RI NSF/EPSCoR Proteomics Facility
Mass Spectrometry Report
Protein Groups and Peptide-Spectrum Matches (PSMs)

Sample: Sample 1186 10
Researcher: Djuro Josic
Data collected: 24 Aug 2011
Results filtering: Unique PSMs; MOWSE Score > 19.4; 10 Proteins/ Group max

MS data file: Sample_1186_10_082611_022855.raw
Instrument type: ESI-FTICR
Search engine: Mascot
Parameter file: N/D
Search database: N/D (269577 entries)
Enzyme specificity: Trypsin (2 missed cleavages allowed)
MS mass tolerance: 20 ppm; MS/MS tolerance 0.5 Da
Fixed modifications: Carbamidomethyl (C)
Var. modifications: [1] Oxidation (M)
Number of spectra: 4852
Input PSMs: 1221 'Target'; 18 'Decoy'; 1.5% FDR
Output PSMs: 1219

UniProt Human Protein IDs

Grp Nr.	*Accession Number*	*Protein Name*	*Protein Score*	*Unique PSMs*	*PSM Serial Nrs.*	*Other Grp.*	*% Seq. Cover.*

1	B4E1B2	cDNA FLJ53691, highly similar to Serotransferrin OS=Homo sapiens PE=2 SV=1	3196.27	64	3 5 19 23 57 79 97 102 105 118 129 136 148 183 206 208 209 231 236 287 309 330 346 351 373 387 391 412 450 456 484 515 576 634 684 718 732 766 782 787 788 791 805 813 814 817 833 842 898 915 928 1025 1043 1090 1096 1121 1125 1135 1145 1152 1170 1172 1173 1215		*61.7*
2	Q5I6Y6	Lamin A/C transcript variant 1 OS=Homo sapiens GN=LMNA PE=2 SV=1	1143.14	26	34 244 275 321 326 350 355 367 380 423 445 472 566 607 695 716 722 843 851 867 930 961 967 1035 1062 1129		*41.1*
	Q5I6Y4	Lamin A/C transcript variant 1 OS=Homo sapiens GN=LMNA PE=2 SV=1	1143.14	26	34 244 275 321 326 350 355 367 380 423 445 472 566 607 695 716 722 843 851 867 930 961 967 1035 1062 1129		*41.1*
	P02545	Prelamin-A/C OS=Homo sapiens GN=LMNA PE=1 SV=1	1143.14	26	34 244 275 321 326 350 355 367 380 423 445 472 566 607 695 716 722 843 851 867 930 961 967 1035 1062 1129		*41.1*
3	P08727	Keratin, type I cytoskeletal 19 OS=Homo sapiens GN=KRT19 PE=1 SV=4	930.85	21	2 25 85 194 280 433 480 487 631 717 846 858 888 946 999 1004 1047 1133 1148 1203 1211		*50.8*
4	P05787	Keratin, type II cytoskeletal 8 OS=Homo sapiens GN=KRT8 PE=1 SV=7	930.59	22	1 71 123 210 296 307 382 553 573 641 670 683 758 784 808 901 909 921 943 970 1207 1213		*35.6*
5	P04075	Fructose-bisphosphate aldolase A OS=Homo sapiens GN=ALDOA PE=1 SV=2	616.74	14	63 143 173 286 291 422 457 465 504 715 981 1003 1157 1190		*36.7*
	J3KPS3	Fructose-bisphosphate aldolase OS=Homo sapiens GN=ALDOA PE=3 SV=1	616.74	14	63 143 173 286 291 422 457 465 504 715 981 1003 1157 1190		*36.7*
6	P60174	Triosephosphate isomerase OS=Homo sapiens GN=TPI1 PE=1 SV=3	610.12	11	20 35 51 184 300 458 463 857 860 889 1042		*45.1*

7	P20700	Lamin-B1 OS=Homo sapiens GN=LMNB1 PE=1 SV=2	578.90	13	39 125 128 205 420 434 476 575 724 891 910 956 1057		*27.8*
8	P11021	78 kDa glucose-regulated protein OS=Homo sapiens GN=HSPA5 PE=1 SV=2	571.50	12	73 139 234 396 477 554 568 660 741 774 996 1208		*24.2*
9	Q5T8M8	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=4 SV=1	540.39	10	11 281 313 318 405 481 571 777 803 874		*35.9*
	P68133	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=1 SV=1	540.39	10	11 281 313 318 405 481 571 777 803 874		*35.9*
	P68032	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE=1 SV=1	540.39	10	11 281 313 318 405 481 571 777 803 874		*35.9*
	B7Z6P1	cDNA FLJ53662, highly similar to Actin, alpha skeletal muscle OS=Homo sapiens PE=2 SV=1	540.39	10	11 281 313 318 405 481 571 777 803 874		*35.9*
	A6NL76	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE=2 SV=2	540.39	10	11 281 313 318 405 481 571 777 803 874		*35.9*
10	Q4VB24	Histone cluster 1, H1e OS=Homo sapiens GN=HIST1H1E PE=2 SV=1	535.92	10	110 196 392 526 656 692 770 1011 1063 1087		*36.7*
	P16402	Histone H1.3 OS=Homo sapiens GN=HIST1H1D PE=1 SV=2	535.92	10	110 196 392 526 656 692 770 1011 1063 1087		*36.7*
	P10412	Histone H1.4 OS=Homo sapiens GN=HIST1H1E PE=1 SV=2	535.92	10	110 196 392 526 656 692 770 1011 1063 1087		*36.7*
	B2R984	cDNA, FLJ94268, highly similar to Homo sapiens histone 1, H1e (HIST1H1E), mRNA OS=Homo sapiens PE=2 SV=1	535.92	10	110 196 392 526 656 692 770 1011 1063 1087		*36.7*
	A3R0T8	Histone 1, H1e OS=Homo sapiens GN=HIST1H1E PE=2 SV=1	535.92	10	110 196 392 526 656 692 770 1011 1063 1087		*36.7*
11	B7Z2X4	cDNA FLJ53327, highly similar to Gelsolin OS=Homo sapiens PE=2 SV=1	529.28	13	252 256 269 299 385 448 482 667 895 896 1024 1112 1166		*22.0*
12	P11142	Heat shock cognate 71 kDa protein OS=Homo sapiens GN=HSPA8 PE=1 SV=1	491.15	12	16 135 161 260 344 613 647 657 759 771 933 1144		*22.9*
	B3KTV0	cDNA FLJ38781 fis, clone LIVER2000216, highly similar to HEAT SHOCK COGNATE 71 kDa PROTEIN OS=Homo sapiens PE=2 SV=1	491.15	12	16 135 161 260 344 613 647 657 759 771 933 1144		*22.9*
13	P10809	60 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPD1 PE=1 SV=2	482.57	10	165 180 317 366 418 506 911 929 1050 1116		*16.5*
	B3GQS7	Mitochondrial heat shock 60kD protein 1 variant 1 OS=Homo sapiens GN=HSPD1 PE=2 SV=1	482.57	10	165 180 317 366 418 506 911 929 1050 1116		*16.5*
14	P02768	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	470.85	10	170 315 414 801 873 897 1001 1074 1177 1188		*17.4*

	F6KPG5	Albumin (Fragment) OS=Homo sapiens PE=2 SV=1	470.85	10	170 315 414 801 873 897 1001 1074 1177 1188		*17.4*
	B4DPP6	cDNA FLJ54371, highly similar to Serum albumin OS=Homo sapiens PE=2 SV=1	470.85	10	170 315 414 801 873 897 1001 1074 1177 1188		*17.4*
	B2RBS8	cDNA, FLJ95666, highly similar to Homo sapiens albumin (ALB), mRNA OS=Homo sapiens PE=2 SV=1	470.85	10	170 315 414 801 873 897 1001 1074 1177 1188		*17.4*
15	Q5VU66	Tropomyosin alpha-3 chain OS=Homo sapiens GN=TPM3 PE=4 SV=1	459.56	10	77 142 283 295 362 488 508 525 1029 1081		*50.4*
	B2RDE1	cDNA, FLJ96568, highly similar to Homo sapiens tropomyosin 3 (TPM3), mRNA OS=Homo sapiens PE=2 SV=1	459.56	10	77 142 283 295 362 488 508 525 1029 1081		*50.4*
16	P16401	Histone H1.5 OS=Homo sapiens GN=HIST1H1B PE=1 SV=3	442.18	8	91 188 311 413 479 536 775 819		*31.9*
17	P07910	Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=1 SV=4	437.56	10	217 279 361 401 754 780 940 1006 1192 1221		*27.5*
	G3V4C1	Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=2 SV=1	437.56	10	217 279 361 401 754 780 940 1006 1192 1221		*27.5*
	G3V2Q1	Heterogeneous nuclear ribonucleoproteins C1/C2 OS=Homo sapiens GN=HNRNPC PE=2 SV=1	437.56	10	217 279 361 401 754 780 940 1006 1192 1221		*27.5*
	A8K9A4	cDNA FLJ75154, highly similar to Homo sapiens heterogeneous nuclear ribonucleoprotein C (C1/C2), mRNA OS=Homo sapiens PE=2 SV=1	437.56	10	217 279 361 401 754 780 940 1006 1192 1221		*27.5*
18	P42167	Lamina-associated polypeptide 2, isoforms beta/gamma OS=Homo sapiens GN=TMPO PE=1 SV=2	399.65	8	140 402 421 549 650 690 778 856		*31.5*
	P42166	Lamina-associated polypeptide 2, isoform alpha OS=Homo sapiens GN=TMPO PE=1 SV=2	399.65	8	140 402 421 549 650 690 778 856		*31.5*
	G5E972	Thymopentin OS=Homo sapiens GN=TMPO PE=4 SV=1	399.65	8	140 402 421 549 650 690 778 856		*31.5*
	A2T926	Thymopentin OS=Homo sapiens GN=TMPO PE=2 SV=1	399.65	8	140 402 421 549 650 690 778 856		*31.5*
19	Q6FGD7	TBCA protein OS=Homo sapiens GN=TBCA PE=2 SV=1	385.12	8	83 94 393 495 730 776 827 1012		*69.0*
	O75347	Tubulin-specific chaperone A OS=Homo sapiens GN=TBCA PE=1 SV=3	385.12	8	83 94 393 495 730 776 827 1012		*69.0*
	E5RJD8	Tubulin-specific chaperone A OS=Homo sapiens GN=TBCA PE=2 SV=1	385.12	8	83 94 393 495 730 776 827 1012		*69.0*
	E5RIW3	Tubulin-specific chaperone A OS=Homo sapiens GN=TBCA PE=2 SV=1	385.12	8	83 94 393 495 730 776 827 1012		*69.0*
20	P19338	Nucleolin OS=Homo sapiens GN=NCL PE=1 SV=3	375.25	9	38 371 496 507 521 623 772 937 1036		*16.6*
21	P09651	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=1 SV=5	368.13	7	168 320 545 591 601 798 1055		*29.6*

	F8W6I7	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=2 SV=1	368.13	7	168 320 545 591 601 798 1055		*29.6*
	F8VXY0	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=2 SV=1	368.13	7	168 320 545 591 601 798 1055		*29.6*
	F8VRQ1	Heterogeneous nuclear ribonucleoprotein A1 OS=Homo sapiens GN=HNRNPA1 PE=2 SV=1	368.13	7	168 320 545 591 601 798 1055		*29.6*
22	Q6DEN2	DPYSL3 protein OS=Homo sapiens GN=DPYSL3 PE=2 SV=1	360.18	7	608 661 688 747 934 1092 1158		*12.6*
23	Q92945	Far upstream element-binding protein 2 OS=Homo sapiens GN=KHSRP PE=1 SV=4	359.80	6	159 603 862 871 914 1098		*9.1*
24	P06733	Alpha-enolase OS=Homo sapiens GN=ENO1 PE=1 SV=2	343.95	10	65 72 268 290 356 769 822 852 983 1189		*27.9*
25	P07737	Profilin-1 OS=Homo sapiens GN=PFN1 PE=1 SV=2	341.64	5	108 701 1022 1068 1214		*32.1*
26	P62937	Peptidyl-prolyl cis-trans isomerase A OS=Homo sapiens GN=PPIA PE=1 SV=2	341.53	6	271 586 616 1089 1097 1142		*41.2*
27	P67809	Nuclease-sensitive element-binding protein 1 OS=Homo sapiens GN=YBX1 PE=1 SV=3	324.05	5	26 92 164 519 1080		*29.9*
28	Q99879	Histone H2B type 1-M OS=Homo sapiens GN=HIST1H2BM PE=1 SV=3	317.99	8	216 261 284 415 737 761 975 1016		*55.8*
	I6L9F7	Histone H2B (Fragment) OS=Homo sapiens GN=HIST1H2BM PE=2 SV=1	317.99	8	216 261 284 415 737 761 975 1016		*55.8*
29	Q9P2E9	Ribosome-binding protein 1 OS=Homo sapiens GN=RRBP1 PE=1 SV=4	300.21	6	124 293 377 708 997 1183		*4.6*
30	P38159	RNA-binding motif protein, X chromosome OS=Homo sapiens GN=RBMX PE=1 SV=3	288.07	7	87 109 162 166 262 338 550		*18.4*
31	Q14103	Heterogeneous nuclear ribonucleoprotein D0 OS=Homo sapiens GN=HNRNPD PE=1 SV=1	283.54	7	179 424 632 764 941 1149 1154		*21.7*
32	P07900	Heat shock protein HSP 90-alpha OS=Homo sapiens GN=HSP90AA1 PE=1 SV=5	282.20	7	126 527 570 643 953 1056 1164		*3.5*
	K9JA46	Epididymis luminal secretory protein 52 OS=Homo sapiens GN=EL52 PE=2 SV=1	282.20	7	126 527 570 643 953 1056 1164		*3.5*
33	Q60FE2	MYH9 variant protein OS=Homo sapiens GN=MYH9 PE=2 SV=1	276.01	6	426 517 605 768 906 932		*4.6*
	P35579	Myosin-9 OS=Homo sapiens GN=MYH9 PE=1 SV=4	276.01	6	426 517 605 768 906 932		*4.6*
34	Q0VAS5	Histone H4 OS=Homo sapiens GN=HIST1H4H PE=2 SV=1	274.00	6	78 237 409 611 965 1010		*52.4*
	P62805	Histone H4 OS=Homo sapiens GN=HIST1H4A PE=1 SV=2	274.00	6	78 237 409 611 965 1010		*52.4*
	B2R4R0	Histone H4 OS=Homo sapiens GN=HIST1H4J PE=2 SV=1	274.00	6	78 237 409 611 965 1010		*52.4*
35	P16949	Stathmin OS=Homo sapiens GN=STMN1 PE=1 SV=3	267.80	6	115 563 639 952 957 1046		*32.9*
	B5BU83	Stathmin OS=Homo sapiens GN=STMN1 PE=2 SV=1	267.80	6	115 563 639 952 957 1046		*32.9*

36	Q4LE64	NUMA1 variant protein (Fragment) OS=Homo sapiens GN=NUMA1 variant protein PE=2 SV=1	265.57	5	6 753 872 1030 1119		*4.7*
	Q14980	Nuclear mitotic apparatus protein 1 OS=Homo sapiens GN=NUMA1 PE=1 SV=2	265.57	5	6 753 872 1030 1119		*4.7*
37	P31947	14-3-3 protein sigma OS=Homo sapiens GN=SFN PE=1 SV=1	264.42	6	9 80 347 398 442 742		*28.6*
38	P04406	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens GN=GAPDH PE=1 SV=3	264.18	5	68 429 699 979 1077		*25.5*
39	Q53F64	Heterogeneous nuclear ribonucleoprotein AB isoform a variant (Fragment) OS=Homo sapiens PE=2 SV=1	264.10	6	44 618 633 671 912 1205		*17.6*
	D6RD18	Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens GN=HNRNPAB PE=2 SV=1	264.10	6	44 618 633 671 912 1205		*17.6*
	D6RBZ0	Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens GN=HNRNPAB PE=2 SV=1	264.10	6	44 618 633 671 912 1205		*17.6*
	D6R9P3	Heterogeneous nuclear ribonucleoprotein A/B OS=Homo sapiens GN=HNRNPAB PE=2 SV=1	264.10	6	44 618 633 671 912 1205		*17.6*
	B4DMY3	cDNA FLJ60713, highly similar to Homo sapiens heterogeneous nuclear ribonucleoprotein A/B (HNRPAB), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1	264.10	6	44 618 633 671 912 1205		*17.6*
40	P06748	Nucleophosmin OS=Homo sapiens GN=NPM1 PE=1 SV=2	263.47	7	59 276 332 539 845 875 1041		*24.5*
41	Q68CT4	Putative uncharacterized protein DKFZp686A1668 OS=Homo sapiens GN=DKFZp686A1668 PE=2 SV=1	258.74	6	167 399 511 904 935 1065		*5.8*
	O75369	Filamin-B OS=Homo sapiens GN=FLNB PE=1 SV=2	258.74	6	167 399 511 904 935 1065		*5.8*
	E7EN95	Filamin-B OS=Homo sapiens GN=FLNB PE=2 SV=1	258.74	6	167 399 511 904 935 1065		*5.8*
42	P61604	10 kDa heat shock protein, mitochondrial OS=Homo sapiens GN=HSPE1 PE=1 SV=2	258.06	4	499 962 1099 1165		*42.2*
43	Q86TY5	Full-length cDNA clone CS0DI041YE05 of Placenta of Homo sapiens (human) OS=Homo sapiens PE=2 SV=1	255.85	7	132 171 406 452 542 1018 1019		*34.8*
	Q6FGL0	LGALS3 protein (Fragment) OS=Homo sapiens GN=LGALS3 PE=2 SV=1	255.85	7	132 171 406 452 542 1018 1019		*34.8*
	Q59FR8	LGALS3 protein variant (Fragment) OS=Homo sapiens PE=2 SV=1	255.85	7	132 171 406 452 542 1018 1019		*34.8*
	P17931	Galectin-3 OS=Homo sapiens GN=LGALS3 PE=1 SV=5	255.85	7	132 171 406 452 542 1018 1019		*34.8*
44	H7BYY1	Tropomyosin 1 (Alpha), isoform CRA_m OS=Homo sapiens GN=TPM1 PE=3 SV=1	255.48	6	425 470 577 750 949 1146		*48.4*
45	Q9Y2W1	Thyroid hormone receptor-associated protein 3 OS=Homo sapiens GN=THRAP3 PE=1 SV=2	254.72	4	75 157 478 1196		*4.3*
46	Q15149	Plectin OS=Homo sapiens GN=PLEC PE=1 SV=3	253.15	6	117 222 500 783 899 1117		*2.5*
47	P05783	Keratin, type I cytoskeletal 18 OS=Homo sapiens GN=KRT18 PE=1 SV=2	250.48	7	43 491 512 589 676 1093 1139		*20.7*

48	P29966	Myristoylated alanine-rich C-kinase substrate OS=Homo sapiens GN=MARCKS PE=1 SV=4	240.65	4	582 696 864 931		*24.7*
49	Q14512	Fibroblast growth factor-binding protein 1 OS=Homo sapiens GN=FGFBP1 PE=1 SV=1	238.69	5	687 815 816 868 995		*16.2*
50	P40925	Malate dehydrogenase, cytoplasmic OS=Homo sapiens GN=MDH1 PE=1 SV=4	234.16	5	257 303 345 1198 1220		*18.0*
51	P63104	14-3-3 protein zeta/delta OS=Homo sapiens GN=YWHAZ PE=1 SV=1	228.76	4	289 546 685 1167		*19.6*
	E7EX29	14-3-3 protein zeta/delta (Fragment) OS=Homo sapiens GN=YWHAZ PE=2 SV=1	228.76	4	289 546 685 1167		*19.6*
	E7ESK7	14-3-3 protein zeta/delta (Fragment) OS=Homo sapiens GN=YWHAZ PE=2 SV=1	228.76	4	289 546 685 1167		*19.6*
	D0PNI1	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein zeta polypeptide OS=Homo sapiens GN=YWHAZ PE=2 SV=1	228.76	4	289 546 685 1167		*19.6*
52	Q5TCU3	Tropomyosin beta chain OS=Homo sapiens GN=TPM2 PE=2 SV=1	221.39	5	107 203 625 828 1045		*35.9*
53	P05067	Amyloid beta A4 protein OS=Homo sapiens GN=APP PE=1 SV=3	215.64	6	93 325 612 712 1106 1147		*8.4*
	H7C0V9	Gamma-secretase C-terminal fragment 59 (Fragment) OS=Homo sapiens GN=APP PE=4 SV=1	215.64	6	93 325 612 712 1106 1147		*8.4*
	E9PG40	Gamma-secretase C-terminal fragment 59 OS=Homo sapiens GN=APP PE=2 SV=1	215.64	6	93 325 612 712 1106 1147		*8.4*
	B4DGD0	cDNA FLJ50491, highly similar to Amyloid beta A4 protein (APP) (ABPP)(Alzheimer disease amyloid protein) (Cerebral vascularamyloid peptide) (CVAP) (Protease nexin-II) (PN-II) (APPI) (PreA4) OS=Homo sapiens PE=2 SV=1	215.64	6	93 325 612 712 1106 1147		*8.4*
54	Q86V58	Fibulin 2 OS=Homo sapiens GN=FBLN2 PE=2 SV=1	215.58	3	762 927 1153		*4.1*
	P98095	Fibulin-2 OS=Homo sapiens GN=FBLN2 PE=1 SV=2	215.58	3	762 927 1153		*4.1*
	F5H1F3	Fibulin-2 OS=Homo sapiens GN=FBLN2 PE=2 SV=1	215.58	3	762 927 1153		*4.1*
	B7Z9B8	cDNA FLJ56912, highly similar to Fibulin-2 OS=Homo sapiens PE=2 SV=1	215.58	3	762 927 1153		*4.1*
55	H7BZJ3	Thioredoxin (Fragment) OS=Homo sapiens GN=PDIA3 PE=2 SV=1	211.51	3	431 693 728		*30.1*
56	P23193	Transcription elongation factor A protein 1 OS=Homo sapiens GN=TCEA1 PE=1 SV=2	211.43	3	121 455 1104		*15.0*
57	Q9UQ80	Proliferation-associated protein 2G4 OS=Homo sapiens GN=PA2G4 PE=1 SV=3	211.05	3	113 193 789		*13.2*
58	P14618	Pyruvate kinase isozymes M1/M2 OS=Homo sapiens GN=PKM PE=1 SV=4	210.70	5	703 1048 1069 1185 1199		*16.4*
59	O43707	Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2	209.95	5	459 619 790 829 1100		*9.4*

60	Q6NZ55	60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=2 SV=1	207.62	4	211 902 998 1075		*18.0*
	P26373	60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=1 SV=4	207.62	4	211 902 998 1075		*18.0*
	A8K4C8	60S ribosomal protein L13 OS=Homo sapiens GN=RPL13 PE=2 SV=1	207.62	4	211 902 998 1075		*18.0*

UniProt Human Protein IDs, *cont.*

Grp Nr.	*Accession Number*	*Protein Name*	*Protein Score*	*Unique PSMs*	*PSM Serial Nrs.*	*Other Grp.*	*% Seq. Cover.*
61	Q7KYM9	ORF protein OS=Homo sapiens GN=ORF PE=2 SV=1	202.95	4	654 823 881 886		*12.0*
	Q59ES8	Heterogeneous nuclear ribonucleoprotein M isoform a variant (Fragment) OS=Homo sapiens PE=2 SV=1	202.95	4	654 823 881 886		*12.0*
	P52272	Heterogeneous nuclear ribonucleoprotein M OS=Homo sapiens GN=HNRNPM PE=1 SV=3	202.95	4	654 823 881 886		*12.0*
62	Q03252	Lamin-B2 OS=Homo sapiens GN=LMNB2 PE=1 SV=3	201.39	5	220 228 672 1031 1124		*12.4*
	J9JID7	Lamin B2, isoform CRA_a OS=Homo sapiens GN=LMNB2 PE=3 SV=1	201.39	5	220 228 672 1031 1124		*12.4*
63	Q9BSV4	SFPQ protein (Fragment) OS=Homo sapiens GN=SFPQ PE=2 SV=2	199.66	5	47 826 916 1072 1082		*12.3*
	P23246	Splicing factor, proline- and glutamine-rich OS=Homo sapiens GN=SFPQ PE=1 SV=2	199.66	5	47 826 916 1072 1082		*12.3*
64	Q9H1E3	Nuclear ubiquitous casein and cyclin-dependent kinase substrate 1 OS=Homo sapiens GN=NUCKS1 PE=1 SV=1	199.41	5	50 417 562 665 710		*20.6*
65	P39019	40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=1 SV=2	199.23	4	29 127 258 532		*24.8*
	B0ZBD0	40S ribosomal protein S19 OS=Homo sapiens GN=RPS19 PE=2 SV=1	199.23	4	29 127 258 532		*24.8*
66	P11940	Polyadenylate-binding protein 1 OS=Homo sapiens GN=PABPC1 PE=1 SV=2	198.02	5	489 537 626 651 1212		*14.9*
	B3KT93	cDNA FLJ37875 fis, clone BRSSN2018771, highly similar to Poly(A)-binding protein 1 OS=Homo sapiens PE=2 SV=1	198.02	5	489 537 626 651 1212		*14.9*
67	P62263	40S ribosomal protein S14 OS=Homo sapiens GN=RPS14 PE=1 SV=3	196.98	5	81 111 473 1049 1191		*24.5*

68	Q5U071	High-mobility group box 2 OS=Homo sapiens PE=2 SV=1	196.43	5	312 388 597 781 1155		*13.0*
	P26583	High mobility group protein B2 OS=Homo sapiens GN=HMGB2 PE=1 SV=2	196.43	5	312 388 597 781 1155		*13.0*
69	Q71DI3	Histone H3.2 OS=Homo sapiens GN=HIST2H3A PE=1 SV=3	195.63	5	28 130 266 725 980		*36.8*
	Q16695	Histone H3.1t OS=Homo sapiens GN=HIST3H3 PE=1 SV=3	195.63	5	28 130 266 725 980		*36.8*
	P84243	Histone H3.3 OS=Homo sapiens GN=H3F3A PE=1 SV=2	195.63	5	28 130 266 725 980		*36.8*
	P68431	Histone H3.1 OS=Homo sapiens GN=HIST1H3A PE=1 SV=2	195.63	5	28 130 266 725 980		*36.8*
	K7EK07	Histone H3 (Fragment) OS=Homo sapiens GN=H3F3B PE=3 SV=1	195.63	5	28 130 266 725 980		*36.8*
	B4E380	Histone H3 OS=Homo sapiens PE=2 SV=1	195.63	5	28 130 266 725 980		*36.8*
	B2R4P9	Histone H3 OS=Homo sapiens GN=H3F3A PE=2 SV=1	195.63	5	28 130 266 725 980		*36.8*
70	P26038	Moesin OS=Homo sapiens GN=MSN PE=1 SV=3	192.97	5	95 323 850 879 1073		*8.8*
71	O94907	Dickkopf-related protein 1 OS=Homo sapiens GN=DKK1 PE=1 SV=1	191.01	4	145 282 468 938		*15.8*
	I1W660	Dickkopf-like protein 1 OS=Homo sapiens GN=DKK1 PE=2 SV=1	191.01	4	145 282 468 938		*15.8*
72	P08107	Heat shock 70 kDa protein 1A/1B OS=Homo sapiens GN=HSPA1A PE=1 SV=5	183.75	4	492 809 1054 1115		*15.9*
	A8K5I0	Heat shock 70kDa protein 1A OS=Homo sapiens GN=HSPA1A PE=2 SV=1	183.75	4	492 809 1054 1115		*15.9*
73	Q04695	Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV=2	177.86	4	485 628 945 1186		*11.1*
74	P00338	L-lactate dehydrogenase A chain OS=Homo sapiens GN=LDHA PE=1 SV=2	175.26	4	580 704 990 1102		*18.7*
75	Q14847	LIM and SH3 domain protein 1 OS=Homo sapiens GN=LASP1 PE=1 SV=2	175.20	4	189 336 617 756		*15.7*
76	Q6IQ15	EEF1A1 protein OS=Homo sapiens GN=EEF1A1 PE=2 SV=1	172.08	4	522 559 739 887		*11.1*
	Q6IPT9	Elongation factor 1-alpha OS=Homo sapiens GN=EEF1A1 PE=2 SV=1	172.08	4	522 559 739 887		*11.1*
	Q6IPS9	Elongation factor 1-alpha OS=Homo sapiens GN=EEF1A1 PE=2 SV=1	172.08	4	522 559 739 887		*11.1*
	Q6IPN6	Elongation factor 1-alpha OS=Homo sapiens GN=EEF1A1 PE=2 SV=1	172.08	4	522 559 739 887		*11.1*
	Q5VTE0	Putative elongation factor 1-alpha-like 3 OS=Homo sapiens GN=EEF1A1P5 PE=5 SV=1	172.08	4	522 559 739 887		*11.1*
	Q53HQ7	Elongation factor 1-alpha (Fragment) OS=Homo sapiens PE=2 SV=1	172.08	4	522 559 739 887		*11.1*

	Q53HM9	Elongation factor 1-alpha (Fragment) OS=Homo sapiens PE=2 SV=1	172.08	4	522 559 739 887		*11.1*
	Q53GE9	Elongation factor 1-alpha (Fragment) OS=Homo sapiens PE=2 SV=1	172.08	4	522 559 739 887		*11.1*
	Q53GA1	Elongation factor 1-alpha (Fragment) OS=Homo sapiens PE=2 SV=1	172.08	4	522 559 739 887		*11.1*
	Q53G85	Elongation factor 1-alpha (Fragment) OS=Homo sapiens PE=2 SV=1	172.08	4	522 559 739 887		*11.1*
77	Q53HU8	Vimentin variant (Fragment) OS=Homo sapiens PE=2 SV=1	171.49	4	370 602 673 1204		*13.5*
	P08670	Vimentin OS=Homo sapiens GN=VIM PE=1 SV=4	171.49	4	370 602 673 1204		*13.5*
	B3KRK8	cDNA FLJ34494 fis, clone HLUNG2005030, highly similar to VIMENTIN OS=Homo sapiens PE=2 SV=1	171.49	4	370 602 673 1204		*13.5*
	B0YJC4	Vimentin OS=Homo sapiens GN=VIM PE=3 SV=1	171.49	4	370 602 673 1204		*13.5*
78	P00558	Phosphoglycerate kinase 1 OS=Homo sapiens GN=PGK1 PE=1 SV=3	163.89	3	226 333 1101		*13.4*
	B7Z7A9	Phosphoglycerate kinase OS=Homo sapiens GN=PGK1 PE=2 SV=1	163.89	3	226 333 1101		*13.4*
79	Q07955	Serine/arginine-rich splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=1 SV=2	163.70	4	96 292 751 837		*13.8*
	J3KTL2	Serine/arginine-rich-splicing factor 1 OS=Homo sapiens GN=SRSF1 PE=4 SV=1	163.70	4	96 292 751 837		*13.8*
80	Q99988	Growth/differentiation factor 15 OS=Homo sapiens GN=GDF15 PE=1 SV=3	162.49	6	61 198 239 241 254 510		*26.6*
81	P35527	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	159.97	2	678 831		*5.8*
82	Q15102	Platelet-activating factor acetylhydrolase IB subunit gamma OS=Homo sapiens GN=PAFAH1B3 PE=1 SV=1	159.38	4	677 709 1009 1113		*18.2*
83	Q5TZP7	APEX nuclease (Multifunctional DNA repair enzyme) 1 OS=Homo sapiens GN=APEX1 PE=2 SV=1	159.03	3	449 719 755		*12.5*
	P27695	DNA-(apurinic or apyrimidinic site) lyase OS=Homo sapiens GN=APEX1 PE=1 SV=2	159.03	3	449 719 755		*12.5*
	G3V5Q1	DNA-(apurinic or apyrimidinic site) lyase (Fragment) OS=Homo sapiens GN=APEX1 PE=2 SV=1	159.03	3	449 719 755		*12.5*
	G3V3M6	DNA-(apurinic or apyrimidinic site) lyase (Fragment) OS=Homo sapiens GN=APEX1 PE=2 SV=1	159.03	3	449 719 755		*12.5*
84	Q6IBA2	PC4 protein OS=Homo sapiens GN=PC4 PE=2 SV=1	158.91	3	319 353 1217		*34.6*
	Q59G24	Activated RNA polymerase II transcription cofactor 4 variant (Fragment) OS=Homo sapiens PE=2 SV=1	158.91	3	319 353 1217		*34.6*
	P53999	Activated RNA polymerase II transcriptional coactivator p15 OS=Homo sapiens GN=SUB1 PE=1 SV=3	158.91	3	319 353 1217		*34.6*
85	P04264	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6	158.02	3	583 925 1033		*4.7*

	H6VRG3	Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1	158.02	3	583 925 1033		*4.7*
	H6VRG2	Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1	158.02	3	583 925 1033		*4.7*
	H6VRG1	Keratin 1 OS=Homo sapiens GN=KRT1 PE=2 SV=1	158.02	3	583 925 1033		*4.7*
	H6VRG0	Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1	158.02	3	583 925 1033		*4.7*
	H6VRF9	Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1	158.02	3	583 925 1033		*4.7*
	H6VRF8	Keratin 1 OS=Homo sapiens GN=KRT1 PE=3 SV=1	158.02	3	583 925 1033		*4.7*
86	Q02790	Peptidyl-prolyl cis-trans isomerase FKBP4 OS=Homo sapiens GN=FKBP4 PE=1 SV=3	156.60	3	493 1122 1159		*5.9*
	B2R9U2	cDNA, FLJ94557, highly similar to Homo sapiens FK506 binding protein 4, 59kDa (FKBP4), mRNA OS=Homo sapiens PE=2 SV=1	156.60	3	493 1122 1159		*5.9*
87	P09874	Poly [ADP-ribose] polymerase 1 OS=Homo sapiens GN=PARP1 PE=1 SV=4	146.47	3	42 882 1008		*4.4*
	B2R5W3	cDNA, FLJ92658, highly similar to Homo sapiens poly (ADP-ribose) polymerase family, member 1 (PARP1), mRNA OS=Homo sapiens PE=2 SV=1	146.47	3	42 882 1008		*4.4*
88	P13639	Elongation factor 2 OS=Homo sapiens GN=EEF2 PE=1 SV=4	142.98	4	52 238 305 1038		*5.2*
89	Q53H03	Nuclear autoantigenic sperm protein isoform 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1	142.50	3	250 773 907		*3.4*
	P49321	Nuclear autoantigenic sperm protein OS=Homo sapiens GN=NASP PE=1 SV=2	142.50	3	250 773 907		*3.4*
90	Q6IBN1	HNRPK protein OS=Homo sapiens GN=HNRPK PE=2 SV=1	142.36	4	982 1014 1151 1179		*13.4*
	Q5EC54	Heterogeneous nuclear ribonucleoprotein K transcript variant OS=Homo sapiens GN=HNRPK PE=2 SV=1	142.36	4	982 1014 1151 1179		*13.4*
	P61978	Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens GN=HNRNPK PE=1 SV=1	142.36	4	982 1014 1151 1179		*13.4*
	B4DUQ1	cDNA FLJ54552, highly similar to Heterogeneous nuclear ribonucleoprotein K OS=Homo sapiens PE=2 SV=1	142.36	4	982 1014 1151 1179		*13.4*
91	P10909	Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	141.32	2	225 242		*9.5*
	H0YC35	Clusterin (Fragment) OS=Homo sapiens GN=CLU PE=3 SV=1	141.32	2	225 242		*9.5*
	E7ETA7	Clusterin OS=Homo sapiens GN=CLU PE=2 SV=1	141.32	2	225 242		*9.5*
	B4DW11	cDNA FLJ57622, highly similar to Clusterin OS=Homo sapiens PE=2 SV=1	141.32	2	225 242		*9.5*
92	Q6LAM1	Heavy chain of factor I (Fragment) OS=Homo sapiens PE=2 SV=1	140.52	2	322 991		*8.4*

93	Q9Y265	RuvB-like 1 OS=Homo sapiens GN=RUVBL1 PE=1 SV=1	139.63	3	4 727 734		*7.7*
	B5BUB1	RuvB-like 1 (Fragment) OS=Homo sapiens GN=RUVBL1 PE=2 SV=1	139.63	3	4 727 734		*7.7*
94	P04792	Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 SV=2	139.63	3	187 427 609		*15.1*
	F8WE04	Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=2 SV=1	139.63	3	187 427 609		*15.1*
95	P08238	Heat shock protein HSP 90-beta OS=Homo sapiens GN=HSP90AB1 PE=1 SV=4	139.34	5	190 531 534 795 1178		*17.4*
	B4DMA2	cDNA FLJ54023, highly similar to Heat shock protein HSP 90-beta OS=Homo sapiens PE=2 SV=1	139.34	5	190 531 534 795 1178		*17.4*
96	Q6FHN3	Nucleoside diphosphate kinase OS=Homo sapiens GN=NME2 PE=2 SV=1	136.96	3	240 469 561		*26.3*
	Q32Q12	Nucleoside diphosphate kinase OS=Homo sapiens GN=NME1-NME2 PE=2 SV=1	136.96	3	240 469 561		*26.3*
	P22392	Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=1 SV=1	136.96	3	240 469 561		*26.3*
	J3KPD9	Nucleoside diphosphate kinase B OS=Homo sapiens GN=NME2 PE=3 SV=1	136.96	3	240 469 561		*26.3*
97	Q15717	ELAV-like protein 1 OS=Homo sapiens GN=ELAVL1 PE=1 SV=2	133.11	2	263 314		*9.6*
	B4DVB8	ELAV-like protein 1 OS=Homo sapiens GN=ELAVL1 PE=2 SV=1	133.11	2	263 314		*9.6*
98	P21741	Midkine OS=Homo sapiens GN=MDK PE=1 SV=1	130.84	3	378 666 705		*32.7*
	E9PPJ5	Midkine (Fragment) OS=Homo sapiens GN=MDK PE=2 SV=1	130.84	3	378 666 705		*32.7*
	E9PLM6	Midkine OS=Homo sapiens GN=MDK PE=2 SV=1	130.84	3	378 666 705		*32.7*
99	Q13435	Splicing factor 3B subunit 2 OS=Homo sapiens GN=SF3B2 PE=1 SV=2	129.92	2	966 1138		*3.4*
100	Q75MT9	Malate dehydrogenase (Fragment) OS=Homo sapiens GN=MDH2 PE=2 SV=1	129.48	3	548 972 1034		*20.7*
	Q6FHZ0	Malate dehydrogenase OS=Homo sapiens GN=MDH2 PE=2 SV=1	129.48	3	548 972 1034		*20.7*
	Q0QF37	Malate dehydrogenase (Fragment) OS=Homo sapiens GN=MDH2 PE=2 SV=1	129.48	3	548 972 1034		*20.7*
	P40926	Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=1 SV=3	129.48	3	548 972 1034		*20.7*
	G3XAL0	Malate dehydrogenase OS=Homo sapiens GN=MDH2 PE=3 SV=1	129.48	3	548 972 1034		*20.7*
	E9PDB2	Malate dehydrogenase, mitochondrial OS=Homo sapiens GN=MDH2 PE=2 SV=1	129.48	3	548 972 1034		*20.7*
	B4DE44	cDNA FLJ52880, highly similar to Malate dehydrogenase, mitochondrial (EC 1.1.1.37) OS=Homo sapiens PE=2 SV=1	129.48	3	548 972 1034		*20.7*

