.5	(+0.0)	2.411	0.331	0.686	3	K.EYFGAFGEIENIEL*PM@DTK#.T
PIR2:JW0079	S13	7848	2	1342.6	(+0.6)	4.309	0.545	1.000	3	K.MFIGGLSWDTSK.K
PIR2:JW0079	S13	7320	2	1372.6	(+0.0)	3.391	0.481	1.000	3	K.M@FIGGL*SWDTSK#.K
PIR2:JW0079	S13	7880	2	1356.6	(-0.0)	3.125	0.450	0.927	3	K.MFIGGL*SWDTSK#.K
PIR2:JW0079	S13	6650	2	1720.9	(-0.7)	3.366	0.326	0.613	3	K.VFVGGL*SPDTSEEQIK#.E
PIR2:JW0079	S14	6498	2	1706.9	(-0.4)	4.177	0.409	1.000	3	K.VFVGGLSPDTSEEQIK.E
PIR2:T08693	S08	9614	2	1532.7	(+0.3)	3.428	0.431	0.963	5	R.LLSSFDFFLTDAR.I
PIR2:T08693	S08	9470	2	1532.7	(+0.0)	3.234	0.444	0.962	5	R.LLSSFDFFLTDAR.I
PIR2:T08693	S08	9320	2	1532.7	(+1.0)	2.740	0.478	0.979	5	R.LLSSFDFFLTDAR.I
PIR2:T08693	S08	9298	2	1550.7	(-0.5)	2.453	0.364	0.878	5	R.L*L*SSFDFFL*TDAR.I

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
PIR2:T08693	S08	9450	2	1550.7	(-0.5)	2.432	0.212	0.588	5	R.L*L*SSFDFFL*TDAR.I
PIR2:T08693	S08	9990	2	1532.7	(-0.2)	2.431	0.370	0.881	5	R.LSSFDFFLTDAR.I
PIR2:T08693	S08	9374	2	1550.7	(-0.3)	2.288	0.319	0.784	5	R.L*L*SSFDFFL*TDAR.I
PIR2:T08693	S08	10298	2	1532.7	(+0.8)	2.270	0.205	0.532	5	R.LSSFDFFLTDAR.I
PIR2:T08693	S08	9748	2	1532.7	(-0.3)	2.226	0.331	0.786	5	R.LSSFDFFLTDAR.I
PIR2:T08693	S13	9226	2	1532.7	(+0.6)	2.398	0.300	0.887	5	R.LSSFDFFLTDAR.I
PIR2:T08693	S14	9360	2	1532.7	(+0.6)	2.778	0.461	0.978	5	R.LSSFDFFLTDAR.I
PIR2:T08693	S15	8894	2	1532.7	(+0.8)	3.658	0.463	1.000	5	R.LSSFDFFLTDAR.I
PIR2:T08693	S15	8920	2	1532.7	(-0.5)	3.084	0.456	0.960	5	R.LSSFDFFLTDAR.I
PIR2:T08693	S15	9010	2	1532.7	(+0.0)	2.522	0.414	0.922	5	R.LSSFDFFLTDAR.I
PIR2:T08693	S08	7126	2	1043.3	(+0.5)	2.228	0.303	0.901	5	R.RL*L*PSL*IGR.H
PIR2:T08693	S09	7452	2	1331.6	(+0.7)	2.938	0.388	0.972	5	K.TVSQIISLQTLK.K
PIR2:T08693	S11	7296	2	1331.6	(+0.6)	2.788	0.443	0.977	5	K.TVSQIISLQTLK.K
PIR2:T08693	S14	7430	2	1331.6	(+0.6)	3.214	0.408	0.980	5	K.TVSQIISLQTLK.K
PIR2:T08693	S15	7198	2	1331.6	(+0.8)	3.135	0.423	0.980	5	K.TVSQIISLQTLK.K
PIR2:T08693	S15	8934	2	1550.7	(-0.7)	2.460	0.412	0.733	5	R.L*L*SSFDFFL*TDAR.I
PIR2:T08694	S13	2392	2	1380.5	(+0.7)	2.582	0.292	0.900	1	K.ASGGSL*QGHDAVL*R.L
PIR2:T08694	S13	5488	2	1558.7	(-0.3)	2.342	0.365	0.861	1	R.LVPVHYDETEAER.E
PIR2:T09073	S04	4433	2	1433.5	(+0.3)	3.031	0.334	0.848	1	K.QDQISGL*SQSEVK#.T
PIR2:T09073	S05	4802	2	1419.5	(+0.3)	3.279	0.357	0.942	1	K.QDQISGLSQSEVK.T
PIR2:T09073	S03	5373	2	1433.6	(-0.2)	2.226	0.430	0.893		K.TL*PADVQNYYSR.R
PIR2:T09073	S05	4794	2	1433.5	(-0.3)	2.566	0.215	0.487	1	K.QDQISGL*SQSEVK#.T
PIR2:T12528	S04	4407	2	1773.9	(+0.0)	3.094	0.448	0.956	2	R.GL*SQNQIQPNQSVTPR.R
PIR2:T12528	S05	4066	2	1314.5	(+0.5)	3.388	0.358	0.470	3	K.SENVDVGKPALGK.S
PIR2:T12528	S05	4764	2	1767.9	(-0.1)	2.901	0.329	0.890	2	R.GLSQNNQIQPNQSVTPR.R
PIR2:T34531	S03	6875	2	1943.1	(-0.2)	2.380	0.310	0.770	5	R.DVPESFTSEAYQWLN.R.S
PIR2:T34531	S03	6869	2	1949.1	(+0.1)	2.359	0.419	0.900	5	R.DVPESFTSEAYQWL*NR.S
PIR2:T34531	S03	6373	2	1272.5	(+0.9)	2.552	0.411	0.968	4	R.SIFTGL*M@IDPR.T
PIR2:T34531	S05	6424	2	1112.3	(+0.9)	2.403	0.474	0.976	6	K.SQSLTFSTK.S
PIR2:T42680	S04	6441	2	1317.5	(+0.6)	2.695	0.479	0.980	4	R.VYSTALSSFLTK.R
PIR2:T42680	S06	5744	2	815.0	(+0.8)	2.252	0.330	0.934	4	K.SPLSALAR.K
SW:ACIN_HUMAN	S06	5016	2	1215.4	(+0.6)	2.632	0.380	0.379	4	R.GLLVDRPSETK.T
SW:ACIN_HUMAN	S06	5022	2	1235.4	(-0.4)	2.377	0.165	0.010	4	R.GL*L*VDRPSETK#.T
SW:ACIN_HUMAN	S07	5012	2	1215.4	(+0.5)	2.224	0.275	0.109	4	R.GLLVDRPSETK.T
SW:ACIN_HUMAN	S05	5592	2	887.1	(+0.3)	2.394	0.329	0.892	2	K.IEELALAK.G
SW:ACIN_HUMAN	S03	5425	2	1304.5	(+0.6)	3.636	0.488	1.000	4	K.KPSISITTESLK.S
SW:ACIN_HUMAN	S03	5421	2	1326.5	(+0.0)	2.616	0.390	0.855	4	K.K#PSISITTESL*K#.S
SW:ACIN_HUMAN	S06	5898	2	1304.5	(+0.5)	2.874	0.534	1.000	4	K.KPSISITTESLK.S
SW:ACIN_HUMAN	S06	5914	2	1326.5	(-0.3)	2.338	0.282	0.595	4	K.K#PSISITTESL*K#.S
SW:ACIN_HUMAN	S06	5428	2	1104.3	(+1.0)	2.678	0.451	0.979	4	K.KVTLGDTLTR.R
SW:ACIN_HUMAN	S04	5895	2	1338.6	(+0.8)	3.462	0.456	1.000	2	K.VPEESVLPVQK.S
SW:ACIN_HUMAN	S05	6688	2	1338.6	(+0.7)	2.764	0.437	0.976	2	K.VPEESVLPVQK.S
SW:ACIN_HUMAN	S06	6648	2	1338.6	(+0.8)	3.129	0.486	1.000	2	K.VPEESVLPVQK.S
SW:ACIN_HUMAN	S06	5352	2	976.1	(+0.8)	2.721	0.393	0.974	4	K.VTLGDTLTR.R
SW:ACIN_HUMAN	S07	5400	2	976.1	(+0.9)	2.201	0.309	0.883	4	K.VTLGDTLTR.R
SW:ACIN_HUMAN	S11	5018	2	1235.4	(+0.1)	2.531	0.337	0.081	4	R.GL*L*VDRPSETK#.T
SW:ACTA_HUMAN	S11	7254	2	1792.0	(+1.0)	3.513	0.451	0.983	16	K.SYELPDGQVITIGNER.F
SW:ACTA_HUMAN	S11	6868	2	1792.0	(-0.5)	2.640	0.435	0.933	16	K.SYELPDGQVITIGNER.F
SW:ACTA_HUMAN	S12	6658	2	1792.0	(+0.9)	3.390	0.567	1.000	16	K.SYELPDGQVITIGNER.F
SW:ACTA_HUMAN	S15	7164	2	1792.0	(-0.4)	2.779	0.247	0.760	16	K.SYELPDGQVITIGNER.F
SW:ACTA_HUMAN	S16	7122	2	1792.0	(-0.7)	2.430	0.422	0.722	16	K.SYELPDGQVITIGNER.F
SW:ACTA_HUMAN	S17	7400	2	1792.0	(-0.5)	2.574	0.427	0.925	16	K.SYELPDGQVITIGNER.F
SW:ACTA_HUMAN	S18	7314	2	1792.0	(+0.6)	3.745	0.382	0.980	16	K.SYELPDGQVITIGNER.F
SW:ACTA_HUMAN	S18	7328	2	1792.0	(-0.9)	2.617	0.366	0.673	16	K.SYELPDGQVITIGNER.F
SW:ACTA_HUMAN	S19	7344	2	1792.0	(+0.8)	3.188	0.537	1.000	16	K.SYELPDGQVITIGNER.F
SW:ACTA_HUMAN	S12	6986	2	1962.2	(+0.9)	3.743	0.346	0.975	6	K.YPIEHGIITNWDDMEK.I
SW:ACTA_HUMAN	S20	6484	2	1792.0	(+0.4)	2.510	0.387	0.948	16	K.SYELPDGQVITIGNER.F
SW:ACTB_HUMAN	S12	7364	2	2216.5	(-0.0)	3.318	0.437	0.959	11	K.DLYANTVLSGGTTMYPGIADR.M

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ACTB_HUMAN	S12	6514	2	1516.7	(+0.7)	2.828	0.453	0.979	10	K.IWHHTFYNELR.V
SW:ACTB_HUMAN	S11	6870	2	1955.3	(-0.8)	3.628	0.548	1.000	5	R.VAPEEHPVLLTEAPLNPK.A
SW:ACTB_HUMAN	S12	6660	2	1955.3	(+0.7)	4.486	0.499	1.000	5	R.VAPEEHPVLLTEAPLNPK.A
SW:ACTB_HUMAN	S13	7058	2	1955.3	(+0.3)	4.020	0.505	1.000	5	R.VAPEEHPVLLTEAPLNPK.A
SW:ACTB_HUMAN	S14	6998	2	1955.3	(-0.6)	3.415	0.510	1.000	5	R.VAPEEHPVLLTEAPLNPK.A
SW:ACTB_HUMAN	S15	6834	2	1955.3	(-0.7)	3.517	0.517	1.000	5	R.VAPEEHPVLLTEAPLNPK.A
SW:ACTB_HUMAN	S19	6874	2	1955.3	(-0.7)	2.773	0.546	0.878	5	R.VAPEEHPVLLTEAPLNPK.A
SW:AURB_HUMAN	S12	5640	2	946.1	(+0.7)	2.318	0.474	0.978	16	K.FGNVYL*AR.E
SW:AURB_HUMAN	S12	6560	2	1531.7	(+0.1)	2.886	0.406	0.935	4	K.FPASVPTGAQDLISK.L
SW:AURB_HUMAN	S13	6812	2	1154.3	(+0.5)	2.844	0.220	0.921	7	R.LYNYFYDR.R
SW:BA1B_HUMAN	S08	7532	2	1815.0	(+1.0)	2.572	0.419	0.962	4	R.AGTGENAPWVVEDELVK.K
SW:BA1B_HUMAN	S03	6559	2	1265.4	(+0.3)	2.407	0.236	0.561	4	K.FSDFL*L*DPYK#.Y
SW:BA1B_HUMAN	S04	6613	2	1245.4	(+0.7)	3.103	0.464	1.000	4	K.FSDFLLDPYK.Y
SW:BA1B_HUMAN	S06	7752	2	1245.4	(+0.2)	2.213	0.491	0.944	4	K.FSDFLLDPYK.Y
SW:BA1B_HUMAN	S11	7858	2	1245.4	(+0.9)	2.331	0.268	0.872	4	K.FSDFLLDPYK.Y
SW:BA1B_HUMAN	S14	8038	2	1245.4	(+0.2)	2.453	0.345	0.889	4	K.FSDFLLDPYK.Y
SW:BA1B_HUMAN	S05	6606	2	940.1	(+0.8)	2.603	0.125	0.657	5	K.GGFLYLNR.V
SW:BA1B_HUMAN	S06	6570	2	952.1	(+0.7)	2.478	0.235	0.897	5	K.GGFL*YL*NR.V
SW:BA1B_HUMAN	S03	5779	2	1298.5	(+0.7)	2.361	0.207	0.738	4	K.IISNVPADSLIR.T
SW:BA1B_HUMAN	S03	5775	2	1304.5	(+0.2)	2.260	0.365	0.855	4	K.IISNVPADSL*IR.T
SW:BA1B_HUMAN	S04	5257	2	1004.1	(+0.6)	2.265	0.319	0.919	4	R.SDLIEVATR.L
SW:BA1B_HUMAN	S05	5798	2	1004.1	(+0.7)	3.210	0.342	0.977	4	R.SDLIEVATR.L
SW:BA1B_HUMAN	S10	6012	2	1004.1	(+0.9)	2.653	0.240	0.912	4	R.SDLIEVATR.L
SW:BA1B_HUMAN	S03	4737	2	1360.5	(-0.4)	2.523	0.412	0.921	5	K.TDNSSLSSPLNPK.L
SW:BA1B_HUMAN	S05	4900	2	1360.5	(+0.3)	3.271	0.398	0.953	5	K.TDNSSLSSPLNPK.L
SW:BA1B_HUMAN	S05	4892	2	1380.5	(-0.3)	2.302	0.229	0.404	5	K.TDNSSL*SSPL*NPK#.L
SW:BA1B_HUMAN	S06	4794	2	1360.5	(+0.5)	3.069	0.436	0.980	5	K.TDNSSLSSPLNPK.L
SW:BA1B_HUMAN	S06	4718	2	1360.5	(+0.3)	2.561	0.439	0.928	5	K.TDNSSLSSPLNPK.L
SW:BA1B_HUMAN	S06	4760	2	1380.5	(-0.8)	2.414	0.184	0.112	5	K.TDNSSL*SSPL*NPK#.L
SW:BA1B_HUMAN	S07	4698	2	1360.5	(+0.5)	3.192	0.524	1.000	5	K.TDNSSLSSPLNPK.L
SW:BA1B_HUMAN	S07	4696	2	1380.5	(-0.2)	2.885	0.425	0.900	5	K.TDNSSL*SSPL*NPK#.L
SW:BA1B_HUMAN	S08	5132	2	1360.5	(-0.0)	2.853	0.399	0.937	5	K.TDNSSLSSPLNPK.L
SW:BA1B_HUMAN	S11	4670	2	1360.5	(+1.0)	3.451	0.559	1.000	5	K.TDNSSLSSPLNPK.L
SW:BA1B_HUMAN	S05	9444	2	1844.1	(+0.2)	2.375	0.525	0.950	4	R.YWLFSDVEVPGLFIEK.G
SW:BA1B_HUMAN	S06	9370	2	1844.1	(+0.8)	3.026	0.540	1.000	4	R.YWLFSDVEVPGLFIEK.G
SW:BA1B_HUMAN	S06	9396	2	1844.1	(-0.6)	2.395	0.314	0.782	4	R.YWLFSDVEVPGLFIEK.G
SW:BA1B_HUMAN	S07	9486	2	1844.1	(-0.4)	2.956	0.402	0.937	4	R.YWLFSDVEVPGLFIEK.G
SW:BA1B_HUMAN	S08	9660	2	1844.1	(+0.6)	3.375	0.562	0.987	4	R.YWLFSDVEVPGLFIEK.G
SW:BA1B_HUMAN	S09	9654	2	1844.1	(-0.0)	3.393	0.421	0.957	4	R.YWLFSDVEVPGLFIEK.G
SW:BA1B_HUMAN	S09	9666	2	1864.1	(+0.2)	2.503	0.356	0.760	4	R.YWL*FSDEVPGL*FIEK#.G
SW:BA1B_HUMAN	S10	10210	2	1844.1	(-0.1)	2.563	0.352	0.847	4	R.YWLFSDVEVPGLFIEK.G
SW:BA1B_HUMAN	S14	9788	2	1844.1	(+0.8)	3.860	0.578	1.000	4	R.YWLFSDVEVPGLFIEK.G
SW:BA1B_HUMAN	S15	5842	2	1004.1	(+0.3)	2.644	0.400	0.944	4	R.SDLIEVATR.L
SW:BAF_HUMAN	S20	8414	2	1350.7	(+0.9)	3.454	0.505	1.000	1	K.AYVVLGQFLVLK.K
SW:BAF_HUMAN	S20	8544	2	1376.7	(+0.3)	2.842	0.398	0.887	1	K.AYVVL*GQFL*VL*K#.K
SW:BAF_HUMAN	S20	8410	2	1376.7	(+0.4)	2.551	0.294	0.839	1	K.AYVVL*GQFL*VL*K#.K
SW:BAF_HUMAN	S20	7668	3	2429.8	(+0.5)	3.870	0.468	0.982	1	R.DFVAEPMGEK#PVGSL*AGIGEVL*GK#.K
SW:BAF_HUMAN	S20	3786	2	937.0	(+1.0)	2.288	0.303	0.934	1	K.K#DEDL*FR.E
SW:BIN4_HUMAN	S07	7832	2	2350.5	(+0.6)	4.597	0.582	1.000	1	R.SELLAEPEPFLEGEDGEDTAK.I
SW:BIN4_HUMAN	S07	6890	2	1197.4	(+0.0)	2.678	0.434	0.948	1	R.GHVAALDWVTK.K
SW:BOP1_HUMAN	S04	7091	3	2392.6	(-0.2)	4.125	0.421	0.993	5	R.DPTPSFYDLWAQEDPNAVLGR.H
SW:BOP1_HUMAN	S05	8592	2	2392.6	(+0.2)	5.109	0.562	1.000	5	R.DPTPSFYDLWAQEDPNAVLGR.H
SW:BOP1_HUMAN	S05	8580	3	2404.6	(+0.8)	3.845	0.430	0.998	5	R.DPTPSFYDL*WAQEDPNAVL*GR.H
SW:BOP1_HUMAN	S06	8512	3	2392.6	(+0.6)	4.978	0.537	1.000	5	R.DPTPSFYDLWAQEDPNAVLGR.H
SW:BOP1_HUMAN	S06	8520	3	2404.6	(+0.5)	4.906	0.523	1.000	5	R.DPTPSFYDL*WAQEDPNAVL*GR.H
SW:BOP1_HUMAN	S08	5446	2	1343.4	(+0.2)	2.742	0.422	0.947	5	R.LAWEQQEPGER.K
SW:BOP1_HUMAN	S09	5458	2	1343.4	(+0.0)	2.664	0.314	0.881	5	R.LAWEQQEPGER.K
SW:BOP1_HUMAN	S04	5047	2	1144.3	(+0.2)	2.237	0.226	0.613	5	R.LTDEQVALVR.R
SW:BOP1_HUMAN	S05	5532	2	1144.3	(+0.7)	3.710	0.388	1.000	5	R.LTDEQVALVR.R
SW:BOP1_HUMAN	S05	5834	2	946.1	(+0.5)	2.348	0.322	0.940	5	R.LWEVATAR.C
SW:BOP1_HUMAN	S05	6828	2	1380.5	(+0.7)	3.526	0.283	0.418	5	R.TRELDQFLDK.M

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:BOP1_HUMAN	S05	7242	2	1239.4	(-0.2)	2.967	0.393	0.948	5	R.VNVDPEDLIPK.L
SW:BOP1_HUMAN	S09	7384	2	1239.4	(+0.7)	2.875	0.263	0.931	5	R.VNVDPEDLIPK.L
SW:BOP1_HUMAN	S11	7222	2	1239.4	(+1.0)	2.848	0.177	0.725	5	R.VNVDPEDLIPK.L
SW:BOP1_HUMAN	S05	4784	2	1149.2	(+0.5)	2.344	0.295	0.913	5	R.WLEAEEER.Q
SW:BOP1_HUMAN	S05	4796	2	1155.2	(+0.1)	2.320	0.173	0.540	5	R.WL*EASEEER.Q
SW:BOP1_HUMAN	S10	4874	2	1149.2	(+0.5)	2.649	0.118	0.678	5	R.WLEAEEER.Q
SW:BOP1_HUMAN	S11	4476	2	1149.2	(+0.5)	2.335	0.407	0.964	5	R.WLEAEEER.Q
SW:BOP1_HUMAN	S12	5406	2	1144.3	(+0.7)	2.818	0.355	0.967	5	R.LTDEQVALVR.R
SW:BP28_HUMAN	S06	8442	2	1237.5	(+0.7)	2.489	0.288	0.908	2	K.LVPDLLAIVQR.K
SW:BP28_HUMAN	S08	10312	3	2237.6	(+0.5)	3.738	0.334	0.986	2	K.NTSELVSSEVYLLSALAALQK.V
SW:BP28_HUMAN	S11	10236	3	2237.6	(+0.8)	4.090	0.395	0.996	2	K.NTSELVSSEVYLLSALAALQK.V
SW:BP28_HUMAN	S06	8542	2	1684.0	(+0.4)	3.132	0.382	0.970	2	K.VNALLPTETFIPVIR.G
SW:BP28_HUMAN	S05	8858	2	1542.9	(+0.2)	3.179	0.336	0.928		K.VSLLNEQFLPLIR.L
SW:BP28_HUMAN	S09	8996	2	1542.9	(+0.9)	2.288	0.274	0.830		K.VSLLNEQFLPLIR.L
SW:BP28_HUMAN	S12	8692	2	1542.9	(+0.3)	2.742	0.305	0.863		K.VSLLNEQFLPLIR.L
SW:BP28_HUMAN	S17	8920	2	1542.9	(+0.9)	2.604	0.253	0.757		K.VSLLNEQFLPLIR.L
SW:BYST_HUMAN	S07	5948	2	1477.8	(-0.2)	2.236	0.129	0.024	4	K.CSIPVL*HSSAAML*K#.I
SW:BYST_HUMAN	S10	8036	2	1135.4	(+0.6)	3.555	0.216	0.962	4	R.FYNLVLLPR.V
SW:BYST_HUMAN	S11	7994	2	1135.4	(+0.5)	3.052	0.182	0.915	4	R.FYNLVLLPR.V
SW:BYST_HUMAN	S14	8196	2	1135.4	(+0.4)	2.320	0.169	0.710	4	R.FYNLVLLPR.V
SW:BYST_HUMAN	S15	7878	2	1135.4	(+0.9)	2.530	0.142	0.687	4	R.FYNLVLLPR.V
SW:CBF_HUMAN	S04	5521	2	984.2	(+1.0)	2.506	0.385	0.961	1	K.ALLVQVVK.L
SW:CBF_HUMAN	S04	7661	3	2401.7	(+1.0)	4.052	0.417	0.997	1	K.GAIDDLQQGELEAFIQNLNLAKE.Y
SW:CBF_HUMAN	S10	10286	3	2401.7	(+0.9)	4.512	0.491	1.000	1	K.GAIDDLQQGELEAFIQNLNLAKE.Y
SW:CBF_HUMAN	S10	10290	3	2433.7	(+0.3)	3.780	0.424	0.985	1	K.GAIDDL*QQGEL*EAFIQNL*NL*AK#.Y
SW:CBF_HUMAN	S12	9322	3	2401.7	(+0.0)	4.135	0.453	0.995	1	K.GAIDDLQQGELEAFIQNLNLAKE.Y
SW:CBF_HUMAN	S14	9824	3	2401.7	(+0.6)	4.503	0.498	1.000	1	K.GAIDDLQQGELEAFIQNLNLAKE.Y
SW:CBX1_HUMAN	S16	7634	2	1750.0	(-0.0)	2.451	0.429*	0.028	2	R.IIGATDSSGEL*M@FL*MK#.W
SW:CBX1_HUMAN	S16	6778	3	2110.3	(+0.8)	4.365	0.520	1.000		K.KVEEVLEEEEEYYVEK.V
SW:CBX1_HUMAN	S17	8310	2	1734.0	(-0.2)	2.632	0.305	0.700	2	R.IIGATDSSGEL*MFL*MK#.W
SW:CBX3_HUMAN	S17	5778	2	1176.3	(+0.6)	3.257	0.460	1.000	3	K.DSDEADLVLAKE
SW:CBX3_HUMAN	S17	5782	2	1196.3	(-0.3)	2.458	0.211	0.482	3	K.DSDEADL*VL*AK#.E
SW:CBX3_HUMAN	S17	5936	2	1176.3	(+0.2)	2.253	0.371	0.870	3	K.DSDEADLVLAKE
SW:CBX3_HUMAN	S16	5900	2	1662.8	(+0.9)	5.286	0.434	1.000	2	K.KVEEAPEEFVVEK.V
SW:CBX3_HUMAN	S17	6194	2	1662.8	(-0.5)	4.902	0.447	1.000	2	K.KVEEAPEEFVVEK.V
SW:CBX3_HUMAN	S17	6188	3	1662.8	(+0.4)	3.764	0.259	0.966	2	K.KVEEAPEEFVVEK.V
SW:CBX3_HUMAN	S19	5798	2	1662.8	(+0.7)	3.180	0.388	0.974	2	K.KVEEAPEEFVVEK.V
SW:CBX3_HUMAN	S17	6240	2	1542.7	(-0.3)	2.771	0.326	0.798	2	K.VEEAPEEFVVEK#.V
SW:CBX3_HUMAN	S17	6514	2	1490.7	(-0.3)	3.315	0.448	0.380	3	K.WKDSDEADLVLAKE
SW:CBX3_HUMAN	S17	6522	2	1518.7	(-0.4)	3.130	0.338	0.127	3	K.WK#DSDEADL*VL*AK#.E
SW:CBX3_HUMAN	S19	5468	2	1176.3	(+1.0)	2.726	0.424*	0.296	3	K.DSDEADLVLAKE
SW:CBX5_HUMAN	S15	5576	2	1190.3	(+0.6)	2.639	0.192	0.820	1	K.DTDEADLVLAKE
SW:CBX5_HUMAN	S16	5604	2	1210.3	(+0.6)	2.270	0.343	0.853	1	K.DTDEADL*VL*AK#.E
SW:CBX5_HUMAN	S15	5448	2	1590.6	(+0.9)	3.709	0.399	0.983	1	K.GFSEEHTWEPEK.N
SW:CBX5_HUMAN	S15	5418	2	1598.6	(-0.2)	3.347	0.390	0.911	1	K.GFSEEHTWEPEK#.N
SW:CBX5_HUMAN	S16	5278	2	1590.6	(-0.4)	2.970	0.290	0.879	1	K.GFSEEHTWEPEK.N
SW:CBX5_HUMAN	S15	6006	2	970.1	(+0.2)	2.226	0.316*	0.045	1	K.GQVEYL*L*K#.W
SW:CBX5_HUMAN	S16	8050	2	1716.1	(-0.3)	2.490	0.237	0.642	1	K.IIGATDSCGDLMLFMK.W
SW:CBX5_HUMAN	S16	1932	2	1342.4	(+0.6)	3.159	0.357	0.945	1	R.K#SNFNSADDIK#.S
SW:CBX5_HUMAN	S15	5932	3	1588.7	(+0.9)	3.882	0.371	0.992	1	R.L*TWHAYPEDAENK#.E
SW:CBX5_HUMAN	S15	5956	2	1574.7	(-0.2)	3.772	0.331	0.950	1	R.LTWHAYPEDAENK.E
SW:CBX5_HUMAN	S16	5772	2	1574.7	(-0.3)	3.842	0.393	0.964	1	R.LTWHAYPEDAENK.E
SW:CBX5_HUMAN	S16	5852	2	1574.7	(-0.3)	3.769	0.433	1.000	1	R.LTWHAYPEDAENK.E
SW:CBX5_HUMAN	S16	5778	2	1588.7	(-1.0)	3.593	0.216	0.486	1	R.L*TWHAYPEDAENK#.E
SW:CBX5_HUMAN	S16	5752	2	1832.0	(-0.6)	2.840	0.443	0.287	1	R.LTWHAYPEDAENKEK.E
SW:CBX5_HUMAN	S15	2076	2	1198.2	(+1.0)	2.570	0.418	0.970	1	K.SNFNSADDIK.S
SW:CBX5_HUMAN	S16	2050	2	1206.2	(+0.8)	2.807	0.463	0.963	1	K.SNFNSADDIK#.S
SW:CBX5_HUMAN	S16	2042	2	1198.2	(+1.0)	2.630	0.509	0.982	1	K.SNFNSADDIK.S
SW:CBX5_HUMAN	S16	4638	2	1198.2	(+0.7)	2.604	0.483	0.980	1	K.SNFNSADDIK.S
SW:CBX5_HUMAN	S16	6312	3	1532.7	(+0.1)	3.727	0.236	0.360	1	K.WK#DTDEADL*VL*AK#.E

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:CBX5_HUMAN	S19	6478	2	1504.7	(-0.7)	2.877	0.185	0.013	1	K.WKDTDEADLVLAKE
SW:CBX5_HUMAN	S19	5378	2	1590.6	(-0.4)	2.590	0.292	0.819	1	K.GFSEEHTWEPEK.N
SW:CBX8_HUMAN	S11	7034	3	2522.8	(-1.0)	3.929	0.393	0.624	1	R.K#EL*PDPSQRPL*GEPSAGL*GEYL*K#.G
SW:CBX8_HUMAN	S11	6306	2	949.1	(+0.9)	2.862	0.371	0.977	1	R.LLAAFEER.E
SW:CBX8_HUMAN	S11	6302	2	961.1	(+0.7)	2.637	0.382	0.973	1	R.L*L*AAFEER.E
SW:CBX8_HUMAN	S11	7290	2	1723.8	(-0.9)	2.859	0.412	0.799	1	K.YSTWEPEENILDAR.L
SW:CBX8_HUMAN	S11	7164	2	982.2	(+0.9)	2.412	0.305	0.867	1	R.VFAAEAL*L*K#.R
SW:CDC2_HUMAN	S14	5548	2	1186.4	(+0.0)	3.106	0.229	0.859	5	K.IGEGTYGVVYK.G
SW:CDC2_HUMAN	S14	7082	2	1331.5	(+0.8)	2.757	0.394	0.968	2	K.NLDENGLDLLSK.M
SW:CG48_HUMAN	S08	1656	2	1660.8	(+0.5)	3.084	0.524	1.000	1	K.AGAGPGGPPQKPAPSSQR.K
SW:CG48_HUMAN	S08	6570	3	2269.5	(-0.2)	3.880	0.393	0.877	2	R.L*K#EEFQHAM@GGVPAWAETTK#.R
SW:CG48_HUMAN	S08	6108	2	1100.2	(+0.7)	2.333	0.361	0.893	2	R.SGYFAL*GNEK#.G
SW:CGB7_HUMAN	S16	2090	2	1341.5	(+0.8)	3.324	0.411	0.391	3	K.AM@EVDIEERPK#.E
SW:CGB7_HUMAN	S16	9116	2	1888.1	(+0.8)	4.051	0.567	1.000	1	R.FYPAEWQDFLDSLQK.R
SW:CGB7_HUMAN	S16	7154	2	1917.2	(-0.6)	4.209	0.395	0.966	3	R.KPYVLNDLEAEASLPEK.K
SW:CGB7_HUMAN	S16	7002	3	2087.3	(-0.6)	4.315	0.377	0.899	3	R.K#PYVL*NDL*EAEASL*PEK#K#.G
SW:CGB7_HUMAN	S16	6536	2	1528.7	(-0.0)	2.682	0.314	0.854	2	R.QNLAEMGLAVDPNR.A
SW:CGB7_HUMAN	S16	5474	2	1556.7	(-0.4)	2.529	0.127	0.342	2	R.QNL*AEM@GL*AVDPNR.A
SW:CHD4_HUMAN	S05	8514	2	1686.9	(+0.6)	2.212	0.136	0.222	1	R.GGGNQVSL*L*NVMV@DL*K#.K
SW:CHD4_HUMAN	S07	5238	3	1864.0	(+0.9)	3.922	0.353	0.961	1	K.IEENSLKEEESIEGEK.E
SW:COF1_HUMAN	S17	6100	2	1338.5	(+0.8)	2.936	0.466	0.983	2	R.YALYDATYETK.E
SW:COF1_HUMAN	S17	6104	2	1352.5	(-0.5)	2.216	0.293	0.591	2	R.YAL*YDATYETK#.E
SW:COF1_HUMAN	S18	7922	2	2167.4	(+0.3)	5.001	0.496	1.000	1	K.EILVGDVGGQTVDDPYATFVK.M
SW:DBPA_HUMAN	S11	6726	2	1796.9	(-0.1)	3.293	0.460	0.506	14	R.SVGDGETVEFDVVEGEK.G
SW:DBPA_HUMAN	S11	5744	2	1295.5	(+0.2)	2.241	0.389	0.794	15	K.EDVVFVHQTAIK#.K
SW:DD10_HUMAN	S05	5428	3	2029.1	(+0.7)	4.372	0.468	0.995	2	K.SAIKDAEEDDDTGGINLHK.A
SW:DD10_HUMAN	S05	8362	2	1098.3	(-0.8)	2.774	0.257	0.634	2	K.ISVLYSFLR.S
SW:DD15_HUMAN	S06	5292	2	1194.3	(+0.8)	2.477	0.455	0.974	1	R.LDLGEDYPSGK.K
SW:DD15_HUMAN	S06	7084	2	1158.4	(+0.4)	3.209	0.435	0.983	1	R.SNLGSVVLQLK.K
SW:DD15_HUMAN	S06	8808	2	1317.6	(+0.1)	2.699	0.375	0.853	2	R.TL*ATDIL*M@GVL*K#.E
SW:DD15_HUMAN	S06	9194	2	1301.6	(-0.6)	2.488	0.321	0.737	2	R.TL*ATDIL*MGVL*K#.E
SW:DD15_HUMAN	S09	9456	2	1275.6	(+0.7)	3.553	0.493	1.000	2	R.TLATDILMGVLK.E
SW:DD15_HUMAN	S11	5440	2	1194.3	(+0.6)	2.461	0.400	0.962	1	R.LDLGEDYPSGK.K
SW:DD17_HUMAN	S07	6452	2	1233.4	(+0.4)	2.491	0.263	0.873	5	K.APIL*IATDVASR.G
SW:DD17_HUMAN	S07	6448	2	1227.4	(+0.8)	2.390	0.339	0.926	5	K.APILIATDVASR.G
SW:DD17_HUMAN	S08	6582	2	1227.4	(+0.7)	3.912	0.520	1.000	5	K.APILIATDVASR.G
SW:DD17_HUMAN	S08	6584	2	1233.4	(+0.3)	2.892	0.433	0.953	5	K.APIL*IATDVASR.G
SW:DD17_HUMAN	S16	6376	2	1227.4	(+1.0)	2.923	0.498	0.984	5	K.APILIATDVASR.G
SW:DD17_HUMAN	S07	7532	2	1079.2	(+0.8)	2.618	0.149	0.784	1	R.DWVLNEFR.S
SW:DD17_HUMAN	S07	7538	2	1085.2	(+0.8)	2.222	0.172	0.654	1	R.DWVL*NEFR.S
SW:DD17_HUMAN	S07	6606	2	1706.8	(-0.7)	2.741	0.172	0.141	1	R.EL*AQQVQQVADDYGK#.C
SW:DD17_HUMAN	S08	6720	2	1706.8	(-0.4)	2.202	0.342	0.634	1	R.EL*AQQVQQVADDYGK#.C
SW:DD17_HUMAN	S07	7144	2	1042.2	(+0.2)	2.359	0.208	0.495	1	R.L*IDFL*ESGK#.T
SW:DD17_HUMAN	S08	6228	2	1375.6	(+0.0)	2.315	0.254	0.696	10	R.M@L*DM@GFEPQIR.K
SW:DD17_HUMAN	S07	4370	2	1340.5	(+0.2)	2.682	0.330	0.799	1	K.VL*EEANQAINPK#.L
SW:DD17_HUMAN	S18	6480	2	1227.4	(+0.7)	2.819	0.265	0.920	5	K.APILIATDVASR.G
SW:DD18_HUMAN	S07	2392	1	701.8	(+0.0)	1.948	0.318	0.000	5	R.DLLAAAK.T
SW:DD18_HUMAN	S06	8722	3	2312.5	(+0.4)	3.778	0.359	0.992	6	R.GLDIPEVDWIVQYDPPDDPK.E
SW:DD18_HUMAN	S06	5088	2	1175.3	(-0.2)	2.201	0.191	0.321	3	K.ISDIQSQL*EK#.L
SW:DD18_HUMAN	S11	5150	2	1175.3	(+0.6)	2.296	0.230	0.675	3	K.ISDIQSQL*EK#.L
SW:DD18_HUMAN	S12	5002	2	1161.3	(+0.3)	2.762	0.194	0.752	3	K.ISDIQSLEK.L
SW:DD18_HUMAN	S15	5122	2	1175.3	(+0.5)	2.486	0.298	0.858	3	K.ISDIQSQL*EK#.L
SW:DD18_HUMAN	S16	5016	2	1161.3	(+0.1)	2.946	0.216	0.834	3	K.ISDIQSLEK.L
SW:DD18_HUMAN	S16	5030	2	1175.3	(+0.1)	2.940	0.258	0.786	3	K.ISDIQSQL*EK#.L
SW:DD18_HUMAN	S17	5516	2	1161.3	(+0.2)	3.123	0.214	0.861	3	K.ISDIQSLEK.L

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:DD18_HUMAN	S17	5524	2	1175.3	(+0.0)	2.528	0.173	0.440	3	K.ISDIQSQL*EK#.L
SW:DD18_HUMAN	S07	5910	2	1053.2	(+0.9)	2.244	0.188	0.045	5	K.SIRPL*L*EGR.D
SW:DD18_HUMAN	S06	7936	2	1442.6	(+0.3)	2.954	0.522	1.000	4	K.VPLSEDFDFSWK.I
SW:DD18_HUMAN	S06	7938	2	1456.6	(-0.1)	2.638	0.337	0.799	4	K.VPL*SEDFDFSWK#.I
SW:DD18_HUMAN	S07	8078	2	1442.6	(-0.0)	2.614	0.478	0.954	4	K.VPLSEDFDFSWK.I
SW:DD18_HUMAN	S07	7982	2	1456.6	(-0.1)	2.517	0.355	0.798	4	K.VPL*SEDFDFSWK#.I
SW:DD18_HUMAN	S08	8186	2	1442.6	(+0.9)	2.835	0.536	1.000	4	K.VPLSEDFDFSWK.I
SW:DD18_HUMAN	S11	8014	2	1442.6	(+0.9)	2.466	0.527	0.981	4	K.VPLSEDFDFSWK.I
SW:DD18_HUMAN	S12	7802	2	1442.6	(+0.4)	3.477	0.543	1.000	4	K.VPLSEDFDFSWK.I
SW:DD18_HUMAN	S12	7804	2	1456.6	(+0.2)	2.414	0.306	0.640	4	K.VPL*SEDFDFSWK#.I
SW:DD18_HUMAN	S14	8222	2	1442.6	(+0.6)	2.588	0.441	0.960	4	K.VPLSEDFDFSWK.I
SW:DD18_HUMAN	S15	7886	2	1456.6	(+0.5)	2.272	0.428	0.918	4	K.VPL*SEDFDFSWK#.I
SW:DD18_HUMAN	S16	7892	2	1456.6	(+0.0)	2.494	0.424	0.868	4	K.VPL*SEDFDFSWK#.I
SW:DD18_HUMAN	S17	8094	2	1456.6	(+0.5)	2.667	0.397	0.935	4	K.VPL*SEDFDFSWK#.I
SW:DD18_HUMAN	S19	5140	2	1161.3	(+0.2)	2.294	0.184	0.519	3	K.ISDIQSQLEK.L
SW:DD21_HUMAN	S01	6228	2	1165.4	(+0.9)	2.503	0.243	0.863	3	R.APQVLVLAPTR.E
SW:DD21_HUMAN	S05	6382	2	1165.4	(-0.7)	2.757	0.439	0.837	3	R.APQVLVLAPTR.E
SW:DD21_HUMAN	S05	6368	2	1177.4	(+0.5)	2.415	0.116	0.524	3	R.APQVL*VL*APTR.E
SW:DD21_HUMAN	S05	7336	2	1669.8	(+0.8)	3.247	0.459	0.982	5	K.EGAFSNFPISEETIK.L
SW:DD21_HUMAN	S05	7346	2	1677.8	(-0.8)	2.408	0.283	0.254	5	K.EGAFSNFPISEETIK#.L
SW:DD21_HUMAN	S09	7474	2	1669.8	(-0.2)	2.688	0.246	0.733	5	K.EGAFSNFPISEETIK.L
SW:DD21_HUMAN	S11	7322	2	1669.8	(+0.2)	2.940	0.388	0.930	5	K.EGAFSNFPISEETIK.L
SW:DD21_HUMAN	S14	7440	2	1669.8	(-0.0)	2.383	0.277	0.701	5	K.EGAFSNFPISEETIK.L
SW:DD21_HUMAN	S10	8204	2	1221.5	(-0.4)	2.427	0.406	0.920	3	R.GVTFLFPIQAK.T
SW:DD21_HUMAN	S11	8146	2	1221.5	(-0.4)	2.313	0.296	0.782	3	R.GVTFLFPIQAK.T
SW:DD21_HUMAN	S13	8264	2	1221.5	(+0.8)	2.625	0.423	0.972	3	R.GVTFLFPIQAK.T
SW:DD21_HUMAN	S14	8332	2	1221.5	(+0.7)	3.665	0.455	1.000	3	R.GVTFLFPIQAK.T
SW:DD21_HUMAN	S06	6500	2	1136.4	(+0.7)	2.485	0.226	0.718	3	R.IGVPSATEIIK#.A
SW:DD21_HUMAN	S09	6840	2	1136.4	(+0.6)	2.223	0.138	0.318	3	R.IGVPSATEIIK#.A
SW:DD21_HUMAN	S14	6770	2	1136.4	(+0.9)	2.365	0.170	0.503	3	R.IGVPSATEIIK#.A
SW:DD21_HUMAN	S15	6602	2	1136.4	(+0.7)	2.241	0.262	0.703	3	R.IGVPSATEIIK#.A
SW:DD21_HUMAN	S05	2228	2	1728.8	(-0.1)	2.621	0.254	0.030	3	K.NEEPSEEEIDAPK#PK#.K
SW:DD21_HUMAN	S05	2082	2	1437.6	(+0.9)	2.292	0.153	0.412	3	K.QDAQSLHGDIPQK.Q
SW:DD21_HUMAN	S06	6258	2	1196.4	(+0.8)	2.542	0.358	0.952	3	K.TAITVEHLAIK.C
SW:DD21_HUMAN	S11	6402	2	1196.4	(+0.4)	2.617	0.413	0.970	3	K.TAITVEHLAIK.C
SW:DD21_HUMAN	S12	8378	2	1280.5	(+0.3)	2.205	0.347	0.708	3	K.TFSFAIPL*IEK#.L
SW:DD21_HUMAN	S16	6342	2	1165.4	(+0.9)	2.698	0.408	0.972	3	R.APQVLVLAPTR.E
SW:DD24_HUMAN	S07	4934	2	1336.4	(+0.4)	2.561	0.336	0.940	2	R.NEATVETLTETK.I
SW:DD24_HUMAN	S15	4016	2	1282.5	(+1.0)	2.491	0.243	0.847	2	R.SLVFANSISCIK.R
SW:DD48_HUMAN	S11	6568	2	1829.1	(+0.8)	5.147	0.521	1.000	7	R.GIYAYGFEKPSAIQQR.A
SW:DD48_HUMAN	S11	1488	2	1404.5	(+0.9)	4.349	0.527	1.000	2	K.GRDVIAQSQSGTGK.T
SW:DD48_HUMAN	S11	4978	2	1470.6	(+0.2)	3.348	0.469	0.966	2	K.LDYGQHVVAGTPGR.V
SW:DD48_HUMAN	S11	4966	2	1476.6	(-0.0)	3.249	0.436	0.959	2	K.L*DYGQHVVAGTPGR.V
SW:DD48_HUMAN	S11	7920	2	1521.8	(-0.1)	4.105	0.502	1.000	2	K.MLVLDEADEMLNK.G
SW:DD48_HUMAN	S11	6270	2	1174.3	(+1.0)	2.780	0.304*	0.367	2	K.RDELTLEGIK.Q
SW:DD48_HUMAN	S11	6160	2	992.2	(+0.4)	2.672	0.391	0.947	2	R.K#GVAINFVK#.N
SW:DDB1_HUMAN	S04	5815	2	1054.2	(+0.2)	2.259	0.201	0.419	2	K.L*VFSNVNL*K#.E
SW:DDB1_HUMAN	S05	6578	2	1054.2	(+0.5)	2.346	0.216	0.696	2	K.L*VFSNVNL*K#.E
SW:DDB1_HUMAN	S05	5672	2	1084.2	(+0.8)	2.390	0.240	0.795	2	R.L*YEWTTTEK#.E
SW:DDB1_HUMAN	S04	6323	2	1099.4	(+0.8)	2.593	0.114	0.557	2	K.YLAIAPPIIK.Q
SW:DDB1_HUMAN	S06	7318	2	1099.4	(+0.8)	2.394	0.324	0.930	2	K.YLAIAPPIIK.Q
SW:DDB1_HUMAN	S07	6642	2	1054.2	(-0.0)	2.451	0.340	0.812	2	K.L*VFSNVNL*K#.E
SW:DDX3_HUMAN	S07	9152	2	1292.5	(+0.2)	3.426	0.565	1.000	2	R.SFLDLLLNATGK.D
SW:DDX3_HUMAN	S07	9138	2	1324.5	(-0.2)	2.527	0.311	0.728	2	R.SFL*L*DL*L*NATGK#.D
SW:DDX3_HUMAN	S08	9338	2	1292.5	(+0.4)	3.380	0.528	1.000	2	R.SFLDLLLNATGK.D
SW:DDX3_HUMAN	S09	9296	2	1292.5	(+0.9)	3.709	0.519	1.000	2	R.SFLDLLLNATGK.D
SW:DDX3_HUMAN	S11	10274	3	2333.7	(+0.8)	4.068	0.389	0.993	2	K.TAAFLLPILSQIYSDGPGEALR.A
SW:DDX3_HUMAN	S15	10138	3	2333.7	(+0.8)	3.910	0.354	0.920	2	K.TAAFLLPILSQIYSDGPGEALR.A
SW:DDX5_HUMAN	S08	5768	2	1396.5	(+0.2)	3.190	0.272	0.906	3	K.NFYQEHPDL*AR.R
SW:DDX5_HUMAN	S08	5774	2	1390.5	(-0.1)	3.181	0.375	0.951	3	K.NFYQEHPDLAR.R

