

Supplemental figure 1.

WiDr-conditioned serum-free media were collected and concentrated using a Quickstand™ tangential-flow system (GE Healthcare). Proteins were reduced by adding β -mercaptoethanol at a final concentration of 1% (v/v), and the denatured protein preparations were filtered through a 0.45 μ m syringe filter. Ten milliliter of protein samples were desalted on a HiPrep 26/10 desalting column (GE Healthcare) and concentrated to a final volume of 1 ml. One milligram of protein was pre-cleared by avidin-agarose beads for 1 hr at room temperature and the pre-cleared proteins were allowed to bind to L-PHA-avidin-agarose beads complex overnight at 4 °C. After extensive washing with PBS, the bound proteins were separated from the beads complex by adding 1 X SDS-PAGE denaturation buffer and boiling briefly. Proteins were resolved on an 8% SDS-PAGE gel and tryptic-digested as described previously. The tryptic peptides were eluted from the gel and sequence-analyzed on a Surveyor system connected to a 7-T LTQ-FT mass spectrometer (Thermo Electron) equipped with a nano-electrospray ion source (Proxeon Biosystems).

The peptide mixtures were loaded onto a C18 trap column (5 μ m, 100 Å, 300 μ m i.d. \times 5 mm) by an autosampler (Surveyor) at a flow of 20 μ L/min for desalting and concentration. The trapped peptides were then back-flushed and separated on a home-made column (length 100 mm) packed with C18 (Aqua, 5 μ m, Phenomenex, CA, USA) in 75-mm silica tubing (8-mm id orifice). The mobile phases, A and B, were composed of 0% and 80% ACN, respectively, each containing 0.5% acetic acid and 0.02% formic acid. The gradient began at 5% B for 15 min, was ramped to 20% B for 3 min, to 50% for 47 min, to 95% for 2 min, and held at 95% for 5 min, to 5 % for 2 min. The column was equilibrated with 5% B for 6 min before the next run. The eluted peptides were directly electrosprayed into the mass spectrometer. The mass spectrometer was controlled by Xcalibur software (ThermoElectron Corp., Home Page Version 2.0 SR1). During gradient elution, 3 ion-trap MS/MS spectra were acquired per data-dependent cycle from a high resolution (R set at 100 000) FTICR master spectrum. Ions selected for MS/MS were dynamically excluded for 60 s. General mass spectrometric conditions were described in Experimental Procedures.

The analyzed sequences were blasted against NCBI nr database and the protein identification was performed on the criteria as described in Experimental Procedures. In this experiment, proteins with at least two peptides, each of which showed score values more than 42 (p -value < 0.05), were considered to be a 'true match'. The identified proteins which derived from WiDr:GnT-V, not WiDr:mock, are listed as follows.

1. α -1-antitrypsin

[gi|177836](#) Mass: 46678 Score: 448 Queries matched: 24
alpha-1-antitrypsin precursor

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 193	508.3107	1014.6069	1014.6073	-0.0004	0	56	0.0024	1	K.SVLGQLGITK.V
<input checked="" type="checkbox"/> 254	545.7881	1089.5617	1089.5607	0.0011	0	27	2.2	1	K.WERPFEVK.D
<input checked="" type="checkbox"/> 256	546.8109	1091.6073	1091.6049	0.0024	0	47	0.02	1	K.LSSWLLMK.Y + Oxidation (M)
<input checked="" type="checkbox"/> 282	555.8046	1109.5946	1109.5968	-0.0022	0	(52)	0.0065	1	K.LSITGTYDLK.S
<input checked="" type="checkbox"/> 283	555.8060	1109.5974	1109.5968	0.0006	0	53	0.0048	1	K.LSITGTYDLK.S
<input checked="" type="checkbox"/> 1268	789.3493	1576.6841	1575.8336	0.8504	0	26	1.8	1	R.DTVEFALVNYIEFK.G
<input checked="" type="checkbox"/> 412	602.3240	1803.9503	1802.9526	0.9976	0	(57)	0.002	1	K.LQHLENELTHDIITK.F
<input checked="" type="checkbox"/> 1964	902.9861	1803.9577	1802.9526	1.0051	0	69	7.7e-005	1	K.LQHLENELTHDIITK.F
<input checked="" type="checkbox"/> 2056	917.1184	1832.2223	1832.9155	-0.6933	0	(0)	5.6e+002	2	K.VFSNGADLSGVTEEAPLK.L
<input checked="" type="checkbox"/> 2057	917.5208	1833.0271	1832.9155	0.1115	0	(16)	15	1	K.VFSNGADLSGVTEEAPLK.L
<input checked="" type="checkbox"/> 2058	917.9562	1833.8978	1832.9155	0.9823	0	(50)	0.0056	1	K.VFSNGADLSGVTEEAPLK.L
<input checked="" type="checkbox"/> 2059	917.9587	1833.9029	1832.9155	0.9874	0	73	3e-005	1	K.VFSNGADLSGVTEEAPLK.L
<input checked="" type="checkbox"/> 2151	931.8188	1861.6230	1862.8170	-1.1940	0	(5)	2e+002	1	K.DTEEEDEFHVDQATTVK.V
<input checked="" type="checkbox"/> 472	621.8342	1862.4807	1862.8170	-0.3363	0	35	0.28	1	K.DTEEEDEFHVDQATTVK.V
<input checked="" type="checkbox"/> 2155	932.3736	1862.7326	1862.8170	-0.0843	0	(22)	4	1	K.DTEEEDEFHVDQATTVK.V
<input checked="" type="checkbox"/> 2158	932.5403	1863.0661	1862.8170	0.2492	0	(30)	0.66	1	K.DTEEEDEFHVDQATTVK.V
<input checked="" type="checkbox"/> 2159	932.5676	1863.1207	1862.8170	0.3037	0	(21)	4.3	1	K.DTEEEDEFHVDQATTVK.V
<input checked="" type="checkbox"/> 2160	932.9210	1863.8275	1862.8170	1.0105	0	(16)	15	1	K.DTEEEDEFHVDQATTVK.V
<input checked="" type="checkbox"/> 2161	932.9365	1863.8585	1862.8170	1.0415	0	(22)	4.2	1	K.DTEEEDEFHVDQATTVK.V
<input checked="" type="checkbox"/> 2990	1130.5845	2259.1544	2258.1326	1.0218	0	61	0.00033	1	K.GTEARAGMFELEIPMSIPPEVK.F
<input checked="" type="checkbox"/> 3016	1138.5698	2275.1251	2274.1275	0.9976	0	(13)	24	2	K.GTEARAGMFELEIPMSIPPEVK.F + Oxidation (M)
<input checked="" type="checkbox"/> 3017	1138.5747	2275.1349	2274.1275	1.0074	0	(40)	0.045	1	K.GTEARAGMFELEIPMSIPPEVK.F + Oxidation (M)
<input checked="" type="checkbox"/> 3018	1138.5765	2275.1385	2274.1275	1.0110	0	(41)	0.036	1	K.GTEARAGMFELEIPMSIPPEVK.F + Oxidation (M)
<input checked="" type="checkbox"/> 3019	1138.5808	2275.1471	2274.1275	1.0196	0	(24)	1.7	1	K.GTEARAGMFELEIPMSIPPEVK.F + Oxidation (M)

2. Angiotensinogen preproprotein

[gi|532198](#) Mass: 53122 Score: 266 Queries matched: 9
angiotensinogen

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 66	542.3051	1082.5956	1082.5219	0.0738	0	13	32	1	R.FMQAVTGWK.T + Oxidation (M)
<input checked="" type="checkbox"/> 88	562.8799	1123.7452	1123.6753	0.0699	0	59	0.0008	1	R.LQAILGVPWK.D
<input checked="" type="checkbox"/> 155	634.9073	1267.8000	1267.7499	0.0501	0	55	0.0022	1	K.ALQDQLVLRK.L
<input checked="" type="checkbox"/> 173	649.4106	1296.8066	1296.7078	0.0989	0	33	0.33	1	K.DPTIFIPAPIQAK.T
<input checked="" type="checkbox"/> 210	719.3930	1436.7714	1436.7034	0.0680	0	69	7.7e-005	1	R.SLDFTELDVAREK.I
<input checked="" type="checkbox"/> 224	765.4443	1528.8740	1528.7530	0.1211	0	5	1.9e+002	2	R.AAMVGLANFLGFR.I + 2 Oxidation (M)
<input checked="" type="checkbox"/> 292	941.1238	1880.2330	1880.0560	0.1771	0	(23)	2.9	1	K.QPFVQGLALYTPVVLPR.S + Pyro-glu (N-term Q)
<input checked="" type="checkbox"/> 298	633.4011	1897.1815	1897.0825	0.0990	0	(28)	0.98	1	K.QPFVQGLALYTPVVLPR.S
<input checked="" type="checkbox"/> 299	949.6218	1897.2290	1897.0825	0.1466	0	30	0.57	1	K.QPFVQGLALYTPVVLPR.S