101	Q8NC51	Plasminogen activator inhibitor 1 RNA-binding protein OS=Homo sapiens GN=SERBP1 PE=1 SV=2	129.10	4	579 610 689 1180		*8.7*
	Q63HR1	Putative uncharacterized protein DKFZp686P17171 OS=Homo sapiens GN=DKFZp686P17171 PE=2 SV=1	129.10	4	579 610 689 1180		*8.7*
	Q5VU21	PAI-1 mRNA-binding protein variant OS=Homo sapiens PE=2 SV=1	129.10	4	579 610 689 1180		*8.7*
	D3DQ70	SERPINE1 mRNA binding protein 1, isoform CRA_d OS=Homo sapiens GN=SERBP1 PE=2 SV=1	129.10	4	579 610 689 1180		*8.7*
	D3DQ69	SERPINE1 mRNA binding protein 1, isoform CRA_c OS=Homo sapiens GN=SERBP1 PE=2 SV=1	129.10	4	579 610 689 1180		*8.7*
102	Q13185	Chromobox protein homolog 3 OS=Homo sapiens GN=CBX3 PE=1 SV=4	127.35	2	614 1193		*14.8*
	A4D177	Chromobox homolog 3 (HP1 gamma homolog, Drosophila) OS=Homo sapiens GN=CBX3 PE=2 SV=1	127.35	2	614 1193		*14.8*
103	Q6MZS5	Putative uncharacterized protein DKFZp686A13234 (Fragment) OS=Homo sapiens GN=DKFZp686A13234 PE=2 SV=1	126.76	3	304 461 518		*6.6*
	Q0VGD6	HNRPR protein (Fragment) OS=Homo sapiens GN=HNRPR PE=2 SV=1	126.76	3	304 461 518		*6.6*
	O43390	Heterogeneous nuclear ribonucleoprotein R OS=Homo sapiens GN=HNRNPR PE=1 SV=1	126.76	3	304 461 518		*6.6*
	B2R7W4	cDNA, FLJ93632, highly similar to Homo sapiens heterogeneous nuclear ribonucleoprotein R (HNRPR), mRNA OS=Homo sapiens PE=2 SV=1	126.76	3	304 461 518		*6.6*

UniProt Human Protein IDs, *cont.*

Grp Nr.	*Accession Number*	*Protein Name*	*Protein Score*	*Unique PSMs*	*PSM Serial Nrs.*	*Other Grp.*	*% Seq. Cover.*
104	Q53GD8	Peptidyl-prolyl cis-trans isomerase (Fragment) OS=Homo sapiens PE=2 SV=1	126.54	3	557 700 1168		*19.6*
	Q00688	Peptidyl-prolyl cis-trans isomerase FKBP3 OS=Homo sapiens GN=FKBP3 PE=1 SV=1	126.54	3	557 700 1168		*19.6*
105	P20674	Cytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens GN=COX5A PE=1 SV=2	126.49	3	340 443 483		*36.2*
	H3BV69	Cytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens GN=COX5A PE=2 SV=1	126.49	3	340 443 483		*36.2*

	H3BRM5	Cytochrome c oxidase subunit 5A, mitochondrial OS=Homo sapiens GN=COX5A PE=2 SV=1	126.49	3	340 443 483		*36.2*
106	B4DTA2	cDNA FLJ60148, highly similar to Homo sapiens heterogeneous nuclear ribonucleoprotein D-like (HNRPDL), transcript variant 2, mRNA OS=Homo sapiens PE=2 SV=1	125.86	3	177 185 629		*10.7*
107	P02765	Alpha-2-HS-glycoprotein OS=Homo sapiens GN=AHSG PE=1 SV=1	125.45	2	106 112		*5.3*
	B7Z8Q2	cDNA FLJ55606, highly similar to Alpha-2-HS-glycoprotein OS=Homo sapiens PE=2 SV=1	125.45	2	106 112		*5.3*
	B7Z556	cDNA FLJ56822, highly similar to Alpha-2-HS-glycoprotein OS=Homo sapiens PE=2 SV=1	125.45	2	106 112		*5.3*
108	Q59FI9	Ribosomal protein L12 variant (Fragment) OS=Homo sapiens PE=2 SV=1	124.82	2	830 1181		*33.0*
	P30050	60S ribosomal protein L12 OS=Homo sapiens GN=RPL12 PE=1 SV=1	124.82	2	830 1181		*33.0*
	D3DS95	HCG21173, isoform CRA_a OS=Homo sapiens GN=hCG_21173 PE=2 SV=1	124.82	2	830 1181		*33.0*
109	Q53T09	Putative uncharacterized protein XRCC5 (Fragment) OS=Homo sapiens GN=XRCC5 PE=2 SV=1	124.75	3	33 122 812		*7.6*
	P13010	X-ray repair cross-complementing protein 5 OS=Homo sapiens GN=XRCC5 PE=1 SV=3	124.75	3	33 122 812		*7.6*
110	Q02818	Nucleobindin-1 OS=Homo sapiens GN=NUCB1 PE=1 SV=4	124.74	3	265 942 984		*8.4*
	B4DZX0	cDNA FLJ52898, highly similar to Nucleobindin-1 OS=Homo sapiens PE=2 SV=1	124.74	3	265 942 984		*8.4*
	A8K7Q1	cDNA FLJ77770, highly similar to Homo sapiens nucleobindin 1 (NUCB1), mRNA OS=Homo sapiens PE=2 SV=1	124.74	3	265 942 984		*8.4*
111	Q9NYD3	Prothymosin alpha OS=Homo sapiens GN=PTMA PE=2 SV=1	124.63	2	67 369		*20.8*
112	Q9UBR2	Cathepsin Z OS=Homo sapiens GN=CTSZ PE=1 SV=1	124.60	2	444 447		*7.3*
	Q5U000	Cathepsin Z OS=Homo sapiens PE=2 SV=1	124.60	2	444 447		*7.3*
113	P35900	Keratin, type I cytoskeletal 20 OS=Homo sapiens GN=KRT20 PE=1 SV=1	123.00	3	192 474 1058		*12.7*
114	Q6NSG7	High-mobility group nucleosome binding domain 1 OS=Homo sapiens GN=HMGN1 PE=2 SV=1	122.35	2	30 327		*35.3*
	P05114	Non-histone chromosomal protein HMG-14 OS=Homo sapiens GN=HMGN1 PE=1 SV=3	122.35	2	30 327		*35.3*
	A6NEL0	Non-histone chromosomal protein HMG-14 OS=Homo sapiens GN=HMGN1 PE=2 SV=1	122.35	2	30 327		*35.3*
115	Q6FI35	Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=2 SV=1	122.26	3	27 334 853		*10.3*
	Q6FHF5	Proliferating cell nuclear antigen (Fragment) OS=Homo sapiens GN=PCNA PE=2 SV=1	122.26	3	27 334 853		*10.3*

	P12004	Proliferating cell nuclear antigen OS=Homo sapiens GN=PCNA PE=1 SV=1	122.26	3	27 334 853		*10.3*
116	P32119	Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=5	121.95	3	368 713 1013		*20.8*
	B4DF70	cDNA FLJ60461, highly similar to Peroxiredoxin-2 (EC 1.11.1.15) OS=Homo sapiens PE=2 SV=1	121.95	3	368 713 1013		*20.8*
117	P51991	Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=1 SV=2	121.58	1	939		*8.1*
	E7EWI9	Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens GN=HNRNPA3 PE=2 SV=1	121.58	1	939		*8.1*
	B4E3E6	cDNA FLJ58832, highly similar to Heterogeneous nuclear ribonucleoprotein A3 OS=Homo sapiens PE=2 SV=1	121.58	1	939		*8.1*
	B4DDB6	Heterogeneous nuclear ribonucleoprotein A3, isoform CRA_a OS=Homo sapiens GN=HNRPA3 PE=2 SV=1	121.58	1	939		*8.1*
118	P22626	Heterogeneous nuclear ribonucleoproteins A2/B1 OS=Homo sapiens GN=HNRNPA2B1 PE=1 SV=2	121.54	4	14 31 799 1130		*14.2*
119	P15924	Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	119.52	3	533 1040 1194		*2.2*
120	P02538	Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 SV=3	117.47	2	642 681		*13.5*
	B4DRU6	cDNA FLJ54657, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1	117.47	2	642 681		*13.5*
	B4DRR0	cDNA FLJ53910, highly similar to Keratin, type II cytoskeletal 6A OS=Homo sapiens PE=2 SV=1	117.47	2	642 681		*13.5*
	A8K2I0	cDNA FLJ78504, highly similar to Homo sapiens keratin 6A (KRT6A), mRNA OS=Homo sapiens PE=2 SV=1	117.47	2	642 681		*13.5*
121	B4E177	cDNA FLJ56368, highly similar to Myosin-14 OS=Homo sapiens PE=2 SV=1	115.64	3	138 528 635		*17.6*
	A1L2Z2	MYH14 protein OS=Homo sapiens GN=MYH14 PE=2 SV=1	115.64	3	138 528 635		*61.7*
122	P01185	Vasopressin-neurophysin 2-copeptin OS=Homo sapiens GN=AVP PE=1 SV=2	115.10	3	430 903 1094		*12.2*
123	P07237	Protein disulfide-isomerase OS=Homo sapiens GN=P4HB PE=1 SV=3	112.91	3	251 255 1085		*5.5*
	B4DNL5	cDNA FLJ59361, highly similar to Protein disulfide-isomerase (EC 5.3.4.1) OS=Homo sapiens PE=2 SV=1	112.91	3	251 255 1085		*5.5*
124	O75475	PC4 and SFRS1-interacting protein OS=Homo sapiens GN=PSIP1 PE=1 SV=1	111.98	2	137 920		*5.7*
125	Q53RR5	Putative uncharacterized protein YWHAQ (Fragment) OS=Homo sapiens GN=YWHAQ PE=2 SV=1	109.42	2	53 191		*29.5*
	P27348	14-3-3 protein theta OS=Homo sapiens GN=YWHAQ PE=1 SV=1	109.42	2	53 191		*29.5*
	E9PG15	14-3-3 protein theta (Fragment) OS=Homo sapiens GN=YWHAQ PE=2 SV=1	109.42	2	53 191		*29.5*
126	Q53SS8	Poly(RC) binding protein 1 OS=Homo sapiens GN=PCBP1 PE=2 SV=1	109.34	2	992 1044		*8.7*

	Q15365	Poly(rC)-binding protein 1 OS=Homo sapiens GN=PCBP1 PE=1 SV=2	109.34	2	992 1044		8.7
127	P36955	Pigment epithelium-derived factor OS=Homo sapiens GN=SERPINF1 PE=1 SV=4	108.46	2	82 513		9.1
	I3L3M1	Pigment epithelium-derived factor OS=Homo sapiens GN=SERPINF1 PE=2 SV=1	108.46	2	82 513		9.1
128	Q53FC7	Heat shock 70kDa protein 6 (HSP70B~) variant (Fragment) OS=Homo sapiens PE=2 SV=1	105.87	2	15 1143		15.1
	P17066	Heat shock 70 kDa protein 6 OS=Homo sapiens GN=HSPA6 PE=1 SV=2	105.87	2	15 1143		15.1
	B3KSM6	cDNA FLJ36606 fis, clone TRACH2015654, highly similar to HEAT SHOCK 70 kDa PROTEIN 6 OS=Homo sapiens PE=2 SV=1	105.87	2	15 1143		15.1
	B2R6X5	cDNA, FLJ93166, highly similar to Homo sapiens heat shock 70kDa protein 6 (HSP70B~) (HSPA6), mRNA OS=Homo sapiens PE=2 SV=1	105.87	2	15 1143		15.1
129	G3V1X9	Chromobox homolog 5 (HP1 alpha homolog, Drosophila), isoform CRA_a OS=Homo sapiens GN=CBX5 PE=4 SV=1	105.71	2	669 1108		19.2
130	P49006	MARCKS-related protein OS=Homo sapiens GN=MARCKSL1 PE=1 SV=2	105.15	2	12 24		18.5
131	Q6IAT9	Proteasome subunit beta type OS=Homo sapiens GN=PSMB6 PE=2 SV=1	104.36	2	389 652		8.4
	P28072	Proteasome subunit beta type-6 OS=Homo sapiens GN=PSMB6 PE=1 SV=4	104.36	2	389 652		8.4
132	Q9UKV3	Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens GN=ACIN1 PE=1 SV=2	104.23	2	141 913		1.7
	E7EQT4	Apoptotic chromatin condensation inducer in the nucleus OS=Homo sapiens GN=ACIN1 PE=2 SV=2	104.23	2	141 913		1.7
	B4DQZ7	cDNA FLJ50838, highly similar to Apoptotic chromatin condensation inducer in thenucleus (Fragment) OS=Homo sapiens PE=2 SV=1	104.23	2	141 913		1.7
133	Q9Y266	Nuclear migration protein nudC OS=Homo sapiens GN=NUDC PE=1 SV=1	104.20	2	592 1053		6.0
134	P00441	Superoxide dismutase [Cu-Zn] OS=Homo sapiens GN=SOD1 PE=1 SV=2	104.04	2	743 994		33.1
135	Q8WVW5	Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1	103.82	3	88 264 1088		33.9
	Q53GK6	Beta actin variant (Fragment) OS=Homo sapiens PE=2 SV=1	103.82	3	88 264 1088		33.9
	Q53G99	Beta actin variant (Fragment) OS=Homo sapiens PE=2 SV=1	103.82	3	88 264 1088		33.9
	Q53G76	Beta actin variant (Fragment) OS=Homo sapiens PE=2 SV=1	103.82	3	88 264 1088		33.9
	Q1KLZ0	HCG15971, isoform CRA_a OS=Homo sapiens GN=PS1TP5BP1 PE=2 SV=1	103.82	3	88 264 1088		33.9

	P63261	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1	103.82	3	88 264 1088		33.9
	P60709	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	103.82	3	88 264 1088		33.9
	B4E3A4	cDNA FLJ57283, highly similar to Actin, cytoplasmic 2 OS=Homo sapiens PE=2 SV=1	103.82	3	88 264 1088		33.9
	B4DVQ0	cDNA FLJ58286, highly similar to Actin, cytoplasmic 2 OS=Homo sapiens PE=2 SV=1	103.82	3	88 264 1088		33.9
136	Q99426	Tubulin-folding cofactor B OS=Homo sapiens GN=TBCB PE=1 SV=2	102.38	2	248 471		10.4
	Q6FGY5	CKAP1 protein OS=Homo sapiens GN=CKAP1 PE=2 SV=1	102.38	2	248 471		10.4
	K7EP07	Tubulin-folding cofactor B (Fragment) OS=Homo sapiens GN=TBCB PE=4 SV=1	102.38	2	248 471		10.4
137	F5GXR3	Parathymosin OS=Homo sapiens GN=PTMS PE=2 SV=1	101.59	2	201 1107		19.2
138	Q3ZCU9	STIP1 protein OS=Homo sapiens GN=STIP1 PE=2 SV=1	101.54	2	535 971		12.1
	P31948	Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=1 SV=1	101.54	2	535 971		12.1
	G3XAD8	Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=4 SV=1	101.54	2	535 971		12.1
	F5H0T1	Stress-induced-phosphoprotein 1 OS=Homo sapiens GN=STIP1 PE=2 SV=1	101.54	2	535 971		12.1
	A8K690	cDNA FLJ76863, highly similar to Homo sapiens stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein) (STIP1), mRNA OS=Homo sapiens PE=2 SV=1	101.54	2	535 971		12.1
139	P09496	Clathrin light chain A OS=Homo sapiens GN=CLTA PE=1 SV=1	101.47	3	224 375 785		10.5
140	Q13263	Transcription intermediary factor 1-beta OS=Homo sapiens GN=TRIM28 PE=1 SV=5	99.16	3	150 746 1163		3.5
	B2R8R5	cDNA, FLJ94025, highly similar to Homo sapiens tripartite motif-containing 28 (TRIM28), mRNA OS=Homo sapiens PE=2 SV=1	99.16	3	150 746 1163		3.5
141	Q6UXA7	Uncharacterized protein C6orf15 OS=Homo sapiens GN=C6orf15 PE=2 SV=3	98.37	2	156 918		5.8
142	P62318	Small nuclear ribonucleoprotein Sm D3 OS=Homo sapiens GN=SNRPD3 PE=1 SV=1	97.96	2	578 1005		10.8
	B4DJP7	Small nuclear ribonucleoprotein Sm D3 OS=Homo sapiens GN=SNRPD3 PE=2 SV=1	97.96	2	578 1005		10.8
143	Q9Y2W2	WW domain-binding protein 11 OS=Homo sapiens GN=WBP11 PE=1 SV=1	97.61	2	200 824		5.3
	F5H721	WW domain-binding protein 11 OS=Homo sapiens GN=WBP11 PE=2 SV=1	97.61	2	200 824		5.3
	B4DY34	cDNA FLJ60194, highly similar to WW domain-binding protein 11 OS=Homo sapiens PE=2 SV=1	97.61	2	200 824		5.3

	B4DMD3	cDNA FLJ58174, highly similar to WW domain-binding protein 11 OS=Homo sapiens PE=2 SV=1	97.61	2	200 824		*5.3*
144	Q9H307	Pinin OS=Homo sapiens GN=PNN PE=1 SV=4	97.43	2	363 638		*3.9*
	A8K964	cDNA FLJ75071, highly similar to Homo sapiens pinin, desmosome associated protein (PNN), mRNA OS=Homo sapiens PE=2 SV=1	97.43	2	363 638		*3.9*
145	Q9NPL4	Enolase (Fragment) OS=Homo sapiens PE=2 SV=1	97.25	1	277		*8.8*
	P13929	Beta-enolase OS=Homo sapiens GN=ENO3 PE=1 SV=5	97.25	1	277		*8.8*
	D3DTL4	Enolase OS=Homo sapiens GN=ENO3 PE=2 SV=1	97.25	1	277		*8.8*
146	P67936	Tropomyosin alpha-4 chain OS=Homo sapiens GN=TPM4 PE=1 SV=3	97.21	3	119 977 1023		*30.2*
147	Q15424	Scaffold attachment factor B1 OS=Homo sapiens GN=SAFB PE=1 SV=4	97.05	2	900 1182		*4.6*
	F5GZU3	Scaffold attachment factor B1 OS=Homo sapiens GN=SAFB PE=2 SV=1	97.05	2	900 1182		*4.6*
	B7ZLP6	SAFB protein OS=Homo sapiens GN=SAFB PE=2 SV=1	97.05	2	900 1182		*4.6*
	B7ZLP5	SAFB protein OS=Homo sapiens GN=SAFB PE=2 SV=1	97.05	2	900 1182		*4.6*
	B7Z5X3	cDNA FLJ59404, highly similar to Scaffold attachment factor B OS=Homo sapiens PE=2 SV=1	97.05	2	900 1182		*4.6*
	B7Z2Z1	cDNA FLJ59523, highly similar to Scaffold attachment factor B OS=Homo sapiens PE=2 SV=1	97.05	2	900 1182		*4.6*
	B7Z2F6	Scaffold attachment factor B1 OS=Homo sapiens GN=SAFB PE=2 SV=1	97.05	2	900 1182		*4.6*
	B7Z1C7	cDNA FLJ59451, highly similar to Scaffold attachment factor B OS=Homo sapiens PE=2 SV=1	97.05	2	900 1182		*4.6*
	A8K329	cDNA FLJ76656, highly similar to Homo sapiens scaffold attachment factor B (SAFB), mRNA OS=Homo sapiens PE=2 SV=1	97.05	2	900 1182		*4.6*
	A0AV56	SAFB protein OS=Homo sapiens GN=SAFB PE=2 SV=1	97.05	2	900 1182		*4.6*
148	P62851	40S ribosomal protein S25 OS=Homo sapiens GN=RPS25 PE=1 SV=1	96.45	2	278 1140		*12.8*
149	Q6FGH5	40S ribosomal protein S21 (Fragment) OS=Homo sapiens GN=RPS21 PE=2 SV=1	96.01	2	86 446		*26.5*
	P63220	40S ribosomal protein S21 OS=Homo sapiens GN=RPS21 PE=1 SV=1	96.01	2	86 446		*26.5*
150	Q01469	Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP5 PE=1 SV=3	95.35	2	357 364		*25.2*
	E7DVW5	Fatty acid binding protein 5 (Psoriasis-associated) OS=Homo sapiens GN=FABP5 PE=2 SV=1	95.35	2	357 364		*25.2*

UniProt Human Protein IDs, *cont.*

Grp Nr.	*Accession Number*	*Protein Name*	*Protein Score*	*Unique PSMs*	*PSM Serial Nrs.*	*Other Grp.*	*% Seq. Cover.*
151	Q53HJ4	Minichromosome maintenance protein 3 variant (Fragment) OS=Homo sapiens PE=2 SV=1	95.10	3	462 1064 1161		*4.1*
	P25205	DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=1 SV=3	95.10	3	462 1064 1161		*4.1*
	J3KQ69	DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=3 SV=1	95.10	3	462 1064 1161		*4.1*
	B4DWW4	DNA replication licensing factor MCM3 OS=Homo sapiens GN=MCM3 PE=2 SV=1	95.10	3	462 1064 1161		*4.1*
	B4DUQ9	cDNA FLJ50873, highly similar to DNA replication licensing factor MCM3 OS=Homo sapiens PE=2 SV=1	95.10	3	462 1064 1161		*4.1*
	B4DS46	cDNA FLJ55751, highly similar to DNA replication licensing factor MCM3 OS=Homo sapiens PE=2 SV=1	95.10	3	462 1064 1161		*4.1*
	B2R7C5	cDNA, FLJ93378, highly similar to Homo sapiens MCM3 minichromosome maintenance deficient 3 (S. cerevisiae) (MCM3), mRNA OS=Homo sapiens PE=2 SV=1	95.10	3	462 1064 1161		*4.1*
152	Q59FV9	PTK7 protein tyrosine kinase 7 isoform a variant (Fragment) OS=Homo sapiens PE=2 SV=1	94.17	2	572 1002		*3.6*
	Q13308	Inactive tyrosine-protein kinase 7 OS=Homo sapiens GN=PTK7 PE=1 SV=2	94.17	2	572 1002		*3.6*
153	Q6FI03	G3BP protein OS=Homo sapiens GN=G3BP PE=2 SV=1	93.77	2	147 1084		*9.4*
	Q5U0Q1	Putative uncharacterized protein DKFZp686L1159 OS=Homo sapiens GN=DKFZp686L1159 PE=2 SV=1	93.77	2	147 1084		*9.4*
	Q32P45	GTPase activating protein (SH3 domain) binding protein 1 OS=Homo sapiens GN=G3BP1 PE=2 SV=1	93.77	2	147 1084		*9.4*
	Q13283	Ras GTPase-activating protein-binding protein 1 OS=Homo sapiens GN=G3BP1 PE=1 SV=1	93.77	2	147 1084		*9.4*
154	P24752	Acetyl-CoA acetyltransferase, mitochondrial OS=Homo sapiens GN=ACAT1 PE=1 SV=1	93.73	1	435		*3.0*
155	P33176	Kinesin-1 heavy chain OS=Homo sapiens GN=KIF5B PE=1 SV=1	93.47	1	735		*1.2*
	D3DRX6	Kinesin family member 5B, isoform CRA_a OS=Homo sapiens GN=KIF5B PE=3 SV=1	93.47	1	735		*1.2*
	C1PHA2	Tyrosine-protein kinase receptor OS=Homo sapiens GN=KIF5B-ALK PE=2 SV=1	93.47	1	735		*1.2*

	A8K048	cDNA FLJ76989, highly similar to Homo sapiens kinesin family member 5B (KIF5B), mRNA (Fragment) OS=Homo sapiens PE=2 SV=1	93.47	1	735		*1.2*
156	Q567R9	CIP29 protein OS=Homo sapiens GN=CIP29 PE=2 SV=1	93.30	2	294 947		*5.5*
	P82979	SAP domain-containing ribonucleoprotein OS=Homo sapiens GN=SARNP PE=1 SV=3	93.30	2	294 947		*5.5*
	H0YHG0	Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=1	93.30	2	294 947		*5.5*
157	Q5JQ13	Vinculin (Fragment) OS=Homo sapiens GN=VCL PE=2 SV=1	92.77	2	464 1110		*2.4*
	P18206	Vinculin OS=Homo sapiens GN=VCL PE=1 SV=4	92.77	2	464 1110		*2.4*
	B4E3Q9	cDNA FLJ59659, highly similar to Vinculin OS=Homo sapiens PE=2 SV=1	92.77	2	464 1110		*2.4*
	B3KXA2	cDNA FLJ45031 fis, clone BRAWH3018548, highly similar to Vinculin OS=Homo sapiens PE=2 SV=1	92.77	2	464 1110		*2.4*
158	Q9Y4K0	Lysyl oxidase homolog 2 OS=Homo sapiens GN=LOXL2 PE=1 SV=1	92.65	3	428 884 1095		*9.8*
159	P02751	Fibronectin OS=Homo sapiens GN=FN1 PE=1 SV=4	91.89	3	103 230 847		*1.3*
	F8W7G7	Ugl-Y3 OS=Homo sapiens GN=FN1 PE=2 SV=1	91.89	3	103 230 847		*1.3*
	E9PE77	Ugl-Y3 OS=Homo sapiens GN=FN1 PE=2 SV=1	91.89	3	103 230 847		*1.3*
	B7ZLF0	Fibronectin 1 OS=Homo sapiens GN=FN1 PE=2 SV=1	91.89	3	103 230 847		*1.3*
	B7ZLE5	FN1 protein OS=Homo sapiens GN=FN1 PE=2 SV=1	91.89	3	103 230 847		*1.3*
160	P35080	Profilin-2 OS=Homo sapiens GN=PFN2 PE=1 SV=3	91.86	1	1171		*4.2*
	G5E9Q6	Profilin OS=Homo sapiens GN=PFN2 PE=3 SV=1	91.86	1	1171		*4.2*
	D3DNI3	Profilin (Fragment) OS=Homo sapiens GN=PFN2 PE=2 SV=1	91.86	1	1171		*4.2*
	D3DNI2	Profilin (Fragment) OS=Homo sapiens GN=PFN2 PE=2 SV=1	91.86	1	1171		*4.2*
	C9JQ45	Profilin OS=Homo sapiens GN=PFN2 PE=2 SV=1	91.86	1	1171		*4.2*
	C9J712	Profilin-2 OS=Homo sapiens GN=PFN2 PE=4 SV=1	91.86	1	1171		*4.2*
	C9J0J7	Profilin-2 OS=Homo sapiens GN=PFN2 PE=4 SV=1	91.86	1	1171		*4.2*
	B4DNH1	Profilin OS=Homo sapiens PE=2 SV=1	91.86	1	1171		*4.2*
161	Q59GB4	Dihydropyrimidinase-like 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1	91.49	2	541 581		*3.1*
	Q53ET2	Dihydropyrimidinase-like 2 variant (Fragment) OS=Homo sapiens PE=2 SV=1	91.49	2	541 581		*3.1*
	Q16555	Dihydropyrimidinase-related protein 2 OS=Homo sapiens GN=DPYSL2 PE=1 SV=1	91.49	2	541 581		*3.1*
162	P30049	ATP synthase subunit delta, mitochondrial OS=Homo sapiens GN=ATP5D PE=1 SV=2	91.40	2	172 1000		*8.9*
163	Q5SYQ9	Retinal dehydrogenase 1 OS=Homo sapiens GN=ALDH1A1 PE=2 SV=1	91.38	2	13 1184		*10.8*
	Q5SYQ8	Retinal dehydrogenase 1 (Fragment) OS=Homo sapiens GN=ALDH1A1 PE=2 SV=1	91.38	2	13 1184		*10.8*
	Q5SYQ7	Retinal dehydrogenase 1 (Fragment) OS=Homo sapiens GN=ALDH1A1 PE=2 SV=1	91.38	2	13 1184		*10.8*

	Q59EJ0	Aldehyde dehydrogenase 1A1 variant (Fragment) OS=Homo sapiens PE=2 SV=1	91.38	2	13 1184		*10.8*
	P00352	Retinal dehydrogenase 1 OS=Homo sapiens GN=ALDH1A1 PE=1 SV=2	91.38	2	13 1184		*10.8*
164	Q8N1G4	Leucine-rich repeat-containing protein 47 OS=Homo sapiens GN=LRRC47 PE=1 SV=1	91.37	1	214		*2.6*
165	Q68CM6	STXBP1 protein OS=Homo sapiens GN=stxbp1 PE=2 SV=1	91.02	1	733		*2.3*
	Q59GC9	Syntaxin binding protein 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1	91.02	1	733		*2.3*
	P61764	Syntaxin-binding protein 1 OS=Homo sapiens GN=STXBP1 PE=1 SV=1	91.02	1	733		*2.3*
	B7Z3F4	cDNA FLJ55070, highly similar to Syntaxin-binding protein 1 OS=Homo sapiens PE=2 SV=1	91.02	1	733		*2.3*
	B7Z2V7	cDNA FLJ54602, highly similar to Syntaxin-binding protein 1 OS=Homo sapiens PE=2 SV=1	91.02	1	733		*2.3*
	B7Z1V5	cDNA FLJ55678, highly similar to Syntaxin-binding protein 1 OS=Homo sapiens PE=2 SV=1	91.02	1	733		*2.3*
166	Q7Z4W8	Heparin-binding protein HBp15 OS=Homo sapiens PE=2 SV=1	90.37	2	199 379		*28.1*
	P35268	60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=1 SV=2	90.37	2	199 379		*28.1*
	K7ERI7	60S ribosomal protein L22 OS=Homo sapiens GN=RPL22 PE=4 SV=1	90.37	2	199 379		*28.1*
	K7EMH1	60S ribosomal protein L22 (Fragment) OS=Homo sapiens GN=RPL22 PE=4 SV=1	90.37	2	199 379		*28.1*
167	Q6ZP45	CDNA FLJ26517 fis, clone KDN07769 OS=Homo sapiens PE=2 SV=1	89.85	1	207		*15.6*
	Q5T6U8	High mobility group AT-hook 1 OS=Homo sapiens GN=HMGA1 PE=4 SV=1	89.85	1	207		*15.6*
	P17096	High mobility group protein HMG-I/HMG-Y OS=Homo sapiens GN=HMGA1 PE=1 SV=3	89.85	1	207		*15.6*
168	Q8WVB5	Metallothionein OS=Homo sapiens GN=MT1X PE=2 SV=1	89.76	2	98 838		*49.2*
	P80297	Metallothionein-1X OS=Homo sapiens GN=MT1X PE=1 SV=1	89.76	2	98 838		*49.2*
169	Q12906	Interleukin enhancer-binding factor 3 OS=Homo sapiens GN=ILF3 PE=1 SV=3	88.71	2	158 1109		*5.8*
	G5E9M5	Interleukin enhancer binding factor 3, 90kDa, isoform CRA_b OS=Homo sapiens GN=ILF3 PE=4 SV=1	88.71	2	158 1109		*5.8*
	F4ZW66	NF110b OS=Homo sapiens PE=2 SV=1	88.71	2	158 1109		*5.8*
	F4ZW65	NF90b OS=Homo sapiens PE=2 SV=1	88.71	2	158 1109		*5.8*
	F4ZW64	NF90a OS=Homo sapiens PE=2 SV=1	88.71	2	158 1109		*5.8*
	A8K590	cDNA FLJ77456, highly similar to Homo sapiens interleukin enhancer binding factor 3, 90kDa (ILF3), transcript variant 2, mRNA OS=Homo sapiens PE=2 SV=1	88.71	2	158 1109		*5.8*
170	Q59EQ2	Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, beta polypeptide variant (Fragment) OS=Homo sapiens PE=2 SV=1	88.53	2	604 627		*44.0*

	Q4VY20	14-3-3 protein beta/alpha (Fragment) OS=Homo sapiens GN=YWHAB PE=4 SV=1	88.53	2	604 627		*44.0*
	Q4VY19	14-3-3 protein beta/alpha (Fragment) OS=Homo sapiens GN=YWHAB PE=4 SV=1	88.53	2	604 627		*44.0*
	P31946	14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=1 SV=3	88.53	2	604 627		*44.0*
	B5BU24	14-3-3 protein beta/alpha OS=Homo sapiens GN=YWHAB PE=2 SV=1	88.53	2	604 627		*44.0*
171	Q16778	Histone H2B type 2-E OS=Homo sapiens GN=HIST2H2BE PE=1 SV=3	88.04	2	395 740		*61.1*
172	Q53G71	Calreticulin variant (Fragment) OS=Homo sapiens PE=2 SV=1	87.97	3	90 215 436		*15.4*
	P27797	Calreticulin OS=Homo sapiens GN=CALR PE=1 SV=1	87.97	3	90 215 436		*15.4*
	K7EJB9	Calreticulin (Fragment) OS=Homo sapiens GN=CALR PE=3 SV=1	87.97	3	90 215 436		*15.4*
173	Q5RKT7	Ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=2 SV=1	87.30	3	301 407 729		*30.1*
	P62979	Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RPS27A PE=1 SV=2	87.30	3	301 407 729		*30.1*
	B2RDW1	Ribosomal protein S27a, isoform CRA_c OS=Homo sapiens GN=RPS27A PE=2 SV=1	87.30	3	301 407 729		*30.1*
174	Q86X29	Lipolysis-stimulated lipoprotein receptor OS=Homo sapiens GN=LSR PE=1 SV=4	86.85	1	663		*2.8*
	A6NDW3	Lipolysis-stimulated lipoprotein receptor OS=Homo sapiens GN=LSR PE=2 SV=1	86.85	1	663		*2.8*
175	Q6IB64	TCEA2 protein OS=Homo sapiens GN=TCEA2 PE=2 SV=1	86.60	1	890		*11.1*
	Q15560	Transcription elongation factor A protein 2 OS=Homo sapiens GN=TCEA2 PE=1 SV=1	86.60	1	890		*11.1*
	B3KNM1	cDNA FLJ14918 fis, clone PLACE1007239, highly similar to Transcription elongation factor A protein 2 OS=Homo sapiens PE=2 SV=1	86.60	1	890		*45.1*
176	Q9NRX4	14 kDa phosphohistidine phosphatase OS=Homo sapiens GN=PHPT1 PE=1 SV=1	85.73	1	1067		*9.6*
	Q6FIE5	PHP14 protein OS=Homo sapiens GN=PHP14 PE=2 SV=1	85.73	1	1067		*9.6*
177	P31431	Syndecan-4 OS=Homo sapiens GN=SDC4 PE=1 SV=2	85.32	2	497 1061		*17.5*
	B4E1S6	Syndecan OS=Homo sapiens GN=SDC4 PE=2 SV=1	85.32	2	497 1061		*17.5*
178	Q76LA1	CSTB protein OS=Homo sapiens GN=CSTB PE=2 SV=1	84.93	2	235 1202		*30.6*
	P04080	Cystatin-B OS=Homo sapiens GN=CSTB PE=1 SV=2	84.93	2	235 1202		*30.6*
179	P07954	Fumarate hydratase, mitochondrial OS=Homo sapiens GN=FH PE=1 SV=3	84.88	1	530		*2.7*
	B1ANK7	Fumarate hydratase OS=Homo sapiens GN=FH PE=2 SV=1	84.88	1	530		*2.7*
180	P30041	Peroxiredoxin-6 OS=Homo sapiens GN=PRDX6 PE=1 SV=3	84.37	2	551 1201		*8.9*
181	D3DND1	CDV3 homolog (Mouse), isoform CRA_a OS=Homo sapiens GN=CDV3 PE=4 SV=1	83.49	3	101 229 919		*10.5*
182	Q7Z2W4	Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=1 SV=3	83.47	1	679		*3.4*

	Q05DV5	ZC3HAV1 protein (Fragment) OS=Homo sapiens GN=ZC3HAV1 PE=2 SV=1	83.47	1	679		*3.4*
	C9J6P4	Zinc finger CCCH-type antiviral protein 1 OS=Homo sapiens GN=ZC3HAV1 PE=2 SV=1	83.47	1	679		*3.4*
	A8K9U6	cDNA FLJ76121, highly similar to Homo sapiens zinc finger CCCH-type, antiviral 1 (ZC3HAV1), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1	83.47	1	679		*3.4*
183	Q06830	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1	82.57	3	163 337 547		*24.6*
	B2R4P2	cDNA, FLJ92164, highly similar to Homo sapiens peroxiredoxin 1 (PRDX1), mRNA OS=Homo sapiens PE=2 SV=1	82.57	3	163 337 547		*24.6*
184	P01034	Cystatin-C OS=Homo sapiens GN=CST3 PE=1 SV=1	81.75	2	821 936		*19.9*
185	Q5VXV3	SET OS=Homo sapiens GN=SET PE=2 SV=1	81.69	2	1111 1175		*11.6*
	Q5VXV2	Protein SET OS=Homo sapiens GN=SET PE=2 SV=2	81.69	2	1111 1175		*11.6*
	Q01105	Protein SET OS=Homo sapiens GN=SET PE=1 SV=3	81.69	2	1111 1175		*11.6*
	B2RCX0	cDNA, FLJ96345, Homo sapiens SET translocation (myeloid leukemia-associated) (SET),mRNA OS=Homo sapiens PE=2 SV=1	81.69	2	1111 1175		*11.6*
186	P14314	Glucosidase 2 subunit beta OS=Homo sapiens GN=PRKCSH PE=1 SV=2	80.98	3	182 540 1052		*25.4*
	K7ELL7	Glucosidase 2 subunit beta OS=Homo sapiens GN=PRKCSH PE=4 SV=1	80.98	3	182 540 1052		*25.4*
	B4DJQ5	cDNA FLJ59211, highly similar to Glucosidase 2 subunit beta OS=Homo sapiens PE=2 SV=1	80.98	3	182 540 1052		*25.4*
	A2VCQ4	PRKCSH protein (Fragment) OS=Homo sapiens GN=PRKCSH PE=2 SV=1	80.98	3	182 540 1052		*25.4*
187	O14737	Programmed cell death protein 5 OS=Homo sapiens GN=PDCD5 PE=1 SV=3	80.91	1	806		*10.1*
	K7ESJ4	Programmed cell death protein 5 OS=Homo sapiens GN=PDCD5 PE=4 SV=1	80.91	1	806		*10.1*
	K7EQA1	Programmed cell death protein 5 OS=Homo sapiens GN=PDCD5 PE=4 SV=1	80.91	1	806		*10.1*
	K7EL31	Programmed cell death protein 5 OS=Homo sapiens GN=PDCD5 PE=4 SV=1	80.91	1	806		*10.1*
	B4DE64	Programmed cell death protein 5 OS=Homo sapiens GN=PDCD5 PE=2 SV=1	80.91	1	806		*10.1*