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:DDX5_HUMAN	S08	7616	2	1130.3	(+0.6)	2.217	0.177	0.641	1	K.QVSDLISVLR.E
SW:DDX5_HUMAN	S08	6546	2	1296.4	(+0.9)	3.484	0.432	1.000	2	R.TTYLVLDEADR.M
SW:DDX5_HUMAN	S08	6414	2	1004.2	(+0.4)	2.210	0.351	0.941	1	K.L*L*QL*VEDR.G
SW:DEK_HUMAN	S10	6486	2	1461.7	(-0.8)	2.777	0.447	0.709		K.L*L*ASANL*EEVTM@K#.Q
SW:DEK_HUMAN	S10	6090	2	1474.7	(-0.7)	2.362	0.239	0.005	2	K.L*L*YNRPGTVSSSL*K#.K
SW:DEK_HUMAN	S10	7434	2	1365.5	(+1.0)	3.536	0.431	1.000	2	K.NVGQFSGFPFEK#.G
SW:DEK_HUMAN	S10	6314	2	1663.8	(+0.8)	3.558	0.516	1.000	1	K.VYENPTYDLTER.K
SW:DEK_HUMAN	S10	6312	2	1669.8	(-0.5)	2.856	0.293	0.867	1	K.VYENPTYDL*TER.K
SW:DEK_HUMAN	S10	6094	2	1448.7	(-0.8)	2.241	0.238	0.008	2	K.LLYNRPGTVSSLK.K
SW:DHX9_HUMAN	S04	6191	2	1032.2	(+0.5)	2.409	0.110	0.636	3	R.DFVNYL*VR.I
SW:DHX9_HUMAN	S08	7308	2	1032.2	(+0.9)	2.514	0.205	0.872	3	R.DFVNYL*VR.I
SW:DHX9_HUMAN	S07	7124	2	1742.9	(-0.2)	2.293	0.134	0.236	3	R.ELDALDANDELTPPLGR.I
SW:DHX9_HUMAN	S13	7288	2	1742.9	(+0.6)	2.363	0.289	0.850	3	R.ELDALDANDELTPPLGR.I
SW:DHX9_HUMAN	S11	10836	2	1403.7	(+0.1)	2.219	0.260	0.644	3	K.ETPFELIEALLK.Y
SW:DHX9_HUMAN	S15	10654	2	1403.7	(-0.3)	2.437	0.206	0.598	3	K.ETPFELIEALLK.Y
SW:DHX9_HUMAN	S04	6153	2	1024.2	(+0.2)	3.167	0.492	1.000	3	R.L*GGIGQFL*AK#.A
SW:DHX9_HUMAN	S08	7240	2	1024.2	(-0.2)	2.738	0.330	0.838	3	R.L*GGIGQFL*AK#.A
SW:DHX9_HUMAN	S10	7204	2	1004.2	(+0.7)	2.991	0.444	0.982	3	R.LGGIGQFLAK.A
SW:DHX9_HUMAN	S10	7216	2	1024.2	(-0.3)	2.669	0.393	0.883	3	R.L*GGIGQFL*AK#.A
SW:DHX9_HUMAN	S11	7152	2	1004.2	(+0.9)	3.234	0.453	1.000	3	R.LGGIGQFLAK.A
SW:DHX9_HUMAN	S06	8656	3	2051.3	(+0.5)	4.190	0.538	1.000	3	K.TTQVPQFILDFFIQNDR.A
SW:DHX9_HUMAN	S04	6909	2	1326.5	(+0.0)	2.347	0.282	0.624	1	K.YPSPFFVFGEK#.I
SW:DHX9_HUMAN	S17	10698	2	1403.7	(-0.4)	2.436	0.276	0.766	3	K.ETPFELIEALLK.Y
SW:DIL2_HUMAN	S05	6134	2	1095.2	(+1.0)	2.587	0.285	0.935	4	K.EVNFTSEL.R.K
SW:DIL2_HUMAN	S05	4466	2	1054.1	(+0.5)	2.228	0.229	0.829	5	K.HQLEEELR.Q
SW:DIL2_HUMAN	S06	6314	2	1067.3	(+0.8)	2.976	0.342	0.966	4	K.LALAGIGQPVK.K
SW:DIL2_HUMAN	S08	6552	2	1067.3	(+0.9)	3.017	0.446	0.982	4	K.LALAGIGQPVK.K
SW:DIL2_HUMAN	S05	4968	3	1921.1	(+0.7)	4.404	0.477	0.998	4	R.M@PTK#EDEEEDPVIK#.A
SW:DIL2_HUMAN	S05	5478	3	1905.1	(+0.2)	3.822	0.418	0.926	4	R.MPTK#EDEEEDPVIK#.A
SW:DIL2_HUMAN	S11	5624	2	1355.5	(+0.3)	2.320	0.458	0.928	5	K.SSDQPLTVPVSPK.F
SW:DIL2_HUMAN	S04	6651	3	2191.4	(+0.7)	4.466	0.475	1.000	5	K.SVAEGLSGSLVQEPFQLATEK.R
SW:DIL2_HUMAN	S05	8058	2	2191.4	(+0.4)	5.644	0.613	1.000	5	K.SVAEGLSGSLVQEPFQLATEK.R
SW:DIL2_HUMAN	S05	8054	2	2217.4	(-0.7)	3.581	0.339	0.670	5	K.SVAEGL*SGSL*VQEPFQL*ATEK#.R
SW:DIL2_HUMAN	S14	5584	2	1355.5	(+0.5)	2.643	0.302	0.921	5	K.SSDQPLTVPVSPK.F
SW:DKC1_HUMAN	S09	8864	2	2110.5	(-0.3)	4.527	0.579	0.906	3	R.ALETLTGALFQRPLIAAVK.R
SW:DKC1_HUMAN	S09	2068	2	1426.6	(+0.1)	2.597	0.435	0.255	3	K.HGKPTDSTPATWK.Q
SW:DKC1_HUMAN	S15	8042	2	1314.6	(+0.7)	2.224	0.234	0.766	3	K.LDTSQWPLLLK.N
SW:DKC1_HUMAN	S09	4610	2	1396.5	(+0.9)	4.003	0.436	0.997	3	R.LHNAIEGGTQLSR.A
SW:DKC1_HUMAN	S09	4520	2	1396.5	(+0.7)	3.678	0.465	1.000	3	R.LHNAIEGGTQLSR.A
SW:DKC1_HUMAN	S09	4708	2	1396.5	(+0.9)	3.287	0.420	0.980	3	R.LHNAIEGGTQLSR.A
SW:DKC1_HUMAN	S09	4690	2	1408.5	(+0.4)	3.223	0.410	0.979	3	R.L*HNAIEGGTQL*SR.A
SW:DKC1_HUMAN	S09	4590	2	1408.5	(+0.6)	2.986	0.376	0.969	3	R.L*HNAIEGGTQL*SR.A
SW:DKC1_HUMAN	S09	4604	2	1408.5	(-0.8)	2.827	0.375	0.761	3	R.L*HNAIEGGTQL*SR.A
SW:DKC1_HUMAN	S09	4512	2	1408.5	(+0.3)	2.721	0.302	0.856	3	R.L*HNAIEGGTQL*SR.A
SW:DKC1_HUMAN	S09	7964	3	2482.8	(+0.7)	5.127	0.529	1.000	3	R.TGFINL*DK#PSNPSSHEVVAWIR.R
SW:DKC1_HUMAN	S09	8000	3	2468.8	(+0.8)	4.856	0.555	0.994	3	R.TGFINLDKPSNPSSHEVVAWIR.R
SW:DKC1_HUMAN	S16	7608	3	2482.8	(+0.9)	4.158	0.434	0.986	3	R.TGFINL*DK#PSNPSSHEVVAWIR.R
SW:DKC1_HUMAN	S16	8042	2	1314.6	(+0.8)	2.991	0.249	0.933	3	K.LDTSQWPLLLK.N
SW:EBP2_HUMAN	S12	5924	2	947.0	(+0.9)	2.438	0.289	0.943	2	R.DLEWVER.L
SW:EBP2_HUMAN	S12	7216	2	2165.4	(+0.7)	4.816	0.548	1.000	2	K.GFSDKLDLFLEGDQKPLAQR.K
SW:EBP2_HUMAN	S12	7262	3	1534.9	(-0.6)	4.244	0.361	0.931	2	R.GLLKPGLNVVLEGP.K
SW:EBP2_HUMAN	S12	6490	2	1630.8	(-0.9)	3.616	0.343	0.094	2	K.LDFLEGDQKPLAQR.K
SW:EBP2_HUMAN	S12	6432	2	1630.8	(+0.7)	2.531	0.160	0.039	2	K.LDFLEGDQKPLAQR.K
SW:EBP2_HUMAN	S12	7044	2	2190.5	(+0.4)	4.017	0.566	1.000	2	R.LDVTLPVPEIGGSEAPAPQNK.D
SW:EBP2_HUMAN	S12	6298	2	1337.5	(-0.5)	3.510	0.288	0.879	2	K.RPTDYFAEMAK#.S
SW:EBP2_HUMAN	S12	5110	2	1353.5	(+0.5)	2.499	0.342	0.892	2	K.RPTDYFAEM@AK#.S
SW:EBP2_HUMAN	S12	7232	2	1534.9	(+0.8)	2.349	0.444	0.353	2	R.GLLKPGLNVVLEGP.K
SW:EF11_HUMAN	S10	6182	2	976.2	(+0.9)	2.585	0.195	0.876	11	R.LPLQDVYK.I
SW:EF11_HUMAN	S15	6054	2	976.2	(+0.7)	2.373	0.205	0.837	11	R.LPLQDVYK.I
SW:EF11_HUMAN	S11	7622	3	2555.0	(-0.7)	3.895	0.409	0.666	9	R.VETGVL*K#PGM@VTFAPVNVVTEVK#.S

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:EF11_HUMAN	S16	5888	2	976.2	(+0.6)	3.054	0.253	0.960	11	R.LPLQDVYK.I
SW:EF2_HUMAN	S12	9360	2	1445.7	(+0.9)	2.249	0.352	0.193	3	K.EGIPALDNFLDKL.-
SW:EF2_HUMAN	S16	8988	3	2221.5	(+0.7)	4.154	0.335	0.993	2	R.ALLELQLEPEELYQTFQR.I
SW:ELV1_HUMAN	S13	5830	2	972.1	(+0.1)	2.366	0.363	0.901	10	R.AINTLNGLR.L
SW:ELV1_HUMAN	S14	6806	2	1231.4	(+0.8)	2.578	0.431	0.972		K.DANL*YISGL*PR.T
SW:ELV1_HUMAN	S13	7420	2	1569.8	(+0.9)	4.900	0.460	1.000		K.NVALLSQLYHSPAR.R
SW:ELV1_HUMAN	S13	7418	2	1587.8	(-0.4)	3.886	0.520	1.000		K.NVAL*L*SQL*YHSPAR.R
SW:ELV1_HUMAN	S14	7438	2	1587.8	(+0.2)	3.849	0.466	1.000		K.NVAL*L*SQL*YHSPAR.R
SW:ELV1_HUMAN	S13	6762	3	2629.8	(+0.5)	4.893	0.354	0.950		R.SEAEAAITSFNGHK#PPGSSEPITVK#.F
SW:ELV1_HUMAN	S13	6876	3	2613.8	(+0.2)	4.561	0.468	0.977		R.SEAEAAITSFNGHKPPGSSEPITVK.F
SW:ELV1_HUMAN	S13	6760	3	2613.8	(-0.3)	4.166	0.445	0.961		R.SEAEAAITSFNGHKPPGSSEPITVK.F
SW:ELV1_HUMAN	S13	7450	2	1354.5	(+0.7)	3.329	0.414	0.980		R.SLFSSIGEVESAK.L
SW:ELV1_HUMAN	S13	7444	2	1368.5	(-0.2)	2.924	0.371	0.868		R.SL*FSSIGEVESAK#.L
SW:ELV1_HUMAN	S14	7454	2	1368.5	(+0.7)	3.903	0.476	1.000		R.SL*FSSIGEVESAK#.L
SW:ELV1_HUMAN	S13	8098	2	2163.5	(+0.0)	2.457	0.447*	0.054		R.TNLIVNYLPQNMTQDEL.R.S
SW:ELV1_HUMAN	S14	7528	2	2197.5	(+0.7)	3.354	0.489*	0.431		R.TNL*IVNYL*PQNM@TQDEL*R.S
SW:ELV1_HUMAN	S14	8158	2	2181.5	(-0.8)	2.280	0.116*	0.009		R.TNL*IVNYL*PQNMTQDEL*R.S
SW:ELV1_HUMAN	S13	5292	2	1189.4	(-0.7)	3.472	0.552	1.000		R.VLVDQTTGLSR.G
SW:ELV1_HUMAN	S14	5146	2	1189.4	(-0.8)	2.234	0.448	0.758		R.VLVDQTTGLSR.G
SW:ELV1_HUMAN	S15	4880	2	1189.4	(+0.6)	2.549	0.406	0.967		R.VLVDQTTGLSR.G
SW:ELV1_HUMAN	S16	4810	2	1189.4	(+0.9)	3.432	0.504	1.000		R.VLVDQTTGLSR.G
SW:ELV1_HUMAN	S16	4794	2	1201.4	(-0.6)	2.597	0.360	0.909		R.VL*VDQTTGL*SR.G
SW:ELV1_HUMAN	S17	5308	2	1189.4	(+0.8)	3.236	0.466	1.000		R.VLVDQTTGLSR.G
SW:ELV1_HUMAN	S17	5286	2	1201.4	(-0.2)	2.662	0.362	0.916		R.VL*VDQTTGL*SR.G
SW:ELV1_HUMAN	S20	4562	2	1189.4	(+0.8)	2.297	0.427	0.961		R.VLVDQTTGLSR.G
SW:EMD_HUMAN	S14	5544	2	1125.2	(+0.8)	3.025	0.390	0.978	1	R.GDADMYDLPK.K
SW:EMD_HUMAN	S14	5410	2	1222.4	(+0.6)	3.076	0.390	0.981	1	K.K#IFEYETQR.R
SW:EMD_HUMAN	S14	6562	2	2162.3	(+0.1)	3.755	0.564	1.000	1	R.LSPSSSAASSYSFSDLNSTR.G
SW:EMD_HUMAN	S14	2542	2	1223.4	(+0.5)	2.478	0.167	0.590	1	K.K#EDAL*L*YQSK#.G
SW:FBRL_HUMAN	S13	5836	2	1542.8	(+0.4)	4.269	0.604	1.000	5	R.DHAVVGVYRPPPK#.V
SW:FBRL_HUMAN	S13	5846	3	1534.8	(-0.7)	4.103	0.586	1.000	5	R.DHAVVGVYRPPPK.V
SW:FBRL_HUMAN	S13	5822	2	1534.8	(-0.1)	3.981	0.579	1.000	5	R.DHAVVGVYRPPPK.V
SW:FBRL_HUMAN	S13	5784	2	1519.6	(-0.1)	3.133	0.407	0.311	5	R.VSISEGDDK#IEYR.A
SW:FBRL_HUMAN	S13	5776	2	1511.6	(+0.0)	2.791	0.375	0.215	5	R.VSISEGDDKIEYR.A
SW:FBRL_HUMAN	S13	7272	2	1255.5	(+0.0)	2.731	0.330	0.897	5	R.IVALNAHTFLR.N
SW:FUS_HUMAN	S09	7224	2	1031.1	(+0.7)	2.795	0.359*	0.275	9	K.AAIDWFDGK#.E
SW:FUS_HUMAN	S07	5054	2	1429.5	(-0.2)	3.932	0.414	1.000	9	K.GEATVSFDDPPSAK#.A
SW:FUS_HUMAN	S07	5058	2	1421.5	(+0.2)	3.589	0.523	1.000	9	K.GEATVSFDDPPSAK#.A
SW:FUS_HUMAN	S08	5346	2	1429.5	(-1.0)	2.665	0.240	0.259	9	K.GEATVSFDDPPSAK#.A
SW:FUS_HUMAN	S10	5316	2	1421.5	(-0.1)	3.587	0.473	1.000	9	K.GEATVSFDDPPSAK#.A
SW:FUS_HUMAN	S10	7122	2	1031.1	(+0.9)	2.437	0.394*	0.133	9	K.AAIDWFDGK#.E
SW:G3P2_HUMAN	S13	9934	3	2597.0	(+0.6)	4.596	0.436	0.998	3	K.VIHDNFGIVEGLMTTVHAITATQK.T
SW:G3P2_HUMAN	S13	6738	2	1426.6	(-0.3)	2.239	0.221	0.149	3	R.GAL*QNIIPASTGAAK#.A
SW:GDIS_HUMAN	S16	7764	3	2976.3	(-0.2)	4.022	0.459	0.944		K.ATFM@VGSYGPRPEEYFL*TPVEEAPK#.G
SW:GDIS_HUMAN	S16	6054	2	1332.5	(-0.6)	2.637	0.446	0.892		K.TL*L*GDGPVVTDPK#.A
SW:GR75_HUMAN	S07	8188	2	1368.6	(+0.3)	2.385	0.475	0.942	3	R.AQFEGIVTDL*IR.R
SW:GR75_HUMAN	S07	7180	3	1666.9	(+0.5)	4.162	0.301	0.979	3	R.VINEPTAAAL*AYGL*DK#.S
SW:GR75_HUMAN	S07	7174	2	1646.9	(+0.6)	2.831	0.226	0.828	3	R.VINEPTAAALAYGLDK.S
SW:GR75_HUMAN	S07	7184	2	1666.9	(-0.6)	2.810	0.274	0.687	3	R.VINEPTAAAL*AYGL*DK#.S
SW:GR75_HUMAN	S07	6580	2	1291.4	(+0.6)	2.654	0.365	0.960	3	K.VQQTVDLDFGR.A
SW:GR75_HUMAN	S12	8004	2	1362.6	(+0.7)	2.542	0.475	0.977	3	R.AQFEGIVTDLIR.R
SW:GR78_HUMAN	S07	7100	2	1412.6	(+0.2)	2.290	0.235	0.384	2	K.EL*EEIVQPIISK#.L
SW:GR78_HUMAN	S06	7152	3	1660.9	(+0.9)	3.910	0.353	0.994	13	R.IINEPTAAAIAYGLDK.R
SW:GR78_HUMAN	S06	7142	2	1660.9	(-0.0)	3.737	0.577	1.000	13	R.IINEPTAAAIAYGLDK.R
SW:GR78_HUMAN	S07	7262	2	1674.9	(+0.1)	2.316	0.235	0.387	13	R.IINEPTAAAIAYGL*DK#.R
SW:GR78_HUMAN	S08	7352	2	1660.9	(+0.1)	2.991	0.451	0.953	13	R.IINEPTAAAIAYGLDK.R
SW:GR78_HUMAN	S09	7434	3	1660.9	(+1.0)	4.594	0.381	0.996	13	R.IINEPTAAAIAYGLDK.R



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:GR78_HUMAN	S13	7396	2	1660.9	(+0.7)	4.312	0.515	1.000	13	R.IINEPTAAAIYGLDK.R
SW:GRWD_HUMAN	S10	8852	3	3333.6	(-0.2)	4.952	0.422	0.995	3	R.DPEAGDVEADPGLADLPQQLLFVHQGETELK.E
SW:GRWD_HUMAN	S10	9278	2	1798.1	(-0.2)	3.363	0.519	1.000	3	R.LLQVVEEPQALAAFLR.D
SW:GSR2_HUMAN	S08	9644	3	2072.3	(+0.9)	4.140	0.485*	0.036	6	R.LAQEPLGLEVDQFLEDVRL
SW:GSR2_HUMAN	S09	9616	3	2072.3	(+0.6)	4.237	0.535*	0.042	6	R.LAQEPLGLEVDQFLEDVRL
SW:GSR2_HUMAN	S09	9658	2	2096.3	(-0.9)	2.829	0.397	0.767	6	R.L*AQEPL*GL*EVDQFL*EDVRL
SW:GSR2_HUMAN	S09	5294	2	1303.4	(-0.4)	2.376	0.268	0.711	6	R.TSGLLSEAPNEK.L
SW:GSR2_HUMAN	S09	2134	2	1206.4	(+0.5)	2.229	0.357	0.861	6	K.DVL*AHQVPNAK#.K
SW:H11_HUMAN	S01	4488	2	1122.2	(-0.3)	3.106	0.460	0.933	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S05	4686	2	1122.2	(+0.2)	2.417	0.254	0.500	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S08	4936	2	1108.2	(+0.5)	2.360	0.401	0.957	12	K.ALAAAGYDVEK.N
SW:H11_HUMAN	S10	4774	2	1122.2	(-0.3)	2.762	0.352	0.832	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S11	5230	2	1108.2	(-0.4)	2.771	0.210	0.761	12	K.ALAAAGYDVEK.N
SW:H11_HUMAN	S12	4492	2	1108.2	(-0.6)	2.804	0.188	0.725	12	K.ALAAAGYDVEK.N
SW:H11_HUMAN	S13	5002	2	1122.2	(+0.1)	3.711	0.464	1.000	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S13	5190	2	1108.2	(+0.8)	3.706	0.501	1.000	12	K.ALAAAGYDVEK.N
SW:H11_HUMAN	S13	4952	2	1108.2	(-0.6)	3.503	0.416	0.966	12	K.ALAAAGYDVEK.N
SW:H11_HUMAN	S13	5080	2	1122.2	(+0.3)	3.477	0.487	1.000	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S13	5428	2	1122.2	(+0.5)	3.355	0.444	1.000	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S13	5160	2	1122.2	(-0.4)	3.259	0.379	0.913	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S13	5110	2	1108.2	(+1.0)	3.224	0.471	1.000	12	K.ALAAAGYDVEK.N
SW:H11_HUMAN	S13	5262	2	1122.2	(+0.7)	2.917	0.413	0.956	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S13	4928	1	1122.2	(-0.7)	2.057	0.314	0.000	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	4986	2	1122.2	(+0.7)	4.130	0.520	1.000	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	4494	2	1122.2	(+0.7)	4.125	0.519	1.000	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	5204	2	1122.2	(+0.6)	4.036	0.465	1.000	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	4582	2	1122.2	(+0.8)	3.856	0.536	1.000	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	5082	2	1122.2	(+0.0)	3.847	0.521	1.000	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	4898	2	1122.2	(+0.7)	3.746	0.499	1.000	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	4398	2	1122.2	(+0.8)	3.731	0.513	1.000	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	4718	2	1122.2	(+0.8)	3.698	0.527	0.997	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	4816	2	1122.2	(+0.7)	3.681	0.501	1.000	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	4306	2	1122.2	(+0.2)	3.678	0.412	1.000	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	9280	2	1108.2	(+0.9)	3.280	0.409	0.982	12	K.ALAAAGYDVEK.N
SW:H11_HUMAN	S14	9358	2	1108.2	(+0.7)	3.229	0.424	0.982	12	K.ALAAAGYDVEK.N
SW:H11_HUMAN	S14	5286	2	1122.2	(-0.0)	3.156	0.465	1.000	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	7722	2	1108.2	(+1.0)	3.108	0.432	0.982	12	K.ALAAAGYDVEK.N
SW:H11_HUMAN	S14	5292	2	1108.2	(+1.0)	2.867	0.449	0.980	12	K.ALAAAGYDVEK.N
SW:H11_HUMAN	S14	8346	2	1122.2	(+0.0)	2.858	0.455	0.921	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	5556	2	1108.2	(+0.7)	2.823	0.442	0.979	12	K.ALAAAGYDVEK.N
SW:H11_HUMAN	S14	5372	2	1108.2	(+0.6)	2.625	0.404	0.969	12	K.ALAAAGYDVEK.N
SW:H11_HUMAN	S14	4402	1	1122.2	(+0.4)	2.539	0.419	0.003	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	7658	2	1122.2	(-0.2)	2.520	0.349	0.805	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	4676	1	1122.2	(+0.4)	2.503	0.431	0.004	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	8030	2	1122.2	(+0.7)	2.476	0.433	0.941	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	9344	2	1122.2	(+1.0)	2.475	0.313	0.860	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	7396	2	1122.2	(+0.7)	2.470	0.293	0.834	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	4818	1	1122.2	(+0.3)	2.449	0.449	0.004	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	4730	1	1122.2	(-0.6)	2.062	0.345	0.000	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	4996	1	1122.2	(-0.7)	1.922	0.215	0.000	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S15	5068	2	1108.2	(+0.1)	3.558	0.412	1.000	12	K.ALAAAGYDVEK.N
SW:H11_HUMAN	S15	5072	2	1122.2	(-0.6)	2.850	0.381	0.884	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S15	4600	2	1122.2	(-0.2)	2.762	0.330	0.828	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S16	4460	2	1122.2	(+0.1)	3.053	0.379	0.900	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S17	4992	2	1122.2	(+0.1)	2.977	0.367	0.887	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S18	4532	2	1122.2	(-0.5)	2.478	0.360	0.810	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S19	5094	2	1122.2	(-0.1)	3.553	0.460	1.000	12	K.AL*AAAGYDVEK#.N
SW:H11_HUMAN	S19	4944	2	1108.2	(+0.3)	2.971	0.337	0.927	12	K.ALAAAGYDVEK.N
SW:H11_HUMAN	S14	2526	2	1593.7	(-0.1)	3.403	0.414	0.334	12	K.AL*AAAGYDVEK#NNSR.I
SW:H11_HUMAN	S14	4288	2	1539.7	(-0.1)	2.376	0.405	0.159	9	K.GTLVQTKGTGASGSFK.L
SW:H11_HUMAN	S13	4524	2	1236.4	(+0.8)	4.194	0.502	1.000	12	K.KALAAAGYDVEK.N
SW:H11_HUMAN	S13	4456	2	1258.4	(+0.2)	3.739	0.514	1.000	12	K.K#AL*AAAGYDVEK#.N
SW:H11_HUMAN	S13	4532	2	1258.4	(+0.0)	3.588	0.498	1.000	12	K.K#AL*AAAGYDVEK#.N

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:H11_HUMAN	S13	4424	2	1236.4	(+0.7)	3.222	0.473	1.000	12	K.KALAAAGYDVEK.N
SW:H11_HUMAN	S13	4610	2	1258.4	(+0.6)	3.188	0.481	1.000	12	K.K#AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	2482	2	1258.4	(+0.1)	3.785	0.486	1.000	12	K.K#AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	5190	3	1258.4	(+0.9)	3.709	0.323	0.987	12	K.K#AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	2560	2	1258.4	(+0.3)	3.646	0.449	0.994	12	K.K#AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	4272	2	1258.4	(+0.6)	3.416	0.486	1.000	12	K.K#AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	4280	2	1236.4	(+0.9)	3.275	0.403	0.980	12	K.KALAAAGYDVEK.N
SW:H11_HUMAN	S14	4202	2	1236.4	(-0.2)	3.226	0.416	0.958	12	K.KALAAAGYDVEK.N
SW:H11_HUMAN	S14	3080	2	1236.4	(+0.8)	3.193	0.508*	0.474	12	K.KALAAAGYDVEK.N
SW:H11_HUMAN	S14	4104	2	1258.4	(+0.1)	2.846	0.328	0.826	12	K.K#AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	4046	2	1236.4	(+1.0)	2.682	0.387	0.964	12	K.KALAAAGYDVEK.N
SW:H11_HUMAN	S14	3066	2	1258.4	(-0.3)	2.677	0.438	0.897	12	K.K#AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	4194	2	1258.4	(+0.9)	2.593	0.321	0.877	12	K.K#AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	4962	2	1236.4	(+0.9)	2.399	0.478	0.974	12	K.KALAAAGYDVEK.N
SW:H11_HUMAN	S14	5158	2	1258.4	(-0.4)	2.360	0.344	0.740	12	K.K#AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	2498	1	1258.4	(-0.8)	2.217	0.313	0.000	12	K.K#AL*AAAGYDVEK#.N
SW:H11_HUMAN	S14	2494	1	1236.4	(-0.8)	2.174	0.332	0.000	12	K.KALAAAGYDVEK.N
SW:H11_HUMAN	S19	4498	2	1108.2	(+0.1)	2.659	0.316	0.882	12	K.ALAAAGYDVEK.N
SW:H12_HUMAN	S14	746	2	875.0	(+0.7)	2.545	0.495	0.392	5	K.AASGEAK#PK#.V
SW:H12_HUMAN	S14	586	2	875.0	(+1.0)	2.462	0.466	0.343	5	K.AASGEAK#PK#.V
SW:H12_HUMAN	S14	826	2	875.0	(+0.7)	2.403	0.467	0.331	5	K.AASGEAK#PK#.V
SW:H12_HUMAN	S14	666	2	875.0	(+0.8)	2.353	0.452	0.301	5	K.AASGEAK#PK#.V
SW:H12_HUMAN	S14	346	2	875.0	(+0.7)	2.301	0.440	0.272	5	K.AASGEAK#PK#.V
SW:H12_HUMAN	S01	5922	2	1199.4	(+0.6)	2.675	0.383	0.963	5	K.ASGPPVSELITK.A
SW:H12_HUMAN	S02	5874	2	1213.4	(-0.1)	2.682	0.431	0.893	5	K.ASGPPVSEL*ITK#.A
SW:H12_HUMAN	S03	5537	2	1199.4	(+0.8)	2.698	0.379	0.963	5	K.ASGPPVSELITK.A
SW:H12_HUMAN	S03	5533	2	1213.4	(-0.1)	2.553	0.295	0.707	5	K.ASGPPVSEL*ITK#.A
SW:H12_HUMAN	S07	6140	2	1199.4	(+0.9)	2.765	0.400	0.970	5	K.ASGPPVSELITK.A
SW:H12_HUMAN	S07	6132	2	1213.4	(+0.1)	2.610	0.440	0.892	5	K.ASGPPVSEL*ITK#.A
SW:H12_HUMAN	S08	6286	2	1199.4	(+0.9)	2.398	0.406	0.942	5	K.ASGPPVSELITK.A
SW:H12_HUMAN	S09	6406	2	1213.4	(+0.0)	2.587	0.430	0.882	5	K.ASGPPVSEL*ITK#.A
SW:H12_HUMAN	S10	6304	2	1213.4	(+0.6)	2.214	0.329	0.807	5	K.ASGPPVSEL*ITK#.A
SW:H12_HUMAN	S11	6192	2	1199.4	(+0.8)	2.410	0.363	0.919	5	K.ASGPPVSELITK.A
SW:H12_HUMAN	S13	6388	2	1213.4	(+0.6)	2.307	0.365	0.874	5	K.ASGPPVSEL*ITK#.A
SW:H12_HUMAN	S14	6080	2	1213.4	(+0.5)	2.552	0.401	0.928	5	K.ASGPPVSEL*ITK#.A
SW:H12_HUMAN	S01	5844	2	1327.6	(+0.2)	3.764	0.471	1.000	5	R.KASGPPVSELITK.A
SW:H12_HUMAN	S01	5830	2	1349.6	(-0.4)	2.673	0.216	0.535	5	R.K#ASGPPVSEL*ITK#.A
SW:H12_HUMAN	S04	5407	2	1327.6	(+0.7)	3.093	0.340	0.964	5	R.KASGPPVSELITK.A
SW:H12_HUMAN	S08	6180	2	1327.6	(+0.7)	2.754	0.408	0.969	5	R.KASGPPVSELITK.A
SW:H12_HUMAN	S09	6296	2	1327.6	(+0.7)	2.970	0.443	0.979	5	R.KASGPPVSELITK.A
SW:H12_HUMAN	S11	6096	2	1327.6	(+0.3)	2.299	0.252	0.639	5	R.KASGPPVSELITK.A
SW:H12_HUMAN	S12	5826	2	1349.6	(-0.0)	2.685	0.295	0.727	5	R.K#ASGPPVSEL*ITK#.A
SW:H12_HUMAN	S13	6272	2	1349.6	(-0.4)	3.727	0.440	1.000	5	R.K#ASGPPVSEL*ITK#.A
SW:H12_HUMAN	S13	6274	2	1327.6	(-0.4)	3.699	0.490	1.000	5	R.KASGPPVSELITK.A
SW:H12_HUMAN	S14	5782	2	1327.6	(+0.7)	3.951	0.472	1.000	5	R.KASGPPVSELITK.A
SW:H12_HUMAN	S14	5900	2	1327.6	(+0.6)	3.746	0.525	1.000	5	R.KASGPPVSELITK.A
SW:H12_HUMAN	S14	5982	2	1327.6	(-0.1)	3.641	0.450	1.000	5	R.KASGPPVSELITK.A
SW:H12_HUMAN	S14	6028	2	1349.6	(+0.1)	3.585	0.441	1.000	5	R.K#ASGPPVSEL*ITK#.A
SW:H12_HUMAN	S14	5778	2	1349.6	(+0.1)	3.515	0.399	0.922	5	R.K#ASGPPVSEL*ITK#.A
SW:H12_HUMAN	S14	5936	2	1349.6	(-0.2)	3.203	0.273	0.802	5	R.K#ASGPPVSEL*ITK#.A
SW:H12_HUMAN	S14	6064	2	1327.6	(-0.3)	3.072	0.379	0.940	5	R.KASGPPVSELITK.A
SW:H12_HUMAN	S14	5948	1	1349.6	(+0.0)	2.192	0.241	0.000	5	R.K#ASGPPVSEL*ITK#.A
SW:H12_HUMAN	S14	5820	1	1327.6	(-1.0)	1.916	0.137	0.000	5	R.KASGPPVSELITK.A
SW:H12_HUMAN	S15	6036	2	1327.6	(-0.0)	3.022	0.317	0.906	5	R.KASGPPVSELITK.A
SW:H12_HUMAN	S16	5906	2	1327.6	(+0.9)	3.553	0.434	0.984	5	R.KASGPPVSELITK.A
SW:H12_HUMAN	S16	5932	2	1349.6	(-0.5)	3.294	0.351	0.887	5	R.K#ASGPPVSEL*ITK#.A
SW:H12_HUMAN	S17	6238	2	1327.6	(+0.4)	3.463	0.531	1.000	5	R.KASGPPVSELITK.A
SW:H12_HUMAN	S18	5992	2	1349.6	(+0.0)	3.607	0.384	0.921	5	R.K#ASGPPVSEL*ITK#.A
SW:H12_HUMAN	S14	1420	1	903.1	(-0.4)	1.938	0.438	0.000	1	K.K#PAAATVTK#.K
SW:H12_HUMAN	S13	2002	2	1487.6	(-0.7)	2.658	0.283*	0.012		-.SETAPAAPAAAPPAEK#.A
SW:H12_HUMAN	S06	5882	2	846.0	(+0.9)	2.237	0.285	0.885	5	R.SGVSLAALK.K
SW:H12_HUMAN	S15	5968	1	866.0	(-0.4)	1.974	0.438	0.000	5	R.SGVSL*AAL*K#.K
SW:H12_HUMAN	S15	5624	2	974.2	(+0.9)	2.486	0.278	0.187	5	R.SGVSLAALKK.A
SW:H12_HUMAN	S16	5500	2	974.2	(+0.8)	2.201	0.189	0.035	5	R.SGVSLAALKK.A
SW:H12_HUMAN	S18	5978	2	1327.6	(+0.7)	3.449	0.399	0.980	5	R.KASGPPVSELITK.A

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:H15_HUMAN	S13	730	1	624.7	(+0.3)	1.944	0.300	0.000	2	K.AAGAGAAK#.R
SW:H15_HUMAN	S14	1356	1	624.7	(+0.0)	2.129	0.334	0.000	2	K.AAGAGAAK#.R
SW:H15_HUMAN	S14	470	1	624.7	(-0.0)	1.909	0.251	0.000	2	K.AAGAGAAK#.R
SW:H15_HUMAN	S09	2278	2	1094.2	(+0.9)	2.447	0.124	0.334	1	K.ALAAGGYDVEK.N
SW:H15_HUMAN	S10	2392	2	1108.2	(+0.6)	3.184	0.464	1.000	1	K.AL*AAGGYDVEK#.N
SW:H15_HUMAN	S13	4190	2	1108.2	(+0.5)	2.983	0.406	0.956	1	K.AL*AAGGYDVEK#.N
SW:H15_HUMAN	S13	4268	2	1108.2	(+0.6)	2.406	0.360	0.894	1	K.AL*AAGGYDVEK#.N
SW:H15_HUMAN	S13	5182	2	1094.2	(+0.5)	2.404	0.291	0.898	1	K.ALAAGGYDVEK.N
SW:H15_HUMAN	S13	5296	2	1108.2	(+0.2)	2.338	0.418*	0.035	1	K.AL*AAGGYDVEK#.N
SW:H15_HUMAN	S14	2534	2	1108.2	(+0.9)	3.206	0.491	1.000	1	K.AL*AAGGYDVEK#.N
SW:H15_HUMAN	S14	2436	2	1094.2	(-0.5)	3.131	0.302	0.920	1	K.ALAAGGYDVEK.N
SW:H15_HUMAN	S14	2574	2	1108.2	(-0.3)	3.076	0.329	0.869	1	K.AL*AAGGYDVEK#.N
SW:H15_HUMAN	S14	4844	2	1094.2	(+0.3)	2.606	0.459	0.951	1	K.ALAAGGYDVEK.N
SW:H15_HUMAN	S14	2518	1	1108.2	(+0.5)	2.091	0.399	0.000	1	K.AL*AAGGYDVEK#.N
SW:H15_HUMAN	S16	2408	2	1108.2	(+0.1)	3.171	0.411	0.921	1	K.AL*AAGGYDVEK#.N
SW:H15_HUMAN	S18	5010	2	1108.2	(+0.5)	2.320	0.308*	0.038	1	K.AL*AAGGYDVEK#.N
SW:H15_HUMAN	S19	2394	2	1108.2	(+0.8)	3.135	0.437	0.966	1	K.AL*AAGGYDVEK#.N
SW:H15_HUMAN	S19	2420	2	1094.2	(+0.5)	2.851	0.359	0.966	1	K.ALAAGGYDVEK.N
SW:H15_HUMAN	S14	5006	2	1579.7	(+0.5)	3.639	0.355	0.475	1	K.AL*AAGGYDVEK#NNSR.I
SW:H15_HUMAN	S14	2356	2	1565.7	(+0.9)	2.784	0.261	0.157	1	K.ALAAGGYDVEK#NNSR.I
SW:H15_HUMAN	S01	6096	2	1213.4	(+0.9)	2.972	0.476	0.983	1	K.ATGPPVSELITK.A
SW:H15_HUMAN	S01	6014	2	1213.4	(+0.8)	2.400	0.423	0.962	1	K.ATGPPVSELITK.A
SW:H15_HUMAN	S02	5950	2	1213.4	(+0.9)	2.451	0.423	0.964	1	K.ATGPPVSELITK.A
SW:H15_HUMAN	S03	5607	2	1213.4	(+1.0)	2.686	0.478	0.979	1	K.ATGPPVSELITK.A
SW:H15_HUMAN	S04	5551	2	1213.4	(+1.0)	2.254	0.516	0.976	1	K.ATGPPVSELITK.A
SW:H15_HUMAN	S08	6368	2	1213.4	(+0.8)	2.272	0.374	0.934	1	K.ATGPPVSELITK.A
SW:H15_HUMAN	S13	6490	2	1213.4	(+0.9)	2.383	0.428	0.963	1	K.ATGPPVSELITK.A
SW:H15_HUMAN	S13	6464	2	1227.4	(+0.5)	2.219	0.410	0.900	1	K.ATGPPVSEL*ITK#.A
SW:H15_HUMAN	S14	6340	2	1213.4	(+0.4)	2.771	0.348	0.957	1	K.ATGPPVSELITK.A
SW:H15_HUMAN	S14	6258	2	1213.4	(+1.0)	2.534	0.421	0.967	1	K.ATGPPVSELITK.A
SW:H15_HUMAN	S15	6248	2	1213.4	(+0.8)	2.264	0.331	0.903	1	K.ATGPPVSELITK.A
SW:H15_HUMAN	S18	6256	2	1213.4	(+0.8)	2.510	0.423	0.950	1	K.ATGPPVSELITK.A
SW:H15_HUMAN	S18	6434	2	1172.4	(-0.0)	2.364	0.266	0.062	1	K.ERNGLSLAALK.K
SW:H15_HUMAN	S13	2310	2	1244.4	(-0.1)	2.688	0.269	0.696	1	K.K#AL*AAGGYDVEK#.N
SW:H15_HUMAN	S14	2328	2	1222.4	(-0.7)	4.071	0.478	1.000	1	K.KALAAGGYDVEK.N
SW:H15_HUMAN	S14	5028	2	1222.4	(+1.0)	3.255	0.454	0.984	1	K.KALAAGGYDVEK.N
SW:H15_HUMAN	S14	2344	2	1244.4	(+0.1)	3.016	0.343	0.864	1	K.K#AL*AAGGYDVEK#.N
SW:H15_HUMAN	S14	4302	2	1244.4	(+0.1)	2.562	0.301	0.722	1	K.K#AL*AAGGYDVEK#.N
SW:H15_HUMAN	S01	5902	2	1363.6	(-0.9)	2.568	0.276	0.325	1	R.K#ATGPPVSEL*ITK#.A
SW:H15_HUMAN	S02	5862	2	1363.6	(+0.0)	2.526	0.349	0.779	1	R.K#ATGPPVSEL*ITK#.A
SW:H15_HUMAN	S03	5519	2	1363.6	(-0.5)	3.003	0.413	0.902	1	R.K#ATGPPVSEL*ITK#.A
SW:H15_HUMAN	S04	5461	2	1363.6	(+0.2)	3.232	0.405	0.912	1	R.K#ATGPPVSEL*ITK#.A
SW:H15_HUMAN	S11	6176	2	1341.6	(+1.0)	2.490	0.433	0.966	1	R.KATGPPVSELITK.A
SW:H15_HUMAN	S12	5906	2	1341.6	(-0.1)	2.820	0.415	0.941	1	R.KATGPPVSELITK.A
SW:H15_HUMAN	S12	5886	2	1363.6	(+0.3)	2.755	0.397	0.870	1	R.K#ATGPPVSEL*ITK#.A
SW:H15_HUMAN	S13	6328	2	1363.6	(+0.0)	4.346	0.548	0.999	1	R.K#ATGPPVSEL*ITK#.A
SW:H15_HUMAN	S14	5924	2	1363.6	(+0.8)	3.785	0.437	1.000	1	R.K#ATGPPVSEL*ITK#.A
SW:H15_HUMAN	S14	5958	3	1363.6	(+0.8)	3.723	0.406	0.994	1	R.K#ATGPPVSEL*ITK#.A
SW:H15_HUMAN	S14	6034	2	1341.6	(+0.7)	3.670	0.394	0.982	1	R.KATGPPVSELITK.A
SW:H15_HUMAN	S14	6156	2	1363.6	(-0.6)	3.664	0.435	1.000	1	R.K#ATGPPVSEL*ITK#.A
SW:H15_HUMAN	S14	6118	2	1341.6	(+0.6)	3.617	0.409	0.979	1	R.KATGPPVSELITK.A
SW:H15_HUMAN	S14	6070	2	1363.6	(+0.0)	3.435	0.416	0.925	1	R.K#ATGPPVSEL*ITK#.A
SW:H15_HUMAN	S15	6144	3	1363.6	(+0.2)	3.860	0.478	1.000	1	R.K#ATGPPVSEL*ITK#.A
SW:H15_HUMAN	S15	6112	2	1341.6	(+0.8)	3.721	0.521	1.000	1	R.KATGPPVSELITK.A
SW:H15_HUMAN	S15	6116	2	1363.6	(+0.8)	2.958	0.414	0.951	1	R.K#ATGPPVSEL*ITK#.A
SW:H15_HUMAN	S15	6136	2	1341.6	(-0.4)	2.873	0.421	0.946	1	R.KATGPPVSELITK.A
SW:H15_HUMAN	S16	6002	2	1341.6	(+0.3)	4.099	0.434	1.000	1	R.KATGPPVSELITK.A
SW:H15_HUMAN	S16	5978	2	1363.6	(+0.4)	2.954	0.471	0.964	1	R.K#ATGPPVSEL*ITK#.A
SW:H15_HUMAN	S17	6298	2	1341.6	(+0.7)	3.769	0.400	0.983	1	R.KATGPPVSELITK.A
SW:H15_HUMAN	S17	6296	2	1363.6	(-0.1)	3.251	0.419	0.918	1	R.K#ATGPPVSEL*ITK#.A
SW:H15_HUMAN	S18	6058	2	1341.6	(+0.8)	4.015	0.317	0.978	1	R.KATGPPVSELITK.A
SW:H15_HUMAN	S14	1310	1	757.9	(-0.2)	2.542	0.477	0.009	1	K.K#PAAAGVK#.K
SW:H15_HUMAN	S14	1230	1	757.9	(-0.2)	2.407	0.542	0.008	1	K.K#PAAAGVK#.K
SW:H15_HUMAN	S14	1240	1	741.9	(-0.2)	2.184	0.332	0.000	1	K.KPAAAGVK.K
SW:H15_HUMAN	S14	1320	1	741.9	(-0.2)	2.163	0.317	0.000	1	K.KPAAAGVK.K