Proteins matching the same set of peptides:

[gi|553181](#) Mass: 36550 Score: 266 Queries matched: 9

angiotensinogen

[gi|15079348](#) Mass: 53080 Score: 266 Queries matched: 9

Angiotensinogen, preproprotein [Homo sapiens]

[gi|55959990](#) Mass: 53121 Score: 266 Queries matched: 9

angiotensinogen (serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitr

3. β -N-acetylhexosaminidase A

[gi|1179460](#) Mass: 56169 Score: 281 Queries matched: 8
N-acetyl-alpha-glucosaminidase prepro-polypeptide
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 114	440.2328	878.4511	878.4497	0.0013	0	28	1.6	1	K.EVIEYAR.L
<input checked="" type="checkbox"/> 413	562.7700	1123.5254	1123.5219	0.0034	0	32	0.58	1	R.EDIPVNYMK.E + Oxidation (M)
<input checked="" type="checkbox"/> 594	626.7861	1251.5577	1251.5554	0.0024	0	47	0.016	1	K.SNPEIQDFMR.K + Oxidation (M)
<input checked="" type="checkbox"/> 722	654.3546	1306.6947	1306.6921	0.0026	0	37	0.15	1	R.GLETFSQLVVK.S
<input checked="" type="checkbox"/> 846	684.8878	1367.7610	1367.7561	0.0048	0	20	8.6	1	K.IQPDIIQVVR.E
<input checked="" type="checkbox"/> 501	598.3013	1791.8820	1791.8791	0.0029	0	20	9.4	1	K.GSYNPVTHIYTAQDVK.E
<input checked="" type="checkbox"/> 2155	984.9902	1967.9658	1967.9516	0.0142	0	66	0.00012	1	K.DFYVVEPLAFEGTPEQK.A
<input checked="" type="checkbox"/> 1024	737.3842	2209.1306	2208.1136	1.0170	0	30	0.73	1	R.HYLPLSSILDITLDVMAYNK.L + Oxidation (M)

Proteins matching the same set of peptides:
[gi|4261632](#) Mass: 60650 Score: 281 Queries matched: 8
lysosomal enzyme beta-N-acetylhexosaminidase A [Homo sapiens]

4. Cathepsin D preprotein

[gi|54697170](#) Mass: 44524 Score: 120 Queries matched: 4
cathepsin D (lysosomal aspartyl protease) [Homo sapiens]
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 1178	768.3847	1534.7549	1534.7548	0.0001	0	59	0.0009	1	R.TMSEVGGSVEDLIAR.G
<input checked="" type="checkbox"/> 1215	776.3824	1550.7502	1550.7497	0.0005	0	(51)	0.0058	1	R.TMSEVGGSVEDLIAR.G + Oxidation (M)
<input checked="" type="checkbox"/> 2399	980.5250	1959.0354	1958.0295	1.0059	0	61	0.00042	1	R.ISVNNVLPVEDNLMQQK.L
<input checked="" type="checkbox"/> 2430	988.5312	1975.0478	1974.0244	1.0234	0	(36)	0.13	1	R.ISVNNVLPVEDNLMQQK.L + Oxidation (M)

5. Cathepsin X precursor

[gi|3294548](#) Mass: 33860 Score: 165 Queries matched: 7
cathepsin Z precursor; CTSZ [Homo sapiens]
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 23	505.7884	1009.5622	1009.4828	0.0794	0	56	0.0015	1	R.VGDYGSLSGR.E
<input checked="" type="checkbox"/> 69	609.3084	1216.6022	1216.5261	0.0762	0	29	0.95	1	R.NSWGEPWGER.G
<input checked="" type="checkbox"/> 98	654.8746	1307.7346	1307.6469	0.0877	0	54	0.0029	1	R.NVDGVNYASITR.N
<input checked="" type="checkbox"/> 99	654.8839	1307.7532	1307.6469	0.1063	0	(25)	2.3	1	R.NVDGVNYASITR.N
100	654.8951	1307.7756	1307.6469	0.1287	0	(10)	75	3	R.NVDGVNYASITR.N
168	631.3468	1891.0186	1890.8822	0.1364	0	(1)	5.4e+002	6	R.YNLAIEEHCTFGDPVIV.- + Propionamide (C)
<input checked="" type="checkbox"/> 169	946.5334	1891.0522	1890.8822	0.1701	0	26	1.6	1	R.YNLAIEEHCTFGDPVIV.- + Propionamide (C)

Proteins matching the same set of peptides:
[gi|3650498](#) Mass: 33921 Score: 165 Queries matched: 7
cathepsin X precursor [Homo sapiens]
[gi|3719219](#) Mass: 32682 Score: 165 Queries matched: 7
preprocathepsin P [Homo sapiens]
[gi|7245729](#) Mass: 31130 Score: 165 Queries matched: 7
Chain B, Crystal Structure Of Human Procathepsin X: A Cysteine Protease With The Proregion Covalent
[gi|7546546](#) Mass: 27132 Score: 165 Queries matched: 7
Chain B, Crystal Structure Of Human Cathepsin X
[gi|22538442](#) Mass: 33846 Score: 165 Queries matched: 7
cathepsin Z preproprotein [Homo sapiens]

6. DDR1 variant protein

[gi|1754536](#) Mass: 101035 Score: 156 Queries matched: 3
 tyrosine kinase DDR

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 1156	711.3499	1420.6852	1420.6834	0.0018	0	68	0.00011	1	K.EEEYLQVDLQR.V
<input checked="" type="checkbox"/> 2095	978.4932	1954.9718	1954.9635	0.0082	0	82	4e-006	1	R.WGQEVISGNEPEGVVLK.D
2450	1123.5590	3367.6551	3367.6288	0.0263	0	7	1e+002	4	K.AREGAPGDGQAAQGPTISYPMLLHVAAQIASGMR.Y + 2 Oxidation (M)

Proteins matching the same set of peptides:
[gi|168533097](#) Mass: 99042 Score: 156 Queries matched: 3
 DDR1 variant protein [Homo sapiens]

7. Dipeptidyl peptidase 7 preproprotein

[gi|6465985](#) Mass: 54281 Score: 256 Queries matched: 8
 quiescent cell proline dipeptidase [Homo sapiens]

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 33	539.3206	1076.6266	1076.5039	0.1227	0	8	1.1e+002	1	R.LDHFNER.F
<input checked="" type="checkbox"/> 43	556.8755	1111.7364	1111.6138	0.1227	0	19	8.4	1	R.GALLVFAEHR.Y
<input checked="" type="checkbox"/> 61	596.3678	1190.7210	1190.6044	0.1167	0	40	0.081	1	K.SLFFGAQSTQR.G
<input checked="" type="checkbox"/> 77	621.3825	1240.7504	1240.6274	0.1231	0	26	1.9	1	K.DLTQLEMFAR.N
<input checked="" type="checkbox"/> 94	647.3699	1292.7252	1292.5884	0.1368	0	54	0.003	1	R.DVTAFEGQSPK.C
<input checked="" type="checkbox"/> 120	699.4277	1396.8408	1396.6986	0.1422	0	41	0.058	1	K.DLELQGYDTR.W
<input checked="" type="checkbox"/> 207	742.7997	2225.3773	2225.1691	0.2081	0	53	0.0027	1	R.GHTELLTVEQALADFELLR.A
<input checked="" type="checkbox"/> 237	1005.6060	3013.7962	3013.4605	0.3357	0	16	11	1	R.NAETVLAMMDYFYPIDFLGPLPANPVK.V + 2 Oxidation (M)

Proteins matching the same set of peptides:
[gi|16877430](#) Mass: 54293 Score: 256 Queries matched: 8
 Dipeptidyl peptidase 7, preproprotein [Homo sapiens]

8. Discoidin receptor tyrosine kinase

[gi|38327632](#) Mass: 97112 Score: 339 Queries matched: 8
 discoidin receptor tyrosine kinase [Homo sapiens]

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 99	428.2568	854.4990	854.4973	0.0017	0	30	0.97	1	R.AVSVPLGGR.V
<input checked="" type="checkbox"/> 330	486.2537	970.4928	970.4906	0.0022	0	46	0.024	1	K.DLGPPMVAR.L + Oxidation (M)
<input checked="" type="checkbox"/> 610	575.2936	1148.5726	1148.5686	0.0040	0	41	0.066	1	R.HNLGGRLGDPR.A
<input checked="" type="checkbox"/> 797	632.8832	1263.7519	1262.7459	1.0061	0	74	3.7e-005	1	R.LHLVALVGTQGR.H
<input checked="" type="checkbox"/> 1175	711.3506	1420.6867	1420.6834	0.0034	0	64	0.00032	1	K.EEEYLQVDLQR.L
<input checked="" type="checkbox"/> 2195	978.4914	1954.9682	1954.9635	0.0047	0	79	6.9e-006	1	R.WGQEVISGNEPEGVVLK.D
2298	1027.7720	2053.5294	2052.9236	0.6058	0	1	3.9e+002	2	R.TIPDSDISASSSWSSTAAR.H
1143	705.3051	2112.8933	2114.0288	-1.1355	1	6	1.9e+002	6	R.NCLVGENETIKIADFGMSR.N