UniProt Human Protein IDs, *cont.*

Grp Nr.	Accession Number	Protein Name	Protein Score	Unique PSMs	PSM Serial Nrs.	Other Grp.	% Seq. Cover.
188	Q9BW30	Tubulin polymerization-promoting protein family member 3 OS=Homo sapiens GN=TPPP3 PE=1 SV=1	79.40	2	697 714		*19.9*
189	Q9UHD8	Septin-9 OS=Homo sapiens GN=SEPT9 PE=1 SV=2	79.39	2	308 989		*5.8*
190	P30040	Endoplasmic reticulum resident protein 29 OS=Homo sapiens GN=ERP29 PE=1 SV=4	78.96	2	466 978		*10.6*
	F8VY02	Endoplasmic reticulum resident protein 29 OS=Homo sapiens GN=ERP29 PE=2 SV=1	78.96	2	466 978		*10.6*
191	Q15818	Neuronal pentraxin-1 OS=Homo sapiens GN=NPTX1 PE=2 SV=2	78.79	1	1083		*3.5*
192	G5E9L5	DEAD (Asp-Glu-Ala-Asp) box polypeptide 17, isoform CRA_a OS=Homo sapiens GN=DDX17 PE=4 SV=1	78.55	1	232		*13.8*
193	Q8N1C8	HSPA9 protein (Fragment) OS=Homo sapiens GN=HSPA9 PE=2 SV=1	77.03	1	917		*5.7*
	P38646	Stress-70 protein, mitochondrial OS=Homo sapiens GN=HSPA9 PE=1 SV=2	77.03	1	917		*5.7*
	D6RJI2	Stress-70 protein, mitochondrial (Fragment) OS=Homo sapiens GN=HSPA9 PE=2 SV=1	77.03	1	917		*5.7*
	D6RA73	Stress-70 protein, mitochondrial (Fragment) OS=Homo sapiens GN=HSPA9 PE=2 SV=1	77.03	1	917		*5.7*
	B7Z4V2	cDNA FLJ51907, highly similar to Stress-70 protein, mitochondrial OS=Homo sapiens PE=2 SV=1	77.03	1	917		*5.7*
	B7Z1V7	cDNA FLJ51811, highly similar to Stress-70 protein, mitochondrial OS=Homo sapiens PE=2 SV=1	77.03	1	917		*5.7*
194	C9JNW5	60S ribosomal protein L24 OS=Homo sapiens GN=RPL24 PE=4 SV=1	76.63	2	7 341		*24.0*
195	Q5HYI3	Putative uncharacterized protein DKFZp686N1815 OS=Homo sapiens GN=DKFZp686N1815 PE=2 SV=1	76.35	1	1037		*7.0*
	P42574	Caspase-3 OS=Homo sapiens GN=CASP3 PE=1 SV=2	76.35	1	1037		*7.0*
	C9JXR7	Caspase-3 subunit p12 (Fragment) OS=Homo sapiens GN=CASP3 PE=2 SV=2	76.35	1	1037		*7.0*
	A8MVM1	Caspase-3 subunit p12 OS=Homo sapiens GN=CASP3 PE=4 SV=2	76.35	1	1037		*7.0*
196	Q9BTM1	Histone H2A.J OS=Homo sapiens GN=H2AFJ PE=1 SV=1	75.80	2	648 1070		*22.3*
	Q99878	Histone H2A type 1-J OS=Homo sapiens GN=HIST1H2AJ PE=1 SV=3	75.80	2	648 1070		*22.3*
	Q96KK5	Histone H2A type 1-H OS=Homo sapiens GN=HIST1H2AH PE=1 SV=3	75.80	2	648 1070		*22.3*
	Q93077	Histone H2A type 1-C OS=Homo sapiens GN=HIST1H2AC PE=1 SV=3	75.80	2	648 1070		*22.3*
	Q7L7L0	Histone H2A type 3 OS=Homo sapiens GN=HIST3H2A PE=1 SV=3	75.80	2	648 1070		*22.3*

	Q6FI13	Histone H2A type 2-A OS=Homo sapiens GN=HIST2H2AA3 PE=1 SV=3	75.80	2	648 1070		*22.3*
	Q16777	Histone H2A type 2-C OS=Homo sapiens GN=HIST2H2AC PE=1 SV=4	75.80	2	648 1070		*22.3*
	Q08AJ9	Histone H2A OS=Homo sapiens GN=HIST1H2AB PE=2 SV=1	75.80	2	648 1070		*22.3*
	P20671	Histone H2A type 1-D OS=Homo sapiens GN=HIST1H2AD PE=1 SV=2	75.80	2	648 1070		*22.3*
	P16104	Histone H2A.x OS=Homo sapiens GN=H2AFX PE=1 SV=2	75.80	2	648 1070		*22.3*
197	P19012	Keratin, type I cytoskeletal 15 OS=Homo sapiens GN=KRT15 PE=1 SV=3	75.62	2	509 1123		*9.0*
198	Q8TEA8	D-tyrosyl-tRNA(Tyr) deacylase 1 OS=Homo sapiens GN=DTD1 PE=1 SV=2	75.53	1	394		*7.7*
	Q496C9	D-tyrosyl-tRNA deacylase 1 homolog (S. cerevisiae) OS=Homo sapiens GN=DTD1 PE=2 SV=1	75.53	1	394		*7.7*
199	Q8NBS9	Thioredoxin domain-containing protein 5 OS=Homo sapiens GN=TXNDC5 PE=1 SV=2	75.25	2	908 973		*4.4*
	Q86UY0	TXNDC5 protein OS=Homo sapiens GN=TXNDC5 PE=2 SV=1	75.25	2	908 973		*4.4*
	Q6EHZ3	Putative uncharacterized protein STRF8 OS=Homo sapiens GN=STRF8 PE=2 SV=1	75.25	2	908 973		*4.4*
	Q658S9	Putative uncharacterized protein DKFZp666I134 (Fragment) OS=Homo sapiens GN=DKFZp666I134 PE=2 SV=1	75.25	2	908 973		*4.4*
200	Q8IY67	Ribonucleoprotein PTB-binding 1 OS=Homo sapiens GN=RAVER1 PE=1 SV=1	75.23	1	644		*13.5*
	K7EKR9	Ribonucleoprotein PTB-binding 1 (Fragment) OS=Homo sapiens GN=RAVER1 PE=4 SV=1	75.23	1	644		*13.5*
	E9PAU2	Ribonucleoprotein PTB-binding 1 OS=Homo sapiens GN=RAVER1 PE=2 SV=1	75.23	1	644		*13.5*
201	Q15651	High mobility group nucleosome-binding domain-containing protein 3 OS=Homo sapiens GN=HMGN3 PE=1 SV=2	75.07	1	460		*38.4*
202	Q92688	Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Homo sapiens GN=ANP32B PE=1 SV=1	74.11	2	861 968		*6.0*
	Q53F35	Acidic (Leucine-rich) nuclear phosphoprotein 32 family, member B variant (Fragment) OS=Homo sapiens PE=2 SV=1	74.11	2	861 968		*6.0*
203	P54652	Heat shock-related 70 kDa protein 2 OS=Homo sapiens GN=HSPA2 PE=1 SV=1	74.02	2	658 1219		*14.6*
204	Q5EK51	Lactoferrin OS=Homo sapiens PE=2 SV=1	73.92	2	926 1150		*3.7*
	Q5DSM0	Growth-inhibiting protein 12 OS=Homo sapiens GN=GIG12 PE=2 SV=1	73.92	2	926 1150		*3.7*
	Q2TUW9	Lactoferrin OS=Homo sapiens PE=2 SV=1	73.92	2	926 1150		*3.7*
	P02788	Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6	73.92	2	926 1150		*3.7*
	E7ER44	Kaliocin-1 OS=Homo sapiens GN=LTF PE=2 SV=1	73.92	2	926 1150		*3.7*
	E7EQB2	Kaliocin-1 (Fragment) OS=Homo sapiens GN=LTF PE=2 SV=1	73.92	2	926 1150		*3.7*
	B7ZAL5	cDNA, FLJ79229, highly similar to Lactotransferrin (EC 3.4.21.-) OS=Homo sapiens PE=2 SV=1	73.92	2	926 1150		*3.7*
	B3VMW0	Lactoferrin OS=Homo sapiens PE=2 SV=1	73.92	2	926 1150		*3.7*

	B3KSL2	cDNA FLJ36533 fis, clone TRACH2004428, highly similar to Lactotransferrin (EC 3.4.21.-) (Fragment) OS=Homo sapiens PE=2 SV=1	73.92	2	926 1150		*3.7*
	B2MV14	Truncated lactoferrin OS=Homo sapiens GN=LTF PE=4 SV=1	73.92	2	926 1150		*3.7*
205	H6VQN8	MHC class II antigen (Fragment) OS=Homo sapiens GN=HLA-C PE=3 SV=1	73.91	1	744		*14.9*
	G3ETQ6	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1	73.91	1	744		*14.9*
	D1FXH2	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1	73.91	1	744		*14.9*
206	F6KRT8	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-B PE=3 SV=1	73.91	1	760		*22.9*
207	A7WPJ2	MHC class I antigen (Fragment) OS=Homo sapiens GN=HLA-C PE=3 SV=1	73.91	1	748		*12.6*
208	Q9NSB2	Keratin, type II cuticular Hb4 OS=Homo sapiens GN=KRT84 PE=2 SV=2	73.18	2	213 1114		*5.0*
209	Q9BU08	Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1	72.88	1	151		*2.0*
	P48643	T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=1 SV=1	72.88	1	151		*2.0*
	E9PCA1	T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=2 SV=1	72.88	1	151		*2.0*
	E7ENZ3	T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=2 SV=1	72.88	1	151		*2.0*
	B7ZAR1	T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=2 SV=1	72.88	1	151		*2.0*
	B4DZT5	cDNA FLJ53116, highly similar to T-complex protein 1 subunit epsilon OS=Homo sapiens PE=2 SV=1	72.88	1	151		*2.0*
	B4DYD8	T-complex protein 1 subunit epsilon OS=Homo sapiens GN=CCT5 PE=2 SV=1	72.88	1	151		*2.0*
	B4DYC8	cDNA FLJ52361, highly similar to T-complex protein 1 subunit epsilon OS=Homo sapiens PE=2 SV=1	72.88	1	151		*2.0*
	B4DXI1	cDNA FLJ54333, highly similar to T-complex protein 1 subunit epsilon OS=Homo sapiens PE=2 SV=1	72.88	1	151		*2.0*
	B4DX08	cDNA FLJ58784, highly similar to T-complex protein 1 subunit epsilon OS=Homo sapiens PE=2 SV=1	72.88	1	151		*2.0*
210	P12277	Creatine kinase B-type OS=Homo sapiens GN=CKB PE=1 SV=1	72.65	2	505 1195		*10.6*
	G3V4N7	Creatine kinase B-type (Fragment) OS=Homo sapiens GN=CKB PE=2 SV=1	72.65	2	505 1195		*10.6*
	B4DP56	cDNA FLJ52237, highly similar to Creatine kinase B-type (EC 2.7.3.2) OS=Homo sapiens PE=2 SV=1	72.65	2	505 1195		*10.6*
211	Q59FC4	Presynaptic protein SAP97 variant (Fragment) OS=Homo sapiens PE=2 SV=1	72.41	1	306		*3.8*
	Q12959	Disks large homolog 1 OS=Homo sapiens GN=DLG1 PE=1 SV=2	72.41	1	306		*3.8*

	E7EQD7	Disks large homolog 1 OS=Homo sapiens GN=DLG1 PE=2 SV=1	72.41	1	306		*3.8*
212	P30086	Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens GN=PEBP1 PE=1 SV=3	71.95	2	924 1086		*8.6*
	D9IAI1	Phosphatidylethanolamine-binding protein 1 OS=Homo sapiens PE=2 SV=1	71.95	2	924 1086		*8.6*
213	Q9BS26	Endoplasmic reticulum resident protein 44 OS=Homo sapiens GN=ERP44 PE=1 SV=1	70.99	1	37		*3.0*
214	Q59EV3	Myosin, heavy polypeptide 7, cardiac muscle, beta variant (Fragment) OS=Homo sapiens PE=2 SV=1	70.51	1	114		*1.6*
	P12883	Myosin-7 OS=Homo sapiens GN=MYH7 PE=1 SV=5	70.51	1	114		*1.6*
	A5YM51	MYH7 protein (Fragment) OS=Homo sapiens GN=MYH7 PE=2 SV=1	70.51	1	114		*1.6*
215	Q5JRS3	Ubiquitin-like modifier-activating enzyme 1 (Fragment) OS=Homo sapiens GN=UBA1 PE=2 SV=1	70.50	1	948		*4.4*
	Q5JRS2	Ubiquitin-like modifier-activating enzyme 1 (Fragment) OS=Homo sapiens GN=UBA1 PE=2 SV=1	70.50	1	948		*4.4*
	Q5JRS1	Ubiquitin-like modifier-activating enzyme 1 (Fragment) OS=Homo sapiens GN=UBA1 PE=2 SV=1	70.50	1	948		*4.4*
	Q5JRS0	Ubiquitin-like modifier-activating enzyme 1 (Fragment) OS=Homo sapiens GN=UBA1 PE=2 SV=1	70.50	1	948		*4.4*
	Q5JRR9	Ubiquitin-like modifier-activating enzyme 1 (Fragment) OS=Homo sapiens GN=UBA1 PE=2 SV=1	70.50	1	948		*4.4*
	P22314	Ubiquitin-like modifier-activating enzyme 1 OS=Homo sapiens GN=UBA1 PE=1 SV=3	70.50	1	948		*4.4*
216	Q8IVT2	Uncharacterized protein C19orf21 OS=Homo sapiens GN=C19orf21 PE=1 SV=1	70.18	2	246 794		*4.4*
217	A7XZE4	Beta tropomyosin isoform OS=Homo sapiens GN=TPM2b PE=2 SV=1	69.61	2	40 149		*34.5*
218	Q9BRP8	Partner of Y14 and mago OS=Homo sapiens GN=WIBG PE=1 SV=1	69.47	1	1132		*14.2*
219	P17980	26S protease regulatory subunit 6A OS=Homo sapiens GN=PSMC3 PE=1 SV=3	69.32	1	410		*2.6*
	A8K781	cDNA FLJ75299, highly similar to Xenopus laevis proteasome (prosome, macropain) 26S subunit, ATPase 3, mRNA OS=Homo sapiens PE=2 SV=1	69.32	1	410		*2.6*
220	P31943	Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=1 SV=4	68.76	2	152 720		*17.9*
	G8JLB6	Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=2 SV=1	68.76	2	152 720		*17.9*
	E9PCY7	Heterogeneous nuclear ribonucleoprotein H OS=Homo sapiens GN=HNRNPH1 PE=2 SV=1	68.76	2	152 720		*17.9*
	D6RBM0	Heterogeneous nuclear ribonucleoprotein H (Fragment) OS=Homo sapiens GN=HNRNPH1 PE=2 SV=1	68.76	2	152 720		*17.9*
221	O43278	Kunitz-type protease inhibitor 1 OS=Homo sapiens GN=SPINT1 PE=1 SV=2	68.61	2	372 863		*5.3*

	H3BVD9	Kunitz-type protease inhibitor 1 (Fragment) OS=Homo sapiens GN=SPINT1 PE=2 SV=1	68.61	2	372 863		5.3
	H3BTQ8	Kunitz-type protease inhibitor 1 (Fragment) OS=Homo sapiens GN=SPINT1 PE=2 SV=1	68.61	2	372 863		5.3
	F5H877	Kunitz-type protease inhibitor 1 OS=Homo sapiens GN=SPINT1 PE=2 SV=1	68.61	2	372 863		5.3
	B4DTF6	cDNA FLJ51604, highly similar to Kunitz-type protease inhibitor 1 OS=Homo sapiens PE=2 SV=1	68.61	2	372 863		5.3
	B2RBU9	cDNA, FLJ95704, highly similar to Homo sapiens serine protease inhibitor, Kunitz type 1 (SPINT1), mRNA OS=Homo sapiens PE=2 SV=1	68.61	2	372 863		5.3
222	Q6KB66	Keratin, type II cytoskeletal 80 OS=Homo sapiens GN=KRT80 PE=1 SV=2	68.59	1	765		2.7
223	Q96ET4	Similar to calcyphosine (Fragment) OS=Homo sapiens PE=2 SV=1	68.35	2	682 1200		10.5
	Q8NF12	FLJ00390 protein (Fragment) OS=Homo sapiens GN=FLJ00390 PE=2 SV=1	68.35	2	682 1200		10.5
	Q13938	Calcyphosin OS=Homo sapiens GN=CAPS PE=1 SV=1	68.35	2	682 1200		10.5
	K7ES72	Calcyphosin (Fragment) OS=Homo sapiens GN=CAPS PE=4 SV=1	68.35	2	682 1200		10.5
	K7EL21	Calcyphosin OS=Homo sapiens GN=CAPS PE=4 SV=1	68.35	2	682 1200		10.5
224	P62280	40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=1 SV=3	68.15	2	204 585		17.8
	M0QZC5	40S ribosomal protein S11 OS=Homo sapiens GN=RPS11 PE=4 SV=1	68.15	2	204 585		17.8
225	Q6P2S0	SRP9 protein OS=Homo sapiens GN=SRP9 PE=2 SV=1	67.94	1	249		22.4
	Q659G3	Putative uncharacterized protein DKFZp564M2223 OS=Homo sapiens GN=DKFZp564M2223 PE=2 SV=1	67.94	1	249		22.4
	P49458	Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=1 SV=2	67.94	1	249		22.4
	E9PE20	Signal recognition particle 9 kDa protein OS=Homo sapiens GN=SRP9 PE=2 SV=1	67.94	1	249		22.4
226	Q9BZ93	Prosomal P27K protein (Fragment) OS=Homo sapiens GN=PSMA6 PE=2 SV=1	67.82	1	745		11.8
	P60900	Proteasome subunit alpha type-6 OS=Homo sapiens GN=PSMA6 PE=1 SV=1	67.82	1	745		11.8
	G3V5Z7	Proteasome subunit alpha type OS=Homo sapiens GN=PSMA6 PE=2 SV=1	67.82	1	745		11.8
	G3V3U4	Proteasome subunit alpha type OS=Homo sapiens GN=PSMA6 PE=2 SV=1	67.82	1	745		11.8
	G3V3I1	Proteasome subunit alpha type OS=Homo sapiens GN=PSMA6 PE=2 SV=1	67.82	1	745		11.8
	G3V295	Proteasome subunit alpha type OS=Homo sapiens GN=PSMA6 PE=2 SV=1	67.82	1	745		11.8
	B4DXJ9	Proteasome (Prosome, macropain) subunit, alpha type, 6, isoform CRA_a OS=Homo sapiens GN=PSMA6 PE=2 SV=1	67.82	1	745		11.8

UniProt Human Protein IDs, *cont.*

Grp Nr.	*Accession Number*	*Protein Name*	*Protein Score*	*Unique PSMs*	*PSM Serial Nrs.*	*Other Grp.*	*% Seq. Cover.*
227	Q5CAQ5	Tumor rejection antigen (Gp96) 1 OS=Homo sapiens GN=TRA1 PE=2 SV=1	66.94	2	959 1162		*9.9*
	P14625	Endoplasmin OS=Homo sapiens GN=HSP90B1 PE=1 SV=1	66.94	2	959 1162		*9.9*
228	Q6EEV6	Small ubiquitin-related modifier 4 OS=Homo sapiens GN=SUMO4 PE=1 SV=2	66.77	1	259		*8.5*
	P61956	Small ubiquitin-related modifier 2 OS=Homo sapiens GN=SUMO2 PE=1 SV=3	66.77	1	259		*8.5*
	P55854	Small ubiquitin-related modifier 3 OS=Homo sapiens GN=SUMO3 PE=1 SV=2	66.77	1	259		*8.5*
	H7BZT4	Uncharacterized protein OS=Homo sapiens PE=4 SV=1	66.77	1	259		*8.5*
	B4DUW4	Small ubiquitin-related modifier 3 OS=Homo sapiens GN=SUMO3 PE=2 SV=1	66.77	1	259		*8.5*
	A8MUA9	SMT3 suppressor of mif two 3 homolog 3 (Yeast), isoform CRA_d OS=Homo sapiens GN=SUMO3 PE=4 SV=1	66.77	1	259		*8.5*
	A8MU27	Small ubiquitin-related modifier 3 OS=Homo sapiens GN=SUMO3 PE=2 SV=1	66.77	1	259		*8.5*
229	Q9Y5B9	FACT complex subunit SPT16 OS=Homo sapiens GN=SUPT16H PE=1 SV=1	66.61	2	523 621		*3.8*
230	Q9H910	Hematological and neurological expressed 1-like protein OS=Homo sapiens GN=HN1L PE=1 SV=1	65.89	1	243		*12.2*
	H3BU16	Hematological and neurological-expressed 1-like protein (Fragment) OS=Homo sapiens GN=HN1L PE=2 SV=1	65.89	1	243		*12.2*
	H3BTV5	Hematological and neurological-expressed 1-like protein (Fragment) OS=Homo sapiens GN=HN1L PE=2 SV=1	65.89	1	243		*12.2*
	H3BMV3	Hematological and neurological-expressed 1-like protein (Fragment) OS=Homo sapiens GN=HN1L PE=2 SV=1	65.89	1	243		*12.2*
	H3BMT0	Hematological and neurological-expressed 1-like protein (Fragment) OS=Homo sapiens GN=HN1L PE=2 SV=1	65.89	1	243		*12.2*
	B4DLH4	Hematological and neurological-expressed 1-like protein OS=Homo sapiens GN=HN1L PE=2 SV=1	65.89	1	243		*12.2*
	B4DL85	cDNA FLJ60660, highly similar to Hematological and neurological expressed1-like protein OS=Homo sapiens PE=2 SV=1	65.89	1	243		*12.2*

	A6NGP5	Hematological and neurological-expressed 1-like protein OS=Homo sapiens GN=HN1L PE=2 SV=2	65.89	1	243		*12.2*
231	Q96IR1	RPS4X protein (Fragment) OS=Homo sapiens GN=RPS4X PE=2 SV=2	65.45	2	358 738		*5.3*
	Q53HV1	Ribosomal protein S4, X-linked X isoform variant (Fragment) OS=Homo sapiens PE=2 SV=1	65.45	2	358 738		*5.3*
	P62701	40S ribosomal protein S4, X isoform OS=Homo sapiens GN=RPS4X PE=1 SV=2	65.45	2	358 738		*5.3*
	B2R491	Ribosomal protein S4, X-linked, isoform CRA_c OS=Homo sapiens GN=RPS4X PE=2 SV=1	65.45	2	358 738		*5.3*
232	B7Z1Y2	Fructose-bisphosphate aldolase OS=Homo sapiens PE=2 SV=1	65.08	1	686		*12.2*
233	Q1JUQ4	FK506 binding protein12 OS=Homo sapiens GN=FKBP12-Exip3 PE=4 SV=1	64.72	1	69		*35.1*
	Q1JUQ3	FK506 binding protein12 OS=Homo sapiens GN=FKBP12-Exin PE=4 SV=1	64.72	1	69		*35.1*
	P62942	Peptidyl-prolyl cis-trans isomerase FKBP1A OS=Homo sapiens GN=FKBP1A PE=1 SV=2	64.72	1	69		*35.1*
234	P14174	Macrophage migration inhibitory factor OS=Homo sapiens GN=MIF PE=1 SV=4	64.14	1	390		*7.8*
	I4AY87	Macrophage migration inhibitory factor (Fragment) OS=Homo sapiens PE=2 SV=1	64.14	1	390		*7.8*
235	P11487	Fibroblast growth factor 3 OS=Homo sapiens GN=FGF3 PE=1 SV=1	63.74	1	45		*4.2*
236	P09429	High mobility group protein B1 OS=Homo sapiens GN=HMGB1 PE=1 SV=3	63.68	2	757 865		*21.0*
	B3KQ05	cDNA FLJ32558 fis, clone SPLEN1000143, highly similar to High mobility group protein B1 OS=Homo sapiens PE=2 SV=1	63.68	2	757 865		*21.0*
237	P27482	Calmodulin-like protein 3 OS=Homo sapiens GN=CALML3 PE=1 SV=2	62.95	1	8		*8.1*
238	B4E259	cDNA FLJ59607, moderately similar to D-dopachrome decarboxylase (EC 4.1.1.84) OS=Homo sapiens PE=2 SV=1	62.87	2	841 893		*17.1*
239	P30101	Protein disulfide-isomerase A3 OS=Homo sapiens GN=PDIA3 PE=1 SV=4	62.41	2	820 1017		*15.5*
	G5EA52	Protein disulfide isomerase family A, member 3, isoform CRA_b OS=Homo sapiens GN=PDIA3 PE=3 SV=1	62.41	2	820 1017		*15.5*
	B3KQT9	cDNA PSEC0175 fis, clone OVARC1000169, highly similar to Protein disulfide-isomerase A3 (EC 5.3.4.1) OS=Homo sapiens PE=2 SV=1	62.41	2	820 1017		*15.5*
	B3KQT2	cDNA PSEC0148 fis, clone PLACE1007202, highly similar to Protein disulfide-isomerase A3 (EC 5.3.4.1) OS=Homo sapiens PE=2 SV=1	62.41	2	820 1017		*15.5*
240	O15230	Laminin subunit alpha-5 OS=Homo sapiens GN=LAMA5 PE=1 SV=8	62.23	1	1028		*8.1*
241	Q96AE4	Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1 PE=1 SV=3	62.01	2	62 595		*8.1*

	Q59FU3	Far upstream element-binding protein variant (Fragment) OS=Homo sapiens PE=2 SV=1	62.01	2	62 595		*8.1*
	E9PEB5	Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1 PE=2 SV=1	62.01	2	62 595		*8.1*
	B4E0X8	cDNA FLJ61021, highly similar to Far upstream element-binding protein 1 OS=Homo sapiens PE=2 SV=1	62.01	2	62 595		*8.1*
	B4DWL1	cDNA FLJ59240, highly similar to Far upstream element-binding protein 1 OS=Homo sapiens PE=2 SV=1	62.01	2	62 595		*8.1*
	B4DT31	Far upstream element-binding protein 1 OS=Homo sapiens GN=FUBP1 PE=2 SV=1	62.01	2	62 595		*8.1*
242	Q14974	Importin subunit beta-1 OS=Homo sapiens GN=KPNB1 PE=1 SV=2	61.41	1	175		*3.4*
	J3QR48	Importin subunit beta-1 (Fragment) OS=Homo sapiens GN=KPNB1 PE=4 SV=1	61.41	1	175		*3.4*
	B2RBR9	cDNA, FLJ95650, highly similar to Homo sapiens karyopherin (importin) beta 1 (KPNB1), mRNA OS=Homo sapiens PE=2 SV=1	61.41	1	175		*3.4*
243	P01308	Insulin OS=Homo sapiens GN=INS PE=1 SV=1	61.39	2	598 1076		*25.5*
	I3WAC9	Preproinsulin OS=Homo sapiens GN=INS PE=3 SV=1	61.39	2	598 1076		*25.5*
	F6MZK5	Insulin (Precursor) OS=Homo sapiens GN=INS PE=2 SV=1	61.39	2	598 1076		*25.5*
	A6XGL2	Insulin OS=Homo sapiens GN=INS PE=3 SV=1	61.39	2	598 1076		*25.5*
244	Q7Z2V5	Putative uncharacterized protein DKFZp686J01190 (Fragment) OS=Homo sapiens GN=DKFZp686J01190 PE=2 SV=1	61.38	1	878		*3.5*
	Q59E92	Putative uncharacterized protein (Fragment) OS=Homo sapiens PE=2 SV=1	61.38	1	878		*3.5*
	P17844	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=1 SV=1	61.38	1	878		*3.5*
	J3QRQ7	Probable ATP-dependent RNA helicase DDX5 (Fragment) OS=Homo sapiens GN=DDX5 PE=4 SV=1	61.38	1	878		*3.5*
	J3QR02	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=4 SV=1	61.38	1	878		*3.5*
	J3KTA4	Probable ATP-dependent RNA helicase DDX5 OS=Homo sapiens GN=DDX5 PE=3 SV=1	61.38	1	878		*3.5*
	J3KRX8	Probable ATP-dependent RNA helicase DDX5 (Fragment) OS=Homo sapiens GN=DDX5 PE=4 SV=1	61.38	1	878		*3.5*
	C1IK54	DEAD box polypeptide 5/ets variant protein 4 fusion protein OS=Homo sapiens GN=DDX5-ETV4 fusion PE=2 SV=1	61.38	1	878		*3.5*
	B5BUE6	ATP-dependent RNA helicase DDX5 (Fragment) OS=Homo sapiens GN=DDX5 PE=2 SV=1	61.38	1	878		*3.5*
	B4DN41	cDNA FLJ53366, highly similar to Probable ATP-dependent RNA helicase DDX5 (EC 3.6.1.-) OS=Homo sapiens PE=2 SV=1	61.38	1	878		*3.5*
245	P61769	Beta-2-microglobulin OS=Homo sapiens GN=B2M PE=1 SV=1	60.93	2	349 1210		*23.8*
	F5H6I0	Beta-2-microglobulin form pI 5.3 OS=Homo sapiens GN=B2M PE=3 SV=1	60.93	2	349 1210		*23.8*

	B4E0X1	cDNA FLJ57067, highly similar to Beta-2-microglobulin OS=Homo sapiens PE=2 SV=1	60.93	2	349 1210		*23.8*
	A6XMH5	Beta-2-microglobulin OS=Homo sapiens PE=3 SV=1	60.93	2	349 1210		*23.8*
246	Q9BW71	HIRA-interacting protein 3 OS=Homo sapiens GN=HIRIP3 PE=1 SV=3	60.88	1	297		*3.6*
	B2R6A9	cDNA, FLJ92868, highly similar to Homo sapiens HIRA interacting protein 3 (HIRIP3), mRNA OS=Homo sapiens PE=2 SV=1	60.88	1	297		*3.6*
247	O43765	Small glutamine-rich tetratricopeptide repeat-containing protein alpha OS=Homo sapiens GN=SGTA PE=1 SV=1	60.84	1	17		*4.5*
	K7EMD6	Small glutamine-rich tetratricopeptide repeat-containing protein alpha (Fragment) OS=Homo sapiens GN=SGTA PE=4 SV=1	60.84	1	17		*4.5*
	B4DEA6	cDNA FLJ56566, highly similar to Small glutamine-rich tetratricopeptiderepeat-containing protein A OS=Homo sapiens PE=2 SV=1	60.84	1	17		*4.5*
248	Q9UMY2	3-phosphoglycerate dehydrogenase (Fragment) OS=Homo sapiens GN=PGDH3 PE=2 SV=1	60.66	1	329		*2.2*
	Q96RV5	3-phosphoglycerate dehydrogenase (Fragment) OS=Homo sapiens PE=2 SV=1	60.66	1	329		*2.2*
	Q8N5M8	PHGDH protein (Fragment) OS=Homo sapiens GN=PHGDH PE=2 SV=3	60.66	1	329		*2.2*
	Q5SZU1	D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=4 SV=1	60.66	1	329		*2.2*
	O43175	D-3-phosphoglycerate dehydrogenase OS=Homo sapiens GN=PHGDH PE=1 SV=4	60.66	1	329		*2.2*
	B3KSC3	cDNA FLJ35987 fis, clone TESTI2014269, highly similar to D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95) OS=Homo sapiens PE=2 SV=1	60.66	1	329		*2.2*
249	Q6X4U4	Sclerostin domain-containing protein 1 OS=Homo sapiens GN=SOSTDC1 PE=1 SV=2	60.38	1	792		*5.3*
	A8MUA6	Sclerostin domain-containing protein 1 OS=Homo sapiens GN=SOSTDC1 PE=2 SV=1	60.38	1	792		*5.3*
	A4D125	Sclerostin domain containing 1 OS=Homo sapiens GN=SOSTDC1 PE=2 SV=1	60.38	1	792		*5.3*
250	C9J7P1	Drebrin-like protein OS=Homo sapiens GN=DBNL PE=2 SV=2	60.26	1	825		*3.2*
	B4DXL9	cDNA FLJ53677, highly similar to Drebrin-like protein OS=Homo sapiens PE=2 SV=1	60.26	1	825		*3.2*
	B4DUF9	cDNA FLJ59432, highly similar to Drebrin-like protein OS=Homo sapiens PE=2 SV=1	60.26	1	825		*3.2*
	B4DDP6	Drebrin-like protein OS=Homo sapiens GN=DBNL PE=2 SV=1	60.26	1	825		*3.2*
	B4DDD6	Drebrin-like protein OS=Homo sapiens GN=DBNL PE=2 SV=1	60.26	1	825		*3.2*
251	Q6FHU3	PSME1 protein (Fragment) OS=Homo sapiens GN=PSME1 PE=2 SV=1	60.10	1	169		*9.9*
	Q06323	Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=1 SV=1	60.10	1	169		*9.9*

	H0YNE3	Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=2 SV=1	60.10	1	169		*9.9*
	A6NJG9	Proteasome activator complex subunit 1 OS=Homo sapiens GN=PSME1 PE=2 SV=2	60.10	1	169		*9.9*
252	Q96IZ0	PRKC apoptosis WT1 regulator protein OS=Homo sapiens GN=PAWR PE=1 SV=1	59.92	1	178		*3.8*
253	P46782	40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=1 SV=4	59.62	1	116		*14.2*
	M0R0R2	40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=4 SV=1	59.62	1	116		*14.2*
	M0R0F0	40S ribosomal protein S5 (Fragment) OS=Homo sapiens GN=RPS5 PE=4 SV=1	59.62	1	116		*14.2*
	M0QZN2	40S ribosomal protein S5 OS=Homo sapiens GN=RPS5 PE=4 SV=1	59.62	1	116		*14.2*
254	Q9BX68	Histidine triad nucleotide-binding protein 2, mitochondrial OS=Homo sapiens GN=HINT2 PE=1 SV=1	59.54	2	223 360		*19.5*
	Q8WYJ5	Protein kinase C inhibitor-2 OS=Homo sapiens PE=2 SV=1	59.54	2	223 360		*19.5*
255	Q53HV6	Niemann-Pick disease, type C2 variant (Fragment) OS=Homo sapiens PE=2 SV=1	58.66	1	227		*9.2*
	P61916	Epididymal secretory protein E1 OS=Homo sapiens GN=NPC2 PE=1 SV=1	58.66	1	227		*9.2*
	J3KMY5	Epididymal secretory protein E1 OS=Homo sapiens GN=NPC2 PE=4 SV=1	58.66	1	227		*9.2*
	H0YIZ1	Epididymal secretory protein E1 (Fragment) OS=Homo sapiens GN=NPC2 PE=4 SV=1	58.66	1	227		*9.2*
	G3V3E8	Epididymal secretory protein E1 OS=Homo sapiens GN=NPC2 PE=2 SV=1	58.66	1	227		*9.2*
	G3V3D1	Epididymal secretory protein E1 (Fragment) OS=Homo sapiens GN=NPC2 PE=2 SV=1	58.66	1	227		*9.2*
	G3V2V8	Epididymal secretory protein E1 (Fragment) OS=Homo sapiens GN=NPC2 PE=2 SV=1	58.66	1	227		*9.2*
	E7EMS2	Epididymal secretory protein E1 OS=Homo sapiens GN=NPC2 PE=2 SV=1	58.66	1	227		*9.2*
	B4DV10	cDNA FLJ59142, highly similar to Epididymal secretory protein E1 OS=Homo sapiens PE=2 SV=1	58.66	1	227		*9.2*
	B4DQV7	Epididymal secretory protein E1 OS=Homo sapiens GN=NPC2 PE=2 SV=1	58.66	1	227		*9.2*
256	Q59EF5	Splicing factor, arginine/serine-rich 4 variant (Fragment) OS=Homo sapiens PE=2 SV=1	58.64	1	637		*3.3*
	Q53F45	Splicing factor, arginine/serine-rich 4 variant (Fragment) OS=Homo sapiens PE=2 SV=1	58.64	1	637		*3.3*
	Q08170	Serine/arginine-rich splicing factor 4 OS=Homo sapiens GN=SRSF4 PE=1 SV=2	58.64	1	637		*3.3*
	A8K644	Splicing factor, arginine/serine-rich 4, isoform CRA_b OS=Homo sapiens GN=SFRS4 PE=2 SV=1	58.64	1	637		*3.3*

257	Q16610	Extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=1 SV=2	58.63	2	564 836		*4.7*
	C8CHS3	Truncated extracellular matrix protein 1 OS=Homo sapiens GN=ECM1 PE=2 SV=1	58.63	2	564 836		*4.7*
258	Q969G3	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens GN=SMARCE1 PE=1 SV=2	58.59	1	810		*2.7*
	J3QR61	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 (Fragment) OS=Homo sapiens GN=SMARCE1 PE=4 SV=1	58.59	1	810		*2.7*
	J3QKS7	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 (Fragment) OS=Homo sapiens GN=SMARCE1 PE=4 SV=1	58.59	1	810		*2.7*
	J3KT85	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 (Fragment) OS=Homo sapiens GN=SMARCE1 PE=4 SV=1	58.59	1	810		*2.7*
	C0IMW8	Smarce1 variant 10 (Fragment) OS=Homo sapiens PE=2 SV=1	58.59	1	810		*2.7*
	C0IMW7	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens GN=SMARCE1 PE=2 SV=1	58.59	1	810		*2.7*
	C0IMW5	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens GN=SMARCE1 PE=2 SV=1	58.59	1	810		*2.7*
	C0IMW4	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens GN=SMARCE1 PE=2 SV=1	58.59	1	810		*2.7*
	B4DGM3	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens GN=SMARCE1 PE=2 SV=1	58.59	1	810		*2.7*
	B4DFR4	SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily E member 1 OS=Homo sapiens GN=SMARCE1 PE=2 SV=1	58.59	1	810		*2.7*

UniProt Human Protein IDs, *cont.*

Grp Nr.	*Accession Number*	*Protein Name*	*Protein Score*	*Unique PSMs*	*PSM Serial Nrs.*	*Other Grp.*	*% Seq. Cover.*