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:H15_HUMAN	S14	1136	1	741.9	(-0.4)	1.950	0.350	0.000	1	K.KPAAAGVK.K
SW:H15_HUMAN	S14	2354	1	769.9	(+0.3)	1.972	0.337	0.000	1	K.KPAGATPK.K
SW:H15_HUMAN	S13	6818	2	887.1	(+0.2)	2.434	0.283	0.834	1	R.NGLSLAALK.K
SW:H15_HUMAN	S14	6654	2	887.1	(+0.6)	2.818	0.171	0.871	1	R.NGLSLAALK.K
SW:H15_HUMAN	S14	6734	2	887.1	(+0.3)	2.732	0.192	0.770	1	R.NGLSLAALK.K
SW:H15_HUMAN	S14	6528	2	887.1	(-0.3)	2.630	0.354	0.924	1	R.NGLSLAALK.K
SW:H15_HUMAN	S15	6572	2	887.1	(-0.2)	2.868	0.273	0.897	1	R.NGLSLAALK.K
SW:H15_HUMAN	S14	2074	2	1607.7	(+0.5)	2.916	0.571	0.999		-.SETAPAETATPAPVEK#.S
SW:H15_HUMAN	S19	4972	2	1094.2	(+0.1)	2.350	0.368	0.883	1	K.ALAAGGYDVEK.N
SW:H1X_HUMAN	S14	6744	2	1342.6	(+0.8)	3.308	0.438	0.983		K.ALVQNDTLLQVK.G
SW:H1X_HUMAN	S14	1786	2	1332.5	(+0.7)	2.470	0.444	0.964		R.GAPAAATAPAPTAHK.A
SW:H1X_HUMAN	S15	1630	2	1332.5	(+0.6)	3.045	0.450	0.979		R.GAPAAATAPAPTAHK.A
SW:H1X_HUMAN	S15	1656	2	1496.7	(+0.6)	2.875	0.482	0.960		R.RGAPAAATAPAPTAHK#.A
SW:H1X_HUMAN	S15	6378	2	1208.4	(-0.8)	2.236	0.347	0.597		K.YSQLVETIR.R
SW:H2AA_HUMAN	S05	6270	2	951.1	(+0.9)	2.314	0.372	0.944	24	R.AGL*QFPVGR.V
SW:H2AA_HUMAN	S06	6234	2	945.1	(+0.9)	3.127	0.315	0.972	24	R.AGLQFPVGR.V
SW:H2AA_HUMAN	S08	6496	2	945.1	(-0.1)	2.314	0.319	0.851	24	R.AGLQFPVGR.V
SW:H2AA_HUMAN	S10	6512	2	945.1	(-0.1)	2.348	0.289	0.820	24	R.AGLQFPVGR.V
SW:H2AA_HUMAN	S18	6332	2	951.1	(-0.5)	2.955	0.323	0.934	24	R.AGL*QFPVGR.V
SW:H2AA_HUMAN	S19	6322	2	951.1	(+0.5)	2.668	0.420	0.977	24	R.AGL*QFPVGR.V
SW:H2AA_HUMAN	S19	6152	2	951.1	(+0.2)	2.446	0.466	0.953	24	R.AGL*QFPVGR.V
SW:H2AA_HUMAN	S19	6646	2	945.1	(+0.4)	2.321	0.342	0.940	24	R.AGLQFPVGR.V
SW:H2AA_HUMAN	S20	5658	2	851.0	(-0.1)	2.313	0.205	0.718	20	R.HLQLAIR.N
SW:H2AA_HUMAN	S19	6234	2	1719.9	(-0.0)	4.648	0.398	1.000	18	R.HL*QL*AIRNDEEL*NK#.L
SW:H2AA_HUMAN	S19	6228	2	1693.9	(+0.7)	4.553	0.487	1.000	18	R.HLQLAIRNDEELNK.L
SW:H2AA_HUMAN	S19	6326	2	1693.9	(+0.5)	4.333	0.386	1.000	18	R.HLQLAIRNDEELNK.L
SW:H2AA_HUMAN	S19	6316	2	1719.9	(-0.4)	4.024	0.390	0.239	18	R.HL*QL*AIRNDEEL*NK#.L
SW:H2AA_HUMAN	S04	7217	2	1932.4	(+0.7)	3.078	0.347	0.961	14	R.VTIAQGGVLPNIQAVLLPK.K
SW:H2AA_HUMAN	S06	8694	2	1932.4	(+0.3)	2.754	0.423	0.934	14	R.VTIAQGGVLPNIQAVLLPK.K
SW:H2AA_HUMAN	S08	8970	2	1932.4	(+0.8)	4.022	0.277	0.968	14	R.VTIAQGGVLPNIQAVLLPK.K
SW:H2AA_HUMAN	S15	8672	2	1932.4	(+0.9)	4.078	0.542	1.000	14	R.VTIAQGGVLPNIQAVLLPK.K
SW:H2AA_HUMAN	S16	8646	2	1932.4	(+0.2)	3.970	0.349	0.954	14	R.VTIAQGGVLPNIQAVLLPK.K
SW:H2AA_HUMAN	S17	8782	2	1932.4	(+0.9)	4.870	0.370	1.000	14	R.VTIAQGGVLPNIQAVLLPK.K
SW:H2AA_HUMAN	S17	9254	2	1932.4	(+0.6)	2.415	0.245	0.790	14	R.VTIAQGGVLPNIQAVLLPK.K
SW:H2AA_HUMAN	S18	8916	2	1932.4	(+0.3)	4.331	0.367	0.964	14	R.VTIAQGGVLPNIQAVLLPK.K
SW:H2AA_HUMAN	S18	8924	3	1958.4	(+0.5)	4.142	0.457	0.998	14	R.VTIAQGGVL*PNIQAVL*L*PK#.K
SW:H2AA_HUMAN	S18	8836	2	1932.4	(+0.5)	4.097	0.371	0.982	14	R.VTIAQGGVLPNIQAVLLPK.K
SW:H2AA_HUMAN	S18	9368	2	1958.4	(+0.1)	2.782	0.272	0.674	14	R.VTIAQGGVL*PNIQAVL*L*PK#.K
SW:H2AA_HUMAN	S18	9210	2	1932.4	(+0.4)	2.689	0.411	0.964	14	R.VTIAQGGVLPNIQAVLLPK.K
SW:H2AA_HUMAN	S18	8832	2	1958.4	(-0.7)	2.478	0.332	0.387	14	R.VTIAQGGVL*PNIQAVL*L*PK#.K
SW:H2AA_HUMAN	S19	13266	3	1932.4	(+0.7)	4.870	0.446	1.000	14	R.VTIAQGGVLPNIQAVLLPK.K
SW:H2AA_HUMAN	S19	8854	3	1958.4	(+0.3)	4.503	0.460	1.000	14	R.VTIAQGGVL*PNIQAVL*L*PK#.K
SW:H2AA_HUMAN	S19	8756	2	1932.4	(+0.5)	4.473	0.269	0.974	14	R.VTIAQGGVLPNIQAVLLPK.K
SW:H2AA_HUMAN	S19	8674	2	1932.4	(+0.5)	4.396	0.336	0.981	14	R.VTIAQGGVLPNIQAVLLPK.K
SW:H2AA_HUMAN	S19	8592	2	1932.4	(+0.5)	4.344	0.277	0.973	14	R.VTIAQGGVLPNIQAVLLPK.K
SW:H2AA_HUMAN	S19	8920	2	1932.4	(+0.2)	4.299	0.376	0.964	14	R.VTIAQGGVLPNIQAVLLPK.K
SW:H2AA_HUMAN	S19	8838	2	1932.4	(+0.4)	4.160	0.305	0.975	14	R.VTIAQGGVLPNIQAVLLPK.K
SW:H2AA_HUMAN	S19	9080	2	1932.4	(+0.8)	4.012	0.292	0.971	14	R.VTIAQGGVLPNIQAVLLPK.K
SW:H2AA_HUMAN	S19	8646	3	1958.4	(+0.5)	3.975	0.449	0.997	14	R.VTIAQGGVL*PNIQAVL*L*PK#.K
SW:H2AA_HUMAN	S19	8942	3	1958.4	(+0.8)	3.933	0.390	0.993	14	R.VTIAQGGVL*PNIQAVL*L*PK#.K
SW:H2AA_HUMAN	S19	9184	3	1958.4	(+1.0)	3.909	0.488	1.000	14	R.VTIAQGGVL*PNIQAVL*L*PK#.K
SW:H2AA_HUMAN	S19	8750	3	1958.4	(+0.3)	3.866	0.415	0.986	14	R.VTIAQGGVL*PNIQAVL*L*PK#.K
SW:H2AA_HUMAN	S19	13046	3	1958.4	(+0.8)	3.818	0.369	0.972	14	R.VTIAQGGVL*PNIQAVL*L*PK#.K
SW:H2AA_HUMAN	S19	11320	3	1932.4	(+0.7)	3.706	0.399	0.996	14	R.VTIAQGGVLPNIQAVLLPK.K
SW:H2AA_HUMAN	S19	8982	2	1958.4	(+0.0)	3.210	0.289	0.799	14	R.VTIAQGGVL*PNIQAVL*L*PK#.K
SW:H2AA_HUMAN	S19	8504	2	1958.4	(-0.5)	2.463	0.288	0.604	14	R.VTIAQGGVL*PNIQAVL*L*PK#.K
SW:H2AA_HUMAN	S20	8282	2	1932.4	(+0.5)	3.225	0.380	0.972	14	R.VTIAQGGVLPNIQAVLLPK.K
SW:H2AA_HUMAN	S20	8550	2	1932.4	(+0.7)	2.241	0.309	0.850	14	R.VTIAQGGVLPNIQAVLLPK.K
SW:H2AC_HUMAN	S19	6586	2	1273.4	(+0.9)	3.341	0.385	0.534	8	R.NDEELNKLLGK.V
SW:H2AC_HUMAN	S19	6746	2	1307.4	(+0.4)	2.951	0.223	0.107	8	R.NDEEL*NK#L*L*GK#.V
SW:H2AC_HUMAN	S19	1084	2	845.9	(-0.2)	2.304	0.250	0.801	14	R.K#GNYAER.V
SW:H2AY_HUMAN	S12	6290	2	2128.3	(-0.7)	3.590	0.512	1.000	5	K.AASADSTTEGTPADGFTVLSTK.S

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:H2AY_HUMAN	S12	6016	2	2128.3	(-0.9)	3.288	0.459	0.867	5	K.AASADSTTEGTPADGFTVLSTK.S
SW:H2AY_HUMAN	S12	6294	2	2142.3	(-0.7)	2.608	0.328	0.421	5	K.AASADSTTEGTPADGFTVL*STK#.S
SW:H2AY_HUMAN	S12	8784	2	1205.4	(+0.4)	2.344	0.378	0.951	6	K.EFVEAVLELR.K
SW:H2AY_HUMAN	S12	6050	2	1357.6	(-0.4)	2.945	0.339	0.109	6	K.GK#L*EAIITPPPAK#.K
SW:H2AY_HUMAN	S12	6062	2	1335.6	(-0.2)	2.815	0.442	0.303	6	K.GKLEAIITPPPAK.K
SW:H2AY_HUMAN	S12	7612	2	1987.3	(-0.7)	3.615	0.521	1.000	6	K.GVTIASGGVLPNIHPELLAK.K
SW:H2AY_HUMAN	S12	5732	2	1150.4	(+0.9)	2.337	0.323	0.915	6	K.LEAIITPPPAK.K
SW:H2AY_HUMAN	S12	6564	2	1817.1	(+0.6)	4.771	0.658	1.000	6	K.NGPLEVAGAAVSAGHGLPAK.F
SW:H2AY_HUMAN	S12	6802	2	1837.1	(+0.7)	4.161	0.568	1.000	6	K.NGPL*EVAGAAVSAGHGL*PAK#.F
SW:H2AY_HUMAN	S12	6582	2	1817.1	(-0.9)	2.712	0.520	0.861	6	K.NGPLEVAGAAVSAGHGLPAK.F
SW:H2AY_HUMAN	S16	6388	2	2128.3	(-0.9)	4.120	0.572	1.000	5	K.AASADSTTEGTPADGFTVLSTK.S
SW:H2AZ_HUMAN	S17	6310	2	1379.6	(+0.5)	3.160	0.430	0.959	1	K.ATIAGGGVIPHIHK#.S
SW:H2AZ_HUMAN	S18	6070	2	1371.6	(+0.8)	3.896	0.464	1.000	1	K.ATIAGGGVIPHIHK.S
SW:H2AZ_HUMAN	S19	5914	2	1379.6	(+0.5)	3.843	0.487	1.000	1	K.ATIAGGGVIPHIHK#.S
SW:H2AZ_HUMAN	S19	6034	2	1379.6	(+0.6)	3.286	0.456	0.966	1	K.ATIAGGGVIPHIHK#.S
SW:H2AZ_HUMAN	S19	5902	2	1371.6	(-0.1)	2.216	0.115	0.175	1	K.ATIAGGGVIPHIHK.S
SW:H2AZ_HUMAN	S01	6258	2	1139.2	(+0.5)	2.801	0.308	0.911	1	R.GDEEL*DSL*IK#.A
SW:H2AZ_HUMAN	S15	6500	2	1119.2	(+0.4)	3.098	0.286	0.960	1	R.GDEELDSLIIK.A
SW:H2AZ_HUMAN	S16	6392	2	1139.2	(+0.0)	2.633	0.287	0.758	1	R.GDEEL*DSL*IK#.A
SW:H2AZ_HUMAN	S17	6716	2	1119.2	(+0.8)	3.346	0.273	0.965	1	R.GDEELDSLIIK.A
SW:H2AZ_HUMAN	S17	6680	2	1139.2	(-0.8)	2.325	0.292	0.338	1	R.GDEEL*DSL*IK#.A
SW:H2AZ_HUMAN	S18	6482	2	1139.2	(+0.1)	2.901	0.210	0.690	1	R.GDEEL*DSL*IK#.A
SW:H2AZ_HUMAN	S19	6452	2	1119.2	(+1.0)	3.748	0.287	0.977	1	R.GDEELDSLIIK.A
SW:H2AZ_HUMAN	S19	6546	2	1119.2	(+0.9)	3.625	0.359	0.982	1	R.GDEELDSLIIK.A
SW:H2AZ_HUMAN	S19	6346	2	1119.2	(+0.5)	2.834	0.327	0.961	1	R.GDEELDSLIIK.A
SW:H2AZ_HUMAN	S19	6466	2	1119.2	(-0.5)	2.640	0.339	0.908	1	R.GDEELDSLIIK.A
SW:H2AZ_HUMAN	S19	6534	2	1139.2	(+0.2)	2.233	0.251	0.514	1	R.GDEEL*DSL*IK#.A
SW:H2AZ_HUMAN	S19	12622	2	2897.3	(-0.5)	3.826	0.517	1.000	1	R.VGATAAVYSAIALEYLTAEVLELAGNASK.D
SW:H2AZ_HUMAN	S20	5832	2	1379.6	(+0.8)	2.816	0.304	0.874	1	K.ATIAGGGVIPHIHK#.S
SW:H2BA_HUMAN	S18	8152	2	1784.1	(+0.0)	2.317	0.154	0.002	27	R.EIQTAVRL*#L*PGEL*AK#.H
SW:H2BA_HUMAN	S18	3190	2	828.9	(-0.7)	2.384	0.318	0.656	28	K.HAVSEGTK.A
SW:H2BA_HUMAN	S18	588	2	836.9	(+0.5)	2.379	0.380	0.920	28	K.HAVSEGTK#.A
SW:H2BA_HUMAN	S18	320	2	836.9	(+0.4)	2.351	0.326	0.891	28	K.HAVSEGTK#.A
SW:H2BA_HUMAN	S18	3752	2	828.9	(-0.6)	2.346	0.282	0.832	28	K.HAVSEGTK.A
SW:H2BA_HUMAN	S18	488	2	828.9	(-0.6)	2.302	0.305	0.850	28	K.HAVSEGTK.A
SW:H2BA_HUMAN	S18	3610	2	828.9	(-0.8)	2.282	0.352	0.682	28	K.HAVSEGTK.A
SW:H2BA_HUMAN	S18	3680	2	828.9	(-0.7)	2.274	0.340	0.656	28	K.HAVSEGTK.A
SW:H2BA_HUMAN	S18	976	2	828.9	(-0.0)	2.260	0.340	0.878	28	K.HAVSEGTK.A
SW:H2BA_HUMAN	S18	686	2	828.9	(-0.5)	2.259	0.304	0.838	28	K.HAVSEGTK.A
SW:H2BA_HUMAN	S18	722	2	836.9	(+0.5)	2.256	0.389	0.910	28	K.HAVSEGTK#.A
SW:H2BA_HUMAN	S18	1076	2	828.9	(-0.6)	2.224	0.297	0.819	28	K.HAVSEGTK.A
SW:H2BA_HUMAN	S18	398	2	836.9	(+0.6)	2.223	0.373	0.908	28	K.HAVSEGTK#.A
SW:H2BA_HUMAN	S18	414	1	836.9	(-0.3)	2.179	0.350	0.000	28	K.HAVSEGTK#.A
SW:H2BA_HUMAN	S18	640	1	836.9	(-0.7)	2.148	0.305	0.000	28	K.HAVSEGTK#.A
SW:H2BA_HUMAN	S18	992	1	836.9	(-0.3)	2.139	0.323	0.000	28	K.HAVSEGTK#.A
SW:H2BA_HUMAN	S18	828	1	836.9	(-0.4)	2.086	0.331	0.000	28	K.HAVSEGTK#.A
SW:H2BA_HUMAN	S18	632	1	828.9	(-0.4)	1.999	0.376	0.000	28	K.HAVSEGTK.A
SW:H2BA_HUMAN	S18	1078	1	836.9	(-0.3)	1.988	0.348	0.000	28	K.HAVSEGTK#.A
SW:H2BA_HUMAN	S18	914	1	836.9	(-0.3)	1.975	0.360	0.000	28	K.HAVSEGTK#.A
SW:H2BA_HUMAN	S18	562	1	836.9	(-0.5)	1.936	0.428	0.000	28	K.HAVSEGTK#.A
SW:H2BA_HUMAN	S01	5442	2	1282.4	(-0.1)	2.973	0.397	0.909	15	R.K#ESYSVYVYK#.V
SW:H2BA_HUMAN	S01	5444	2	1266.4	(+0.7)	2.914	0.473	0.984	15	R.KESYSVYVYK.V
SW:H2BA_HUMAN	S15	5676	2	1282.4	(+0.1)	2.458	0.285	0.701	15	R.K#ESYSVYVYK#.V
SW:H2BA_HUMAN	S16	5552	2	1282.4	(+0.2)	2.922	0.400	0.907	15	R.K#ESYSVYVYK#.V
SW:H2BA_HUMAN	S16	5524	2	1266.4	(+0.0)	2.540	0.424	0.941	15	R.KESYSVYVYK.V
SW:H2BA_HUMAN	S18	5516	2	1282.4	(+0.4)	3.243	0.434	0.988	15	R.K#ESYSVYVYK#.V
SW:H2BA_HUMAN	S18	5602	2	1282.4	(+0.5)	3.167	0.476	0.986	15	R.K#ESYSVYVYK#.V
SW:H2BA_HUMAN	S18	5752	2	1266.4	(+1.0)	3.130	0.467	1.000	15	R.KESYSVYVYK.V
SW:H2BA_HUMAN	S18	5684	2	1282.4	(+0.3)	3.030	0.421	0.923	15	R.K#ESYSVYVYK#.V
SW:H2BA_HUMAN	S18	5672	2	1266.4	(+1.0)	2.994	0.532	1.000	15	R.KESYSVYVYK.V
SW:H2BA_HUMAN	S18	5764	2	1282.4	(+0.2)	2.840	0.381	0.787	15	R.K#ESYSVYVYK#.V
SW:H2BA_HUMAN	S18	5408	2	1282.4	(+0.4)	2.833	0.417	0.956	15	R.K#ESYSVYVYK#.V
SW:H2BA_HUMAN	S18	5500	2	1266.4	(+0.9)	2.681	0.472	0.981	15	R.KESYSVYVYK.V
SW:H2BA_HUMAN	S18	5418	2	1266.4	(-0.5)	2.497	0.337	0.889	15	R.KESYSVYVYK.V

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:H2BA_HUMAN	S18	5514	1	1282.4	(+0.1)	2.137	0.180	0.000	15	R.K#ESYSVYVYK#.V
SW:H2BA_HUMAN	S19	5436	2	1282.4	(-0.4)	2.541	0.245	0.643	15	R.K#ESYSVYVYK#.V
SW:H2BA_HUMAN	S20	5232	2	1266.4	(+0.2)	2.651	0.389	0.935	15	R.KESYSVYVYK.V
SW:H2BA_HUMAN	S20	5306	2	1282.4	(+0.2)	2.557	0.351	0.830	15	R.K#ESYSVYVYK#.V
SW:H2BA_HUMAN	S20	5230	2	1282.4	(+0.1)	2.334	0.322	0.730	15	R.K#ESYSVYVYK#.V
SW:H2BA_HUMAN	S15	6830	2	954.2	(-0.1)	2.297	0.101	0.299	28	R.LLLPGELAK.H
SW:H2BA_HUMAN	S18	2138	2	1509.7	(+0.8)	2.984	0.461	0.530	29	K.VLKQVHPDTGISSK.A
SW:H2BA_HUMAN	S18	2134	2	1531.7	(+0.2)	2.647	0.365	0.092	29	K.VL*K#QVHPDTGISSK#.A
SW:H2BA_HUMAN	S20	7628	2	1784.1	(-0.0)	2.267	0.211	0.010	27	R.EIQTAVRL*L*L*PGEL*AK#.H
SW:H4_HUMAN	S19	1740	2	1135.2	(-0.4)	3.464	0.364	0.959	2	R.DAVTYTEHAK.R
SW:H4_HUMAN	S19	4412	2	1135.2	(-0.7)	3.429	0.341	0.843	2	R.DAVTYTEHAK.R
SW:H4_HUMAN	S19	2408	2	1135.2	(+0.6)	3.037	0.337	0.970	2	R.DAVTYTEHAK.R
SW:H4_HUMAN	S19	2910	2	1143.2	(+1.0)	2.895	0.450	0.965	2	R.DAVTYTEHAK#.R
SW:H4_HUMAN	S19	2486	2	1135.2	(+0.6)	2.855	0.368	0.971	2	R.DAVTYTEHAK.R
SW:H4_HUMAN	S19	2838	2	1143.2	(+0.8)	2.655	0.459	0.959	2	R.DAVTYTEHAK#.R
SW:H4_HUMAN	S19	2052	2	1143.2	(+0.6)	2.567	0.406	0.942	2	R.DAVTYTEHAK#.R
SW:H4_HUMAN	S19	3050	2	1143.2	(-0.1)	2.560	0.217	0.580	2	R.DAVTYTEHAK#.R
SW:H4_HUMAN	S19	4396	2	1135.2	(+0.9)	2.560	0.215	0.854	2	R.DAVTYTEHAK.R
SW:H4_HUMAN	S19	1818	2	1143.2	(+0.4)	2.487	0.417	0.941	2	R.DAVTYTEHAK#.R
SW:H4_HUMAN	S19	4486	2	1143.2	(+0.3)	2.303	0.301	0.676	2	R.DAVTYTEHAK#.R
SW:H4_HUMAN	S19	1738	2	1143.2	(-0.9)	2.273	0.221	0.174	2	R.DAVTYTEHAK#.R
SW:H4_HUMAN	S19	2866	2	1135.2	(+0.8)	2.268	0.222	0.780	2	R.DAVTYTEHAK.R
SW:H4_HUMAN	S19	4138	2	1143.2	(+0.7)	2.249	0.357	0.876	2	R.DAVTYTEHAK#.R
SW:H4_HUMAN	S20	1578	2	1143.2	(+0.9)	2.409	0.316	0.864	2	R.DAVTYTEHAK#.R
SW:H4_HUMAN	S01	5248	2	1326.5	(-0.0)	2.757	0.221	0.067	2	R.DNIQGITKPAIR.R
SW:H4_HUMAN	S01	5244	2	1334.5	(-0.5)	2.299	0.292	0.066	2	R.DNIQGITK#PAIR.R
SW:H4_HUMAN	S03	5075	2	1326.5	(+0.3)	2.992	0.200	0.075	2	R.DNIQGITKPAIR.R
SW:H4_HUMAN	S16	5256	2	1326.5	(+0.0)	2.828	0.257	0.103	2	R.DNIQGITKPAIR.R
SW:H4_HUMAN	S16	5264	2	1334.5	(-0.6)	2.425	0.309	0.094	2	R.DNIQGITK#PAIR.R
SW:H4_HUMAN	S17	5732	2	1326.5	(-0.1)	2.643	0.225	0.059	2	R.DNIQGITKPAIR.R
SW:H4_HUMAN	S17	5724	2	1334.5	(+0.0)	2.395	0.302	0.085	2	R.DNIQGITK#PAIR.R
SW:H4_HUMAN	S18	5260	2	1334.5	(+0.7)	2.849	0.351	0.365	2	R.DNIQGITK#PAIR.R
SW:H4_HUMAN	S19	5298	2	1326.5	(+0.9)	3.396	0.247	0.306	2	R.DNIQGITKPAIR.R
SW:H4_HUMAN	S19	5466	2	1326.5	(+0.3)	3.231	0.206	0.105	2	R.DNIQGITKPAIR.R
SW:H4_HUMAN	S19	5382	2	1326.5	(+0.8)	3.021	0.198	0.153	2	R.DNIQGITKPAIR.R
SW:H4_HUMAN	S19	5370	2	1334.5	(+0.2)	2.893	0.353	0.218	2	R.DNIQGITK#PAIR.R
SW:H4_HUMAN	S19	5452	2	1334.5	(-0.6)	2.296	0.289	0.063	2	R.DNIQGITK#PAIR.R
SW:H4_HUMAN	S20	5122	2	1326.5	(-0.2)	2.723	0.197	0.049	2	R.DNIQGITKPAIR.R
SW:H4_HUMAN	S20	5018	2	1326.5	(+0.1)	2.709	0.254	0.086	2	R.DNIQGITKPAIR.R
SW:H4_HUMAN	S20	4932	2	1326.5	(+0.5)	2.643	0.209	0.102	2	R.DNIQGITKPAIR.R
SW:H4_HUMAN	S20	4980	2	1334.5	(+0.3)	2.487	0.360	0.155	2	R.DNIQGITK#PAIR.R
SW:H4_HUMAN	S20	5062	2	1334.5	(+0.3)	2.474	0.292	0.087	2	R.DNIQGITK#PAIR.R
SW:H4_HUMAN	S19	9254	2	1387.7	(+0.4)	3.807	0.496	1.000	2	R.GVLKVFLENVIR.D
SW:H4_HUMAN	S01	5840	2	1181.3	(+0.8)	3.835	0.438	1.000	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S01	5908	2	1187.3	(+0.7)	3.456	0.457	1.000	2	R.ISGL*YEETR.G
SW:H4_HUMAN	S01	5834	2	1187.3	(+0.1)	2.560	0.425	0.943	2	R.ISGL*YEETR.G
SW:H4_HUMAN	S01	5870	2	1181.3	(-0.6)	2.203	0.157	0.377	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S03	5507	2	1181.3	(+0.5)	3.255	0.455	1.000	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S04	5429	2	1181.3	(+0.5)	2.558	0.408	0.970	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S16	5986	2	1187.3	(-0.0)	2.293	0.224	0.637	2	R.ISGL*YEETR.G
SW:H4_HUMAN	S16	5908	2	1187.3	(+0.5)	2.263	0.389	0.950	2	R.ISGL*YEETR.G
SW:H4_HUMAN	S16	5918	2	1181.3	(-0.1)	2.230	0.374	0.879	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S17	6282	2	1187.3	(+0.1)	2.330	0.391	0.907	2	R.ISGL*YEETR.G
SW:H4_HUMAN	S17	6254	2	1181.3	(+0.7)	2.247	0.291	0.857	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S18	6010	2	1187.3	(+0.9)	3.170	0.449	1.000	2	R.ISGL*YEETR.G
SW:H4_HUMAN	S19	12782	2	1181.3	(+0.8)	3.701	0.467	1.000	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S19	11616	2	1181.3	(+0.9)	3.634	0.432	1.000	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S19	12856	2	1181.3	(+0.9)	3.476	0.475	1.000	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S19	13004	2	1181.3	(+0.5)	3.459	0.498	1.000	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S19	13074	2	1187.3	(+1.0)	3.442	0.431	0.932	2	R.ISGL*YEETR.G
SW:H4_HUMAN	S19	6350	2	1181.3	(+0.0)	3.415	0.464	0.990	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S19	11142	2	1181.3	(+0.9)	3.368	0.404	0.983	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S19	6342	2	1187.3	(+0.1)	3.363	0.430	1.000	2	R.ISGL*YEETR.G
SW:H4_HUMAN	S19	11546	2	1181.3	(+0.8)	3.363	0.409	0.984	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S19	12706	2	1181.3	(+0.9)	3.346	0.413	0.984	2	R.ISGLIYEETR.G

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:H4_HUMAN	S19	13076	2	1181.3	(+0.9)	3.331	0.440	1.000	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S19	11876	2	1181.3	(+0.7)	3.309	0.431	1.000	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S19	12928	2	1181.3	(+0.6)	3.307	0.451	1.000	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S19	11780	2	1181.3	(+0.9)	3.280	0.412	0.983	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S19	10814	2	1181.3	(+0.9)	3.267	0.418	0.983	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S19	6688	2	1187.3	(-0.2)	3.235	0.392	0.960	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	12478	2	1181.3	(+0.8)	3.187	0.446	1.000	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S19	13270	2	1181.3	(+1.0)	3.160	0.400	0.979	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S19	11070	2	1181.3	(+0.8)	3.156	0.429	0.983	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S19	6512	2	1181.3	(+0.7)	3.127	0.407	0.981	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S19	6100	2	1181.3	(-0.3)	3.122	0.308	0.930	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S19	12228	2	1181.3	(+0.6)	3.106	0.400	0.980	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S19	10488	2	1187.3	(+0.4)	3.085	0.422	0.982	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	6422	2	1187.3	(+0.8)	3.072	0.358	0.975	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	11350	2	1187.3	(+0.9)	3.018	0.426	0.981	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	6174	2	1187.3	(+0.3)	3.004	0.489	1.000	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	6180	2	1181.3	(-0.4)	2.936	0.343	0.934	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S19	7412	2	1187.3	(+0.8)	2.930	0.397	0.977	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	7240	2	1187.3	(+0.7)	2.927	0.310	0.960	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	12042	2	1181.3	(+0.4)	2.919	0.412	0.979	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S19	6094	2	1187.3	(+0.4)	2.904	0.459	0.983	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	10704	2	1187.3	(+0.5)	2.856	0.370	0.972	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	11726	2	1187.3	(+0.1)	2.844	0.463	0.962	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	10560	2	1187.3	(+0.3)	2.831	0.459	0.961	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	12146	2	1181.3	(+0.6)	2.825	0.373	0.971	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S19	5844	2	1187.3	(+0.7)	2.814	0.476	0.983	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	11174	2	1187.3	(+0.2)	2.774	0.457	0.959	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	10634	2	1187.3	(+0.4)	2.774	0.401	0.975	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	13546	2	1187.3	(+0.0)	2.722	0.373	0.933	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	12956	2	1187.3	(-0.2)	2.695	0.363	0.925	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	11964	2	1181.3	(+0.8)	2.647	0.423	0.975	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S19	12660	2	1187.3	(-0.0)	2.646	0.318	0.893	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	7650	2	1187.3	(+0.5)	2.628	0.411	0.969	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	10950	2	1187.3	(+0.4)	2.621	0.381	0.965	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	12166	2	1187.3	(-0.0)	2.612	0.338	0.904	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	11858	2	1187.3	(+0.7)	2.596	0.450	0.977	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	6504	2	1187.3	(+0.9)	2.574	0.402	0.969	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	10800	2	1187.3	(-0.2)	2.565	0.252	0.801	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	12304	2	1187.3	(-0.2)	2.534	0.334	0.891	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	12410	2	1187.3	(+0.2)	2.527	0.449	0.949	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	9922	2	1181.3	(+0.9)	2.467	0.366	0.955	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S19	10122	2	1187.3	(+0.3)	2.442	0.409	0.928	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	6002	2	1187.3	(-0.6)	2.390	0.290	0.813	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	6262	2	1181.3	(-0.5)	2.346	0.260	0.746	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S19	6258	2	1187.3	(-0.3)	2.339	0.282	0.785	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	10310	2	1187.3	(-0.4)	2.298	0.313	0.822	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S19	12036	2	1187.3	(-0.7)	2.265	0.341	0.596	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S20	5882	2	1181.3	(+0.9)	3.391	0.451	1.000	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S20	5686	2	1181.3	(+0.9)	3.389	0.495	1.000	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S20	5396	2	1187.3	(+0.7)	3.114	0.403	0.981	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S20	12142	2	1187.3	(+0.6)	3.072	0.353	0.970	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S20	5688	2	1187.3	(+0.7)	2.827	0.440	0.980	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S20	5552	2	1187.3	(+0.8)	2.780	0.434	0.979	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S20	12374	2	1187.3	(+0.8)	2.774	0.322	0.957	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S20	5282	2	1187.3	(+0.7)	2.541	0.444	0.975	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S20	5794	2	1181.3	(+0.2)	2.466	0.478	0.953	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S20	5862	2	1187.3	(+0.4)	2.444	0.480	0.978	2	R.ISGL*IYEETR.G
SW:H4_HUMAN	S20	5702	2	1181.3	(-0.9)	2.305	0.196	0.249	2	R.ISGLIYEETR.G
SW:H4_HUMAN	S01	6528	2	1477.8	(+0.3)	2.776	0.404	0.878	2	R.K#TVTAM@DVVYAL*K#.R
SW:H4_HUMAN	S19	7600	2	1461.8	(-0.1)	4.790	0.580*	0.567	2	R.K#TVTAMDVVYAL*K#.R
SW:H4_HUMAN	S19	7598	3	1461.8	(+0.7)	4.013	0.361	0.994	2	R.K#TVTAMDVVYAL*K#.R
SW:H4_HUMAN	S19	7692	2	1461.8	(-0.8)	2.564	0.244	0.234	2	R.K#TVTAMDVVYAL*K#.R
SW:H4_HUMAN	S20	6412	2	1477.8	(-0.2)	3.677	0.483	1.000	2	R.K#TVTAM@DVVYAL*K#.R
SW:H4_HUMAN	S20	7154	2	1461.8	(-0.2)	3.262	0.382	0.903	2	R.K#TVTAMDVVYAL*K#.R
SW:H4_HUMAN	S19	6308	2	1337.5	(+0.5)	2.910	0.324	0.959	2	K.RISGLIYEETR.G
SW:H4_HUMAN	S19	6212	2	1343.5	(-0.1)	2.741	0.218	0.767	2	K.RISGL*IYEETR.G

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:H4_HUMAN	S01	7418	2	1325.6	(+0.5)	2.757	0.477	0.962	2	K.TVTAMDVVYAL*K#.R
SW:H4_HUMAN	S16	7770	2	1311.6	(+0.7)	2.247	0.431	0.957	2	K.TVTAMDVVYALK.R
SW:H4_HUMAN	S19	12978	2	1325.6	(+0.8)	3.421	0.524*	0.399	2	K.TVTAMDVVYAL*K#.R
SW:H4_HUMAN	S19	12822	2	1325.6	(+0.7)	3.237	0.491*	0.328	2	K.TVTAMDVVYAL*K#.R
SW:H4_HUMAN	S19	7930	2	1325.6	(+0.3)	3.094	0.509	1.000	2	K.TVTAMDVVYAL*K#.R
SW:H4_HUMAN	S19	10500	2	1325.6	(+0.9)	3.075	0.470*	0.267	2	K.TVTAMDVVYAL*K#.R
SW:H4_HUMAN	S19	11094	2	1325.6	(+0.8)	3.049	0.492*	0.258	2	K.TVTAMDVVYAL*K#.R
SW:H4_HUMAN	S19	12894	2	1325.6	(+0.5)	3.045	0.505	1.000	2	K.TVTAMDVVYAL*K#.R
SW:H4_HUMAN	S19	8056	2	1311.6	(+0.9)	3.037	0.464	0.983	2	K.TVTAMDVVYALK.R
SW:H4_HUMAN	S19	13028	2	1311.6	(+0.9)	2.661	0.392	0.965	2	K.TVTAMDVVYALK.R
SW:H4_HUMAN	S19	10734	2	1325.6	(+0.8)	2.632	0.427*	0.125	2	K.TVTAMDVVYAL*K#.R
SW:H4_HUMAN	S19	10732	2	1311.6	(+0.4)	2.630	0.451	0.975	2	K.TVTAMDVVYALK.R
SW:H4_HUMAN	S19	11302	2	1325.6	(+0.3)	2.598	0.460	0.902	2	K.TVTAMDVVYAL*K#.R
SW:H4_HUMAN	S19	13058	2	1325.6	(+0.8)	2.560	0.437	0.943	2	K.TVTAMDVVYAL*K#.R
SW:H4_HUMAN	S19	8040	2	1325.6	(+0.4)	2.491	0.415	0.930	2	K.TVTAMDVVYAL*K#.R
SW:H4_HUMAN	S19	11812	2	1325.6	(+0.2)	2.472	0.366*	0.042	2	K.TVTAMDVVYAL*K#.R
SW:H4_HUMAN	S19	10144	2	1325.6	(+0.3)	2.457	0.471*	0.041	2	K.TVTAMDVVYAL*K#.R
SW:H4_HUMAN	S19	8086	2	1325.6	(-0.8)	2.407	0.433	0.621	2	K.TVTAMDVVYAL*K#.R
SW:H4_HUMAN	S19	11180	2	1325.6	(-0.0)	2.406	0.493	0.903	2	K.TVTAMDVVYAL*K#.R
SW:H4_HUMAN	S19	11132	2	1311.6	(+0.4)	2.382	0.423	0.961	2	K.TVTAMDVVYALK.R
SW:H4_HUMAN	S19	10940	2	1325.6	(+0.9)	2.367	0.414	0.920	2	K.TVTAMDVVYAL*K#.R
SW:H4_HUMAN	S19	10858	2	1325.6	(+0.4)	2.346	0.426	0.924	2	K.TVTAMDVVYAL*K#.R
SW:H4_HUMAN	S19	10140	2	1311.6	(+0.5)	2.306	0.434	0.961	2	K.TVTAMDVVYALK.R
SW:H4_HUMAN	S19	7094	2	1341.6	(+0.1)	2.278	0.354	0.733	2	K.TVTAM@DVVYAL*K#.R
SW:H4_HUMAN	S19	13310	2	1325.6	(+0.5)	2.235	0.420	0.909	2	K.TVTAMDVVYAL*K#.R
SW:H4_HUMAN	S19	7034	2	996.2	(-0.7)	2.856	0.257	0.661	2	K.VFL*ENVIR.D
SW:H4_HUMAN	S19	7204	2	996.2	(+0.9)	2.553	0.256	0.924	2	K.VFL*ENVIR.D
SW:H4_HUMAN	S20	5710	1	1181.3	(-0.8)	1.907	0.224	0.000	2	R.ISGLIYEETR.G
SW:HBA_HUMAN	S19	7156	2	1835.0	(+0.4)	4.058	0.619	1.000	7	K.TYFPHFDLSHGSAQVK.G
SW:HBA_HUMAN	S19	5394	2	1530.6	(-0.3)	2.478	0.156	0.387	5	K.VGAHAGEYGAEALER.M
SW:HBA_HUMAN	S19	7488	2	1072.3	(+0.4)	2.224	0.392	0.953	7	R.MFLSFPTTK.T
SW:HC66_HUMAN	S08	5112	2	1762.9	(-0.5)	3.012	0.289	0.866	1	R.ELEIESQTEEQPTTK.Q
SW:HC66_HUMAN	S08	8036	2	1093.3	(+0.2)	3.129	0.401	0.962	1	K.GELAWIYK.N
SW:HC66_HUMAN	S08	7946	2	1093.3	(+0.6)	2.753	0.343	0.957	1	K.GELAWIYK.N
SW:HC66_HUMAN	S08	4186	2	1162.2	(+0.5)	2.890	0.288	0.893	3	K.SQEDTEAVFK#.K
SW:HC66_HUMAN	S08	4318	2	1154.2	(+0.6)	2.597	0.434	0.975	3	K.SQEDTEAVFK.K
SW:HC66_HUMAN	S08	4090	2	1154.2	(+1.0)	2.491	0.389	0.958	3	K.SQEDTEAVFK.K
SW:HC66_HUMAN	S08	6756	2	993.1	(+0.7)	2.409	0.273	0.931	4	K.YL*DWAYR.S
SW:HC66_HUMAN	S08	7970	2	1107.3	(+0.2)	2.212	0.266	0.578	1	K.GEL*AWIYK#.N
SW:HDA1_HUMAN	S08	5816	3	2270.4	(+0.5)	5.637	0.304	0.993	3	K.L*HISPSNM@TNQNTNEYL*EK#.I
SW:HDA1_HUMAN	S08	6380	3	2254.4	(-0.0)	4.105	0.245	0.806	3	K.L*HISPSNMTNQNTNEYL*EK#.I
SW:HDA1_HUMAN	S09	5920	3	2270.4	(-0.4)	5.343	0.387	0.991	3	K.L*HISPSNM@TNQNTNEYL*EK#.I
SW:HDA1_HUMAN	S09	6508	3	2254.4	(+0.5)	4.848	0.388	0.997	3	K.L*HISPSNMTNQNTNEYL*EK#.I
SW:HDA1_HUMAN	S08	6354	2	1159.3	(+0.9)	2.852	0.326	0.966	3	K.YYAVNYPLR.D
SW:HDA1_HUMAN	S08	6358	2	1165.3	(+0.5)	2.660	0.348	0.964	3	K.YYAVNYPL*R.D
SW:HDA1_HUMAN	S09	6486	2	1165.3	(+0.7)	2.821	0.337	0.967	3	K.YYAVNYPL*R.D
SW:HDA1_HUMAN	S15	6518	2	1375.5	(+0.8)	2.837	0.434	0.974	5	K.YGEYFPGTGLDLR.D
SW:HMG2_HUMAN	S15	6196	2	1593.7	(-0.4)	3.268	0.468*	0.256	3	K.KHPDSSVNFAEFSK.K
SW:HMG2_HUMAN	S15	4098	2	1296.4	(+0.7)	2.974	0.304	0.916	3	K.L*GEM@WSEQSAK#.D
SW:HMG2_HUMAN	S15	5596	2	1280.4	(+0.7)	2.756	0.322	0.907	3	K.L*GEMWSEQSAK#.D
SW:HMG2_HUMAN	S15	4026	2	1296.4	(+0.1)	2.697	0.418	0.893	3	K.L*GEM@WSEQSAK#.D
SW:HMG2_HUMAN	S15	4838	2	1326.4	(+0.6)	2.889	0.379	0.936	3	K.SEHPGL*SIGDTAK#.K
SW:HMG2_HUMAN	S15	4768	2	1312.4	(+0.6)	2.706	0.428	0.972	3	K.SEHPGLSIGDTAK.K
SW:HMG2_HUMAN	S15	3952	2	1296.4	(+0.1)	2.625	0.426	0.892	3	K.L*GEM@WSEQSAK#.D
SW:HS72_HUMAN	S07	7406	2	1266.4	(-0.0)	2.630	0.347*	0.157	5	R.FEEL*NADL*FR.G
SW:HS72_HUMAN	S10	7454	2	1254.4	(+0.6)	3.124	0.439	0.984	5	R.FEELNADLFR.G
SW:HS72_HUMAN	S11	7396	2	1254.4	(+0.7)	2.500	0.300	0.926	5	R.FEELNADLFR.G
SW:HS72_HUMAN	S07	7272	2	1082.2	(+0.5)	2.703	0.396	0.974	7	K.LLQDFFNGK.E
SW:HS72_HUMAN	S07	7256	2	1102.2	(-0.1)	2.250	0.276	0.623	7	K.L*L*QDFFNGK#.E
SW:HS72_HUMAN	S07	2410	2	1692.7	(+0.2)	4.365	0.436	1.000	5	K.STAGDTHLGGEDFDNR.M
SW:HS72_HUMAN	S07	3996	2	1692.7	(-0.0)	3.739	0.453	1.000	5	K.STAGDTHLGGEDFDNR.M



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:HS72_HUMAN	S07	4074	2	1692.7	(+0.7)	3.511	0.359	0.974	5	K.STAGDTHLGGEDFDNR.M
SW:HS72_HUMAN	S07	3872	2	1692.7	(+0.6)	3.229	0.426	0.978	5	K.STAGDTHLGGEDFDNR.M
SW:HS72_HUMAN	S07	3788	2	1692.7	(+0.9)	3.006	0.443	0.977	5	K.STAGDTHLGGEDFDNR.M
SW:HS72_HUMAN	S07	4022	2	1698.7	(+0.5)	2.494	0.325	0.911	5	K.STAGDTHL*GGEDFDNR.M
SW:HS72_HUMAN	S07	3900	2	1698.7	(+0.3)	2.380	0.272	0.688	5	K.STAGDTHL*GGEDFDNR.M
SW:HS72_HUMAN	S11	2356	2	1692.7	(+0.6)	2.601	0.386	0.945	5	K.STAGDTHLGGEDFDNR.M
SW:HS72_HUMAN	S13	4912	2	1692.7	(-0.1)	3.628	0.468	1.000	5	K.STAGDTHLGGEDFDNR.M
SW:HS7C_HUMAN	S07	6964	2	1212.4	(+0.4)	3.108	0.506	1.000	2	K.DAGTIAGL*NVL*R.I
SW:HS7C_HUMAN	S07	6970	2	1200.4	(+1.0)	2.875	0.308	0.947	2	K.DAGTIAGLNVL.R.I
SW:HS7C_HUMAN	S07	5544	2	1674.8	(-0.5)	3.742	0.448*	0.236	1	K.NQVAM@NPTNTVFDK#.R
SW:HS7C_HUMAN	S07	6202	2	1650.8	(-0.5)	2.989	0.457	0.955	1	K.NQVAMNPTNTVFDK.R
SW:HS7C_HUMAN	S07	8716	3	2275.5	(+0.6)	3.841	0.433	0.996	2	K.SINPDEAVAYGAAVQAAIL*SGDK#.S
SW:HS7C_HUMAN	S16	6838	2	1200.4	(+0.6)	2.406	0.416	0.961	2	K.DAGTIAGLNVL.R.I
SW:HS9A_HUMAN	S03	5991	2	1243.4	(+0.6)	2.575	0.463	0.976	15	K.ADLINNLGTIAK.S
SW:HS9A_HUMAN	S07	6942	2	1243.4	(+1.0)	2.850	0.192	0.851	15	K.ADLINNLGTIAK.S
SW:HS9A_HUMAN	S10	7010	2	1243.4	(+0.7)	3.283	0.404	0.980	15	K.ADLINNLGTIAK.S
SW:HS9A_HUMAN	S11	6928	2	1243.4	(+0.9)	3.834	0.400	1.000	15	K.ADLINNLGTIAK.S
SW:HS9A_HUMAN	S14	7058	2	1243.4	(+0.7)	4.015	0.441	1.000	15	K.ADLINNLGTIAK.S
SW:HS9A_HUMAN	S15	6888	2	1243.4	(+0.7)	2.693	0.392	0.966	15	K.ADLINNLGTIAK.S
SW:HS9A_HUMAN	S16	6798	2	1243.4	(+0.7)	2.572	0.427	0.970	15	K.ADLINNLGTIAK.S
SW:HS9A_HUMAN	S06	4868	2	1292.4	(+0.4)	2.581	0.319	0.932	6	R.ELISNSSDALDK.I
SW:HS9A_HUMAN	S11	4848	2	1292.4	(+0.7)	2.961	0.419	0.977	6	R.ELISNSSDALDK.I
SW:HS9A_HUMAN	S06	6740	2	1526.7	(-0.1)	2.942	0.168	0.646	13	R.GVVDESDL*PL*NISR.E
SW:HS9A_HUMAN	S09	7066	2	1514.7	(+0.7)	2.406	0.356*	0.109	13	R.GVVDESDLPLNISR.E
SW:HS9A_HUMAN	S11	6872	2	1514.7	(+0.4)	2.588	0.439*	0.162	13	R.GVVDESDLPLNISR.E
SW:HS9A_HUMAN	S06	6188	2	1834.9	(-0.6)	4.054	0.474	1.000	6	R.NPDDITNEEYGEFYK.S
SW:HS9A_HUMAN	S14	7196	2	1350.6	(+0.7)	2.553	0.373*	0.169	4	R.TLTIVDTGIGMTK.A
SW:HS9A_HUMAN	S19	4982	2	1292.4	(+0.4)	2.471	0.277	0.883	6	R.ELISNSSDALDK.I
SW:HS9B_HUMAN	S06	7158	2	1081.2	(+0.2)	2.280	0.336	0.863	4	R.APFDLFENK.K
SW:HS9B_HUMAN	S06	6264	2	1848.9	(+0.6)	5.233	0.588	1.000	5	R.NPDDITQEEYGEFYK.S
SW:HS9B_HUMAN	S06	5586	2	1169.3	(+0.6)	2.240	0.431	0.927	5	K.SIYYITGESK#.E
SW:IF41_HUMAN	S11	6492	2	1060.2	(+0.8)	2.218	0.279	0.874	1	K.EELTLEGIR.Q
SW:IF41_HUMAN	S11	5242	2	1395.5	(+0.7)	4.128	0.575	1.000	4	K.GYDVIAQAQSGTGK.T
SW:IF41_HUMAN	S11	7390	2	1115.4	(+0.5)	2.825	0.451	0.981	6	R.VLITDLLAR.G
SW:IF41_HUMAN	S16	7212	2	1115.4	(+0.7)	2.601	0.344	0.948	6	R.VLITDLLAR.G
SW:IF6_HUMAN	S16	6616	3	2104.3	(+0.8)	4.387	0.488	1.000	1	R.HGL*L*VPNNTTDQEL*QHIR.N
SW:IF6_HUMAN	S16	6512	3	2104.3	(+0.1)	3.889	0.377	0.986	1	R.HGL*L*VPNNTTDQEL*QHIR.N
SW:IF6_HUMAN	S16	5394	2	1525.7	(-0.3)	3.626	0.438*	0.375	1	K.L*NEAQPSTIATSMR.D
SW:IF6_HUMAN	S16	2142	2	1541.7	(+0.6)	3.501	0.420*	0.522	1	K.L*NEAQPSTIATSM@R.D
SW:IF6_HUMAN	S16	5392	2	1519.7	(-0.4)	3.396	0.451*	0.298	1	K.LNEAQPSTIATSMR.D
SW:IF6_HUMAN	S16	8886	2	2585.9	(-0.1)	3.125	0.452	0.957	1	K.TSIEDQDELSSLLQVPLVAGTVNR.G
SW:IF6_HUMAN	S16	8890	2	2609.9	(+0.2)	2.627	0.337	0.862	1	K.TSIEDQDEL*SSL*L*QVPL*VAGTVNR.G
SW:IF6_HUMAN	S17	6818	3	2086.3	(+0.5)	4.168	0.527	1.000	1	R.HGLLVNNTTDQELQHIR.N
SW:ILF3_HUMAN	S06	6472	2	1041.2	(+1.0)	2.530	0.390	0.931	17	K.AYAAL*AAL*EK#.L
SW:ILF3_HUMAN	S09	6804	2	1021.2	(+0.4)	3.341	0.357	0.979	17	K.AYAALAALK.L
SW:ILF3_HUMAN	S10	6688	2	1021.2	(+0.2)	3.328	0.347	0.952	17	K.AYAALAALK.L
SW:ILF3_HUMAN	S05	4734	2	1198.3	(+0.9)	2.407	0.348	0.938	13	K.EATDAIGHLDR.Q
SW:ILF3_HUMAN	S06	4498	2	1198.3	(+1.0)	2.352	0.289	0.887	13	K.EATDAIGHLDR.Q
SW:ILF3_HUMAN	S07	4276	2	1198.3	(+1.0)	2.604	0.286	0.896	13	K.EATDAIGHLDR.Q
SW:ILF3_HUMAN	S10	4768	2	1198.3	(+0.7)	2.270	0.273	0.820	13	K.EATDAIGHLDR.Q
SW:ILF3_HUMAN	S12	4496	2	1198.3	(+0.9)	2.784	0.340	0.959	13	K.EATDAIGHLDR.Q
SW:ILF3_HUMAN	S05	5312	2	1369.5	(-0.5)	2.458	0.335	0.859	14	R.EDITQSAQHALR.L
SW:ILF3_HUMAN	S05	5314	2	1375.5	(+0.1)	2.435	0.288	0.788	14	R.EDITQSAQHAL*R.L
SW:ILF3_HUMAN	S06	5282	2	1369.5	(+0.9)	3.083	0.333	0.965	14	R.EDITQSAQHALR.L
SW:ILF3_HUMAN	S06	5280	2	1375.5	(+0.2)	2.839	0.410	0.944	14	R.EDITQSAQHAL*R.L
SW:ILF3_HUMAN	S11	5426	2	1369.5	(+0.3)	3.081	0.347	0.933	14	R.EDITQSAQHALR.L
SW:ILF3_HUMAN	S10	7400	2	1415.6	(+0.7)	2.316	0.191	0.445	17	K.LFPDTPLALDANK.K
SW:ILF3_HUMAN	S05	4960	2	1074.2	(+0.8)	2.268	0.309	0.913	23	K.NPVMELNEK.R
SW:ILF3_HUMAN	S07	4840	2	1074.2	(+0.9)	2.207	0.138	0.445	23	K.NPVMELNEK.R
SW:ILF3_HUMAN	S08	5212	2	1074.2	(+0.4)	2.408	0.292	0.919	23	K.NPVMELNEK.R