Proteins matching the same set of peptides:
[gi|56206533](#) Mass: 101063 Score: 339 Queries matched: 8
 discoidin domain receptor family, member 1 [Homo sapiens]

9. Dystroglycan 1 precursor

[gi|4758116](#) Mass: 97520 Score: 292 Queries matched: 10
dystroglycan 1 precursor [Homo sapiens]

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 196	455.7781	909.5417	909.5396	0.0021	0	32	0.64	1	K.LVPVNNR.L
<input checked="" type="checkbox"/> 671	608.3412	1214.6678	1214.6659	0.0020	0	60	0.00084	1	K.VVENGALLSVK.L
<input checked="" type="checkbox"/> 673	608.8344	1215.6543	1214.6659	0.9884	0	(35)	0.26	1	K.VVENGALLSVK.L
<input checked="" type="checkbox"/> 168	446.2123	1335.6152	1335.6129	0.0023	0	(16)	26	1	R.SFSEVELHNMK.L + Oxidation (M)
<input checked="" type="checkbox"/> 926	668.8161	1335.6176	1335.6129	0.0048	0	34	0.32	1	R.SFSEVELHNMK.L + Oxidation (M)
<input checked="" type="checkbox"/> 1575	821.9706	1641.9267	1641.9189	0.0079	0	103	3.5e-008	1	R.VTIPTDLIRSSGDIK.V
2297	1055.1807	2108.3468	2109.0465	-0.6997	0	(0)	4.7e+002	4	R.EGAMSAQLGYPVVGWHIANK.K + Pyro-glu (N-term E)
<input checked="" type="checkbox"/> 1125	715.6941	2144.0604	2143.0520	1.0085	0	56	0.0019	1	R.EGAMSAQLGYPVVGWHIANK.K + Oxidation (M)
<input checked="" type="checkbox"/> 2466	1123.4207	3367.2401	3368.6272	-1.3871	0	2	2.8e+002	1	R.LGANGSHIPQTSSVFSIEVYEDHSDLSQSVR.T
2842	1248.0724	3741.1953	3740.8739	0.3214	1	4	1.5e+002	5	R.TASDPGPEVSSACRADEPVTLVTLVDLADLTKMTPK.Q

10. Galectin 3 binding protein

[gi|5031863](#) Mass: 65289 Score: 402 Queries matched: 12
galectin 3 binding protein [Homo sapiens]

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 32	413.7266	825.4386	825.4384	0.0002	0	26	2.4	1	R.VEIFYR.G
<input checked="" type="checkbox"/> 151	488.2900	974.5655	974.5648	0.0007	0	51	0.0091	1	R.IDITLSSVK.C
<input checked="" type="checkbox"/> 85	442.8896	1325.6470	1325.6462	0.0008	0	39	0.15	1	R.ASHEEVEGLVEK.I
<input checked="" type="checkbox"/> 705	678.3931	1354.7716	1354.7707	0.0008	0	(23)	4.7	1	R.SDLAVPSELALLK.A
<input checked="" type="checkbox"/> 706	678.3935	1354.7724	1354.7707	0.0017	0	56	0.002	1	R.SDLAVPSELALLK.A
<input checked="" type="checkbox"/> 1318	796.9006	1591.7866	1591.7841	0.0024	0	68	0.00012	1	R.ELSEALGQIEDSQR.G
<input checked="" type="checkbox"/> 228	531.6035	1591.7887	1591.7841	0.0046	0	(46)	0.027	1	R.ELSEALGQIEDSQR.G
<input checked="" type="checkbox"/> 2812	1081.5159	2161.0172	2161.0116	0.0056	0	(108)	7.6e-009	1	R.IYTSPTWSAEVTDSSWSAR.K
<input checked="" type="checkbox"/> 2815	1082.0173	2162.0201	2161.0116	1.0085	0	120	4.7e-010	1	R.IYTSPTWSAEVTDSSWSAR.K
<input checked="" type="checkbox"/> 1565	841.3998	2521.1775	2520.1750	1.0025	0	29	0.84	1	R.YYPYQSETPQHPSELEQDK.R
<input checked="" type="checkbox"/> 3510	1399.6370	2797.2594	2798.2560	-0.9967	0	14	13	1	R.AREGQSGPIMLDEVQCTGTERSLADCK.S
<input checked="" type="checkbox"/> 3515	1407.6285	2813.2425	2814.2509	-1.0084	0	(11)	25	1	R.AREGQSGPIMLDEVQCTGTERSLADCK.S + Oxidation (M)

11. Granulin isoform 1 precursor

[gi|4504151](#) Mass: 63500 Score: 272 Queries matched: 15
granulin isoform 1 precursor [Homo sapiens]

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 74	430.7350	859.4555	859.4552	0.0003	0	21	11	1	K.WPTLSR.H
<input checked="" type="checkbox"/> 281	501.7769	1001.5393	1001.5393	0.0000	0	62	0.00069	1	R.GSEIVAGLEK.M
<input checked="" type="checkbox"/> 333	518.7930	1035.5715	1035.5713	0.0002	0	47	0.022	1	K.LPAHTVGDVK.C
<input checked="" type="checkbox"/> 84	437.2385	1308.6937	1308.6938	-0.0002	1	27	2.6	1	R.YDAPLRDPAALR.Q
<input checked="" type="checkbox"/> 169	463.9243	1388.7512	1387.7459	1.0053	0	30	1.1	1	K.EVVSQAQATFLAR.S
<input checked="" type="checkbox"/> 247	486.6086	1456.8040	1456.8038	0.0002	0	(48)	0.018	1	K.APAHLSLDPQALK.R
<input checked="" type="checkbox"/> 1166	729.9111	1457.8077	1456.8038	1.0039	0	57	0.0022	1	K.APAHLSLDPQALK.R
<input checked="" type="checkbox"/> 332	518.3177	1551.9314	1550.6428	1.2886	0	1	9.5e+002	8	R.QHCCPAGYTCNVK.A + Carbamidomethyl (C); Propionamide (C)
1785	855.4391	1708.8636	1709.7171	-0.8535	1	10	89	7	R.SRCPDGTCCLELPSGK.Y + Propionamide (C)
506	574.3955	1720.1647	1720.7596	-0.5949	1	5	3.4e+002	8	R.QHCCPAGYTCNVKAR.S + Propionamide (C)
2226	985.4889	1968.9632	1968.7851	0.1781	1	1	6.1e+002	10	R.QGNACCPYRQGVCCADR.R + Propionamide (C); Pyro-glu (N-term Q)
1948	902.9556	2705.8449	2707.0380	-1.1932	1	7	2.1e+002	2	K.DVECEGGHFCNDNQTCRRHR.Q + Carbamidomethyl (C); 3 Propionamide
<input checked="" type="checkbox"/> 2461	1068.5088	3202.5045	3202.3472	0.1573	0	9	1.1e+002	1	R.CPDGQFCPVACCLDPGGASYSCRRLLDK.W + 2 Carbamidomethyl (C); Prop
2509	1086.3984	3256.1735	3255.5311	0.6424	1	2	5.3e+002	7	R.VHCCPHGAFCDLVHTRCITPTGTPLAK.K + 3 Carbamidomethyl (C); Propi
2857	1267.1160	3798.3261	3797.4952	0.8309	0	5	2.2e+002	5	K.YGCCPMPNATCCSDHLHCCPQDTVCDLIQSK.C + 6 Carbamidomethyl (C); Pr