259	Q86VP6	Cullin-associated NEDD8-dissociated protein 1 OS=Homo sapiens GN=CAND1 PE=1 SV=2	58.34	2	381 1091		*4.6*
	A8K8U1	cDNA FLJ77762, highly similar to Homo sapiens cullin-associated and neddylation-dissociated 1 (CAND1), mRNA OS=Homo sapiens PE=2 SV=1	58.34	2	381 1091		*4.6*
260	P09012	U1 small nuclear ribonucleoprotein A OS=Homo sapiens GN=SNRPA PE=1 SV=3	57.99	1	298		*7.8*
	M0R2B8	U1 small nuclear ribonucleoprotein A (Fragment) OS=Homo sapiens GN=SNRPA PE=4 SV=1	57.99	1	298		*7.8*
	M0R221	U1 small nuclear ribonucleoprotein A (Fragment) OS=Homo sapiens GN=SNRPA PE=4 SV=1	57.99	1	298		*7.8*
	M0R0G9	U1 small nuclear ribonucleoprotein A OS=Homo sapiens GN=SNRPA PE=4 SV=1	57.99	1	298		*7.8*
	M0QZG7	U1 small nuclear ribonucleoprotein A (Fragment) OS=Homo sapiens GN=SNRPA PE=4 SV=1	57.99	1	298		*7.8*
	M0QXK2	U1 small nuclear ribonucleoprotein A (Fragment) OS=Homo sapiens GN=SNRPA PE=4 SV=1	57.99	1	298		*7.8*
	B2R802	cDNA, FLJ93681, highly similar to Homo sapiens small nuclear ribonucleoprotein polypeptide A (SNRPA), mRNA OS=Homo sapiens PE=2 SV=1	57.99	1	298		*7.8*
261	Q96IH1	Fascin (Fragment) OS=Homo sapiens GN=FSCN1 PE=2 SV=1	57.99	2	374 1039		*9.5*
	Q16658	Fascin OS=Homo sapiens GN=FSCN1 PE=1 SV=3	57.99	2	374 1039		*9.5*
	J3KNT0	Fascin OS=Homo sapiens GN=FSCN1 PE=3 SV=1	57.99	2	374 1039		*9.5*
	B3KTA3	Fascin OS=Homo sapiens PE=2 SV=1	57.99	2	374 1039		*9.5*
262	Q53EM5	Transketolase variant (Fragment) OS=Homo sapiens PE=2 SV=1	57.21	1	120		*5.9*
	P29401	Transketolase OS=Homo sapiens GN=TKT PE=1 SV=3	57.21	1	120		*5.9*
	B4E022	Transketolase OS=Homo sapiens GN=TKT PE=2 SV=1	57.21	1	120		*5.9*
	B4DVU1	cDNA FLJ53217, highly similar to Transketolase (EC 2.2.1.1) OS=Homo sapiens PE=2 SV=1	57.21	1	120		*5.9*
	B3KSI4	cDNA FLJ36348 fis, clone THYMU2007025, highly similar to TRANSKETOLASE (EC 2.2.1.1) OS=Homo sapiens PE=2 SV=1	57.21	1	120		*5.9*
	B3KPZ8	cDNA FLJ32530 fis, clone SMINT2000185, highly similar to TRANSKETOLASE (EC 2.2.1.1) OS=Homo sapiens PE=2 SV=1	57.21	1	120		*5.9*
263	Q96B58	Nucleolysin TIA-1 isoform p40 OS=Homo sapiens GN=TIA1 PE=2 SV=1	57.01	1	348		*7.5*
	Q59G98	TIA1 protein variant (Fragment) OS=Homo sapiens PE=2 SV=1	57.01	1	348		*7.5*
	P31483	Nucleolysin TIA-1 isoform p40 OS=Homo sapiens GN=TIA1 PE=1 SV=3	57.01	1	348		*7.5*
	F8W8I6	Nucleolysin TIA-1 isoform p40 OS=Homo sapiens GN=TIA1 PE=2 SV=1	57.01	1	348		*7.5*
	E5RGV5	Nucleolysin TIA-1 isoform p40 OS=Homo sapiens GN=TIA1 PE=2 SV=1	57.01	1	348		*7.5*

	E5RG67	Nucleolysin TIA-1 isoform p40 OS=Homo sapiens GN=TIA1 PE=2 SV=1	57.01	1	348		*7.5*
264	P51858	Hepatoma-derived growth factor OS=Homo sapiens GN=HDGF PE=1 SV=1	56.96	1	514		*7.1*
	B2RDE8	cDNA, FLJ96580, highly similar to Homo sapiens hepatoma-derived growth factor (high-mobility group protein 1-like) (HDGF), mRNA OS=Homo sapiens PE=2 SV=1	56.96	1	514		*7.1*
265	P37802	Transgelin-2 OS=Homo sapiens GN=TAGLN2 PE=1 SV=3	56.65	1	1136		*5.5*
266	P62861	40S ribosomal protein S30 OS=Homo sapiens GN=FAU PE=1 SV=1	56.51	2	186 440		*11.2*
	E9PR30	40S ribosomal protein S30 OS=Homo sapiens GN=FAU PE=2 SV=1	56.51	2	186 440		*11.2*
267	Q53F91	Villin 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1	56.35	1	854		*10.3*
	P09327	Villin-1 OS=Homo sapiens GN=VIL1 PE=1 SV=4	56.35	1	854		*10.3*
268	Q6P452	Annexin OS=Homo sapiens GN=ANXA4 PE=2 SV=1	56.14	1	352		*4.6*
	Q6LES2	Annexin (Fragment) OS=Homo sapiens GN=ANXA4 PE=2 SV=1	56.14	1	352		*4.6*
	P09525	Annexin A4 OS=Homo sapiens GN=ANXA4 PE=1 SV=4	56.14	1	352		*4.6*
	B4E1S2	Annexin OS=Homo sapiens PE=2 SV=1	56.14	1	352		*4.6*
	B4DE02	Annexin OS=Homo sapiens PE=2 SV=1	56.14	1	352		*4.6*
	B4DDZ4	Annexin OS=Homo sapiens PE=2 SV=1	56.14	1	352		*4.6*
	B4DDF9	Annexin OS=Homo sapiens GN=ANXA4 PE=2 SV=1	56.14	1	352		*4.6*
269	Q8TB01	Similar to cytoskeleton-associated protein 4 (Fragment) OS=Homo sapiens PE=2 SV=1	56.12	1	555		*4.8*
	Q6NWZ1	CKAP4 protein (Fragment) OS=Homo sapiens GN=CKAP4 PE=2 SV=1	56.12	1	555		*4.8*
	Q07065	Cytoskeleton-associated protein 4 OS=Homo sapiens GN=CKAP4 PE=1 SV=2	56.12	1	555		*4.8*
	B3KVX6	cDNA FLJ41699 fis, clone HCHON2004776, highly similar to Homo sapiens cytoskeleton-associated protein 4 (CKAP4), mRNA OS=Homo sapiens PE=2 SV=1	56.12	1	555		*4.8*
270	P10599	Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3	55.87	1	958		*21.0*
	H9ZYJ2	Thioredoxin OS=Homo sapiens GN=TXN PE=2 SV=1	55.87	1	958		*21.0*
271	Q13740	CD166 antigen OS=Homo sapiens GN=ALCAM PE=1 SV=2	55.49	2	866 894		*2.0*
	F5GXJ9	CD166 antigen OS=Homo sapiens GN=ALCAM PE=2 SV=1	55.49	2	866 894		*2.0*
	B4DX43	cDNA FLJ52980, highly similar to CD166 antigen OS=Homo sapiens PE=2 SV=1	55.49	2	866 894		*2.0*
	B3KNN9	cDNA FLJ30070 fis, clone ASTRO2000046, highly similar to CD166 ANTIGEN OS=Homo sapiens PE=2 SV=1	55.49	2	866 894		*2.0*
272	Q68D11	Putative uncharacterized protein DKFZp686K23100 OS=Homo sapiens GN=DKFZp686K23100 PE=2 SV=1	54.90	2	802 804		*2.7*
	P43243	Matrin-3 OS=Homo sapiens GN=MATR3 PE=1 SV=2	54.90	2	802 804		*2.7*
	A8MXP9	Matrin-3 OS=Homo sapiens GN=MATR3 PE=4 SV=1	54.90	2	802 804		*2.7*

273	Q9UIS4	Small nuclear ribonucleoprotein-associated protein OS=Homo sapiens GN=SNRPB PE=2 SV=1	54.44	1	1134		*3.3*
	Q6LBS1	Small nuclear ribonucleoprotein-associated protein (Fragment) OS=Homo sapiens PE=2 SV=1	54.44	1	1134		*3.3*
	Q66K91	Small nuclear ribonucleoprotein-associated protein OS=Homo sapiens GN=SNRPB PE=2 SV=1	54.44	1	1134		*3.3*
	Q5XPV6	Small nuclear ribonucleoprotein-associated protein OS=Homo sapiens PE=2 SV=1	54.44	1	1134		*3.3*
	Q53HE7	Small nuclear ribonucleoprotein-associated protein (Fragment) OS=Homo sapiens PE=2 SV=1	54.44	1	1134		*3.3*
	Q15182	Small nuclear ribonucleoprotein-associated protein OS=Homo sapiens GN=SNRPB PE=2 SV=1	54.44	1	1134		*3.3*
	P63162	Small nuclear ribonucleoprotein-associated protein N OS=Homo sapiens GN=SNRPN PE=1 SV=1	54.44	1	1134		*3.3*
	P14678	Small nuclear ribonucleoprotein-associated proteins B and B~ OS=Homo sapiens GN=SNRPB PE=1 SV=2	54.44	1	1134		*3.3*
	J3QLE5	Small nuclear ribonucleoprotein-associated protein N (Fragment) OS=Homo sapiens GN=SNRPN PE=4 SV=1	54.44	1	1134		*3.3*
	B4DVS0	Small nuclear ribonucleoprotein-associated protein OS=Homo sapiens GN=SNRPB PE=2 SV=1	54.44	1	1134		*3.3*
274	P33316	Deoxyuridine 5~-triphosphate nucleotidohydrolase, mitochondrial OS=Homo sapiens GN=DUT PE=1 SV=4	54.38	1	354		*10.0*
	H0YNW5	Deoxyuridine 5~-triphosphate nucleotidohydrolase, mitochondrial OS=Homo sapiens GN=DUT PE=2 SV=1	54.38	1	354		*10.0*
	H0YKC5	Deoxyuridine 5~-triphosphate nucleotidohydrolase, mitochondrial (Fragment) OS=Homo sapiens GN=DUT PE=2 SV=1	54.38	1	354		*10.0*
275	Q14697	Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=1 SV=3	53.99	1	944		*2.0*
	F5H6X6	Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=2 SV=1	53.99	1	944		*2.0*
	E9PKU7	Neutral alpha-glucosidase AB OS=Homo sapiens GN=GANAB PE=2 SV=1	53.99	1	944		*2.0*
	B4DZ53	cDNA FLJ59643, highly similar to Neutral alpha-glucosidase AB OS=Homo sapiens PE=2 SV=1	53.99	1	944		*2.0*
	B4DSM6	cDNA FLJ54057, highly similar to Neutral alpha-glucosidase AB OS=Homo sapiens PE=2 SV=1	53.99	1	944		*2.0*
	B4DJ30	cDNA FLJ61290, highly similar to Neutral alpha-glucosidase AB OS=Homo sapiens PE=2 SV=1	53.99	1	944		*2.0*
	B4DIW2	cDNA FLJ54035, highly similar to Neutral alpha-glucosidase AB OS=Homo sapiens PE=2 SV=1	53.99	1	944		*2.0*
276	Q13409	Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC1I2 PE=1 SV=3	53.79	1	702		*2.2*
	F8W8S0	Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC1I2 PE=2 SV=1	53.79	1	702		*2.2*

	B7ZA04	Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens GN=DYNC1I2 PE=2 SV=1	53.79	1	702		2.2
	B4DPZ3	cDNA FLJ53290, highly similar to Cytoplasmic dynein 1 intermediate chain 2 OS=Homo sapiens PE=2 SV=1	53.79	1	702		2.2
277	B4DLR3	cDNA FLJ54020, highly similar to Heterogeneous nuclear ribonucleoprotein U OS=Homo sapiens PE=2 SV=1	53.70	2	84 974		4.4
278	P06703	Protein S100-A6 OS=Homo sapiens GN=S100A6 PE=1 SV=1	53.43	1	1216		8.9
279	Q6MZV5	Putative uncharacterized protein DKFZp686M09245 OS=Homo sapiens GN=DKFZp686M09245 PE=2 SV=1	53.28	1	567		2.2
	P48444	Coatomer subunit delta OS=Homo sapiens GN=ARCN1 PE=1 SV=1	53.28	1	567		2.2
	B0YIW6	Archain 1, isoform CRA_a OS=Homo sapiens GN=ARCN1 PE=4 SV=1	53.28	1	567		2.2
	B0YIW5	Archain 1, isoform CRA_b OS=Homo sapiens GN=ARCN1 PE=2 SV=1	53.28	1	567		2.2
280	Q68E00	Putative uncharacterized protein DKFZp686G2045 (Fragment) OS=Homo sapiens GN=DKFZp686G2045 PE=2 SV=2	53.27	1	1206		5.1
	Q16186	Proteasomal ubiquitin receptor ADRM1 OS=Homo sapiens GN=ADRM1 PE=1 SV=2	53.27	1	1206		5.1
281	Q16527	Cysteine and glycine-rich protein 2 OS=Homo sapiens GN=CSRP2 PE=1 SV=3	53.20	1	1174		4.2
	F8VW96	Cysteine and glycine-rich protein 2 OS=Homo sapiens GN=CSRP2 PE=2 SV=1	53.20	1	1174		61.7
282	Q86UE4	Protein LYRIC OS=Homo sapiens GN=MTDH PE=1 SV=2	53.15	1	335		1.7
	E5RJU9	Protein LYRIC OS=Homo sapiens GN=MTDH PE=2 SV=1	53.15	1	335		1.7
283	Q9Y4G6	Talin-2 OS=Homo sapiens GN=TLN2 PE=1 SV=4	53.00	1	1218		1.2
284	Q96CT7	Coiled-coil domain-containing protein 124 OS=Homo sapiens GN=CCDC124 PE=1 SV=1	52.82	1	1156		4.5
285	P09455	Retinol-binding protein 1 OS=Homo sapiens GN=RBP1 PE=1 SV=2	52.78	2	668 869		18.5
	A8K2Q0	cDNA FLJ76382, highly similar to Homo sapiens retinol binding protein 1, cellular (RBP1), mRNA OS=Homo sapiens PE=2 SV=1	52.78	2	668 869		18.5
286	Q71UI9	Histone H2A.V OS=Homo sapiens GN=H2AFV PE=1 SV=3	52.74	1	624		1.0
	C9J0D1	Histone H2A OS=Homo sapiens GN=H2AFV PE=2 SV=1	52.74	1	624		1.0
	A8MQC5	Histone H2A OS=Homo sapiens GN=H2AFV PE=2 SV=3	52.74	1	624		16.6
287	P37108	Signal recognition particle 14 kDa protein OS=Homo sapiens GN=SRP14 PE=1 SV=2	52.67	1	146		14.8
	H0YLA2	Signal recognition particle 14 kDa protein OS=Homo sapiens GN=SRP14 PE=2 SV=1	52.67	1	146		14.8
288	P50238	Cysteine-rich protein 1 OS=Homo sapiens GN=CRIP1 PE=1 SV=3	52.54	2	155 752		31.2
289	P17540	Creatine kinase S-type, mitochondrial OS=Homo sapiens GN=CKMT2 PE=1 SV=2	52.43	1	408		5.7

	B2R8A3	cDNA, FLJ93805, highly similar to Homo sapiens creatine kinase, mitochondrial 2 (sarcomeric) (CKMT2), nuclear gene encoding mitochondrial protein, mRNA OS=Homo sapiens PE=2 SV=1	52.43	1	408		*5.7*
290	Q5XKE5	Keratin, type II cytoskeletal 79 OS=Homo sapiens GN=KRT79 PE=1 SV=2	52.28	1	675		*4.5*
291	P62807	Histone H2B type 1-C/E/F/G/I OS=Homo sapiens GN=HIST1H2BC PE=1 SV=4	52.07	1	397		*61.1*
	B2R4S9	Histone H2B OS=Homo sapiens GN=HIST1H2BF PE=2 SV=1	52.07	1	397		*61.1*
292	Q8N4D0	Carcinoembryonic antigen-related cell adhesion molecule 5 OS=Homo sapiens GN=CEACAM5 PE=2 SV=1	51.69	1	849		*5.2*
	Q53G30	Carcinoembryonic antigen-related cell adhesion molecule 5 variant (Fragment) OS=Homo sapiens PE=2 SV=1	51.69	1	849		*5.2*
	P06731	Carcinoembryonic antigen-related cell adhesion molecule 5 OS=Homo sapiens GN=CEACAM5 PE=1 SV=3	51.69	1	849		*5.2*
	M0R3J1	Carcinoembryonic antigen-related cell adhesion molecule 5 (Fragment) OS=Homo sapiens GN=CEACAM5 PE=4 SV=1	51.69	1	849		*5.2*
	H9KVA7	Carcinoembryonic antigen-related cell adhesion molecule 5 OS=Homo sapiens GN=CEACAM5 PE=4 SV=2	51.69	1	849		*5.2*
293	P13647	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=3	51.56	1	64		*4.2*
294	P62269	40S ribosomal protein S18 OS=Homo sapiens GN=RPS18 PE=1 SV=3	51.35	1	1026		*61.7*
295	Q9UPN4	5-azacytidine-induced protein 1 OS=Homo sapiens GN=AZI1 PE=1 SV=3	51.34	2	960 986		*3.6*
	I3L2J8	5-azacytidine-induced protein 1 OS=Homo sapiens GN=AZI1 PE=2 SV=1	51.34	2	960 986		*3.6*
	B2RN10	5-azacytidine induced 1 OS=Homo sapiens GN=AZI1 PE=2 SV=1	51.34	2	960 986		*3.6*

UniProt Human Protein IDs, *cont.*

Grp Nr.	*Accession Number*	*Protein Name*	*Protein Score*	*Unique PSMs*	*PSM Serial Nrs.*	*Other Grp.*	*% Seq. Cover.*
296	Q9UKE5	TRAF2 and NCK-interacting protein kinase OS=Homo sapiens GN=TNIK PE=1 SV=1	50.98	1	590		*3.7*
	F5H865	TRAF2 and NCK-interacting protein kinase OS=Homo sapiens GN=TNIK PE=2 SV=1	50.98	1	590		*3.7*

	F5H5M9	TRAF2 and NCK-interacting protein kinase OS=Homo sapiens GN=TNIK PE=2 SV=1	50.98	1	590		*3.7*
297	Q15637	Splicing factor 1 OS=Homo sapiens GN=SF1 PE=1 SV=4	50.98	1	818		*1.6*
	B4DX42	Splicing factor 1 OS=Homo sapiens GN=SF1 PE=2 SV=1	50.98	1	818		*1.6*
	B4DSE4	cDNA FLJ54056, highly similar to Splicing factor 1 OS=Homo sapiens PE=2 SV=1	50.98	1	818		*1.6*
	B4DJU4	cDNA FLJ53344, highly similar to Splicing factor 1 OS=Homo sapiens PE=2 SV=1	50.98	1	818		*1.6*
298	O00533	Neural cell adhesion molecule L1-like protein OS=Homo sapiens GN=CHL1 PE=1 SV=4	50.80	1	1137		*3.4*
299	Q9Y6E0	Serine/threonine-protein kinase 24 OS=Homo sapiens GN=STK24 PE=1 SV=1	50.70	1	691		*5.8*
	Q6P0Y1	Serine/threonine kinase 24 (STE20 homolog, yeast) OS=Homo sapiens GN=STK24 PE=2 SV=1	50.70	1	691		*5.8*
	Q6FG81	STK24 protein (Fragment) OS=Homo sapiens GN=STK24 PE=2 SV=1	50.70	1	691		*5.8*
	Q5U0E6	Serine/threonine kinase 24 (STE20 homolog, yeast) OS=Homo sapiens GN=STK24 PE=2 SV=1	50.70	1	691		*5.8*
	B4DT57	cDNA FLJ61383, highly similar to Serine/threonine-protein kinase 24 (EC 2.7.11.1) OS=Homo sapiens PE=2 SV=1	50.70	1	691		*5.8*
	B4DR80	Serine/threonine-protein kinase 24 12 kDa subunit OS=Homo sapiens GN=STK24 PE=2 SV=1	50.70	1	691		*5.8*
300	E7ERI3	Threonine--tRNA ligase, cytoplasmic OS=Homo sapiens GN=TARS PE=2 SV=1	50.55	1	844		*2.8*
	B4DKZ9	cDNA FLJ55705, highly similar to Threonyl-tRNA synthetase, cytoplasmic (EC 6.1.1.3) OS=Homo sapiens PE=2 SV=1	50.55	1	844		*2.8*
301	Q6FHV6	ENO2 protein OS=Homo sapiens GN=ENO2 PE=2 SV=1	50.22	1	70		*9.8*
	P09104	Gamma-enolase OS=Homo sapiens GN=ENO2 PE=1 SV=3	50.22	1	70		*9.8*
	F5H0C8	Enolase OS=Homo sapiens GN=ENO2 PE=2 SV=1	50.22	1	70		*9.8*
	B7Z2X9	Enolase OS=Homo sapiens GN=ENO2 PE=2 SV=1	50.22	1	70		*9.8*
	A8K3B0	cDNA FLJ77877, highly similar to Human ENO2 neuron specific (gamma) enolase OS=Homo sapiens PE=2 SV=1	50.22	1	70		*9.8*
302	P69905	Hemoglobin subunit alpha OS=Homo sapiens GN=HBA1 PE=1 SV=2	49.94	1	839		*26.8*
	I1VZV6	Hemoglobin alpha 1 OS=Homo sapiens GN=HBA1 PE=3 SV=1	49.94	1	839		*26.8*
	E9M4D4	Hemoglobin alpha-1 globin chain (Fragment) OS=Homo sapiens GN=HBA1 PE=3 SV=1	49.94	1	839		*26.8*
	E1B2D1	Hemoglobin alpha-1 globin chain variant (Fragment) OS=Homo sapiens GN=HBA1 PE=3 SV=1	49.94	1	839		*26.8*
	D1MGQ2	Alpha-2 globin chain OS=Homo sapiens GN=HBA2 PE=2 SV=1	49.94	1	839		*26.8*
303	Q13573	SNW domain-containing protein 1 OS=Homo sapiens GN=SNW1 PE=1 SV=1	49.72	1	41		*6.8*

	G3V3A4	SNW domain-containing protein 1 OS=Homo sapiens GN=SNW1 PE=2 SV=1	49.72	1	41		6.8
	B7Z9X2	cDNA, FLJ78986, highly similar to SNW domain-containing protein 1 OS=Homo sapiens PE=2 SV=1	49.72	1	41		6.8
	B4DY36	cDNA FLJ51388, highly similar to SNW domain-containing protein 1 OS=Homo sapiens PE=2 SV=1	49.72	1	41		6.8
304	P13521	Secretogranin-2 OS=Homo sapiens GN=SCG2 PE=1 SV=2	49.23	1	840		4.4
	B4DQJ6	cDNA FLJ51276, highly similar to Secretogranin-2 OS=Homo sapiens PE=2 SV=1	49.23	1	840		4.4
305	P55209	Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=1 SV=1	49.19	2	574 1187		13.0
	H0YIV4	Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens GN=NAP1L1 PE=2 SV=1	49.19	2	574 1187		13.0
	H0YHC3	Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens GN=NAP1L1 PE=2 SV=1	49.19	2	574 1187		13.0
	H0YH88	Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens GN=NAP1L1 PE=3 SV=1	49.19	2	574 1187		13.0
	F8W543	Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=2 SV=1	49.19	2	574 1187		13.0
	F8W118	Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens GN=NAP1L1 PE=2 SV=1	49.19	2	574 1187		13.0
	F8W0J6	Nucleosome assembly protein 1-like 1 OS=Homo sapiens GN=NAP1L1 PE=2 SV=1	49.19	2	574 1187		13.0
	F8W020	Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens GN=NAP1L1 PE=2 SV=1	49.19	2	574 1187		13.0
	F8VY35	Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens GN=NAP1L1 PE=2 SV=1	49.19	2	574 1187		13.0
	F8VVB5	Nucleosome assembly protein 1-like 1 (Fragment) OS=Homo sapiens GN=NAP1L1 PE=2 SV=1	49.19	2	574 1187		13.0
306	Q13242	Serine/arginine-rich splicing factor 9 OS=Homo sapiens GN=SRSF9 PE=1 SV=1	48.74	2	99 416		12.0
	B4DFT9	cDNA FLJ56571, highly similar to Splicing factor, arginine/serine-rich 9 OS=Homo sapiens PE=2 SV=1	48.74	2	99 416		12.0
	A8K3M9	cDNA FLJ76387, highly similar to Homo sapiens splicing factor, arginine/serine-rich 9 (SFRS9), mRNA OS=Homo sapiens PE=2 SV=1	48.74	2	99 416		12.0
307	Q12904	Aminoacyl tRNA synthase complex-interacting multifunctional protein 1 OS=Homo sapiens GN=AIMP1 PE=1 SV=2	48.47	1	1078		2.6
308	P62316	Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2 PE=1 SV=1	48.29	1	1118		12.8
	K7ERG4	Small nuclear ribonucleoprotein Sm D2 OS=Homo sapiens GN=SNRPD2 PE=4 SV=1	48.29	1	1118		12.8
309	Q3MHD2	Protein LSM12 homolog OS=Homo sapiens GN=LSM12 PE=1 SV=2	48.05	1	538		7.2
	B4DUG4	cDNA FLJ51308 OS=Homo sapiens PE=4 SV=1	48.05	1	538		7.2

310	B7Z351	cDNA FLJ54682, highly similar to Osteopontin OS=Homo sapiens PE=2 SV=1	47.99	1	655		*13.5*
311	Q9BZM5	NKG2D ligand 2 OS=Homo sapiens GN=ULBP2 PE=1 SV=1	47.88	1	707		*4.9*
	Q8IZX9	NKG2D ligand 2 (Fragment) OS=Homo sapiens PE=2 SV=1	47.88	1	707		*4.9*
	Q6H3X3	Retinoic acid early transcript 1G protein OS=Homo sapiens GN=RAET1G PE=1 SV=1	47.88	1	707		*4.9*
	Q5VY80	Retinoic acid early transcript 1L protein OS=Homo sapiens GN=RAET1L PE=2 SV=1	47.88	1	707		*4.9*
	Q4V9S8	Retinoic acid early transcript 1G OS=Homo sapiens GN=RAET1G PE=2 SV=1	47.88	1	707		*4.9*
	J7HHH7	Retinoic acid early transcript 1H (Fragment) OS=Homo sapiens GN=RAET1L PE=4 SV=1	47.88	1	707		*4.9*
	J7HHG3	Retinoic acid early transcript 1G (Fragment) OS=Homo sapiens GN=RAET1G PE=4 SV=1	47.88	1	707		*4.9*
	J7HEN7	Retinoic acid early transcript 1L (Fragment) OS=Homo sapiens GN=RAET1L PE=4 SV=1	47.88	1	707		*4.9*
	J7HEM2	Retinoic acid early transcript 1G (Fragment) OS=Homo sapiens GN=RAET1G PE=4 SV=1	47.88	1	707		*4.9*
	J7HBD2	Retinoic acid early transcript 1L (Fragment) OS=Homo sapiens GN=RAET1L PE=4 SV=1	47.88	1	707		*4.9*
312	Q6FG59	CDC37 protein OS=Homo sapiens GN=CDC37 PE=2 SV=1	47.86	1	645		*5.8*
	Q16543	Hsp90 co-chaperone Cdc37 OS=Homo sapiens GN=CDC37 PE=1 SV=1	47.86	1	645		*5.8*
	K7EQA9	Hsp90 co-chaperone Cdc37 (Fragment) OS=Homo sapiens GN=CDC37 PE=4 SV=1	47.86	1	645		*5.8*
	K7EKQ2	Hsp90 co-chaperone Cdc37 (Fragment) OS=Homo sapiens GN=CDC37 PE=4 SV=1	47.86	1	645		*5.8*
313	Q96IF9	VCP protein (Fragment) OS=Homo sapiens GN=VCP PE=2 SV=2	47.22	1	584		*6.7*
	P55072	Transitional endoplasmic reticulum ATPase OS=Homo sapiens GN=VCP PE=1 SV=4	47.22	1	584		*6.7*
314	B4DFW2	Metalloproteinase inhibitor 2 OS=Homo sapiens GN=TIMP2 PE=2 SV=1	47.21	1	987		*3.6*
315	P25705	ATP synthase subunit alpha, mitochondrial OS=Homo sapiens GN=ATP5A1 PE=1 SV=1	47.20	1	1079		*4.0*
	K7ENP3	ATP synthase subunit alpha OS=Homo sapiens GN=ATP5A1 PE=3 SV=1	47.20	1	1079		*4.0*
	K7ENJ4	ATP synthase subunit alpha, mitochondrial (Fragment) OS=Homo sapiens GN=ATP5A1 PE=4 SV=1	47.20	1	1079		*4.0*
	K7EK77	ATP synthase subunit alpha, mitochondrial (Fragment) OS=Homo sapiens GN=ATP5A1 PE=3 SV=1	47.20	1	1079		*4.0*
	K7EK63	ATP synthase subunit alpha OS=Homo sapiens GN=ATP5A1 PE=3 SV=1	47.20	1	1079		*4.0*
	B4DY56	ATP synthase subunit alpha OS=Homo sapiens PE=2 SV=1	47.20	1	1079		*4.0*
316	K7EJP1	ATP synthase subunit alpha, mitochondrial (Fragment) OS=Homo sapiens GN=ATP5A1 PE=4 SV=1	47.20	1	1066		*5.8*

317	Q9Y3E8	CGI-150 protein OS=Homo sapiens GN=C17orf25 PE=2 SV=1	47.07	1	316		4.5
	Q9HC38	Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 PE=1 SV=1	47.07	1	316		4.5
	I3L3Q4	Glyoxalase domain-containing protein 4 (Fragment) OS=Homo sapiens GN=GLOD4 PE=2 SV=1	47.07	1	316		4.5
	B7Z403	Glyoxalase domain-containing protein 4 OS=Homo sapiens GN=GLOD4 PE=2 SV=1	47.07	1	316		4.5
	B4DX01	cDNA FLJ59092 OS=Homo sapiens PE=2 SV=1	47.07	1	316		4.5
	B3KV49	cDNA FLJ16128 fis, clone BRACE2038269, moderately similar to Bombyx mori cytosolic juvenile hormone binding protein 36 kDa subunit (cJHBP) mRNA OS=Homo sapiens PE=2 SV=1	47.07	1	316		4.5
	A8K8F0	cDNA FLJ76436 OS=Homo sapiens PE=2 SV=1	47.07	1	316		4.5
318	M0QYQ9	Splicing factor U2AF 65 kDa subunit (Fragment) OS=Homo sapiens GN=U2AF2 PE=4 SV=1	47.03	1	383		15.7
319	Q9H7G6	cDNA: FLJ20897 fis, clone ADKA03573 OS=Homo sapiens PE=2 SV=1	46.64	1	134		34.8
	Q71RH4	FP1047 OS=Homo sapiens PE=2 SV=1	46.64	1	134		36.8
	E9PRY8	Elongation factor 1-delta OS=Homo sapiens GN=EEF1D PE=2 SV=1	46.64	1	134		1.7
	D3DWK1	Eukaryotic translation elongation factor 1 delta (Guanine nucleotide exchange protein), isoform CRA_b OS=Homo sapiens GN=EEF1D PE=3 SV=1	46.64	1	134		1.7
	B2RAR6	cDNA, FLJ95068, highly similar to Homo sapiens eukaryotic translation elongation factor 1 delta (guanine nucleotide exchange protein) (EEF1D), transcript variant 1, mRNA OS=Homo sapiens PE=2 SV=1	46.64	1	134		1.7
320	Q5T8U3	60S ribosomal protein L7a (Fragment) OS=Homo sapiens GN=RPL7A PE=4 SV=1	46.57	1	1160		12.0
	P62424	60S ribosomal protein L7a OS=Homo sapiens GN=RPL7A PE=1 SV=2	46.57	1	1160		12.0
321	P60660	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=1 SV=2	46.49	1	694		23.0
	J3KND3	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=4 SV=1	46.49	1	694		23.0
	G8JLA2	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=2 SV=1	46.49	1	694		23.0
	G3V1V0	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=4 SV=1	46.49	1	694		23.0
	F8W1R7	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=2 SV=1	46.49	1	694		23.0
	F8VZV5	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=2 SV=1	46.49	1	694		23.0
	B7Z6Z4	Myosin light polypeptide 6 OS=Homo sapiens GN=MYL6 PE=2 SV=1	46.49	1	694		23.0

322	P33240	Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=1 SV=1	46.20	1	212		1.8
	E9PID8	Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=2 SV=1	46.20	1	212		1.8
	E7EWR4	Cleavage stimulation factor subunit 2 OS=Homo sapiens GN=CSTF2 PE=2 SV=1	46.20	1	212		1.8
	B4DUD5	cDNA FLJ58787, highly similar to Cleavage stimulation factor 64 kDa subunit OS=Homo sapiens PE=2 SV=1	46.20	1	212		1.8
	B3V096	BetaCstF-64 variant 2 OS=Homo sapiens GN=CSTF2 PE=2 SV=1	46.20	1	212		1.8
323	P25786	Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=1 SV=1	46.03	2	615 877		8.8
	F5GX11	Proteasome subunit alpha type-1 OS=Homo sapiens GN=PSMA1 PE=2 SV=1	46.03	2	615 877		8.8
324	P23528	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3	45.99	1	630		32.9
	G3V1A4	Cofilin 1 (Non-muscle), isoform CRA_a OS=Homo sapiens GN=CFL1 PE=4 SV=1	45.99	1	630		32.9
	E9PP50	Cofilin-1 (Fragment) OS=Homo sapiens GN=CFL1 PE=2 SV=1	45.99	1	630		32.9
	E9PK25	Cofilin-1 OS=Homo sapiens GN=CFL1 PE=2 SV=1	45.99	1	630		32.9
325	Q6IQ49	Protein SDE2 homolog OS=Homo sapiens GN=SDE2 PE=1 SV=1	45.82	1	221		2.0

UniProt Human Protein IDs, *cont.*

Grp Nr.	Accession Number	Protein Name	Protein Score	Unique PSMs	PSM Serial Nrs.	Other Grp.	% Seq. Cover.
326	Q3KQZ8	EPRS protein (Fragment) OS=Homo sapiens GN=EPRS PE=2 SV=1	45.74	1	569		0.9
	P07814	Bifunctional glutamate/proline--tRNA ligase OS=Homo sapiens GN=EPRS PE=1 SV=5	45.74	1	569		0.9
	H6WCP5	EPRSN1 OS=Homo sapiens PE=2 SV=1	45.74	1	569		0.9
	B4DKX5	cDNA FLJ56021, highly similar to Bifunctional aminoacyl-tRNA synthetase[Includes: Glutamyl-tRNA synthetase (EC 6.1.1.17) (Fragment) OS=Homo sapiens PE=2 SV=1	45.74	1	569		0.9
327	P02790	Hemopexin OS=Homo sapiens GN=HPX PE=1 SV=2	45.39	1	1007		4.1
328	Q9H299	SH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo sapiens GN=SH3BGRL3 PE=1 SV=1	45.38	1	302		3.9

	Q86Z22	Putative uncharacterized protein OS=Homo sapiens PE=2 SV=1	45.38	1	302		3.9
	Q5T123	SH3 domain-binding glutamic acid-rich-like protein 3 OS=Homo sapiens GN=SH3BGRL3 PE=2 SV=1	45.38	1	302		3.9
	D3DPK5	SH3 domain binding glutamic acid-rich protein like 3, isoform CRA_a (Fragment) OS=Homo sapiens GN=SH3BGRL3 PE=2 SV=1	45.38	1	302		3.9
329	Q6FGX5	TIMP metallopeptidase inhibitor 1, isoform CRA_a OS=Homo sapiens GN=TIMP1 PE=2 SV=1	45.34	1	270		6.7
	Q5H9A7	Metalloproteinase inhibitor 1 OS=Homo sapiens GN=TIMP1 PE=2 SV=1	45.34	1	270		6.7
	P01033	Metalloproteinase inhibitor 1 OS=Homo sapiens GN=TIMP1 PE=1 SV=1	45.34	1	270		6.7
	H0Y789	Metalloproteinase inhibitor 1 (Fragment) OS=Homo sapiens GN=TIMP1 PE=4 SV=1	45.34	1	270		6.7
	B3KQF4	cDNA FLJ90373 fis, clone NT2RP2004606, highly similar to Metalloproteinase inhibitor 1 OS=Homo sapiens PE=2 SV=1	45.34	1	270		6.7
330	O00115	Deoxyribonuclease-2-alpha OS=Homo sapiens GN=DNASE2 PE=1 SV=2	44.93	1	880		5.5
	K7ENE5	Deoxyribonuclease-2-alpha (Fragment) OS=Homo sapiens GN=DNASE2 PE=4 SV=1	44.93	1	880		5.5
	C0LQF2	Deoxyribonuclease II (Fragment) OS=Homo sapiens PE=2 SV=1	44.93	1	880		5.5
	B7Z4K6	Deoxyribonuclease-2-alpha OS=Homo sapiens GN=DNASE2 PE=2 SV=1	44.93	1	880		5.5
	B3KQS9	cDNA PSEC0141 fis, clone PLACE1005913, highly similar to Deoxyribonuclease-2-alpha (EC 3.1.22.1) OS=Homo sapiens PE=2 SV=1	44.93	1	880		5.5
331	P05455	Lupus La protein OS=Homo sapiens GN=SSB PE=1 SV=2	44.91	1	1103		10.8
	B5BUB5	Autoantigen La (Fragment) OS=Homo sapiens GN=SSB PE=2 SV=1	44.91	1	1103		10.8
332	Q05639	Elongation factor 1-alpha 2 OS=Homo sapiens GN=EEF1A2 PE=1 SV=1	44.87	1	905		5.8
333	Q71UA6	Neutral amino acid transporter OS=Homo sapiens GN=SLC1A5 PE=2 SV=1	44.74	1	556		2.7
	Q59ES3	Solute carrier family 1 (Neutral amino acid transporter), member 5 variant (Fragment) OS=Homo sapiens PE=2 SV=1	44.74	1	556		2.7
	Q15758	Neutral amino acid transporter B(0) OS=Homo sapiens GN=SLC1A5 PE=1 SV=2	44.74	1	556		2.7
	M0QXM4	Neutral amino acid transporter B(0) OS=Homo sapiens GN=SLC1A5 PE=4 SV=1	44.74	1	556		2.7
	E9PC01	Neutral amino acid transporter B(0) OS=Homo sapiens GN=SLC1A5 PE=2 SV=1	44.74	1	556		2.7
	B7ZB81	cDNA, FLJ79445, highly similar to Neutral amino acid transporter B(0) OS=Homo sapiens PE=2 SV=1	44.74	1	556		2.7