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ILF3_HUMAN	S05	6952	2	1911.1	(-0.7)	2.641	0.381	0.706	10	K.VLAGETLSVNDPPDVLDR.Q
SW:ILF3_HUMAN	S05	6256	2	1057.3	(+0.7)	2.743	0.427	0.977	14	K.VLGMDPLPSK.M
SW:ILF3_HUMAN	S05	6258	2	1077.3	(+0.4)	2.551	0.405	0.940	14	K.VL*GMDPL*PSK#.M
SW:ILF3_HUMAN	S05	5038	2	1093.3	(-0.4)	2.363	0.233	0.531	14	K.VL*GM@DPL*PSK#.M
SW:ILF3_HUMAN	S06	6214	2	1057.3	(+1.0)	2.581	0.328	0.948	14	K.VLGMDPLPSK.M
SW:ILF3_HUMAN	S07	4964	2	1093.3	(-0.1)	2.488	0.144	0.336	14	K.VL*GM@DPL*PSK#.M
SW:ILF3_HUMAN	S10	5204	2	1093.3	(+0.1)	2.431	0.351	0.803	14	K.VL*GM@DPL*PSK#.M
SW:ILF3_HUMAN	S05	4978	2	1472.6	(-0.4)	2.872	0.207	0.720	17	K.VL*QDM@GL*PTGAEGR.D
SW:ILF3_HUMAN	S05	6092	2	1456.6	(-0.1)	2.779	0.246	0.773	17	K.VL*QDMGL*PTGAEGR.D
SW:ILF3_HUMAN	S05	6090	2	1444.6	(-0.1)	2.261	0.188	0.400	17	K.VLQDMGLPTGAEGR.D
SW:ILF3_HUMAN	S06	4890	2	1472.6	(-0.0)	3.246	0.312	0.914	17	K.VL*QDM@GL*PTGAEGR.D
SW:ILF3_HUMAN	S07	4904	2	1472.6	(-0.1)	3.214	0.315	0.914	17	K.VL*QDM@GL*PTGAEGR.D
SW:ILF3_HUMAN	S12	5540	2	985.2	(+0.7)	2.263	0.203	0.764	14	R.LAAFGQLHK.V
SW:IMA2_HUMAN	S09	9174	2	2186.6	(+0.8)	2.585	0.357	0.264	3	R.NKNPAPPIDAVEQILPTLVR.L
SW:IMA2_HUMAN	S09	9532	2	1944.3	(+0.9)	2.628	0.371	0.940	3	K.NPAPPIDAVEQILPTLVR.L
SW:IMA2_HUMAN	S09	6252	2	955.2	(+0.7)	2.346	0.269	0.803	3	K.TGVVPQL*VK#.L
SW:IMA2_HUMAN	S10	8092	2	1550.9	(-0.5)	2.471	0.367	0.824	3	K.LLGASELPIVTPALR.A
SW:K020_HUMAN	S07	8746	2	1445.7	(+0.7)	2.431	0.500	0.977	5	K.VFLDFFTYAPPK.L
SW:K020_HUMAN	S12	8588	2	1445.7	(-0.0)	2.573	0.221	0.696	5	K.VFLDFFTYAPPK.L
SW:K020_HUMAN	S10	8064	2	1074.4	(+0.9)	2.301	0.174	0.713	2	K.VLLYLLSPR.D
SW:K020_HUMAN	S14	8202	2	1074.4	(+0.4)	2.519	0.281	0.925	2	K.VLLYLLSPR.D
SW:K020_HUMAN	S14	10298	2	1970.3	(+0.4)	2.251	0.431	0.949	2	K.QIIIEISSLPSIVNDK.Y
SW:K117_HUMAN	S10	6864	2	1090.3	(+0.6)	3.439	0.455	1.000	3	R.L*QGVASSL*FR.G
SW:K117_HUMAN	S10	6860	2	1078.3	(+0.8)	3.310	0.470	1.000	3	R.LGQVASSLFR.G
SW:K117_HUMAN	S10	5606	3	2458.6	(+0.6)	4.516	0.523	1.000	3	K.RNEEEESTSQIERPLSQEPAK.K
SW:K117_HUMAN	S10	6722	2	1124.3	(+0.7)	2.366	0.343	0.937	1	R.SVFGNLPYK.V
SW:K179_HUMAN	S06	5318	3	2219.4	(+0.9)	4.723	0.560	1.000	1	K.HHL*QPENPGPGGAAPSL*EQNR.G
SW:K179_HUMAN	S06	5300	3	2207.4	(+0.9)	4.563	0.342	0.994	1	K.HHLQPENPGPGGAAPSL*EQNR.G
SW:K179_HUMAN	S05	5326	2	1114.3	(+0.7)	2.847	0.256	0.925	1	K.SILVSPTGPSR.V
SW:K179_HUMAN	S10	5522	2	1114.3	(+0.5)	2.823	0.199	0.870	1	K.SILVSPTGPSR.V
SW:K179_HUMAN	S11	5378	2	1114.3	(+0.6)	2.680	0.286	0.916	1	K.SILVSPTGPSR.V
SW:K179_HUMAN	S06	4470	2	1605.8	(+0.4)	3.832	0.394	0.981	1	K.SSTATHPPGPAVQLNK.T
SW:K179_HUMAN	S06	4394	2	1605.8	(+0.4)	2.563	0.300	0.898	1	K.SSTATHPPGPAVQLNK.T
SW:K179_HUMAN	S06	4510	2	1619.8	(+0.7)	2.352	0.283	0.678	1	K.SSTATHPPGPAVQL*NK#.T
SW:K179_HUMAN	S06	4398	2	1619.8	(+0.2)	2.218	0.380	0.723	1	K.SSTATHPPGPAVQL*NK#.T
SW:K179_HUMAN	S06	2230	2	1357.5	(+0.6)	2.762	0.400	0.934	1	K.TPTSSPASSPL*VAK#.K
SW:K179_HUMAN	S06	7064	2	1001.2	(+0.4)	2.293	0.287	0.838	2	K.VFL*DVL*M@K#.E
SW:K179_HUMAN	S06	6432	2	2030.2	(+0.6)	5.091	0.590	1.000	2	K.VGDGDLSAEEIPENEVSLR.R
SW:K179_HUMAN	S12	5182	2	1114.3	(+0.8)	2.780	0.255	0.917	1	K.SILVSPTGPSR.V
SW:K1M5_HUMAN	S01	5790	2	1244.4	(+0.2)	2.221	0.326	0.805	3	R.QLVEDINGLR.R
SW:K1M5_HUMAN	S11	5226	2	1001.2	(+0.3)	2.205	0.148	0.389	2	R.LVVEIDNAK.L
SW:KU70_HUMAN	S07	6772	2	1028.2	(+0.1)	2.430	0.425	0.887	1	R.L*GSL*VDEFK#.E
SW:KU70_HUMAN	S07	9966	3	2424.8	(+0.6)	3.998	0.361	0.993	1	R.NLEALALDLMEPEQAVDLTLPK.V
SW:KU70_HUMAN	S07	6720	2	1704.8	(-0.5)	2.648	0.356	0.890	2	R.SDSFENPVLQQHFR.N
SW:KU70_HUMAN	S07	6830	2	1652.8	(+1.0)	3.388	0.482	1.000	1	R.TFNTSTGGLLLPSDTK.R
SW:KU70_HUMAN	S14	7594	2	1574.8	(-0.7)	2.331	0.355	0.573	1	K.NIYVLQELDNPGAK.R
SW:KU86_HUMAN	S06	6010	3	2244.3	(+0.5)	4.103	0.522	1.000	1	K.DQVTAQEIQDNHEDGPTAK.K
SW:KU86_HUMAN	S06	6026	2	1110.3	(+0.5)	2.738	0.324	0.951	1	R.LGGHGSPFLK.G
SW:KU86_HUMAN	S06	9472	3	2348.6	(-0.2)	4.040	0.369	0.972	1	K.YAPTEAQL*NAVDAL*IDSMSL*AK#.K
SW:KU86_HUMAN	S11	9650	3	2348.6	(+0.6)	4.286	0.392	0.995	1	K.YAPTEAQL*NAVDAL*IDSMSL*AK#.K
SW:LAM1_HUMAN	S06	8158	2	1447.6	(+0.6)	2.489	0.123	0.524	2	R.IESLSSQLSNLQK.E
SW:LAM1_HUMAN	S07	5412	2	1066.2	(+0.1)	2.501	0.194	0.453	2	K.DAAL*ATAL*GDK#.K
SW:MA32_HUMAN	S15	7938	2	1698.9	(-0.1)	3.267	0.271	0.153	1	K.AFVDFLSDEIKEER.K
SW:MA32_HUMAN	S15	7944	2	1712.9	(+0.5)	3.073	0.391	0.447	1	K.AFVDFL*SDEIK#EER.K
SW:MA32_HUMAN	S15	8006	2	2302.6	(+0.4)	4.551	0.500	1.000	2	K.VEEQEPEL*STPNFVVEVIK#.N
SW:MA32_HUMAN	S15	8030	2	1298.5	(+0.4)	2.556	0.435	0.947	1	K.AFVDFL*SDEIK#.E

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:MAT3_HUMAN	S05	2070	2	1337.4	(+0.8)	2.893	0.440	0.976		R.GNL*GAGNGNL*QGPR.H
SW:MAT3_HUMAN	S05	6340	2	1639.8	(-0.2)	2.861	0.310	0.868	1	R.GPSL*NPVL*DYDHGSR.S
SW:MAT3_HUMAN	S05	8016	2	1978.3	(+0.8)	3.728	0.484	1.000	3	R.IGPYQPNVPVGDYVIPK#.T
SW:MAT3_HUMAN	S05	8018	2	1970.3	(+0.6)	3.631	0.475	1.000	3	R.IGPYQPNVPVGDYVIPK.T
SW:MAT3_HUMAN	S08	8106	2	1970.3	(+0.7)	4.320	0.515	1.000	3	R.IGPYQPNVPVGDYVIPK.T
SW:MAT3_HUMAN	S05	9022	2	1621.0	(+0.6)	3.392	0.322	0.966	1	K.ITPENLPQILLQLK.R
SW:MAT3_HUMAN	S06	8974	2	1621.0	(+0.4)	2.777	0.292	0.921	1	K.ITPENLPQILLQLK.R
SW:MAT3_HUMAN	S08	9254	2	1621.0	(+0.1)	3.479	0.324	0.934	1	K.ITPENLPQILLQLK.R
SW:MAT3_HUMAN	S09	9222	2	1621.0	(-0.5)	2.521	0.182	0.514	1	K.ITPENLPQILLQLK.R
SW:MAT3_HUMAN	S10	9280	2	1621.0	(-0.1)	2.338	0.272	0.688	1	K.ITPENLPQILLQLK.R
SW:MAT3_HUMAN	S11	9130	2	1621.0	(+0.9)	2.816	0.390	0.965	1	K.ITPENLPQILLQLK.R
SW:MAT3_HUMAN	S12	8878	2	1621.0	(+0.6)	3.009	0.324	0.953	1	K.ITPENLPQILLQLK.R
SW:MAT3_HUMAN	S13	9236	2	1621.0	(+0.5)	2.943	0.401	0.971	1	K.ITPENLPQILLQLK.R
SW:MAT3_HUMAN	S14	9376	2	1621.0	(+0.2)	2.652	0.331	0.868	1	K.ITPENLPQILLQLK.R
SW:MAT3_HUMAN	S05	4566	2	1372.5	(-0.6)	2.844	0.314	0.894	1	R.RTEEGPTL*SYGR.D
SW:MAT3_HUMAN	S04	4161	2	1216.3	(+0.4)	2.215	0.349	0.918	1	R.TEEGPTL*SYGR.D
SW:MAT3_HUMAN	S05	4476	2	1210.3	(+0.4)	2.684	0.469	0.975	1	R.TEEGPTLSYGR.D
SW:MAT3_HUMAN	S05	4528	2	1216.3	(+0.7)	2.449	0.429	0.968	1	R.TEEGPTL*SYGR.D
SW:MAT3_HUMAN	S05	4450	2	1216.3	(+0.6)	2.380	0.371	0.947	1	R.TEEGPTL*SYGR.D
SW:MAT3_HUMAN	S10	4326	2	1210.3	(+0.1)	2.622	0.433	0.945	1	R.TEEGPTLSYGR.D
SW:MAT3_HUMAN	S10	4324	2	1216.3	(+0.7)	2.544	0.377	0.959	1	R.TEEGPTL*SYGR.D
SW:MAT3_HUMAN	S12	4120	2	1210.3	(+0.7)	2.624	0.451	0.976	1	R.TEEGPTLSYGR.D
SW:MAT3_HUMAN	S12	4156	2	1216.3	(+0.6)	2.407	0.401	0.959	1	R.TEEGPTL*SYGR.D
SW:MAT3_HUMAN	S13	4662	2	1210.3	(+1.0)	2.772	0.393	0.971	1	R.TEEGPTLSYGR.D
SW:MAT3_HUMAN	S15	8972	2	1621.0	(+0.4)	2.217	0.225	0.682	1	K.ITPENLPQILLQLK.R
SW:MEC2_HUMAN	S07	6156	2	1114.3	(+0.5)	2.518	0.259	0.877	2	R.SVQETVLPK.K
SW:MEC2_HUMAN	S07	1998	2	1338.5	(+0.6)	2.692	0.465	0.953	2	K.TQPAVATAATAAEK#.Y
SW:MEC2_HUMAN	S07	2002	2	1330.5	(+0.5)	2.446	0.381	0.944	2	K.TQPAVATAATAAEK.Y
SW:MEC2_HUMAN	S07	6522	2	1324.5	(-0.0)	2.292	0.327	0.663	2	K.YDVYL*INPQGK#.A
SW:MEC2_HUMAN	S07	6162	2	1128.3	(-0.2)	2.286	0.257	0.558	2	R.SVQETVL*PIK#.K
SW:MGN_HUMAN	S18	5694	2	1174.3	(+0.0)	2.957	0.271	0.881	1	K.IGSLIDVNQSK.D
SW:MGN_HUMAN	S18	7852	2	1308.5	(+0.6)	2.883	0.323	0.927	2	R.VFYLL*VQDL*K#.C
SW:MLN_HUMAN	S19	5166	2	1355.5	(+0.4)	2.650	0.393*	0.204	7	R.ALGNPTNAEVLK.V
SW:MLN_HUMAN	S19	6562	2	1545.6	(+1.0)	3.224	0.511	1.000	8	K.DQGTIEDYVEGLR.V
SW:MLN_HUMAN	S19	5174	2	1375.5	(-0.6)	2.496	0.220	0.470	7	R.AL*GNPTNAEVL*K#.V
SW:MLRM_HUMAN	S17	5772	2	1229.3	(+0.4)	3.461	0.365	0.980	5	K.LNGTDPEDVIR.N
SW:MLRM_HUMAN	S17	6554	2	1416.5	(+0.9)	3.186	0.462	1.000	2	R.FTDEEVDLYR.E
SW:MP10_HUMAN	S05	8360	3	2163.6	(+0.9)	3.766	0.319	0.900	1	K.LDALSNFHFIPKPPVPEIK.V
SW:MP10_HUMAN	S05	7816	2	1569.8	(-0.3)	2.455	0.208	0.587		K.LSEMEAYLENIEK.E
SW:MP10_HUMAN	S05	8000	2	1599.8	(+0.6)	3.443	0.455*	0.537		K.LSLAEIYEQEYIK.L
SW:MP10_HUMAN	S05	4754	2	910.0	(+0.2)	2.282	0.225	0.492	1	K.SSQAFFSK#.L
SW:MP10_HUMAN	S05	2220	2	1661.7	(+0.7)	4.344	0.369	0.968		K.TAEENPEHVEIQK#.M
SW:MP10_HUMAN	S12	2098	2	1653.7	(+0.5)	2.620	0.167	0.644		K.TAEENPEHVEIQK.M
SW:MTA2_HUMAN	S07	5704	3	2173.3	(+0.5)	4.638	0.478	0.999	2	R.GHLRPEAQLSPYTTSANR.A
SW:MTA2_HUMAN	S07	5446	2	1180.4	(+0.5)	2.309	0.301	0.160	2	K.DLVAQAPLKP.T
SW:NNP1_HUMAN	S10	6102	2	1259.4	(+0.2)	3.172	0.393	0.951		R.AAGGFTHDELLK.V
SW:NNP1_HUMAN	S10	7606	2	1872.1	(-0.6)	2.869	0.403	0.932	3	K.LQDLAGGIFPEDEIPEK.A
SW:NNP1_HUMAN	S10	6302	2	1394.6	(-0.4)	2.472	0.281	0.078	3	R.TK#DSL*VL*NNITR.G
SW:NNP1_HUMAN	S10	5370	2	1388.5	(-0.6)	2.271	0.185	0.419	3	K.VGAEELTADQNLK.F
SW:NNP1_HUMAN	S10	6952	2	1392.6	(+0.1)	2.557	0.182	0.491		R.VQLPPEIQLAQR.L
SW:NNP1_HUMAN	S10	6966	2	1404.6	(-0.7)	2.218	0.301	0.425		R.VQL*PPEIQL*AQR.L
SW:NO56_HUMAN	S07	4492	2	1189.3	(+0.6)	2.992	0.367	0.972	5	K.AQLGLGHSYSR.A
SW:NO56_HUMAN	S07	4572	2	1189.3	(+0.6)	2.701	0.319	0.947	5	K.AQLGLGHSYSR.A
SW:NO56_HUMAN	S07	4414	2	1189.3	(-0.4)	2.529	0.416	0.933	5	K.AQLGLGHSYSR.A
SW:NO56_HUMAN	S07	4464	2	1201.3	(+0.3)	2.408	0.320	0.843	5	K.AQL*GL*GHSYSR.A
SW:NO56_HUMAN	S07	1876	2	1415.5	(+0.5)	2.610	0.555	0.983	3	K.EEPVSSGPEEAVGK.S
SW:NO56_HUMAN	S07	5224	2	925.1	(+0.7)	2.396	0.310	0.939	5	R.L*AQFIGNR.R
SW:NO56_HUMAN	S08	5480	2	925.1	(+0.8)	2.463	0.285	0.932	5	R.L*AQFIGNR.R

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:NO56_HUMAN	S15	5218	2	925.1	(+0.3)	2.603	0.296	0.896	5	R.L*AQFIGNR.R
SW:NO56_HUMAN	S07	5266	2	1127.3	(-0.8)	2.258	0.176	0.104	2	K.L*EEL*TMDGAK#.A
SW:NO56_HUMAN	S07	6134	2	1309.6	(+0.2)	3.431	0.457	1.000	4	R.LIAHAGSLTNLAK.Y
SW:NO56_HUMAN	S07	6130	2	1335.6	(-0.3)	3.108	0.273*	0.131	4	R.L*IAHAGSL*TNL*AK#.Y
SW:NO56_HUMAN	S08	6278	2	1309.6	(+0.1)	2.440	0.450	0.933	4	R.LIAHAGSLTNLAK.Y
SW:NO56_HUMAN	S12	5966	2	1309.6	(+0.6)	2.472	0.487	0.975	4	R.LIAHAGSLTNLAK.Y
SW:NO56_HUMAN	S13	6428	2	1309.6	(+0.9)	2.528	0.515	0.980	4	R.LIAHAGSLTNLAK.Y
SW:NO56_HUMAN	S08	6578	2	1151.4	(+0.9)	2.315	0.172	0.370	2	R.LLLETHLPSK.K
SW:NO56_HUMAN	S01	6454	2	1312.5	(+0.5)	2.772	0.452	0.979	4	R.LSFYETGEIPR.K
SW:NO56_HUMAN	S17	5908	2	918.1	(+0.5)	2.301	0.256	0.764	5	K.VL*L*GVGDPK#.I
SW:NO56_HUMAN	S07	5278	2	953.1	(+0.8)	2.662	0.356	0.970	5	R.VVSLSEYR.Q
SW:NO56_HUMAN	S08	5488	2	953.1	(+0.9)	2.441	0.332	0.952	5	R.VVSLSEYR.Q
SW:NO56_HUMAN	S09	5514	2	953.1	(+0.7)	2.232	0.396	0.960	5	R.VVSLSEYR.Q
SW:NO56_HUMAN	S01	6078	2	1377.6	(+0.7)	3.395	0.533	1.000	5	K.YPASTVQILGAEK.A
SW:NO56_HUMAN	S08	6386	2	1377.6	(-0.3)	4.393	0.502	1.000	5	K.YPASTVQILGAEK.A
SW:NO56_HUMAN	S10	6420	2	1377.6	(+0.9)	2.741	0.428	0.973	5	K.YPASTVQILGAEK.A
SW:NO56_HUMAN	S13	6542	2	1391.6	(+0.1)	2.975	0.419	0.903	5	K.YPASTVQIL*GAEK#.A
SW:NO56_HUMAN	S13	6538	2	1377.6	(-0.0)	2.223	0.294	0.711	5	K.YPASTVQILGAEK.A
SW:NO56_HUMAN	S16	6166	2	1391.6	(-0.3)	2.664	0.183	0.436	5	K.YPASTVQIL*GAEK#.A
SW:NO56_HUMAN	S17	6462	2	1377.6	(+0.7)	3.103	0.500	1.000	5	K.YPASTVQILGAEK.A
SW:NO56_HUMAN	S20	5956	2	1391.6	(+0.2)	3.222	0.402	0.910	5	K.YPASTVQIL*GAEK#.A
SW:NOG1_HUMAN	S07	7420	2	1052.2	(+0.2)	2.485	0.218	0.738	4	K.DFIDLTLSK.T
SW:NOG1_HUMAN	S07	8350	3	2350.7	(+0.3)	4.995	0.389	0.984	3	K.IPEIWEGHNIADYIDPAIM@K#.K
SW:NOG1_HUMAN	S07	6710	2	1061.3	(-0.0)	2.959	0.341	0.877	4	K.L*AL*GQINIAK#.N
SW:NOG1_HUMAN	S12	6538	2	1041.3	(+1.0)	3.233	0.503	1.000	4	K.LALGQINIAK.N
SW:NOG1_HUMAN	S07	7098	2	1162.4	(+0.9)	2.851	0.373	0.972	4	R.LSQILTDFPK.L
SW:NOG1_HUMAN	S10	7160	2	1162.4	(+0.2)	2.809	0.326	0.916	4	R.LSQILTDFPK.L
SW:NOG1_HUMAN	S17	6916	2	1041.3	(+0.9)	3.046	0.394	0.979	4	K.LALGQINIAK.N
SW:NOL1_HUMAN	S05	5318	2	1391.5	(+0.4)	2.521	0.406	0.958	2	K.GADSELSTVPSVTK.T
SW:NOL1_HUMAN	S09	5616	2	1391.5	(+0.6)	3.146	0.488	0.984	2	K.GADSELSTVPSVTK.T
SW:NOL1_HUMAN	S10	5542	2	1391.5	(+0.5)	2.358	0.388	0.941	2	K.GADSELSTVPSVTK.T
SW:NOL1_HUMAN	S11	5446	2	1391.5	(-0.7)	2.329	0.242	0.283	2	K.GADSELSTVPSVTK.T
SW:NOL1_HUMAN	S12	5200	2	1391.5	(+0.4)	2.848	0.408	0.970	2	K.GADSELSTVPSVTK.T
SW:NOL1_HUMAN	S05	4428	2	1402.5	(+0.5)	2.840	0.416	0.971	2	K.GTDTQTPAVLSPSK.T
SW:NOL1_HUMAN	S05	7208	2	1027.3	(+0.8)	2.923	0.245	0.942	2	R.IQDIVGILR.D
SW:NOL1_HUMAN	S07	7222	2	1027.3	(+0.9)	3.210	0.211	0.945	2	R.IQDIVGILR.D
SW:NOL1_HUMAN	S07	7236	2	1033.3	(+0.5)	2.589	0.283	0.934	2	R.IQDIVGIL*R.D
SW:NOL1_HUMAN	S09	7388	2	1027.3	(+1.0)	3.289	0.188	0.939	2	R.IQDIVGILR.D
SW:NOL1_HUMAN	S07	4792	2	1458.6	(+0.6)	4.592	0.565	1.000	2	K.NTGIVILANDANAER.L
SW:NOL1_HUMAN	S15	7156	2	1027.3	(+0.8)	2.819	0.110	0.769	2	R.IQDIVGILR.D
SW:NOP5_HUMAN	S08	4388	2	1265.4	(-0.0)	2.312	0.299	0.627	3	K.EAHEPL*AVADAK#.L
SW:NOP5_HUMAN	S08	4416	2	1251.4	(+1.0)	2.219	0.269	0.815	3	K.EAHEPLAVADAK.L
SW:NOP5_HUMAN	S09	9884	2	1935.2	(-1.0)	2.642	0.235	0.227	2	K.FQDTAEAL*AAFTAL*MEGK#.I
SW:NOP5_HUMAN	S15	9644	3	1935.2	(+0.7)	4.456	0.439	0.998	2	K.FQDTAEAL*AAFTAL*MEGK#.I
SW:NOP5_HUMAN	S16	9608	3	1915.2	(+0.9)	4.830	0.556	1.000	2	K.FQDTAEALAAFTALMEGK.I
SW:NOP5_HUMAN	S08	5776	2	1325.5	(-0.5)	2.608	0.349	0.887	3	K.HAASTVQILGAEK.A
SW:NOP5_HUMAN	S12	5398	2	1325.5	(+0.4)	3.164	0.533	1.000	3	K.HAASTVQILGAEK.A
SW:NOP5_HUMAN	S14	5590	2	1325.5	(-0.5)	3.276	0.387	0.948	3	K.HAASTVQILGAEK.A
SW:NOP5_HUMAN	S09	2018	2	1576.7	(+0.9)	3.738	0.452	1.000	2	K.IEQVDKEDEITEK.K
SW:NOP5_HUMAN	S09	7298	2	1353.6	(+0.1)	2.383	0.345	0.734	3	R.L*IAHAGSL*L*NL*AK#.H
SW:NOP5_HUMAN	S12	6930	2	1321.6	(+0.6)	3.213	0.349*	0.442	3	R.LIAHAGSLLNLAK.H
SW:NOP5_HUMAN	S14	7268	2	1321.6	(+0.1)	3.026	0.364*	0.205	3	R.LIAHAGSLLNLAK.H
SW:NOP5_HUMAN	S08	6822	2	1138.3	(+0.1)	2.687	0.293	0.803	2	K.L*QEVDL*WK#.E
SW:NOP5_HUMAN	S09	6914	2	1118.3	(-0.4)	2.943	0.325	0.934	2	K.LQEVDLWK.E
SW:NOP5_HUMAN	S09	6920	2	1138.3	(+0.1)	2.766	0.313	0.842	2	K.L*QEVDL*WK#.E
SW:NOP5_HUMAN	S17	6894	2	1118.3	(+0.8)	2.591	0.290	0.927	2	K.LQEVDLWK.E
SW:NOP5_HUMAN	S09	6974	2	1399.6	(-0.3)	2.964	0.436	0.953	2	R.SQMDGLIPGVEPR.E
SW:NOP5_HUMAN	S08	6606	2	1328.5	(-0.4)	3.217	0.288	0.926	3	R.TQLYEYLQNR.M
SW:NOP5_HUMAN	S08	6602	2	1340.5	(-0.4)	2.239	0.141	0.348	3	R.TQL*YEYL*QNR.M
SW:NOP5_HUMAN	S09	6708	2	1328.5	(+0.6)	2.297	0.476	0.974	3	R.TQLYEYLQNR.M
SW:NOP5_HUMAN	S09	6728	2	1340.5	(-0.9)	2.293	0.140	0.135	3	R.TQL*YEYL*QNR.M
SW:NOP5_HUMAN	S14	6650	2	1328.5	(+0.4)	2.237	0.253	0.826	3	R.TQLYEYLQNR.M
SW:NOP5_HUMAN	S09	5682	3	2123.2	(+0.6)	5.725	0.600	1.000	2	K.VEEEEEEKVAEEETSVK.K

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:NOP5_HUMAN	S17	6904	2	1138.3	(-0.2)	2.568	0.269	0.734	2	K.L*QEVDL*WK#.E
SW:NP14_HUMAN	S05	1402	2	1212.4	(+0.8)	2.352	0.366	0.164	4	K.VAGGAAPSKPASAK.K
SW:NP14_HUMAN	S09	10228	2	1689.1	(+0.2)	3.442	0.486	1.000	3	R.VVPSDLYPLVLGFLR.D
SW:NP14_HUMAN	S11	10186	2	1689.1	(+0.6)	2.926	0.547	1.000	3	R.VVPSDLYPLVLGFLR.D
SW:NP14_HUMAN	S14	10462	2	1689.1	(-0.2)	2.854	0.414	0.936	3	R.VVPSDLYPLVLGFLR.D
SW:NPM_HUMAN	S13	7890	2	2160.4	(+0.7)	5.422	0.498	0.994	12	K.DEL*HIVEAEAMNYEGSPIK#.V
SW:NPM_HUMAN	S13	7888	2	2146.4	(+0.2)	5.354	0.554	1.000	12	K.DELHIVEAEAMNYEGSPIK.V
SW:NPM_HUMAN	S13	10180	3	2160.4	(+0.6)	4.652	0.469	1.000	12	K.DEL*HIVEAEAMNYEGSPIK#.V
SW:NPM_HUMAN	S13	11344	3	2160.4	(+0.3)	4.515	0.511	1.000	12	K.DEL*HIVEAEAMNYEGSPIK#.V
SW:NPM_HUMAN	S13	7518	3	2176.4	(-0.7)	4.380	0.440	0.975	12	K.DEL*HIVEAEAM@NYEGSPIK#.V
SW:NPM_HUMAN	S13	10502	3	2160.4	(+0.4)	4.250	0.490	1.000	12	K.DEL*HIVEAEAMNYEGSPIK#.V
SW:NPM_HUMAN	S13	7990	2	2160.4	(-0.2)	4.214	0.463	1.000	12	K.DEL*HIVEAEAMNYEGSPIK#.V
SW:NPM_HUMAN	S13	12814	3	2146.4	(+0.9)	4.211	0.380	0.996	12	K.DELHIVEAEAMNYEGSPIK.V
SW:NPM_HUMAN	S13	10674	3	2160.4	(+0.5)	4.176	0.391	0.995	12	K.DEL*HIVEAEAMNYEGSPIK#.V
SW:NPM_HUMAN	S13	8012	3	2160.4	(+0.7)	4.122	0.390	0.994	12	K.DEL*HIVEAEAMNYEGSPIK#.V
SW:NPM_HUMAN	S13	11804	3	2146.4	(+0.6)	3.976	0.452	0.998	12	K.DELHIVEAEAMNYEGSPIK.V
SW:NPM_HUMAN	S13	10998	3	2146.4	(-0.0)	3.947	0.473	0.996	12	K.DELHIVEAEAMNYEGSPIK.V
SW:NPM_HUMAN	S13	10182	3	2146.4	(+0.6)	3.901	0.401	0.997	12	K.DELHIVEAEAMNYEGSPIK.V
SW:NPM_HUMAN	S13	12726	3	2146.4	(+0.7)	3.881	0.449	0.998	12	K.DELHIVEAEAMNYEGSPIK.V
SW:NPM_HUMAN	S13	10404	3	2146.4	(-0.0)	3.822	0.365	0.981	12	K.DELHIVEAEAMNYEGSPIK.V
SW:NPM_HUMAN	S13	7874	3	2146.4	(+1.0)	3.817	0.485	0.999	12	K.DELHIVEAEAMNYEGSPIK.V
SW:NPM_HUMAN	S13	11956	3	2160.4	(+0.5)	3.801	0.288	0.950	12	K.DEL*HIVEAEAMNYEGSPIK#.V
SW:NPM_HUMAN	S13	11468	3	2146.4	(+0.3)	3.792	0.424	0.992	12	K.DELHIVEAEAMNYEGSPIK.V
SW:NPM_HUMAN	S13	7878	3	2160.4	(+1.0)	3.782	0.374	0.991	12	K.DEL*HIVEAEAMNYEGSPIK#.V
SW:NPM_HUMAN	S13	11244	3	2160.4	(+0.7)	3.741	0.399	0.994	12	K.DEL*HIVEAEAMNYEGSPIK#.V
SW:NPM_HUMAN	S13	11690	3	2146.4	(+0.3)	3.710	0.462	0.995	12	K.DELHIVEAEAMNYEGSPIK.V
SW:NPM_HUMAN	S13	11072	3	2160.4	(+0.7)	3.706	0.353	0.984	12	K.DEL*HIVEAEAMNYEGSPIK#.V
SW:NPM_HUMAN	S18	7786	3	2146.4	(+0.9)	3.778	0.426	0.997	12	K.DELHIVEAEAMNYEGSPIK.V
SW:NPM_HUMAN	S19	7436	3	2176.4	(+0.9)	4.007	0.491	1.000	12	K.DEL*HIVEAEAM@NYEGSPIK#.V
SW:NPM_HUMAN	S13	4988	3	3725.3	(+0.6)	4.874	0.579	1.000	9	K.LAADEDDDDDEEDDDDDDDDDDFDDEEAEEK.A
SW:NPM_HUMAN	S13	4806	3	3725.3	(+0.2)	3.705	0.536	1.000	9	K.LAADEDDDDDEEDDDDDDDDDDFDDEEAEEK.A
SW:NPM_HUMAN	S13	9002	2	2228.7	(-0.3)	3.924	0.529	1.000	13	K.MSVQPTVSLGGFEITPPVVL.R
SW:NPM_HUMAN	S14	8996	2	2256.7	(+0.7)	4.844	0.619	1.000	13	K.M@SVQPTVSL*GGFEITPPVVL*R.L
SW:NPM_HUMAN	S17	8728	2	2256.7	(+0.8)	4.873	0.608	1.000	13	K.M@SVQPTVSL*GGFEITPPVVL*R.L
SW:NPM_HUMAN	S18	8800	2	2256.7	(+0.5)	5.351	0.645	1.000	13	K.M@SVQPTVSL*GGFEITPPVVL*R.L
SW:NPM_HUMAN	S18	8790	3	2256.7	(+0.6)	3.727	0.406	0.996	13	K.M@SVQPTVSL*GGFEITPPVVL*R.L
SW:NPM_HUMAN	S18	8994	2	2228.7	(-0.4)	3.021	0.427	0.948	13	K.MSVQPTVSLGGFEITPPVVL.R
SW:NPM_HUMAN	S13	8340	2	1843.0	(+0.8)	3.700	0.404	0.982	9	R.M@TDQEIQL*WQWR.K
SW:NPM_HUMAN	S13	8380	2	1821.0	(-0.8)	3.069	0.213	0.481	9	R.MTDQEIQLWQWR.K
SW:NPM_HUMAN	S14	8454	2	1843.0	(-0.9)	2.866	0.340	0.702	9	R.M@TDQEIQL*WQWR.K
SW:NPM_HUMAN	S19	8284	2	1843.0	(-0.4)	3.921	0.330	0.951	9	R.M@TDQEIQL*WQWR.K
SW:NPM_HUMAN	S12	2342	2	1569.6	(+0.9)	3.148	0.328	0.963	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	S13	4760	2	1569.6	(+1.0)	4.052	0.409	1.000	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	S13	4272	2	1569.6	(+0.3)	3.829	0.326	0.951	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	S13	4606	2	1569.6	(+0.3)	3.807	0.430	1.000	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	S13	4670	2	1581.6	(+0.6)	3.658	0.434	1.000	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	S13	2496	2	1569.6	(+0.3)	3.637	0.402	0.962	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	S13	2642	2	1569.6	(+0.9)	3.588	0.367	0.979	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	S13	4918	2	1569.6	(-0.0)	3.566	0.302	0.933	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	S13	4112	2	1569.6	(+0.9)	3.533	0.366	0.978	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	S13	4072	2	1581.6	(+0.1)	3.523	0.449	1.000	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	S13	4374	2	1569.6	(-0.6)	3.482	0.372	0.948	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	S13	4564	2	1581.6	(+0.5)	3.482	0.464	1.000	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	S13	4528	2	1569.6	(+1.0)	3.471	0.427	0.983	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	S13	3888	2	1569.6	(-0.2)	3.465	0.380	0.954	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	S13	3088	2	1569.6	(-0.3)	3.430	0.332	0.939	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	S13	4748	2	1581.6	(+0.6)	3.395	0.353	0.974	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	S13	3208	2	1569.6	(-0.4)	3.329	0.301	0.919	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	S13	2998	2	1569.6	(-0.2)	3.316	0.324	0.930	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	S13	4838	2	1569.6	(+0.4)	3.293	0.459	0.984	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	S13	4462	2	1581.6	(+0.1)	3.231	0.381	0.947	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	S13	3722	2	1569.6	(-0.1)	3.190	0.389	0.948	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	S13	4592	2	1581.6	(-0.9)	3.179	0.401	0.834	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	S13	4892	2	1581.6	(+0.6)	3.112	0.373	0.972	12	K.VDNDENEHQL*SL*R.T

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:NPM_HUMAN	S13	4146	2	1581.6	(+0.3)	3.006	0.448	0.957	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	S13	3818	2	1581.6	(+0.4)	3.005	0.457	0.981	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	S13	3584	2	1581.6	(+0.3)	2.964	0.445	0.955	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	S13	3540	2	1569.6	(-0.0)	2.923	0.381	0.934	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	S13	3394	2	1581.6	(+0.1)	2.865	0.371	0.925	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	S13	2382	2	1569.6	(+0.9)	2.864	0.290	0.933	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	S13	2928	2	1581.6	(+0.7)	2.832	0.437	0.976	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	S13	3296	2	1581.6	(-0.7)	2.798	0.333	0.690	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	S13	3340	2	1569.6	(-0.5)	2.796	0.364	0.917	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	S13	2858	2	1581.6	(+0.2)	2.792	0.271	0.830	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	S13	4308	2	1581.6	(-0.7)	2.782	0.321	0.663	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	S13	2942	2	1581.6	(-0.7)	2.739	0.268	0.533	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	S13	3844	2	1581.6	(-1.0)	2.643	0.188	0.289	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	S13	3226	2	1581.6	(-0.1)	2.593	0.246	0.738	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	S13	3748	2	1581.6	(-0.4)	2.575	0.251	0.742	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	S13	3084	2	1581.6	(-0.9)	2.567	0.299	0.547	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	S13	4232	2	1581.6	(-0.8)	2.499	0.197	0.259	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	S13	2384	2	1581.6	(+0.5)	2.414	0.391	0.950	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	S13	3678	2	1581.6	(-0.9)	2.387	0.214	0.256	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	S13	3484	2	1581.6	(+0.8)	2.375	0.367	0.936	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	S13	3516	2	1581.6	(-1.0)	2.341	0.162	0.138	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	S13	2420	2	1569.6	(-0.5)	2.338	0.100	0.204	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	S14	2434	2	1569.6	(+0.3)	2.526	0.277	0.778	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	S17	4120	2	1569.6	(+0.8)	3.327	0.311	0.964	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	S17	4048	2	1569.6	(+0.9)	2.721	0.334	0.945	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	S17	4198	2	1569.6	(+0.8)	2.477	0.300	0.900	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	S18	2220	2	1569.6	(+0.8)	3.490	0.350	0.975	12	K.VDNDENEHQLSLR.T
SW:NPM_HUMAN	S18	2222	2	1581.6	(+0.5)	2.632	0.408	0.965	12	K.VDNDENEHQL*SL*R.T
SW:NPM_HUMAN	S19	2348	2	1581.6	(+0.3)	2.890	0.476	0.960	12	K.VDNDENEHQL*SL*R.T
SW:NUCL_HUMAN	S05	7470	2	1649.8	(-0.3)	2.876	0.380	0.926	3	K.FGYVDFESAEDLEK.A
SW:NUCL_HUMAN	S05	7570	2	1649.8	(+0.1)	2.332	0.137	0.278	3	K.FGYVDFESAEDLEK.A
SW:NUCL_HUMAN	S08	7510	2	1649.8	(-0.1)	2.844	0.400	0.933	3	K.FGYVDFESAEDLEK.A
SW:NUCL_HUMAN	S11	7388	2	1649.8	(+0.3)	3.676	0.579	0.999	3	K.FGYVDFESAEDLEK.A
SW:NUCL_HUMAN	S05	7460	2	1562.6	(+1.0)	4.346	0.449	1.000	5	K.GFGFVDFNSEEDAK.E
SW:NUCL_HUMAN	S05	7382	2	1562.6	(+0.0)	2.702	0.369	0.906	5	K.GFGFVDFNSEEDAK.E
SW:NUCL_HUMAN	S05	7764	2	1570.6	(+0.1)	2.597	0.438	0.878	5	K.GFGFVDFNSEEDAK#.E
SW:NUCL_HUMAN	S05	7368	2	1570.6	(+0.6)	2.444	0.424	0.923	5	K.GFGFVDFNSEEDAK#.E
SW:NUCL_HUMAN	S05	7660	2	1570.6	(+0.4)	2.419	0.281	0.755	5	K.GFGFVDFNSEEDAK#.E
SW:NUCL_HUMAN	S05	9086	2	1570.6	(+0.2)	2.373	0.288	0.461	5	K.GFGFVDFNSEEDAK#.E
SW:NUCL_HUMAN	S06	7238	2	1570.6	(+0.3)	3.295	0.525	1.000	5	K.GFGFVDFNSEEDAK#.E
SW:NUCL_HUMAN	S12	7122	2	1570.6	(+0.5)	3.250	0.510	1.000	5	K.GFGFVDFNSEEDAK#.E
SW:NUCL_HUMAN	S12	6628	2	949.1	(+0.5)	2.216	0.170	0.537	4	K.GIAYIEFK#.T
SW:NUCL_HUMAN	S04	4095	2	1323.4	(+0.7)	2.685	0.383	0.963	4	K.GLSEDTTEETLK.E
SW:NUCL_HUMAN	S05	4352	2	1323.4	(+0.6)	2.916	0.380	0.970	4	K.GLSEDTTEETLK.E
SW:NUCL_HUMAN	S05	4484	2	1323.4	(+0.5)	2.600	0.389	0.962	4	K.GLSEDTTEETLK.E
SW:NUCL_HUMAN	S05	4436	2	1343.4	(+0.4)	2.476	0.475	0.952	4	K.GL*SEDTTEETL*K#.E
SW:NUCL_HUMAN	S08	4700	2	1323.4	(+0.2)	2.939	0.414	0.949	4	K.GLSEDTTEETLK.E
SW:NUCL_HUMAN	S08	4680	2	1343.4	(+0.1)	2.532	0.438	0.883	4	K.GL*SEDTTEETL*K#.E
SW:NUCL_HUMAN	S09	2338	2	1323.4	(+0.6)	2.250	0.318	0.889	4	K.GLSEDTTEETLK.E
SW:NUCL_HUMAN	S10	2424	2	1323.4	(+0.5)	2.458	0.336	0.931	4	K.GLSEDTTEETLK.E
SW:NUCL_HUMAN	S12	4026	2	1323.4	(+0.8)	3.176	0.402	0.978	4	K.GLSEDTTEETLK.E
SW:NUCL_HUMAN	S12	4028	2	1343.4	(+0.0)	2.659	0.490	0.919	4	K.GL*SEDTTEETL*K#.E
SW:NUCL_HUMAN	S12	3954	2	1323.4	(+0.5)	2.643	0.351	0.952	4	K.GLSEDTTEETLK.E
SW:NUCL_HUMAN	S12	4102	2	1343.4	(-0.0)	2.514	0.317	0.737	4	K.GL*SEDTTEETL*K#.E
SW:NUCL_HUMAN	S12	4040	2	1323.4	(-0.7)	2.508	0.380	0.712	4	K.GLSEDTTEETLK.E
SW:NUCL_HUMAN	S13	4460	2	1343.4	(-0.3)	2.590	0.301	0.730	4	K.GL*SEDTTEETL*K#.E
SW:NUCL_HUMAN	S15	4168	2	1323.4	(+0.6)	3.010	0.339	0.964	4	K.GLSEDTTEETLK.E
SW:NUCL_HUMAN	S15	4180	2	1343.4	(-0.6)	2.698	0.395	0.870	4	K.GL*SEDTTEETL*K#.E
SW:NUCL_HUMAN	S15	4094	2	1323.4	(+0.4)	2.602	0.389	0.962	4	K.GLSEDTTEETLK.E
SW:NUCL_HUMAN	S15	4242	2	1323.4	(-0.4)	2.389	0.324	0.831	4	K.GLSEDTTEETLK.E
SW:NUCL_HUMAN	S15	4106	2	1343.4	(+0.1)	2.287	0.438	0.850	4	K.GL*SEDTTEETL*K#.E
SW:NUCL_HUMAN	S16	3986	2	1323.4	(+0.7)	2.850	0.341	0.958	4	K.GLSEDTTEETLK.E
SW:NUCL_HUMAN	S16	3898	2	1323.4	(+0.3)	2.250	0.384	0.873	4	K.GLSEDTTEETLK.E
SW:NUCL_HUMAN	S05	10072	2	1595.7	(+0.9)	3.001	0.489	0.983	4	K.GYAFIEFASFEDAK.E
SW:NUCL_HUMAN	S05	9826	2	1595.7	(+0.6)	2.768	0.347	0.950	4	K.GYAFIEFASFEDAK.E