12. Heat shock 70 kDa protein 8 isoform 1

[gi|5729877](#) Mass: 70854 Score: 719 Queries matched: 28
 heat shock 70kDa protein 8 isoform 1 [Homo sapiens]
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
46	424.3323	846.6500	847.4334	-0.7834	1	15	39	6	R.LRTACER.A
<input checked="" type="checkbox"/> 478	600.3412	1198.6679	1198.6669	0.0010	0	(54)	0.0037	1	K.DAGTIAGLNVL.R.I
<input checked="" type="checkbox"/> 479	600.3412	1198.6679	1198.6669	0.0010	0	63	0.00043	1	K.DAGTIAGLNVL.R.I
<input checked="" type="checkbox"/> 480	600.3422	1198.6699	1198.6669	0.0030	0	(60)	0.00094	1	K.DAGTIAGLNVL.R.I
<input checked="" type="checkbox"/> 552	614.8181	1227.6217	1227.6207	0.0010	0	55	0.0024	1	K.VETIANDQGN.R.T
<input checked="" type="checkbox"/> 618	626.8167	1251.6189	1252.6087	-0.9899	0	(36)	0.25	1	R.FEELNADLFR.G
<input checked="" type="checkbox"/> 619	627.3109	1252.6073	1252.6087	-0.0015	0	52	0.0053	1	R.FEELNADLFR.G
<input checked="" type="checkbox"/> 622	627.3770	1252.7394	1252.6087	0.1306	0	(28)	1.3	1	R.FEELNADLFR.G
<input checked="" type="checkbox"/> 623	627.7886	1253.5627	1253.5598	0.0029	0	59	0.001	1	R.FDDAVVQSDMK.H
<input checked="" type="checkbox"/> 1279	744.3562	1486.6979	1486.6940	0.0039	0	55	0.0023	1	R.TTPSYVAFETTER.L
<input checked="" type="checkbox"/> 1701	808.8509	1615.6872	1615.7803	-0.0931	0	81	5.8e-006	1	K.SFYPEEVSSMVLTK.M
<input checked="" type="checkbox"/> 1807	825.4003	1648.7861	1648.7879	-0.0017	0	(82)	4.8e-006	1	K.NQVAMNPTNTVFDAK.R
<input checked="" type="checkbox"/> 1832	829.9614	1657.9082	1658.8879	-0.9797	0	(36)	0.16	1	R.IINEPTAARIAYGLDK.K
<input checked="" type="checkbox"/> 1833	829.9745	1657.9345	1658.8879	-0.9533	0	(22)	4.1	1	R.IINEPTAARIAYGLDK.K
<input checked="" type="checkbox"/> 1835	830.4492	1658.8838	1658.8879	-0.0041	0	(89)	8.8e-007	1	R.IINEPTAARIAYGLDK.K
<input checked="" type="checkbox"/> 1836	830.4502	1658.8858	1658.8879	-0.0020	0	102	4.7e-008	1	R.IINEPTAARIAYGLDK.K
<input checked="" type="checkbox"/> 1837	830.4504	1658.8862	1658.8879	-0.0017	0	(94)	2.7e-007	1	R.IINEPTAARIAYGLDK.K
<input checked="" type="checkbox"/> 1838	830.4515	1658.8884	1658.8879	0.0005	0	(98)	1.1e-007	1	R.IINEPTAARIAYGLDK.K
<input checked="" type="checkbox"/> 1839	830.8245	1659.6344	1658.8879	0.7465	0	(69)	8.4e-005	1	R.IINEPTAARIAYGLDK.K
<input checked="" type="checkbox"/> 1841	830.9476	1659.8806	1658.8879	0.9927	0	(77)	1.3e-005	1	R.IINEPTAARIAYGLDK.K
<input checked="" type="checkbox"/> 1842	830.9527	1659.8908	1658.8879	1.0030	0	(84)	2.5e-006	1	R.IINEPTAARIAYGLDK.K
<input checked="" type="checkbox"/> 1843	830.9560	1659.8974	1658.8879	1.0096	0	(83)	3.5e-006	1	R.IINEPTAARIAYGLDK.K
<input checked="" type="checkbox"/> 1844	831.0821	1660.1496	1658.8879	1.2618	0	(40)	0.066	1	R.IINEPTAARIAYGLDK.K
<input checked="" type="checkbox"/> 1845	831.1986	1660.3827	1658.8879	1.4948	0	(80)	7.5e-006	1	R.IINEPTAARIAYGLDK.K
<input checked="" type="checkbox"/> 1858	833.3976	1664.7806	1664.7828	-0.0022	0	92	5.1e-007	1	K.NQVAMNPTNTVFDAK.R +
<input checked="" type="checkbox"/> 461	596.6694	1786.9863	1786.9828	0.0035	1	33	0.49	1	R.IINEPTAARIAYGLDK.V
<input checked="" type="checkbox"/> 1384	754.3890	2260.1453	2259.1382	1.0071	0	(54)	0.0028	1	K.SINPDEVRYGARVQARILS
<input checked="" type="checkbox"/> 3221	1131.0869	2260.1593	2259.1382	1.0211	0	120	4.1e-010	1	K.SINPDEVRYGARVQARILS

Proteins matching the same set of peptides:
[gi|24234686](#) Mass: 53484 Score: 719 Queries matched: 28

13. Heat shock protein gp96 precursor

[gi|15010550](#) Mass: 90138 Score: 562 Queries matched: 21
 heat shock protein gp96 precursor [Homo sapiens]
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 105	482.2984	962.5823	962.5800	0.0022	0	42	0.063	1	K.LIINSLYK.N
<input checked="" type="checkbox"/> 129	497.2672	992.5199	992.5178	0.0021	0	43	0.056	1	R.SGYLLPDTK.A
<input checked="" type="checkbox"/> 186	541.2769	1080.5392	1080.5352	0.0040	0	49	0.011	1	K.FRFQREVNR.M
<input checked="" type="checkbox"/> 260	572.3160	1142.6175	1142.5607	0.0568	1	12	61	5	R.GLFDEYGSKK.S
<input checked="" type="checkbox"/> 312	594.3446	1186.6747	1186.6710	0.0037	0	58	0.0014	1	K.SILFVPTSAPR.G
<input checked="" type="checkbox"/> 433	638.3256	1274.6366	1274.6354	0.0012	0	54	0.0035	1	R.ELISNASDALDK.I
<input checked="" type="checkbox"/> 812	743.3809	1484.7473	1484.7470	0.0002	0	56	0.0021	1	K.GVVDSDLLPLNVS.R.E
<input checked="" type="checkbox"/> 905	758.8624	1515.7102	1514.7041	1.0060	1	12	46	2	K.IADDKYNDTFWK.E
<input checked="" type="checkbox"/> 931	763.0728	1524.1311	1524.7195	-0.5884	0	(11)	54	1	K.EEASDYLELDTIK.N
<input checked="" type="checkbox"/> 932	763.3680	1524.7214	1524.7195	0.0019	0	76	1.7e-005	1	K.EEASDYLELDTIK.N
<input checked="" type="checkbox"/> 1583	861.3754	1720.7363	1720.7349	0.0014	0	59	0.00094	1	K.TETVEEPMEEEEAAK.E
<input checked="" type="checkbox"/> 1617	867.5812	1733.1478	1733.7479	-0.6001	0	7	1.3e+002	1	-.DDEVVDVGTVEEDLGGK.S
<input checked="" type="checkbox"/> 1622	867.5840	1733.1534	1733.7479	-0.5945	0	(2)	4e+002	8	-.DDEVVDVGTVEEDLGGK.S
<input checked="" type="checkbox"/> 1653	869.3707	1736.7269	1736.7298	-0.0029	0	(39)	0.086	1	K.TETVEEPMEEEEAAK.E + Oxidation (M)
<input checked="" type="checkbox"/> 1787	890.9893	1779.9641	1778.8120	1.1521	1	4	2.8e+002	3	R.RVFIPDDFHDMPK.Y + 2 Oxidation (M)
<input checked="" type="checkbox"/> 2108	939.9741	1877.9336	1877.9352	-0.0016	0	(34)	0.21	1	K.YSQFINFPIYVWSSK.T
<input checked="" type="checkbox"/> 2109	939.9741	1877.9337	1877.9352	-0.0015	0	(32)	0.33	1	K.YSQFINFPIYVWSSK.T
<input checked="" type="checkbox"/> 2110	939.9749	1877.9353	1877.9352	0.0001	0	(32)	0.38	1	K.YSQFINFPIYVWSSK.T
<input checked="" type="checkbox"/> 2113	940.4802	1878.9459	1877.9352	1.0107	0	98	9.3e-008	1	K.YSQFINFPIYVWSSK.T
<input checked="" type="checkbox"/> 2114	940.4810	1878.9475	1877.9352	1.0123	0	(12)	35	1	K.YSQFINFPIYVWSSK.T
<input checked="" type="checkbox"/> 2326	971.8185	2912.4338	2913.4847	-1.0509	1	1	4.5e+002	5	K.VEKTVMDVWELMNDIKPIWQRPSK.E + Oxidation (M)

14. Heparan sulfate proteoglycan perlecan

[gi1184427](#) Mass: 468525 Score: 175 Queries matched: 5
heparan sulfate proteoglycan