	B4DWS4	Neutral amino acid transporter B(0) OS=Homo sapiens GN=SLC1A5 PE=2 SV=1	44.74	1	556		*2.7*
	B4DR77	cDNA FLJ58403, highly similar to Neutral amino acid transporter B(0) OS=Homo sapiens PE=2 SV=1	44.74	1	556		*2.7*
	B4DE27	cDNA FLJ58765, highly similar to Neutral amino acid transporter B(0) OS=Homo sapiens PE=2 SV=1	44.74	1	556		*2.7*
334	Q9BXP5	Serrate RNA effector molecule homolog OS=Homo sapiens GN=SRRT PE=1 SV=1	44.48	1	74		*24.2*
335	J3KNE3	Platelet-activating factor acetylhydrolase IB subunit beta (Fragment) OS=Homo sapiens GN=PAFAH1B2 PE=4 SV=1	44.36	1	274		*10.3*
336	P62826	GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=1 SV=3	44.32	1	664		*4.3*
	J3KQE5	GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=RAN PE=4 SV=1	44.32	1	664		*4.3*
	F5H018	GTP-binding nuclear protein Ran (Fragment) OS=Homo sapiens GN=RAN PE=2 SV=1	44.32	1	664		*4.3*
	B5MDF5	GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=4 SV=1	44.32	1	664		*4.3*
	B4DV51	GTP-binding nuclear protein Ran OS=Homo sapiens GN=RAN PE=2 SV=1	44.32	1	664		*4.3*
337	P09382	Galectin-1 OS=Homo sapiens GN=LGALS1 PE=1 SV=2	44.07	1	36		*7.4*
338	Q86Y82	Syntaxin-12 OS=Homo sapiens GN=STX12 PE=1 SV=1	43.85	1	144		*8.5*
	Q6LEU0	STX12 protein (Fragment) OS=Homo sapiens GN=STX12 PE=2 SV=1	43.85	1	144		*8.5*
	B1AJQ6	Syntaxin-12 (Fragment) OS=Homo sapiens GN=STX12 PE=4 SV=1	43.85	1	144		*8.5*
339	Q8NFU3	Thiosulfate sulfurtransferase/rhodanese-like domain-containing protein 1 OS=Homo sapiens GN=TSTD1 PE=1 SV=3	43.84	1	922		*7.8*
340	Q9NXZ6	BMP and activin membrane-bound inhibitor homolog OS=Homo sapiens GN=nma PE=2 SV=1	43.80	1	253		*3.5*
	Q53G66	BMP and activin membrane-bound inhibitor homolog (Fragment) OS=Homo sapiens PE=2 SV=1	43.80	1	253		*3.5*
	Q13145	BMP and activin membrane-bound inhibitor homolog OS=Homo sapiens GN=BAMBI PE=1 SV=1	43.80	1	253		*3.5*
	A8K3M4	BMP and activin membrane-bound inhibitor homolog OS=Homo sapiens PE=2 SV=1	43.80	1	253		*3.5*
341	Q9UKM9	RNA-binding protein Raly OS=Homo sapiens GN=RALY PE=1 SV=1	43.73	1	640		*9.5*
	Q5QPM2	RNA-binding protein Raly (Fragment) OS=Homo sapiens GN=RALY PE=4 SV=1	43.73	1	640		*9.5*
	Q5QPM1	RNA-binding protein Raly (Fragment) OS=Homo sapiens GN=RALY PE=4 SV=1	43.73	1	640		*9.5*
	Q5QPM0	RNA-binding protein Raly (Fragment) OS=Homo sapiens GN=RALY PE=4 SV=1	43.73	1	640		*9.5*

	Q5QPL9	RNA-binding protein Raly (Fragment) OS=Homo sapiens GN=RALY PE=4 SV=1	43.73	1	640		*9.5*
	Q53GL6	RNA binding protein (Autoantigenic, hnRNP-associated with lethal yellow) long isoform variant (Fragment) OS=Homo sapiens GN=RALY PE=2 SV=1	43.73	1	640		*9.5*
	B4DSJ1	cDNA FLJ56677, highly similar to RNA-binding protein Raly OS=Homo sapiens PE=2 SV=1	43.73	1	640		*9.5*
	A8K4T9	cDNA FLJ77421, highly similar to Homo sapiens autoantigen p542 mRNA OS=Homo sapiens PE=2 SV=1	43.73	1	640		*9.5*
342	Q86SE5	RNA-binding Raly-like protein OS=Homo sapiens GN=RALYL PE=1 SV=2	43.73	1	834		*7.2*
	G3V129	Putative uncharacterized protein LOC138046 OS=Homo sapiens GN=RALYL PE=4 SV=1	43.73	1	834		*7.2*
	B3KT61	RNA-binding Raly-like protein OS=Homo sapiens GN=RALYL PE=2 SV=1	43.73	1	834		*7.2*
	B3KSX3	cDNA FLJ37224 fis, clone BRAMY2000052, moderately similar to RNA-binding protein Raly OS=Homo sapiens PE=2 SV=1	43.73	1	834		*7.2*
343	P35659	Protein DEK OS=Homo sapiens GN=DEK PE=1 SV=1	43.62	1	46		*8.0*
344	Q5T081	CHC1 protein OS=Homo sapiens GN=RCC1 PE=2 SV=1	43.27	1	501		*2.4*
	P18754	Regulator of chromosome condensation OS=Homo sapiens GN=RCC1 PE=1 SV=1	43.27	1	501		*2.4*
	C9JW69	Regulator of chromosome condensation (Fragment) OS=Homo sapiens GN=RCC1 PE=2 SV=1	43.27	1	501		*2.4*
345	Q92823	Neuronal cell adhesion molecule OS=Homo sapiens GN=NRCAM PE=1 SV=3	42.88	1	793		*1.3*
	Q75ML9	Putative uncharacterized protein NRCAM (Fragment) OS=Homo sapiens GN=NRCAM PE=2 SV=1	42.88	1	793		*1.3*
	Q4KMQ7	NRCAM protein OS=Homo sapiens GN=NRCAM PE=2 SV=1	42.88	1	793		*1.3*
	Q14CA1	NRCAM protein OS=Homo sapiens GN=NRCAM PE=2 SV=1	42.88	1	793		*1.3*
	F8W775	Neuronal cell adhesion molecule OS=Homo sapiens GN=NRCAM PE=2 SV=1	42.88	1	793		*1.3*
	C9JYY6	Neuronal cell adhesion molecule OS=Homo sapiens GN=NRCAM PE=2 SV=2	42.88	1	793		*1.3*
	C9JH43	Neuronal cell adhesion molecule (Fragment) OS=Homo sapiens GN=NRCAM PE=2 SV=1	42.88	1	793		*1.3*
	C9JF43	Neuronal cell adhesion molecule (Fragment) OS=Homo sapiens GN=NRCAM PE=2 SV=1	42.88	1	793		*1.3*
	C9J8B6	Neuronal cell adhesion molecule (Fragment) OS=Homo sapiens GN=NRCAM PE=4 SV=1	42.88	1	793		*1.3*
	B7Z670	cDNA FLJ61703, highly similar to Neuronal cell adhesion molecule (Fragment) OS=Homo sapiens PE=2 SV=1	42.88	1	793		*1.3*
346	Q5TDH0	Protein DDI1 homolog 2 OS=Homo sapiens GN=DDI2 PE=1 SV=1	42.87	1	154		*8.7*
	H0YII4	Protein DDI1 homolog 2 (Fragment) OS=Homo sapiens GN=DDI2 PE=2 SV=1	42.87	1	154		*8.7*

	H0YI90	Protein DDI1 homolog 2 (Fragment) OS=Homo sapiens GN=DDI2 PE=4 SV=1	42.87	1	154		*8.7*
347	Q8TDH9	Biogenesis of lysosome-related organelles complex 1 subunit 5 OS=Homo sapiens GN=BLOC1S5 PE=1 SV=1	42.80	1	376		*7.4*
	H3BN57	Uncharacterized protein (Fragment) OS=Homo sapiens PE=4 SV=1	42.80	1	376		*7.4*
348	P12956	X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=1 SV=2	42.65	1	870		*7.0*
	B4DE32	cDNA FLJ53970, highly similar to ATP-dependent DNA helicase 2 subunit 1 (EC3.6.1.-) OS=Homo sapiens PE=2 SV=1	42.65	1	870		*7.0*
	B2RDN9	cDNA, FLJ96699, highly similar to Homo sapiens thyroid autoantigen 70kDa (Ku antigen) (G22P1), mRNA OS=Homo sapiens PE=2 SV=1	42.65	1	870		*7.0*
	B1AHC9	X-ray repair cross-complementing protein 6 OS=Homo sapiens GN=XRCC6 PE=4 SV=1	42.65	1	870		*7.0*
	B1AHC8	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa), isoform CRA_b OS=Homo sapiens GN=XRCC6 PE=2 SV=1	42.65	1	870		*7.0*
349	Q6FH91	TNNC1 protein OS=Homo sapiens GN=TNNC1 PE=2 SV=1	42.42	1	1120		*11.2*
	P63316	Troponin C, slow skeletal and cardiac muscles OS=Homo sapiens GN=TNNC1 PE=1 SV=1	42.42	1	1120		*11.2*
350	Q5BJH1	PSAP protein OS=Homo sapiens GN=PSAP PE=2 SV=1	42.41	1	1209		*3.6*
	Q59EN5	Prosaposin variant (Fragment) OS=Homo sapiens PE=2 SV=1	42.41	1	1209		*3.6*
	Q53FJ5	Prosaposin (Variant Gaucher disease and variant metachromatic leukodystrophy) variant (Fragment) OS=Homo sapiens PE=2 SV=1	42.41	1	1209		*3.6*
	P07602	Proactivator polypeptide OS=Homo sapiens GN=PSAP PE=1 SV=2	42.41	1	1209		*3.6*
	C9JIZ6	Saposin-D OS=Homo sapiens GN=PSAP PE=2 SV=1	42.41	1	1209		*3.6*
	B4DRB7	cDNA FLJ54136, highly similar to Proactivator polypeptide OS=Homo sapiens PE=2 SV=1	42.41	1	1209		*3.6*
	B1AVU8	Saposin-D OS=Homo sapiens GN=PSAP PE=2 SV=1	42.41	1	1209		*3.6*
351	Q08211	ATP-dependent RNA helicase A OS=Homo sapiens GN=DHX9 PE=1 SV=4	42.28	1	267		*36.8*
352	Q8N4C6	Ninein OS=Homo sapiens GN=NIN PE=1 SV=4	42.02	1	976		*2.5*
	Q5XUU0	Ninein isoform 6 OS=Homo sapiens GN=NIN PE=2 SV=1	42.02	1	976		*2.5*
	H9KV85	Ninein (Fragment) OS=Homo sapiens GN=NIN PE=4 SV=1	42.02	1	976		*2.5*
	H0YEL6	Ninein (Fragment) OS=Homo sapiens GN=NIN PE=4 SV=1	42.02	1	976		*2.5*
	H0YDJ4	Ninein (Fragment) OS=Homo sapiens GN=NIN PE=4 SV=1	42.02	1	976		*2.5*
	F8W6D3	Ninein OS=Homo sapiens GN=NIN PE=2 SV=1	42.02	1	976		*2.5*
	E9PN67	Ninein OS=Homo sapiens GN=NIN PE=4 SV=1	42.02	1	976		*2.5*
	C9J066	Ninein OS=Homo sapiens GN=NIN PE=2 SV=1	42.02	1	976		*2.5*

353	Q6NTA2	HNRNPL protein (Fragment) OS=Homo sapiens GN=HNRNPL PE=2 SV=2	41.42	1	721		*3.6*
	P14866	Heterogeneous nuclear ribonucleoprotein L OS=Homo sapiens GN=HNRNPL PE=1 SV=2	41.42	1	721		*3.6*
	M0QXS5	Heterogeneous nuclear ribonucleoprotein L (Fragment) OS=Homo sapiens GN=HNRNPL PE=4 SV=1	41.42	1	721		*3.6*
	B2R959	cDNA, FLJ94229, highly similar to Homo sapiens heterogeneous nuclear ribonucleoprotein L (HNRPL),mRNA OS=Homo sapiens PE=2 SV=1	41.42	1	721		*3.6*
354	Q9Y371	Endophilin-B1 OS=Homo sapiens GN=SH3GLB1 PE=1 SV=1	41.39	1	58		*2.0*
	Q9NR46	Endophilin-B2 OS=Homo sapiens GN=SH3GLB2 PE=1 SV=1	41.39	1	58		*2.0*
	F8WFB9	Endophilin-B2 OS=Homo sapiens GN=SH3GLB2 PE=2 SV=1	41.39	1	58		*2.0*
	B7ZC39	Endophilin-B2 OS=Homo sapiens GN=SH3GLB2 PE=2 SV=1	41.39	1	58		*2.0*
	B7ZC38	Endophilin-B2 OS=Homo sapiens GN=SH3GLB2 PE=2 SV=1	41.39	1	58		*2.0*

UniProt Human Protein IDs, *cont.*

Grp Nr.	*Accession Number*	*Protein Name*	*Protein Score*	*Unique PSMs*	*PSM Serial Nrs.*	*Other Grp.*	*% Seq. Cover.*
355	Q2NNQ8	FER-1-like protein 4 OS=Homo sapiens GN=FER1L4 PE=2 SV=1	41.32	1	600		*7.9*
	A9Z1Z3	Fer-1-like protein 4 OS=Homo sapiens GN=FER1L4 PE=2 SV=1	41.32	1	600		*7.9*
356	Q92973	Transportin-1 OS=Homo sapiens GN=TNPO1 PE=1 SV=2	41.25	1	848		*9.4*
	J3KPU5	Transportin-1 OS=Homo sapiens GN=TNPO1 PE=4 SV=1	41.25	1	848		*9.4*
	E7EW37	Transportin-1 OS=Homo sapiens GN=TNPO1 PE=2 SV=1	41.25	1	848		*9.4*
	B4DSC0	Transportin-1 OS=Homo sapiens GN=TNPO1 PE=2 SV=1	41.25	1	848		*9.4*
357	Q9BY44	Eukaryotic translation initiation factor 2A OS=Homo sapiens GN=EIF2A PE=1 SV=3	41.24	1	438		*5.2*
	F8WAE5	Eukaryotic translation initiation factor 2A OS=Homo sapiens GN=EIF2A PE=2 SV=1	41.24	1	438		*5.2*
	B4DQ14	Eukaryotic translation initiation factor 2A OS=Homo sapiens GN=EIF2A PE=2 SV=1	41.24	1	438		*5.2*
	B4DF96	Eukaryotic translation initiation factor 2A OS=Homo sapiens GN=EIF2A PE=2 SV=1	41.24	1	438		*5.2*
358	Q6P6D7	Phosphoglycerate mutase 1 (Brain) OS=Homo sapiens GN=PGAM1 PE=2 SV=1	41.13	2	21 1020		*6.3*

	Q6FHU2	HCG2015269, isoform CRA_a (Fragment) OS=Homo sapiens GN=PGAM1 PE=2 SV=1	41.13	2	21 1020		*6.3*
	Q6FHK8	PGAM1 protein OS=Homo sapiens GN=PGAM1 PE=2 SV=1	41.13	2	21 1020		*6.3*
	Q53G35	Phosphoglycerate mutase (Fragment) OS=Homo sapiens PE=2 SV=1	41.13	2	21 1020		*6.3*
	Q0D2Q6	Phosphoglycerate mutase 1 (Brain) OS=Homo sapiens GN=PGAM1 PE=2 SV=1	41.13	2	21 1020		*6.3*
	P18669	Phosphoglycerate mutase 1 OS=Homo sapiens GN=PGAM1 PE=1 SV=2	41.13	2	21 1020		*6.3*
	P15259	Phosphoglycerate mutase 2 OS=Homo sapiens GN=PGAM2 PE=1 SV=3	41.13	2	21 1020		*6.3*
	B7Z9E5	cDNA, FLJ78809, highly similar to Phosphoglycerate mutase 1 (EC 5.4.2.1) OS=Homo sapiens PE=2 SV=1	41.13	2	21 1020		*6.3*
	B4DMJ7	HCG2015269, isoform CRA_c OS=Homo sapiens GN=hCG_2015269 PE=2 SV=1	41.13	2	21 1020		*6.3*
	B4DKL5	cDNA FLJ51983, highly similar to Phosphoglycerate mutase 1 (EC 5.4.2.1) OS=Homo sapiens PE=2 SV=1	41.13	2	21 1020		*6.3*
359	Q5SWC8	Heterochromatin protein 1-binding protein 3 (Fragment) OS=Homo sapiens GN=HP1BP3 PE=2 SV=1	40.95	1	954		*32.9*
	Q5SSJ5	Heterochromatin protein 1-binding protein 3 OS=Homo sapiens GN=HP1BP3 PE=1 SV=1	40.95	1	954		*32.9*
360	Q13884	Beta-1-syntrophin OS=Homo sapiens GN=SNTB1 PE=1 SV=3	40.91	1	1015		*1.7*
361	Q8IX12	Cell division cycle and apoptosis regulator protein 1 OS=Homo sapiens GN=CCAR1 PE=1 SV=2	40.87	1	835		*1.4*
	F5H3E1	Cell division cycle and apoptosis regulator protein 1 OS=Homo sapiens GN=CCAR1 PE=4 SV=1	40.87	1	835		*1.4*
	F5H2E6	Cell division cycle and apoptosis regulator protein 1 (Fragment) OS=Homo sapiens GN=CCAR1 PE=2 SV=1	40.87	1	835		*1.4*
	F5H1H2	Cell division cycle and apoptosis regulator protein 1 (Fragment) OS=Homo sapiens GN=CCAR1 PE=2 SV=1	40.87	1	835		*1.4*
362	Q9BS10	Similar to ribosomal protein S8 (Fragment) OS=Homo sapiens PE=2 SV=1	40.87	1	736		*4.3*
	Q5JR95	40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=4 SV=1	40.87	1	736		*4.3*
	Q5JR94	40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=2 SV=1	40.87	1	736		*4.3*
	P62241	40S ribosomal protein S8 OS=Homo sapiens GN=RPS8 PE=1 SV=2	40.87	1	736		*4.3*
363	P60953	Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=1 SV=2	40.83	1	969		*7.3*
	E7ETU3	Cell division control protein 42 homolog OS=Homo sapiens GN=CDC42 PE=2 SV=1	40.83	1	969		*7.3*
	B7ZAY4	cDNA, FLJ79348, highly similar to Cell division control protein 42 homolog OS=Homo sapiens PE=2 SV=1	40.83	1	969		*7.3*
	B4E1U9	cDNA FLJ54776, highly similar to Cell division control protein 42 homolog OS=Homo sapiens PE=2 SV=1	40.83	1	969		*7.3*

	B4DMH5	cDNA FLJ55107, highly similar to Cell division control protein 42 homolog OS=Homo sapiens PE=2 SV=1	40.83	1	969		*7.3*
364	P62306	Small nuclear ribonucleoprotein F OS=Homo sapiens GN=SNRPF PE=1 SV=1	40.80	1	859		*9.3*
365	O75947	ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H PE=1 SV=3	40.75	1	197		*15.7*
	F5H608	ATP synthase subunit d, mitochondrial OS=Homo sapiens GN=ATP5H PE=4 SV=2	40.75	1	197		*15.7*
	A0PJH2	ATP5H protein (Fragment) OS=Homo sapiens GN=ATP5H PE=2 SV=1	40.75	1	197		*15.7*
366	O76013	Keratin, type I cuticular Ha6 OS=Homo sapiens GN=KRT36 PE=1 SV=1	40.68	1	807		*4.3*
367	O76015	Keratin, type I cuticular Ha8 OS=Homo sapiens GN=KRT38 PE=2 SV=3	40.68	1	796		*3.9*
368	Q4J6C0	PPM1B beta isoform variant 6 (Fragment) OS=Homo sapiens GN=PPM1B PE=2 SV=1	40.51	1	273		*11.3*
369	I3L2L6	Serine/arginine repetitive matrix protein 2 OS=Homo sapiens GN=SRRM2 PE=2 SV=1	40.38	1	832		*5.8*
370	Q59G88	Coronin (Fragment) OS=Homo sapiens PE=3 SV=1	40.14	1	365		*2.9*
	P31146	Coronin-1A OS=Homo sapiens GN=CORO1A PE=1 SV=4	40.14	1	365		*2.9*
371	Q6P2Q9	Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens GN=PRPF8 PE=1 SV=2	40.11	1	622		*1.0*
	Q53GM6	U5 snRNP-specific protein variant (Fragment) OS=Homo sapiens PE=2 SV=1	40.11	1	622		*1.0*
	B4DK16	cDNA FLJ57882, highly similar to Pre-mRNA-processing-splicing factor 8 OS=Homo sapiens PE=2 SV=1	40.11	1	622		*1.0*
372	Q9H173	Nucleotide exchange factor SIL1 OS=Homo sapiens GN=SIL1 PE=1 SV=1	39.68	1	56		*6.4*
	D6RIU8	Nucleotide exchange factor SIL1 (Fragment) OS=Homo sapiens GN=SIL1 PE=2 SV=1	39.68	1	56		*6.4*
	D6RG16	Nucleotide exchange factor SIL1 (Fragment) OS=Homo sapiens GN=SIL1 PE=2 SV=1	39.68	1	56		*6.4*
	D6REA1	Nucleotide exchange factor SIL1 OS=Homo sapiens GN=SIL1 PE=2 SV=1	39.68	1	56		*6.4*
	D6RBP7	Nucleotide exchange factor SIL1 (Fragment) OS=Homo sapiens GN=SIL1 PE=2 SV=1	39.68	1	56		*6.4*
	D6RAI3	Nucleotide exchange factor SIL1 (Fragment) OS=Homo sapiens GN=SIL1 PE=2 SV=1	39.68	1	56		*6.4*
373	Q5W0S5	UV excision repair protein RAD23 homolog B (Fragment) OS=Homo sapiens GN=RAD23B PE=2 SV=1	39.61	1	558		*8.9*
	Q53F10	UV excision repair protein RAD23 homolog B variant (Fragment) OS=Homo sapiens PE=2 SV=1	39.61	1	558		*8.9*
	P54727	UV excision repair protein RAD23 homolog B OS=Homo sapiens GN=RAD23B PE=1 SV=1	39.61	1	558		*8.9*
	B4DEA3	cDNA FLJ56531, highly similar to UV excision repair protein RAD23 homolog B OS=Homo sapiens PE=2 SV=1	39.61	1	558		*8.9*

374	Q93045	Stathmin-2 OS=Homo sapiens GN=STMN2 PE=1 SV=3	39.39	1	202		*11.9*
	E5RGX5	Stathmin OS=Homo sapiens GN=STMN2 PE=2 SV=1	39.39	1	202		*11.9*
	B7Z4N6	cDNA FLJ53062, highly similar to Stathmin-2 OS=Homo sapiens PE=2 SV=1	39.39	1	202		*11.9*
375	Q1JQ76	Ribosomal protein (Fragment) OS=Homo sapiens GN=RPL10A PE=2 SV=1	39.30	1	552		*11.7*
	P62906	60S ribosomal protein L10a OS=Homo sapiens GN=RPL10A PE=1 SV=2	39.30	1	552		*11.7*
376	Q5TC02	Sodium/potassium-transporting ATPase subunit alpha-1 (Fragment) OS=Homo sapiens GN=ATP1A1 PE=4 SV=1	38.75	1	89		*4.9*
	Q5TC01	Sodium/potassium-transporting ATPase subunit alpha-1 (Fragment) OS=Homo sapiens GN=ATP1A1 PE=4 SV=1	38.75	1	89		*4.9*
377	Q5VTU8	ATP synthase subunit epsilon-like protein, mitochondrial OS=Homo sapiens GN=ATP5EP2 PE=3 SV=1	38.74	1	963		*15.7*
	P56381	ATP synthase subunit epsilon, mitochondrial OS=Homo sapiens GN=ATP5E PE=1 SV=2	38.74	1	963		*15.7*
378	Q71UM5	40S ribosomal protein S27-like OS=Homo sapiens GN=RPS27L PE=1 SV=3	38.61	1	153		*8.0*
	P42677	40S ribosomal protein S27 OS=Homo sapiens GN=RPS27 PE=1 SV=3	38.61	1	153		*8.0*
	H0YMV8	40S ribosomal protein S27 OS=Homo sapiens GN=RPS27L PE=2 SV=1	38.61	1	153		*8.0*
	C9J1C5	40S ribosomal protein S27 OS=Homo sapiens GN=RPS27L PE=3 SV=1	38.61	1	153		*8.0*
	A4D1G5	40S ribosomal protein S27 OS=Homo sapiens GN=LOC392748 PE=3 SV=1	38.61	1	153		*8.0*
379	P08758	Annexin A5 OS=Homo sapiens GN=ANXA5 PE=1 SV=2	38.60	1	596		*4.5*
	E7ENQ5	Annexin OS=Homo sapiens GN=ANXA5 PE=2 SV=1	38.60	1	596		*4.5*
	D6RBL5	Annexin OS=Homo sapiens GN=ANXA5 PE=2 SV=1	38.60	1	596		*4.5*
	D6RBE9	Annexin OS=Homo sapiens GN=ANXA5 PE=2 SV=1	38.60	1	596		*4.5*
380	Q6NZ52	Ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=2 SV=1	38.49	1	104		*14.2*
	P46776	60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=1 SV=2	38.49	1	104		*14.2*
	E9PLX7	60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=2 SV=1	38.49	1	104		*14.2*
	E9PJD9	60S ribosomal protein L27a OS=Homo sapiens GN=RPL27A PE=3 SV=1	38.49	1	104		*14.2*
381	E7EVA0	Microtubule-associated protein OS=Homo sapiens GN=MAP4 PE=2 SV=1	38.48	1	176		*1.6*
382	P62837	Ubiquitin-conjugating enzyme E2 D2 OS=Homo sapiens GN=UBE2D2 PE=1 SV=1	38.23	1	543		*9.3*
	P61077	Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=1 SV=1	38.23	1	543		*9.3*

	H9KV45	Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=2 SV=1	38.23	1	543		*9.3*
	D6RFM0	Ubiquitin-conjugating enzyme E2 D2 (Fragment) OS=Homo sapiens GN=UBE2D2 PE=2 SV=1	38.23	1	543		*9.3*
	D6RAW0	Ubiquitin-conjugating enzyme E2 D3 (Fragment) OS=Homo sapiens GN=UBE2D3 PE=2 SV=1	38.23	1	543		*9.3*
	D6RAH7	Ubiquitin-conjugating enzyme E2 D3 OS=Homo sapiens GN=UBE2D3 PE=3 SV=1	38.23	1	543		*9.3*
383	Q9NZT1	Calmodulin-like protein 5 OS=Homo sapiens GN=CALML5 PE=1 SV=2	38.21	1	1032		*11.6*
	Q53H37	Calmodulin-like skin protein variant (Fragment) OS=Homo sapiens PE=2 SV=1	38.21	1	1032		*11.6*
384	Q9P013	Spliceosome-associated protein CWC15 homolog OS=Homo sapiens GN=CWC15 PE=1 SV=2	38.19	1	10		*4.8*
385	Q9UG16	Putative uncharacterized protein DKFZp564P0562 (Fragment) OS=Homo sapiens GN=DKFZp564P0562 PE=2 SV=1	38.10	1	560		*2.0*
386	P49411	Elongation factor Tu, mitochondrial OS=Homo sapiens GN=TUFM PE=1 SV=2	37.98	1	524		*2.4*
387	P62888	60S ribosomal protein L30 OS=Homo sapiens GN=RPL30 PE=1 SV=2	37.71	1	502		*7.0*
	E5RI99	60S ribosomal protein L30 (Fragment) OS=Homo sapiens GN=RPL30 PE=2 SV=1	37.71	1	502		*7.0*
388	P09497	Clathrin light chain B OS=Homo sapiens GN=CLTB PE=1 SV=1	37.69	1	467		*3.5*
389	Q6T598	Cellular nucleic acid binding protein (Fragment) OS=Homo sapiens PE=2 SV=1	37.63	1	1027		*8.1*
	Q4JGY1	Cellular nucleic acid binding protein beta variant 1 OS=Homo sapiens GN=ZNF9 PE=2 SV=1	37.63	1	1027		*8.1*
	P62633	Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP PE=1 SV=1	37.63	1	1027		*8.1*
	B4DP17	Cellular nucleic acid-binding protein OS=Homo sapiens GN=CNBP PE=2 SV=1	37.63	1	1027		*8.1*
390	P21796	Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens GN=VDAC1 PE=1 SV=2	37.54	1	18		*4.2*
	B4DEI3	cDNA FLJ57715, highly similar to Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens PE=2 SV=1	37.54	1	18		*4.2*
	B3KTS5	cDNA FLJ38670 fis, clone HSYRA2000190, highly similar to Voltage-dependent anion-selective channel protein 1 OS=Homo sapiens PE=2 SV=1	37.54	1	18		*4.2*
391	Q8NBJ4	Golgi membrane protein 1 OS=Homo sapiens GN=GOLM1 PE=1 SV=1	37.31	1	310		*4.0*
	B3KNK9	Golgi phosphoprotein 2, isoform CRA_a OS=Homo sapiens GN=GOLPH2 PE=2 SV=1	37.31	1	310		*4.0*

UniProt Human Protein IDs, *cont.*

Grp Nr.	*Accession Number*	*Protein Name*	*Protein Score*	*Unique PSMs*	*PSM Serial Nrs.*	*Other Grp.*	*% Seq. Cover.*
392	Q53XX5	Cold inducible RNA binding protein OS=Homo sapiens GN=CIRBP PE=2 SV=1	37.13	1	1071		*22.3*
	Q14011	Cold-inducible RNA-binding protein OS=Homo sapiens GN=CIRBP PE=1 SV=1	37.13	1	1071		*22.3*
	K7EQR7	Cold-inducible RNA-binding protein OS=Homo sapiens GN=CIRBP PE=4 SV=1	37.13	1	1071		*22.3*
	K7EPM4	Cold-inducible RNA-binding protein OS=Homo sapiens GN=CIRBP PE=4 SV=1	37.13	1	1071		*22.3*
	K7EMY9	Cold-inducible RNA-binding protein (Fragment) OS=Homo sapiens GN=CIRBP PE=4 SV=1	37.13	1	1071		*22.3*
	D6W5Y5	Cold inducible RNA binding protein, isoform CRA_c OS=Homo sapiens GN=CIRBP PE=4 SV=1	37.13	1	1071		*22.3*
	B4E2X2	Cold-inducible RNA-binding protein OS=Homo sapiens GN=CIRBP PE=2 SV=1	37.13	1	1071		*22.3*
393	Q14624	Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=1 SV=4	36.94	1	646		*0.6*
	B7ZKJ8	35 kDa inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens GN=ITIH4 PE=2 SV=1	36.94	1	646		*0.6*
	B7Z544	cDNA FLJ51742, highly similar to Inter-alpha-trypsin inhibitor heavy chain H4 OS=Homo sapiens PE=2 SV=1	36.94	1	646		*0.6*
	B2RMS9	Inter-alpha (Globulin) inhibitor H4 (Plasma Kallikrein-sensitive glycoprotein) OS=Homo sapiens GN=ITIH4 PE=2 SV=1	36.94	1	646		*0.6*
394	Q9Y3Z5	Putative uncharacterized protein DKFZp564B112 (Fragment) OS=Homo sapiens GN=DKFZp564B112 PE=2 SV=2	36.73	1	1176		*2.0*
	Q9UK43	Chondrosarcoma-associated protein 2 OS=Homo sapiens GN=CSA2 PE=2 SV=1	36.73	1	1176		*2.0*
	Q9H4P6	Clone TCCCIA00142 mRNA sequence OS=Homo sapiens PE=2 SV=1	36.73	1	1176		*2.0*
	Q95HA6	IK cytokine, down-regulator of HLA II OS=Homo sapiens GN=IK PE=2 SV=1	36.73	1	1176		*2.0*
	Q13123	Protein Red OS=Homo sapiens GN=IK PE=1 SV=3	36.73	1	1176		*2.0*
	E7EQZ7	Protein Red (Fragment) OS=Homo sapiens GN=IK PE=2 SV=1	36.73	1	1176		*2.0*

	D6REL4	Protein Red (Fragment) OS=Homo sapiens GN=IK PE=2 SV=1	36.73	1	1176		*2.0*
	D6RCQ4	Protein Red (Fragment) OS=Homo sapiens GN=IK PE=2 SV=1	36.73	1	1176		*2.0*
	D6RAY9	Protein Red (Fragment) OS=Homo sapiens GN=IK PE=2 SV=1	36.73	1	1176		*2.0*
	B2R5Y4	cDNA, FLJ92684, highly similar to Homo sapiens IK cytokine, down-regulator of HLA II (IK), mRNA OS=Homo sapiens PE=2 SV=1	36.73	1	1176		*2.0*
395	H0Y5B4	60S ribosomal protein L36a (Fragment) OS=Homo sapiens GN=RPL36A PE=3 SV=1	36.72	1	606		*6.9*
396	A6NHZ5	Leucine-rich repeat-containing protein 14B OS=Homo sapiens GN=LRRC14B PE=3 SV=3	36.59	1	100		*12.0*
397	Q5JQF8	Polyadenylate-binding protein 1-like 2 OS=Homo sapiens GN=PABPC1L2A PE=2 SV=1	36.33	1	520		*16.5*
398	Q2M1N2	Laminin, gamma 2 OS=Homo sapiens GN=LAMC2 PE=2 SV=1	36.23	1	1105		*0.7*
	Q13753	Laminin subunit gamma-2 OS=Homo sapiens GN=LAMC2 PE=1 SV=2	36.23	1	1105		*0.7*
399	P56385	ATP synthase subunit e, mitochondrial OS=Homo sapiens GN=ATP5I PE=1 SV=2	36.22	1	233		*14.5*
400	O95218	Zinc finger Ran-binding domain-containing protein 2 OS=Homo sapiens GN=ZRANB2 PE=1 SV=2	36.20	1	342		*2.4*
401	Q6IPX4	40S ribosomal protein S16 OS=Homo sapiens GN=RPS16 PE=2 SV=1	36.14	1	66		*15.1*
402	P31150	Rab GDP dissociation inhibitor alpha OS=Homo sapiens GN=GDI1 PE=1 SV=2	36.09	1	359		*4.6*
	B4DHX4	cDNA FLJ52902, highly similar to Rab GDP dissociation inhibitor alpha OS=Homo sapiens PE=2 SV=1	36.09	1	359		*4.6*
403	Q13429	Insulin-like growth factor I (Fragment) OS=Homo sapiens GN=IGF-I PE=2 SV=1	35.99	1	1051		*9.5*
	P05019	Insulin-like growth factor I OS=Homo sapiens GN=IGF1 PE=1 SV=1	35.99	1	1051		*16.5*
	E9PD02	Insulin-like growth factor I OS=Homo sapiens GN=IGF1 PE=3 SV=1	35.99	1	1051		*16.5*
404	O75525	KH domain-containing, RNA-binding, signal transduction-associated protein 3 OS=Homo sapiens GN=KHDRBS3 PE=1 SV=1	35.89	1	529		*6.6*
405	Q9P258	Protein RCC2 OS=Homo sapiens GN=RCC2 PE=1 SV=2	35.89	1	328		*3.3*
	A5PLK7	RCC2 protein (Fragment) OS=Homo sapiens GN=RCC2 PE=2 SV=1	35.89	1	328		*3.3*
406	Q6UW32	Insulin growth factor-like family member 1 OS=Homo sapiens GN=IGFL1 PE=1 SV=1	35.87	1	516		*9.1*
407	Q8WX77	Insulin-like growth factor-binding protein-like 1 OS=Homo sapiens GN=IGFBPL1 PE=2 SV=1	35.85	1	439		*4.3*

408	Q96DV6	40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=2 SV=1	35.56	1	441		*3.2*
	P62753	40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=1 SV=1	35.56	1	441		*3.2*
	A2A3R7	40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=2 SV=1	35.56	1	441		*3.2*
	A2A3R6	40S ribosomal protein S6 OS=Homo sapiens GN=RPS6 PE=2 SV=1	35.56	1	441		*3.2*
409	Q92598	Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=1 SV=1	35.35	1	181		*3.7*
	B4DYH1	Heat shock 105kDa/110kDa protein 1, isoform CRA_b OS=Homo sapiens GN=HSPH1 PE=2 SV=1	35.35	1	181		*3.7*
	B4DY72	Heat shock protein 105 kDa OS=Homo sapiens GN=HSPH1 PE=2 SV=1	35.35	1	181		*3.7*
	B4DF68	cDNA FLJ55325, highly similar to Heat-shock protein 105 kDa OS=Homo sapiens PE=2 SV=1	35.35	1	181		*3.7*
410	L0R512	Alternative protein NCAM2 OS=Homo sapiens GN=NCAM2 PE=4 SV=1	35.24	1	160		*21.4*
411	B4DEX9	cDNA FLJ56687, highly similar to Serotransferrin OS=Homo sapiens PE=2 SV=1	35.09	1	411		*37.7*
412	O75937	DnaJ homolog subfamily C member 8 OS=Homo sapiens GN=DNAJC8 PE=1 SV=2	35.01	1	1059		*8.7*
413	Q99733	Nucleosome assembly protein 1-like 4 OS=Homo sapiens GN=NAP1L4 PE=1 SV=1	34.98	1	811		*4.8*
	F5HFY4	Nucleosome assembly protein 1-like 4 OS=Homo sapiens GN=NAP1L4b PE=2 SV=1	34.98	1	811		*4.8*
	E9PS34	Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens GN=NAP1L4 PE=2 SV=1	34.98	1	811		*4.8*
	E9PNW0	Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens GN=NAP1L4 PE=2 SV=1	34.98	1	811		*4.8*
	E9PNJ7	Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens GN=NAP1L4 PE=2 SV=1	34.98	1	811		*4.8*
	E9PKT8	Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens GN=NAP1L4 PE=2 SV=1	34.98	1	811		*4.8*
	E9PJJ2	Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens GN=NAP1L4 PE=2 SV=1	34.98	1	811		*4.8*
	C9JZI7	Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens GN=NAP1L4 PE=2 SV=1	34.98	1	811		*4.8*
	C9J6D1	Nucleosome assembly protein 1-like 4 (Fragment) OS=Homo sapiens GN=NAP1L4 PE=2 SV=1	34.98	1	811		*4.8*
	B7ZB83	cDNA, FLJ79447, highly similar to Nucleosome assembly protein 1-like 4 OS=Homo sapiens PE=2 SV=1	34.98	1	811		*4.8*
414	Q86XW9	Thioredoxin domain-containing protein 6 OS=Homo sapiens GN=NME9 PE=1 SV=1	34.96	1	386		*2.4*

