

Supplemental Table. Identities of proteins in 165 spots from 2D gel.

From **"POET: Using proteomics to screen pools of open reading frames for protein expression"**, by Gillette, et al.

Spots with a letter suffix contained more than one protein. 170 spots were picked for identification by MS. Two were lost in processing. Three spots contained 9, 11, and 16 different proteins, each identified by a single peptide, and were judged unreliable and omitted from the table. Thus proteins identified from 165 spots are included in this table. Note that spot numbers do not correspond to lane numbers in the main text.

Spot #	Swiss Prot ID	Protein ID	Organism	Total peptides	# different peptides	MW ¹
001	P02931	Outer membrane protein F precursor (Porin ompF) (Outer membrane protein 1A) (Outer membrane protein IA) (Outer membrane protein B)	E. coli	106	12	39333
002a	O44739	Bag1 (Human) homolog protein 1 (BAG-family molecular chaperone regulator-1)	C. elegans	61	13	24010
002b	P02931	Outer membrane protein F precursor	E. coli	37	11	39333

		(Porin ompF) (Outer membrane protein 1A) (Outer membrane protein IA) (Outer membrane protein B)				
003	P02931	Outer membrane protein F precursor (Porin ompF) (Outer membrane protein 1A) (Outer membrane protein IA) (Outer membrane protein B)	E. coli	109	11	39333
004	P30856	FKBP-type peptidyl-prolyl cis-trans isomerase slyD (EC 5.2.1.8) (PPIase) (Rotamase) (Histidine-rich protein) (WHP)	E. coli	58	6	20853
005	P30856	FKBP-type peptidyl-prolyl cis-trans isomerase slyD (EC 5.2.1.8) (PPIase) (Rotamase) (Histidine-rich protein) (WHP)	E. coli	67	6	20853
006	O17406	Hypothetical protein F09G2.9	C. elegans	88	25	44287
007a	P03020	Catabolite gene activator (cAMP receptor protein) (cAMP-regulatory protein)	E. coli	7	6	23640
007b	P34477	Probable ubiquitin-conjugating enzyme E2 7 (EC 6.3.2.19) (Ubiquitin-protein ligase 7) (Ubiquitin carrier protein 7)	C. elegans	7	4	18938
008	Q9XVI9	Hypothetical protein T12D8.6	C. elegans	23	5	15971

009	P33918	Ribosomal small subunit pseudouridine synthase A (EC 4.2.1.70) (16S pseudouridylate 516 synthase) (16S pseudouridine 516 synthase) (Uracil hydrolyase)	E. coli	51	11	25865
010	P02934	Outer membrane protein A precursor (Outer membrane protein II*)	E. coli	79	18	37201
011	P02931	Outer membrane protein F precursor (Porin ompF) (Outer membrane protein 1A) (Outer membrane protein IA) (Outer membrane protein B)	E. coli	104	11	39333
012	O17850	Machado-Joseph disease-like protein	C. elegans	44	16	35863
13a	P49596	Probable protein phosphatase 2C T23F11.1 (EC 3.1.3.16) (PP2C)	C. elegans	31	10	39064
13b	Q93375	C. elegans TAP-1 protein (Corresponding sequence C44H4.5) (TAB1-like protein TAP-1)	C. elegans	24	10	43469
014	Q93375	C. elegans TAP-1 protein (Corresponding sequence C44H4.5) (TAB1-like protein TAP-1)	C. elegans	28	11	43469
015	Q22871	Skp1p homolog (SKR-12) (Skp1 related (Ubiquitin ligase complex	C. elegans	28	6	18926

		component) protein 12)				
016	P02392	50S ribosomal protein L7/L12 (L8)	E. coli	23	6	12164
017	P09372	GrpE protein (HSP-70 cofactor) (Heat shock protein B25.3) (HSP24)	E. coli	15	5	21798
018	O17850	Machado-Joseph disease-like protein	C. elegans	15	6	35863
019a	P49596	Probable protein phosphatase 2C T23F11.1 (EC 3.1.3.16) (PP2C)	C. elegans	39	11	39064
019b	Q93375	C. elegans TAP-1 protein (Corresponding sequence C44H4.5) (TAB1-like protein TAP-1)	C. elegans	20	9	43469
020	P49596	Probable protein phosphatase 2C T23F11.1 (EC 3.1.3.16) (PP2C)	C. elegans	4	2	39064
021	O02592	PTL-1A protein (Protein with tau-like repeats protein 1, isoform a)	C. elegans	32	8	49416
022	Q93375	C. elegans TAP-1 protein (Corresponding sequence C44H4.5) (TAB1-like protein TAP-1)	C. elegans	42	11	43469
023	O02592	PTL-1A protein (Protein with tau-like repeats protein 1, isoform a)	C. elegans	27	10	49416
024a	Q93510	Hypothetical protein F15D4.2	C. elegans	7	5	20017
024b	Q9TXJ0	Cam kinase protein 1	C. elegans	5	4	39124
025	Q09665	Troponin C, isoform 2	C. elegans	28	8	18227