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
1228	780.4374	1558.8602	1557.8838	0.9764	1	5	2.3e+002	3	R.VTVTSEGGRTLIIR.D
<input checked="" type="checkbox"/> 1368	805.9386	1609.8626	1609.8562	0.0064	0	39	0.094	1	R.SLPEVPETIELEVR.T
<input checked="" type="checkbox"/> 1588	845.9407	1689.8668	1689.8685	-0.0017	0	81	6.9e-006	1	K.GSVYIGGAPDVATLTGGR.F
<input checked="" type="checkbox"/> 1983	906.0103	1810.0061	1809.8883	0.1178	0	43	0.03	1	R.EVSEAVVDTLESEYLK.I
<input checked="" type="checkbox"/> 3336	1272.7888	2543.5631	2542.2889	1.2742	1	13	19	1	K.FEIKITFRPDSADGMILLYGQK.R

Proteins matching the same set of peptides:

[gi11602963](#) Mass: 466304 Score: 175 Queries matched: 5
heparan sulfate proteoglycan perlecan [Homo sapiens]

[gi162859979](#) Mass: 468528 Score: 175 Queries matched: 5
heparan sulfate proteoglycan 2 [Homo sapiens]

15. Hexosaminidase B preproprotein

[gi1179462](#) Mass: 64321 Score: 268 Queries matched: 6
N-acetyl-beta-glucosaminidase prepro-polypeptide

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 263	550.3394	1098.6643	1098.6648	-0.0005	0	52	0.0062	1	K.VLDIATINK.G
<input checked="" type="checkbox"/> 334	578.3253	1154.6361	1154.6335	0.0026	1	57	0.0017	1	K.KLESEYIQK.V
<input checked="" type="checkbox"/> 386	595.8062	1189.5978	1189.5979	-0.0001	0	40	0.088	1	K.VEPLDFGGTQK.Q
<input checked="" type="checkbox"/> 428	606.8544	1211.6943	1211.6914	0.0029	0	32	0.54	1	K.LAPGTIVEVWK.D
<input checked="" type="checkbox"/> 859	711.8491	1421.6837	1421.6826	0.0010	0	55	0.0026	1	K.GSIVWQEVFDDK.R
<input checked="" type="checkbox"/> 1405	812.7331	2435.1775	2434.1692	1.0083	0	32	0.46	1	K.EISEVFPDQFIHLGGDEVEFK.C

Proteins matching the same set of peptides:

[gi1867691](#) Mass: 61808 Score: 268 Queries matched: 6
beta-hexosaminidase beta-subunit

[gi116924217](#) Mass: 63071 Score: 268 Queries matched: 6
Hexosaminidase B, preproprotein [Homo sapiens]

[gi130749656](#) Mass: 58081 Score: 268 Queries matched: 6
Chain B, Human Lysosomal Beta-Hexosaminidase Isoform B In Complex With Intermediate Analogue Nag-Th

[gi138492604](#) Mass: 58821 Score: 268 Queries matched: 6
Chain F, Human Beta-Hexosaminidase B

16. Human Fc γ binding protein

[gi15080756](#) Mass: 301609 Score: 112 Queries matched: 3
Human Fc gamma BP [AA 1-2843] [Homo sapiens]

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 570	590.3652	1178.7159	1178.7135	0.0024	0	59	0.0011	1	K.LPVVLANGQIR.A
<input checked="" type="checkbox"/> 745	631.3373	1260.6600	1259.6550	1.0050	0	57	0.0019	1	R.VAYDLVYYVR.V
2099	978.7813	2933.3221	2933.5345	-0.2124	1	1	4.2e+002	4	K.AYPRLLISSLSSESPASVSIQSADNTSK.K

Proteins matching the same set of peptides:

[gi14503681](#) Mass: 571718 Score: 108 Queries matched: 3
Fc fragment of IgG binding protein [Homo sapiens]

17. Ig kappa chain V-III

[gi|106586](#) Mass: 23037 Score: 154 Queries matched: 5
Ig kappa chain V-III (KAU cold agglutinin) - human
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
271	752.2289	1502.4432	1501.7512	0.6921	0	(8)	1.1e+002	2	K.DSTYLSSTLTLSK.A
<input checked="" type="checkbox"/> 272	752.2354	1502.4562	1501.7512	0.7050	0	43	0.036	1	K.DSTYLSSTLTLSK.A
<input checked="" type="checkbox"/> 273	752.2454	1502.4763	1501.7512	0.7251	0	(6)	2e+002	1	K.DSTYLSSTLTLSK.A
<input checked="" type="checkbox"/> 1892	1068.9955	2135.9764	2134.9614	1.0150	0	109	6.6e-009	1	K.VDNALQSGNSQESVTEQDSK.D
350	759.9188	2276.7346	2276.1549	0.5798	1	3	3.9e+002	8	K.VYAGEVTHQGLSSPVTKSFNR.G

18. Laminin γ1 precursor

[gi|126369](#) Mass: 177492 Score: 333 Queries matched: 12
Laminin gamma-1 chain precursor (Laminin B2 chain)
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
16	464.2624	926.5102	927.4298	-0.9195	0	9	85	5	K.QEADDIVR.V + Pyro-glu (N-term Q)
<input checked="" type="checkbox"/> 92	687.4029	1372.7912	1372.6946	0.0966	0	35	0.24	1	K.TEQQTADQLLAR.A
<input checked="" type="checkbox"/> 109	721.9606	1441.9066	1441.7776	0.1291	0	56	0.0016	1	R.LSÆEDLVLEGAGLR.V
<input checked="" type="checkbox"/> 112	726.8530	1451.6914	1451.6164	0.0750	0	30	0.6	1	R.DGSEASLEWSSER.Q
<input checked="" type="checkbox"/> 118	748.4277	1494.8408	1494.6990	0.1418	0	63	0.00032	1	R.LNTPGDEVFNDPK.V
<input checked="" type="checkbox"/> 121	755.9399	1509.8652	1509.7463	0.1189	0	30	0.65	1	R.QDIAVISDSYFPR.Y
<input checked="" type="checkbox"/> 126	773.4544	1544.8942	1544.7430	0.1512	0	13	38	1	R.NTIEETGNLÆQAR.A
<input checked="" type="checkbox"/> 132	800.9741	1599.9336	1599.8104	0.1233	0	49	0.0076	1	R.DTLQEQANDILNMLK.D
166	985.0474	1968.0802	1967.9146	0.1657	0	11	49	2	R.TFÆVTDLDNEVNNMLK.Q + Oxidation (M)
<input checked="" type="checkbox"/> 169	995.6028	1989.1910	1989.0418	0.1492	0	16	14	1	R.VSVPLIAQGNSTPSETTVK.Y
<input checked="" type="checkbox"/> 213	965.5185	2893.5337	2893.3651	0.1686	0	46	0.014	1	K.LQELSLIANLGTGDEMVDQAFEDR.L
216	970.8697	2909.5873	2909.3600	0.2273	0	(12)	34	2	K.LQELSLIANLGTGDEMVDQAFEDR.L + Oxidation (M)

Proteins matching the same set of peptides:
[gi|9845498](#) Mass: 177459 Score: 333 Queries matched: 12
laminin, gamma 1 precursor [Homo sapiens]

19. Legumain preproprotein

[gi|1890050](#) Mass: 49351 Score: 244 Queries matched: 7
cysteine protease [Homo sapiens]
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 786	669.3062	1336.5978	1336.5929	0.0049	0	55	0.0025	1	K.LMNTNDLEESR.Q + Oxidation (M)
228	489.2389	1464.6948	1464.6878	0.0070	1	34	0.46	2	R.KLMNTNDLEESR.Q + Oxidation (M)
1110	748.3658	1494.7170	1494.6085	0.1085	1	4	2.9e+002	10	R.ESSYACYDEKR.S + Pyro-glu (N-term E)
585	646.6599	1936.9579	1936.9530	0.0049	0	(6)	2.3e+002	3	K.DYTGEDVTPQNFVAVLR.G
<input checked="" type="checkbox"/> 1900	969.9907	1937.9669	1936.9530	1.0139	0	69	6.4e-005	1	K.DYTGEDVTPQNFVAVLR.G
<input checked="" type="checkbox"/> 2024	1029.5625	2057.1104	2056.1051	1.0053	0	82	3.2e-006	1	K.IVSLLAÆSEÆVEQLLSER.A
<input checked="" type="checkbox"/> 864	686.7138	2057.1196	2056.1051	1.0145	0	(51)	0.0058	1	K.IVSLLAÆSEÆVEQLLSER.A

Proteins matching the same set of peptides:
[gi|56682964](#) Mass: 49379 Score: 244 Queries matched: 7
legumain preproprotein [Homo sapiens]

20. Met proto-oncogene precursor

[gi|125484](#) Mass: 155427 Score: 131 Queries matched: 2
 Hepatocyte growth factor receptor precursor (Met proto-oncogene tyrosine kinase) (c-met) (HGF recep

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 207	702.3608	1402.7071	1402.7052	0.0020	0	85	2.5e-006	1	K.GDLTIANLGTSEGR.F
<input checked="" type="checkbox"/> 237	720.8741	1439.7336	1439.7296	0.0040	0	46	0.018	1	R.EDPIVYIEIHPK.S