415	B3KRZ1	cDNA FLJ35128 fis, clone PLACE6008768, moderately similar to Insulin-like growth factor-binding protein 3 OS=Homo sapiens PE=2 SV=1	34.82	1	437		*15.4*
416	A0N4V7	HCG2039797 (Fragment) OS=Homo sapiens GN=Tcr-alpha PE=4 SV=1	34.78	1	324		*38.1*
417	E5RK99	Collagen triple helix repeat-containing protein 1 OS=Homo sapiens GN=CTHRC1 PE=2 SV=1	34.77	1	1126		*61.7*
418	P11388	DNA topoisomerase 2-alpha OS=Homo sapiens GN=TOP2A PE=1 SV=3	34.77	1	247		*4.4*
419	P16615	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 OS=Homo sapiens GN=ATP2A2 PE=1 SV=1	34.73	1	786		*5.1*
	H7C5W9	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2 (Fragment) OS=Homo sapiens GN=ATP2A2 PE=3 SV=1	34.73	1	786		*5.1*
420	Q567R0	UQCRH protein OS=Homo sapiens GN=UQCRH PE=2 SV=1	34.19	1	706		*8.2*
	P07919	Cytochrome b-c1 complex subunit 6, mitochondrial OS=Homo sapiens GN=UQCRH PE=1 SV=2	34.19	1	706		*8.2*
421	Q15233	Non-POU domain-containing octamer-binding protein OS=Homo sapiens GN=NONO PE=1 SV=4	34.11	1	403		*4.9*
	A8K525	cDNA FLJ76817, highly similar to Homo sapiens non-POU domain containing, octamer-binding (NONO), mRNA OS=Homo sapiens PE=2 SV=1	34.11	1	403		*4.9*
422	Q9NQW1	Protein transport protein Sec31B OS=Homo sapiens GN=SEC31B PE=1 SV=1	34.06	1	54		*29.5*
423	Q6DCA8	BCLAF1 protein (Fragment) OS=Homo sapiens GN=BCLAF1 PE=2 SV=1	33.95	1	343		*2.8*
	E9PQN2	Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=2 SV=1	33.95	1	343		*2.8*
	E9PKI6	Bcl-2-associated transcription factor 1 OS=Homo sapiens GN=BCLAF1 PE=4 SV=1	33.95	1	343		*2.8*
	E9PK09	Bcl-2-associated transcription factor 1 (Fragment) OS=Homo sapiens GN=BCLAF1 PE=2 SV=1	33.95	1	343		*2.8*
424	Q53H26	Transferrin variant (Fragment) OS=Homo sapiens PE=2 SV=1	33.82	1	339		*60.6*
425	O15347	High mobility group protein B3 OS=Homo sapiens GN=HMGB3 PE=1 SV=4	33.81	1	680		*11.4*
	E7ES08	High mobility group protein B3 (Fragment) OS=Homo sapiens GN=HMGB3 PE=2 SV=1	33.81	1	680		*11.4*
	E7EQU1	High mobility group protein B3 (Fragment) OS=Homo sapiens GN=HMGB3 PE=2 SV=1	33.81	1	680		*11.4*
426	Q8N8K9	Uncharacterized protein KIAA1958 OS=Homo sapiens GN=KIAA1958 PE=1 SV=1	33.75	1	1197		*1.1*
	B7ZKW6	KIAA1958 protein OS=Homo sapiens GN=KIAA1958 PE=2 SV=1	33.75	1	1197		*1.1*
427	Q8IWR8	Ribosomal protein L19 (Fragment) OS=Homo sapiens PE=2 SV=1	33.32	1	486		*15.5*
	Q53G49	Ribosomal protein L19 (Fragment) OS=Homo sapiens PE=2 SV=1	33.32	1	486		*15.5*

	P84098	60S ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=1 SV=1	33.32	1	486		*15.5*
	J3QR09	Ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=3 SV=1	33.32	1	486		*15.5*
	J3KTE4	Ribosomal protein L19 OS=Homo sapiens GN=RPL19 PE=3 SV=1	33.32	1	486		*15.5*
428	O15400	Syntaxin-7 OS=Homo sapiens GN=STX7 PE=1 SV=4	33.13	1	779		*4.2*
	B4DH37	cDNA FLJ53760, highly similar to Syntaxin-7 OS=Homo sapiens PE=2 SV=1	33.13	1	779		*4.2*
429	P09936	Ubiquitin carboxyl-terminal hydrolase isozyme L1 OS=Homo sapiens GN=UCHL1 PE=1 SV=2	33.09	1	763		*3.6*
	D6RE83	Ubiquitin carboxyl-terminal hydrolase isozyme L1 OS=Homo sapiens GN=UCHL1 PE=2 SV=1	33.09	1	763		*3.6*
	B2RD14	cDNA, FLJ96414, highly similar to Homo sapiens ubiquitin carboxyl-terminal esterase L1 (ubiquitin thiolesterase) (UCHL1), mRNA OS=Homo sapiens PE=2 SV=1	33.09	1	763		*3.6*
	A6NLJ7	Ubiquitin carboxyl-terminal esterase L1 (Ubiquitin thiolesterase), isoform CRA_a OS=Homo sapiens GN=UCHL1 PE=2 SV=1	33.09	1	763		*3.6*
430	P14854	Cytochrome c oxidase subunit 6B1 OS=Homo sapiens GN=COX6B1 PE=1 SV=2	32.91	1	498		*17.5*
431	P35609	Alpha-actinin-2 OS=Homo sapiens GN=ACTN2 PE=1 SV=1	32.74	1	985		*5.7*
432	Q8WXI7	Mucin-16 OS=Homo sapiens GN=MUC16 PE=1 SV=2	32.62	1	1060		*8.7*
433	M0QZ39	Upstream stimulatory factor 2 (Fragment) OS=Homo sapiens GN=USF2 PE=4 SV=1	32.58	1	800		*14.2*
434	Q7Z3T9	Putative uncharacterized protein DKFZp686J1169 OS=Homo sapiens GN=DKFZp686J1169 PE=2 SV=1	32.52	1	245		*1.3*
	Q7LBX6	Neuropilin 2 OS=Homo sapiens GN=NRP2 PE=2 SV=1	32.52	1	245		*1.3*
	O60462	Neuropilin-2 OS=Homo sapiens GN=NRP2 PE=1 SV=2	32.52	1	245		*1.3*
	F5H2X3	Neuropilin-2 OS=Homo sapiens GN=NRP2 PE=2 SV=1	32.52	1	245		*1.3*
	F5H1G4	Neuropilin-2 OS=Homo sapiens GN=NRP2 PE=2 SV=1	32.52	1	245		*1.3*
	B7ZL68	Neuropilin 2 OS=Homo sapiens GN=NRP2 PE=2 SV=1	32.52	1	245		*1.3*

UniProt Human Protein IDs, *cont.*

Grp Nr.	*Accession Number*	*Protein Name*	*Protein Score*	*Unique PSMs*	*PSM Serial Nrs.*	*Other Grp.*	*% Seq. Cover.*

435	Q15366	Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=1 SV=1	32.52	1	60		*6.9*
	H3BRU6	Poly(rC)-binding protein 2 (Fragment) OS=Homo sapiens GN=PCBP2 PE=4 SV=1	32.52	1	60		*6.9*
	G3V0E8	Poly(RC) binding protein 2, isoform CRA_f OS=Homo sapiens GN=PCBP2 PE=4 SV=1	32.52	1	60		*6.9*
	F8VZX2	Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=2 SV=1	32.52	1	60		*6.9*
	B4DXP5	Poly(rC)-binding protein 2 OS=Homo sapiens GN=PCBP2 PE=2 SV=1	32.52	1	60		*6.9*
	B4DRD7	cDNA FLJ54752, highly similar to Poly(rC)-binding protein 2 OS=Homo sapiens PE=2 SV=1	32.52	1	60		*6.9*
436	Q5U0A0	Proteasome subunit alpha type OS=Homo sapiens PE=2 SV=1	32.47	1	195		*7.9*
	P28066	Proteasome subunit alpha type-5 OS=Homo sapiens GN=PSMA5 PE=1 SV=3	32.47	1	195		*7.9*
437	Q92597	Protein NDRG1 OS=Homo sapiens GN=NDRG1 PE=1 SV=1	32.39	1	674		*3.9*
	Q8N959	cDNA FLJ38330 fis, clone FCBBF3025280, highly similar to NDRG1 PROTEIN OS=Homo sapiens PE=2 SV=1	32.39	1	674		*3.9*
	Q597H1	Transformation-related protein 14 OS=Homo sapiens GN=TRG14 PE=2 SV=1	32.39	1	674		*3.9*
	Q53EU7	N-myc downstream regulated gene 1 variant (Fragment) OS=Homo sapiens PE=2 SV=1	32.39	1	674		*3.9*
	E9PDL6	Protein NDRG1 OS=Homo sapiens GN=NDRG1 PE=2 SV=2	32.39	1	674		*3.9*
	E7ESM1	Protein NDRG1 OS=Homo sapiens GN=NDRG1 PE=2 SV=1	32.39	1	674		*3.9*
	E5RJY1	Protein NDRG1 OS=Homo sapiens GN=NDRG1 PE=2 SV=1	32.39	1	674		*3.9*
	B7Z5Z7	cDNA FLJ53648, highly similar to Protein NDRG1 OS=Homo sapiens PE=2 SV=1	32.39	1	674		*3.9*
	B7Z505	cDNA FLJ53637, highly similar to Protein NDRG1 OS=Homo sapiens PE=2 SV=1	32.39	1	674		*3.9*
	B7Z4H0	cDNA FLJ59927, moderately similar to Protein NDRG1 OS=Homo sapiens PE=2 SV=1	32.39	1	674		*3.9*
438	Q96L21	60S ribosomal protein L10-like OS=Homo sapiens GN=RPL10L PE=1 SV=3	31.68	1	285		*55.8*
	P27635	60S ribosomal protein L10 OS=Homo sapiens GN=RPL10 PE=1 SV=4	31.68	1	285		*55.8*
439	Q99497	Protein DJ-1 OS=Homo sapiens GN=PARK7 PE=1 SV=2	31.35	1	587		*33.1*
	K7ELW0	Protein DJ-1 OS=Homo sapiens GN=PARK7 PE=4 SV=1	31.35	1	587		*33.1*
440	P61812	Transforming growth factor beta-2 OS=Homo sapiens GN=TGFB2 PE=1 SV=1	31.02	1	1127		*4.6*
	B2R7T2	cDNA, FLJ93591, highly similar to Homo sapiens transforming growth factor, beta 2 (TGFB2), mRNA OS=Homo sapiens PE=2 SV=1	31.02	1	1127		*4.6*
441	Q9NRL2	Bromodomain adjacent to zinc finger domain protein 1A OS=Homo sapiens GN=BAZ1A PE=1 SV=2	30.99	1	726		*3.2*

	Q59G54	Bromodomain adjacent to zinc finger domain, 1A isoform b variant (Fragment) OS=Homo sapiens PE=2 SV=1	30.99	1	726		*3.2*
	D3DS96	Bromodomain adjacent to zinc finger domain, 1A, isoform CRA_c OS=Homo sapiens GN=BAZ1A PE=2 SV=1	30.99	1	726		*3.2*
	B3KND8	cDNA FLJ14383 fis, clone HEMBA1002035, highly similar to Bromodomain adjacent to zinc finger domain protein 1A OS=Homo sapiens PE=2 SV=1	30.99	1	726		*3.2*
442	Q53GL5	Isocitrate dehydrogenase [NADP] (Fragment) OS=Homo sapiens PE=2 SV=1	30.95	1	855		*2.5*
	Q13584	Isocitrate dehydrogenase [NADP] OS=Homo sapiens PE=2 SV=1	30.95	1	855		*2.5*
	P48735	Isocitrate dehydrogenase [NADP], mitochondrial OS=Homo sapiens GN=IDH2 PE=1 SV=2	30.95	1	855		*2.5*
	B4DFL2	Isocitrate dehydrogenase [NADP] OS=Homo sapiens GN=IDH2 PE=2 SV=1	30.95	1	855		*2.5*
443	Q96MU7	YTH domain-containing protein 1 OS=Homo sapiens GN=YTHDC1 PE=1 SV=3	30.95	1	767		*2.7*
	J3QR07	YTH domain-containing protein 1 OS=Homo sapiens GN=YTHDC1 PE=4 SV=1	30.95	1	767		*2.7*
444	Q6NUR7	Ezrin OS=Homo sapiens GN=EZR PE=2 SV=1	30.36	1	649		*7.2*
	P15311	Ezrin OS=Homo sapiens GN=EZR PE=1 SV=4	30.36	1	649		*7.2*
	E7EQR4	Ezrin OS=Homo sapiens GN=EZR PE=2 SV=2	30.36	1	649		*7.2*
	B7Z5V2	cDNA FLJ54141, highly similar to Ezrin OS=Homo sapiens PE=2 SV=1	30.36	1	649		*7.2*
	B7Z437	cDNA FLJ53435, highly similar to Ezrin OS=Homo sapiens PE=2 SV=1	30.36	1	649		*7.2*
	B2R6J2	cDNA, FLJ92973, highly similar to Homo sapiens villin 2 (ezrin) (VIL2), mRNA OS=Homo sapiens PE=2 SV=1	30.36	1	649		*7.2*
445	O14974	Protein phosphatase 1 regulatory subunit 12A OS=Homo sapiens GN=PPP1R12A PE=1 SV=1	30.36	1	698		*3.7*
	H0YHI8	Protein phosphatase 1 regulatory subunit 12A (Fragment) OS=Homo sapiens GN=PPP1R12A PE=4 SV=1	30.36	1	698		*3.7*
	B2RAH5	cDNA, FLJ94919, highly similar to Homo sapiens protein phosphatase 1, regulatory (inhibitor) subunit 12A (PPP1R12A), mRNA OS=Homo sapiens PE=2 SV=1	30.36	1	698		*3.7*
446	Q5U077	L-lactate dehydrogenase OS=Homo sapiens GN=LDHB PE=2 SV=1	30.36	1	49		*6.3*
	P07195	L-lactate dehydrogenase B chain OS=Homo sapiens GN=LDHB PE=1 SV=2	30.36	1	49		*6.3*
447	P55060	Exportin-2 OS=Homo sapiens GN=CSE1L PE=1 SV=3	30.10	1	1169		*2.1*
	F8W904	Exportin-2 OS=Homo sapiens GN=CSE1L PE=2 SV=1	30.10	1	1169		*2.1*
	A3RLL6	Cellular apoptosis susceptibility protein variant 2 OS=Homo sapiens GN=CSE1L-2 PE=2 SV=1	30.10	1	1169		*2.1*
448	Q96M42	Putative uncharacterized protein encoded by LINC00479 OS=Homo sapiens GN=LINC00479 PE=5 SV=2	30.10	1	723		*4.9*

449	Q6ZWH5	Serine/threonine-protein kinase Nek10 OS=Homo sapiens GN=NEK10 PE=2 SV=3	30.10	1	400		*5.8*
450	Q9UQM3	Alpha-tubulin (Fragment) OS=Homo sapiens PE=2 SV=1	30.06	1	490		*1.8*
	Q9BQE3	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C PE=1 SV=1	30.06	1	490		*1.8*
	Q71U36	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=1 SV=1	30.06	1	490		*1.8*
	Q53GA7	Tubulin alpha 6 variant (Fragment) OS=Homo sapiens PE=2 SV=1	30.06	1	490		*1.8*
	Q1ZYQ1	Tubulin, alpha 2 OS=Homo sapiens GN=TUBA2 PE=2 SV=1	30.06	1	490		*1.8*
	Q13748	Tubulin alpha-3C/D chain OS=Homo sapiens GN=TUBA3C PE=1 SV=3	30.06	1	490		*1.8*
	P68366	Tubulin alpha-4A chain OS=Homo sapiens GN=TUBA4A PE=1 SV=1	30.06	1	490		*1.8*
	P68363	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B PE=1 SV=1	30.06	1	490		*1.8*
	G3V1U9	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=3 SV=1	30.06	1	490		*1.8*
	F8VXZ4	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A PE=2 SV=1	30.06	1	490		*1.8*
451	Q9UMX0	Ubiquilin-1 OS=Homo sapiens GN=UBQLN1 PE=1 SV=2	29.98	1	731		*2.5*
	B3KNI8	cDNA FLJ14670 fis, clone NT2RP2003272, highly similar to Ubiquilin-1 OS=Homo sapiens PE=2 SV=1	29.98	1	731		*2.5*
	B3KNI2	cDNA FLJ14650 fis, clone NT2RP2002185, highly similar to Ubiquilin-1 OS=Homo sapiens PE=2 SV=1	29.98	1	731		*2.5*
452	P42765	3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=1 SV=2	29.56	1	636		*3.3*
	K7EME0	3-ketoacyl-CoA thiolase, mitochondrial OS=Homo sapiens GN=ACAA2 PE=3 SV=1	29.56	1	636		*3.3*
	B3KNP8	cDNA FLJ30111 fis, clone BNGH42000360, highly similar to 3-ketoacyl-CoA thiolase, mitochondrial (EC 2.3.1.16) OS=Homo sapiens PE=2 SV=1	29.56	1	636		*3.3*
	B2RB23	cDNA, FLJ95265, highly similar to Homo sapiens acetyl-Coenzyme A acyltransferase 2 (mitochondrial 3-oxoacyl-Coenzyme A thiolase) (ACAA2), nuclear gene encoding mitochondrial protein, mRNA OS=Homo sapiens PE=2 SV=1	29.56	1	636		*3.3*
453	E5RGS7	Uncharacterized protein OS=Homo sapiens PE=2 SV=1	29.26	1	993		*7.5*
	B3KPU0	cDNA FLJ32186 fis, clone PLACE6002011, highly similar to PDZ and LIM domain protein 2 OS=Homo sapiens PE=2 SV=1	29.26	1	993		*7.5*
454	Q5SSV3	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 (Fragment) OS=Homo sapiens GN=DDAH2 PE=4 SV=1	29.18	1	876		*8.0*
	Q5SRR8	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 (Fragment) OS=Homo sapiens GN=DDAH2 PE=4 SV=2	29.18	1	876		*8.0*
	O95865	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 OS=Homo sapiens GN=DDAH2 PE=1 SV=1	29.18	1	876		*8.0*

	H0Y7N1	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 (Fragment) OS=Homo sapiens GN=DDAH2 PE=4 SV=1	29.18	1	876		*8.0*
	A3KGN5	N(G),N(G)-dimethylarginine dimethylaminohydrolase 2 (Fragment) OS=Homo sapiens GN=DDAH2 PE=2 SV=1	29.18	1	876		*8.0*
455	O75944	Aconitase (Fragment) OS=Homo sapiens GN=ACON PE=2 SV=1	28.54	1	76		*5.5*
456	Q86W61	VCAN protein OS=Homo sapiens GN=VCAN PE=2 SV=1	28.37	1	451		*12.5*
	Q59FG9	Chondroitin sulfate proteoglycan 2 (Versican) variant (Fragment) OS=Homo sapiens PE=2 SV=1	28.37	1	451		*12.5*
	P13611	Versican core protein OS=Homo sapiens GN=VCAN PE=1 SV=3	28.37	1	451		*35.9*
	E9PF17	Versican core protein OS=Homo sapiens GN=VCAN PE=2 SV=2	28.37	1	451		*12.5*
	D6RGZ6	Versican core protein (Fragment) OS=Homo sapiens GN=VCAN PE=2 SV=1	28.37	1	451		*61.7*
457	Q71V99	Peptidyl-prolyl cis-trans isomerase OS=Homo sapiens PE=2 SV=1	28.19	1	892		*35.4*
458	Q9UNX3	60S ribosomal protein L26-like 1 OS=Homo sapiens GN=RPL26L1 PE=1 SV=1	28.01	1	659		*15.2*
	Q6IBH6	RPL26 protein OS=Homo sapiens GN=RPL26 PE=2 SV=1	28.01	1	659		*15.2*
	P61254	60S ribosomal protein L26 OS=Homo sapiens GN=RPL26 PE=1 SV=1	28.01	1	659		*15.2*
	J3QRI7	60S ribosomal protein L26 (Fragment) OS=Homo sapiens GN=RPL26 PE=4 SV=1	28.01	1	659		*15.2*
	J3QQV1	60S ribosomal protein L26 OS=Homo sapiens GN=RPL26 PE=4 SV=1	28.01	1	659		*15.2*
	J3QQQ9	KRAB-A domain-containing protein 2 OS=Homo sapiens GN=KRBA2 PE=4 SV=1	28.01	1	659		*15.2*
	J3KTJ8	60S ribosomal protein L26 (Fragment) OS=Homo sapiens GN=RPL26 PE=4 SV=1	28.01	1	659		*15.2*
	E5RIT6	60S ribosomal protein L26-like 1 (Fragment) OS=Homo sapiens GN=RPL26L1 PE=2 SV=1	28.01	1	659		*15.2*
459	Q13765	Nascent polypeptide-associated complex subunit alpha OS=Homo sapiens GN=NACA PE=1 SV=1	27.94	1	797		*5.2*
	H0YHX9	Nascent polypeptide-associated complex subunit alpha (Fragment) OS=Homo sapiens GN=NACA PE=2 SV=1	27.94	1	797		*5.2*
	F8W1N5	Nascent polypeptide-associated complex subunit alpha (Fragment) OS=Homo sapiens GN=NACA PE=2 SV=1	27.94	1	797		*5.2*
	F8W0W4	Nascent polypeptide-associated complex subunit alpha (Fragment) OS=Homo sapiens GN=NACA PE=2 SV=1	27.94	1	797		*5.2*
	F8VZJ2	Nascent polypeptide-associated complex subunit alpha OS=Homo sapiens GN=NACA PE=2 SV=1	27.94	1	797		*5.2*
	F8VZ58	Nascent polypeptide-associated complex subunit alpha (Fragment) OS=Homo sapiens GN=NACA PE=2 SV=1	27.94	1	797		*5.2*
	F8VNW4	Nascent polypeptide-associated complex subunit alpha (Fragment) OS=Homo sapiens GN=NACA PE=2 SV=1	27.94	1	797		*5.2*

	E9PAV3	Nascent polypeptide-associated complex subunit alpha OS=Homo sapiens GN=NACA PE=2 SV=1	27.94	1	797		*5.2*
	B2R4P8	HCG2016482, isoform CRA_b OS=Homo sapiens GN=hCG_2016482 PE=2 SV=1	27.94	1	797		*5.2*

UniProt Human Protein IDs, *cont.*

Grp Nr.	*Accession Number*	*Protein Name*	*Protein Score*	*Unique PSMs*	*PSM Serial Nrs.*	*Other Grp.*	*% Seq. Cover.*
460	O00479	High mobility group nucleosome-binding domain-containing protein 4 OS=Homo sapiens GN=HMGN4 PE=1 SV=3	27.76	1	988		*37.8*
461	Q08380	Galectin-3-binding protein OS=Homo sapiens GN=LGALS3BP PE=1 SV=1	27.47	1	711		*4.7*
	B4DVE1	cDNA FLJ53478, highly similar to Galectin-3-binding protein OS=Homo sapiens PE=2 SV=1	27.47	1	711		*4.7*
462	P25398	40S ribosomal protein S12 OS=Homo sapiens GN=RPS12 PE=1 SV=3	27.27	1	544		*18.9*
463	Q07654	Trefoil factor 3 OS=Homo sapiens GN=TFF3 PE=1 SV=1	27.12	1	331		*28.8*
464	Q9UMS4	Pre-mRNA-processing factor 19 OS=Homo sapiens GN=PRPF19 PE=1 SV=1	26.26	1	32		*6.0*
	F5H2I0	Pre-mRNA-processing factor 19 (Fragment) OS=Homo sapiens GN=PRPF19 PE=2 SV=1	26.26	1	32		*6.0*
	F5GY56	Pre-mRNA-processing factor 19 (Fragment) OS=Homo sapiens GN=PRPF19 PE=2 SV=1	26.26	1	32		*6.0*
465	Q7Z434	Mitochondrial antiviral-signaling protein OS=Homo sapiens GN=MAVS PE=1 SV=2	26.19	1	432		*2.4*
466	Q96T88	E3 ubiquitin-protein ligase UHRF1 OS=Homo sapiens GN=UHRF1 PE=1 SV=1	26.16	1	48		*3.4*
467	P60866	40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=1 SV=1	25.92	1	923		*18.8*
	G3XAN0	40S ribosomal protein S20 OS=Homo sapiens GN=RPS20 PE=4 SV=1	25.92	1	923		*18.8*
468	C9JB55	Serotransferrin (Fragment) OS=Homo sapiens GN=TF PE=2 SV=1	25.77	1	1131		*31.6*
469	F6TR96	TRIO and F-actin-binding protein (Fragment) OS=Homo sapiens GN=TRIOBP PE=2 SV=1	25.67	1	494		*4.2*
470	Q59H49	Polypyrimidine tract-binding protein 1 isoform c variant (Fragment) OS=Homo sapiens PE=2 SV=1	25.65	1	1141		*11.4*

	P26599	Polypyrimidine tract-binding protein 1 OS=Homo sapiens GN=PTBP1 PE=1 SV=1	25.65	1	1141		*11.4*
	K7ES59	Polypyrimidine tract-binding protein 1 (Fragment) OS=Homo sapiens GN=PTBP1 PE=4 SV=1	25.65	1	1141		*11.4*
	K7ELW5	Polypyrimidine tract-binding protein 1 (Fragment) OS=Homo sapiens GN=PTBP1 PE=4 SV=1	25.65	1	1141		*11.4*
	K7EKJ7	Polypyrimidine tract-binding protein 1 (Fragment) OS=Homo sapiens GN=PTBP1 PE=4 SV=1	25.65	1	1141		*11.4*
471	Q13151	Heterogeneous nuclear ribonucleoprotein A0 OS=Homo sapiens GN=HNRNPA0 PE=1 SV=1	25.35	1	218		*7.9*
472	O75822	Eukaryotic translation initiation factor 3 subunit J OS=Homo sapiens GN=EIF3J PE=1 SV=2	25.21	1	964		*3.9*
	F5H425	Eukaryotic translation initiation factor 3 subunit J OS=Homo sapiens GN=EIF3J PE=2 SV=1	25.21	1	964		*3.9*
	B4DUI3	Eukaryotic translation initiation factor 3 subunit J OS=Homo sapiens GN=EIF3J PE=2 SV=1	25.21	1	964		*3.9*
473	E9PD68	Dihydropyrimidinase-related protein 1 OS=Homo sapiens GN=CRMP1 PE=2 SV=1	25.17	1	653		*8.4*
474	O95750	Fibroblast growth factor 19 OS=Homo sapiens GN=FGF19 PE=1 SV=1	25.17	1	565		*7.4*
475	A5A3E0	POTE ankyrin domain family member F OS=Homo sapiens GN=POTEF PE=1 SV=2	24.99	1	883		*4.4*
476	P41219	Peripherin OS=Homo sapiens GN=PRPH PE=1 SV=2	24.81	1	593		*29.6*
	B3KWQ6	cDNA FLJ43599 fis, clone SMINT2017781, highly similar to PERIPHERIN OS=Homo sapiens PE=2 SV=1	24.81	1	593		*6.0*
477	P16070	CD44 antigen OS=Homo sapiens GN=CD44 PE=1 SV=3	24.71	1	174		*4.2*
	H0YDX6	CD44 antigen (Fragment) OS=Homo sapiens GN=CD44 PE=4 SV=1	24.71	1	174		*4.2*
	H0YDW7	CD44 antigen (Fragment) OS=Homo sapiens GN=CD44 PE=2 SV=1	24.71	1	174		*4.2*
	H0YD17	CD44 antigen (Fragment) OS=Homo sapiens GN=CD44 PE=4 SV=1	24.71	1	174		*4.2*
	H0YD13	CD44 antigen (Fragment) OS=Homo sapiens GN=CD44 PE=2 SV=1	24.71	1	174		*4.2*
	H0YCV9	CD44 antigen (Fragment) OS=Homo sapiens GN=CD44 PE=2 SV=1	24.71	1	174		*4.2*
	H0Y5E4	CD44 antigen (Fragment) OS=Homo sapiens GN=CD44 PE=4 SV=1	24.71	1	174		*4.2*
	H0Y2P0	CD44 antigen (Fragment) OS=Homo sapiens GN=CD44 PE=2 SV=1	24.71	1	174		*4.2*
	E7EPC6	CD44 antigen OS=Homo sapiens GN=CD44 PE=2 SV=2	24.71	1	174		*4.2*
	C1PHC4	CD44 molecule (Fragment) OS=Homo sapiens GN=CD44 PE=2 SV=1	24.71	1	174		*4.2*
478	I6L997	GRIA2 protein (Fragment) OS=Homo sapiens GN=GRIA2 PE=2 SV=1	24.70	1	1128		*0.8*

479	O14745	Na(+)/H(+) exchange regulatory cofactor NHE-RF1 OS=Homo sapiens GN=SLC9A3R1 PE=1 SV=4	24.68	1	662		*2.8*
	J3QRP6	Na(+)/H(+) exchange regulatory cofactor NHE-RF1 (Fragment) OS=Homo sapiens GN=SLC9A3R1 PE=4 SV=1	24.68	1	662		*2.8*
	B2R6A3	cDNA, FLJ92860, highly similar to Homo sapiens solute carrier family 9 (sodium/hydrogen exchanger), member 3 regulator 1 (SLC9A3R1), mRNA OS=Homo sapiens PE=2 SV=1	24.68	1	662		*2.8*
480	O75367	Core histone macro-H2A.1 OS=Homo sapiens GN=H2AFY PE=1 SV=4	24.59	1	453		*8.3*
481	Q6PKH8	ANP32A protein (Fragment) OS=Homo sapiens GN=ANP32A PE=2 SV=1	24.52	1	599		*7.9*
	Q1AHP8	Hepatopoietin PCn127 OS=Homo sapiens PE=2 SV=1	24.52	1	599		*7.9*
	Q08AJ6	ANP32A protein OS=Homo sapiens GN=ANP32A PE=2 SV=1	24.52	1	599		*7.9*
	P39687	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens GN=ANP32A PE=1 SV=1	24.52	1	599		*7.9*
	H0YN26	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Homo sapiens GN=ANP32A PE=2 SV=1	24.52	1	599		*7.9*
482	Q53GS9	U4/U6.U5 tri-snRNP-associated protein 2 OS=Homo sapiens GN=USP39 PE=1 SV=2	24.49	1	503		*2.3*
	G5E9H0	U4/U6.U5 tri-snRNP-associated protein 2 OS=Homo sapiens GN=USP39 PE=4 SV=1	24.49	1	503		*2.3*
	F8WC91	U4/U6.U5 tri-snRNP-associated protein 2 OS=Homo sapiens GN=USP39 PE=2 SV=1	24.49	1	503		*2.3*
	B9A018	U4/U6.U5 tri-snRNP-associated protein 2 OS=Homo sapiens GN=USP39 PE=2 SV=1	24.49	1	503		*2.3*
	B8ZZD1	U4/U6.U5 tri-snRNP-associated protein 2 OS=Homo sapiens GN=USP39 PE=2 SV=1	24.49	1	503		*2.3*
	B3KM40	cDNA FLJ10185 fis, clone HEMBA1004509, highly similar to U4/U6.U5 tri-snRNP-associated protein 2 OS=Homo sapiens PE=2 SV=1	24.49	1	503		*2.3*
483	Q6IAX6	3~-phosphoadenosine 5~-phosphosulfate synthase 1 OS=Homo sapiens GN=PAPSS1 PE=2 SV=1	24.38	1	454		*8.3*
	O43252	Bifunctional 3~-phosphoadenosine 5~-phosphosulfate synthase 1 OS=Homo sapiens GN=PAPSS1 PE=1 SV=2	24.38	1	454		*34.8*
484	Q8TEA6	CDNA FLJ23731 fis, clone HEP14545 OS=Homo sapiens PE=2 SV=1	24.36	1	288		*3.5*
	Q8NFH3	Nucleoporin Nup43 OS=Homo sapiens GN=NUP43 PE=1 SV=1	24.36	1	288		*3.5*
	B3KTT0	cDNA FLJ38675 fis, clone IMR322000243, highly similar to Nucleoporin Nup43 OS=Homo sapiens PE=2 SV=1	24.36	1	288		*3.5*
	A0PJK4	NUP43 protein (Fragment) OS=Homo sapiens GN=NUP43 PE=2 SV=1	24.36	1	288		*3.5*
485	Q15459	Splicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1 PE=1 SV=1	23.99	1	133		*1.7*

	E9PAW1	Splicing factor 3A subunit 1 OS=Homo sapiens GN=SF3A1 PE=2 SV=1	23.99	1	133		*1.7*
	B4E091	cDNA FLJ55438, highly similar to Splicing factor 3 subunit 1 OS=Homo sapiens PE=2 SV=1	23.99	1	133		*1.7*
486	Q96PU4	E3 ubiquitin-protein ligase UHRF2 OS=Homo sapiens GN=UHRF2 PE=1 SV=1	23.98	1	749		*12.6*
487	P55145	Mesencephalic astrocyte-derived neurotrophic factor OS=Homo sapiens GN=MANF PE=1 SV=3	23.58	1	272		*11.3*
	H7C2D6	Mesencephalic astrocyte-derived neurotrophic factor (Fragment) OS=Homo sapiens GN=MANF PE=4 SV=1	23.58	1	272		*11.3*
	A8K878	cDNA FLJ77177, highly similar to Homo sapiens arginine-rich, mutated in early stage tumors (ARMET), mRNA OS=Homo sapiens PE=2 SV=1	23.58	1	272		*11.3*
488	P62917	60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=1 SV=2	23.49	1	131		*36.8*
	G3V1A1	60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=4 SV=1	23.49	1	131		*36.8*
	E9PKZ0	60S ribosomal protein L8 OS=Homo sapiens GN=RPL8 PE=4 SV=1	23.49	1	131		*36.8*
	B4DVG7	cDNA FLJ53750, highly similar to 60S ribosomal protein L8 OS=Homo sapiens PE=2 SV=1	23.49	1	131		*36.8*
489	Q15843	NEDD8 OS=Homo sapiens GN=NEDD8 PE=1 SV=1	23.11	1	588		*18.0*
	F8VSA6	NEDD8 OS=Homo sapiens GN=NEDD8 PE=4 SV=1	23.11	1	588		*18.0*
	E9PS38	Protein NEDD8-MDP1 OS=Homo sapiens GN=NEDD8-MDP1 PE=2 SV=1	23.11	1	588		*18.0*
	E9PL57	Protein NEDD8-MDP1 (Fragment) OS=Homo sapiens GN=NEDD8-MDP1 PE=2 SV=1	23.11	1	588		*18.0*
490	Q8WWM7	Ataxin-2-like protein OS=Homo sapiens GN=ATXN2L PE=1 SV=2	22.63	1	475		*41.1*
	Q63ZY4	ATXN2L protein OS=Homo sapiens GN=ATXN2L PE=2 SV=1	22.63	1	475		*41.1*
	H3BUF6	Ataxin-2-like protein OS=Homo sapiens GN=ATXN2L PE=2 SV=1	22.63	1	475		*12.7*
491	Q6IAW5	CALU protein OS=Homo sapiens GN=CALU PE=2 SV=1	22.56	1	951		*4.1*
	O43852	Calumenin OS=Homo sapiens GN=CALU PE=1 SV=2	22.56	1	951		*4.1*
	B3KQF5	cDNA FLJ90381 fis, clone NT2RP2005035, highly similar to Calumenin OS=Homo sapiens PE=2 SV=1	22.56	1	951		*4.1*
	B3KNG6	cDNA FLJ14554 fis, clone NT2RM2001839, highly similar to Calumenin OS=Homo sapiens PE=2 SV=1	22.56	1	951		*4.1*
492	Q15819	Ubiquitin-conjugating enzyme E2 variant 2 OS=Homo sapiens GN=UBE2V2 PE=1 SV=4	22.50	1	955		*22.1*
	H0YBP9	Ubiquitin-conjugating enzyme E2 variant 2 (Fragment) OS=Homo sapiens GN=UBE2V2 PE=4 SV=1	22.50	1	955		*22.1*
	G3V113	Ubiquitin-conjugating enzyme E2 variant 2 OS=Homo sapiens GN=UBE2V2 PE=4 SV=1	22.50	1	955		*22.1*
	A0M8W4	Ubiquitin-conjugating enzyme E2 variant 2 OS=Homo sapiens GN=UBE2V2 PE=2 SV=1	22.50	1	955		*22.1*

493	B7Z6N2	cDNA FLJ56154, highly similar to Gelsolin OS=Homo sapiens PE=2 SV=1	22.47	1	419		*18.4*
494	P27824	Calnexin OS=Homo sapiens GN=CANX PE=1 SV=2	21.87	1	404		*1.9*
	B4E2T8	Calnexin OS=Homo sapiens GN=CANX PE=2 SV=1	21.87	1	404		*1.9*
	B4DGP8	Calnexin OS=Homo sapiens GN=CANX PE=2 SV=1	21.87	1	404		*1.9*
495	Q14151	Scaffold attachment factor B2 OS=Homo sapiens GN=SAFB2 PE=1 SV=1	21.56	1	55		*4.5*
496	Q8N355	IGL@ protein OS=Homo sapiens GN=IGL@ PE=2 SV=1	21.26	1	950		*11.1*
497	Q59GL1	Synaptotagmin binding, cytoplasmic RNA interacting protein variant (Fragment) OS=Homo sapiens PE=2 SV=1	20.80	1	22		*6.4*
	Q05CK9	SYNCRIP protein (Fragment) OS=Homo sapiens GN=SYNCRIP PE=2 SV=1	20.80	1	22		*6.4*
	O60506	Heterogeneous nuclear ribonucleoprotein Q OS=Homo sapiens GN=SYNCRIP PE=1 SV=2	20.80	1	22		*6.4*
	B7Z645	Synaptotagmin binding, cytoplasmic RNA interacting protein, isoform CRA_b OS=Homo sapiens GN=SYNCRIP PE=2 SV=1	20.80	1	22		*6.4*
	B2R8Z8	cDNA, FLJ94136, highly similar to Homo sapiens synaptotagmin binding, cytoplasmic RNA interacting protein (SYNCRIP), mRNA OS=Homo sapiens PE=2 SV=1	20.80	1	22		*6.4*
498	Q9BTQ7	Similar to ribosomal protein L23 (Fragment) OS=Homo sapiens PE=2 SV=1	20.75	1	620		*13.4*
	P62829	60S ribosomal protein L23 OS=Homo sapiens GN=RPL23 PE=1 SV=1	20.75	1	620		*13.4*
499	H0YB22	40S ribosomal protein S14 (Fragment) OS=Homo sapiens GN=RPS14 PE=4 SV=1	20.54	1	384		*23.3*
500	Q13813	Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=1 SV=3	20.22	1	885		*4.6*
	B4DGT1	cDNA FLJ59116, highly similar to Spectrin alpha chain, brain OS=Homo sapiens PE=2 SV=1	20.22	1	885		*4.6*
	A6NG51	Spectrin alpha chain, non-erythrocytic 1 OS=Homo sapiens GN=SPTAN1 PE=2 SV=2	20.22	1	885		*4.6*
501	F5H0B0	Tumor protein D52 OS=Homo sapiens GN=TPD52 PE=2 SV=1	20.04	1	1021		*14.7*
	A5Y5A3	PC1/MRPS28 fusion protein OS=Homo sapiens PE=2 SV=1	20.04	1	1021		*14.7*

Note: Number of proteins per group ≤ 10.