026	Q20728	Hypothetical protein F53F4.3 in chromosome V	C. elegans	17	9	25440
027	P02934	Outer membrane protein A precursor (Outer membrane protein II*)	E. coli	31	12	37201
028a	Q18212	Probable ATP-dependent RNA helicase p47 homolog	C. elegans	16	9	48492
028b	O45418	C. elegans FKB-6 protein (Corresponding sequence F31D4.3)	C. elegans	14	11	48059
029a	P91328	Paralysed arrest at two-fold protein 10 (Troponin C)	C. elegans	12	4	18516
029b	Q93375	C. elegans TAP-1 protein (Corresponding sequence C44H4.5) (TAB1-like protein TAP-1)	C. elegans	7	7	43469
030	P05055	Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8) (Polynucleotide phosphorylase) (PNPase)	E. coli	31	18	77101
031	Q09974	Hypothetical protein C17G10.2	C. elegans	32	16	49050
032	Q9XVI9	Hypothetical protein T12D8.6	C. elegans	13	7	15971
033	Q19007	Hypothetical protein D2096.8	C. elegans	40	10	35665
034	Q19007	Hypothetical protein D2096.8	C. elegans	5	5	35665
035	P32168	ATP-dependent hsl protease ATP-binding subunit hslU (Heat shock protein hslU)	E. coli	73	23	49593
036	O02592	PTL-1A protein (Protein with tau-like repeats protein 1,	C. elegans	42	13	49416

		isoform a)				
037	P05055	Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8) (Polynucleotide phosphorylase) (PNPase)	E. coli	37	17	77101
038	Q20728	Hypothetical protein F53F4.3 in chromosome V	C. elegans	30	11	25440
039	O02592	PTL-1A protein (Protein with tau-like repeats protein 1, isoform a)	C. elegans	64	16	49416
040a	P33918	Ribosomal small subunit pseudouridine synthase A (EC 4.2.1.70) (16S pseudouridylate 516 synthase) (16S pseudouridine 516 synthase) (Uracil hydrolyase)	E. coli	18	9	25865
040b	Q93573	Translationally controlled tumor protein homolog (TCTP)	C. elegans	8	6	20542
041	O44739	Bag1 (Human) homolog protein 1 (BAG-family molecular chaperone regulator-1)	C. elegans	30	11	24010
042	O17850	Machado-Joseph disease-like protein	C. elegans	33	11	35863
043a	P91328	Paralysed arrest at two-fold protein 10 (Troponin C)	C. elegans	11	6	18516
043b	P04630	Calmodulin-like protein	C. elegans	6	2	18707
043c	Q09665	Troponin C, isoform 2	C. elegans	6	3	18227
044	P30856	FKBP-type peptidyl-prolyl cis-trans	E. coli	15	3	20853

		isomerase slyD (EC 5.2.1.8) (PPIase) (Rotamase) (Histidine-rich protein) (WHP)				
045	P30856	FKBP-type peptidyl-prolyl cis-trans isomerase slyD (EC 5.2.1.8) (PPIase) (Rotamase) (Histidine-rich protein) (WHP)	E. coli	57	3	20853
046	P32168	ATP-dependent hsl protease ATP-binding subunit hslU (Heat shock protein hslU)	E. coli	89	26	49593
047	Q22871	Skp1p homolog (SKR-12) (Skp1 related (Ubiquitin ligase complex component) protein 12)	C. elegans	70	6	18926
048	Q09974	Hypothetical protein C17G10.2	C. elegans	38	12	49050
049a	Q09974	Hypothetical protein C17G10.2	C. elegans	24	15	49050
049b	Q27371	Troponin T	C. elegans	11	10	47041
050a	P02928	Maltose-binding periplasmic protein precursor (Maltodextrin-binding protein) (MMBP)	E. coli	9	8	43387
050b	Q23680	Probable vacuolar ATP synthase subunit F (EC 3.6.3.14) (V-ATPase F subunit) (Vacuolar proton pump F subunit) (V-ATPase 14 kDa subunit)	C. elegans	5	3	13312
051	P05055	Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8)	E. coli	52	25	77101