Proteins matching the same set of peptides:

[gi|307196](#) Mass: 157611 Score: 131 Queries matched: 2
 MET proto-oncogene protein

[gi|2078456](#) Mass: 84489 Score: 131 Queries matched: 2
 receptor protein tyrosine kinase [Homo sapiens]

[gi|51095116](#) Mass: 155441 Score: 131 Queries matched: 2
 met proto-oncogene (hepatocyte growth factor receptor) [Homo sapiens]

21. N-acetylgalactosamine-6-sulfatase

[gi|4503899](#) Mass: 57989 Score: 113 Queries matched: 4
 N-acetylgalactosamine-6-sulfatase precursor [Homo sapiens]

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
175	797.5389	1593.0632	1592.9249	0.1383	0	7	1.2e+002	2	R.AIDGLNLLPTLLQGR.L
<input checked="" type="checkbox"/> 228	606.0135	1815.0187	1814.8838	0.1348	0	(42)	0.04	1	R.FPLSFASAEYQEALSR.I
<input checked="" type="checkbox"/> 229	908.5168	1815.0190	1814.8838	0.1352	0	61	0.00044	1	R.FPLSFASAEYQEALSR.I
<input checked="" type="checkbox"/> 306	875.5475	2623.6207	2623.3744	0.2463	0	44	0.022	1	R.HAYTPOEIVGGIPDSEQLPELLK.K

Proteins matching the same set of peptides:

[gi|34526537](#) Mass: 51082 Score: 113 Queries matched: 4
 FLJ00319 protein [Homo sapiens]

22. N-acetylglucosamine-6-sulfatase

[gi|4504061](#) Mass: 62042 Score: 363 Queries matched: 15
 N-acetylglucosamine-6-sulfatase precursor

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 217	493.2820	984.5494	984.5491	0.0003	0	56	0.0027	1	K.TIDPELLGK.M
<input checked="" type="checkbox"/> 284	519.7606	1037.5066	1037.5069	-0.0004	0	(20)	12	1	R.QLYEFDIK.V + Pyro-glu (N-term Q)
<input checked="" type="checkbox"/> 310	525.2795	1048.5445	1048.5454	-0.0008	0	56	0.0032	1	K.AFQNVFAPR.N
<input checked="" type="checkbox"/> 316	528.2747	1054.5348	1054.5335	0.0013	0	26	2.5	1	R.QLYEFDIK.V
<input checked="" type="checkbox"/> 873	676.3266	1350.6386	1350.6415	-0.0028	0	68	0.00015	1	R.SDVLVEYQGEGR.N
1102	729.3085	1456.6025	1457.6135	-1.0110	0	9	1.3e+002	5	R.LMLQSCSGPTCR.T + 2 Oxidation (M)
<input checked="" type="checkbox"/> 1209	745.8912	1489.7678	1489.7632	0.0046	0	(55)	0.0031	1	K.TQMDGMSLLPILR.G + Oxidation (M)
<input checked="" type="checkbox"/> 239	502.9275	1505.7606	1505.7582	0.0024	0	(38)	0.19	1	K.TQMDGMSLLPILR.G + 2 Oxidation (M)
<input checked="" type="checkbox"/> 1255	753.8887	1505.7628	1505.7582	0.0046	0	(54)	0.0042	1	K.TQMDGMSLLPILR.G + 2 Oxidation (M)
<input checked="" type="checkbox"/> 1257	754.3914	1506.7682	1505.7582	1.0100	0	59	0.0011	1	K.TQMDGMSLLPILR.G + 2 Oxidation (M)
1380	773.0526	1544.0907	1544.8086	-0.7179	0	(9)	1.1e+002	2	R.WQTLLSVDDLVEK.L
<input checked="" type="checkbox"/> 271	515.9438	1544.8095	1544.8086	0.0009	0	(43)	0.054	1	R.WQTLLSVDDLVEK.L
<input checked="" type="checkbox"/> 1386	773.4141	1544.8136	1544.8086	0.0050	0	79	1.2e-005	1	R.WQTLLSVDDLVEK.L
982	698.6896	2093.0469	2092.8985	0.1484	1	5	3.1e+002	4	K.MNYRLMLQSCSGPTCR.T + 2 Oxidation (M); Propionamide
2042	912.1074	2733.3003	2734.3246	-1.0244	1	4	3.8e+002	8	K.IQEPNTFPAILRSMCGYQTFVAGK.Y + Oxidation (M)

23. Prosaposin

[gi|220064](#) Mass: 58445 Score: 162 Queries matched: 8
sphingolipid activator proteins [Homo sapiens]

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
633	630.3361	1258.6577	1259.6254	-0.9677	0	(10)	82	8	K.EMPMQTLVPAK.V + Oxidation (M)
646	630.4136	1258.8127	1259.6254	-0.8126	0	15	29	5	K.EMPMQTLVPAK.V + Oxidation (M)
<input checked="" type="checkbox"/> 1155	717.9344	1433.8542	1433.8493	0.0049	0	9	88	1	K.NVIPALELVEPIK.K
<input checked="" type="checkbox"/> 1536	781.9803	1561.9461	1561.9443	0.0019	1	58	0.0012	1	K.NVIPALELVEPIK.H
<input checked="" type="checkbox"/> 214	521.9906	1562.9500	1561.9443	1.0057	1	(19)	12	1	K.NVIPALELVEPIK.H
1752	815.9373	1629.8600	1628.8629	0.9970	1	15	23	2	K.EMPMQTLVPAKVASK.N
<input checked="" type="checkbox"/> 364	577.3387	1728.9944	1728.9913	0.0031	0	(54)	0.0036	1	K.EIVDSYLPVILDIK.G
<input checked="" type="checkbox"/> 2008	865.5078	1729.0011	1728.9913	0.0098	0	70	7.6e-005	1	K.EIVDSYLPVILDIK.G

Proteins matching the same set of peptides:

[gi|337760](#) Mass: 58429 Score: 162 Queries matched: 8
cerebroside sulfate activator protein

[gi|337765](#) Mass: 58058 Score: 162 Queries matched: 8
cerebroside sulfate activator protein

[gi|337767](#) Mass: 58301 Score: 162 Queries matched: 8
cerebroside sulfate activator protein

[gi|48145609](#) Mass: 58058 Score: 162 Queries matched: 8
PSAP [Homo sapiens]

[gi|57209715](#) Mass: 58074 Score: 162 Queries matched: 8
prosaposin (variant Gaucher disease and variant metachromatic leukodystrophy) [Homo sapiens]

24. Protective protein for β -galactosidase

[gi|2098348](#) Mass: 51406 Score: 167 Queries matched: 2
Chain B, Physiological Dimer Hpp Precursor

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 739	685.8345	1369.6545	1369.6513	0.0032	0	84	2.9e-006	1	K.YGDSGEQIAGFVK.E
<input checked="" type="checkbox"/> 1265	788.9230	1575.8315	1575.8256	0.0059	0	82	4.1e-006	1	K.DTVVVQDLGNIET.R.L

Proteins matching the same set of peptides:

[gi|3191969](#) Mass: 54431 Score: 167 Queries matched: 2
PPCB [Homo sapiens]

[gi|4505989](#) Mass: 54461 Score: 167 Queries matched: 2
protective protein for beta-galactosidase [Homo sapiens]

[gi|12653639](#) Mass: 54318 Score: 167 Queries matched: 2
Protective protein for beta-galactosidase [Homo sapiens]

25. Protein-tyrosine kinase-related receptor PTK7 precursor

[gi|2136061](#) Mass: 118331 Score: 155 Queries matched: 5
protein-tyrosine kinase-related receptor PTK7 precursor - human

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
103	596.8533	1191.6920	1191.5554	0.1367	0	(7)	1.7e+002	3	R.NQMLISED.SR.F
<input checked="" type="checkbox"/> 108	604.8456	1207.6766	1207.5503	0.1264	0	30	0.75	1	R.NQMLISED.SR.F + Oxidation (M)
<input checked="" type="checkbox"/> 128	633.4556	1264.8966	1264.7503	0.1464	0	53	0.0033	1	R.VVLAPODVVVVAR.Y
<input checked="" type="checkbox"/> 213	574.0142	1719.0208	1718.8528	0.1679	0	44	0.025	1	K.GLPEPSVWMEHAGVR.L
<input checked="" type="checkbox"/> 300	748.7713	2243.2921	2243.0607	0.2314	0	30	0.58	1	R.ADGSSLPEWVTDNAGTLHFA.R.V

Proteins matching the same set of peptides:

[gi|8134650](#) Mass: 118186 Score: 155 Queries matched: 5
Tyrosine-protein kinase-like 7 precursor (Colon carcinoma kinase 4) (CCK-4)