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:NUCL_HUMAN	S05	10246	2	1595.7	(+0.7)	2.577	0.377	0.951	4	K.GYAFIEFASFEDAK.E
SW:NUCL_HUMAN	S05	10640	2	1595.7	(+0.5)	2.225	0.439	0.953	4	K.GYAFIEFASFEDAK.E
SW:NUCL_HUMAN	S05	5640	2	1001.1	(-0.6)	2.691	0.430	0.954	3	K.NDLAVVDVR.I
SW:NUCL_HUMAN	S06	5620	2	1001.1	(+0.5)	2.719	0.129	0.779	3	K.NDLAVVDVR.I
SW:NUCL_HUMAN	S07	5690	2	1001.1	(+0.9)	3.116	0.322	0.973	3	K.NDLAVVDVR.I
SW:NUCL_HUMAN	S08	5848	2	1001.1	(+0.8)	3.270	0.303	0.973	3	K.NDLAVVDVR.I
SW:NUCL_HUMAN	S09	5930	2	1007.1	(+0.1)	2.661	0.381	0.938	3	K.NDL*AVVDVR.I
SW:NUCL_HUMAN	S10	5826	2	1001.1	(+0.7)	2.618	0.190	0.854	3	K.NDLAVVDVR.I
SW:NUCL_HUMAN	S11	5786	2	1001.1	(+0.5)	2.939	0.354	0.974	3	K.NDLAVVDVR.I
SW:NUCL_HUMAN	S17	5968	2	1001.1	(+0.2)	2.960	0.377	0.952	3	K.NDLAVVDVR.I
SW:NUCL_HUMAN	S05	6162	2	946.1	(+0.6)	2.470	0.209	0.732	3	K.TGISDVFAK#.N
SW:NUCL_HUMAN	S10	6396	2	946.1	(+0.8)	2.653	0.235	0.833	3	K.TGISDVFAK#.N
SW:NUCL_HUMAN	S09	9552	3	2502.8	(-0.6)	3.730	0.490	0.996	4	K.TLVLSNLSYSATEETLQEVFEK.A
SW:NUCL_HUMAN	S13	9536	3	2534.8	(-0.5)	4.409	0.520	1.000	4	K.TL*VL*SNL*SYSATEETL*QEVFEK#.A
SW:NUCL_HUMAN	S15	9272	3	2534.8	(+0.9)	4.292	0.439	0.997	4	K.TL*VL*SNL*SYSATEETL*QEVFEK#.A
SW:NUCL_HUMAN	S17	9382	3	2502.8	(+0.8)	3.990	0.470	0.998	4	K.TLVLSNLSYSATEETLQEVFEK.A
SW:NUCL_HUMAN	S04	7365	3	2333.6	(-0.6)	4.512	0.421	0.991	3	K.VEGTEPTTAFNL*FVGNL*NFNK#.S
SW:NUCL_HUMAN	S05	8946	3	2333.6	(+0.5)	5.038	0.480	1.000	3	K.VEGTEPTTAFNL*FVGNL*NFNK#.S
SW:NUCL_HUMAN	S05	9020	3	2333.6	(+0.9)	4.670	0.427	0.997	3	K.VEGTEPTTAFNL*FVGNL*NFNK#.S
SW:NUCL_HUMAN	S05	9048	3	2313.6	(-0.2)	4.314	0.411	0.993	3	K.VEGTEPTTAFNL*FVGNL*NFNK#.S
SW:NUCL_HUMAN	S05	8956	2	2313.6	(+0.0)	4.297	0.568	1.000	3	K.VEGTEPTTAFNL*FVGNL*NFNK#.S
SW:NUCL_HUMAN	S05	8940	3	2313.6	(+0.7)	4.227	0.437	0.998	3	K.VEGTEPTTAFNL*FVGNL*NFNK#.S
SW:NUCL_HUMAN	S06	8892	3	2313.6	(+0.7)	5.043	0.488	0.999	3	K.VEGTEPTTAFNL*FVGNL*NFNK#.S
SW:NUCL_HUMAN	S08	9166	3	2333.6	(+1.0)	4.488	0.370	0.994	3	K.VEGTEPTTAFNL*FVGNL*NFNK#.S
SW:NUCL_HUMAN	S08	9162	3	2313.6	(+0.5)	3.857	0.417	0.996	3	K.VEGTEPTTAFNL*FVGNL*NFNK#.S
SW:NUCL_HUMAN	S08	9238	3	2313.6	(+0.5)	3.785	0.415	0.997	3	K.VEGTEPTTAFNL*FVGNL*NFNK#.S
SW:NUCL_HUMAN	S09	9126	3	2333.6	(+0.8)	5.042	0.447	1.000	3	K.VEGTEPTTAFNL*FVGNL*NFNK#.S
SW:NUCL_HUMAN	S09	9122	3	2313.6	(+0.9)	4.230	0.469	0.999	3	K.VEGTEPTTAFNL*FVGNL*NFNK#.S
SW:NUCL_HUMAN	S09	9196	3	2313.6	(+0.7)	4.170	0.430	0.998	3	K.VEGTEPTTAFNL*FVGNL*NFNK#.S
SW:NUCL_HUMAN	S15	8898	3	2313.6	(+0.9)	3.807	0.353	0.991	3	K.VEGTEPTTAFNL*FVGNL*NFNK#.S
SW:NUCL_HUMAN	S15	6134	2	1058.3	(+0.8)	2.942	0.313	0.395	4	K.VTLDWAKPK.G
SW:NUCL_HUMAN	S20	8952	3	2502.8	(+0.8)	4.727	0.576	1.000	4	K.TLVLSNLSYSATEETLQEVFEK.A
SW:PCNA_HUMAN	S14	7878	2	2076.2	(+0.3)	3.212	0.454	0.960		R.AEDNADTLALVFEAPNQEK.V
SW:PCNA_HUMAN	S14	5318	2	1308.4	(+0.8)	2.963	0.460	0.962		K.FSASGEL*GNGNIK#.L
SW:PEBB_HUMAN	S16	6308	2	1805.9	(-0.6)	4.594	0.562	1.000	3	R.AQQEDALAQQAFEEAR.R
SW:PEBB_HUMAN	S17	6582	2	1805.9	(+0.4)	5.432	0.568	0.979	3	R.AQQEDALAQQAFEEAR.R
SW:PEBB_HUMAN	S17	6586	2	1811.9	(+0.6)	4.630	0.576	1.000	3	R.AQQEDAL*AAQAFEEAR.R
SW:PEBB_HUMAN	S16	6284	2	1341.4	(+0.1)	3.029	0.374	0.301	4	R.SK#FENEEFFR.K
SW:PEBB_HUMAN	S16	6296	2	1333.4	(-0.4)	2.520	0.296	0.117	4	R.SK#FENEEFFR.K
SW:PEBB_HUMAN	S17	6568	2	1333.4	(+0.1)	2.877	0.258	0.135	4	R.SK#FENEEFFR.K
SW:PEBB_HUMAN	S16	5624	2	1016.2	(+0.8)	3.052	0.412	0.981	2	R.VSLLAVTGK.K
SW:PEBB_HUMAN	S17	6570	2	1341.4	(-0.6)	2.839	0.379	0.273	4	R.SK#FENEEFFR.K
SW:PESC_HUMAN	S08	6126	2	973.2	(+0.9)	3.455	0.396*	0.674		K.LAALSASLAR.V
SW:PESC_HUMAN	S08	7782	2	1081.2	(+0.9)	2.214	0.147	0.584		K.L*QL*SL*ADFR.R
SW:PESC_HUMAN	S15	7544	2	1063.2	(+0.9)	2.572	0.308	0.945		K.LQLSLADFR.R
SW:PESC_HUMAN	S07	6044	2	1112.2	(-0.1)	2.455	0.210	0.676		R.SFGGEVSWDK.S
SW:PESC_HUMAN	S07	7576	2	1096.3	(+1.0)	2.724	0.326	0.960		R.YPTFIDALR.D
SW:PESC_HUMAN	S08	7684	2	1096.3	(+0.6)	2.799	0.248	0.933		R.YPTFIDALR.D
SW:PESC_HUMAN	S08	7694	2	1102.3	(+1.0)	2.513	0.293	0.932		R.YPTFIDAL*R.D
SW:PESC_HUMAN	S15	7512	2	1096.3	(-0.2)	2.481	0.313	0.858		R.YPTFIDALR.D
SW:PESC_HUMAN	S17	7742	2	1096.3	(+0.1)	2.632	0.293	0.883		R.YPTFIDALR.D
SW:PP1A_HUMAN	S13	7100	2	1640.8	(+0.9)	5.188	0.486	1.000	8	R.AHQVVEDGYEFFAK.R
SW:PP1A_HUMAN	S13	7096	2	1648.8	(+0.2)	4.887	0.425	1.000	8	R.AHQVVEDGYEFFAK#.R
SW:PP1A_HUMAN	S13	8176	2	1199.4	(+0.8)	3.146	0.357	0.978	8	K.YPENFFLLR.G
SW:PP1G_HUMAN	S13	7212	2	1072.2	(+1.0)	3.265	0.312	0.974	3	K.LNIDSIIQR.L
SW:PP1G_HUMAN	S13	5064	2	1243.4	(+0.9)	2.494	0.321	0.938	3	K.NVQLQENEIR.G
SW:PPIA_HUMAN	S18	7456	2	1070.2	(+0.9)	2.780	0.420	0.959	4	R.VSFEL*FADK#.V
SW:PPIA_HUMAN	S18	6818	2	1169.3	(+0.6)	2.503	0.259	0.831	2	K.FEDENFIL*K#.H
SW:PPIB_HUMAN	S17	6502	2	1475.7	(+0.8)	3.868	0.594	1.000	2	K.HYGPVWVSMANAGK.D

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:PPIB_HUMAN	S17	7350	2	1365.5	(+0.9)	3.398	0.554	1.000	2	K.TVDNFVALATGEK.G
SW:PPIB_HUMAN	S17	6156	2	1032.2	(+1.0)	3.718	0.494	1.000	2	K.VLEGMEVVR.K
SW:PPIB_HUMAN	S17	5800	2	1499.7	(-0.3)	3.388	0.446	0.929	2	K.HYGPWVSM@ANAGK#.D
SW:PRO1_HUMAN	S19	8324	2	1645.0	(+0.4)	2.559	0.102	0.434	2	K.TFVNITPAEVGVLVGK.D
SW:PRO1_HUMAN	S20	7760	2	1645.0	(+0.5)	3.907	0.455	1.000	2	K.TFVNITPAEVGVLVGK.D
SW:PRO1_HUMAN	S20	5502	2	1380.5	(+0.6)	2.556	0.508	0.979	2	K.STGGAPTFFNVTVTK.T
SW:PTB_HUMAN	S09	7192	2	932.2	(+0.5)	2.585	0.358*	0.373	6	K.VTNLLMLK.G
SW:PTB_HUMAN	S10	6138	2	1121.3	(+0.9)	2.261	0.261	0.707	3	K.VL*FSSNGGVVK#.G
SW:PWP2_HUMAN	S06	8936	2	1428.8	(+0.5)	2.591	0.328	0.933	2	R.AGTLLPVIQFLQK.S
SW:PWP2_HUMAN	S07	9006	2	1428.8	(+0.3)	2.374	0.261	0.616	2	R.AGTLLPVIQFLQK.S
SW:PWP2_HUMAN	S09	9160	2	1428.8	(+0.6)	2.535	0.411	0.962	2	R.AGTLLPVIQFLQK.S
SW:PWP2_HUMAN	S12	8842	2	1428.8	(+0.8)	3.434	0.414	0.982	2	R.AGTLLPVIQFLQK.S
SW:PWP2_HUMAN	S06	6526	2	1535.7	(+0.7)	2.665	0.309	0.923	2	K.EGDFNNLTAAAFHK.K
SW:PWP2_HUMAN	S03	5683	2	1225.4	(+0.7)	2.848	0.364	0.967	2	K.LVQEALEAVPR.G
SW:PWP2_HUMAN	S03	5675	2	1237.4	(-0.0)	2.285	0.223	0.600	2	K.L*VQEALEAVPR.G
SW:PWP2_HUMAN	S12	4898	2	974.1	(+0.4)	2.346	0.220	0.740	2	K.SDTLPLATR.Y
SW:PWP2_HUMAN	S05	8646	2	1794.0	(+0.5)	4.391	0.476	1.000	2	R.VLFDPFELDTSVTPGR.V
SW:PWP2_HUMAN	S06	8568	2	1794.0	(-0.1)	2.917	0.385	0.927	2	R.VLFDPFELDTSVTPGR.V
SW:PWP2_HUMAN	S06	8578	2	1806.0	(-0.2)	2.474	0.394	0.894	2	R.VL*FDPFEL*DTSVTPGR.V
SW:PWP2_HUMAN	S12	8476	2	1806.0	(+0.3)	2.268	0.408	0.879	2	R.VL*FDPFEL*DTSVTPGR.V
SW:PWP2_HUMAN	S15	8580	2	1794.0	(-0.3)	2.349	0.279	0.694	2	R.VLFDPFELDTSVTPGR.V
SW:R10A_HUMAN	S16	7196	2	1513.7	(+0.4)	3.441	0.410	0.963	2	K.K#YDAFL*ASESL*IK#.Q
SW:R10A_HUMAN	S16	7178	2	1485.7	(+0.4)	3.213	0.506	1.000	2	K.KYDAFLASESLIK.Q
SW:R10A_HUMAN	S16	6478	2	1637.9	(-0.2)	3.017	0.290	0.780	2	K.FPSL*L*THNENM@VAK#.V
SW:RALY_HUMAN	S13	6276	2	1154.3	(+0.8)	3.443	0.399	0.984	3	K.KSDVETIFSK.Y
SW:RALY_HUMAN	S13	6278	2	1170.3	(-0.0)	2.883	0.327	0.857	3	K.K#SDVETIFSK#.Y
SW:RALY_HUMAN	S15	6366	2	989.1	(+1.0)	2.435	0.161	0.743	3	K.SNIDALLSR.L
SW:RAN_HUMAN	S15	6296	2	1303.4	(+0.7)	2.216	0.435*	0.051	4	K.FNVWDTAGQEKF.F
SW:RAN_HUMAN	S15	5046	2	1016.2	(+0.9)	3.400	0.218	0.944	5	K.LVLVGDGGTGK.T
SW:RAN_HUMAN	S15	5434	2	1016.2	(+0.5)	2.213	0.246	0.746	5	K.LVLVGDGGTGK.T
SW:RAN_HUMAN	S16	5690	2	1229.3	(+0.1)	2.432	0.228	0.551	5	K.NL*QYYDISAK#.S
SW:RAN_HUMAN	S15	8376	2	1786.0	(-0.2)	3.412	0.444	0.377	5	K.SNYNFEKPFLLWLAR.K
SW:RAN_HUMAN	S16	5682	2	1215.3	(+0.8)	2.343	0.294	0.901	5	K.NLQYYDISAK.S
SW:RB8A_HUMAN	S17	6598	2	1366.5	(+0.6)	2.721	0.568	1.000	1	K.GYTLVEYETYK.E
SW:RB8A_HUMAN	S17	6600	2	1380.5	(-0.9)	2.448	0.185	0.147	1	K.GYTL*VEYETYK#.E
SW:RB8A_HUMAN	S17	5364	2	965.1	(+0.1)	2.354	0.249	0.645	1	K.FAEYGEIK#.N
SW:RBB4_HUMAN	S10	6064	2	1137.2	(+0.8)	3.845	0.567	1.000	1	K.GEFGGFGSVSGK#.I
SW:RBB4_HUMAN	S10	6060	2	1129.2	(+0.7)	3.453	0.462	1.000	1	K.GEFGGFGSVSGK.I
SW:RBB4_HUMAN	S10	6114	2	1137.2	(-0.6)	3.251	0.434	0.927	1	K.GEFGGFGSVSGK#.I
SW:RBB4_HUMAN	S11	5986	2	1129.2	(+0.8)	3.650	0.482	1.000	1	K.GEFGGFGSVSGK.I
SW:RBB4_HUMAN	S11	5988	2	1137.2	(+0.5)	3.595	0.547	1.000	1	K.GEFGGFGSVSGK#.I
SW:RBB4_HUMAN	S17	6180	2	1129.2	(+0.5)	2.990	0.453	0.981	1	K.GEFGGFGSVSGK.I
SW:RBB4_HUMAN	S10	7420	3	2895.1	(+0.0)	4.470	0.487	1.000	1	K.IGEEQSPEDAEDGPPPEL*L*FIHGGHTAK#.I
SW:RBB4_HUMAN	S10	7418	3	2875.1	(+0.4)	3.897	0.406	0.996	1	K.IGEEQSPEDAEDGPPPELLFIHGGHTAK.I
SW:RBB4_HUMAN	S11	7394	3	2875.1	(+0.5)	3.733	0.343	0.986	1	K.IGEEQSPEDAEDGPPPELLFIHGGHTAK.I
SW:RBB4_HUMAN	S15	7292	3	2875.1	(+0.4)	4.061	0.490	0.999	1	K.IGEEQSPEDAEDGPPPELLFIHGGHTAK.I
SW:RBB4_HUMAN	S10	6976	2	935.1	(+1.0)	2.243	0.271	0.905	3	K.LMIWDR.S
SW:RBB4_HUMAN	S15	6798	2	1131.3	(+0.4)	2.726	0.170	0.822	2	R.RLNVDLSK.I
SW:RBB4_HUMAN	S18	6928	2	1131.3	(+0.7)	2.689	0.127	0.764	2	R.RLNVDLSK.I
SW:RBB4_HUMAN	S09	7258	2	1486.6	(-1.0)	2.375	0.403	0.537	2	K.TPSSDVL*VFDYTK#.H
SW:RBB4_HUMAN	S10	7114	2	1486.6	(-0.9)	2.992	0.424	0.716	2	K.TPSSDVL*VFDYTK#.H
SW:RBB4_HUMAN	S11	7070	2	1472.6	(+0.5)	2.545	0.507	0.979	2	K.TPSSDVLVFDYTK.H
SW:RBB4_HUMAN	S14	7190	2	1486.6	(+0.6)	3.658	0.515	1.000	2	K.TPSSDVL*VFDYTK#.H
SW:RBB4_HUMAN	S14	7186	2	1472.6	(+0.3)	2.407	0.372	0.879	2	K.TPSSDVLVFDYTK.H
SW:RBB4_HUMAN	S15	7002	2	1472.6	(+0.4)	2.297	0.516	0.976	2	K.TPSSDVLVFDYTK.H
SW:RBB4_HUMAN	S16	6938	2	1486.6	(-0.6)	3.074	0.446	0.920	2	K.TPSSDVL*VFDYTK#.H
SW:RBB4_HUMAN	S17	7216	2	1486.6	(-0.7)	3.000	0.419	0.711	2	K.TPSSDVL*VFDYTK#.H
SW:RBB4_HUMAN	S17	7206	2	1472.6	(-0.3)	2.867	0.483	0.960	2	K.TPSSDVLVFDYTK.H



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:RBB4_HUMAN	S19	6802	2	1131.3	(+0.3)	2.378	0.147	0.493	2	R.RLNVDLSK.I
SW:RCC1_HUMAN	S11	7796	2	1420.6	(+0.3)	3.027	0.382	0.886	1	R.DNNGVIGL*L*EPMK#.K
SW:RCC1_HUMAN	S11	7788	2	1400.6	(+0.9)	2.764	0.425	0.973	1	R.DNNGVIGLLEPMK.K
SW:RCC1_HUMAN	S11	2052	2	1336.5	(+0.7)	2.581	0.411	0.964	1	R.DTSVEGSEMVPVK.V
SW:RCC1_HUMAN	S11	7234	2	1669.0	(+0.5)	4.198	0.499	1.000	1	K.SM@VPVQVQL*DVPVVK#.V
SW:RCC1_HUMAN	S11	8112	2	1018.2	(+0.4)	2.263	0.331	0.936	1	R.VFL*WGSFR.D
SW:RCC1_HUMAN	S11	6226	2	946.1	(-0.5)	2.530	0.420	0.949	1	R.VPEL*FANR.G
SW:RCC1_HUMAN	S11	6204	2	952.1	(+1.0)	2.215	0.452	0.972	1	R.VPEL*FANR.G
SW:RCC1_HUMAN	S16	6052	2	946.1	(+0.8)	2.586	0.334	0.961	1	R.VPEL*FANR.G
SW:RCC1_HUMAN	S11	5342	3	1900.0	(+1.0)	4.265	0.451	0.999	1	K.VVQVSAGDSHTAALTDDGR.V
SW:RCC1_HUMAN	S16	6058	2	952.1	(+0.5)	2.321	0.368	0.957	1	R.VPEL*FANR.G
SW:RFC2_HUMAN	S12	4670	2	1446.6	(-0.1)	4.034	0.317	0.953	2	K.LNEIVGNEDTVSR.L
SW:RFC2_HUMAN	S12	5278	2	1031.2	(+0.9)	3.346	0.324	0.977	3	K.LTDAQILTR.L
SW:RFC2_HUMAN	S17	5790	2	1031.2	(-0.0)	2.204	0.275	0.748	3	K.LTDAQILTR.L
SW:RFC4_HUMAN	S13	9130	3	3088.4	(+0.3)	7.208	0.536	1.000	2	K.DLIDEGHAATQLVNLQHDVVVNNLSDK.Q
SW:RFC4_HUMAN	S13	8696	2	2047.3	(-0.5)	2.817	0.215*	0.115	2	K.SLEGADLPNLLFYGGPGTGK.T
SW:RFC4_HUMAN	S13	7118	2	1326.6	(+0.9)	3.534	0.476	1.000	1	K.VITDIAGVIPAEL.I
SW:RFC4_HUMAN	S13	8044	2	1120.3	(+0.3)	2.382	0.421	0.935	2	R.EL*FGPEL*FR.L
SW:RL11_HUMAN	S17	6880	2	1567.8	(-1.0)	2.857	0.248	0.335	4	K.VL*EQL*TGQTPVFSK#.A
SW:RL11_HUMAN	S17	6416	2	990.2	(+0.9)	2.843	0.303	0.959	3	K.YDGIL*PGK#.-
SW:RL21_HUMAN	S17	6546	2	1641.9	(-0.5)	4.605	0.556	1.000	2	R.VYNVTQHAVGIVVVK.Q
SW:RL21_HUMAN	S17	6538	3	1649.9	(+0.8)	3.865	0.410	0.996	2	R.VYNVTQHAVGIVVVK#.Q
SW:RL21_HUMAN	S17	6906	2	1244.5	(+1.0)	2.663	0.472	0.980	3	K.HGVVPLATYMR.I
SW:RL22_HUMAN	S19	5622	2	1243.4	(+0.8)	2.572	0.497	0.979	2	K.AGNLGGGVVTIER.S
SW:RL22_HUMAN	S18	6266	2	1208.4	(+0.9)	3.529	0.471	1.000	2	K.ITVTSEVPFSK.R
SW:RL22_HUMAN	S19	6282	2	1208.4	(+0.5)	2.558	0.415	0.969	2	K.ITVTSEVPFSK.R
SW:RL2B_HUMAN	S17	6024	2	1087.3	(-0.3)	2.570	0.304	0.791	3	K.K#L*YDIDVAK#.V
SW:RL2B_HUMAN	S17	4552	2	1242.4	(+0.8)	3.443	0.444	1.000	3	K.VNTLIRPDGEK.K
SW:RL2B_HUMAN	S17	4466	2	1242.4	(+0.9)	2.824	0.451	0.530	3	K.VNTLIRPDGEK.K
SW:RL2B_HUMAN	S17	4508	2	1256.4	(+0.3)	2.423	0.358	0.071	3	K.VNTL*IRPDGEK#.K
SW:RL3_HUMAN	S11	1800	2	1343.3	(+0.6)	2.461	0.251	0.851	6	K.NNASTDYDLSK.S
SW:RL3_HUMAN	S11	6512	2	996.1	(+0.4)	2.283	0.345	0.938	4	R.HGSL*GFL*PR.K
SW:RL4_HUMAN	S11	1774	2	971.1	(+0.3)	3.662	0.557	1.000	1	K.AAAAAAAL*QAK#.S
SW:RL4_HUMAN	S11	6702	2	1281.5	(+0.8)	3.186	0.432	0.984	2	R.KLDELYGTWR.K
SW:RL4_HUMAN	S11	1848	2	957.1	(-0.8)	2.258	0.201	0.217	1	K.AAAAAAALQAK.S
SW:RL6_HUMAN	S13	9994	2	1538.9	(+0.1)	2.908	0.443	0.948	7	R.ASITPGTIL*IIL*TGR.H
SW:RL6_HUMAN	S13	5254	2	1341.4	(+0.9)	3.047	0.327	0.933	6	R.HQEGEIFDTEK#.E
SW:RL6_HUMAN	S13	5288	2	1333.4	(+0.7)	2.623	0.338	0.949	6	R.HQEGEIFDTEK.E
SW:RL6_HUMAN	S13	2394	2	1307.5	(+0.9)	2.768	0.273	0.109	7	K.VL*ATVTK#PVGGDK#.N
SW:RL6_HUMAN	S13	9984	2	1526.9	(+0.3)	2.524	0.462	0.937	7	R.ASITPGTILILTGR.H
SW:RLA0_HUMAN	S13	6712	2	977.1	(+0.8)	2.831	0.464	0.968	1	R.GNVGFVFTK#.E
SW:RLA0_HUMAN	S13	7378	2	1218.4	(+0.4)	3.289	0.115	0.863	2	K.IIQLDDYPK.C
SW:RLA0_HUMAN	S13	8394	2	1314.5	(+0.8)	3.431	0.394	0.981	2	K.TSFFQALGITTK.I
SW:RLA0_HUMAN	S13	8396	2	1328.5	(+1.0)	3.015	0.440	0.961	2	K.TSFFQAL*GITTK#.I
SW:RLA0_HUMAN	S13	8474	2	1314.5	(+0.3)	2.567	0.464	0.948	2	K.TSFFQALGITTK.I
SW:RLA2_HUMAN	S19	5898	2	2776.1	(-0.3)	2.854	0.355	0.905		K.LASVPAGGAVAVSAAPGSAAPAAGSAPAAAEK.K
SW:RLA2_HUMAN	S19	7416	2	1265.4	(+0.7)	3.609	0.353	0.958		K.NIEDVIAQGIGK#.L
SW:RLA2_HUMAN	S19	8446	3	1896.1	(+0.5)	3.701	0.496	1.000		R.YVASYL*L*AAL*GGNSSPSAK#.D
SW:RLA2_HUMAN	S19	8436	2	1870.1	(+1.0)	2.708	0.446	0.972		R.YVASYLLAALGGNSSPSAK.D
SW:ROA0_HUMAN	S14	8146	3	2193.3	(-0.8)	4.381	0.528	1.000	1	K.GDVAEGDL*IEHFSQFGTVEK#.A
SW:ROA0_HUMAN	S14	7714	2	1709.9	(+0.8)	4.613	0.433	1.000	2	K.L*FIGGL*NVQTSSEGL*R.G
SW:ROA0_HUMAN	S15	7426	2	1691.9	(+0.7)	3.689	0.416	0.982	2	K.LFIGGLNVQTSSEGLR.G

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta M$	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ROA1_HUMAN	S12	5038	2	1058.1	(+0.2)	2.330	0.469*	0.062	1	R.DYFEQYGK#.I
SW:ROA1_HUMAN	S13	5554	2	1050.1	(-0.7)	2.524	0.454*	0.056	1	R.DYFEQYGK.I
SW:ROA1_HUMAN	S13	5678	1	1058.1	(+0.4)	2.219	0.394*	0.000	1	R.DYFEQYGK#.I
SW:ROA1_HUMAN	S18	5116	2	1050.1	(+0.9)	2.518	0.418*	0.332	1	R.DYFEQYGK.I
SW:ROA1_HUMAN	S18	5128	2	1058.1	(+0.8)	2.224	0.347*	0.094	1	R.DYFEQYGK#.I
SW:ROA1_HUMAN	S13	7504	2	1708.8	(+0.6)	4.552	0.443	1.000	3	R.GFAFVTFDDHDSVDK#.I
SW:ROA1_HUMAN	S13	7764	2	1700.8	(-1.0)	3.524	0.337	0.793	3	R.GFAFVTFDDHDSVDK.I
SW:ROA1_HUMAN	S13	7686	2	1700.8	(+0.3)	3.423	0.499	1.000	3	R.GFAFVTFDDHDSVDK.I
SW:ROA1_HUMAN	S13	7988	2	1700.8	(-0.1)	3.339	0.321	0.909	3	R.GFAFVTFDDHDSVDK.I
SW:ROA1_HUMAN	S13	8136	2	1700.8	(+0.5)	2.222	0.196	0.577	3	R.GFAFVTFDDHDSVDK.I
SW:ROA1_HUMAN	S14	7554	2	1708.8	(-0.5)	4.867	0.622	1.000	3	R.GFAFVTFDDHDSVDK#.I
SW:ROA1_HUMAN	S14	7550	2	1700.8	(+1.0)	4.686	0.556	1.000	3	R.GFAFVTFDDHDSVDK.I
SW:ROA1_HUMAN	S14	7636	2	1708.8	(+0.0)	4.677	0.519	1.000	3	R.GFAFVTFDDHDSVDK#.I
SW:ROA1_HUMAN	S14	7662	2	1700.8	(-0.1)	4.507	0.517	1.000	3	R.GFAFVTFDDHDSVDK.I
SW:ROA1_HUMAN	S14	7894	2	1700.8	(+0.3)	2.743	0.365	0.902	3	R.GFAFVTFDDHDSVDK.I
SW:ROA1_HUMAN	S17	7528	2	1700.8	(-0.3)	3.952	0.470	1.000	3	R.GFAFVTFDDHDSVDK.I
SW:ROA1_HUMAN	S13	8444	2	1786.0	(+0.9)	5.218	0.465	1.000	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	10178	2	1786.0	(+0.4)	4.597	0.427	1.000	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	10412	2	1786.0	(+0.2)	4.259	0.388	0.964	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	11638	2	1786.0	(+0.4)	4.099	0.422	1.000	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	9288	2	1786.0	(-0.4)	3.980	0.450	1.000	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	8366	2	1786.0	(+0.0)	3.851	0.431	1.000	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	10508	2	1786.0	(+0.7)	3.610	0.496	1.000	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	12044	2	1786.0	(+0.9)	3.610	0.368	0.977	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	11286	2	1786.0	(+0.4)	3.543	0.404	0.980	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	11002	2	1786.0	(+0.6)	3.455	0.485	1.000	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	12142	2	1786.0	(+0.4)	3.407	0.421	0.980	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	8606	2	1786.0	(+0.4)	3.360	0.396	0.976	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	10686	2	1786.0	(+0.4)	3.356	0.344	0.968	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	10610	2	1786.0	(+0.2)	3.352	0.402	0.952	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	8632	2	1786.0	(-0.8)	3.148	0.373	0.786	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	11974	2	1786.0	(+0.8)	3.084	0.344	0.960	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	10340	2	1786.0	(+0.7)	3.078	0.376	0.968	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	11358	2	1786.0	(+0.6)	2.975	0.427	0.975	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	11712	2	1786.0	(+0.2)	2.953	0.408	0.939	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	11462	2	1786.0	(+0.0)	2.895	0.358	0.911	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	12770	2	1786.0	(-0.1)	2.772	0.221	0.703	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	10256	2	1786.0	(-0.5)	2.667	0.360	0.890	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	9462	2	1786.0	(+0.2)	2.612	0.342	0.865	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	9600	2	1786.0	(+0.3)	2.511	0.403	0.905	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	11210	2	1786.0	(+0.0)	2.496	0.100	0.230	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	12992	2	1786.0	(+0.5)	2.475	0.374	0.940	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	10938	2	1804.0	(+0.6)	2.416	0.344	0.916	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	S13	9378	2	1786.0	(-0.0)	2.413	0.270	0.696	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	12418	2	1786.0	(+0.3)	2.408	0.392	0.884	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	9122	2	1786.0	(-0.1)	2.367	0.284	0.712	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	8808	2	1786.0	(+0.1)	2.359	0.278	0.695	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	9206	2	1786.0	(+0.2)	2.244	0.493	0.932	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S14	8578	2	1786.0	(-0.1)	4.088	0.370	0.961	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S14	8608	2	1804.0	(+0.4)	3.350	0.465	0.983	1	K.L*FIGGL*SFETTDESL*R.S
SW:ROA1_HUMAN	S14	11554	2	1786.0	(+0.8)	3.265	0.387	0.974	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S14	12844	2	1786.0	(+0.7)	3.185	0.456	0.981	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S14	10084	2	1786.0	(+0.1)	3.160	0.393	0.943	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S14	9536	2	1786.0	(+0.1)	2.964	0.363	0.917	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S14	9992	2	1786.0	(-0.2)	2.899	0.447	0.949	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S14	9614	2	1786.0	(-0.3)	2.775	0.285	0.823	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S14	12124	2	1786.0	(+0.5)	2.737	0.374	0.955	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S14	11046	2	1786.0	(+0.0)	2.712	0.186	0.588	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S14	9056	2	1786.0	(+0.2)	2.697	0.435	0.936	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S14	10966	2	1786.0	(-0.2)	2.624	0.381	0.901	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S14	12294	2	1786.0	(-0.0)	2.588	0.316	0.830	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S14	12500	2	1786.0	(+0.1)	2.519	0.370	0.880	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S14	8804	2	1786.0	(-0.1)	2.483	0.314	0.804	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S14	10558	2	1786.0	(-0.3)	2.483	0.316	0.807	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S14	11472	2	1786.0	(-0.6)	2.480	0.380	0.883	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S14	11630	2	1786.0	(+0.2)	2.463	0.343	0.841	1	K.LFIGGLSFETTDESLR.S

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ROA1_HUMAN	S14	13072	2	1786.0	(-0.3)	2.463	0.135	0.314	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S14	12046	2	1786.0	(-0.5)	2.425	0.323	0.804	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S14	11182	2	1786.0	(-0.2)	2.414	0.243	0.627	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S14	10894	2	1786.0	(-0.1)	2.404	0.382	0.873	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S14	8530	2	1804.0	(-0.2)	2.403	0.380	0.872	1	K.L*FIGGL*SFETTDESLR.S
SW:ROA1_HUMAN	S14	10634	2	1786.0	(-0.6)	2.401	0.162	0.368	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S14	10814	2	1786.0	(-0.6)	2.378	0.420	0.903	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S14	11936	2	1786.0	(-0.6)	2.359	0.286	0.713	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S14	10166	2	1786.0	(-0.8)	2.287	0.376	0.590	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S14	9884	2	1786.0	(+0.2)	2.258	0.258	0.598	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S14	11808	2	1786.0	(+0.5)	2.255	0.375	0.920	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S16	8130	2	1786.0	(-0.3)	3.435	0.351	0.939	1	K.LFIGGLSFETTDESLR.S
SW:ROA1_HUMAN	S13	5746	2	1637.8	(+0.4)	3.012	0.427	0.477	3	R.SSGPYGGGGQYFAK#PR.N
SW:ROA1_HUMAN	S13	5772	2	1637.8	(-0.8)	2.896	0.316	0.041	3	R.SSGPYGGGGQYFAK#PR.N
SW:ROA1_HUMAN	S14	5456	2	1629.8	(-0.2)	3.616	0.477	1.000	3	R.SSGPYGGGGQYFAKPR.N
SW:ROA1_HUMAN	S19	8316	2	1786.0	(-0.2)	5.022	0.432	1.000	1	K.LFIGGLSFETTDESLR.S
SW:ROA2_HUMAN	S15	5364	2	1059.1	(+0.5)	2.617	0.285	0.898	2	R.DYFEEYGK#.I
SW:ROA2_HUMAN	S12	7206	2	1696.8	(-0.1)	3.219	0.396	0.946	2	R.GFGFVTFDDHDPVDK.I
SW:ROA2_HUMAN	S13	7402	2	1696.8	(-0.1)	4.967	0.466	0.999	2	R.GFGFVTFDDHDPVDK.I
SW:ROA2_HUMAN	S13	7600	2	1696.8	(+0.9)	4.203	0.515	1.000	2	R.GFGFVTFDDHDPVDK.I
SW:ROA2_HUMAN	S13	7520	2	1696.8	(-0.4)	4.171	0.497	1.000	2	R.GFGFVTFDDHDPVDK.I
SW:ROA2_HUMAN	S14	7576	2	1696.8	(+1.0)	3.821	0.476	1.000	2	R.GFGFVTFDDHDPVDK.I
SW:ROA2_HUMAN	S15	7330	2	1704.8	(+0.2)	3.453	0.437	0.926	2	R.GFGFVTFDDHDPVDK#.I
SW:ROA2_HUMAN	S15	7320	2	1696.8	(-0.1)	3.039	0.476	0.960	2	R.GFGFVTFDDHDPVDK.I
SW:ROA2_HUMAN	S16	7296	2	1696.8	(-0.3)	4.284	0.477	1.000	2	R.GFGFVTFDDHDPVDK.I
SW:ROA2_HUMAN	S16	7306	2	1704.8	(-0.2)	3.748	0.509	1.000	2	R.GFGFVTFDDHDPVDK#.I
SW:ROA2_HUMAN	S17	7562	2	1696.8	(+0.8)	4.175	0.459	1.000	2	R.GFGFVTFDDHDPVDK.I
SW:ROA2_HUMAN	S13	8370	2	1928.2	(-0.1)	3.470	0.254	0.865	2	R.KLFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S01	7780	2	1800.0	(+0.3)	3.401	0.464	0.965	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S12	8278	2	1800.0	(+0.5)	3.030	0.504	0.983	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S12	8168	2	1818.0	(-0.3)	2.564	0.357	0.874	2	K.L*FIGGL*SFETTEESLR.N
SW:ROA2_HUMAN	S12	8178	2	1800.0	(-0.8)	2.314	0.262	0.311	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	8562	2	1800.0	(+0.8)	5.158	0.431	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	8642	2	1800.0	(+1.0)	4.734	0.443	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	9558	2	1800.0	(+1.0)	4.625	0.384	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	8566	2	1818.0	(-0.4)	4.570	0.532	1.000	2	K.L*FIGGL*SFETTEESLR.N
SW:ROA2_HUMAN	S13	8722	2	1800.0	(+0.9)	4.482	0.443	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	11010	2	1800.0	(+1.0)	4.246	0.467	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	10360	2	1800.0	(+0.5)	4.141	0.445	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	10744	2	1800.0	(+0.7)	4.110	0.345	0.979	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	9244	2	1800.0	(+0.8)	4.074	0.448	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	10286	2	1800.0	(-0.1)	4.060	0.405	0.965	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	13298	2	1800.0	(+0.5)	4.048	0.509	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	11112	2	1800.0	(+0.6)	4.015	0.386	0.982	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	11848	2	1800.0	(+0.5)	4.005	0.413	0.984	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	12122	2	1800.0	(+0.6)	3.974	0.425	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	10940	2	1800.0	(+0.6)	3.928	0.433	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	11488	2	1800.0	(+0.5)	3.870	0.474	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	12054	2	1800.0	(+0.5)	3.861	0.396	0.982	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	13166	2	1800.0	(+0.5)	3.845	0.438	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	8820	2	1818.0	(-0.6)	3.828	0.462	1.000	2	K.L*FIGGL*SFETTEESLR.N
SW:ROA2_HUMAN	S13	11916	2	1800.0	(+0.7)	3.774	0.425	0.983	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	9910	2	1800.0	(+0.4)	3.740	0.477	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	11780	2	1800.0	(+0.3)	3.726	0.400	0.960	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	10584	2	1800.0	(-0.5)	3.669	0.325	0.938	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	11640	2	1800.0	(+0.9)	3.664	0.440	0.984	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	11262	2	1800.0	(+0.8)	3.567	0.473	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	8928	2	1800.0	(-0.1)	3.564	0.476	1.000	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	11016	2	1818.0	(-0.5)	3.538	0.487	1.000	2	K.L*FIGGL*SFETTEESLR.N
SW:ROA2_HUMAN	S13	10868	2	1800.0	(-0.9)	3.529	0.458	0.879	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	12450	2	1800.0	(+0.3)	3.506	0.426	0.960	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	11514	2	1818.0	(+0.5)	3.447	0.501	1.000	2	K.L*FIGGL*SFETTEESLR.N
SW:ROA2_HUMAN	S13	11708	2	1800.0	(+0.3)	3.435	0.439	0.961	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	9986	2	1800.0	(+0.4)	3.432	0.432	0.981	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	11986	2	1800.0	(+0.3)	3.431	0.415	0.957	2	K.LFIGGLSFETTEESLR.N

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ROA2_HUMAN	S13	10630	2	1818.0	(+0.1)	3.429	0.512	1.000	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	10832	2	1800.0	(+0.4)	3.427	0.338	0.968	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	11290	2	1818.0	(-0.5)	3.412	0.532	1.000	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	8484	2	1800.0	(-0.3)	3.387	0.424	0.958	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	12728	2	1800.0	(+0.5)	3.383	0.432	0.981	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	8796	2	1800.0	(-0.7)	3.323	0.403	0.834	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	11042	2	1800.0	(-0.8)	3.294	0.402	0.831	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	10474	2	1800.0	(-0.7)	3.282	0.428	0.849	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	12798	2	1800.0	(+0.3)	3.278	0.435	0.956	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	10154	2	1800.0	(-0.5)	3.276	0.434	0.957	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	12800	2	1818.0	(-0.4)	3.244	0.481	0.964	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	12962	2	1800.0	(+0.5)	3.233	0.438	0.980	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	9644	2	1800.0	(+1.0)	3.229	0.430	0.979	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	10786	2	1818.0	(-0.0)	3.209	0.455	0.959	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	10470	2	1818.0	(-0.7)	3.165	0.435	0.844	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	9828	2	1818.0	(+0.6)	3.135	0.466	0.981	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	12660	2	1800.0	(+0.7)	3.064	0.397	0.972	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	10324	2	1818.0	(-0.9)	3.063	0.392	0.796	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	12192	2	1800.0	(+0.2)	3.056	0.386	0.934	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	10396	2	1818.0	(-0.4)	3.055	0.444	0.954	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	13364	2	1800.0	(+0.9)	3.034	0.489	0.982	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	12156	2	1818.0	(-0.2)	3.022	0.420	0.946	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	10874	2	1818.0	(-0.5)	2.982	0.412	0.942	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	9006	2	1800.0	(+0.2)	2.971	0.373	0.925	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	10248	2	1818.0	(-0.6)	2.946	0.414	0.941	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	10060	2	1800.0	(-0.7)	2.946	0.416	0.806	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	12592	2	1800.0	(+0.2)	2.931	0.462	0.954	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	10946	2	1818.0	(-0.4)	2.925	0.395	0.932	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	9522	2	1818.0	(+0.1)	2.901	0.424	0.942	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	11672	2	1818.0	(-0.0)	2.870	0.400	0.931	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	10166	2	1818.0	(-0.9)	2.868	0.455	0.832	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	11600	2	1818.0	(-0.2)	2.867	0.467	0.953	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	10714	2	1818.0	(-0.9)	2.804	0.393	0.758	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	11842	2	1818.0	(-0.1)	2.755	0.488	0.955	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	12448	2	1818.0	(-0.7)	2.734	0.450	0.812	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	11984	2	1818.0	(+0.2)	2.722	0.433	0.937	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	12990	2	1818.0	(-0.2)	2.701	0.455	0.944	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	10546	2	1818.0	(-0.9)	2.693	0.380	0.716	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	11366	2	1818.0	(-0.6)	2.685	0.359	0.891	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	13576	2	1800.0	(+0.3)	2.680	0.422	0.930	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	12320	2	1818.0	(-0.3)	2.669	0.372	0.899	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	8930	2	1818.0	(-0.7)	2.649	0.320	0.587	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	11744	2	1818.0	(-0.6)	2.614	0.484	0.949	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	9820	2	1800.0	(-0.1)	2.594	0.451	0.937	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	13074	2	1818.0	(-0.7)	2.579	0.361	0.653	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	13232	2	1800.0	(-0.2)	2.530	0.433	0.925	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	10672	2	1800.0	(-0.8)	2.512	0.224	0.292	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	9612	2	1818.0	(-0.2)	2.455	0.426	0.915	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	9736	2	1800.0	(+0.1)	2.410	0.375	0.868	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	10002	2	1818.0	(-0.2)	2.399	0.402	0.892	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	9086	2	1818.0	(+0.1)	2.321	0.345	0.813	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	13228	2	1818.0	(-0.3)	2.306	0.442	0.910	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	12056	2	1818.0	(-0.1)	2.271	0.394	0.865	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S13	9852	2	1818.0	(-0.6)	2.269	0.351	0.809	2	K.L*FIGGL*SFETTEESL*R.N
SW:ROA2_HUMAN	S20	7880	2	1800.0	(+0.3)	2.751	0.412	0.930	2	K.LFIGGLSFETTEESLR.N
SW:ROA2_HUMAN	S13	6580	3	1901.1	(+0.2)	4.111	0.434	0.969	2	K.L*FVGGIK#EDTEEHL*R.D
SW:ROA2_HUMAN	S12	5162	2	1096.2	(+0.5)	2.449	0.261	0.843	2	R.NYYEQWGK#.L
SW:ROA2_HUMAN	S12	5250	2	1088.2	(+0.1)	2.380	0.337	0.880	2	R.NYYEQWGK.L
SW:ROA2_HUMAN	S13	5640	2	1088.2	(-0.4)	2.930	0.286	0.924	2	R.NYYEQWGK.L
SW:ROA2_HUMAN	S13	5878	2	1096.2	(+0.9)	2.299	0.320	0.877	2	R.NYYEQWGK#.L
SW:ROA2_HUMAN	S16	5242	2	1096.2	(+0.8)	2.265	0.343	0.891	2	R.NYYEQWGK#.L
SW:ROA2_HUMAN	S18	5246	2	1088.2	(+1.0)	2.286	0.336	0.941	2	R.NYYEQWGK.L
SW:ROA2_HUMAN	S18	5254	2	1096.2	(+0.6)	2.233	0.410	0.930	2	R.NYYEQWGK#.L
SW:ROA2_HUMAN	S12	5444	2	1070.2	(+0.3)	2.736	0.394	0.947		K.TL*ETVPL*ER.K
SW:ROA2_HUMAN	S13	5944	2	1070.2	(+0.6)	2.590	0.357	0.963		K.TL*ETVPL*ER.K
SW:ROA2_HUMAN	S20	4958	2	1096.2	(+0.9)	2.220	0.383	0.914	2	R.NYYEQWGK#.L

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	$\Delta$ M	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ROA3_HUMAN	S12	5034	2	1050.2	(+0.7)	2.452	0.445*	0.010	2	R.DYFEKYGK.I
SW:ROA3_HUMAN	S13	5506	2	1050.2	(+0.5)	2.376	0.478*	0.008	2	R.DYFEKYGK.I
SW:ROA3_HUMAN	S14	5334	2	1050.2	(+0.8)	2.524	0.468*	0.012	2	R.DYFEKYGK.I
SW:ROA3_HUMAN	S15	2258	2	1381.6	(+0.1)	2.264	0.193	0.018	2	R.EDSVKPGAHLTVK.K
SW:ROA3_HUMAN	S12	7854	2	1900.1	(-0.6)	3.219	0.457	0.960	2	R.KLFIGGLSFETDDSLR.E
SW:ROA3_HUMAN	S12	8838	2	1772.0	(+0.5)	3.414	0.452	0.983	2	K.LFIGGLSFETDDSLR.E
SW:ROA3_HUMAN	S12	8246	2	1772.0	(+0.4)	3.340	0.363	0.965	2	K.LFIGGLSFETDDSLR.E
SW:ROA3_HUMAN	S12	8400	2	1772.0	(+0.5)	2.995	0.396	0.970	2	K.LFIGGLSFETDDSLR.E
SW:ROA3_HUMAN	S12	9206	2	1772.0	(+0.4)	2.926	0.291	0.929	2	K.LFIGGLSFETDDSLR.E
SW:ROA3_HUMAN	S12	8754	2	1772.0	(+0.6)	2.601	0.366	0.945	2	K.LFIGGLSFETDDSLR.E
SW:ROA3_HUMAN	S12	9630	2	1772.0	(+0.4)	2.578	0.345	0.932	2	K.LFIGGLSFETDDSLR.E
SW:ROA3_HUMAN	S12	8892	2	1790.0	(-0.4)	2.331	0.306	0.747	2	K.L*FIGGL*SFETDDSL*R.E
SW:ROA3_HUMAN	S12	9718	2	1772.0	(+0.7)	2.307	0.437	0.955	2	K.LFIGGLSFETDDSLR.E
SW:ROA3_HUMAN	S12	8654	2	1772.0	(+0.4)	2.307	0.177	0.560	2	K.LFIGGLSFETDDSLR.E
SW:ROA3_HUMAN	S12	8432	2	1790.0	(+0.4)	2.294	0.299	0.849	2	K.L*FIGGL*SFETDDSL*R.E
SW:ROA3_HUMAN	S12	10424	2	1772.0	(+0.0)	2.276	0.289	0.689	2	K.LFIGGLSFETDDSLR.E
SW:ROA3_HUMAN	S13	8418	2	1772.0	(+0.0)	4.234	0.407	1.000	2	K.LFIGGLSFETDDSLR.E
SW:ROA3_HUMAN	S13	8542	2	1772.0	(+0.4)	2.392	0.357	0.923	2	K.LFIGGLSFETDDSLR.E
SW:ROA3_HUMAN	S16	2232	2	1381.6	(+1.0)	2.442	0.217	0.072	2	R.EDSVKPGAHLTVK.K
SW:ROCL_HUMAN	S12	5914	2	1124.3	(-0.5)	3.399	0.211	0.893	8	K.KSDVEAIFSK.Y
SW:ROCL_HUMAN	S12	5898	2	1140.3	(+0.7)	2.636	0.304	0.889	8	K.K#SDVEAIFSK#.Y
SW:ROCL_HUMAN	S13	6364	2	1124.3	(-0.8)	3.242	0.230	0.680	8	K.KSDVEAIFSK.Y
SW:ROCL_HUMAN	S13	6434	2	1140.3	(+0.8)	3.042	0.393	0.958	8	K.K#SDVEAIFSK#.Y
SW:ROCL_HUMAN	S13	6352	2	1140.3	(+0.4)	2.657	0.293	0.882	8	K.K#SDVEAIFSK#.Y
SW:ROCL_HUMAN	S16	6018	2	1124.3	(+1.0)	3.271	0.236	0.950	8	K.KSDVEAIFSK.Y
SW:ROCL_HUMAN	S16	6026	2	1140.3	(+0.5)	2.820	0.440	0.961	8	K.K#SDVEAIFSK#.Y
SW:ROCL_HUMAN	S17	6338	2	1140.3	(+0.4)	2.870	0.333	0.931	8	K.K#SDVEAIFSK#.Y
SW:ROCL_HUMAN	S12	4652	2	1101.3	(-0.6)	2.700	0.336	0.193	9	K.LKGGDDLQAIK.Q
SW:ROCL_HUMAN	S12	4706	2	1129.3	(-0.1)	2.460	0.303	0.061	9	K.L*K#GDDL*QAIK#.Q
SW:ROCL_HUMAN	S13	5172	2	1129.3	(-0.2)	2.620	0.211	0.032	9	K.L*K#GDDL*QAIK#.Q
SW:ROCL_HUMAN	S13	5092	2	1129.3	(+0.2)	2.306	0.351	0.072	9	K.L*K#GDDL*QAIK#.Q
SW:ROCL_HUMAN	S11	6246	2	996.1	(+0.9)	2.589	0.223	0.888	8	K.SDVEAIFSK.Y
SW:ROCL_HUMAN	S15	6208	2	996.1	(+1.0)	2.788	0.277	0.947	8	K.SDVEAIFSK.Y
SW:ROCL_HUMAN	S16	6078	2	996.1	(+0.9)	2.621	0.350	0.962	8	K.SDVEAIFSK.Y
SW:ROCL_HUMAN	S16	6084	2	1004.1	(+0.8)	2.506	0.209	0.745	8	K.SDVEAIFSK#.Y
SW:ROCL_HUMAN	S12	6762	2	1186.3	(+0.3)	2.202	0.174	0.276	9	K.VDSL*L*ENL*EK#.I
SW:ROCL_HUMAN	S14	7122	2	1186.3	(+0.3)	2.327	0.231	0.506	9	K.VDSL*L*ENL*EK#.I
SW:ROCL_HUMAN	S01	7250	2	1337.6	(+0.4)	2.398	0.309	0.826	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S12	12219	2	1317.6	(+0.3)	2.525	0.358	0.891	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S13	13170	2	1317.6	(+0.9)	3.679	0.457	1.000	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S13	12566	2	1317.6	(+0.8)	3.415	0.469	1.000	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S13	12496	2	1317.6	(+0.6)	3.380	0.460	1.000	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S13	11716	2	1317.6	(+0.5)	3.359	0.387	0.979	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S13	10894	2	1317.6	(+0.7)	3.353	0.429	0.983	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S13	11038	2	1317.6	(+0.9)	3.334	0.526	1.000	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S13	10108	2	1317.6	(+0.7)	3.276	0.436	0.983	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S13	10376	2	1317.6	(+0.8)	3.272	0.345	0.972	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S13	11188	2	1317.6	(+1.0)	3.218	0.460	0.984	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S13	12384	2	1317.6	(+0.5)	3.214	0.499	1.000	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S13	8028	2	1317.6	(+0.0)	3.210	0.452	0.964	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S13	11334	2	1317.6	(+0.6)	3.106	0.454	0.982	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S13	7894	2	1337.6	(+0.2)	3.105	0.398	0.907	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	12936	2	1317.6	(+0.6)	3.078	0.452	0.982	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S13	12174	2	1317.6	(+0.4)	3.078	0.423	0.979	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S13	12014	2	1317.6	(+0.5)	3.031	0.468	0.983	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S13	7972	2	1337.6	(+0.3)	3.004	0.433	0.916	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	9578	2	1317.6	(+0.7)	2.989	0.460	0.982	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S13	12310	2	1317.6	(+1.0)	2.986	0.424	0.978	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S13	12242	2	1317.6	(+0.5)	2.944	0.397	0.974	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S13	10822	2	1317.6	(+0.3)	2.938	0.415	0.950	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S13	9338	2	1317.6	(+1.0)	2.934	0.463	0.981	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S13	12712	2	1317.6	(+0.3)	2.890	0.436	0.953	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S13	12644	2	1317.6	(+0.2)	2.882	0.490	0.963	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S13	11322	2	1337.6	(+0.5)	2.854	0.412	0.950	9	R.VFIGNL*NTL*VVK#.K