Group Nr.

By the rule of parsimony, we have gathered all proteins sharing the same identified peptides into a single group.

Accession Nr.

The accession number from the searched database (DB).

Protein Name

The protein name in the DB.

Protein Score

Sum of the contributing peptide scores.

NOTE: This score can only be used to support the identification of **one** protein per group.
Unique PSMs.

The number of unique peptide-spectrum matches that contribute to the protein assignment.
PSM Serial Nrs.

Sequential number of assigned peptide (in the following table.)
Other Grp.

If the protein is assigned to another group, that (those) group number(s).
% Seq. Cover.

Percent sequence coverage of this protein.

Assigned Peptides

#	*Sequence*	*PTM Site*	*Nr. Scans*	*Mascot Score*	*Expectation*	*Isolated Mass*	*Delta Mass*	*Charge State*	*Matched Ions*	*Scan Nr.*
1	R.GELAIKDANAK.L		2	29.900	0.18	565.32	2.7	2	'8/20	2222
2	R.IVLQIDNAR.L		3	36.330	0.018	521.31	-2.2	2	'7/16	3317
3	K.CSTSSLLEACTFRRP.-		8	35.450	0.033	595.62	0.6	3	'7/28	4184
4	K.QAASGLVGQENAR.E		1	64.290	5.4e-005	650.83	0.1	2	'10/24	1903
5	K.DCHLAQVPSHTVVAR.S		12	60.080	0.00015	845.43	-2.5	2	'21/28	3175
6	R.LQNALNEQR.V		2	51.060	0.00082	543.29	0.2	2	'8/16	1707
7	R.QINWTVLYR.R		1	44.280	0.0055	596.83	1.1	2	'6/16	5138
8	R.SLGQNPTEAELR.D		1	62.950	6.2e-005	657.84	-0.8	2	'7/22	2690
9	R.NLLSVAYKNVVGGQR.A		2	87.270	1.7e-007	809.46	0.6	2	'10/28	5568
10	R.QTTQDAPEEVR.N		1	38.190	0.014	637.30	0.5	2	'6/20	1247
11	R.HQGVMVGMGQKDSYVGDEAQSKR.G	0.00001001000000000000000.0	3	41.680	0.017	635.55	-1.1	4	'22/44	3160
12	R.GDVTAEEAAGASPAK.A		1	63.940	2.9e-005	687.33	-4.6	2	'10/28	1657
13	R.YCAGWADKIQGR.T		1	38.830	0.014	475.56	-0.6	3	'13/22	3903
14	R.SGRGGNFGFGDSR.G		1	24.260	0.26	438.54	0.5	3	'10/24	3295
15	R.LSKEEVER.M		2	39.760	0.018	495.27	2.3	2	'6/14	1673

16	R.IINEPTAAAIAYGLDKK.V		1	26.130	0.23	596.67	-0.7	3	'12/32	4557
17	K.LGNYAGAVQDCER.A		1	60.840	5.7e-005	726.83	-1.2	2	'9/24	2501
18	K.YQIDPDACFSAK.V		1	37.540	0.01	707.82	-2.2	2	'10/22	3626
19	K.EACVHKILR.Q		2	28.150	0.2	375.88	-3.2	3	'6/16	3433
20	K.FFVGGNWK.M		3	23.770	0.37	477.75	0.2	2	'7/14	4485
21	K.RVLIAAHGNSLR.G		1	20.430	0.37	436.26	3.2	3	'9/22	3952
22	K.VADSSKGPDEAKIK.A		1	20.800	1.5	361.95	0.0	4	'17/26	2027
23	K.INHCRFDEFFSEGCAPGSK.K		2	19.750	0.31	565.25	-4.5	4	'13/36	5532
24	K.AAATPESQEPQAK.G		1	41.210	0.008	664.33	1.6	2	'9/24	1037
25	K.SRLEQEIATYR.S		1	23.390	0.67	455.91	2.4	3	'13/20	4374
26	K.AADPPAENSSAPEAEQGGAE.-		1	80.720	1.8e-007	949.41	0.0	2	'21/38	1661
27	R.LVQGSILKK.V		1	30.170	0.029	329.22	-1.0	3	'6/16	2909
28	K.STELLIR.K		2	37.120	0.031	416.25	0.7	2	'10/12	3008
29	R.RVLQALEGLK.M		1	54.960	0.00015	563.85	2.4	2	'6/18	4991
30	K.EDLPAENGETK.T		1	52.400	0.00028	601.78	-1.8	2	'7/20	1415
31	R.GGNFGFGDSR.G		1	47.870	0.00096	507.23	-0.9	2	'7/18	2942
32	R.QELSHALYQHDAACR.V		1	26.260	0.2	450.46	-0.1	4	'7/28	3457
33	K.IKTLFPLIEAK.K		1	31.710	0.013	424.94	-1.0	3	'6/20	5637
34	R.TLEGELHDLRGQVAK.L		1	26.060	0.33	555.97	2.6	3	'9/28	4797
35	K.VVFEQTK.V		3	24.640	0.48	425.74	0.1	2	'5/12	1847
36	K.DGGAWGTEQR.E		1	44.070	0.0014	538.74	0.2	2	'8/18	1872
37	R.VDCDQHSDIAQR.Y		2	70.990	3.8e-006	722.32	0.8	2	'15/22	1489
38	R.LELQGPR.G		1	34.040	0.029	406.73	-0.2	2	'6/12	2239
39	K.CKAEHDQLLLNYAK.K		1	40.830	0.012	568.29	0.9	3	'18/26	4816
40	R.ARQLEEELR.T		1	35.610	0.076	381.88	-0.2	3	'9/16	2982
41	R.TSNEVQYDQR.L		1	49.720	0.00058	620.28	-2.0	2	'6/18	1199
42	K.TLGDFAAEYAK.S		1	56.270	0.00032	593.29	-3.3	2	'7/20	4110
43	R.AQYDELAR.K		2	36.760	0.023	483.24	-1.1	2	'6/14	2118
44	K.EVYQQQQYGSGGR.G		1	52.970	0.0004	750.35	1.9	2	'9/24	1669
45	R.LGSQLEASAH.-		1	63.740	3.7e-005	506.76	-2.1	2	'9/18	1871
46	R.SGVNSELVKR.I		2	43.620	0.0079	363.54	-0.3	3	'12/18	2212
47	R.STGKGIVEFASKPAAR.K		1	29.880	0.12	405.48	0.2	4	'12/30	3812
48	R.TAEQSCDQKLTNTNR.A		1	26.160	0.22	589.28	-0.5	3	'15/28	1548
49	R.GLTSVINQK.L		1	30.360	0.15	480.28	3.2	2	'5/16	2698
50	K.TSTSPPPEKSGDEGSEDEAPSGED.-		2	21.370	0.054	1202.99	-0.7	2	'12/46	1424
51	R.KQSLGELIGTLNAAK.V		2	30.550	0.069	514.97	0.3	3	'8/28	5464
52	R.CLYASVLTAQPR.L		1	55.540	0.00042	689.86	2.6	2	'9/22	4160

53	R.NLLSVAYKNVVGGRR.S		2	29.260	0.073	549.32	0.1	3	'16/28	5644
54	R.KNEPIIK.V		2	34.060	0.028	421.26	0.2	2	'6/12	2406
55	K.DQDELKPGPTNR.S		1	21.560	0.78	457.23	0.3	3	'5/22	1753
56	R.LNLQTGER.E		1	39.680	0.02	465.75	-0.3	2	'7/14	1942
57	K.DLLFKDSAHGFLK.V		2	45.220	0.0044	497.60	-1.0	3	'8/24	5502
58	R.AVQFTEEK.F		1	41.390	0.0091	476.24	1.5	2	'7/14	1755
59	K.GPSSVEDIK.A		1	52.650	0.00077	466.24	-4.8	2	'7/16	1677
60	K.IANPVEGSTDR.Q		1	32.520	0.065	579.79	2.2	2	'8/20	1954
61	R.AALPEGLPEASR.L		1	36.580	0.035	605.83	1.1	2	'9/22	3174
62	R.IGGNEGIDVPIPR.F		1	29.170	0.17	668.86	-5.9	2	'10/24	4132
63	K.ADDGRPFPQVIK.S		1	28.110	0.25	448.24	0.8	3	'20/22	3726
64	R.ISISTSGGSFR.N		1	51.560	0.00087	556.29	-0.1	2	'9/20	3061
65	K.KLNVTEQEKIDK.L		2	46.290	0.0032	482.27	-0.4	3	'9/22	2742
66	M.PSKGPLQSVQVFGR.K		1	36.140	0.03	500.62	-0.6	3	'5/26	4855
67	R.AAEDDEDDDVDTQKQKTDEDD.-		3	75.810	2.2e-007	799.66	15.0	3	'12/40	1356
68	M.GKVKVGVNGFGR.I		1	21.890	0.46	406.58	-0.2	3	'6/22	3607
69	M.GVQVETISPGDGR.T		1	64.720	4.4e-005	657.84	0.5	2	'10/24	2510
70	R.IEEELGDEAR.F		1	50.220	0.00064	580.77	-0.3	2	'8/18	2058
71	K.TLNNKFASFIDKVR.F		14	42.060	0.0061	551.64	0.1	3	'15/26	5602
72	K.YNQLLR.I		2	26.510	0.34	403.73	0.5	2	'4/10	2340
73	R.IINEPTAAAIAYGLDKR.E		1	35.720	0.028	606.00	-0.6	3	'15/32	4702
74	R.ESLSEEEAQK.M		1	44.480	0.0027	575.27	-0.7	2	'8/18	1214
75	R.ASAVSELSPR.E		1	74.160	7.9e-006	508.77	-1.1	2	'9/18	2327
76	K.HPNGTQETILLNHTFNETQIEWFR.A		2	28.540	0.16	732.11	0.5	4	'31/46	6197
77	K.TIDDLEDK.L		4	24.330	0.67	474.73	0.1	2	'4/14	1978
78	K.VFLENVIR.D		1	48.610	0.0014	495.29	1.3	2	'7/14	4715
79	K.NPDPWAK.N		2	25.140	0.23	414.21	0.2	2	'5/12	2359
80	K.SNEEGSEEKGPEVR.E		2	63.710	2.5e-005	773.85	1.2	2	'9/26	1472
81	K.ELGITALHIK.L		4	20.000	0.43	365.56	0.3	3	'11/18	4558
82	R.DTDTGALLFIGK.I		1	80.210	1.4e-006	625.84	-0.1	2	'17/22	5259
83	K.DLEEAEEYKEAR.L		1	72.340	5.5e-006	741.34	-0.6	2	'9/22	2412
84	K.VSELKEELK.K		1	27.860	0.27	358.87	-0.5	3	'9/16	2828
85	R.QSSATSSFGGLGGGSVR.F		1	125.830	3.6e-011	777.88	-0.3	2	'12/32	3080
86	K.ADGIVSKNF.-		1	46.350	0.0033	475.75	0.4	2	'8/16	2957
87	K.DSYSSRDYPSSR.D		1	28.590	0.047	473.88	0.1	3	'11/22	1496
88	R.VAPEEHPVLLTEAPLNPK.A		2	37.290	0.018	652.03	-0.9	3	'16/34	4676
89	K.YGTDLSR.G		2	38.750	0.0096	406.20	0.7	2	'6/12	1483

90	K.NVLINKDIR.C		1	19.980	0.79	362.22	0.8	3	'7/16	3204
91	K.ALAAGGYDVEKNNSR.I		2	97.390	2.8e-008	782.89	-0.4	2	'12/28	2496
92	K.GAEAANVTGPGGVPVQGSK.Y		1	106.060	4.7e-009	848.44	-1.2	2	'17/36	2324
93	K.AVIQHFQEK.V		1	20.170	1.2	367.20	1.0	3	'11/16	2785
94	R.ILENEKDLEEAEEYK.E		1	43.640	0.0051	617.96	-3.6	3	'8/28	3679
95	K.ESEAVEWQQK.A		1	43.250	0.0037	617.29	-3.5	2	'6/18	2218
96	R.VEFPR.S		1	26.110	0.42	324.18	0.2	2	'4/8	2207
97	K.KSCHTAVGR.T		2	35.950	0.025	339.17	-0.6	3	'8/16	1710
98	K.CAQGCICKGTSDKCSCCA.-		1	32.830	0.00052	708.27	-0.3	3	'21/34	2071
99	R.VEFPR.T		1	26.110	0.42	324.18	0.2	2	'4/8	2207
100	R.VADLTGIR.D		1	36.590	0.044	422.74	-12.7	2	'4/14	1850
101	K.EVDYSGLR.V		1	37.160	0.034	469.73	0.0	2	'6/14	2409
102	R.EGTCPEAPTDECKPVKWCALSHHER.L		2	28.720	0.096	749.34	-0.9	4	'19/48	4728
103	R.ISCTIANR.C		1	48.130	0.0028	467.74	-0.6	2	'7/14	1519
104	K.IKSVGGACVLVA.-		1	38.490	0.021	587.34	0.3	2	'8/22	3808
105	R.LKCDEWSVNSVGK.I		6	73.100	7.4e-006	761.37	-0.4	2	'10/24	3345
106	K.CDSSPDSAEDVRK.V		2	46.740	0.0004	489.21	-0.1	3	'16/24	1162
107	K.TIDDLEETLASAK.E		1	89.820	1.4e-007	703.36	-1.4	2	'11/24	4733
108	R.TKSTGGAPTFNVTVTK.T		1	41.170	0.013	536.96	1.2	3	'9/30	3134
109	R.DGYGGSRDSYSSSR.S		1	45.120	0.00063	498.55	0.3	3	'15/26	1561
110	K.KALAAAGYDVEKNNSR.I		2	65.350	4.9e-005	569.63	0.2	3	'20/30	2979
111	R.CKELGITALHIK.L		2	28.470	0.11	346.45	-0.7	4	'11/22	4745
112	K.CDSSPDSAEDVR.K		2	78.710	1.9e-007	669.27	4.0	2	'9/22	1205
113	R.AFFSEVER.R		1	52.100	0.00046	492.74	0.9	2	'7/14	3759
114	R.ELEEISERLEEAGGATSVQIEMNK.K	0.000000000000000000000100.0	4	70.510	8.9e-006	893.43	-2.0	3	'26/46	5056
115	K.RASGQAFELILSPR.S		1	37.230	0.024	515.62	-1.1	3	'10/26	5386
116	R.VNQAIWLLCTGAR.E		1	59.620	0.00018	751.40	-2.8	2	'8/24	5332
117	K.AALEEVER.L		1	45.770	0.0042	458.74	0.0	2	'7/14	1958
118	K.LHDRNTYEKYLGEEYVK.A		6	36.750	0.03	719.69	-0.6	3	'22/32	5039
119	K.TIDDLEEK.L		2	34.760	0.048	481.74	0.4	2	'6/14	1979
120	R.DAIAQAVR.G		2	57.210	0.00023	422.24	-0.1	2	'6/14	1977
121	K.QSTDEEVTSLAK.S		1	83.960	5.3e-007	654.32	6.5	2	'9/22	2445
122	K.SQIPLSK.I		1	22.150	1.3	386.73	1.0	2	'4/12	1940
123	K.YEELQSLAGKHGDDLRR.T		2	22.030	0.95	497.51	0.8	4	'17/32	4116
124	K.LLSLTQAK.E		1	30.170	0.069	437.28	13.6	2	'4/14	2911

125	K.DAALATALGDKK.S		1	60.030	0.0003	587.33	-0.9	2	'8/22	2879
126	K.LSELLR.Y		1	29.590	0.25	365.73	0.3	2	'4/10	2851
127	R.VLQALEGLK.M		1	49.400	0.00084	485.80	-2.3	2	'7/16	4052
128	R.EYEAALNSK.D		1	56.490	0.00024	512.75	-0.6	2	'7/16	1622
129	K.DSGFQMNQLR.G		3	56.880	0.00016	598.28	-3.1	2	'8/18	3468
130	R.RYQKSTELLIR.K		2	41.470	0.0043	469.61	-0.6	3	'6/20	4454
131	K.GIVKDIIHDPGRGAPLAK.V		1	23.490	0.21	465.02	0.6	4	'18/34	5684
132	R.QSVFPFESGKPFK.I		1	41.050	0.011	499.93	0.7	3	'6/24	5248
133	K.IGEEEIQKPEEK.V		1	23.990	0.49	476.91	-1.0	3	'12/22	2034
134	K.SLAGSSGPGASSGTSGDHGELVVR.I		1	46.640	0.0025	729.02	-1.3	3	'15/46	3341
135	R.LSKEDIER.M		4	50.010	0.0017	495.27	2.3	2	'7/14	1673
136	K.DKEACVHKILR.Q		6	47.480	0.0021	456.92	0.1	3	'8/20	3638
137	K.AVDITTPK.A		1	54.400	0.00073	422.74	0.7	2	'5/14	1850
138	R.VAEQAANDLR.A		2	29.150	0.16	543.78	-0.1	2	'9/18	1764
139	K.NQLTSNPENTVFDAK.R		2	90.450	1.8e-007	839.41	-1.6	2	'11/28	3497
140	R.SSTPLPTISSSAENTR.Q		1	78.940	5.4e-006	824.41	-1.7	2	'12/30	3005
141	K.TTSPLEEEER.E		1	48.270	0.0013	595.78	1.1	2	'8/18	1920
142	R.KLVIIEGDLER.T		4	63.080	4.6e-005	642.88	-2.3	2	'7/20	4551
143	R.LQSIGTENTEENRR.F		1	25.150	0.56	549.61	-0.2	3	'7/26	2032
144	R.ISQATAQIK.N		1	43.850	0.007	480.28	-0.5	2	'8/16	1408
145	R.SSDCASGLCCAR.H		1	69.350	6.2e-007	672.26	0.3	2	'8/22	1544
146	K.KGTVEGFEPADNKCLLR.A		2	52.670	0.0009	645.33	-0.2	3	'19/32	4178
147	R.TFSWASVTSK.N		1	24.000	0.39	557.28	1.7	2	'6/18	4141
148	K.DYELLCLDGTRK.S		2	44.330	0.0064	741.87	-1.1	2	'8/22	4399
149	R.QLEEELR.T		1	34.000	0.062	458.74	-0.4	2	'6/12	2204
150	R.VLVNDAQKVTEGQQER.L		1	46.620	0.0029	605.32	-0.6	3	'18/30	2732
151	R.IADGYEQAAR.V		1	72.880	7.8e-006	547.27	2.4	2	'9/18	1750
152	R.IGHRYIEIFK.S		2	24.860	0.4	425.91	-0.7	3	'8/18	5727
153	R.LTEGCSFR.R		1	38.610	0.009	485.23	-0.5	2	'7/14	1912
154	R.VLVEQQQDR.A		1	42.870	0.0065	557.80	-1.3	2	'7/16	1549
155	K.CNKEVYFAER.V		1	25.580	0.2	439.21	0.6	3	'7/18	3052
156	R.SIGVVEEK.V		1	40.200	0.023	430.74	-0.2	2	'7/14	1802
157	K.AEEYTEETEER.E		1	71.650	1e-006	693.29	-1.8	2	'7/20	1452
158	K.AYAALAALEK.L		1	66.800	2.6e-005	510.79	0.3	2	'13/18	4074
159	R.SVSLTGAPESVQK.A		2	51.740	0.0012	651.85	-2.6	2	'10/24	2474
160	K.LQAELEGIK.R		1	35.240	0.044	500.79	-0.6	2	'6/16	3078
161	K.VEIIANDQGNR.T		5	66.110	3.2e-005	614.82	-0.2	2	'8/20	2085

162	K.VEQATKPSFESGR.R		1	30.670	0.12	479.24	-1.9	3	'10/24	1991
163	R.GLFIIDDKGILR.Q		2	29.640	0.064	453.94	-1.0	3	'7/22	5762
164	R.EDGNEEDKENQGDETQGQQPPQRR.Y		3	37.200	0.0077	696.81	-0.7	4	'12/46	1389
165	K.NAGVEGSLIVEK.I		1	47.470	0.0031	608.33	0.0	2	'8/22	3088
166	K.AIKVEQATKPSFESGR.R		1	28.230	0.2	437.74	2.7	4	'14/30	3132
167	R.VEVGKDQEFTVDTR.G		1	22.830	2.2	541.61	4.6	3	'9/26	2917
168	K.SESPKEPEQLR.K		2	39.500	0.014	433.89	0.1	3	'13/20	1934
169	K.TENLLGSYFPK.K		1	60.100	0.00027	634.83	-3.7	2	'8/20	5024
170	K.LVTDLTK.V		5	42.480	0.0066	395.24	-1.0	2	'6/12	2289
171	R.VIVCNTKLDNNWGR.E		1	38.190	0.024	563.62	-1.0	3	'13/26	3697
172	R.IEANEALVK.A		1	57.950	0.00026	493.78	0.2	2	'8/16	2246
173	R.IVAPGKGILAADESTGSIAKR.L		1	21.620	0.37	514.30	-0.3	4	'19/40	4739
174	R.YGFIEGHVVIPR.I		1	24.710	0.52	462.92	0.3	3	'10/22	5121
175	R.VLANPGNSQVAR.V		1	61.410	7.5e-005	613.34	-0.7	2	'9/22	1963
176	K.TTTAAAVASTGPSSR.S		1	38.480	0.024	689.35	1.0	2	'8/28	1508
177	R.SRGFGFVLFK.D		2	30.080	0.15	579.33	0.3	2	'7/18	6090
178	K.STTSVSEEDVSSR.Y		1	59.920	7e-005	692.32	-0.4	2	'9/24	1438
179	R.SRGFGFVLFK.E		2	30.080	0.15	579.33	0.3	2	'7/18	6090
180	R.VTDALNATR.A		1	65.110	6.4e-005	480.76	0.3	2	'6/16	1641
181	K.SLDQDPVVR.A		1	35.350	0.033	514.77	0.3	2	'6/16	2210
182	K.ILIEDWKK.A		1	26.940	0.28	348.87	-0.3	3	'4/14	3960
183	R.KSVEEYANCHLAR.A		2	87.200	2.1e-007	526.25	-2.1	3	'19/24	3263
184	R.GWLKSNVSDAVAQSTR.I		3	56.760	0.00038	573.63	-0.3	3	'15/30	4767
185	R.FGEVVDCTIK.T		1	56.700	0.00026	584.29	-0.9	2	'6/18	3400
186	R.FVNVVPTFGKK.K		1	30.140	0.069	412.58	-0.3	3	'8/20	4355
187	R.RVPFSLLR.G		1	22.620	0.34	494.31	-0.3	2	'5/14	5409
188	R.KATGPPVSELITK.A		1	58.510	0.00012	447.60	0.6	3	'10/24	4029
189	K.QQSELQSQVR.Y		1	48.430	0.0022	601.81	3.3	2	'9/18	1590
190	K.KHLEINPDHPIVETLR.Q		1	21.840	0.61	478.52	-0.9	4	'8/30	5290
191	K.AVTEQGAELSNEER.N		1	80.160	9.7e-007	766.86	-1.4	2	'9/26	1921
192	R.CVLQIDNAK.L		1	37.400	0.04	530.78	-0.1	2	'10/16	2744
193	K.ALLQSSASR.K		1	34.550	0.06	466.76	-1.1	2	'8/16	1885
194	R.APSIHGGSGGRGVSVSSAR.F		1	23.860	0.63	435.48	0.5	4	'14/36	2994
195	R.AIGSASEGAQSSLQEVYHK.S		1	32.470	0.07	654.66	-1.3	3	'14/36	3246
196	K.ASGPPVSELITK.A		1	20.290	1.2	599.83	-8.3	2	'8/22	3597
197	K.AIASSLKSWNETLTSR.L		1	40.750	0.013	588.65	0.0	3	'17/30	4862

198	R.QLSLARPQAPALHLR.L		2	19.450	0.51	418.50	-0.3	4	'13/28	4926
199	R.VVANSKESYELR.Y		1	31.500	0.099	465.58	-0.1	3	'9/22	2396
200	K.SEDDSAVPLAK.A		1	56.890	0.0002	566.28	-4.2	2	'14/20	2049
201	K.SVEAAAELSAKDLK.E		1	40.690	0.015	477.93	0.0	3	'13/26	3266
202	K.ALEENNNFSK.M		1	39.390	0.012	583.28	0.9	2	'5/18	1610
203	K.ATDAEADVASLNRR.I		5	42.300	0.0086	496.92	-0.3	3	'8/26	2500
204	R.YYKNIGLGFKTPK.E		1	35.150	0.042	382.97	0.1	4	'15/24	4788
205	R.LAVYIDKVR.S		1	24.700	0.16	359.55	-0.2	3	'9/16	3509
206	K.YLGEEYVK.A		2	32.790	0.049	500.75	-0.1	2	'11/14	3283
207	K.EEEEGISQESSEEEQ.-		1	89.850	4.9e-009	869.84	-0.2	2	'12/28	1792
208	K.SVIPSDGPSVACVK.K		12	57.990	0.00019	708.36	0.1	2	'7/26	3267
209	K.KASYLDCIR.A		8	44.470	0.0045	563.29	-2.5	2	'6/16	3350
210	K.SYKVSTSGPR.A		2	44.810	0.0045	541.29	0.4	2	'9/18	1828
211	R.NKSTESLQANVQR.L		1	58.450	0.00026	492.26	0.3	3	'16/24	2176
212	K.LCVQNSPQEAR.N		1	46.200	0.0022	651.31	-4.2	2	'13/20	1625
213	K.AQYEEVAR.R		1	25.690	0.3	483.24	-1.1	2	'6/14	2118
214	R.EGGDGEEQDVGDAGR.L		1	91.370	5.3e-009	745.80	1.2	2	'11/28	1232
215	R.QIDNPDYK.G		1	20.620	0.95	496.74	1.9	2	'4/14	1373
216	R.EIQTAVR.L		3	23.010	1.2	408.73	-0.6	2	'5/12	1285
217	K.EAEEGEDDRDSANGEDDS.-		1	56.580	2.2e-006	970.35	-0.9	2	'12/34	978
218	K.AVPKEDIYSGGGGGGSR.S		1	25.350	0.61	536.26	-0.9	3	'11/32	2434
220	R.AELDEVNKSAK.K		1	28.820	0.23	401.88	0.2	3	'8/20	1650
221	R.VAEVAPEER.E		1	45.820	0.0024	500.26	0.1	2	'5/16	1360
222	R.ELEQLGR.Q		1	26.720	0.61	422.73	0.7	2	'5/12	1624
223	K.AQQATPGGAAPTIFSR.I		1	24.080	0.86	786.91	0.6	2	'17/30	3526
224	R.SVLISLK.Q		1	26.690	0.094	380.25	-0.7	2	'4/12	3677
225	R.ELDESLQVAER.L		1	56.480	0.00028	644.82	-1.4	2	'7/20	3068
226	R.GCITIIGGGDTATCCAK.W		1	85.000	6.8e-007	877.90	1.4	2	'12/32	3309
227	K.EVNVSPCPTQPCQLSK.G		1	58.660	0.00016	922.44	-0.2	2	'15/30	2702
228	R.AGGPATPLSPTR.L		1	37.700	0.021	562.81	0.2	2	'7/22	2261
229	K.AVTKDEDEWK.E		1	23.990	0.43	407.53	0.4	3	'7/18	2026
230	R.IGDTWSK.K		1	22.020	1.1	403.71	0.1	2	'6/12	1992
231	K.DYELLCLDGTR.K		2	56.250	0.00023	677.82	-0.5	2	'14/20	4981
232	R.SSQSSSQQFSGIGR.S		2	78.550	1.3e-006	728.34	-0.5	2	'10/26	2188
233	R.ELAEDDSILK.-		1	36.220	0.039	566.79	0.1	2	'7/18	3288
234	K.VLEDSDLKK.S		1	29.730	0.21	349.53	0.2	3	'7/16	2023

235	K.SQVVAGTNYFIK.V		1	60.310	0.00012	663.86	-0.5	2	'9/22	3826
236	K.ASYLDCIR.A		12	40.660	0.0082	499.24	1.2	2	'7/14	3399
237	R.ISGLIYEETR.G		1	61.790	9.9e-005	590.81	0.9	2	'8/18	3663
238	R.RCLYASVLTAQPR.L		1	25.250	0.46	512.28	1.4	3	'6/24	4464
239	R.ILTPEVR.L		2	21.540	0.47	414.25	0.5	2	'5/12	2657
240	R.GLVGEIIKR.F		2	43.480	0.0028	492.81	-1.0	2	'7/16	4617
241	R.ASFPGPSELHSEDSR.F		1	20.140	0.57	539.25	-0.3	3	'6/28	3207
242	R.EILSVDCSTNNPSQAK.L		1	84.840	3.2e-007	881.92	-1.1	2	'12/30	2722
243	K.TSDIFGSPVTATSR.L		1	65.890	3.8e-005	719.86	-3.3	2	'10/26	3701
244	R.LQLELSKVR.E		1	32.890	0.035	362.56	0.7	3	'7/16	3738
245	R.TTWASSSSPNDR.T		1	32.520	0.039	654.80	1.3	2	'7/22	1655
246	R.GTPAGTTPGASQAPK.A		1	25.700	0.62	670.84	1.3	2	'9/28	1299
247	K.IIIENKPK.K		1	34.770	0.014	477.80	-11.7	2	'5/14	3949
248	R.LGEYEDVSR.V		1	70.890	6.8e-006	534.25	-0.7	2	'7/16	2100
249	M.PQYQTWEEFSR.A		1	67.940	9.9e-006	735.83	-3.6	2	'8/20	4221
250	K.SIEVIENR.M		1	32.490	0.11	480.26	-0.2	2	'10/14	2377
251	K.ALAPEYAK.A		2	22.860	1	431.74	-0.7	2	'10/14	1879
252	K.SEDCFILDHGKDGK.I		4	38.870	0.0093	540.92	0.1	3	'14/26	3356
253	K.SELSACFSR.L		1	43.800	0.0023	528.74	-2.1	2	'7/16	2857
254	R.YEDLLTR.L		1	41.360	0.008	455.24	0.2	2	'6/12	3107
255	R.EADDIVNWLK.K		1	37.490	0.024	601.80	-2.2	2	'7/18	5397
256	K.AGKEPGLQIWR.V		2	32.980	0.05	418.90	0.5	3	'9/20	4726
257	K.VIVVGNPANTNCLTASK.S		1	83.140	7.6e-007	879.46	-0.8	2	'12/32	3417
258	K.DVNQQEFVR.A		1	39.110	0.019	567.78	0.4	2	'6/16	2422
259	K.VAGQDGSVVQFK.I		1	66.770	3.8e-005	617.83	0.6	2	'10/22	2810
260	K.EIAEAYLGK.T		1	21.450	1.2	497.27	-0.8	2	'4/16	3066
261	R.KESYSVYVYKVLK.Q		4	44.340	0.004	535.97	-0.4	3	'8/24	4987
262	R.DDGYSTKDSYSSR.D		1	28.230	0.22	494.21	0.7	3	'14/24	1383
263	R.VLVDQTTGLSR.G		1	75.100	4.9e-006	594.83	-0.4	2	'7/20	2751
264	K.QEYDESGPSIVHRK.C		4	19.560	1.3	411.95	-3.0	4	'15/26	2969
265	R.FEEELAAR.E		1	35.380	0.04	482.74	0.2	2	'7/14	2381
266	R.EIAQDFKTDLR.F		2	53.620	0.00067	668.35	-0.7	2	'9/20	3574
267	R.DFVNYLVR.I		1	42.280	0.0086	513.27	-1.5	2	'6/14	5027
268	R.NFRNPLAK.-		2	22.420	1.1	480.27	-1.5	2	'7/14	3511
269	M.VVEHPEFLK.A		1	20.920	0.81	366.54	0.4	3	'11/16	3650
270	R.EPGLCTWQSLR.S		1	45.340	0.0037	673.83	0.7	2	'8/20	4421
271	K.GFGYKGSCFHR.I		1	43.330	0.0027	439.20	-1.1	3	'11/20	4090
272	R.FYQDLKDR.D		1	23.580	0.41	362.19	-0.8	3	'6/14	2691
273	R.VNGSLAVSR.A		2	40.510	0.02	451.76	1.1	2	'7/16	1613

274	K.IIVLGLLPR.G		1	44.360	5.1e-005	497.34	-2.0	2	'6/16	5744
275	R.LQEKEDLQELNDR.L		1	44.220	0.019	543.94	0.0	3	'15/24	2861
276	K.GGSLPKVEAK.F		1	26.300	0.29	329.19	0.5	3	'12/18	2044
277	K.VNQIGSVTESIQACK.L		1	97.250	3.1e-008	817.41	0.2	2	'12/28	3524
278	R.AQVIYTR.N		1	37.370	0.02	425.74	0.2	2	'6/12	1726
279	K.VDSLLENLEK.I		3	48.720	0.0026	580.31	0.8	2	'13/18	4556
280	K.DAEAWFTSR.T		1	44.560	0.0027	541.75	-0.3	2	'7/16	4331
281	K.IIAPPERK.Y		6	27.690	0.066	308.53	0.2	3	'5/14	2001
282	K.GQEGSVCLR.S		1	32.880	0.054	503.24	-0.2	2	'7/16	1706
283	R.AREQAEAEVASLNRR.I		2	25.500	0.44	425.73	0.0	4	'8/28	3110
284	R.EIQTAVRLLLPGELAK.H		3	35.080	0.007	584.35	-0.9	3	'11/30	5725
285	K.IRIFDLGR.K		2	31.680	0.056	330.53	0.0	3	'6/14	5227
286	K.ELSDIAHR.I		1	28.770	0.13	314.17	0.7	3	'5/14	2054
287	R.FDEFFSEGCAPGSKKDSSLCK.L		2	19.370	0.45	599.77	-0.1	4	'15/40	4961
288	R.QGTMPVSLLK.A	0.0001000000.0	4	24.360	0.59	545.31	7.0	2	'8/18	3553
289	R.NLLSVAYKNVVGARR.S		6	25.740	0.12	553.99	0.6	3	'11/28	5661
290	R.LAKYNQLLR.I		1	24.810	0.19	373.56	-0.4	3	'6/16	4009
291	M.PYQYPALTPEQK.K		1	37.130	0.031	717.87	-1.2	2	'7/22	3321
292	R.SHEGETAYIR.V		2	30.570	0.1	581.78	6.5	2	'7/18	2305
293	R.NTDVAQSPEAPK.Q		1	57.070	0.0002	628.81	0.5	2	'14/22	1308
294	K.ITSEIPQTER.M		1	37.160	0.053	587.31	0.0	2	'12/18	1989
295	R.IQLVEEELDRAQER.L		15	33.940	0.061	576.64	-0.3	3	'8/26	4209
296	K.YEELQSLAGK.H		1	62.530	9.2e-005	569.29	-3.6	2	'15/18	3091
297	R.EESEESEAEPVQR.T		2	60.880	2.2e-005	759.83	-1.0	2	'9/24	1284
298	K.EVSSATNALR.S		1	57.990	0.00039	524.28	0.9	2	'8/18	1719
299	K.AALKTASDFITK.M		2	72.300	5.8e-006	422.57	-0.1	3	'9/22	3902
300	K.TATPQQAQEVHEK.L		6	75.060	4.8e-006	733.87	0.6	2	'10/24	1434
301	K.CCLTYCFNKPEDK.-		1	30.790	0.015	578.91	-1.0	3	'10/24	3386
302	R.VYSTSVTGSR.E		1	45.380	0.0031	528.77	-1.0	2	'9/18	1463
303	K.FVEGLPINDFSR.E		1	40.930	0.013	697.36	-0.1	2	'16/22	5014
304	R.TGYTLDVTTGQR.K		2	74.280	5.2e-006	656.33	-1.0	2	'10/22	3021
305	M.VNFTVDQIR.A		1	42.170	0.0096	546.30	-1.4	2	'7/16	3630
306	K.IITGGAAAQDGR.L		1	72.410	8.5e-006	565.30	-0.6	2	'9/22	1618
307	K.IETRDGKLVSESSDVLPK.-		1	34.560	0.039	494.02	0.6	4	'10/34	4129
308	K.QVENAGAIGPSR.F		1	36.280	0.025	599.81	-1.4	2	'7/22	1742
309	K.SASDLTWDNLK.G		4	63.680	6.2e-005	625.31	-0.2	2	'8/20	4010
310	R.VLQDQLK.T		1	37.310	0.03	422.25	0.5	2	'6/12	1937
311	K.KALAAGGYDVEKNNSR.I		2	60.200	0.00015	564.96	0.8	3	'13/30	2863

312	K.SEHPGLSIGDTAKK.L		1	35.120	0.041	360.69	0.6	4	'14/26	2938
313	K.LCYVALDFENEMATAASSSSLEK.S	0.00000000000100000000000.0	3	97.150	1.2e-008	851.39	0.2	3	'22/44	5097
314	R.SLFSSIGEVESAK.L		1	58.010	0.00021	677.35	-0.4	2	'10/24	4888
315	K.YLYEIAR.R		2	34.480	0.041	464.25	-0.1	2	'6/12	3474
316	R.ALLGYADNQCK.L		1	47.070	0.0018	626.80	-2.8	2	'14/20	3050
317	K.VGGTSDVEVNEKK.D		1	40.000	0.017	454.57	-0.8	3	'14/24	1423
318	K.AGFAGDDAPR.A		5	70.860	5.2e-006	488.73	-0.1	2	'9/18	1825
319	K.EQISDIDDAVR.K		1	53.340	0.00048	630.81	0.8	2	'8/20	3076
320	R.DYFEQYGK.I		1	31.650	0.032	525.23	-0.7	2	'6/14	3228
321	K.EGDLIAAQAR.L		1	43.670	0.0057	522.28	-0.3	2	'7/18	2360
322	-.KVTYTSQEDLVEKK.C		1	49.800	0.0013	556.63	1.2	3	'11/26	2648
323	K.ALTSELANAR.D		1	64.260	7.1e-005	523.29	-0.1	2	'9/18	2664
324	K.GITLSVRP.-		2	34.780	0.029	421.76	0.0	2	'4/14	2706
325	R.WYFDVTEGK.C		1	32.980	0.032	572.77	-0.3	2	'8/16	4814
326	R.ARLQLELSKVR.E		1	26.530	0.09	328.96	0.3	4	'8/20	4469
327	K.TEESPASDEAGEKEAK.S		2	69.950	4.1e-006	839.38	-0.4	2	'11/30	1167
328	K.AGGAAVVITEPEHTK.E		1	35.890	0.043	493.93	-3.0	3	'12/28	2684
329	R.GGIVDEGALLR.A		1	60.660	0.00012	550.31	1.4	2	'9/20	4121
330	K.EDPQTFYYAVAVVKK.D		6	58.300	0.00022	879.46	0.0	2	'11/28	4707
331	R.VDCGYPHVTPK.E		1	27.120	0.18	424.87	1.9	3	'9/20	2466
332	K.TPKGPSSVEDIKAK.M		2	50.590	0.0036	486.27	-1.1	3	'10/26	2746
333	K.SLLGKDVLFLK.D		2	34.460	0.011	616.88	-1.8	2	'16/20	5742
334	K.CAGNEDIITLR.A		1	62.960	6e-005	631.31	-1.9	2	'8/20	3579
335	R.EDLPVNTSK.T		1	53.150	0.00072	501.76	0.4	2	'6/16	1737
336	K.GFSVVADTPELQR.I		1	52.800	0.00088	709.87	-2.0	2	'16/24	4053
337	R.TIAQDYGVLK.A		1	30.010	0.21	554.31	0.0	2	'8/18	3537
338	R.DSYESYGNSR.S		1	50.270	8.2e-005	589.24	-1.4	2	'8/18	1510
339	R.KPVEEYANCHLAR.A		1	33.820	0.054	397.45	0.4	4	'11/24	3265
340	R.RLNDFASTVR.I		1	41.230	0.011	589.82	-0.1	2	'13/18	3656
341	R.TDGKVFQFLNAK.C		1	32.350	0.084	456.58	-1.0	3	'12/22	5090
342	K.CGNVNFAR.R		1	36.200	0.022	469.22	1.9	2	'7/14	1941
343	K.TIAPQNAPR.D		2	33.950	0.044	484.27	-0.2	2	'8/16	1344
344	K.VCNPIITK.L		2	22.630	1.2	472.77	-0.4	2	'5/14	2344
345	K.ESAFEFLSSA.-		1	31.860	0.046	544.25	-2.5	2	'5/18	5949
346	R.KCSTSSLLEACTFR.R		2	35.670	0.025	553.93	-0.2	3	'7/26	4034
347	R.YLAEVATGDDKKR.I		1	23.300	0.7	367.20	0.3	4	'15/24	3071
348	K.DTSSSTVVSTQR.S		1	57.010	0.00021	634.31	0.9	2	'9/22	1223
349	K.IQVYSR.H		1	30.210	0.12	383.22	-0.4	2	'5/10	1627