26. Protein tyrosine phosphatase kappa

[gi|1479976](#) Mass: 162127 Score: 359 Queries matched: 13
protein tyrosine phosphatase [Homo sapiens]

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 18	515.8237	1029.6328	1029.5277	0.1052	0	35	0.26	1	K.MILTNPGR.K
<input checked="" type="checkbox"/> 22	523.3309	1044.6472	1045.5226	-0.8753	0	(24)	3.3	1	K.MILTNPGR.K + Oxidation (M)
<input checked="" type="checkbox"/> 39	555.8320	1109.6494	1109.5353	0.1142	0	11	56	1	K.SLQGTSEENK.I
<input checked="" type="checkbox"/> 86	633.9402	1265.8658	1265.7455	0.1203	0	65	0.0002	1	K.GLNPGTLNILVR.V
<input checked="" type="checkbox"/> 154	562.9880	1685.9422	1685.8049	0.1373	0	35	0.22	1	K.LWHLDPDTEYEIR.V
<input checked="" type="checkbox"/> 189	661.0405	1980.0997	1979.9047	0.1950	0	33	0.32	1	R.MTSGSWTETHAVNAPTYK.L
<input checked="" type="checkbox"/> 195	666.3761	1996.1065	1995.8996	0.2069	0	(28)	0.91	1	R.MTSGSWTETHAVNAPTYK.L + Oxidation (M)
<input checked="" type="checkbox"/> 199	672.7570	2015.2492	2015.0588	0.1904	0	40	0.062	1	K.GAPISRYQIVVEELMPHR.T
<input checked="" type="checkbox"/> 205	1036.1237	2070.2328	2069.9979	0.2349	0	18	10	1	R.SGYIAIDDIQVLSYPCDK.S + Propionamide (C)
<input checked="" type="checkbox"/> 217	1091.6416	2181.2686	2181.0688	0.1998	0	17	13	1	K.ESEETIIQTDEDPVGPVPVK.S
<input checked="" type="checkbox"/> 228	765.7963	2294.3671	2294.1430	0.2241	0	35	0.21	1	K.EPLDPNGIITQYEISYSSIR.S
<input checked="" type="checkbox"/> 233	770.8033	2309.3881	2309.1638	0.2243	1	48	0.0083	1	R.KESEETIIQTDEDPVGPVPVK.S
<input checked="" type="checkbox"/> 261	933.9048	2798.6926	2798.3550	0.3375	0	29	0.72	1	R.AELAVSTFWPNEYQVIFEREVSQGR.S

Proteins matching the same set of peptides:
[gi|57160745](#) Mass: 161998 Score: 359 Queries matched: 13
PTPRK [Homo sapiens]
[gi|17439347](#) Mass: 162100 Score: 356 Queries matched: 13
protein-tyrosine-phosphatase (EC 3.1.3.48) receptor-type - human

27. Ribonuclease T2 precursor

[gi|5231228](#) Mass: 29462 Score: 420 Queries matched: 32
ribonuclease T2 precursor [Homo sapiens]

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 69	437.2289	872.4433	872.4426	0.0008	0	(19)	15	2	K.DLLPEMR.A
<input checked="" type="checkbox"/> 84	445.2259	888.4372	888.4375	-0.0003	0	22	8.1	2	K.DLLPEMR.A + Oxidation (M)
<input checked="" type="checkbox"/> 85	445.2261	888.4377	888.4375	0.0002	0	(22)	8.2	3	K.DLLPEMR.A + Oxidation (M)
<input checked="" type="checkbox"/> 272	563.3302	1124.6458	1124.6441	0.0018	0	53	0.005	1	R.ELDLSVLLK.L + Pyro-glu (N-term E)
<input checked="" type="checkbox"/> 275	563.8222	1125.6299	1124.6441	0.9858	0	(18)	19	5	R.ELDLSVLLK.L + Pyro-glu (N-term E)
<input checked="" type="checkbox"/> 291	572.3350	1142.6554	1142.6546	0.0007	0	(47)	0.022	1	R.ELDLSVLLK.L
<input checked="" type="checkbox"/> 292	572.8250	1143.6355	1142.6546	0.9808	0	(13)	64	6	R.ELDLSVLLK.L
<input checked="" type="checkbox"/> 293	572.8265	1143.6384	1142.6546	0.9838	0	(15)	38	3	R.ELDLSVLLK.L
<input checked="" type="checkbox"/> 294	572.8269	1143.6393	1142.6546	0.9846	0	(30)	1	1	R.ELDLSVLLK.L
<input checked="" type="checkbox"/> 295	572.8270	1143.6395	1142.6546	0.9849	0	(15)	34	6	R.ELDLSVLLK.L
<input checked="" type="checkbox"/> 296	572.8272	1143.6399	1142.6546	0.9852	0	(15)	33	2	R.ELDLSVLLK.L
<input checked="" type="checkbox"/> 469	631.8244	1261.6343	1261.6342	0.0000	0	(39)	0.12	1	R.SWPFNLEEIK.D
<input checked="" type="checkbox"/> 470	631.8244	1261.6343	1261.6342	0.0000	0	48	0.018	1	R.SWPFNLEEIK.D
<input checked="" type="checkbox"/> 471	632.3169	1262.6192	1261.6342	0.9850	0	(33)	0.56	1	R.SWPFNLEEIK.D
<input checked="" type="checkbox"/> 780	707.8330	1413.6515	1412.6684	0.9831	0	(26)	2.8	1	K.QEVWLANGAESR.G + Pyro-glu (N-term Q)
<input checked="" type="checkbox"/> 781	707.8339	1413.6533	1412.6684	0.9849	0	40	0.11	1	K.QEVWLANGAESR.G + Pyro-glu (N-term Q)
<input checked="" type="checkbox"/> 782	707.8345	1413.6544	1412.6684	0.9860	0	(32)	0.65	1	K.QEVWLANGAESR.G + Pyro-glu (N-term Q)
<input checked="" type="checkbox"/> 816	716.3464	1430.6782	1429.6949	0.9833	0	(30)	1.1	1	K.QEVWLANGAESR.G
<input checked="" type="checkbox"/> 817	716.3464	1430.6783	1429.6949	0.9834	0	(35)	0.31	1	K.QEVWLANGAESR.G
<input checked="" type="checkbox"/> 819	716.3483	1430.6820	1429.6949	0.9871	0	(25)	3.4	1	K.QEVWLANGAESR.G
<input checked="" type="checkbox"/> 1052	759.8701	1517.7257	1517.7224	0.0033	0	59	0.0011	1	R.VCEDGPFYPPPK.K + Propionamide (C)
<input checked="" type="checkbox"/> 224	538.9233	1613.7482	1612.7627	0.9855	0	(45)	0.038	1	K.HGTCAQVDALNSQK.K + Propionamide (C)
<input checked="" type="checkbox"/> 225	538.9239	1613.7500	1612.7627	0.9873	0	(63)	0.00059	1	K.HGTCAQVDALNSQK.K + Propionamide (C)
<input checked="" type="checkbox"/> 1350	807.8836	1613.7527	1612.7627	0.9899	0	63	0.00045	1	K.HGTCAQVDALNSQK.K + Propionamide (C)
<input checked="" type="checkbox"/> 377	600.6335	1798.8786	1798.8746	0.0040	0	33	0.54	1	K.LIMVQHWPETVCEK.I + Oxidation (M); Propionamide (C)
<input checked="" type="checkbox"/> 413	613.9616	1838.8630	1838.8628	0.0002	0	(40)	0.11	1	R.DPPDYWTIHGLWPK.S
<input checked="" type="checkbox"/> 1907	920.4389	1838.8633	1838.8628	0.0005	0	(62)	0.00051	1	R.DPPDYWTIHGLWPK.S
<input checked="" type="checkbox"/> 414	613.9620	1838.8643	1838.8628	0.0015	0	(28)	1.6	1	R.DPPDYWTIHGLWPK.S
<input checked="" type="checkbox"/> 1911	920.9407	1839.8669	1838.8628	1.0041	0	69	0.00011	1	R.DPPDYWTIHGLWPK.S
<input checked="" type="checkbox"/> 429	619.3825	1855.1257	1854.9879	0.1378	0	19	14	1	K.LGIKPSINYQVDFK.D
<input checked="" type="checkbox"/> 798	712.0315	2133.0727	2132.0612	1.0115	1	15	33	2	R.SWPFNLEEIKDLLPEMR.A + Oxidation (M)
<input checked="" type="checkbox"/> 1988	933.8796	2798.6171	2798.3830	0.2341	0	7	1.8e+002	1	K.IQCLPPSQDEEVQTIGIQLCLTK.Q + 2 Carbamidomethyl (C)

28. Tissue inhibitor of metalloproteinase-1

[gi|31189](#) Mass: 23182 Score: 119 Queries matched: 6
unnamed protein product [Homo sapiens]