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ROCL_HUMAN	S13	13008	2	1337.6	(+0.2)	2.794	0.303	0.784	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	10384	2	1337.6	(+0.3)	2.699	0.400	0.874	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	10304	2	1337.6	(+0.1)	2.686	0.412	0.881	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	9258	2	1317.6	(+0.7)	2.671	0.498	0.981	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S13	11048	2	1337.6	(+0.1)	2.665	0.399	0.869	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	10460	2	1337.6	(+0.4)	2.587	0.402	0.932	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	8276	2	1317.6	(+0.1)	2.582	0.420	0.934	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S13	10216	2	1317.6	(-0.5)	2.575	0.358	0.897	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S13	8674	2	1337.6	(+0.1)	2.557	0.427	0.878	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	12932	2	1337.6	(-0.1)	2.534	0.284	0.678	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	11978	2	1337.6	(+0.5)	2.519	0.314	0.834	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	12850	2	1337.6	(+0.7)	2.499	0.347	0.886	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	11510	2	1337.6	(-0.5)	2.495	0.337	0.766	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	12356	2	1337.6	(+0.3)	2.490	0.326	0.746	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	11580	2	1337.6	(+0.2)	2.458	0.356	0.786	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	12774	2	1337.6	(+0.3)	2.441	0.288	0.653	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	9954	2	1337.6	(+0.1)	2.431	0.417	0.852	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	10900	2	1337.6	(+0.6)	2.426	0.386	0.908	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	11908	2	1337.6	(-0.2)	2.425	0.265	0.589	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	12288	2	1337.6	(-0.1)	2.412	0.326	0.723	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	8212	2	1337.6	(+0.0)	2.406	0.388	0.818	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	13404	2	1337.6	(+0.8)	2.404	0.394	0.911	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	7814	2	1337.6	(-0.4)	2.398	0.331	0.728	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	12114	2	1337.6	(+0.4)	2.381	0.341	0.862	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	13104	2	1337.6	(+0.7)	2.342	0.324	0.833	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	10970	2	1337.6	(-0.4)	2.335	0.282	0.594	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	11814	2	1337.6	(-0.3)	2.320	0.228	0.434	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	11248	2	1337.6	(+0.1)	2.305	0.237	0.453	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	10824	2	1337.6	(+0.1)	2.285	0.277	0.558	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	11392	2	1337.6	(+0.7)	2.258	0.345	0.842	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	10580	2	1337.6	(-0.1)	2.243	0.220	0.371	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	11718	2	1337.6	(+0.0)	2.231	0.190	0.281	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	11464	2	1337.6	(+0.8)	2.226	0.304	0.768	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S13	12704	2	1337.6	(+0.1)	2.213	0.251	0.446	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S14	7882	2	1317.6	(-0.0)	3.047	0.361	0.937	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S14	7844	2	1337.6	(-0.2)	2.949	0.384	0.888	9	R.VFIGNL*NTL*VVK#.K
SW:ROCL_HUMAN	S17	7790	2	1317.6	(+0.9)	2.472	0.427	0.966	9	R.VFIGNLNTLVVK.K
SW:ROCL_HUMAN	S19	7742	2	1337.6	(+0.1)	2.333	0.228	0.441	9	R.VFIGNL*NTL*VVK#.K
SW:ROC_HUMAN	S13	6128	2	1546.6	(+0.6)	2.949	0.269	0.130	7	R.GDDQL*EL*IK#DDEK#.E
SW:ROC_HUMAN	S13	6130	2	1518.6	(-0.0)	2.712	0.279	0.099	7	R.GDDQLELIKDDEK.E
SW:ROC_HUMAN	S12	7086	2	1720.0	(-0.6)	4.274	0.534	1.000	6	R.M@IAGQVL*DINL*AAEPK#.V
SW:ROC_HUMAN	S12	7522	2	1684.0	(+0.1)	3.744	0.499	1.000	6	R.MIAGQVLDINLAAEPK.V
SW:ROC_HUMAN	S13	7836	2	1684.0	(+0.7)	4.887	0.490	1.000	6	R.MIAGQVLDINLAAEPK.V
SW:ROC_HUMAN	S13	8018	3	1684.0	(+0.3)	4.863	0.351	0.992	6	R.MIAGQVLDINLAAEPK.V
SW:ROC_HUMAN	S13	7426	3	1720.0	(+0.6)	4.444	0.421	0.997	6	R.M@IAGQVL*DINL*AAEPK#.V
SW:ROC_HUMAN	S13	7982	2	1684.0	(+0.6)	4.289	0.440	1.000	6	R.MIAGQVLDINLAAEPK.V
SW:ROC_HUMAN	S13	7508	2	1720.0	(-0.1)	4.051	0.499	1.000	6	R.M@IAGQVL*DINL*AAEPK#.V
SW:ROC_HUMAN	S13	8094	2	1684.0	(-0.4)	3.966	0.447	1.000	6	R.MIAGQVLDINLAAEPK.V
SW:ROC_HUMAN	S13	7428	2	1720.0	(-1.0)	3.779	0.475	1.000	6	R.M@IAGQVL*DINL*AAEPK#.V
SW:ROC_HUMAN	S13	7850	2	1684.0	(-0.7)	3.631	0.426	0.869	6	R.MIAGQVLDINLAAEPK.V
SW:ROC_HUMAN	S14	7450	2	1720.0	(-0.5)	3.883	0.483	1.000	6	R.M@IAGQVL*DINL*AAEPK#.V
SW:ROD_HUMAN	S11	8382	2	2162.4	(-1.0)	2.651	0.287	0.508	10	R.EYFGGFGEVESIELPMDNK.T
SW:ROD_HUMAN	S11	7924	2	2192.4	(-1.0)	2.583	0.192	0.137	10	R.EYFGGFGEVESIEL*PM@DNK#.T
SW:ROD_HUMAN	S10	8408	2	929.1	(+0.6)	2.286	0.403*	0.112	14	R.GFGFVL*FK#.E
SW:ROD_HUMAN	S11	8302	2	929.1	(+0.6)	2.351	0.422*	0.134	14	R.GFGFVL*FK#.E
SW:ROD_HUMAN	S13	8452	2	915.1	(-0.3)	2.560	0.337	0.918	14	R.GFGFVLFK.E
SW:ROD_HUMAN	S10	6492	2	1489.7	(+0.1)	4.746	0.469	1.000	10	K.IFVGGLSPDTPPEEK.I
SW:ROD_HUMAN	S12	6148	2	1489.7	(+0.7)	3.911	0.470	1.000	10	K.IFVGGLSPDTPPEEK.I
SW:ROD_HUMAN	S13	6610	2	1503.7	(-0.1)	2.324	0.186	0.272	10	K.IFVGGL*SPDTPPEEK#.I
SW:ROD_HUMAN	S15	6350	2	1503.7	(-0.9)	2.738	0.203	0.206	10	K.IFVGGL*SPDTPPEEK#.I
SW:ROD_HUMAN	S15	6346	2	1489.7	(-0.1)	2.694	0.346	0.887	10	K.IFVGGLSPDTPPEEK.I
SW:ROD_HUMAN	S11	7776	2	1356.6	(-0.2)	3.835	0.488	1.000	9	K.MFIGGLSWDTTK.K
SW:ROD_HUMAN	S11	7214	2	1386.6	(+0.3)	2.842	0.277	0.753	9	K.M@FIGGL*SWDTTK#.K
SW:ROD_HUMAN	S11	7750	2	1370.6	(+0.8)	2.613	0.380	0.923	9	K.MFIGGL*SWDTTK#.K

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ROD_HUMAN	S12	7006	2	1386.6	(-0.4)	2.571	0.299	0.720	9	K.M@FIGGL*SWDTTK#.K
SW:ROD_HUMAN	S12	7554	2	1370.6	(+0.7)	2.279	0.450	0.930	9	K.MFIGGL*SWDTTK#.K
SW:ROD_HUMAN	S16	6242	2	1489.7	(-0.3)	3.251	0.292	0.901	10	K.IFVGGLSPDTPPEEK.I
SW:ROF_HUMAN	S11	8840	2	1998.2	(+0.8)	3.399	0.467	0.984	2	K.ATENDIYNFFSPLNPVR.V
SW:ROF_HUMAN	S12	8536	2	2004.2	(+0.8)	3.655	0.522	1.000	2	K.ATENDIYNFFSPL*NPVR.V
SW:ROF_HUMAN	S13	8854	2	1998.2	(-0.4)	2.886	0.460	0.952	2	K.ATENDIYNFFSPLNPVR.V
SW:ROF_HUMAN	S14	9028	2	2004.2	(-0.1)	2.956	0.326	0.893	2	K.ATENDIYNFFSPL*NPVR.V
SW:ROF_HUMAN	S14	9026	2	1998.2	(+0.4)	2.941	0.404	0.970	2	K.ATENDIYNFFSPLNPVR.V
SW:ROF_HUMAN	S15	8628	2	1998.2	(+0.1)	4.245	0.429	1.000	2	K.ATENDIYNFFSPLNPVR.V
SW:ROF_HUMAN	S15	8634	2	2004.2	(+1.0)	4.176	0.541	1.000	2	K.ATENDIYNFFSPL*NPVR.V
SW:ROF_HUMAN	S16	8612	2	1998.2	(+0.4)	3.883	0.496	1.000	2	K.ATENDIYNFFSPLNPVR.V
SW:ROF_HUMAN	S11	8480	2	1869.1	(+0.6)	3.373	0.437	0.981	1	K.ITGEAFVQFASQELA EK.A
SW:ROF_HUMAN	S16	8382	2	1869.1	(+0.0)	4.343	0.516	1.000	1	K.ITGEAFVQFASQELA EK.A
SW:ROF_HUMAN	S17	8760	2	1998.2	(+0.9)	4.649	0.501	1.000	2	K.ATENDIYNFFSPLNPVR.V
SW:ROG_HUMAN	S11	6658	2	1456.6	(-0.4)	2.382	0.104	0.131	3	K.L*FIGGL*NTTETNEK#.A
SW:ROG_HUMAN	S12	6450	2	1436.6	(+0.8)	2.439	0.219	0.774	3	K.LFIGGLNTTETNEK.A
SW:ROG_HUMAN	S14	6774	2	1436.6	(+0.5)	2.750	0.218	0.853	3	K.LFIGGLNTTETNEK.A
SW:ROG_HUMAN	S11	1818	2	1444.6	(+0.5)	2.833	0.433	0.478	2	K.VEQATK#PSFESGR.R
SW:ROG_HUMAN	S15	6622	2	1436.6	(+0.4)	3.201	0.349	0.969	3	K.LFIGGLNTTETNEK.A
SW:ROH1_HUMAN	S10	7452	2	1335.5	(+0.9)	3.752	0.453	1.000		K.SNNVEMDWVLK.H
SW:ROH1_HUMAN	S10	7370	2	1335.5	(-0.0)	3.178	0.229	0.869		K.SNNVEMDWVLK.H
SW:ROH1_HUMAN	S10	7398	2	1349.5	(-0.4)	2.716	0.216	0.609		K.SNNVEMDWVL*K#.H
SW:ROH1_HUMAN	S10	6650	2	1365.5	(+0.2)	2.660	0.308	0.778		K.SNNVEM@DWVL*K#.H
SW:ROH1_HUMAN	S10	7838	2	1851.0	(+0.5)	4.213	0.560	1.000	1	R.STGEAFVQFASQEIAEK#.A
SW:ROH1_HUMAN	S10	7836	2	1843.0	(-0.5)	4.018	0.462	1.000	1	R.STGEAFVQFASQEIAEK.A
SW:ROH1_HUMAN	S10	7914	2	1843.0	(-0.4)	3.181	0.365	0.932	1	R.STGEAFVQFASQEIAEK.A
SW:ROH1_HUMAN	S10	10138	2	1843.0	(+0.6)	3.046	0.415	0.972	1	R.STGEAFVQFASQEIAEK.A
SW:ROH1_HUMAN	S10	10912	2	1843.0	(+0.7)	3.036	0.323	0.951	1	R.STGEAFVQFASQEIAEK.A
SW:ROH1_HUMAN	S10	9900	2	1843.0	(+0.5)	2.983	0.357	0.960	1	R.STGEAFVQFASQEIAEK.A
SW:ROH1_HUMAN	S10	9528	2	1843.0	(+0.2)	2.979	0.288	0.860	1	R.STGEAFVQFASQEIAEK.A
SW:ROH1_HUMAN	S10	12880	2	1843.0	(+0.5)	2.797	0.383	0.961	1	R.STGEAFVQFASQEIAEK.A
SW:ROH1_HUMAN	S10	11604	2	1843.0	(+0.9)	2.703	0.269	0.887	1	R.STGEAFVQFASQEIAEK.A
SW:ROH1_HUMAN	S10	12286	2	1843.0	(+0.4)	2.503	0.381	0.936	1	R.STGEAFVQFASQEIAEK.A
SW:ROH1_HUMAN	S10	11856	2	1843.0	(+0.5)	2.494	0.430	0.962	1	R.STGEAFVQFASQEIAEK.A
SW:ROH1_HUMAN	S10	11014	2	1843.0	(+0.7)	2.463	0.424	0.959	1	R.STGEAFVQFASQEIAEK.A
SW:ROH1_HUMAN	S10	12738	2	1843.0	(+0.4)	2.358	0.380	0.933	1	R.STGEAFVQFASQEIAEK.A
SW:ROH1_HUMAN	S10	9948	2	1851.0	(+0.5)	2.338	0.451	0.925	1	R.STGEAFVQFASQEIAEK#.A
SW:ROH1_HUMAN	S10	12374	2	1843.0	(+0.8)	2.314	0.408	0.944	1	R.STGEAFVQFASQEIAEK.A
SW:ROH1_HUMAN	S10	9446	2	1851.0	(+0.1)	2.277	0.226	0.344	1	R.STGEAFVQFASQEIAEK#.A
SW:ROH1_HUMAN	S10	11336	2	1843.0	(-0.1)	2.254	0.334	0.777	1	R.STGEAFVQFASQEIAEK.A
SW:ROH1_HUMAN	S10	11204	2	1843.0	(+0.7)	2.213	0.323	0.863	1	R.STGEAFVQFASQEIAEK.A
SW:ROH1_HUMAN	S11	7814	2	1851.0	(+0.5)	3.628	0.510	1.000	1	R.STGEAFVQFASQEIAEK#.A
SW:ROH1_HUMAN	S12	7596	2	1843.0	(+0.8)	4.149	0.355	0.981	1	R.STGEAFVQFASQEIAEK.A
SW:ROH1_HUMAN	S14	7994	2	1843.0	(+0.7)	3.486	0.422	0.981	1	R.STGEAFVQFASQEIAEK.A
SW:ROH1_HUMAN	S14	7998	2	1851.0	(-0.3)	3.032	0.337	0.832	1	R.STGEAFVQFASQEIAEK#.A
SW:ROH1_HUMAN	S15	7686	2	1851.0	(+1.0)	4.875	0.536	1.000	1	R.STGEAFVQFASQEIAEK#.A
SW:ROH1_HUMAN	S15	7678	2	1843.0	(-0.5)	2.732	0.453	0.944	1	R.STGEAFVQFASQEIAEK.A
SW:ROH1_HUMAN	S16	7680	2	1843.0	(-0.4)	4.107	0.453	1.000	1	R.STGEAFVQFASQEIAEK.A
SW:ROH1_HUMAN	S16	7684	2	1851.0	(-0.4)	3.572	0.503	1.000	1	R.STGEAFVQFASQEIAEK#.A
SW:ROH1_HUMAN	S17	7912	2	1843.0	(+1.0)	4.989	0.384	1.000	1	R.STGEAFVQFASQEIAEK.A
SW:ROH1_HUMAN	S17	7924	2	1851.0	(-0.0)	4.065	0.511	1.000	1	R.STGEAFVQFASQEIAEK#.A
SW:ROH3_HUMAN	S13	8852	2	1920.1	(+0.9)	3.518	0.559	1.000	6	R.ATENDIANFFSPLNPIR.V
SW:ROH3_HUMAN	S13	8884	2	1920.1	(-0.9)	2.968	0.386	0.776	6	R.ATENDIANFFSPLNPIR.V
SW:ROH3_HUMAN	S13	8870	2	1926.1	(+0.9)	2.964	0.360	0.960	6	R.ATENDIANFFSPL*NPPIR.V
SW:ROH3_HUMAN	S14	9024	2	1920.1	(+1.0)	3.241	0.486	0.984	6	R.ATENDIANFFSPLNPIR.V
SW:ROH3_HUMAN	S14	9050	2	1920.1	(-0.9)	2.319	0.307	0.430	6	R.ATENDIANFFSPLNPIR.V
SW:ROH3_HUMAN	S13	5986	2	2220.3	(+0.3)	4.086	0.566	1.000	4	R.M@GM@GNNYSGGYGTPDGL*GGYGR.G
SW:ROH3_HUMAN	S13	6018	2	2220.3	(-1.0)	3.131	0.408	0.815	4	R.M@GM@GNNYSGGYGTPDGL*GGYGR.G
SW:ROH3_HUMAN	S13	6704	2	1272.4	(+0.8)	3.541	0.465	1.000	2	R.STGEAFVQFASK.E
SW:ROH3_HUMAN	S13	6642	2	1280.4	(-0.1)	3.345	0.358	0.902	2	R.STGEAFVQFASK#.E
SW:ROH3_HUMAN	S13	6808	2	1280.4	(+0.3)	2.698	0.303	0.762	2	R.STGEAFVQFASK#.E
SW:ROH3_HUMAN	S18	6380	2	1280.4	(+0.1)	2.321	0.219	0.408	2	R.STGEAFVQFASK#.E

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ROK_HUMAN	S09	6244	2	888.0	(-0.9)	2.390	0.298	0.410	1	K.DL*AGSIIGK#.G
SW:ROK_HUMAN	S09	7580	2	1918.2	(+0.7)	4.613	0.497	1.000	1	R.GSYGDLGGPIITTQVTIPK.D
SW:ROK_HUMAN	S09	7582	2	1932.2	(+0.0)	4.186	0.443	1.000	1	R.GSYGDL*GGPIITTQVTIPK#.D
SW:ROK_HUMAN	S12	7238	2	1918.2	(+0.8)	4.556	0.527	1.000	1	R.GSYGDLGGPIITTQVTIPK.D
SW:ROK_HUMAN	S14	7602	2	1932.2	(-0.6)	2.379	0.387	0.779	1	R.GSYGDL*GGPIITTQVTIPK#.D
SW:ROK_HUMAN	S09	2122	2	1266.3	(+0.6)	2.704	0.317	0.946	1	K.IDEPL*EGSEDR.I
SW:ROK_HUMAN	S10	2186	2	1260.3	(+0.7)	2.435	0.393	0.958	1	K.IDEPLEGESEDR.I
SW:ROK_HUMAN	S13	8406	3	2590.9	(-0.1)	4.758	0.511	1.000	1	R.IITITGTQDQIQNAQYLLQNSVK.Q
SW:ROK_HUMAN	S14	8510	3	2590.9	(+1.0)	5.691	0.577	1.000	1	R.IITITGTQDQIQNAQYLLQNSVK.Q
SW:ROK_HUMAN	S16	8138	3	2590.9	(+0.7)	4.742	0.626	1.000	1	R.IITITGTQDQIQNAQYLLQNSVK.Q
SW:ROK_HUMAN	S09	5518	2	1107.2	(-0.2)	3.285	0.336	0.953	1	R.NTDEMVELR.I
SW:ROK_HUMAN	S09	5498	2	1113.2	(+0.4)	2.369	0.106	0.547	1	R.NTDEMVEL*R.I
SW:ROK_HUMAN	S09	5434	2	1107.2	(+0.4)	2.243	0.129	0.390	1	R.NTDEMVELR.I
SW:ROK_HUMAN	S10	5408	2	1107.2	(+0.5)	2.637	0.112	0.708	1	R.NTDEMVELR.I
SW:ROK_HUMAN	S19	5204	2	1113.2	(+0.5)	2.683	0.269	0.935	1	R.NTDEMVEL*R.I
SW:ROK_HUMAN	S09	5192	2	1580.7	(-0.4)	4.190	0.515	1.000	1	K.RPAEDMEEEEQAFK.R
SW:ROK_HUMAN	S10	5134	3	1744.9	(+0.3)	3.919	0.447	0.973	1	K.RPAEDMEEEEQAFK#R.S
SW:ROK_HUMAN	S09	5006	2	1054.3	(+1.0)	2.621	0.317	0.288	1	R.VVLIGGKPD.R.V
SW:ROK_HUMAN	S09	4928	2	1054.3	(+1.0)	2.213	0.221	0.037	1	R.VVLIGGKPD.R.V
SW:ROK_HUMAN	S12	4732	2	1054.3	(+0.1)	2.358	0.232	0.030	1	R.VVLIGGKPD.R.V
SW:ROK_HUMAN	S19	5200	2	1107.2	(+0.7)	2.671	0.192	0.868	1	R.NTDEMVELR.I
SW:ROL_HUMAN	S09	7076	2	1649.9	(-0.1)	2.749	0.299	0.736	1	R.AITHL*NNNFMFGQK#.L
SW:ROL_HUMAN	S07	5872	3	2905.9	(-0.3)	4.657	0.501	1.000	1	K.NDQDTWDYTNPNL*SGQGDPGSNPKNR.Q
SW:ROL_HUMAN	S07	5870	3	2891.9	(+0.6)	3.871	0.417	0.976	1	K.NDQDTWDYTNPNLSGQGDPGSNPKNR.Q
SW:ROL_HUMAN	S08	5990	3	2905.9	(+0.8)	5.025	0.463	1.000	1	K.NDQDTWDYTNPNL*SGQGDPGSNPKNR.Q
SW:ROL_HUMAN	S09	6116	3	2891.9	(+1.0)	4.942	0.591	1.000	1	K.NDQDTWDYTNPNLSGQGDPGSNPKNR.Q
SW:ROL_HUMAN	S09	6114	3	2905.9	(+0.5)	4.487	0.476	1.000	1	K.NDQDTWDYTNPNL*SGQGDPGSNPKNR.Q
SW:ROL_HUMAN	S10	6042	3	2905.9	(-0.0)	4.836	0.366	0.925	1	K.NDQDTWDYTNPNL*SGQGDPGSNPKNR.Q
SW:ROL_HUMAN	S10	6040	3	2891.9	(+0.0)	4.377	0.544	1.000	1	K.NDQDTWDYTNPNLSGQGDPGSNPKNR.Q
SW:ROL_HUMAN	S11	5956	3	2891.9	(+0.1)	4.358	0.564	1.000	1	K.NDQDTWDYTNPNLSGQGDPGSNPKNR.Q
SW:ROL_HUMAN	S11	5958	3	2905.9	(+0.2)	4.314	0.431	0.958	1	K.NDQDTWDYTNPNL*SGQGDPGSNPKNR.Q
SW:ROL_HUMAN	S12	5660	3	2905.9	(+0.2)	4.771	0.516	1.000	1	K.NDQDTWDYTNPNL*SGQGDPGSNPKNR.Q
SW:ROL_HUMAN	S12	5662	3	2891.9	(+0.4)	4.156	0.488	1.000	1	K.NDQDTWDYTNPNLSGQGDPGSNPKNR.Q
SW:ROL_HUMAN	S13	6154	3	2905.9	(+0.4)	4.930	0.486	1.000	1	K.NDQDTWDYTNPNL*SGQGDPGSNPKNR.Q
SW:ROL_HUMAN	S08	7892	2	1910.1	(-0.6)	2.888	0.318	0.784	1	K.SDAL*ETL*GFL*NHYQM@K#.N
SW:ROL_HUMAN	S13	6152	3	2891.9	(+0.5)	4.129	0.569	1.000	1	K.NDQDTWDYTNPNLSGQGDPGSNPKNR.Q
SW:ROM_HUMAN	S01	7394	2	1265.5	(+0.5)	2.963	0.320	0.960	6	R.AFITNIPFDVK.W
SW:ROM_HUMAN	S04	6607	2	1265.5	(+0.5)	2.668	0.206	0.849	6	R.AFITNIPFDVK.W
SW:ROM_HUMAN	S13	7994	2	1273.5	(+0.8)	2.253	0.230	0.625	6	R.AFITNIPFDVK#.W
SW:ROM_HUMAN	S14	8036	2	1265.5	(-0.8)	3.505	0.382	0.864	6	R.AFITNIPFDVK.W
SW:ROM_HUMAN	S16	7726	2	1273.5	(+1.0)	2.893	0.401	0.952	6	R.AFITNIPFDVK#.W
SW:ROM_HUMAN	S17	7948	2	1273.5	(+1.0)	2.530	0.428	0.943	6	R.AFITNIPFDVK#.W
SW:ROM_HUMAN	S05	6570	2	1115.3	(+0.6)	2.493	0.173	0.757	9	R.INEILSNALK.R
SW:ROM_HUMAN	S07	6598	2	1135.3	(+0.4)	2.436	0.155	0.531	9	R.INEIL*SNAL*K#.R
SW:ROM_HUMAN	S08	6742	2	1135.3	(+0.3)	2.500	0.109	0.247	9	R.INEIL*SNAL*K#.R
SW:ROM_HUMAN	S12	6426	2	1115.3	(+0.4)	2.663	0.173	0.816	9	R.INEILSNALK.R
SW:ROM_HUMAN	S07	4984	2	1164.3	(+0.5)	2.677	0.325	0.948	9	R.M@GAGM@GFL*ER.M
SW:ROM_HUMAN	S07	5062	2	1164.3	(+0.1)	2.633	0.409	0.937	9	R.M@GAGM@GFL*ER.M
SW:ROM_HUMAN	S07	2188	2	1422.6	(+0.4)	3.047	0.201	0.860	6	R.M@GL*AM@GGGGGASFDR.A
SW:ROM_HUMAN	S07	5312	2	1466.7	(-0.2)	2.994	0.227	0.775	8	R.M@GPAM@GPAL*GAGIER.M
SW:ROM_HUMAN	S16	5192	2	1466.7	(-0.3)	2.767	0.213	0.682	8	R.M@GPAM@GPAL*GAGIER.M
SW:ROM_HUMAN	S17	5680	2	1466.7	(-0.2)	2.714	0.177	0.562	8	R.M@GPAM@GPAL*GAGIER.M
SW:ROM_HUMAN	S07	5744	2	1658.9	(-0.5)	3.399	0.455	0.963	9	R.M@GPL*GL*DHM@ASSIER.M
SW:ROM_HUMAN	S14	8262	2	1790.0	(-0.1)	2.421	0.354	0.735	6	K.VGEVTVYVEL*L*M@DAEGK#.S
SW:ROM_HUMAN	S17	7942	2	1265.5	(+0.4)	2.480	0.466	0.975	6	R.AFITNIPFDVK.W
SW:ROR_HUMAN	S08	7058	2	928.1	(+0.9)	2.617	0.213	0.868	9	K.AGPIWDLR.L
SW:ROR_HUMAN	S05	8454	2	1610.8	(+0.7)	3.257	0.436	0.981	2	R.DLYEDELVPLFEK.A
SW:ROR_HUMAN	S06	8358	2	1610.8	(+0.4)	3.494	0.484	1.000	2	R.DLYEDELVPLFEK.A
SW:ROR_HUMAN	S07	8386	2	1610.8	(-0.1)	2.802	0.281	0.844	2	R.DLYEDELVPLFEK.A
SW:ROR_HUMAN	S08	8580	2	1610.8	(+0.5)	3.132	0.472	0.983	2	R.DLYEDELVPLFEK.A
SW:ROR_HUMAN	S08	8574	2	1636.8	(+0.4)	2.845	0.270	0.851	2	R.DL*YEDEL*VPL*FEK#.A
SW:ROR_HUMAN	S12	8228	2	1610.8	(+0.6)	3.022	0.469	0.982	2	R.DLYEDELVPLFEK.A



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ROR_HUMAN	S15	8330	2	1610.8	(+0.6)	3.191	0.450	0.982	2	R.DLYEDELVPLFEK.A
SW:ROR_HUMAN	S07	6280	2	875.1	(+0.9)	2.285	0.309	0.862	9	R.L*FVGSIPK#.N
SW:ROR_HUMAN	S08	6540	2	1274.5	(+0.2)	2.531	0.397	0.924	2	R.L*MMDPL*SGQNR.G
SW:ROR_HUMAN	S06	8248	2	1481.7	(-0.3)	3.068	0.296	0.811	2	R.NL*ATTVTEEIL*EK#.S
SW:ROR_HUMAN	S07	8298	2	1481.7	(+0.2)	3.144	0.397	0.903	2	R.NL*ATTVTEEIL*EK#.S
SW:ROR_HUMAN	S12	8122	2	1481.7	(-0.1)	2.581	0.180	0.391	2	R.NL*ATTVTEEIL*EK#.S
SW:ROR_HUMAN	S13	8472	2	1481.7	(-0.4)	3.263	0.388	0.906	2	R.NL*ATTVTEEIL*EK#.S
SW:ROR_HUMAN	S16	8214	2	1481.7	(-0.5)	2.327	0.150	0.204	2	R.NL*ATTVTEEIL*EK#.S
SW:ROR_HUMAN	S07	5492	2	1312.4	(+0.3)	2.614	0.446	0.945	8	R.TGYTLDDVTTGQR.K
SW:ROR_HUMAN	S08	5662	2	1312.4	(+0.2)	2.615	0.418	0.935	8	R.TGYTLDDVTTGQR.K
SW:ROR_HUMAN	S08	5688	2	1318.4	(+0.8)	2.293	0.376	0.937	8	R.TGYTL*DVTTGQR.K
SW:ROR_HUMAN	S07	6940	2	1338.5	(+0.7)	3.634	0.364	0.550	2	K.TKENILEEFSK.V
SW:ROR_HUMAN	S08	7026	2	1360.5	(-0.3)	2.828	0.142	0.019	2	K.TK#ENIL*EEFSK#.V
SW:ROR_HUMAN	S08	7012	2	1338.5	(+0.6)	2.693	0.348	0.340	2	K.TKENILEEFSK.V
SW:ROR_HUMAN	S08	7008	2	1360.5	(+0.9)	2.283	0.301	0.083	2	K.TK#ENIL*EEFSK#.V
SW:ROR_HUMAN	S14	7044	2	1360.5	(-0.8)	2.210	0.250	0.005	2	K.TK#ENIL*EEFSK#.V
SW:ROR_HUMAN	S15	6866	2	1338.5	(+0.7)	2.391	0.352	0.262	2	K.TKENILEEFSK.V
SW:ROR_HUMAN	S15	6860	2	1360.5	(+0.5)	2.280	0.249	0.049	2	K.TK#ENIL*EEFSK#.V
SW:ROR_HUMAN	S16	6800	2	1360.5	(+0.6)	3.163	0.430	0.390	2	K.TK#ENIL*EEFSK#.V
SW:ROR_HUMAN	S07	5816	2	1090.3	(+0.3)	2.615	0.387	0.872	1	K.TL*IEAGL*PQK#.V
SW:ROR_HUMAN	S08	7494	3	2508.8	(+0.8)	4.018	0.433	0.998	2	K.YGGPPPSVYSGVQPGIGTEVFVGK.I
SW:ROR_HUMAN	S17	8498	2	1610.8	(+0.9)	3.982	0.471	1.000	2	R.DLYEDELVPLFEK.A
SW:ROU_HUMAN	S11	4970	2	1022.2	(+0.2)	2.344	0.264	0.673	7	K.DLPEHAVLK.M
SW:ROU_HUMAN	S05	8708	3	2740.1	(+0.6)	4.617	0.427	0.989	6	K.EK#PYFFPIPEEYTFIQNVPL*EDR.V
SW:ROU_HUMAN	S05	8772	3	2726.1	(+0.8)	4.207	0.385	0.973	6	K.EKPYFFPIPEEYTFIQNVPLEDR.V
SW:ROU_HUMAN	S06	8564	3	2726.1	(+0.5)	5.712	0.481	0.998	6	K.EKPYFFPIPEEYTFIQNVPLEDR.V
SW:ROU_HUMAN	S07	8638	3	2726.1	(+0.7)	5.202	0.457	1.000	6	K.EKPYFFPIPEEYTFIQNVPLEDR.V
SW:ROU_HUMAN	S07	8646	3	2740.1	(-0.1)	4.408	0.423	0.961	6	K.EK#PYFFPIPEEYTFIQNVPL*EDR.V
SW:ROU_HUMAN	S12	8354	3	2740.1	(+0.8)	4.893	0.443	0.992	6	K.EK#PYFFPIPEEYTFIQNVPL*EDR.V
SW:ROU_HUMAN	S12	8352	3	2726.1	(+0.2)	4.008	0.476	0.974	6	K.EKPYFFPIPEEYTFIQNVPLEDR.V
SW:ROU_HUMAN	S13	8678	3	2740.1	(+0.6)	4.078	0.243	0.567	6	K.EK#PYFFPIPEEYTFIQNVPL*EDR.V
SW:ROU_HUMAN	S01	6398	2	1300.4	(+0.1)	3.181	0.334	0.893	5	R.GYFEYIEENK#.Y
SW:ROU_HUMAN	S03	5835	2	1292.4	(+0.9)	3.491	0.346	0.980	5	R.GYFEYIEENK.Y
SW:ROU_HUMAN	S04	5817	2	1300.4	(+0.3)	2.765	0.338	0.851	5	R.GYFEYIEENK#.Y
SW:ROU_HUMAN	S04	5809	2	1292.4	(+0.6)	2.488	0.303	0.927	5	R.GYFEYIEENK.Y
SW:ROU_HUMAN	S05	6584	2	1300.4	(+1.0)	2.490	0.350	0.906	5	R.GYFEYIEENK#.Y
SW:ROU_HUMAN	S07	6666	2	1300.4	(+0.5)	3.176	0.329	0.946	5	R.GYFEYIEENK#.Y
SW:ROU_HUMAN	S08	6768	2	1292.4	(-0.2)	3.018	0.355	0.943	5	R.GYFEYIEENK.Y
SW:ROU_HUMAN	S08	6766	2	1300.4	(-0.3)	2.334	0.351	0.778	5	R.GYFEYIEENK#.Y
SW:ROU_HUMAN	S10	6770	2	1300.4	(+0.2)	3.334	0.363	0.917	5	R.GYFEYIEENK#.Y
SW:ROU_HUMAN	S11	6688	2	1300.4	(-0.7)	2.620	0.280	0.427	5	R.GYFEYIEENK#.Y
SW:ROU_HUMAN	S13	6888	2	1292.4	(+0.8)	2.988	0.362	0.973	5	R.GYFEYIEENK.Y
SW:ROU_HUMAN	S14	6814	2	1300.4	(+0.1)	2.929	0.277	0.810	5	R.GYFEYIEENK#.Y
SW:ROU_HUMAN	S17	6858	2	1300.4	(+0.0)	2.771	0.249	0.729	5	R.GYFEYIEENK#.Y
SW:ROU_HUMAN	S17	6854	2	1292.4	(+0.8)	2.769	0.319	0.956	5	R.GYFEYIEENK.Y
SW:ROU_HUMAN	S05	3944	2	1267.4	(+0.6)	2.731	0.435*	0.012	6	K.LLEQYKEESK.K
SW:ROU_HUMAN	S05	3740	2	1295.4	(-0.5)	2.457	0.356	0.093	6	K.L*L*EQYK#EESK#.K
SW:ROU_HUMAN	S05	3814	2	1295.4	(+0.4)	2.356	0.247	0.062	6	K.L*L*EQYK#EESK#.K
SW:ROU_HUMAN	S05	3610	2	1295.4	(+0.1)	2.312	0.393	0.101	6	K.L*L*EQYK#EESK#.K
SW:ROU_HUMAN	S13	2306	2	1267.4	(+0.7)	2.855	0.383*	0.016	6	K.LLEQYKEESK.K
SW:ROU_HUMAN	S15	2244	2	1267.4	(+0.7)	2.298	0.321*	0.004	6	K.LLEQYKEESK.K
SW:ROU_HUMAN	S06	5150	2	858.0	(+0.9)	2.501	0.175*	0.394	6	K.LNTLLQR.A
SW:ROU_HUMAN	S11	5192	2	858.0	(+0.8)	2.266	0.217*	0.241	6	K.LNTLLQR.A
SW:ROU_HUMAN	S04	5423	3	3168.3	(-0.8)	5.380	0.514	1.000	3	R.L*QAAL*DDEEAGGRPAM@EPGNGL*DL*GGDSAGR.S
SW:ROU_HUMAN	S05	6202	3	3168.3	(+0.5)	6.346	0.525	0.999	3	R.L*QAAL*DDEEAGGRPAM@EPGNGL*DL*GGDSAGR.S
SW:ROU_HUMAN	S05	6044	3	3168.3	(+0.6)	5.400	0.582	1.000	3	R.L*QAAL*DDEEAGGRPAM@EPGNGL*DL*GGDSAGR.S
SW:ROU_HUMAN	S05	6432	3	3152.3	(+0.1)	5.371	0.510	1.000	3	R.L*QAAL*DDEEAGGRPAMEPGNGL*DL*GGDSAGR.S
SW:ROU_HUMAN	S05	6512	3	3152.3	(-0.3)	5.166	0.454	1.000	3	R.L*QAAL*DDEEAGGRPAMEPGNGL*DL*GGDSAGR.S
SW:ROU_HUMAN	S07	6500	3	3128.3	(+0.9)	6.780	0.563	1.000	3	R.LQAALDDEEAGGRPAMEPGNGLDLGGDSAGR.S
SW:ROU_HUMAN	S07	6102	3	3168.3	(+0.1)	5.327	0.540	1.000	3	R.L*QAAL*DDEEAGGRPAM@EPGNGL*DL*GGDSAGR.S
SW:ROU_HUMAN	S08	6250	3	3168.3	(+0.1)	5.691	0.586	1.000	3	R.L*QAAL*DDEEAGGRPAM@EPGNGL*DL*GGDSAGR.S
SW:ROU_HUMAN	S08	6642	3	3128.3	(-0.1)	4.710	0.528	1.000	3	R.LQAALDDEEAGGRPAMEPGNGLDLGGDSAGR.S
SW:ROU_HUMAN	S09	6388	3	3168.3	(-0.0)	5.095	0.548	1.000	3	R.L*QAAL*DDEEAGGRPAM@EPGNGL*DL*GGDSAGR.S
SW:ROU_HUMAN	S01	6310	2	1648.8	(+0.7)	4.756	0.456	1.000	6	R.NFILDQTNVSAQAQR.R
SW:ROU_HUMAN	S01	6306	2	1654.8	(+0.3)	4.266	0.518	1.000	6	R.NFIL*DQTNVSAQAQR.R

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:ROU_HUMAN	S05	6456	2	1648.8	(-0.0)	2.767	0.243	0.749	6	R.NFILDQTNVSAQAQR.R
SW:ROU_HUMAN	S06	6430	2	1648.8	(+0.8)	4.498	0.428	1.000	6	R.NFILDQTNVSAQAQR.R
SW:ROU_HUMAN	S08	6656	3	1654.8	(+0.8)	4.337	0.421	0.999	6	R.NFIL*DQTNVSAQAQR.R
SW:ROU_HUMAN	S13	6802	2	1654.8	(+0.3)	4.757	0.480	1.000	6	R.NFIL*DQTNVSAQAQR.R
SW:ROU_HUMAN	S13	6788	2	1648.8	(+0.8)	4.435	0.446	1.000	6	R.NFILDQTNVSAQAQR.R
SW:ROU_HUMAN	S14	6684	2	1648.8	(+0.4)	4.560	0.476	1.000	6	R.NFILDQTNVSAQAQR.R
SW:ROU_HUMAN	S05	5554	2	1049.2	(+0.6)	2.656	0.310	0.945	7	K.NGQDLGVAFK.I
SW:ROU_HUMAN	S06	5510	2	1049.2	(-0.4)	2.264	0.286	0.671	7	K.NGQDLGVAFK.I
SW:ROU_HUMAN	S07	5566	2	1049.2	(+0.9)	2.694	0.419	0.975	7	K.NGQDLGVAFK.I
SW:ROU_HUMAN	S07	5524	2	1063.2	(+0.5)	2.223	0.126	0.313	7	K.NGQDL*GVAFK#.I
SW:ROU_HUMAN	S07	5584	2	1049.2	(-0.5)	2.212	0.178	0.275	7	K.NGQDLGVAFK.I
SW:ROU_HUMAN	S08	5780	2	1049.2	(+0.1)	2.718	0.374	0.933	7	K.NGQDLGVAFK.I
SW:ROU_HUMAN	S10	5766	2	1063.2	(-0.1)	2.273	0.156	0.264	7	K.NGQDL*GVAFK#.I
SW:ROU_HUMAN	S10	5772	2	1049.2	(-0.1)	2.223	0.235	0.543	7	K.NGQDLGVAFK.I
SW:ROU_HUMAN	S15	5556	2	1049.2	(-0.2)	2.229	0.227	0.612	7	K.NGQDLGVAFK.I
SW:ROU_HUMAN	S06	7406	2	1715.9	(+1.0)	2.337	0.390	0.937	4	K.SSGPTSLFAVTVAPPGAR.Q
SW:ROU_HUMAN	S01	6086	2	1413.6	(+0.3)	2.701	0.349	0.826	6	K.YNIL*GTNTIM@DK#.M
SW:ROU_HUMAN	S04	5999	2	1383.6	(+0.8)	2.468	0.318	0.920	6	K.YNILGTNTIMDK.M
SW:ROU_HUMAN	S04	5567	2	1413.6	(+0.2)	2.284	0.301	0.620	6	K.YNIL*GTNTIM@DK#.M
SW:ROU_HUMAN	S06	6172	2	1413.6	(+0.0)	2.302	0.196	0.332	6	K.YNIL*GTNTIM@DK#.M
SW:ROU_HUMAN	S19	8516	3	2726.1	(-0.0)	3.919	0.400	0.924	6	K.EKPYFPIPEEYTFIQNVPLEDR.V
SW:RRP5_HUMAN	S06	4902	2	1227.3	(+0.2)	2.464	0.198	0.649	1	K.FQEAGELYNR.M
SW:RRP5_HUMAN	S05	5328	2	1131.3	(-0.7)	2.433	0.135	0.170	1	R.IEEALMDPGR.Q
SW:RRP5_HUMAN	S07	5328	2	1131.3	(+0.7)	2.395	0.245	0.857	1	R.IEEALMDPGR.Q
SW:RRP5_HUMAN	S06	8736	2	1232.5	(+0.6)	2.347	0.176	0.677	2	R.IPLLLTSLSFK.V
SW:RRP5_HUMAN	S12	8632	2	1232.5	(+1.0)	2.971	0.467	0.980	2	R.IPLLLTSLSFK.V
SW:RRP5_HUMAN	S14	7610	2	1170.4	(+0.5)	2.844	0.510	1.000	2	K.AINIGQLVDVK.V
SW:RRS1_HUMAN	S11	9070	2	2083.4	(+0.0)	3.085	0.271	0.856	1	R.DNTQLLINQLWQLPTER.V
SW:RRS1_HUMAN	S11	8520	2	2192.4	(+0.3)	4.217	0.478	1.000	1	K.EWL*IEVPGNADPL*EDQFAK#.R
SW:RRS1_HUMAN	S11	7602	2	1498.7	(+0.9)	2.513	0.213	0.786	2	R.KFQPLFGDFAAEK.K
SW:RRS1_HUMAN	S11	7580	2	1520.7	(-0.5)	2.478	0.264	0.586	2	R.K#FQPL*FGDFAAEK#.K
SW:RRS1_HUMAN	S11	8516	2	2172.4	(-0.9)	2.431	0.279	0.403	1	K.EWLVIEVPGNADPLEDQFAK.R
SW:RS13_HUMAN	S18	8774	2	1695.0	(+0.7)	2.908	0.384	0.965	1	K.GLAPDLPEDLYHLIK.K
SW:RS13_HUMAN	S18	7212	2	1382.7	(-0.1)	2.637	0.299	0.838	2	K.KGLTPSQIGVILR.D
SW:RS14_HUMAN	S18	7068	2	2266.4	(-0.0)	5.343	0.534	1.000		K.ADRDESSPYAAMLAQAQDVAQR.C
SW:RS14_HUMAN	S18	1808	2	1055.2	(+0.9)	3.238	0.311	0.967		K.TPGPGAQSALR.A
SW:RS14_HUMAN	S19	6910	2	1095.3	(+0.9)	2.382	0.422	0.966		K.ELGITALHIK.L
SW:RS24_HUMAN	S18	8126	2	1682.9	(+0.3)	3.913	0.484	1.000	2	K.TTGFGMIYDSLDAK.K
SW:RS24_HUMAN	S18	6560	2	1237.5	(-0.1)	2.440	0.301	0.825	2	K.QMVIDVLHPGK.A
SW:RS25_HUMAN	S18	6582	2	973.2	(+1.0)	2.892	0.329	0.968		R.AALQELLSK.G
SW:RS25_HUMAN	S18	7174	2	1076.3	(+1.0)	3.138	0.475	0.997		K.LNNLVLFDAK.A
SW:RS25_HUMAN	S18	7176	2	1102.3	(+0.7)	2.367	0.324	0.878		K.L*NNL*VL*FDK#.A
SW:RS25_HUMAN	S18	5856	2	1085.3	(+1.0)	2.202	0.254	0.781		K.LITPAVVSR.L
SW:RS27_HUMAN	S19	5100	2	1294.4	(+0.0)	2.274	0.259	0.690	3	K.DLLHPSPEEEK.R
SW:RS27_HUMAN	S20	6092	2	1558.8	(-0.1)	3.365	0.216	0.744	4	R.L*VQSPNSYFM@DVK#.C
SW:RS27_HUMAN	S20	4618	2	1450.6	(+0.8)	2.780	0.439	0.490	3	K.DLLHPSPEEEKR.K
SW:RS2_HUMAN	S14	5164	2	1034.2	(+0.9)	2.416	0.417	0.931	5	R.GTGIVSAPVPK#.K
SW:RS2_HUMAN	S14	7828	2	1387.6	(+0.1)	2.555	0.473	0.953	7	K.TYSYLTPLDWK.E
SW:RS2_HUMAN	S15	9016	2	1552.9	(+0.6)	2.781	0.298	0.931	6	K.SLEEIYLFSLPIK.E
SW:RS4_HUMAN	S15	8444	2	1887.2	(+0.7)	3.056	0.465	0.980	2	R.TDITYPAGFMDVISIDK.T
SW:RS4_HUMAN	S15	7088	2	1005.2	(+0.7)	2.875	0.425	0.963	2	R.L*SNIFVIGK#.G
SW:RS7_HUMAN	S17	8774	2	1352.7	(+0.3)	2.473	0.442*	0.042	1	K.AIIIFVVPQL*#.S
SW:RS7_HUMAN	S17	9280	3	3332.7	(+0.8)	4.667	0.347	0.961	1	K.IVKPNGEKPDFEFESGISQALLELEMNSDLK.A
SW:RS7_HUMAN	S17	9170	3	3332.7	(-0.2)	4.115	0.332	0.796	1	K.IVKPNGEKPDFEFESGISQALLELEMNSDLK.A
SW:RS7_HUMAN	S17	9326	2	2368.7	(-0.0)	5.270	0.606	1.000	1	R.TLTAHVDAILEDLVFPSEIVGK.R
SW:RS7_HUMAN	S17	9196	2	1391.5	(+0.7)	2.231	0.478	0.970	1	K.DVNFEPFEPQL*.-