		(Polynucleotide phosphorylase) (PNPase)				
052	P02934	Outer membrane protein A precursor (Outer membrane protein II*)	E. coli	50	17	37201
053	P36546	Outer membrane protein X precursor	E. coli	41	8	18603
054a	O17850	Machado-Joseph disease-like protein	C. elegans	7	6	35863
054b	P02934	Outer membrane protein A precursor (Outer membrane protein II*)	E. coli	6	5	37201
054c	P36546	Outer membrane protein X precursor	E. coli	6	6	18603
055a	Q9U2Z5	Hypothetical protein Y106G6H.14	C. elegans	31	12	24107
055b	P53806	Calcipressin-like protein (Down Syndrome candidate region 1-like protein)	C. elegans	10	6	23030
055c	P36546	Outer membrane protein X precursor	E. coli	8	5	18603
056a	O45418	C. elegans FKB-6 protein (Corresponding sequence F31D4.3)	C. elegans	13	11	48059
056b	Q18212	Probable ATP-dependent RNA helicase p47 homolog	C. elegans	13	8	48492
057	P04475	Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70)	E. coli	78	32	68983
058	Q93375	C. elegans TAP-1 protein (Corresponding sequence C44H4.5) (TAB1-like protein TAP-1)	C. elegans	46	12	43469
059	P41932	14-3-3-like protein 1	C.	34	11	28162

			elegans			
060	P41932	14-3-3-like protein 1	C. elegans	43	13	28162
061a	P29209	16 kDa heat shock protein A	E. coli	4	3	15774
061b	O18152	Hypothetical protein T28D6.4	C. elegans	2	1	108633
061c	Q9N4P0	Hypothetical protein ZK355.3	C. elegans	2	1	19974
063	O01504	Hypothetical protein C37A2.7	C. elegans	4	4	10813
064	P02931	Outer membrane protein F precursor (Porin ompF) (Outer membrane protein 1A) (Outer membrane protein IA) (Outer membrane protein B)	E. coli	48	10	39333
065a	P09372	GrpE protein (HSP-70 cofactor) (Heat shock protein B25.3) (HSP24)	E. coli	4	1	21798
065b	P02931	Outer membrane protein F precursor (Porin ompF) (Outer membrane protein 1A) (Outer membrane protein IA) (Outer membrane protein B)	E. coli	4	4	39333
066	P09372	GrpE protein (HSP-70 cofactor) (Heat shock protein B25.3) (HSP24)	E. coli	7	3	21798
067a	P10983	Actin 1/3	C. elegans	10	8	41795
067b	P02306	Histone H4	C. elegans	4	4	11238
068	P36546	Outer membrane protein X precursor	E. coli	58	6	18603
069	P32168	ATP-dependent hsl protease ATP-binding subunit hslU (Heat	E. coli	32	14	49593

		shock protein hslU)				
070a	P49596	Probable protein phosphatase 2C T23F11.1 (EC 3.1.3.16) (PP2C)	C. elegans	8	8	39064
070 b	Q93375	C. elegans TAP-1 protein (Corresponding sequence C44H4.5) (TAB1-like protein TAP-1)	C. elegans	7	7	43469
071a	Q20655	14-3-3-like protein 2	C. elegans	10	6	28067
071 b	Q93375	C. elegans TAP-1 protein (Corresponding sequence C44H4.5) (TAB1-like protein TAP-1)	C. elegans	5	4	43469
072	P33918	Ribosomal small subunit pseudouridine synthase A (EC 4.2.1.70) (16S pseudouridylate 516 synthase) (16S pseudouridine 516 synthase) (Uracil hydrolyase)	E. coli	11	7	25865
073a	P45968	Hypothetical protein T09A5.8 in chromosome III	C. elegans	4	4	37736
073 b	P09371	Fatty acid metabolism regulator protein	E. coli	3	3	26837
074	P19625	Myosin regulatory light chain 1	C. elegans	11	5	18617
075	P30856	FKBP-type peptidyl-prolyl cis-trans isomerase slyD (EC 5.2.1.8) (PPIase) (Rotamase) (Histidine-rich protein) (WHP)	E. coli	17	4	20853