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 144	497.2670	992.5195	992.5178	0.0017	0	45	0.034	1	R.SEEFLIAGK.L
<input checked="" type="checkbox"/> 561	617.3123	1232.6101	1232.6149	-0.0048	0	(15)	32	5	K.GFQALGDARDIR.F
<input checked="" type="checkbox"/> 562	617.3150	1232.6155	1232.6149	0.0006	0	(61)	0.00082	1	K.GFQALGDARDIR.F
<input checked="" type="checkbox"/> 563	617.3152	1232.6159	1232.6149	0.0010	0	74	3.4e-005	1	K.GFQALGDARDIR.F
<input checked="" type="checkbox"/> 564	617.3153	1232.6161	1232.6149	0.0012	0	(71)	7.5e-005	1	K.GFQALGDARDIR.F
<input checked="" type="checkbox"/> 565	617.3156	1232.6166	1232.6149	0.0017	0	(37)	0.2	1	K.GFQALGDARDIR.F

Proteins matching the same set of peptides:

[gi|220125](#) Mass: 18808 Score: 119 Queries matched: 6
tissue inhibitor of metalloproteinases [Homo sapiens]

[gi|4140013](#) Mass: 20609 Score: 119 Queries matched: 6
Chain D, Mmp-3TIMP-1 Complex

[gi|34811011](#) Mass: 14243 Score: 119 Queries matched: 6
Chain B, Orientation In Solution Of Mmp-3 Catalytic Domain And N- Timp-1 From Residual Dipolar Coup

[gi|57210053](#) Mass: 23156 Score: 119 Queries matched: 6
tissue inhibitor of metalloproteinase 1 (erythroid potentiating activity, collagenase inhibitor) [H

29. Tumor-associated calcium signal transducer 1

[gi|4505059](#) Mass: 34880 Score: 204 Queries matched: 18
tumor-associated calcium signal transducer 1 precursor [Homo sapiens]

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> 1093	945.9434	1889.8722	1889.8683	0.0039	0	(117)	1.2e-009	1	K.TQNDVDIADVAYYFEK.D
<input checked="" type="checkbox"/> 1094	945.9449	1889.8753	1889.8683	0.0071	0	(104)	2.4e-008	1	K.TQNDVDIADVAYYFEK.D
<input checked="" type="checkbox"/> 1095	945.9457	1889.8768	1889.8683	0.0085	0	(104)	2.4e-008	1	K.TQNDVDIADVAYYFEK.D
<input checked="" type="checkbox"/> 1096	945.9464	1889.8781	1889.8683	0.0099	0	(111)	4.2e-009	1	K.TQNDVDIADVAYYFEK.D
<input checked="" type="checkbox"/> 1098	946.3539	1890.6933	1889.8683	0.8251	0	(94)	2.2e-007	1	K.TQNDVDIADVAYYFEK.D
<input checked="" type="checkbox"/> 1099	946.4418	1890.8690	1889.8683	1.0007	0	123	3.1e-010	1	K.TQNDVDIADVAYYFEK.D
<input checked="" type="checkbox"/> 1100	946.4426	1890.8706	1889.8683	1.0023	0	(104)	2.4e-008	1	K.TQNDVDIADVAYYFEK.D
<input checked="" type="checkbox"/> 1101	946.4434	1890.8722	1889.8683	1.0039	0	(59)	0.00077	1	K.TQNDVDIADVAYYFEK.D
<input checked="" type="checkbox"/> 1102	946.4454	1890.8763	1889.8683	1.0080	0	(87)	1.3e-006	1	K.TQNDVDIADVAYYFEK.D
<input checked="" type="checkbox"/> 1103	946.4493	1890.8840	1889.8683	1.0157	0	(109)	6.5e-009	1	K.TQNDVDIADVAYYFEK.D
<input checked="" type="checkbox"/> 2954	1435.7000	2869.3854	2868.3738	1.0115	0	(54)	0.0012	1	K.MDLTVNGEQLDLDPGQTLIYYVDEK.A
<input checked="" type="checkbox"/> 2955	1435.7002	2869.3858	2868.3738	1.0120	0	(42)	0.02	1	K.MDLTVNGEQLDLDPGQTLIYYVDEK.A
<input checked="" type="checkbox"/> 2956	1435.7026	2869.3907	2868.3738	1.0169	0	(54)	0.0012	1	K.MDLTVNGEQLDLDPGQTLIYYVDEK.A
<input checked="" type="checkbox"/> 2957	1435.7043	2869.3941	2868.3738	1.0203	0	67	5.6e-005	1	K.MDLTVNGEQLDLDPGQTLIYYVDEK.A
<input checked="" type="checkbox"/> 1156	957.5814	2869.7223	2868.3738	1.3484	0	(26)	1.3	1	K.MDLTVNGEQLDLDPGQTLIYYVDEK.A
<input checked="" type="checkbox"/> 2985	1443.7085	2885.4024	2884.3688	1.0337	0	(10)	33	1	K.MDLTVNGEQLDLDPGQTLIYYVDEK.A + Oxidation (M)
<input checked="" type="checkbox"/> 1412	999.5244	2995.5512	2996.4688	-0.9176	1	9	75	1	K.KMDLTVNGEQLDLDPGQTLIYYVDEK.A
<input checked="" type="checkbox"/> 2299	1173.2487	3516.7241	3516.1243	0.5999	1	6	1.1e+002	1	K.APEFSMQLKAGVIRIVVVVIRVAVGIVLVISR.K

Proteins matching the same set of peptides:

[gi|49457558](#) Mass: 34910 Score: 204 Queries matched: 18
TACSTD1 [Homo sapiens]

30. Zn- α -2-glycoprotein

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Peptide
<input checked="" type="checkbox"/> gi 38026		Mass: 34714	Score: 510	Queries matched: 14					Zn-alpha2-glycoprotein [Homo sapiens]
<input type="checkbox"/> Check to include this hit in error tolerant search or archive report									
<input checked="" type="checkbox"/> 231	464.7255	927.4365	927.4338	0.0027	0	35	0.32	1	K.DYIEFNK.E
<input checked="" type="checkbox"/> 302	495.7464	989.4782	989.4753	0.0030	0	22	6.8	2	K.SQPMGLWR.Q + Oxidation (M)
<input checked="" type="checkbox"/> 521	564.2902	1126.5658	1126.5618	0.0040	0	55	0.0038	1	R.AGEVQEPFLR.G
<input checked="" type="checkbox"/> 594	588.3002	1174.5859	1175.5321	-0.9462	0	11	67	3	K.CLAYDFYPGK.I
<input checked="" type="checkbox"/> 791	638.8214	1275.6281	1275.6247	0.0034	0	45	0.027	1	K.YEAEFVYVQR.A
<input checked="" type="checkbox"/> 198	456.9005	1367.6795	1367.6755	0.0041	1	(44)	0.043	1	K.AREDIFMETLK.D + Oxidation (M)
<input checked="" type="checkbox"/> 1006	684.8477	1367.6808	1367.6755	0.0053	1	69	0.00011	1	K.AREDIFMETLK.D + Oxidation (M)
<input checked="" type="checkbox"/> 1082	704.5203	1407.0261	1407.7285	-0.7024	0	(13)	37	1	R.YSLTYIYTGLSK.H
<input checked="" type="checkbox"/> 1084	704.8745	1407.7345	1407.7285	0.0059	0	86	1.9e-006	1	R.YSLTYIYTGLSK.H
<input checked="" type="checkbox"/> 1288	758.3850	1514.7555	1514.7517	0.0037	1	63	0.00038	1	K.QKWEAEFVYVQR.A + Pyro-glu (N-term Q)
<input checked="" type="checkbox"/> 610	592.9709	1775.8908	1774.8849	1.0059	0	24	3.4	1	R.QDPPSVVVTSHQAPGEK.K
<input checked="" type="checkbox"/> 1819	892.4813	1782.9480	1781.9352	1.0128	0	(26)	1.8	1	K.EIPAWVFPDPAQITK.Q
<input checked="" type="checkbox"/> 615	595.3238	1782.9495	1781.9352	1.0144	0	35	0.33	1	K.EIPAWVFPDPAQITK.Q
<input checked="" type="checkbox"/> 2787	1202.6101	2403.2057	2402.2018	1.0038	0	64	0.00014	1	K.HVEDVPAFQRLGSLNDLQEFR.Y
Proteins matching the same set of peptides:									
gi 141596		Mass: 33851	Score: 510	Queries matched: 14					Zinc-alpha-2-glycoprotein precursor (Zn-alpha-2-glycoprotein) (Zn-alpha-2-GP)
gi 4502337		Mass: 34237	Score: 510	Queries matched: 14					alpha-2-glycoprotein 1, zinc [Homo sapiens]