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:RS8_HUMAN	S16	6558	2	1527.7	(-0.3)	2.257	0.176	0.236	1	K.ISSL*L*EEQFQQGK#.L
SW:RS8_HUMAN	S16	5740	2	1315.5	(+0.9)	2.445	0.295	0.907	1	K.LTPEEEEEILNK.K
SW:RS8_HUMAN	S20	6312	2	1507.7	(-0.0)	3.736	0.512	1.000	1	K.ISSLLLEEQFQQGK.L
SW:RS9_HUMAN	S16	6630	2	1051.2	(-0.1)	2.433	0.271	0.817	3	R.L*FEGNAL*L*R.R
SW:RS9_HUMAN	S16	5828	2	921.1	(+0.9)	2.935	0.356	0.977	4	K.LIGEYGLR.N
SW:RS9_HUMAN	S17	6176	2	921.1	(+0.7)	2.398	0.208	0.848	4	K.LIGEYGLR.N
SW:RS9_HUMAN	S16	4946	2	1020.2	(+0.9)	2.444	0.335	0.953	3	R.RLQTQVFK.L
SW:RS9_HUMAN	S17	6934	2	1051.2	(+0.6)	2.354	0.299	0.917	3	R.L*FEGNAL*L*R.R
SW:RT23_HUMAN	S16	6802	2	1109.3	(+0.9)	3.080	0.282	0.958		R.LETVGSIFSR.T
SW:RT23_HUMAN	S16	6806	2	1115.3	(+1.0)	2.858	0.422	0.979		R.L*ETVGSIFSR.T
SW:RT23_HUMAN	S16	7772	2	1213.4	(+1.0)	2.379	0.377	0.953	3	R.AFDLFPNPK.S
SW:RU2A_HUMAN	S15	5782	2	1126.3	(+0.6)	3.066	0.337	0.968	2	K.GLLQSGQIPGR.E
SW:RU2A_HUMAN	S15	5784	2	1138.3	(+0.3)	2.710	0.322	0.613	2	K.GL*L*QSGQIPGR.E
SW:RU2A_HUMAN	S15	6190	2	1459.6	(-0.0)	2.716	0.456	0.947	2	K.NAIANASTLAEVER.L
SW:RU2A_HUMAN	S15	6184	2	1465.6	(-0.0)	2.582	0.345	0.871	2	K.NAIANASTL*AEVER.L
SW:RU2A_HUMAN	S15	7664	2	1084.3	(+1.0)	2.202	0.114	0.462	2	K.SL*TYL*SIL*R.N
SW:RUN1_HUMAN	S09	5008	3	2381.5	(+0.6)	3.896	0.310	0.971	4	R.ASL*NHSTAFNPQPQSQM@QDTR.Q
SW:RUN1_HUMAN	S09	5730	3	2365.5	(+0.1)	3.824	0.301	0.932	4	R.ASL*NHSTAFNPQPQSQMQDTR.Q
SW:RUN1_HUMAN	S09	6908	2	1163.3	(+0.9)	2.743	0.406	0.493	3	R.LEEAVWRPY.-
SW:RUN1_HUMAN	S10	6810	2	1169.3	(+0.1)	3.116	0.427	0.391	3	R.L*EEAVWRPY.-
SW:RUN1_HUMAN	S10	6834	2	1783.0	(-0.2)	2.332	0.237	0.401	13	K.M@SEAL*PL*GAPDAGAAL*AGK#.L
SW:RUV1_HUMAN	S10	8520	2	1689.0	(+0.4)	3.588	0.538	1.000	1	R.ALESSIAPIVIFASNR.G
SW:RUV1_HUMAN	S10	8518	2	1695.0	(+0.1)	2.729	0.419	0.931	1	R.AL*ESSIAPIVIFASNR.G
SW:RUV1_HUMAN	S10	5794	2	1081.3	(+0.6)	2.948	0.451	0.980	1	R.AVLLAGPPGTGK.T
SW:RUV1_HUMAN	S10	5974	2	1086.2	(+0.6)	2.802	0.478	0.965	1	K.GL*GL*DESL*AK#.Q
SW:RUV1_HUMAN	S10	5978	2	1060.2	(+0.6)	2.707	0.444	0.977	1	K.GLGLDESLAK.Q
SW:RUV2_HUMAN	S10	6704	2	1156.3	(+1.0)	3.539	0.383	0.982	2	R.GLGLDDALEPR.Q
SW:RUV2_HUMAN	S10	5976	2	1043.2	(+1.0)	2.411	0.215	0.838	3	K.TEAL*TQAFR.R
SW:RUV2_HUMAN	S10	6262	2	1081.3	(+0.5)	2.396	0.232	0.839	2	R.AAGVVL*EM@IR.E
SW:RUXE_HUMAN	S20	7658	2	1352.7	(+1.0)	2.763	0.510	0.984	2	K.VM@VQPINL*IFR.Y
SW:RUXE_HUMAN	S20	8060	2	1336.7	(+1.0)	2.556	0.321	0.937	2	K.VMVQPINL*IFR.Y
SW:RUXE_HUMAN	S20	6224	2	1261.4	(+0.6)	2.434	0.453	0.970	2	K.GDNITLLQSVSN.-
SW:S3B2_HUMAN	S04	6297	3	2407.7	(+0.1)	4.157	0.398	0.985	7	K.K#IEEAM@DGSETPQL*FTVL*PEK#.R
SW:S3B2_HUMAN	S04	4965	2	1245.4	(+0.2)	2.806	0.370	0.926	4	K.L*AEIGAPIQGNR.E
SW:S3B2_HUMAN	S04	4985	2	1239.4	(+0.6)	2.785	0.298	0.937	4	K.LAEIGAPIQGNR.E
SW:S3B2_HUMAN	S04	4607	2	1321.4	(+0.9)	3.315	0.467	1.000	5	R.VGEPVAL*SEEER.L
SW:S3B2_HUMAN	S04	4617	2	1315.4	(-0.2)	3.009	0.455	0.961	5	R.VGEPVALSEEER.L
SW:S3B2_HUMAN	S04	4631	2	1321.4	(-0.4)	2.474	0.380	0.902	5	R.VGEPVAL*SEEER.L
SW:S3B3_HUMAN	S03	6269	2	1316.5	(+0.4)	2.608	0.381	0.960	1	R.FL*AVGL*VDNTRV.I
SW:S3B3_HUMAN	S05	6280	2	1489.6	(+0.8)	3.023	0.485	0.982	1	R.TVLDPVTGDLSDTR.T
SW:S3B3_HUMAN	S05	6274	2	1501.6	(-0.2)	2.366	0.393	0.883	1	R.TVL*DPVTGDL*SDTR.T
SW:SFR1_HUMAN	S14	6682	2	1263.5	(+0.5)	3.248	0.401	0.981	4	R.IYVGNL*PPDIR.T
SW:SFR1_HUMAN	S14	6802	2	1257.5	(+0.8)	3.243	0.447	0.984	4	R.IYVGNLPPDIR.T
SW:SFR1_HUMAN	S14	6852	2	1263.5	(+0.7)	2.866	0.300	0.949	4	R.IYVGNL*PPDIR.T
SW:SFR1_HUMAN	S14	7104	2	1257.5	(+0.6)	2.814	0.359	0.965	4	R.IYVGNLPPDIR.T
SW:SFR1_HUMAN	S14	6966	2	1257.5	(+0.6)	2.773	0.412	0.974	4	R.IYVGNLPPDIR.T
SW:SFR1_HUMAN	S14	7016	2	1263.5	(+1.0)	2.519	0.223	0.839	4	R.IYVGNL*PPDIR.T
SW:SFR1_HUMAN	S14	6932	2	1263.5	(+0.7)	2.251	0.239	0.786	4	R.IYVGNL*PPDIR.T
SW:SFR1_HUMAN	S14	6480	2	1258.4	(+1.0)	2.751	0.454	0.537	4	R.TKDIEDVFYK.Y
SW:SFR1_HUMAN	S14	7236	2	1689.9	(-0.9)	2.213	0.147	0.038	4	R.VVVSGL*PPSGSWQDL*K#.D
SW:SFR1_HUMAN	S14	6798	1	1037.1	(-0.6)	1.943	0.326	0.000	4	K.DIEDVFYK#.Y
SW:SFR3_HUMAN	S16	6456	2	1050.2	(+0.2)	2.381	0.367	0.906	1	R.AFGYYGPL*R.S
SW:SFR3_HUMAN	S16	6460	2	1044.2	(+0.4)	2.376	0.435	0.972	1	R.AFGYYGPLR.S
SW:SFR3_HUMAN	S18	6514	2	1050.2	(+0.8)	2.251	0.374	0.948	1	R.AFGYYGPL*R.S

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:SFR3_HUMAN	S17	2390	2	1249.4	(+0.5)	2.755	0.426	0.974	1	K.VYVGNLGNNGNK.T
SW:SFR3_HUMAN	S17	4748	2	1249.4	(+0.9)	2.593	0.233	0.854	1	K.VYVGNLGNNGNK.T
SW:SFR3_HUMAN	S17	5198	2	1263.4	(+0.9)	2.280	0.361	0.865	1	K.VYVGNL*GNNGNK#.T
SW:SFR3_HUMAN	S17	5888	2	1878.1	(+0.4)	3.913	0.400	0.567	1	K.VYVGNLGNNGNKTELER.A
SW:SFR3_HUMAN	S20	6248	2	1044.2	(+0.8)	2.640	0.377	0.969	1	R.AFGYYGPLR.S
SW:SFR4_HUMAN	S10	4970	2	1324.4	(+0.7)	3.156	0.455*	0.297	10	R.DADDAVYEL*NGK#.D
SW:SFR4_HUMAN	S10	5318	2	1310.4	(-0.1)	2.738	0.409	0.939	10	R.DADDAVYELNGK.D
SW:SFR4_HUMAN	S12	5308	2	1324.4	(+0.8)	3.284	0.443*	0.346	10	R.DADDAVYEL*NGK#.D
SW:SFR4_HUMAN	S12	5328	2	1310.4	(+0.4)	2.502	0.278*	0.171	10	R.DADDAVYELNGK.D
SW:SFR4_HUMAN	S06	5652	2	1031.2	(+0.5)	2.310	0.298	0.910	11	R.LIVENLSSR.C
SW:SFR4_HUMAN	S07	5728	2	1043.2	(+0.1)	2.388	0.360	0.902	11	R.L*IVENL*SSR.C
SW:SFR4_HUMAN	S10	5894	2	1043.2	(+0.3)	2.792	0.374	0.943	11	R.L*IVENL*SSR.C
SW:SFR4_HUMAN	S11	5822	2	1043.2	(+0.1)	2.484	0.360	0.914	11	R.L*IVENL*SSR.C
SW:SFR4_HUMAN	S12	5546	2	1031.2	(-0.6)	2.222	0.207	0.586	11	R.LIVENLSSR.C
SW:SFR4_HUMAN	S13	6066	2	1043.2	(+0.5)	2.597	0.377	0.968	11	R.L*IVENL*SSR.C
SW:SFR4_HUMAN	S17	6002	2	1043.2	(+0.1)	2.218	0.326	0.837	11	R.L*IVENL*SSR.C
SW:SFR5_HUMAN	S10	4960	2	1311.3	(+0.3)	3.390	0.391	0.957	3	R.DADDAVYELD GK.E
SW:SFR5_HUMAN	S11	4568	2	1311.3	(+1.0)	2.550	0.374	0.955	3	R.DADDAVYELD GK.E
SW:SFR5_HUMAN	S12	5758	2	876.0	(+0.6)	2.451	0.240	0.880	2	R.VSWQDLK.D
SW:SFR7_HUMAN	S14	6628	2	1080.2	(+0.8)	2.603	0.287	0.937	5	R.AFSYYGPL*R.T
SW:SFR7_HUMAN	S19	6604	2	1074.2	(+0.9)	2.526	0.287	0.930	5	R.AFSYYGPLR.T
SW:SFR7_HUMAN	S20	6214	2	1074.2	(+0.8)	2.650	0.262	0.928	5	R.AFSYYGPLR.T
SW:SFR7_HUMAN	S13	5206	2	1136.3	(+0.8)	3.289	0.424	0.820	5	K.VYVGNLGTGAGK.G
SW:SFR7_HUMAN	S13	5122	2	1136.3	(+0.4)	3.202	0.497	1.000	5	K.VYVGNLGTGAGK.G
SW:SFR7_HUMAN	S13	5118	2	1150.3	(+0.6)	2.785	0.468	0.961	5	K.VYVGNL*GTGAGK#.G
SW:SFR7_HUMAN	S14	4854	2	1136.3	(+0.5)	2.768	0.327	0.949	5	K.VYVGNLGTGAGK.G
SW:SFR7_HUMAN	S14	4974	2	1136.3	(-0.1)	2.465	0.254	0.688	5	K.VYVGNLGTGAGK.G
SW:SFR7_HUMAN	S14	5094	2	1136.3	(+0.4)	2.443	0.211	0.736	5	K.VYVGNLGTGAGK.G
SW:SFR7_HUMAN	S14	4928	2	1150.3	(+0.4)	2.438	0.496	0.955	5	K.VYVGNL*GTGAGK#.G
SW:SFR7_HUMAN	S14	4894	2	1136.3	(-0.8)	2.295	0.182	0.173	5	K.VYVGNLGTGAGK.G
SW:SFR7_HUMAN	S19	4794	2	1150.3	(+0.5)	2.488	0.431	0.938	5	K.VYVGNL*GTGAGK#.G
SW:SFR7_HUMAN	S20	4442	2	1150.3	(+0.9)	2.395	0.434	0.718	5	K.VYVGNL*GTGAGK#.G
SW:SFR9_HUMAN	S15	6682	2	1139.3	(-0.2)	2.918	0.291	0.904		K.DGVGMVEYLR.K
SW:SFR9_HUMAN	S15	7438	2	1043.2	(+0.9)	2.630	0.228	0.914		K.DLEDLFYK.Y
SW:SFR9_HUMAN	S15	7434	2	1063.2	(+0.8)	2.376	0.307	0.879		K.DL*EDL*FYK#.Y
SW:SFR9_HUMAN	S15	7084	2	1300.5	(+1.0)	2.214	0.430	0.360		R.EKDLEDLFYK.Y
SW:SFR9_HUMAN	S15	6348	2	1247.4	(-0.6)	2.355	0.349	0.866		R.IYVGNLPTDVR.E
SW:SFR9_HUMAN	S15	5018	2	1155.3	(+0.3)	2.679	0.321	0.910		R.KEDMEYALR.K
SW:SFR9_HUMAN	S15	5016	2	1169.3	(+0.3)	2.400	0.319	0.869		R.K#EDMEYAL*R.K
SW:SFR9_HUMAN	S15	7238	2	1709.9	(-0.3)	3.234	0.423	0.912		R.VL*VSL*PPSGSWQDL*K#.D
SW:SFR9_HUMAN	S15	7420	2	1683.9	(+0.6)	2.813	0.401	0.966		R.VLVSLPPSGSWQDLK.D
SW:SFR9_HUMAN	S16	6590	2	1139.3	(-0.0)	3.051	0.260	0.895		K.DGVGMVEYLR.K
SW:SMD1_HUMAN	S19	5654	3	2240.5	(+0.5)	3.902	0.386	0.992	1	K.NGTQVHGTTITGVDVSM@NTHL*K#.A
SW:SMD1_HUMAN	S19	6714	2	1555.8	(+0.3)	3.406	0.456	1.000	1	K.NREPVQLETLSIR.G
SW:SMD1_HUMAN	S19	10630	2	2288.7	(+0.2)	3.820	0.469	1.000	1	R.YFILPDSLPLDTLLVDVEPK.V
SW:SMD1_HUMAN	S19	6718	2	1567.8	(-0.8)	2.666	0.188	0.010	1	K.NREPVQL*ETL*SIR.G
SW:SN21_HUMAN	S07	5318	2	1135.3	(+0.9)	3.638	0.286	0.975	2	R.L*DSIVIQQGR.L
SW:SN21_HUMAN	S15	5294	2	1129.3	(+0.2)	2.649	0.171	0.659	2	R.LDSIVIQQGR.L
SW:SN21_HUMAN	S04	5549	2	1117.3	(+0.9)	2.822	0.206	0.907	2	R.VL*IFSQM@TR.L
SW:SN21_HUMAN	S07	7142	2	1095.3	(+1.0)	2.933	0.448	0.983	2	R.VLIFSQMTR.L
SW:SN21_HUMAN	S08	7228	2	1095.3	(+1.0)	2.951	0.455	0.984	2	R.VLIFSQMTR.L
SW:SN21_HUMAN	S06	5564	2	1122.3	(+0.2)	2.625	0.204	0.759	2	R.YL*VIDEAHR.I
SW:SN21_HUMAN	S07	5620	2	1116.3	(+0.7)	2.661	0.209	0.886	2	R.YLVIDEAHR.I
SW:SN21_HUMAN	S08	5802	2	1116.3	(+0.5)	2.592	0.166	0.810	2	R.YLVIDEAHR.I
SW:SN21_HUMAN	S09	5864	2	1116.3	(+0.8)	2.489	0.230	0.876	2	R.YLVIDEAHR.I
SW:SN21_HUMAN	S10	5804	2	1122.3	(-0.1)	2.649	0.261	0.853	2	R.YL*VIDEAHR.I
SW:SN21_HUMAN	S10	5792	2	1116.3	(+0.7)	2.509	0.147	0.740	2	R.YLVIDEAHR.I
SW:SN21_HUMAN	S15	5302	2	1135.3	(+0.4)	2.265	0.163	0.626	2	R.L*DSIVIQQGR.L
SW:SNW1_HUMAN	S08	6520	2	1135.3	(+0.6)	3.304	0.346	0.977	5	K.LAEALYIADR.K

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:SNW1_HUMAN	S08	8456	3	2783.1	(-0.5)	3.734	0.526	1.000	1	R.L*L*EDFGDGGAFPEIHVAQYPL*DM@GR.K
SW:SNW1_HUMAN	S08	4924	2	1555.7	(+0.8)	3.307	0.457	0.982	1	R.YTPSQQGVAFNMSGAK.Q
SW:SNW1_HUMAN	S08	4920	2	1563.7	(-1.0)	2.493	0.378	0.495	1	R.YTPSQQGVAFNMSGAK#.Q
SW:SON_HUMAN	S01	6436	2	1355.5	(+0.3)	4.156	0.527	1.000	9	R.AGIEGPLLASDVGR.D
SW:SON_HUMAN	S01	6432	2	1367.5	(+0.1)	3.355	0.444	0.962	9	R.AGIEGPL*L*ASDVGR.D
SW:SON_HUMAN	S03	5865	2	1355.5	(+0.5)	4.599	0.538	1.000	9	R.AGIEGPLLASDVGR.D
SW:SON_HUMAN	S03	5869	2	1367.5	(+0.6)	3.515	0.502	1.000	9	R.AGIEGPL*L*ASDVGR.D
SW:SON_HUMAN	S04	5847	2	1355.5	(+0.6)	3.765	0.472	1.000	9	R.AGIEGPLLASDVGR.D
SW:SON_HUMAN	S04	5845	2	1367.5	(+0.2)	3.100	0.346	0.923	9	R.AGIEGPL*L*ASDVGR.D
SW:SON_HUMAN	S05	6622	2	1355.5	(+1.0)	2.528	0.465	0.972	9	R.AGIEGPLLASDVGR.D
SW:SON_HUMAN	S05	6620	2	1367.5	(-0.1)	2.347	0.288	0.729	9	R.AGIEGPL*L*ASDVGR.D
SW:SON_HUMAN	S06	6594	2	1367.5	(+0.2)	2.699	0.294	0.832	9	R.AGIEGPL*L*ASDVGR.D
SW:SON_HUMAN	S04	6355	2	1373.5	(+0.7)	2.524	0.364	0.946	8	K.ESDQTLAALLSPK.E
SW:SON_HUMAN	S05	6956	2	1632.8	(+0.5)	4.157	0.426	1.000	7	K.FDSEPSAVALLPTR.A
SW:SON_HUMAN	S04	6709	2	1858.2	(-0.6)	2.713	0.340	0.877	7	K.ILDSFAAAPVPTTTLV.LK.S
SW:SON_HUMAN	S04	6281	3	3146.5	(-1.0)	4.345	0.399	0.699	7	R.L*PEQPVDVPSEIADSSM@TRPQEL*PEL*PK#.T
SW:SON_HUMAN	S05	7916	3	3104.5	(+0.4)	4.721	0.472	0.993	7	R.LPEQPVDVPSEIADSSMTRPQELPEL.PK.T
SW:SON_HUMAN	S05	7578	3	3146.5	(-0.0)	4.669	0.402	0.921	7	R.L*PEQPVDVPSEIADSSM@TRPQEL*PEL*PK#.T
SW:SON_HUMAN	S03	5245	2	1235.3	(+1.0)	2.551	0.176	0.738	9	K.SGGATIEELTEK.C
SW:SON_HUMAN	S05	5612	2	1235.3	(+0.9)	2.789	0.442	0.977	9	K.SGGATIEELTEK.C
SW:SON_HUMAN	S05	5616	2	1249.3	(+0.3)	2.266	0.220	0.383	9	K.SGGATIEEL*TEK#.C
SW:SON_HUMAN	S07	7014	2	1632.8	(+0.7)	2.873	0.430	0.973	7	K.FDSEPSAVALLPTR.A
SW:SSRP_HUMAN	S07	6920	2	1206.4	(-0.7)	2.212	0.160	0.127		K.ASSGLLYPLER.G
SW:SSRP_HUMAN	S09	7098	2	1224.4	(-0.1)	2.332	0.334	0.844		K.ASSGL*L*YPL*ER.G
SW:SSRP_HUMAN	S11	6914	2	1206.4	(+0.9)	3.262	0.347	0.974		K.ASSGLLYPLER.G
SW:SSRP_HUMAN	S11	6922	2	1224.4	(+0.4)	2.303	0.393	0.950		K.ASSGL*L*YPL*ER.G
SW:SSRP_HUMAN	S06	6456	2	956.1	(+1.0)	2.494	0.217	0.754		K.GWNWGTVK#.F
SW:SSRP_HUMAN	S13	6800	2	956.1	(+0.9)	2.313	0.190	0.600		K.GWNWGTVK#.F
SW:SSRP_HUMAN	S06	6006	2	969.2	(+0.8)	2.571	0.346	0.964		K.IPYTTVL*R.L
SW:SSRP_HUMAN	S08	6222	2	969.2	(+0.8)	2.253	0.307	0.920		K.IPYTTVL*R.L
SW:SSRP_HUMAN	S09	6340	2	969.2	(+0.9)	2.378	0.382	0.964		K.IPYTTVL*R.L
SW:SSRP_HUMAN	S10	6250	2	969.2	(+0.8)	2.278	0.369	0.954		K.IPYTTVL*R.L
SW:SSRP_HUMAN	S17	6284	2	963.2	(+1.0)	2.229	0.243	0.850		K.IPYTTVLR.L
SW:SSRP_HUMAN	S07	7000	2	968.1	(+0.4)	2.587	0.196	0.782		K.L*FDFVNAK#.K
SW:SSRP_HUMAN	S09	7220	2	954.1	(+0.3)	2.321	0.224	0.676		K.LFDFVNAK.K
SW:SSRP_HUMAN	S10	7086	2	968.1	(+0.2)	2.622	0.359	0.862		K.L*FDFVNAK#.K
SW:SSRP_HUMAN	S11	7024	2	954.1	(-0.5)	2.398	0.309	0.841		K.LFDFVNAK.K
SW:SSRP_HUMAN	S06	4782	2	1412.6	(+0.6)	2.686	0.366	0.959		K.NM@SGSL*YEM@VSR.V
SW:SSRP_HUMAN	S07	4678	2	1412.6	(+0.7)	2.643	0.426	0.971		K.NM@SGSL*YEM@VSR.V
SW:SSRP_HUMAN	S07	4728	2	1412.6	(-0.6)	2.615	0.135	0.465		K.NM@SGSL*YEM@VSR.V
SW:SSRP_HUMAN	S06	6126	3	1370.5	(-0.4)	3.712	0.259	0.912		K.SDHDPGISITDLSK.K
SW:SSRP_HUMAN	S07	6200	2	1370.5	(+0.7)	2.607	0.331	0.936		K.SDHDPGISITDLSK.K
SW:SSRP_HUMAN	S07	6198	2	1384.5	(+0.7)	2.227	0.298	0.740		K.SDHDPGISITDL*SK#.K
SW:SSRP_HUMAN	S10	6374	2	1370.5	(+0.9)	2.322	0.333	0.906		K.SDHDPGISITDLSK.K
SW:SSRP_HUMAN	S16	6128	2	1370.5	(-0.2)	2.921	0.337	0.910		K.SDHDPGISITDLSK.K
SW:SSRP_HUMAN	S06	7336	2	1701.9	(+1.0)	3.940	0.492	1.000		K.VDNIQAGELTEGIWR.R
SW:SSRP_HUMAN	S06	7342	2	1707.9	(+0.9)	3.238	0.499	1.000		K.VDNIQAGEL*TEGIWR.R
SW:SSRP_HUMAN	S07	7444	2	1701.9	(+0.7)	3.920	0.447	1.000		K.VDNIQAGELTEGIWR.R
SW:SSRP_HUMAN	S18	7524	2	1701.9	(-0.0)	3.842	0.429	0.966		K.VDNIQAGELTEGIWR.R
SW:T150_HUMAN	S04	4941	3	2056.2	(+0.7)	4.525	0.505	1.000	3	K.ASESSKPWPDATYGTGSASR.A
SW:T150_HUMAN	S04	4917	3	2064.2	(+0.9)	4.280	0.435	0.989	3	K.ASESSK#PWPDATYGTGSASR.A
SW:T150_HUMAN	S07	5448	3	2056.2	(+0.6)	3.940	0.490	1.000	3	K.ASESSKPWPDATYGTGSASR.A
SW:T150_HUMAN	S07	5444	3	2064.2	(+0.3)	3.922	0.336	0.820	3	K.ASESSK#PWPDATYGTGSASR.A
SW:T150_HUMAN	S04	5115	2	1423.5	(+0.6)	2.845	0.446	0.980	1	R.EEEWDPEYTPK.S
SW:T150_HUMAN	S04	5131	2	985.2	(+0.9)	2.562	0.348	0.959	5	K.SPLQSVVVR.R
SW:T150_HUMAN	S04	5135	2	991.2	(+0.7)	2.379	0.150	0.634	5	K.SPL*QSVVVR.R
SW:T150_HUMAN	S05	5652	2	991.2	(+0.2)	2.429	0.169	0.532	5	K.SPL*QSVVVR.R
SW:T150_HUMAN	S07	5676	2	991.2	(+0.6)	2.349	0.261	0.882	5	K.SPL*QSVVVR.R
SW:T150_HUMAN	S08	5622	3	2064.2	(+0.6)	3.933	0.468	0.991	3	K.ASESSK#PWPDATYGTGSASR.A
SW:TBA1_HUMAN	S10	8150	2	1702.9	(+0.0)	4.831	0.478	1.000	5	R.AVFVDLEPTVIDEVR.T
SW:TBA1_HUMAN	S10	8160	2	1708.9	(-0.5)	3.852	0.430	1.000	5	R.AVFVDL*EPTVIDEVR.T
SW:TBA1_HUMAN	S11	8106	2	1702.9	(+0.7)	2.427	0.420	0.956	5	R.AVFVDLEPTVIDEVR.T

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:TBA1_HUMAN	S14	8312	2	1702.9	(-0.1)	2.904	0.302	0.865	5	R.AVFVDLEPTVIDEVR.T
SW:TBA1_HUMAN	S16	7972	2	1702.9	(+0.5)	4.174	0.495	1.000	5	R.AVFVDLEPTVIDEVR.T
SW:TBA1_HUMAN	S17	8176	3	1702.9	(+1.0)	4.382	0.442	0.970	5	R.AVFVDLEPTVIDEVR.T
SW:TBA1_HUMAN	S19	8186	2	1702.9	(+0.4)	3.636	0.451	0.983	5	R.AVFVDLEPTVIDEVR.T
SW:TBA1_HUMAN	S09	5910	2	1016.2	(+0.4)	2.998	0.275	0.952	13	K.DVNAAIATIK.T
SW:TBA1_HUMAN	S10	5828	2	1024.2	(-0.3)	2.606	0.148	0.404	13	K.DVNAAIATIK#.T
SW:TBA1_HUMAN	S10	5918	2	1016.2	(+1.0)	2.419	0.294	0.912	13	K.DVNAAIATIK.T
SW:TBA1_HUMAN	S11	5776	2	1016.2	(+0.8)	3.204	0.335	0.974	13	K.DVNAAIATIK.T
SW:TBA1_HUMAN	S12	5478	2	1016.2	(+0.9)	2.390	0.339	0.938	13	K.DVNAAIATIK.T
SW:TBA1_HUMAN	S15	5688	2	1016.2	(+0.0)	2.643	0.341	0.909	13	K.DVNAAIATIK.T
SW:TBA1_HUMAN	S16	5508	2	1016.2	(+0.7)	2.747	0.246	0.917	13	K.DVNAAIATIK.T
SW:TBA1_HUMAN	S17	5948	2	1016.2	(+0.9)	3.376	0.284	0.969	13	K.DVNAAIATIK.T
SW:TBA1_HUMAN	S17	5958	2	1024.2	(-0.0)	2.532	0.104	0.248	13	K.DVNAAIATIK#.T
SW:TBA1_HUMAN	S10	7816	2	1086.3	(-0.5)	2.987	0.357	0.947	5	K.EIIDLVLDLDR.I
SW:TBA1_HUMAN	S10	7798	2	1086.3	(+0.8)	2.252	0.301	0.903	5	K.EIIDLVLDLDR.I
SW:TBA1_HUMAN	S11	7760	2	1086.3	(+0.5)	2.310	0.268	0.882	5	K.EIIDLVLDLDR.I
SW:TBA1_HUMAN	S12	7562	2	1086.3	(+0.5)	2.280	0.374	0.950	5	K.EIIDLVLDLDR.I
SW:TBA1_HUMAN	S13	7922	2	1086.3	(+0.6)	2.223	0.292	0.890	5	K.EIIDLVLDLDR.I
SW:TBA1_HUMAN	S10	7930	2	1758.1	(+0.9)	3.123	0.535	1.000	15	R.IHFPLATYAPVISAEEK.A
SW:TBA1_HUMAN	S10	10068	2	1488.8	(+0.8)	3.844	0.513	1.000	9	R.LISQIVSSITASLR.F
SW:TBA1_HUMAN	S10	10166	2	1488.8	(+0.9)	3.799	0.513	1.000	9	R.LISQIVSSITASLR.F
SW:TBA1_HUMAN	S10	10332	2	1488.8	(+0.4)	3.227	0.461	0.983	9	R.LISQIVSSITASLR.F
SW:TBA1_HUMAN	S10	10088	2	1500.8	(+0.7)	3.160	0.583	1.000	9	R.L*ISQIVSSITASL*R.F
SW:TBA1_HUMAN	S10	10440	2	1488.8	(-0.1)	2.939	0.454	0.954	9	R.LISQIVSSITASLR.F
SW:TBA1_HUMAN	S10	10186	2	1500.8	(+0.6)	2.928	0.508	0.983	9	R.L*ISQIVSSITASL*R.F
SW:TBA1_HUMAN	S14	9766	2	1488.8	(+0.2)	3.341	0.454	0.963	9	R.LISQIVSSITASLR.F
SW:TBA1_HUMAN	S15	9362	2	1488.8	(+1.0)	3.524	0.523	1.000	9	R.LISQIVSSITASLR.F
SW:TBA1_HUMAN	S16	9348	2	1488.8	(+0.5)	3.470	0.471	1.000	9	R.LISQIVSSITASLR.F
SW:TBA1_HUMAN	S10	6330	2	1731.9	(-0.4)	2.497	0.215	0.034	16	R.NL*DIERPTYTNL*NR.L
SW:TBA1_HUMAN	S10	7612	2	2017.1	(-0.7)	3.662	0.426	0.771	10	K.TIGGGDDSFNTFFSETGAGK#.H
SW:TBA1_HUMAN	S10	7608	2	2009.1	(-0.6)	2.512	0.446	0.924	10	K.TIGGGDDSFNTFFSETGAGK.H
SW:TBA1_HUMAN	S14	7750	2	2009.1	(+0.9)	3.726	0.552	1.000	10	K.TIGGGDDSFNTFFSETGAGK.H
SW:TBA1_HUMAN	S16	7452	2	2009.1	(-0.9)	3.563	0.423	0.864	10	K.TIGGGDDSFNTFFSETGAGK.H
SW:TBA1_HUMAN	S18	7654	2	2009.1	(+0.7)	4.001	0.605	1.000	10	K.TIGGGDDSFNTFFSETGAGK.H
SW:TBA1_HUMAN	S10	6886	2	1826.1	(+0.8)	3.500	0.538	1.000	19	K.VGINYQPPTVPPGGDLAK.V
SW:TBA1_HUMAN	S11	6834	2	1826.1	(+0.3)	2.306	0.280	0.679	19	K.VGINYQPPTVPPGGDLAK.V
SW:TBA1_HUMAN	S15	6778	2	1826.1	(-0.4)	2.804	0.462	0.950	19	K.VGINYQPPTVPPGGDLAK.V
SW:TBA1_HUMAN	S17	6988	2	1826.1	(+0.8)	3.593	0.542	1.000	19	K.VGINYQPPTVPPGGDLAK.V
SW:TBA1_HUMAN	S20	7144	2	2009.1	(-0.5)	3.250	0.505	1.000	10	K.TIGGGDDSFNTFFSETGAGK.H
SW:TBB1_HUMAN	S10	7530	2	1628.9	(+0.3)	2.340	0.190*	0.040	13	R.AIL*VDL*EPGTMDSVR.S
SW:TBB1_HUMAN	S10	5450	2	1447.6	(-0.1)	3.056	0.200	0.793	16	K.EVDEQMLNVQNK.N
SW:TBB1_HUMAN	S10	2016	2	1477.6	(+0.5)	2.880	0.336	0.920	16	K.EVDEQM@L*NVQNK#.N
SW:TBB1_HUMAN	S10	6286	2	1131.3	(+0.7)	2.811	0.330	0.961	32	R.FPGQLNADLR.K
SW:TBB1_HUMAN	S10	6446	2	1131.3	(+1.0)	2.701	0.347	0.961	32	R.FPGQLNADLR.K
SW:TBB1_HUMAN	S15	6210	2	1131.3	(+0.8)	2.804	0.333	0.946	32	R.FPGQLNADLR.K
SW:TBB1_HUMAN	S10	9308	2	1972.2	(-0.1)	2.645	0.301	0.820	19	K.GHYTEGAEL*VDSVL*DVVR.K
SW:TBB1_HUMAN	S10	9412	2	1972.2	(-0.8)	2.497	0.352	0.609	19	K.GHYTEGAEL*VDSVL*DVVR.K
SW:TBB1_HUMAN	S10	6806	2	1320.6	(-0.6)	2.220	0.348	0.824	17	R.IMNTFSVVPSPK.V
SW:TBB1_HUMAN	S10	6348	2	1344.6	(+0.3)	2.206	0.157	0.190	17	R.IM@NTFSVVPSPK#.V
SW:TBB1_HUMAN	S10	5410	2	1302.4	(+0.9)	2.783	0.385	0.966	4	R.ISVYYNEATGGK.Y
SW:TBB1_HUMAN	S10	5404	2	1310.4	(+0.1)	2.438	0.428	0.864	4	R.ISVYYNEATGGK#.Y
SW:TBB1_HUMAN	S14	5300	2	1302.4	(+0.8)	3.281	0.408	0.969	4	R.ISVYYNEATGGK.Y
SW:TBB1_HUMAN	S19	5122	2	1310.4	(-0.0)	2.242	0.409	0.809	4	R.ISVYYNEATGGK#.Y
SW:TBB1_HUMAN	S10	6730	2	1166.4	(+0.6)	2.631	0.421	0.974	31	K.L*AVNM@VPFPR.L
SW:TBB1_HUMAN	S10	7984	2	1649.9	(-0.9)	3.015	0.380	0.786	20	R.L*HFFM@PGFAPL*TSR.G
SW:TBB1_HUMAN	S10	8802	2	1621.9	(+1.0)	2.841	0.586	1.000	20	R.LHFFMPGFAPLTSR.G
SW:TBB1_HUMAN	S10	7934	2	1705.9	(-0.5)	2.614	0.332	0.760	26	K.NSSYFVEWIPNNVK#.T
SW:TBB1_HUMAN	S10	8836	3	2808.1	(+0.7)	7.145	0.564	1.000	13	R.SGPFQIFRPDNFVFGQSGAGNNWAK#.G
SW:TBB1_HUMAN	S10	8760	3	2808.1	(+0.7)	5.813	0.560	0.978	13	R.SGPFQIFRPDNFVFGQSGAGNNWAK#.G
SW:TBB1_HUMAN	S10	8730	3	2800.1	(+0.1)	4.150	0.465	0.970	13	R.SGPFQIFRPDNFVFGQSGAGNNWAK.G
SW:TBB1_HUMAN	S13	8736	3	2800.1	(+0.9)	4.487	0.484	0.997	13	R.SGPFQIFRPDNFVFGQSGAGNNWAK.G
SW:TBB1_HUMAN	S20	8130	3	2800.1	(+0.8)	3.828	0.477	0.989	13	R.SGPFQIFRPDNFVFGQSGAGNNWAK.G
SW:TBB1_HUMAN	S20	4762	2	1302.4	(+0.2)	2.440	0.360	0.881	4	R.ISVYYNEATGGK.Y
SW:TBL3_HUMAN	S06	7688	3	1696.9	(+0.9)	4.163	0.422	0.998	2	K.SPGLYFLTAGDQGLR.V

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:TBL3_HUMAN	S06	5966	2	1362.5	(+0.8)	2.341	0.416	0.952	2	R.GTQLLSGSDGLVK.L
SW:TCP4_HUMAN	S18	7740	2	1500.7	(-0.4)	3.228	0.276	0.895	2	K.GISLNPEQWSQLK.E
SW:TCP4_HUMAN	S18	7472	2	1628.9	(+0.6)	2.866	0.486	0.981	2	R.KGISLNPEQWSQLK.E
SW:TCP4_HUMAN	S18	7722	2	1500.7	(+1.0)	2.604	0.365	0.951	2	K.GISLNPEQWSQLK.E
SW:THO4_HUMAN	S14	7218	2	1211.4	(+0.1)	2.937	0.366*	0.158		K.M@DMSL*DDIHK#.L
SW:THO4_HUMAN	S14	7070	3	2036.2	(+0.9)	4.846	0.520	1.000	1	K.QQLSAEELDAQLDAYNAR.M
SW:THO4_HUMAN	S14	7080	2	2036.2	(+0.8)	3.759	0.531	1.000	1	K.QQLSAEELDAQLDAYNAR.M
SW:THO4_HUMAN	S14	5640	2	1238.3	(+0.5)	3.621	0.528	1.000		R.SL*GTADVHFER.K
SW:THO4_HUMAN	S14	5638	2	1232.3	(+1.0)	2.992	0.377	0.974		R.SLGTADVHFER.K
SW:THO4_HUMAN	S15	5698	2	1238.3	(+0.3)	2.851	0.448	0.957		R.SL*GTADVHFER.K
SW:THO4_HUMAN	S15	5780	2	1238.3	(+0.3)	2.618	0.553	1.000		R.SL*GTADVHFER.K
SW:THPA_HUMAN	S09	6450	3	2571.7	(+0.2)	5.160	0.627	0.998	7	K.GPPDFSSDEEREPTVLGSGAAAAGR.S
SW:THPA_HUMAN	S10	6354	3	2571.7	(+0.1)	4.539	0.570	1.000	7	K.GPPDFSSDEEREPTVLGSGAAAAGR.S
SW:THPA_HUMAN	S14	6298	3	2577.7	(+0.1)	4.035	0.399	0.915	7	K.GPPDFSSDEEREPTVL*GSGAAAAGR.S
SW:THPA_HUMAN	S09	1754	2	1252.4	(+0.1)	2.934	0.343	0.213	7	R.NRPPLPAGTNSK.G
SW:THPA_HUMAN	S09	1740	2	1266.4	(-0.7)	2.363	0.335	0.016	7	R.NRPPL*PAGTNSK#.G
SW:THPA_HUMAN	S01	6678	2	1375.6	(+0.4)	3.440	0.384	0.980	1	-.PEFLEDPSVLTK.D
SW:THPA_HUMAN	S10	7068	2	1375.6	(+0.9)	4.018	0.321	0.980	1	-.PEFLEDPSVLTK.D
SW:THPA_HUMAN	S14	7134	2	1375.6	(+0.0)	4.543	0.425	1.000	1	-.PEFLEDPSVLTK.D
SW:THPA_HUMAN	S09	6188	2	1710.9	(-0.3)	2.973	0.410	0.940	7	K.SEL*VANNVTL*PAGEQR.K
SW:THPA_HUMAN	S09	6162	2	1698.9	(-0.5)	2.863	0.334	0.890	7	K.SELVANNVTLPAGEQR.K
SW:THPA_HUMAN	S10	6080	2	1698.9	(-0.5)	2.550	0.321	0.829	7	K.SELVANNVTLPAGEQR.K
SW:THPA_HUMAN	S09	5842	2	1654.8	(+0.7)	3.151	0.412	0.976	7	R.SSTPL*PTISSAENTR.Q
SW:THPA_HUMAN	S10	5764	2	1654.8	(+0.0)	2.975	0.268	0.835	7	R.SSTPL*PTISSAENTR.Q
SW:THPA_HUMAN	S10	5758	2	1648.8	(-0.4)	2.605	0.366	0.887	7	R.SSTPLPTISSAENTR.Q
SW:THPA_HUMAN	S12	5414	2	1648.8	(-0.3)	2.759	0.416	0.932	7	R.SSTPLPTISSAENTR.Q
SW:THPA_HUMAN	S14	7138	2	1395.6	(-0.1)	3.087	0.444	0.924	1	-.PEFL*EDPSVL*TK#.D
SW:TOP1_HUMAN	S05	6654	2	1121.3	(-0.3)	2.950	0.363	0.891	4	K.AEEVATFFAK#.M
SW:TOP1_HUMAN	S08	6804	2	1113.3	(+1.0)	2.816	0.468	0.982	4	K.AEEVATFFAK.M
SW:TOP1_HUMAN	S10	6794	2	1121.3	(+0.6)	2.972	0.426	0.963	4	K.AEEVATFFAK#.M
SW:TOP1_HUMAN	S10	7288	2	1755.0	(+1.0)	3.450	0.377	0.975	4	K.GPVFAPPYEPLPENVK.F
SW:TOP1_HUMAN	S05	7260	2	1356.6	(-0.0)	2.599	0.372	0.910	6	K.HLQDLMEGLTAK.V
SW:TOP1_HUMAN	S05	1778	2	1446.5	(-0.3)	3.549	0.299	0.145	7	K.L*EVQATDREENK#.Q
SW:TOP1_HUMAN	S05	1676	2	1168.3	(-0.4)	2.251	0.307	0.695	7	K.M@L*DHEYTTK#.E
SW:TOP1_HUMAN	S10	7276	2	1769.0	(-0.5)	2.389	0.321	0.628	4	K.GPVFAPPYEPL*PENVK#.F
SW:TP2A_HUMAN	S05	6562	2	1109.3	(+0.6)	2.775	0.336	0.391	6	R.DK#YGVFPL*R.G
SW:TP2A_HUMAN	S05	6558	2	1095.3	(+0.9)	2.420	0.317	0.253	6	R.DKYGVFPLR.G
SW:TP2A_HUMAN	S06	6496	2	1095.3	(+0.8)	2.735	0.343	0.392	6	R.DKYGVFPLR.G
SW:TP2A_HUMAN	S06	6514	2	1109.3	(+0.7)	2.343	0.316	0.228	6	R.DK#YGVFPL*R.G
SW:TP2A_HUMAN	S07	6592	2	1095.3	(+0.5)	2.235	0.265	0.125	6	R.DKYGVFPLR.G
SW:TP2A_HUMAN	S08	6722	2	1109.3	(+0.1)	2.716	0.368	0.255	6	R.DK#YGVFPL*R.G
SW:TP2A_HUMAN	S08	6750	2	1095.3	(+0.4)	2.633	0.402	0.460	6	R.DKYGVFPLR.G
SW:TP2A_HUMAN	S04	1865	2	1624.8	(+0.9)	3.173	0.464	0.551	3	R.DPALNSGVSQKPDPAK.T
SW:TP2A_HUMAN	S05	1966	2	1624.8	(+0.8)	3.945	0.485	1.000	3	R.DPALNSGVSQKPDPAK.T
SW:TP2A_HUMAN	S05	1974	2	1646.8	(+0.8)	2.765	0.537	0.404	3	R.DPAL*NSGVSQK#PDKPAK#.T
SW:TP2A_HUMAN	S07	1822	2	1646.8	(-0.0)	2.212	0.244	0.013	3	R.DPAL*NSGVSQK#PDKPAK#.T
SW:TP2A_HUMAN	S04	7799	2	1808.0	(-0.4)	2.440	0.144	0.331	3	K.EDLATFIEELEAVEAK.E
SW:TP2A_HUMAN	S05	9630	2	1808.0	(+0.4)	3.219	0.555	1.000	3	K.EDLATFIEELEAVEAK.E
SW:TP2A_HUMAN	S06	9588	3	1828.0	(-0.4)	3.822	0.389	0.983	3	K.EDL*ATFIEEL*EAVEAK#.E
SW:TP2A_HUMAN	S06	9578	2	1828.0	(+0.0)	2.717	0.396	0.851	3	K.EDL*ATFIEEL*EAVEAK#.E
SW:TP2A_HUMAN	S08	9848	2	1808.0	(+0.8)	4.063	0.565	1.000	3	K.EDLATFIEELEAVEAK.E
SW:TP2A_HUMAN	S09	9870	2	1828.0	(-0.2)	3.296	0.371	0.887	3	K.EDL*ATFIEEL*EAVEAK#.E
SW:TP2A_HUMAN	S11	9756	2	1828.0	(-0.4)	2.444	0.264	0.531	3	K.EDL*ATFIEEL*EAVEAK#.E
SW:TP2A_HUMAN	S12	9492	3	1828.0	(+0.8)	4.256	0.427	0.998	3	K.EDL*ATFIEEL*EAVEAK#.E
SW:TP2A_HUMAN	S12	9502	2	1828.0	(-0.0)	2.710	0.299	0.710	3	K.EDL*ATFIEEL*EAVEAK#.E
SW:TP2A_HUMAN	S15	9648	2	1828.0	(-0.3)	2.209	0.443	0.818	3	K.EDL*ATFIEEL*EAVEAK#.E
SW:TP2A_HUMAN	S16	9612	2	1808.0	(+0.7)	2.280	0.413	0.944	3	K.EDLATFIEELEAVEAK.E
SW:TP2A_HUMAN	S04	1967	2	1328.5	(+0.1)	2.703	0.491	0.353	3	K.EKQDEQVGLPGK.G
SW:TP2A_HUMAN	S05	2056	2	1350.5	(+0.8)	2.261	0.370	0.135	3	K.EK#QDEQVGL*PGK#.G
SW:TP2A_HUMAN	S06	1918	2	1350.5	(-0.5)	2.285	0.213	0.014	3	K.EK#QDEQVGL*PGK#.G
SW:TP2A_HUMAN	S09	1908	2	1328.5	(+0.5)	3.135	0.354	0.434	3	K.EKQDEQVGLPGK.G