077	P05055	Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8) (Polynucleotide phosphorylase) (PNPase)	E. coli	14	12	77101
078	Q93375	C. elegans TAP-1 protein (Corresponding sequence C44H4.5) (TAB1-like protein TAP-1)	C. elegans	9	8	43469
079	P30856	FKBP-type peptidyl-prolyl cis-trans isomerase slyD (EC 5.2.1.8) (PPIase) (Rotamase) (Histidine-rich protein) (WHP)	E. coli	1	1	20853
080	P10408	Preprotein translocase secA subunit	E. coli	14	10	102023
081	Q20655	14-3-3-like protein 2	C. elegans	9	5	28067
082	Q20728	Hypothetical protein F53F4.3 in chromosome V	C. elegans	6	4	25440
083	P33918	Ribosomal small subunit pseudouridine synthase A (EC 4.2.1.70) (16S pseudouridylate 516 synthase) (16S pseudouridine 516 synthase) (Uracil hydrolase)	E. coli	12	9	25865
084	P06975	Ferric uptake regulation protein (Ferric uptake regulator)	E. coli	7	4	16795
085	O17850	Machado-Joseph disease-like protein	C. elegans	18	9	35863
086	O17850	Machado-Joseph	C.	16	10	35863

		disease-like protein	elegans			
087	O17850	Machado-Joseph disease-like protein	C. elegans	13	10	35863
088	Q20340	Hypothetical protein F42F12.4	C. elegans	8	7	21188
089	P06977	Glyceraldehyde 3-phosphate dehydrogenase A (EC 1.2.1.12) (GAPDH-A)	E. coli	12	5	35401
090a	P30856	FKBP-type peptidyl-prolyl cis-trans isomerase slyD (EC 5.2.1.8) (PPIase) (Rotamase) (Histidine-rich protein) (WHP)	E. coli	27	4	20853
090 b	Q93375	C. elegans TAP-1 protein (Corresponding sequence C44H4.5) (TAB1-like protein TAP-1)	C. elegans	14	11	43469
091a	P05055	Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8) (Polynucleotide phosphorylase) (PNPase)	E. coli	30	16	77101
091 b	Q93375	C. elegans TAP-1 protein (Corresponding sequence C44H4.5) (TAB1-like protein TAP-1)	C. elegans	9	8	43469
092	Q93375	C. elegans TAP-1 protein (Corresponding sequence C44H4.5) (TAB1-like protein TAP-1)	C. elegans	28	11	43469
093	P32168	ATP-dependent hsl protease ATP-binding subunit hslU (Heat shock protein hslU)	E. coli	37	13	49593

094	P91913	60S acidic ribosomal protein P1	C. elegans	4	4	11283
095	P10408	Preprotein translocase secA subunit	E. coli	28	18	102023
096a	Q09974	Hypothetical protein C17G10.2	C. elegans	12	12	49050
096b	Q27371	Troponin T	C. elegans	6	6	47041
097	P06982	DNA gyrase subunit B (EC 5.99.1.3)	E. coli	24	20	89818
098	Q09665	Troponin C, isoform 2	C. elegans	8	5	18227
099a	O17406	Hypothetical protein F09G2.9	C. elegans	7	5	44287
099b	Q20563	Taf (Tbp-associated transcription factor) family protein 11.1	C. elegans	5	1	37788
100	Q20563	Taf (Tbp-associated transcription factor) family protein 11.1	C. elegans	11	5	37788
102	P06138	Cell division protein ftsZ	E. coli	28	14	40324
103a	P04630	Calmodulin-like protein	C. elegans	6	4	18707
103b	P30856	FKBP-type peptidyl-prolyl cis-trans isomerase slyD (EC 5.2.1.8) (PPIase) (Rotamase) (Histidine-rich protein) (WHP)	E. coli	5	2	20853
104a	P30856	FKBP-type peptidyl-prolyl cis-trans isomerase slyD (EC 5.2.1.8) (PPIase) (Rotamase) (Histidine-rich protein) (WHP)	E. coli	13	2	20853
104b	P04630	Calmodulin-like protein	C. elegans	9	4	18707
105	P02931	Outer membrane protein F precursor (Porin ompF) (Outer	E. coli	26	8	39333