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:TP2A_HUMAN	S09	1922	2	1350.5	(+0.9)	2.842	0.424	0.318	3	K.EK#QDEQVGL*PGK#.G
SW:TP2A_HUMAN	S10	2008	2	1328.5	(-0.6)	2.240	0.175	0.015	3	K.EKQDEQVGLPGK.G
SW:TP2A_HUMAN	S11	1870	2	1328.5	(+0.6)	2.549	0.422	0.410	3	K.EKQDEQVGLPGK.G
SW:TP2A_HUMAN	S01	6682	2	1449.5	(-0.2)	2.891	0.388	0.939	7	K.EL*IL*FSNSDNER.S
SW:TP2A_HUMAN	S03	6047	2	1449.5	(+0.5)	3.323	0.438	0.983	7	K.EL*IL*FSNSDNER.S
SW:TP2A_HUMAN	S04	6043	2	1437.5	(+0.9)	3.009	0.454	0.981	7	K.ELILFSNSDNER.S
SW:TP2A_HUMAN	S04	6041	2	1449.5	(+0.0)	2.667	0.333	0.888	7	K.EL*IL*FSNSDNER.S
SW:TP2A_HUMAN	S05	6928	2	1437.5	(-0.3)	2.324	0.261	0.694	7	K.ELILFSNSDNER.S
SW:TP2A_HUMAN	S08	7080	2	1449.5	(-0.1)	2.626	0.257	0.786	7	K.EL*IL*FSNSDNER.S
SW:TP2A_HUMAN	S09	7164	2	1449.5	(-0.3)	2.722	0.283	0.846	7	K.EL*IL*FSNSDNER.S
SW:TP2A_HUMAN	S10	7058	2	1437.5	(-0.4)	2.923	0.411	0.948	7	K.ELILFSNSDNER.S
SW:TP2A_HUMAN	S10	7054	2	1449.5	(-0.1)	2.258	0.222	0.555	7	K.EL*IL*FSNSDNER.S
SW:TP2A_HUMAN	S11	6982	2	1449.5	(+0.2)	3.084	0.349	0.934	7	K.EL*IL*FSNSDNER.S
SW:TP2A_HUMAN	S12	6768	2	1437.5	(+0.8)	2.427	0.461	0.972	7	K.ELILFSNSDNER.S
SW:TP2A_HUMAN	S12	6766	2	1449.5	(+0.3)	2.375	0.332	0.838	7	K.EL*IL*FSNSDNER.S
SW:TP2A_HUMAN	S14	7114	2	1437.5	(+0.7)	4.151	0.456	0.991	7	K.ELILFSNSDNER.S
SW:TP2A_HUMAN	S14	7112	2	1449.5	(+0.2)	3.243	0.398	0.955	7	K.EL*IL*FSNSDNER.S
SW:TP2A_HUMAN	S15	6934	2	1449.5	(+0.2)	2.219	0.304	0.748	7	K.EL*IL*FSNSDNER.S
SW:TP2A_HUMAN	S16	6860	2	1449.5	(+0.2)	2.807	0.290	0.867	7	K.EL*IL*FSNSDNER.S
SW:TP2A_HUMAN	S17	7152	2	1437.5	(+0.5)	3.070	0.392	0.976	7	K.ELILFSNSDNER.S
SW:TP2A_HUMAN	S05	5340	2	1524.7	(-0.0)	2.351	0.187	0.307	3	K.EQVL*EPM@*NGTEK#.T
SW:TP2A_HUMAN	S16	8476	2	1405.7	(+1.0)	2.448	0.449	0.968	3	K.EWLLGMLGAESAK.L
SW:TP2A_HUMAN	S17	8640	2	1405.7	(+0.5)	2.543	0.473	0.975	3	K.EWLLGMLGAESAK.L
SW:TP2A_HUMAN	S04	6881	2	1350.6	(+0.5)	3.010	0.424	0.957	3	R.FL*EEFITPIVK#.V
SW:TP2A_HUMAN	S06	8178	2	1336.6	(+0.9)	2.483	0.381	0.957	3	R.FLEEFITPIVK.V
SW:TP2A_HUMAN	S13	8416	2	1350.6	(+0.6)	3.372	0.363	0.958	3	R.FL*EEFITPIVK#.V
SW:TP2A_HUMAN	S13	8410	2	1336.6	(+1.0)	3.290	0.447	1.000	3	R.FLEEFITPIVK.V
SW:TP2A_HUMAN	S14	8524	2	1350.6	(+0.2)	3.417	0.324	0.876	3	R.FL*EEFITPIVK#.V
SW:TP2A_HUMAN	S14	8534	2	1336.6	(-0.9)	2.281	0.304	0.487	3	R.FLEEFITPIVK.V
SW:TP2A_HUMAN	S16	8142	2	1336.6	(+0.6)	2.433	0.343	0.938	3	R.FLEEFITPIVK.V
SW:TP2A_HUMAN	S12	7228	2	1627.8	(+0.0)	2.420	0.303	0.769	6	K.GFQQISFVNSIATSK.G
SW:TP2A_HUMAN	S01	5546	2	1388.6	(+0.2)	3.760	0.623	1.000	5	R.HVDYVADQIVTK.L
SW:TP2A_HUMAN	S01	5552	2	1396.6	(+0.7)	3.708	0.626	1.000	5	R.HVDYVADQIVTK#.L
SW:TP2A_HUMAN	S03	5271	2	1396.6	(+0.8)	4.260	0.596	1.000	5	R.HVDYVADQIVTK#.L
SW:TP2A_HUMAN	S03	5267	2	1388.6	(+0.9)	4.245	0.602	1.000	5	R.HVDYVADQIVTK.L
SW:TP2A_HUMAN	S04	5161	2	1396.6	(+0.1)	4.309	0.603	1.000	5	R.HVDYVADQIVTK#.L
SW:TP2A_HUMAN	S04	5147	2	1388.6	(+0.9)	4.183	0.479	1.000	5	R.HVDYVADQIVTK.L
SW:TP2A_HUMAN	S04	5167	2	1388.6	(-0.5)	3.633	0.546	1.000	5	R.HVDYVADQIVTK.L
SW:TP2A_HUMAN	S05	5696	2	1396.6	(-0.5)	3.392	0.412	0.926	5	R.HVDYVADQIVTK#.L
SW:TP2A_HUMAN	S05	5664	2	1396.6	(+1.0)	2.566	0.409	0.933	5	R.HVDYVADQIVTK#.L
SW:TP2A_HUMAN	S07	5726	2	1396.6	(-0.0)	3.991	0.486	1.000	5	R.HVDYVADQIVTK#.L
SW:TP2A_HUMAN	S07	5708	2	1388.6	(+0.0)	3.861	0.576	1.000	5	R.HVDYVADQIVTK.L
SW:TP2A_HUMAN	S08	5872	2	1388.6	(-0.1)	3.481	0.528	1.000	5	R.HVDYVADQIVTK.L
SW:TP2A_HUMAN	S09	6012	2	1396.6	(+0.9)	3.732	0.518	1.000	5	R.HVDYVADQIVTK#.L
SW:TP2A_HUMAN	S10	5884	2	1396.6	(-0.1)	3.423	0.409	0.926	5	R.HVDYVADQIVTK#.L
SW:TP2A_HUMAN	S10	5878	2	1388.6	(-0.1)	2.719	0.487	0.959	5	R.HVDYVADQIVTK.L
SW:TP2A_HUMAN	S11	5804	2	1396.6	(+0.0)	3.885	0.411	1.000	5	R.HVDYVADQIVTK#.L
SW:TP2A_HUMAN	S12	5504	2	1388.6	(+0.6)	4.141	0.584	1.000	5	R.HVDYVADQIVTK.L
SW:TP2A_HUMAN	S12	5518	2	1396.6	(-0.2)	3.947	0.465	1.000	5	R.HVDYVADQIVTK#.L
SW:TP2A_HUMAN	S15	5702	2	1388.6	(-0.1)	4.027	0.563	1.000	5	R.HVDYVADQIVTK.L
SW:TP2A_HUMAN	S15	5712	2	1396.6	(-0.0)	3.895	0.508	1.000	5	R.HVDYVADQIVTK#.L
SW:TP2A_HUMAN	S16	5538	2	1388.6	(+0.5)	3.912	0.560	1.000	5	R.HVDYVADQIVTK.L
SW:TP2A_HUMAN	S17	5966	2	1388.6	(+0.1)	3.873	0.573	1.000	5	R.HVDYVADQIVTK.L
SW:TP2A_HUMAN	S19	5584	2	1396.6	(-0.0)	3.320	0.474	1.000	5	R.HVDYVADQIVTK#.L
SW:TP2A_HUMAN	S20	5336	2	1388.6	(+0.7)	4.393	0.567	1.000	5	R.HVDYVADQIVTK.L
SW:TP2A_HUMAN	S20	5342	2	1396.6	(+0.6)	4.339	0.612	1.000	5	R.HVDYVADQIVTK#.L
SW:TP2A_HUMAN	S05	7322	2	1462.6	(+0.9)	2.608	0.397	0.962	9	K.IFDEILVNAADNK.Q
SW:TP2A_HUMAN	S08	7374	3	1476.6	(+0.4)	3.878	0.216	0.831	9	K.IFDEIL*VNAADNK#.Q
SW:TP2A_HUMAN	S13	7424	2	1462.6	(-0.1)	3.004	0.383	0.939	9	K.IFDEILVNAADNK.Q
SW:TP2A_HUMAN	S14	7426	2	1462.6	(+0.9)	2.624	0.389	0.960	9	K.IFDEILVNAADNK.Q
SW:TP2A_HUMAN	S14	7446	2	1476.6	(-0.3)	2.407	0.263	0.553	9	K.IFDEIL*VNAADNK#.Q
SW:TP2A_HUMAN	S15	7192	2	1462.6	(+0.1)	3.029	0.427	0.953	9	K.IFDEILVNAADNK.Q
SW:TP2A_HUMAN	S16	7148	2	1462.6	(+0.8)	2.492	0.380	0.950	9	K.IFDEILVNAADNK.Q
SW:TP2A_HUMAN	S01	5898	3	2287.4	(+0.6)	4.344	0.448	0.990	3	K.IKNENTEGSPQEDGVELEGLK.Q
SW:TP2A_HUMAN	S03	5473	3	2315.4	(+0.1)	4.291	0.476	1.000	3	K.IK#NENTEGSPQEDGVEL*EGL*K#.Q
SW:TP2A_HUMAN	S04	5403	3	2287.4	(+0.8)	5.058	0.481	1.000	3	K.IKNENTEGSPQEDGVELEGLK.Q



Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:TP2A_HUMAN	S04	5405	3	2315.4	(-0.5)	4.036	0.339	0.756	3	K.IK#NENTEGSPQEDGVEL*EGL*K#.Q
SW:TP2A_HUMAN	S05	5994	3	2287.4	(+0.8)	5.151	0.487	1.000	3	K.IKNENTEGSPQEDGVELEGLK.Q
SW:TP2A_HUMAN	S05	5890	3	2287.4	(+0.5)	4.114	0.483	0.986	3	K.IKNENTEGSPQEDGVELEGLK.Q
SW:TP2A_HUMAN	S06	5950	3	2287.4	(+0.7)	5.041	0.511	1.000	3	K.IKNENTEGSPQEDGVELEGLK.Q
SW:TP2A_HUMAN	S06	5952	3	2315.4	(-0.0)	4.624	0.380	0.908	3	K.IK#NENTEGSPQEDGVEL*EGL*K#.Q
SW:TP2A_HUMAN	S08	6188	3	2287.4	(+0.7)	5.138	0.421	0.991	3	K.IKNENTEGSPQEDGVELEGLK.Q
SW:TP2A_HUMAN	S08	6190	3	2315.4	(-0.3)	4.062	0.439	0.939	3	K.IK#NENTEGSPQEDGVEL*EGL*K#.Q
SW:TP2A_HUMAN	S09	6318	3	2315.4	(-0.7)	4.507	0.442	0.847	3	K.IK#NENTEGSPQEDGVEL*EGL*K#.Q
SW:TP2A_HUMAN	S10	6212	3	2287.4	(+1.0)	4.708	0.543	0.996	3	K.IKNENTEGSPQEDGVELEGLK.Q
SW:TP2A_HUMAN	S11	6112	3	2287.4	(+0.7)	4.361	0.515	1.000	3	K.IKNENTEGSPQEDGVELEGLK.Q
SW:TP2A_HUMAN	S05	4142	2	1773.0	(-0.8)	2.255	0.276	0.192	7	K.IM@IM@TDQDQDGSNIK#.G
SW:TP2A_HUMAN	S05	4018	2	1773.0	(+0.6)	2.246	0.326	0.776	7	K.IM@IM@TDQDQDGSNIK#.G
SW:TP2A_HUMAN	S06	2150	2	1773.0	(+0.4)	2.763	0.484	0.958	7	K.IM@IM@TDQDQDGSNIK#.G
SW:TP2A_HUMAN	S07	2184	2	1773.0	(+0.2)	2.267	0.298	0.548	7	K.IM@IM@TDQDQDGSNIK#.G
SW:TP2A_HUMAN	S12	7968	2	1533.8	(+0.1)	3.383	0.484	1.000	3	R.KEWLLGMLGAESAK.L
SW:TP2A_HUMAN	S13	8304	2	1533.8	(+0.7)	2.614	0.516	0.980	3	R.KEWLLGMLGAESAK.L
SW:TP2A_HUMAN	S06	7586	2	1469.7	(-0.3)	2.881	0.335	0.919	7	R.KEWLTNFMEDR.R
SW:TP2A_HUMAN	S06	6568	2	1499.7	(-0.5)	2.347	0.110	0.282	7	R.K#EWL*TNFM@EDR.R
SW:TP2A_HUMAN	S06	7592	2	1483.7	(+0.8)	2.270	0.282	0.862	7	R.K#EWL*TNFMEDR.R
SW:TP2A_HUMAN	S08	6784	2	1499.7	(-0.1)	2.264	0.229	0.606	7	R.K#EWL*TNFM@EDR.R
SW:TP2A_HUMAN	S13	7712	2	1469.7	(+0.8)	2.612	0.245	0.838	7	R.KEWLTNFMEDR.R
SW:TP2A_HUMAN	S15	7478	2	1469.7	(+0.6)	2.770	0.281	0.933	7	R.KEWLTNFMEDR.R
SW:TP2A_HUMAN	S18	7644	2	1469.7	(+0.9)	2.205	0.404	0.947	7	R.KEWLTNFMEDR.R
SW:TP2A_HUMAN	S05	7990	2	1236.5	(+0.9)	2.555	0.424	0.973	3	K.KYDTVLDILR.D
SW:TP2A_HUMAN	S09	7932	2	1236.5	(+0.2)	2.569	0.348	0.906	3	K.KYDTVLDILR.D
SW:TP2A_HUMAN	S16	7588	2	1236.5	(+0.8)	3.043	0.404	0.980	3	K.KYDTVLDILR.D
SW:TP2A_HUMAN	S17	7824	2	1236.5	(+0.3)	2.232	0.388	0.891	3	K.KYDTVLDILR.D
SW:TP2A_HUMAN	S05	7696	2	1721.0	(+0.5)	3.050	0.573	1.000	3	R.LMDGEEPLPMLPSYK.N
SW:TP2A_HUMAN	S06	6638	2	1779.0	(-0.7)	2.493	0.323	0.372	3	R.L*M@DGEEPL*PM@L*PSYK#.N
SW:TP2A_HUMAN	S05	9286	3	2562.8	(+0.5)	4.308	0.433	0.994	5	K.M@YVPAL*IFGQL*L*TSSNYDDDEK#.K
SW:TP2A_HUMAN	S06	9230	3	2562.8	(-0.1)	3.932	0.381	0.975	5	K.M@YVPAL*IFGQL*L*TSSNYDDDEK#.K
SW:TP2A_HUMAN	S08	9522	3	2562.8	(+0.3)	3.761	0.343	0.942	5	K.M@YVPAL*IFGQL*L*TSSNYDDDEK#.K
SW:TP2A_HUMAN	S06	8196	2	1965.2	(-0.9)	2.234	0.192	0.073	3	K.QEM@AFYSL*PEFEFEWK#.S
SW:TP2A_HUMAN	S04	5675	2	1554.8	(+0.5)	2.849	0.306	0.888	7	K.QIM@ENAEINNIK#.I
SW:TP2A_HUMAN	S15	6460	2	1554.8	(+0.8)	2.309	0.123	0.268	7	K.QIM@ENAEINNIK#.I
SW:TP2A_HUMAN	S06	1804	2	1781.0	(+0.9)	2.450	0.450	0.391	3	K.RDPALNSGVSQKPDPAK.T
SW:TP2A_HUMAN	S16	5246	2	832.9	(+0.7)	2.208	0.208	0.781	8	K.SPSDLWK.E
SW:TP2A_HUMAN	S01	6084	2	1277.4	(+1.0)	3.734	0.499	1.000	3	K.SVVSLEADDVK.G
SW:TP2A_HUMAN	S03	5603	2	1277.4	(+0.8)	3.701	0.532	1.000	3	K.SVVSLEADDVK.G
SW:TP2A_HUMAN	S03	5605	2	1291.4	(-0.7)	2.461	0.372	0.523	3	K.SVVSLEADDVK#.G
SW:TP2A_HUMAN	S04	5563	2	1277.4	(+0.9)	2.758	0.568	1.000	3	K.SVVSLEADDVK.G
SW:TP2A_HUMAN	S04	5559	2	1291.4	(-0.2)	2.548	0.291	0.697	3	K.SVVSLEADDVK#.G
SW:TP2A_HUMAN	S07	6260	2	1277.4	(+1.0)	3.742	0.518	1.000	3	K.SVVSLEADDVK.G
SW:TP2A_HUMAN	S07	6288	2	1277.4	(-0.3)	3.331	0.453	1.000	3	K.SVVSLEADDVK.G
SW:TP2A_HUMAN	S07	6278	2	1291.4	(-0.8)	2.680	0.265	0.359	3	K.SVVSLEADDVK#.G
SW:TP2A_HUMAN	S08	6412	2	1277.4	(+0.4)	3.759	0.555	1.000	3	K.SVVSLEADDVK.G
SW:TP2A_HUMAN	S10	6436	2	1277.4	(+0.8)	2.554	0.323	0.932	3	K.SVVSLEADDVK.G
SW:TP2A_HUMAN	S11	6336	2	1277.4	(+0.8)	3.519	0.553	1.000	3	K.SVVSLEADDVK.G
SW:TP2A_HUMAN	S03	5787	2	1141.3	(-0.2)	2.921	0.479	0.963	6	K.TL*AVSGL*GVVGR.D
SW:TP2A_HUMAN	S05	6500	2	1129.3	(+1.0)	3.881	0.541	1.000	6	K.TLAVSGLGVVGR.D
SW:TP2A_HUMAN	S05	6736	2	1129.3	(-0.4)	2.279	0.112	0.229	6	K.TLAVSGLGVVGR.D
SW:TP2A_HUMAN	S06	6486	2	1129.3	(-0.9)	2.999	0.519	1.000	6	K.TLAVSGLGVVGR.D
SW:TP2A_HUMAN	S06	6480	2	1141.3	(+0.4)	2.745	0.591	1.000	6	K.TL*AVSGL*GVVGR.D
SW:TP2A_HUMAN	S08	6734	2	1129.3	(-0.3)	3.280	0.451	0.965	6	K.TLAVSGLGVVGR.D
SW:TP2A_HUMAN	S08	6686	2	1141.3	(+0.2)	2.958	0.592	0.992	6	K.TL*AVSGL*GVVGR.D
SW:TP2A_HUMAN	S08	6866	2	1129.3	(-0.4)	2.436	0.333	0.852	6	K.TLAVSGLGVVGR.D
SW:TP2A_HUMAN	S09	6948	2	1129.3	(-0.3)	2.308	0.296	0.763	6	K.TLAVSGLGVVGR.D
SW:TP2A_HUMAN	S10	6700	2	1141.3	(-0.1)	3.119	0.552	1.000	6	K.TL*AVSGL*GVVGR.D
SW:TP2A_HUMAN	S11	6622	2	1141.3	(+0.6)	2.883	0.628	1.000	6	K.TL*AVSGL*GVVGR.D
SW:TP2A_HUMAN	S13	6822	2	1129.3	(+0.9)	4.173	0.519	1.000	6	K.TLAVSGLGVVGR.D
SW:TP2A_HUMAN	S14	6710	2	1129.3	(+0.4)	3.563	0.466	1.000	6	K.TLAVSGLGVVGR.D
SW:TP2A_HUMAN	S16	6462	2	1129.3	(+0.8)	4.215	0.437	1.000	6	K.TLAVSGLGVVGR.D
SW:TP2A_HUMAN	S17	6756	2	1129.3	(+0.7)	3.426	0.468	1.000	6	K.TLAVSGLGVVGR.D
SW:TP2A_HUMAN	S18	6538	2	1129.3	(+0.9)	3.909	0.469	1.000	6	K.TLAVSGLGVVGR.D
SW:TP2A_HUMAN	S19	6656	2	1129.3	(+0.6)	3.911	0.470	1.000	6	K.TLAVSGLGVVGR.D
SW:TP2A_HUMAN	S04	5389	2	1082.2	(+0.7)	2.484	0.362	0.959	3	K.TPPL*ITDYR.E

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:TP2A_HUMAN	S04	5421	2	1076.2	(-0.0)	2.257	0.421	0.924	3	K.TPPLITDYR.E
SW:TP2A_HUMAN	S05	5966	2	1076.2	(-0.4)	2.567	0.408	0.942	3	K.TPPLITDYR.E
SW:TP2A_HUMAN	S05	5952	2	1082.2	(+0.9)	2.270	0.423	0.965	3	K.TPPL*ITDYR.E
SW:TP2A_HUMAN	S06	5912	2	1082.2	(+1.0)	2.273	0.423	0.965	3	K.TPPL*ITDYR.E
SW:TP2A_HUMAN	S08	6166	2	1082.2	(+0.4)	2.367	0.457	0.975	3	K.TPPL*ITDYR.E
SW:TP2A_HUMAN	S09	6262	2	1076.2	(+0.9)	2.748	0.320	0.960	3	K.TPPLITDYR.E
SW:TP2A_HUMAN	S13	6298	2	1082.2	(+0.8)	2.322	0.413	0.965	3	K.TPPL*ITDYR.E
SW:TP2A_HUMAN	S13	6292	2	1076.2	(+0.9)	2.316	0.333	0.934	3	K.TPPLITDYR.E
SW:TP2A_HUMAN	S15	6038	2	1076.2	(-0.1)	2.356	0.453	0.945	3	K.TPPLITDYR.E
SW:TP2A_HUMAN	S16	5878	2	1076.2	(+0.7)	2.395	0.306	0.927	3	K.TPPLITDYR.E
SW:TP2A_HUMAN	S03	5349	2	1229.4	(+0.6)	2.742	0.313	0.947	3	K.TQMAEVLPSPR.G
SW:TP2A_HUMAN	S04	5217	2	1229.4	(+0.9)	3.001	0.412	0.978	3	K.TQMAEVLPSPR.G
SW:TP2A_HUMAN	S04	5221	2	1235.4	(+0.2)	2.610	0.369	0.916	3	K.TQMAEVL*PSPR.G
SW:TP2A_HUMAN	S05	4546	2	1251.4	(+0.3)	2.473	0.281	0.803	3	K.TQM@AEVL*PSPR.G
SW:TP2A_HUMAN	S06	4160	2	1251.4	(+0.2)	2.512	0.353	0.894	3	K.TQM@AEVL*PSPR.G
SW:TP2A_HUMAN	S06	8004	2	1928.2	(+0.4)	4.001	0.486	0.923	5	R.VTIDPENNLISIWNNKG.G
SW:TP2A_HUMAN	S10	8430	2	1928.2	(-0.2)	2.369	0.412	0.896	5	R.VTIDPENNLISIWNNKG.G
SW:TP2A_HUMAN	S11	8086	2	1928.2	(+0.4)	3.365	0.505	1.000	5	R.VTIDPENNLISIWNNKG.G
SW:TP2A_HUMAN	S11	8084	2	1942.2	(-0.2)	2.225	0.313	0.570	5	R.VTIDPENNL*ISIWNNKG#.G
SW:TP2A_HUMAN	S12	7886	2	1942.2	(+0.4)	3.102	0.434	0.956	5	R.VTIDPENNL*ISIWNNKG#.G
SW:TP2A_HUMAN	S14	8292	2	1942.2	(+0.2)	2.276	0.266	0.402	5	R.VTIDPENNL*ISIWNNKG#.G
SW:TP2A_HUMAN	S15	7958	2	1928.2	(+0.3)	3.631	0.509	1.000	5	R.VTIDPENNLISIWNNKG.G
SW:TP2A_HUMAN	S05	8032	2	1120.3	(+0.6)	2.324	0.261	0.877	3	K.YDTV*DLR.D
SW:TP2A_HUMAN	S06	7856	2	1120.3	(+0.9)	2.587	0.293	0.939	3	K.YDTV*DLR.D
SW:TP2A_HUMAN	S07	7928	2	1120.3	(+0.9)	2.306	0.363	0.948	3	K.YDTV*DLR.D
SW:TP2A_HUMAN	S09	8110	2	1108.3	(+0.8)	2.694	0.357	0.967	3	K.YDVLDIR.D
SW:TP2A_HUMAN	S10	8002	2	1120.3	(+0.7)	2.264	0.204	0.767	3	K.YDTV*DLR.D
SW:TP2A_HUMAN	S12	7756	2	1120.3	(+0.6)	2.222	0.234	0.810	3	K.YDTV*DLR.D
SW:TP2A_HUMAN	S11	7784	2	1330.6	(+0.6)	2.420	0.376	0.949	3	R.YIFTM@L*SSL*AR.L
SW:TP2A_HUMAN	S14	9000	2	1302.6	(+0.8)	2.451	0.274	0.868	3	R.YIFTMLSSLAR.L
SW:TP2A_HUMAN	S06	7140	2	1685.8	(-0.2)	2.642	0.277	0.641	3	K.YSGPEDDAAISL*AFSK#.K
SW:TP2A_HUMAN	S20	6624	2	1437.5	(+0.9)	3.070	0.396	0.976	7	K.ELILFSNSDNER.S
SW:TP2B_HUMAN	S05	4918	2	1189.4	(+0.8)	2.283	0.176	0.027	3	K.DKLDGVALK.V
SW:TP2B_HUMAN	S07	4726	2	1189.4	(+0.8)	2.257	0.180	0.027	3	K.DKLDGVALK.V
SW:TP2B_HUMAN	S10	5024	2	1217.4	(+0.1)	2.435	0.281	0.043	3	K.DK#L*DETGVAL*K#.V
SW:TP2B_HUMAN	S06	8164	2	1116.4	(+0.7)	3.190	0.289	0.968	3	K.DLIQMLVQR.G
SW:TP2B_HUMAN	S04	7035	2	1379.5	(-0.1)	2.922	0.396	0.943	4	K.EDLAAFVEELDK.V
SW:TP2B_HUMAN	S05	8494	2	1379.5	(+0.6)	2.831	0.491	0.982	4	K.EDLAAFVEELDK.V
SW:TP2B_HUMAN	S06	8392	2	1379.5	(+0.4)	2.802	0.457	0.979	4	K.EDLAAFVEELDK.V
SW:TP2B_HUMAN	S07	8992	2	1530.8	(+0.3)	3.236	0.437	0.960	3	K.HGFLEEFITPIVK.A
SW:TP2B_HUMAN	S15	8564	2	1530.8	(+0.5)	4.481	0.497	1.000	3	K.HGFLEEFITPIVK.A
SW:TP2B_HUMAN	S15	8566	2	1544.8	(+0.4)	3.846	0.473	1.000	3	K.HGFL*EEFITPIVK#.A
SW:TP2B_HUMAN	S16	8534	2	1544.8	(+1.0)	3.335	0.520	1.000	3	K.HGFL*EEFITPIVK#.A
SW:TP2B_HUMAN	S06	6246	2	1265.4	(+0.6)	2.726	0.258	0.923	3	K.HLTYNDFINK.E
SW:TP2B_HUMAN	S06	6262	2	1279.4	(-0.5)	2.274	0.202	0.393	3	K.HL*TYNDFINK#.E
SW:TP2B_HUMAN	S07	6340	2	1265.4	(+0.5)	2.940	0.238	0.931	3	K.HLTYNDFINK.E
SW:TP2B_HUMAN	S09	6594	2	1265.4	(+0.7)	3.364	0.232	0.954	3	K.HLTYNDFINK.E
SW:TP2B_HUMAN	S11	6396	2	1265.4	(+0.6)	3.243	0.250	0.955	3	K.HLTYNDFINK.E
SW:TP2B_HUMAN	S15	6352	2	1265.4	(+0.8)	2.691	0.114	0.696	3	K.HLTYNDFINK.E
SW:TP2B_HUMAN	S06	6028	2	1358.5	(+0.2)	3.081	0.456	0.962	3	R.HVDYVVDQVVGK.L
SW:TP2B_HUMAN	S08	6266	2	1358.5	(-0.6)	2.716	0.396	0.932	3	R.HVDYVVDQVVGK.L
SW:TP2B_HUMAN	S10	6292	2	1358.5	(+0.7)	2.738	0.518	0.983	3	R.HVDYVVDQVVGK.L
SW:TP2B_HUMAN	S12	5904	2	1358.5	(+0.5)	3.270	0.535	1.000	3	R.HVDYVVDQVVGK.L
SW:TP2B_HUMAN	S13	6412	2	1366.5	(+0.8)	2.243	0.303	0.771	3	R.HVDYVVDQVVGK#.L
SW:TP2B_HUMAN	S16	6006	2	1358.5	(+0.4)	4.151	0.576	1.000	3	R.HVDYVVDQVVGK.L
SW:TP2B_HUMAN	S03	5771	2	1237.4	(+0.1)	2.575	0.328	0.864	3	K.KYETVQDILK.E
SW:TP2B_HUMAN	S04	5765	2	1237.4	(+0.7)	2.427	0.316	0.928	3	K.KYETVQDILK.E
SW:TP2B_HUMAN	S06	6446	2	1237.4	(+0.0)	2.546	0.200	0.689	3	K.KYETVQDILK.E
SW:TP2B_HUMAN	S10	6656	2	1237.4	(+0.8)	2.205	0.315	0.864	3	K.KYETVQDILK.E
SW:TP2B_HUMAN	S14	2010	2	1109.3	(-0.8)	2.694	0.401	0.794	4	K.LAQEAAGLHK.V
SW:TP2B_HUMAN	S07	7334	3	1701.9	(-0.1)	4.100	0.334	0.967	3	R.L*HGL*PEQFL*YGTATK#.H
SW:TP2B_HUMAN	S09	7446	3	1701.9	(+0.6)	3.734	0.400	0.995	3	R.L*HGL*PEQFL*YGTATK#.H
SW:TP2B_HUMAN	S11	7288	3	1701.9	(+0.8)	3.748	0.235	0.904	3	R.L*HGL*PEQFL*YGTATK#.H
SW:TP2B_HUMAN	S13	8414	2	1358.6	(+0.1)	2.563	0.104	0.341	3	R.LLFPVDDNLLK.F
SW:TP2B_HUMAN	S13	8402	2	1390.6	(-0.3)	2.430	0.292	0.658	3	R.L*L*FPAVDDNL*L*K#.F

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:TP2B_HUMAN	S03	5733	2	1277.5	(+0.3)	2.632	0.468	0.955	4	R.NTVEITEL*PVR.T
SW:TP2B_HUMAN	S04	5701	2	1271.5	(+0.9)	2.244	0.456	0.966	4	R.NTVEITELPVR.T
SW:TP2B_HUMAN	S08	6610	2	1271.5	(-0.4)	2.837	0.351	0.924	4	R.NTVEITELPVR.T
SW:TP2B_HUMAN	S11	6528	2	1271.5	(+0.9)	3.293	0.416	0.982	4	R.NTVEITELPVR.T
SW:TP2B_HUMAN	S11	6536	2	1277.5	(+0.5)	2.617	0.452	0.977	4	R.NTVEITEL*PVR.T
SW:TP2B_HUMAN	S12	6308	2	1277.5	(+0.7)	2.491	0.409	0.965	4	R.NTVEITEL*PVR.T
SW:TP2B_HUMAN	S13	6740	2	1271.5	(+0.4)	3.110	0.354	0.972	4	R.NTVEITELPVR.T
SW:TP2B_HUMAN	S15	6486	2	1271.5	(+0.8)	2.246	0.441	0.962	4	R.NTVEITELPVR.T
SW:TP2B_HUMAN	S16	6382	2	1271.5	(+1.0)	2.233	0.484	0.971	4	R.NTVEITELPVR.T
SW:TP2B_HUMAN	S05	7012	2	1501.7	(+0.5)	2.841	0.420	0.446	3	R.SIPSLVDGFKPGQR.K
SW:TP2B_HUMAN	S03	6009	2	1141.3	(-0.0)	3.586	0.466	1.000	3	K.SL*AVSGL*GVIGR.D
SW:TP2B_HUMAN	S08	7068	2	1141.3	(+0.3)	3.444	0.454	0.993	3	K.SL*AVSGL*GVIGR.D
SW:TP2B_HUMAN	S09	7144	2	1141.3	(+0.6)	3.436	0.503	1.000	3	K.SL*AVSGL*GVIGR.D
SW:TP2B_HUMAN	S12	6756	2	1129.3	(+1.0)	4.101	0.472	1.000	3	K.SLAVSGLGVIGR.D
SW:TP2B_HUMAN	S16	6822	2	1129.3	(+0.0)	3.752	0.415	1.000	3	K.SLAVSGLGVIGR.D
SW:TP2B_HUMAN	S04	6807	2	1853.0	(-0.3)	3.883	0.432	1.000	5	K.SQDFGNLFSFPSYSQK.S
SW:TP2B_HUMAN	S05	8226	2	1867.0	(-0.9)	2.563	0.422	0.603	5	K.SQDFGNL*FSFPSYSQK#.S
SW:TP2B_HUMAN	S07	8128	2	1867.0	(+0.2)	3.587	0.398	0.917	5	K.SQDFGNL*FSFPSYSQK#.S
SW:TP2B_HUMAN	S07	8134	2	1853.0	(-0.4)	3.542	0.458	0.966	5	K.SQDFGNLFSFPSYSQK.S
SW:TP2B_HUMAN	S04	5121	2	1008.2	(+0.6)	2.431	0.201	0.746	4	K.TPALISDYK.E
SW:TP2B_HUMAN	S05	5624	2	1022.2	(+0.4)	2.316	0.304	0.845	4	K.TPAL*ISDYK#.E
SW:TP2B_HUMAN	S07	5674	2	1022.2	(+0.5)	2.766	0.243	0.865	4	K.TPAL*ISDYK#.E
SW:TP2B_HUMAN	S08	5852	2	1008.2	(+0.2)	2.432	0.280	0.782	4	K.TPALISDYK.E
SW:TP2B_HUMAN	S09	5942	2	1022.2	(+0.8)	2.550	0.319	0.901	4	K.TPAL*ISDYK#.E
SW:TP2B_HUMAN	S11	5764	2	1022.2	(-0.2)	2.254	0.278	0.582	4	K.TPAL*ISDYK#.E
SW:TP2B_HUMAN	S14	5676	2	1008.2	(+0.5)	2.599	0.368	0.966	4	K.TPALISDYK.E
SW:TP2B_HUMAN	S16	5522	2	1008.2	(-0.0)	2.414	0.432	0.934	4	K.TPALISDYK.E
SW:TP2B_HUMAN	S17	5964	2	1008.2	(+0.2)	2.472	0.201	0.696	4	K.TPALISDYK.E
SW:TP2B_HUMAN	S17	5974	2	1022.2	(+0.4)	2.443	0.279	0.843	4	K.TPAL*ISDYK#.E
SW:TP2B_HUMAN	S05	8152	2	1887.1	(+0.5)	3.161	0.517	1.000	2	K.VSIDPESNIISWNNKG.G
SW:TP2B_HUMAN	S07	9758	3	2488.8	(+0.3)	3.925	0.587	1.000	3	K.VYVPALIFGQLLTSSNYDDDEK.K
SW:TP2B_HUMAN	S12	9574	3	2488.8	(+0.9)	3.973	0.488	0.999	3	K.VYVPALIFGQLLTSSNYDDDEK.K
SW:TP2B_HUMAN	S15	9720	3	2488.8	(+0.5)	3.915	0.474	0.999	3	K.VYVPALIFGQLLTSSNYDDDEK.K
SW:TP2B_HUMAN	S20	4430	2	1189.4	(+1.0)	2.561	0.229	0.101	3	K.DKLDDETGVALK.V
SW:U2AF_HUMAN	S09	8188	3	1833.1	(+0.7)	3.856	0.181	0.735	1	K.L*FIGGL*PNYL*NDDQVK#.E
SW:U2AF_HUMAN	S09	8186	2	1807.1	(-0.4)	2.567	0.274	0.755	1	K.LFIGGLPNYLNDDQVK.E
SW:U2AF_HUMAN	S09	7278	3	2160.4	(-0.6)	4.620	0.368	0.983	1	R.L*GGL*TAQAPGNPVL*AVQINQDK#.N
SW:U2AF_HUMAN	S09	8294	2	1050.2	(+0.7)	2.491	0.271	0.927	1	K.NFAFL*EFR.S
SW:U2AF_HUMAN	S09	8184	2	1833.1	(+0.5)	2.409	0.296	0.768	1	K.L*FIGGL*PNYL*NDDQVK#.E
SW:U3P2_HUMAN	S10	1740	2	1408.5	(+0.8)	2.594	0.424	0.970	1	R.GTHQL*YSTSHDR.S
SW:U3P2_HUMAN	S10	1742	2	1402.5	(+0.4)	2.331	0.273	0.852	1	R.GTHQLYSTSHDR.S
SW:U3P2_HUMAN	S10	5602	2	2077.1	(-0.9)	4.277	0.358	0.866	1	R.KPEEEEEEELEETAQEK.K
SW:U3P2_HUMAN	S10	5610	2	2099.1	(-0.9)	4.089	0.319	0.708	1	R.K#PEEEEEEELE*EETAQEK#.K
SW:U3P2_HUMAN	S11	5548	3	2077.1	(+0.9)	4.150	0.376	0.997	1	R.KPEEEEEEELEETAQEK.K
SW:U3P2_HUMAN	S10	4716	2	1130.3	(+0.1)	2.265	0.318	0.107	1	R.LKEDVLEQR.G
SW:U3P2_HUMAN	S10	4876	2	1130.3	(+0.8)	2.239	0.253	0.113	1	R.LKEDVLEQR.G
SW:U3P2_HUMAN	S15	5400	3	2077.1	(+0.2)	3.836	0.340	0.975	1	R.KPEEEEEEELEETAQEK.K
SW:U520_HUMAN	S06	7026	2	1025.2	(+0.7)	2.451	0.305	0.924	4	R.GPVLALVAR.A
SW:U520_HUMAN	S04	5363	2	1118.2	(-0.2)	2.428	0.127	0.319	5	K.YAQAGFEGFK.T
SW:U520_HUMAN	S14	5720	2	1190.4	(+0.1)	2.391	0.286	0.691	3	R.IVALSSLSNAK.D
SW:UBF1_HUMAN	S06	6460	2	1049.2	(+0.6)	2.620	0.310	0.956	2	K.DYEVEL*L*R.F
SW:UBF1_HUMAN	S10	6690	2	1049.2	(+0.9)	2.468	0.295	0.938	2	K.DYEVEL*L*R.F
SW:UBF1_HUMAN	S11	6610	2	1049.2	(+0.5)	2.400	0.334	0.950	2	K.DYEVEL*L*R.F
SW:UBF1_HUMAN	S05	5932	2	1517.6	(-0.8)	2.292	0.269	0.376	2	R.FL*ESL*PEEEQQR.V
SW:UBF1_HUMAN	S08	6138	2	1505.6	(-0.3)	2.331	0.166	0.417	2	R.FLESLPEEEQQR.V
SW:UBF1_HUMAN	S12	5286	2	1583.7	(-0.2)	3.900	0.409	1.000	2	R.FREDHPDLIQNAK.K
SW:UBF1_HUMAN	S06	8068	2	1610.8	(+0.1)	3.095	0.413	0.949	2	R.TLTELILDAQEHVK.N
SW:UBF1_HUMAN	S10	8210	2	1610.8	(+0.4)	2.472	0.345	0.926	2	R.TLTELILDAQEHVK.N
SW:UBF1_HUMAN	S05	5880	2	1445.6	(+0.2)	2.393	0.282	0.643	2	K.TPQQL*WYTHEK#.K
SW:UBF1_HUMAN	S12	7924	2	1610.8	(+0.7)	3.472	0.365	0.975	2	R.TLTELILDAQEHVK.N
SW:VIME_HUMAN	S15	5544	2	1324.4	(+0.8)	2.521	0.400	0.964	6	R.EEAENTLQSF.R

Entry Name <sup>a</sup>	Slice# <sup>b</sup>	Scan#	+	(M+H) <sup>+</sup>	ΔM	XCorr	dCn	pcomp <sup>c</sup>	Dup# <sup>d</sup>	Peptide <sup>e</sup>
SW:VIME_HUMAN	S12	4676	2	1094.2	(+0.4)	3.112	0.262	0.951	7	K.FADLSEANR.N
SW:VIME_HUMAN	S10	8018	2	1202.4	(+0.3)	3.007	0.284	0.832	5	K.IL*L*AEL*EQL*K#.G
SW:VIME_HUMAN	S10	8032	2	1202.4	(-0.9)	2.625	0.237	0.331	5	K.IL*L*AEL*EQL*K#.G
SW:VIME_HUMAN	S15	5428	2	1429.6	(-0.7)	2.490	0.331	0.576	3	R.SLYASSPGGVYATR.S
SW:VRK1_HUMAN	S11	6288	3	3137.3	(-0.0)	5.562	0.472	0.998	1	K.EIEESKEPGVEDTEWSNTQTEEEAIQTR.S
SW:VRK1_HUMAN	S11	6290	3	3145.3	(+0.2)	4.932	0.511	1.000	1	K.EIEESK#EPGVEDTEWSNTQTEEEAIQTR.S
SW:VRK1_HUMAN	S11	7040	2	1768.0	(-0.5)	2.948	0.382	0.239	1	K.LLDYTEKPLYENLR.D
SW:VRK1_HUMAN	S12	6842	2	1768.0	(+0.6)	2.588	0.375	0.309	1	K.LLDYTEKPLYENLR.D
SW:VRK1_HUMAN	S11	7582	2	1787.0	(+0.9)	5.176	0.641*	0.856	1	K.NPDQVYLVLDYGLAYR.Y
SW:VRK1_HUMAN	S11	6440	2	1340.5	(+0.2)	2.387	0.438	0.241	1	R.YRENIASLMDK.C
SW:VRK1_HUMAN	S18	7136	2	1768.0	(+0.8)	2.434	0.350	0.226	1	K.LLDYTEKPLYENLR.D
SW:WD12_HUMAN	S10	6202	2	1363.5	(-0.9)	2.901	0.179	0.240	3	K.APL*YDL*AAHEDK#.V
SW:WD12_HUMAN	S10	6194	2	1343.5	(+0.5)	2.520	0.534	0.982	3	K.APLYDLAAHEDK.V
SW:WD12_HUMAN	S10	7222	2	1469.6	(+0.6)	4.353	0.441	0.998	3	K.GAEEWIL*TGSDYDK.T
SW:WD12_HUMAN	S10	7224	2	1483.6	(-0.0)	3.162	0.409	0.910	3	K.GAEEWIL*TGSDYDK#.T
SW:WD12_HUMAN	S10	2290	2	1558.6	(+0.9)	5.403	0.661	1.000	3	R.GHAGSVDSIAVDGSGTK.F
SW:WD12_HUMAN	S10	2272	2	1566.6	(+0.4)	4.872	0.627	1.000	3	R.GHAGSVDSIAVDGSGTK#.F
SW:WD12_HUMAN	S10	6154	2	1120.2	(+0.7)	2.956	0.338	0.968	2	R.VWDVESGSLK.S
SW:WD12_HUMAN	S10	10572	2	2678.0	(-0.6)	3.883	0.431	1.000	3	K.YAVDDVPFISIPAASEIADL*SNIINK#.L
SW:WD12_HUMAN	S17	7304	2	1483.6	(+0.8)	2.627	0.432	0.943	3	K.GAEEWIL*TGSDYDK#.T
SW:WDR3_HUMAN	S10	7942	2	1148.3	(+0.2)	2.589	0.304	0.872	1	K.DAITQALFLR.E
SW:WDR3_HUMAN	S10	4912	2	1162.3	(+0.6)	2.623	0.360	0.957	1	R.LITGASDSELR.V
SW:WDR3_HUMAN	S05	6172	2	1397.6	(-0.0)	2.484	0.179	0.030	2	R.TREPL*IL*EEER.E
SW:WDR3_HUMAN	S17	5136	2	1162.3	(+0.8)	2.476	0.291	0.908	1	R.LITGASDSELR.V
SWN:BRIX_HUMAN	S12	7952	3	3527.1	(+0.3)	4.993	0.599	1.000	1	K.TLLPHDPTADVFTPAEEKPIEQWVKPEPK.V
SWN:BRIX_HUMAN	S12	8474	2	1317.6	(+0.7)	2.752	0.318	0.949	1	K.ELLIQIFSTPR.Y
SWN:DD27_HUMAN	S05	7860	2	1069.3	(+0.9)	2.749	0.294	0.945	8	R.EAIVAAL*L*TR.T
SWN:DD27_HUMAN	S05	7712	2	1593.8	(-0.1)	3.393	0.335	0.934	7	R.IFVNSNTDVAPFLR.Q
SWN:DD27_HUMAN	S05	7720	2	1599.8	(-0.0)	2.648	0.288	0.813	7	R.IFVNSNTDVAPFL*R.Q
SWN:DD27_HUMAN	S09	7774	2	1593.8	(+0.4)	2.227	0.256	0.763	7	R.IFVNSNTDVAPFLR.Q
SWN:DD27_HUMAN	S05	7558	2	1525.6	(+0.4)	2.441	0.429	0.929	5	R.SADFNPDFVFTEK#.E
SWN:DD27_HUMAN	S05	5968	2	1370.5	(+0.8)	2.513	0.248	0.858	8	K.SVFDEELTNTSK.K
SWN:DD27_HUMAN	S16	7652	2	1057.3	(+0.9)	3.206	0.348	0.976	8	R.EAIVAALLTR.T
SWN:INCE_HUMAN	S04	5657	3	2510.6	(-0.1)	4.281	0.423	0.994		K.QAVSEL*DEEQHL*EDEEL*QPPR.S
SWN:INCE_HUMAN	S06	6362	3	2510.6	(+0.7)	3.879	0.367	0.993		K.QAVSEL*DEEQHL*EDEEL*QPPR.S
SWN:INCE_HUMAN	S08	5982	2	1060.2	(-0.2)	2.260	0.333	0.748		R.L*L*NVEVPQK#.V
SWN:PHFE_HUMAN	S04	4321	2	1322.4	(+0.6)	3.072	0.417	0.979		K.NSAEEEEVLSEK.Q
SWN:PHFE_HUMAN	S04	4329	2	1336.4	(-0.1)	2.623	0.320	0.748		K.NSAEEEEVL*SSEK#.Q
SWN:PHFE_HUMAN	S07	4152	2	1322.4	(-0.5)	2.257	0.364	0.813		K.NSAEEEEVLSEK.Q
SWN:PHFE_HUMAN	S06	8326	2	1287.5	(+0.9)	3.227	0.383	0.977		R.SEGQGIWALLGR.I
SWN:PHFE_HUMAN	S07	8376	2	1287.5	(+0.9)	2.622	0.395	0.964		R.SEGQGIWALLGR.I
SWN:PHFE_HUMAN	S15	8306	2	1287.5	(+0.7)	2.417	0.429	0.965		R.SEGQGIWALLGR.I
SWN:ROAA_HUMAN	S12	8198	2	2245.5	(+0.3)	3.615	0.382	0.912	3	R.EYFGFGEIEAIEL*PM@DPK#.L
SWN:ROAA_HUMAN	S12	7120	2	1328.5	(+0.6)	2.850	0.466	0.980	3	K.MFVGGLSWDTSK.K
SWN:SM1A_HUMAN	S07	6686	2	1072.2	(+0.7)	2.448	0.278	0.915	3	R.TAL*FEEISR.S
SWN:SM1A_HUMAN	S07	6708	2	1020.2	(-0.2)	2.264	0.161	0.232	2	K.L*IEIENFK#.S
SWN:TXL2_HUMAN	S12	8914	2	1578.8	(+0.7)	3.139	0.371	0.972	2	K.YEISSVPTFLFFK.N
SWN:TXL2_HUMAN	S12	4804	2	1287.4	(+0.6)	2.414	0.437	0.966	2	K.LEAEGVPEVSEK.Y

<sup>a</sup> Entry name in NCBI, SWISS-Prot or PIR databases

<sup>b</sup> Slice number and color code: H (High Salt, Blue), R (mRIPA, Green), and S (SDS, Red)

<sup>c</sup> pcomp: Computed peptide probability

<sup>d</sup> Dup#: Duplicated numbers of proteins with the designated peptide

<sup>e</sup> May include multiple occurrence of same peptides