		membrane protein 1A) (Outer membrane protein IA) (Outer membrane protein B)				
106	P02931	Outer membrane protein F precursor (Porin ompF) (Outer membrane protein 1A) (Outer membrane protein IA) (Outer membrane protein B)	E. coli	16	8	39333
107a	Q19007	Hypothetical protein D2096.8	C. elegans	18	10	35665
107b	P04475	Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70)	E. coli	14	12	68983
107c	Q22866	Tropomyosin isoforms 1/2	C. elegans	14	11	33003
108a	Q22866	Tropomyosin isoforms 1/2	C. elegans	14	12	33003
108b	Q19007	Hypothetical protein D2096.8	C. elegans	13	11	35665
109	Q22866	Tropomyosin isoforms 1/2	C. elegans	25	11	33003
110a	Q22866	Tropomyosin isoforms 1/2	C. elegans	24	18	33003
110b	Q19007	Hypothetical protein D2096.8	C. elegans	16	10	35665
111a	Q19007	Hypothetical protein D2096.8	C. elegans	21	12	35665
111b	Q22866	Tropomyosin isoforms 1/2	C. elegans	13	11	33003
112	Q19007	Hypothetical protein D2096.8	C. elegans	17	11	35665
113a	Q19007	Hypothetical protein D2096.8	C. elegans	3	3	35665
113b	P04475	Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa	E. coli	2	2	68983

		protein) (HSP70)				
114	Q9NAM6	C. elegans SKR-10 protein (Corresponding sequence Y105C5B.13)	C. elegans	25	3	20901
115	Q19007	Hypothetical protein D2096.8	C. elegans	4	4	35665
116a	P04475	Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70)	E. coli	2	2	68983
116 b	Q27371	Troponin T	C. elegans	2	1	47041
117	P04475	Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70)	E.coli	83	29	68983
118	P06139	60 kDa chaperonin (Protein Cpn60) (groEL protein)	E.coli	106	16	57197
119a	P06139	60 kDa chaperonin (Protein Cpn60) (groEL protein)	E. coli	8	7	57197
119 b	P04475	Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70)	E. coli	6	6	68983
120a	Q23280	Hypothetical 19.4 kDa protein ZC395.10 in chromosome III	C. elegans	8	5	19431
120 b	P06139	60 kDa chaperonin (Protein Cpn60) (groEL protein)	E. coli	7	5	57197
121	Q19007	Hypothetical protein D2096.8	C. elegans	26	12	35665
122	P00824	ATP synthase beta chain (EC 3.6.3.14)	E. coli	25	16	50194
123	P00824	ATP synthase beta chain (EC 3.6.3.14)	E. coli	30	14	50194

124	P49596	Probable protein phosphatase 2C T23F11.1 (EC 3.1.3.16) (PP2C)	C. elegans	17	9	39064
125	O17406	Hypothetical protein F09G2.9	C. elegans	20	16	44287
126	P06959	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12) (E2)	E. coli	17	13	65964
127	P00574	DNA-directed RNA polymerase alpha chain (EC 2.7.7.6) (RNAP alpha subunit) (Transcriptase alpha chain) (RNA polymerase alpha subunit)	E. coli	13	9	36511
128a	P03017	RecA protein (Recombinase A)	E. coli	11	6	37842
128b	Q93375	C. elegans TAP-1 protein (Corresponding sequence C44H4.5) (TAB1-like protein TAP-1)	C. elegans	8	6	43469
128c	P49596	Probable protein phosphatase 2C T23F11.1 (EC 3.1.3.16) (PP2C)	C. elegans	7	6	39064
129	P02997	Elongation factor Ts (EF-Ts)	E. coli	8	4	30292
130	P41932	14-3-3-like protein 1	C. elegans	13	7	28162
131	P02934	Outer membrane protein A precursor (Outer membrane protein II*)	E. coli	21	11	37201
132	Q20728	Hypothetical protein F53F4.3 in chromosome V	C. elegans	11	9	25440

133	P13519	Rod shape-determining protein mreB	E. coli	22	8	36953
134	Q27371	Troponin T	C. elegans	15	9	47041
135	Q27371	Troponin T	C. elegans	16	11	47041
136	Q27371	Troponin T	C. elegans	17	10	47041
137	Q27371	Troponin T	C. elegans	10	7	47041
138	Q09974	Hypothetical protein C17G10.2	C. elegans	4	3	49050
139	Q22871	Skp1p homolog (SKR-12) (Skp1 related (Ubiquitin ligase complex component) protein 12)	C. elegans	4	2	18926
140	Q93573	Translationally controlled tumor protein homolog (TCTP)	C. elegans	17	10	20542
141	P06975	Ferric uptake regulation protein (Ferric uptake regulator)	E. coli	10	3	16795
142	P06975	Ferric uptake regulation protein (Ferric uptake regulator)	E. coli	12	3	16795
143a	Q18225	Hypothetical protein C26E6.2	C. elegans	2	1	52067
143b	P91152	Hypothetical protein C43E11.3	C. elegans	2	1	183461
143c	Q9N323	Hypothetical protein Y59H11AR.2	C. elegans	2	1	126363
144	Q09974	Hypothetical protein C17G10.2	C. elegans	12	8	49050
145	P00822	ATP synthase alpha chain (EC 3.6.3.14)	E. coli	20	12	55222
146	P00391	Dihydrolipoamide dehydrogenase (EC 1.8.1.4) (E3	E. coli	14	11	50557

		component of pyruvate and 2-oxoglutarate dehydrogenases complexes) (Glycine cleavage system L protein)				
148	P02995	Translation initiation factor IF-2	E. coli	13	9	97350
149	P02995	Translation initiation factor IF-2	E. coli	12	9	97350
150	P06982	DNA gyrase subunit B (EC 5.99.1.3)	E. coli	16	13	89818
152a	P00955	Threonyl-tRNA synthetase (EC 6.1.1.3) (Threonine--tRNA ligase) (ThrRS)	E. coli	3	3	74014
152b	O01448	Hypothetical protein	C. elegans	2	2	43957
152c	Q22310	Hypothetical protein T07E3.4	C. elegans	2	1	48744
152d	P30844	Sensor protein basS/pmrB (EC 2.7.3.-)	E. coli	2	1	41029
153a	P00955	Threonyl-tRNA synthetase (EC 6.1.1.3) (Threonine--tRNA ligase) (ThrRS)	E. coli	3	2	74014
153b	Q8WTK1	Hypothetical protein Y51F10.4	C. elegans	2	1	65690
154	P00391	Dihydrolipoamide dehydrogenase (EC 1.8.1.4) (E3 component of pyruvate and 2-oxoglutarate dehydrogenases complexes) (Glycine cleavage system L protein)	E. coli	17	10	50557
155	P00822	ATP synthase alpha chain (EC 3.6.3.14)	E. coli	21	8	55222
156	O17850	Machado-Joseph disease-like protein	C. elegans	9	5	35863

157	Q9N588	Hypothetical protein Y110A7A.4	C. elegans	5	3	35452
158	P06977	Glyceraldehyde 3-phosphate dehydrogenase A (EC 1.2.1.12) (GAPDH-A)	E. coli	10	5	35401
159	P34477	Probable ubiquitin-conjugating enzyme E2 7 (EC 6.3.2.19) (Ubiquitin-protein ligase 7) (Ubiquitin carrier protein 7)	C. elegans	4	4	18938
160a	P03020	Catabolite gene activator (cAMP receptor protein) (cAMP-regulatory protein)	E. coli	6	4	23640
160b	O61817	Hypothetical protein B0511.7	C. elegans	6	3	33951
160c	Q93713	C. elegans CPN-1 protein (Corresponding sequence F43G9.9)	C. elegans	3	2	21066
161a	Q23680	Probable vacuolar ATP synthase subunit F (EC 3.6.3.14) (V-ATPase F subunit) (Vacuolar proton pump F subunit) (V-ATPase 14 kDa subunit)	C. elegans	11	4	13312
161b	Q18742	C. elegans HIS-36 protein (Corresponding sequence C50F4.6)	C. elegans	6	3	10292
162	P25521	Hfq protein (Host factor-I protein) (HF-I) (HF-1)	E. coli	11	5	11035
163a	P02364	30S ribosomal protein S10	E. coli	5	3	11735
163b	P02371	30S ribosomal protein S15	E. coli	5	3	10137
164	P08622	Chaperone protein dnaJ (Heat shock	E. coli	15	7	40969

		protein J) (HSP40)				
165	Q9N588	Hypothetical protein Y110A7A.4	C. elegans	18	7	35452
166	O44739	Bag1 (Human) homolog protein 1 (BAG-family molecular chaperone regulator-1)	C. elegans	14	6	24010
167	O01803	Rab family protein 11.1	C. elegans	6	5	23429
168	P03020	Catabolite gene activator (cAMP receptor protein) (cAMP-regulatory protein)	E. coli	17	7	23640
169	P03020	Catabolite gene activator (cAMP receptor protein) (cAMP-regulatory protein)	E. coli	24	8	23640
170	P45968	Hypothetical protein T09A5.8 in chromosome III	C. elegans	20	9	37736

¹ Predicted from SwissProt IDs submitted to <http://us.expasy.org/sprot/sprot-retrieve-list.html>, 02Oct04.