350	R.SLETENAGLR.L		1	47.540	0.0029	545.28	-0.5	2	'7/18	2141
351	R.SETKDLLFR.D		4	33.450	0.062	554.80	0.2	2	'7/16	3727
352	R.ISQTYQQQYGR.S		1	56.140	0.00023	686.34	-1.8	2	'8/20	1788
353	K.VLIDIR.E		1	24.510	0.4	364.74	0.5	2	'5/10	3617
354	R.IAQLICER.I		1	54.380	0.00087	501.77	-0.3	2	'7/14	2922
355	K.AQNTWGCGNSLR.T		1	63.150	3e-005	682.31	0.1	2	'9/22	2645
356	R.IEEELGSK.A		1	29.330	0.2	452.73	-0.6	2	'6/14	1442
357	K.TESTLKTTQFSCTLGEK.F		1	40.300	0.035	644.32	0.3	3	'17/32	3292
358	R.IGVITNR.E		1	37.130	0.043	386.74	0.0	2	'4/12	2090
359	R.KQNDVFGEAEQ.-		1	36.090	0.018	632.79	0.6	2	'6/20	2628
360	K.AEGLGDGYR.L		1	35.460	0.026	469.22	-5.0	2	'7/16	1941
361	K.LKGDDLQAIKK.E		4	45.800	0.0022	410.25	-0.2	3	'8/20	2871
362	K.IQVLQQQADDAEER.A		4	83.810	5.9e-007	821.90	-0.4	2	'9/26	2772
363	R.DLEGAVSR.L		1	42.850	0.016	423.72	-0.2	2	'6/14	1915
364	K.TTQFSCTLGEK.F		1	55.050	0.00025	636.30	4.1	2	'9/20	2559
365	R.AAPEASGTPSSDAVSR.L		1	40.140	0.0083	751.86	1.5	2	'9/30	1447
366	K.ISKGANPVEIR.R		2	31.290	0.057	395.23	-2.0	3	'11/20	2677
367	R.SGAQASSTPLSPTRITR.L		1	38.550	0.019	577.31	3.5	3	'9/32	2946
368	R.GLFIIDGKGVLR.Q		1	36.010	0.012	644.39	-0.6	2	'12/22	5739
369	K.EVVEEAENGR.D		2	48.820	0.00084	566.27	-1.0	2	'9/18	1398
370	R.FANYIDKVR.F		1	28.290	0.18	375.87	0.4	3	'10/16	3829
371	K.ALELTGLKVFGNEIK.L		1	32.300	0.036	544.65	-0.6	3	'10/28	5698
372	R.EEECILACR.G		1	37.340	0.014	590.26	-1.5	2	'6/16	2699
373	K.DSGFQMNQLR.G	0.0000010000.0	3	61.620	3.1e-005	606.28	-0.6	2	'8/18	2248
374	R.YFGGTEDR.L		1	26.470	0.061	472.71	1.4	2	'5/14	1962
375	R.LQSEPESIRK.W		1	25.740	0.44	396.22	-0.5	3	'12/18	1817
376	R.LQAANDSVCR.L		1	42.800	0.0052	567.27	-0.4	2	'5/18	1303
377	K.LLATEQEDAAVAK.S		1	67.520	3.1e-005	679.86	0.7	2	'10/24	2476
378	R.YNAQCQETIR.V		1	50.720	0.0006	641.80	0.3	2	'6/18	1639
379	K.AGNLGGGVVTIER.S		1	58.870	0.00018	621.84	-0.9	2	'10/24	3251
380	R.VAVEEVDEEGKFVR.L		1	24.090	0.58	535.94	-0.4	3	'9/26	3297
381	K.TVSPALISR.F		2	29.260	0.19	472.28	4.8	2	'7/16	2711
382	K.AQYEDIANRSR.A		1	20.470	1.7	441.55	0.2	3	'4/20	2174
383	-.EDFDEFER.Q		1	47.030	0.00017	543.72	-0.6	2	'7/14	4400
384	-.IMKVK.A	0.01000.0	1	20.540	0.64	317.70	-5.4	2	'4/8	2552
385	R.YIETDPANR.D		2	30.840	0.1	539.76	-0.8	2	'8/16	1652
386	K.AGEEAFEK.L		1	34.960	0.025	440.71	1.3	2	'5/14	1960

387	K.HQTVPQNTGGKNPDPWAK.N		6	40.270	0.014	659.00	-0.1	3	'10/34	3210
388	K.YEKDIAAYR.A		4	62.070	7.5e-005	564.79	-0.1	2	'8/16	2625
389	R.QVLLGDQIPK.F		1	42.060	0.0038	555.83	0.9	2	'8/18	3635
390	K.LLCGLLAER.L		1	64.140	7.4e-005	522.80	-0.2	2	'8/16	4790
391	K.SASDLTWDNLKGK.K		4	66.580	3.5e-005	717.86	0.0	2	'9/24	3531
392	K.ALAAAGYDVEK.N		2	54.330	0.00088	554.29	1.6	2	'8/20	2509
393	R.ILENEKDLEEAEEYKEAR.L		1	29.660	0.14	552.77	-0.2	4	'17/34	3618
394	R.SASSGAEGDVSSEREP.-		1	75.530	9.6e-007	782.84	2.2	2	'12/30	1506
395	R.KESYSIYVYK.V		1	49.510	0.0016	640.33	-0.2	2	'6/18	3444
396	K.SQIFSTASDNQPTVTIK.V		2	67.730	4.6e-005	918.97	-0.3	2	'8/32	3740
397	K.HAVSEGTKAVTKYTSSK.-		4	52.070	0.00089	598.65	1.7	3	'18/32	3125
398	K.GEELSCEER.N		1	28.010	0.026	554.73	1.4	2	'6/16	1240
399	K.VEPAVDTSR.I		1	24.330	0.48	487.25	0.4	2	'4/16	1195
400	K.LILPNKQK.N		2	30.100	0.018	477.31	-11.7	2	'4/14	4361
401	K.SDVEAIFSK.Y		3	43.430	0.0052	498.25	-2.6	2	'6/16	3706
402	K.SELVANNVTLPAGEQR.K		1	59.950	0.00014	849.44	-1.0	2	'9/30	3404
403	R.FACHSASLTVR.N		1	34.110	0.056	416.88	-1.0	3	'8/20	3237
404	K.AEEDEILNRSPR.N		1	21.870	0.75	476.91	-2.2	3	'6/22	2670
405	K.DSYVGDEAQSKR.G		6	60.220	7.4e-005	677.82	-0.1	2	'9/22	1516
406	K.LDNNWGR.E		2	34.250	0.025	437.71	-0.3	2	'5/12	2065
407	K.IQDKEGIPPDQQR.L		2	20.410	1.5	508.60	-0.3	3	'12/24	1918
408	K.TVGMVAGDEESYEVFADLFDPVIK.L	0.000100000000000000000000.0	1	52.430	0.00061	883.09	-1.1	3	'20/46	6641
409	R.DNIQGITKPAIR.R		1	22.440	0.49	442.59	2.0	3	'8/22	2913
410	R.CTDDFNGAQCK.A		1	69.320	6.3e-007	658.26	0.0	2	'9/20	1384
411	K.KSCHTGLGR.S		2	35.090	0.03	339.17	-0.6	3	'7/16	1710
412	K.KSASDLTWDNLK.G		4	68.310	2.4e-005	689.36	2.1	2	'8/22	3717
413	R.NGLSLAALKK.A		2	52.640	0.00041	507.82	0.8	2	'8/18	3664
414	K.KVPQVSTPTLVEVSR.N		12	76.710	1.3e-006	820.47	1.0	2	'9/28	3848
415	K.HAVSEGTKAVTKYTSSK.C		2	52.070	0.00089	598.65	1.7	3	'18/32	3125
416	R.HGLVPFAFVR.F		1	22.630	0.86	571.83	-1.7	2	'4/18	5944
417	K.SGDEGSEDEAPSGED.-		1	73.130	4.9e-008	740.76	0.9	2	'12/28	1118
418	K.VGGTSDVEVNEKKDR.V		1	42.530	0.01	408.96	-0.2	4	'8/28	1886
419	M.NTGLTR.L		1	22.470	1	331.19	5.6	2	'4/10	3735
420	K.IGDTSVSYK.Y		1	53.230	0.00048	485.25	-0.2	2	'6/16	1754

421	M.PEFLEDPSVLTK.D		1	73.240	8.9e-006	687.86	-2.0	2	'10/22	4680
422	K.VLAAVYK.A		3	40.470	0.0057	382.24	0.3	2	'6/12	2482
423	R.EEFKELK.A		1	25.860	0.36	308.17	-0.2	3	'6/12	2477
424	K.IFVGGLSPDTPEEKIR.E		1	27.680	0.25	586.65	-1.3	3	'7/30	4529
425	K.SIDDLEEK.V		5	46.230	0.0043	474.73	-0.1	2	'6/14	2097
426	K.VAAYDKLEK.T		1	35.100	0.036	346.19	-0.1	3	'11/16	2317
427	R.LFDQAFGLPR.L		1	67.160	3.2e-005	582.31	-0.4	2	'8/18	5224
428	R.AILSTYRK.R		1	19.540	0.71	317.86	-0.3	3	'6/14	2926
429	K.IISNASCTTNCLAPLAK.V		2	126.470	3.5e-011	917.46	-0.4	2	'12/32	3556
430	R.QCLPCGPGGK.G		1	31.520	0.034	537.25	0.4	2	'8/18	1901
431	-.SDVLELTDDNFESR.I		1	82.460	3.6e-007	820.38	-0.5	2	'10/26	4628
432	K.VSASTVPTDGSSR.N		1	26.190	0.3	632.31	-0.2	2	'9/24	1353
433	R.TEELNREVAGHTEQLQMSR.S	0.0000000000000000100.0	1	29.870	0.1	561.77	2.2	4	'15/36	3213
434	R.AKLQIELGK.C		1	36.380	0.021	333.88	0.8	3	'6/16	3367
435	R.NEQDAYAINSYTR.S		1	93.730	2.6e-008	772.85	-0.3	2	'19/24	2968
436	K.EQFLDGDGWTSR.W		1	47.370	0.0021	705.82	1.3	2	'8/22	4266
437	K.FLNVLSPR.G		1	34.820	0.049	473.28	1.0	2	'6/14	4618
438	R.SDKSPDLAPTPAPQSTPR.N		1	41.240	0.012	622.32	1.2	3	'16/34	2370
439	R.CLGAEGASCGGR.A		1	35.850	0.0057	597.75	-1.3	2	'7/22	1545
440	R.FVNVVPTFGK.K		1	26.370	0.28	554.31	-0.9	2	'4/18	4518
441	K.LIEVDDER.K		1	35.560	0.034	494.75	1.4	2	'6/14	2269
442	K.GAVEKGEELSCEER.N		1	26.440	0.19	531.58	0.6	3	'13/26	2440
443	R.LNDFASTVR.I		1	45.210	0.004	511.77	-0.4	2	'8/16	2774
444	R.VGDYGSLSGR.E		1	65.650	2.8e-005	505.75	-0.1	2	'8/18	2272
445	R.LAVYIDR.V		1	34.730	0.038	425.24	-0.6	2	'6/12	3041
446	K.TYAICGAIR.R		1	49.660	0.0013	512.77	0.9	2	'8/16	3112
447	R.NVDGVNYASITR.N		1	58.950	0.00021	654.83	1.1	2	'9/22	3138
448	K.TASDFITK.M		2	53.610	0.00036	441.73	0.3	2	'7/14	2226
449	K.NAGFTPQER.Q		1	21.880	0.79	510.25	3.2	2	'6/16	1708
450	K.GDVAFVK.H		2	45.190	0.0041	368.21	-0.4	2	'6/12	2217
451	R.AQCGGGLLGVR.T		1	28.370	0.22	544.28	-10.8	2	'8/20	3302
452	R.GNDVAFHFNPR.F		2	67.590	1.7e-005	637.31	0.4	2	'12/20	3775
453	K.AGVIFPVGR.M		1	24.590	0.78	458.27	-0.7	2	'6/16	3978
454	K.AWTVLTEYYK.S		1	24.380	0.68	637.33	3.2	2	'6/18	5110
455	K.NCTYTQVQTR.S		2	40.870	0.0054	635.80	-0.6	2	'12/18	1498
456	R.FDEFFSEGCAPGSKK.D		4	63.940	2.7e-005	853.38	-0.2	2	'11/28	4378
457	K.GILAADESTGSIAK.R		1	74.220	7.4e-006	666.85	0.1	2	'11/26	3111

458	R.IIYGGSVTGATCK.E		6	100.910	1.3e-008	663.84	0.5	2	'11/24	2635
459	R.KTFTAWCNSHLR.K		2	49.060	0.002	507.59	0.2	3	'8/22	4437
460	K.AEEAQKTESVDNEGE.-		1	75.070	7.2e-007	818.35	0.1	2	'20/28	1166
461	K.VQESTKGPDEAKIK.A		1	26.620	0.35	383.21	1.8	4	'11/26	2047
462	R.YVLCTAPR.A		1	33.670	0.062	490.25	-1.3	2	'7/14	2557
463	K.IAVAAQNCYK.V		3	49.840	0.0017	569.29	1.1	2	'7/18	1924
464	R.ELTPQVVSAAR.I		1	37.820	0.037	585.83	-0.3	2	'8/20	2829
465	K.ENLKAAQEEYVKR.A		2	48.320	0.0061	526.61	-0.2	3	'11/24	2906
466	K.SLNILTAFQK.K		1	50.740	0.00074	567.83	0.1	2	'8/18	5396
467	K.DLEEWNQR.Q		1	37.690	0.0091	545.25	1.2	2	'7/14	3082
468	R.CYCGEGLSCR.I		1	45.910	6.7e-005	631.24	-0.1	2	'8/18	2167
469	R.GDFCIQVGR.N		2	60.370	9.7e-005	526.25	-1.6	2	'7/16	3456
470	R.SLQEQADAAEER.A		2	58.650	9.1e-005	673.81	0.0	2	'9/22	1927
471	K.AQASSIPVGSR.C		1	31.490	0.13	536.79	2.8	2	'8/20	1597
472	R.SVGGSGGGSFGDNLVTR.S		1	75.410	4.5e-006	783.88	0.8	2	'9/32	3443
473	K.TPGPGAQSALR.A		2	70.920	8.5e-006	527.79	-0.7	2	'9/20	2124
474	R.SQIKDAQLQNAR.C		1	39.490	0.018	457.92	-0.9	3	'12/22	2081
475	R.EIESSPQYR.L		1	22.630	0.6	554.77	-0.1	2	'5/16	1557
476	R.CQSLTEDLEFRK.S		1	43.470	0.0051	509.25	-0.4	3	'9/22	3791
477	K.KKELEEIVQPIISK.L		1	28.950	0.046	552.00	-2.2	3	'8/26	5271
478	R.EEKDNIQPTTE.-		1	43.010	0.0039	652.30	0.2	2	'6/20	1364
479	K.ALAAGGYDVEK.N		1	55.850	0.00036	547.28	-0.9	2	'7/20	2367
480	R.SEVTDLR.R		1	32.460	0.086	410.21	-0.4	2	'4/12	1689
481	K.IWHHTFYNELR.V		5	38.910	0.018	505.92	-0.3	3	'9/20	5627
482	K.AGALNSNDAFVLK.T		4	75.600	4.6e-006	660.35	-2.0	2	'10/24	3962
483	K.IIDAALR.A		1	40.050	0.012	386.24	0.3	2	'5/12	2584
484	K.IECVSAETTEDCIAK.I		4	82.100	3.2e-007	863.39	0.1	2	'9/28	2717
485	K.FETEQALR.L		1	25.850	0.42	497.25	0.2	2	'6/14	2325
486	K.LLADQAEAR.R		1	33.320	0.057	493.77	1.3	2	'5/16	1899
487	K.FETEQALR.M		1	25.850	0.42	497.25	0.2	2	'6/14	2325
488	K.TIDDLEDKLK.C		4	27.790	0.3	397.22	1.8	3	'11/18	3459
489	R.IVATKPLYVALAQR.K		1	36.030	0.006	514.98	-1.0	3	'11/26	5186
490	R.LSVDYGKK.S		1	30.060	0.097	303.84	0.1	3	'6/14	1865
491	R.AQIFANTVDNAR.I		2	67.500	3.2e-005	660.34	-0.4	2	'9/22	3145
492	R.QATKDAGVIAGLNVLR.I		2	48.870	0.00081	542.65	-2.3	3	'11/30	5067
493	K.SNTAGSQSQVETEA.-		1	78.260	5.6e-007	704.81	0.1	2	'17/26	1348
494	R.GLGAPLTEDQQ.-		1	25.670	0.25	564.78	-6.6	2	'4/20	1541
495	R.LEAAYLDLQR.I		1	66.230	3.8e-005	596.32	-0.3	2	'8/18	3998

496	K.GLSEDTTEETLK.E		1	55.580	0.00043	661.82	0.0	2	'9/22	2410
497	R.AGSGSQVPTEPK.K		1	44.830	0.0034	579.29	-0.2	2	'12/22	1211
498	R.AEGTFPGKI.-		1	32.910	0.092	460.25	7.5	2	'11/16	3079
499	R.DGDILGKYVD.-		1	45.400	0.0034	547.77	0.1	2	'5/18	4250
500	K.SLAAEEEAAR.Q		1	62.480	7.6e-005	523.76	-0.7	2	'8/18	1785
501	R.LGLGEGAEEK.S		1	43.270	0.0067	501.76	2.4	2	'7/18	2230
502	K.SLESINSR.L		1	37.710	0.03	453.24	0.9	2	'5/14	1698
503	R.EAPASVVPFVR.V		1	24.490	0.54	586.33	-3.1	2	'6/20	4240
504	R.LQSIGTENTEENR.R		1	64.640	3.4e-005	745.86	-0.1	2	'10/24	1805
505	K.VLTPELYAELR.A		1	48.630	0.0018	652.37	0.7	2	'9/20	4900
506	K.LSDGVAVLK.V		1	58.100	0.00026	451.27	-0.3	2	'8/16	2872
507	K.GIAYIEFK.T		1	30.980	0.071	470.76	0.1	2	'5/14	4285
508	K.LEEAEKAADESER.G		28	60.100	0.00017	738.84	-0.1	2	'7/24	1644
509	K.ITMQNLNDR.L	0.001000000.0	1	34.940	0.043	560.77	-0.5	2	'8/16	1450
510	R.ALFRLSPTASR.S		1	23.420	0.58	406.90	-0.4	3	'11/20	4489
511	K.SSFLVDCSK.A		1	52.770	0.00034	521.75	-0.6	2	'13/16	2888
512	R.IVDGKVVSETNDTK.V		1	20.110	1.6	502.27	-0.1	3	'10/26	2294
513	K.LSYEGEVTK.S		1	28.250	0.2	513.26	-1.5	2	'7/16	2045
514	K.CGDLVFAK.M		1	56.960	0.00022	455.23	-3.0	2	'7/14	3220
515	R.DDTVCLAK.L		4	40.620	0.01	461.22	0.0	2	'8/14	1747
516	K.LINQNCDSAR.T		1	35.870	0.023	595.78	-1.0	2	'7/18	1294
517	R.EEILAQAKENEK.K		2	22.090	1.5	467.91	0.2	3	'8/22	2455
518	K.AGPIWDLR.L		2	25.860	0.28	464.26	-0.9	2	'5/14	4775
519	K.NEGSESAPEGQAQQR.R		1	42.330	0.0028	794.36	2.8	2	'9/28	1021
520	K.FSPAGPILSIR.I		1	36.330	0.031	579.34	-0.8	2	'7/20	4923
521	K.TEADAEKTFEEK.Q		2	53.000	0.00069	699.32	-1.8	2	'10/22	1974
522	R.QTVAVGVIKAVDKK.A		1	22.710	0.11	364.73	-0.3	4	'7/26	4098
523	R.AALLTER.T		1	38.290	0.08	387.23	0.9	2	'6/12	2154
524	K.YEEIDNAPEER.A		1	37.980	0.0055	682.80	0.1	2	'6/20	2004
525	K.HIAEEADRKYEEVAR.K		6	21.240	1.1	454.73	1.3	4	'16/28	3519
526	K.GTGASGSFKLNK.K		6	35.970	0.035	583.81	-0.1	2	'9/22	2475
527	K.FENLCK.I		1	20.980	0.84	405.69	0.0	2	'5/10	1793
528	K.AAILEEK.R		2	37.160	0.1	387.23	15.5	2	'4/12	2154
529	R.LVNQEIEK.F		1	35.890	0.04	486.77	2.3	2	'7/14	1653
530	R.AAAEVNQDYGLDPK.I		1	84.880	3.3e-007	745.86	-1.0	2	'9/26	2686
531	K.FENLCK.L		1	20.980	0.84	405.69	0.0	2	'5/10	1793
532	M.PGVTVKDVNQQEFVR.A		1	55.760	0.0004	572.64	-1.2	3	'11/28	3622
533	K.NQCTQVVQER.E		1	49.600	0.001	631.30	1.7	2	'6/18	1394
534	R.LSELLR.Y		1	29.590	0.25	365.73	0.3	2	'4/10	2851

535	R.LAYINPDLALEEK.N		1	54.950	0.00053	744.90	3.0	2	'11/24	4699
536	K.RKATGPPVSELITK.A		1	22.960	0.23	499.63	0.6	3	'13/26	4988
537	K.FSPAGPILSIR.V		2	36.330	0.031	579.34	-0.8	2	'7/20	4923
538	R.SQAQQPQKEAALSS.-		1	48.050	0.0022	736.87	0.3	2	'9/26	1560
539	K.GPSSVEDIKAK.M		1	25.620	0.5	377.54	-1.8	3	'7/20	1902
540	K.EQHQKLWEEQLAAAK.A		2	29.840	0.32	452.99	-0.4	4	'13/28	4943
541	K.SSAEVIAQAR.K		1	64.430	6.9e-005	516.28	-0.6	2	'8/18	1780
542	R.MLITILGTVKPNANR.I		1	22.340	0.35	547.65	-3.0	3	'9/28	5584
543	R.SQWSPALTISK.V		1	38.230	0.03	609.33	-3.4	2	'7/20	3887
544	K.DVIEEYFK.C		1	27.270	0.16	521.76	-0.1	2	'5/14	4844
545	K.SESPKEPEQLRK.L		1	22.370	1.4	476.59	-0.6	3	'8/22	2140
546	R.NLLSVAYKNVVGAR.R		6	51.480	0.00051	752.44	-0.7	2	'8/26	5689
547	R.GLFIIDDK.G		2	22.920	0.66	460.76	1.2	2	'5/14	4768
548	K.TIIPLISQCTPK.V		1	54.040	0.00045	685.89	1.8	2	'15/22	4629
549	K.SELVANNVTLPAGEQRK.D		1	38.950	0.016	609.33	0.4	3	'11/32	3272
550	K.LFIGGLNTETNEK.A		1	76.960	3e-006	718.38	0.7	2	'10/24	4117
551	R.DFTPVCTTELGR.A		1	64.140	3.6e-005	698.33	-0.4	2	'9/22	3846
552	K.FSVCVLGDQQHCDEAK.A		1	39.300	0.0046	631.61	1.2	3	'13/30	3787
553	R.DGKLVSESSDVLPK.-		3	75.140	4.7e-006	737.39	-0.7	2	'10/26	3479
554	K.VTHAVVTVPAYFNDAQR.Q		1	37.880	0.027	630.00	0.1	3	'6/32	4386
555	R.QTESLESLLSK.S		1	56.120	0.00042	617.83	-0.5	2	'7/20	4528
556	R.STEPELIQVK.S		1	44.740	0.0099	572.32	-0.4	2	'7/18	3143
557	K.TANKDHLVTAYNHLFETK.R		1	38.150	0.022	526.27	-1.2	4	'18/34	5492
558	K.TLQQQTFK.I		1	39.610	0.018	497.27	-0.1	2	'7/14	1948
559	K.LEDGPKFLK.S		1	40.710	0.014	349.53	0.0	3	'8/16	4218
560	R.SLQQLAEER.S		2	38.100	0.026	537.28	2.7	2	'7/16	2944
561	R.TFIAIKPDGVQR.G		1	33.110	0.071	448.93	0.7	3	'5/22	3813
562	R.LKATVTPSPVKGK.G		2	27.070	0.057	442.61	0.0	3	'5/24	2675
563	K.SHEAEVLKQLAEKR.E		1	31.340	0.078	410.23	0.1	4	'13/26	4783
564	R.FCEAEFSVK.T		1	32.370	0.028	558.76	-0.2	2	'7/16	3402
565	R.HLYTSGPHGLSSCFLR.I		1	25.170	0.39	611.30	-2.8	3	'11/30	5524
566	R.LKDLEALLNSK.E		2	49.370	0.0018	622.37	-1.5	2	'9/20	5048
567	K.VTQVDGNSPVR.F		1	53.280	0.00056	586.30	-3.9	2	'8/20	1552
568	R.TWNDPSVQQDIK.F		1	71.700	8.2e-006	715.85	-0.9	2	'9/22	3085
569	R.VAVQGDVVR.E		1	45.740	0.0029	471.77	-1.4	2	'8/16	1861
570	K.ADLINNLGTIAK.S		2	56.990	0.00036	621.86	-0.5	2	'15/22	4438

571	K.LCYVALDFENEMATAASSSSLEK.S		3	92.880	3.7e-008	1268.58	-0.7	2	'14/44	6057
572	R.LQDSGTFQCVAR.D		1	46.650	0.0036	691.33	-0.2	2	'8/22	2725
573	R.SYTSGPGSR.I		1	25.900	0.15	456.22	2.6	2	'4/16	1176
574	K.YAVLYQPLFDKR.F		1	20.040	1.3	504.95	1.3	3	'13/22	5178
575	K.ALYETELADAR.R		1	80.980	1.1e-006	626.32	2.8	2	'8/20	3449
576	R.WCAVSEHEATK.C		21	63.970	2.2e-005	659.30	0.5	2	'9/20	2301
577	R.QLEEQLR.I		4	40.850	0.012	458.25	2.1	2	'5/12	1987
578	R.VAQLEQVYIRGSK.I		1	29.470	0.12	497.62	-0.4	3	'12/24	3567
579	R.FEKPLEEK.G		1	21.590	1.2	340.52	-0.9	3	'8/14	2522
580	K.NRVIGSGCNLDSAR.F		2	28.530	0.22	506.92	6.5	3	'5/26	3089
581	R.IVAPPGGR.A		1	27.060	0.14	383.73	0.7	2	'4/14	1419
582	K.VNGDASPAAAESGAK.E		1	53.730	0.00043	672.83	3.6	2	'10/28	1196
583	K.SISISVAR.G		1	29.310	0.16	416.75	0.7	2	'5/14	2655
584	K.LAGESESNLR.K		1	47.220	0.0029	538.27	0.1	2	'9/18	1727
585	R.ILSGVVTK.M		1	33.000	0.027	408.76	0.4	2	'6/14	2543
586	K.KITIADCGQLE.-		1	74.710	5.7e-006	624.32	0.2	2	'9/20	3305
587	R.ALVILAK.G		1	31.350	0.033	364.26	0.3	2	'6/12	3455
588	K.EGIPPQQQR.L		2	23.110	0.63	526.78	3.7	2	'8/16	1243
589	R.STFSTNYR.S		2	25.990	0.21	488.23	0.1	2	'5/14	1956
590	R.TSSGSSSSSSTPSSQPSSQGGSQPGSQAGSSER.T		1	50.980	0.00013	1020.11	0.6	3	'20/64	1212
591	R.SSGPYGGGGQYFAKPR.N		2	97.520	2.1e-008	814.90	0.9	2	'12/30	3602
592	K.ELTDEEAER.L		1	65.140	2e-005	546.25	-0.4	2	'7/16	1310
593	R.LEEETRK.R		1	24.810	0.57	452.73	-13.0	2	'4/12	1442
595	R.GTPQQIDYAR.Q		1	32.840	0.079	574.79	2.2	2	'8/18	1949
596	K.ALLLLCGEDD.-		1	38.600	0.016	559.77	0.1	2	'5/18	5484
597	K.IKSEHPGLSIGDTAK.K		2	49.220	0.0019	518.28	-0.1	3	'10/28	3564
598	R.GIVEQCCTSICSLYQLENYCN.-		1	34.470	0.0055	871.03	-1.8	3	'18/40	5671
599	K.LELSDNR.V		1	24.520	1.1	423.72	0.5	2	'3/12	1676
600	R.LEEQLGR.G		1	41.320	0.021	422.73	0.7	2	'5/12	1624
601	R.NQGGYGGSSSSSSYGSGRRF.-		1	36.660	0.0071	666.63	0.1	3	'13/38	3024
602	R.QDVDNASLAR.L		1	29.400	0.14	544.77	-1.4	2	'8/18	1534
603	K.AINQQTGAFVEISR.Q		1	96.360	3.9e-008	767.41	0.8	2	'9/26	3675
604	K.AVTEQGHELSNEER.N		1	52.840	0.00068	533.58	-0.9	3	'16/26	2022
605	R.NAEQYKDQADKASTR.L		2	47.670	0.002	575.61	-0.3	3	'17/28	1859
606	R.LECVEPNCR.S		1	36.720	0.0073	588.76	-0.5	2	'7/16	1672
607	K.EDLQELNDR.L		1	38.970	0.006	566.26	-14.2	2	'6/16	2312

608	R.IVAPPGGR.S		2	27.060	0.14	383.73	0.7	2	'4/14	1419
609	R.QLSSGVSEIR.H		1	49.850	0.0018	538.29	-1.4	2	'9/18	2348
610	K.SAAQAAAQTNSNAAGKQLRK.E		1	21.580	0.99	497.27	0.1	4	'17/38	2260
611	K.TVTAMDVVYALKR.Q	0.0000100000000.0	2	49.320	0.0012	741.90	-1.1	2	'9/24	4601
612	K.VESLEQEAANER.Q		1	51.290	0.00065	687.83	1.5	2	'8/22	2465
613	K.IQKLLQDFFNGK.E		2	35.940	0.026	484.27	-0.3	3	'6/22	6006
614	K.VEEAEPEEFVVEK.V		1	62.160	6.8e-005	767.37	-1.0	2	'17/24	3520
615	K.AQPAQPADEPAEK.A		1	23.380	0.57	676.33	1.8	2	'9/24	1089
616	K.TEWLDGKHVVFGK.V		6	66.400	3.7e-005	758.40	-1.2	2	'15/24	4868
617	K.TQDQISNIK.Y		1	27.800	0.33	523.78	-1.1	2	'9/16	1614
618	K.IFVGGLNPEATEEK.I		1	77.910	2.6e-006	752.39	0.6	2	'11/26	3969
619	R.TINEVENQILTR.D		2	68.330	2.3e-005	715.39	0.1	2	'9/22	4044
620	K.NLYIISVK.G		1	20.750	0.41	475.29	3.9	2	'5/14	4242
621	R.LTEQKGEQQIQK.A		1	28.320	0.23	477.26	-0.1	3	'8/22	1611
622	K.EQSQLTATQTR.T		1	40.110	0.015	631.82	-1.0	2	'8/20	1245
623	K.TGISDVFAK.N		1	39.260	0.014	469.25	2.0	2	'7/16	3804
624	R.AGLQFPVGR.I		2	52.740	0.0011	472.77	0.0	2	'13/16	3768
625	K.HIAEDSDRKYEEVAR.K		2	31.040	0.1	455.22	-0.6	4	'14/28	3045
626	K.EFSPFGTITSAK.V		1	48.600	0.0016	642.83	-3.3	2	'7/22	4633
627	R.VISSIEQK.T		6	35.690	0.047	452.26	0.0	2	'6/14	1791
628	R.TKFETEQALR.L		1	34.670	0.049	408.22	-2.9	3	'10/18	2967
629	R.GFGFVLFK.D		1	39.080	0.016	457.76	-1.1	2	'6/14	5971
630	R.YALYDATYETK.E		1	45.990	0.0021	669.32	0.6	2	'9/20	3441
631	R.TKFETEQALR.M		1	34.670	0.049	408.22	-2.9	3	'10/18	2967
632	R.GFGFVLFK.E		1	39.080	0.016	457.76	-1.1	2	'6/14	5971
633	K.EVYQQQQYGSGGRGNR.N		1	26.530	0.2	609.62	-0.3	3	'7/30	2153
634	K.HSTIFENLANKADR.D		6	60.960	0.00013	539.28	-1.4	3	'17/26	4909
635	K.LAQAEEQLEQETR.E		2	49.330	0.0015	772.88	-0.3	2	'7/24	2759
636	R.EECDKYALQSQQR.W		1	29.560	0.071	552.26	1.3	3	'11/24	2035
637	R.LIVENLSSR.C		2	58.640	0.00021	515.80	0.7	2	'8/16	3248
638	K.LEVQAEEER.K		1	54.580	0.00039	551.77	-0.7	2	'7/16	1696
639	K.DLSLEEIQK.K		2	38.020	0.029	537.79	-1.5	2	'7/16	3693
640	R.VFIGNLNTALVK.K		1	43.730	0.0025	644.89	0.4	2	'14/22	4840
641	K.AQYEDIANR.S		1	58.630	0.00012	540.26	-0.1	2	'6/16	1945
642	R.SRGSGGLGGACGGAGFGSR.S		1	46.640	0.0013	556.59	-3.6	3	'11/36	3388
643	K.TLVSVTK.E		2	21.760	0.48	374.23	0.5	2	'3/12	1913
644	K.SGAEVEAGDAAER.R		1	75.230	1.6e-006	631.29	0.4	2	'10/24	1312

645	R.LQAEAQQLR.K		1	47.860	0.0021	528.79	-0.2	2	'6/16	1857
646	R.LCVDPR.H		1	36.940	0.011	380.19	-0.4	2	'5/10	1804
647	R.QATKDAGTIAGLNVLR.I		1	70.590	8.8e-006	543.31	2.5	3	'15/30	4411
648	R.AGLQFPVGR.V		2	52.740	0.0011	472.77	0.0	2	'13/16	3768
649	R.ALQLEEER.K		1	30.360	0.13	494.26	1.1	2	'7/14	2315
650	K.YGVNPGPIVGTTRK.L		1	31.960	0.091	486.94	0.5	3	'13/26	3368
651	R.ITRYQGVNLYVK.N		1	22.500	0.42	485.28	1.8	3	'15/22	3907
652	R.TTTGSYIANR.V		1	62.300	6.7e-005	542.28	0.6	2	'8/18	1623
653	K.YATPAPSAK.S		1	25.170	0.52	453.24	0.3	2	'4/16	1217
654	K.FESPEVAER.A		1	48.710	0.0013	532.26	0.2	2	'8/16	2209
655	R.ISHELDSASSEVN.-		1	47.990	0.00095	694.32	-0.4	2	'7/24	2279
656	R.SGVSLAALKK.A		2	60.990	4.7e-005	487.31	0.2	2	'9/18	3030
657	K.VQVEYKGETK.S		2	47.890	0.0024	590.81	-0.2	2	'12/18	1632
658	K.VQVEYKGETK.T		2	47.890	0.0024	590.81	-0.2	2	'12/18	1632
659	K.YVIYIER.V		1	28.010	0.16	478.27	0.1	2	'5/12	3687
660	K.ELEEIVQPIISK.L		1	48.840	0.0013	699.40	-0.4	2	'14/22	4682
661	R.GAPLVVICQGK.I		1	47.420	0.002	571.32	-3.2	2	'13/20	3373
662	R.LVEPGSPAEK.A		1	24.680	0.38	513.78	0.7	2	'5/18	1651
663	R.DTDSSVASEVR.S		1	86.850	1.8e-007	583.27	0.9	2	'9/20	1786
664	K.NLQYYDISAK.S		1	44.320	0.0041	607.81	-0.4	2	'8/18	3365
665	K.EEDEEPESPPEK.K		1	32.190	0.01	707.80	-0.6	2	'6/22	1200
666	K.FENWGACDGGTGTK.V		1	57.490	2.5e-005	750.31	-0.7	2	'12/26	2867
667	R.ANSAGATRAVEVLPK.A		2	33.410	0.058	495.28	-0.8	3	'16/28	3200
668	R.ALDVNVALRK.I		1	19.640	0.86	366.89	0.4	3	'9/18	3320
669	K.SNFSNSADDIK.S		2	58.950	6.4e-005	599.27	-6.2	2	'8/20	1984
670	K.FASFIDKVR.F		9	34.580	0.036	361.54	-0.4	3	'10/16	4396
671	K.FGEVVDCTIK.M		1	56.700	0.00026	584.29	-0.9	2	'6/18	3400
672	K.ISEKEEVTTR.E		1	54.020	0.00067	397.88	-0.1	3	'11/18	1492
673	R.RQVDQLTNDKAR.V		1	66.310	3.8e-005	481.93	-0.1	3	'8/22	2220
674	R.TASGSSVTSLDGTR.S		1	32.390	0.092	669.83	-0.8	2	'10/26	1952
675	K.YEELQVTAGK.H		1	52.280	0.00098	569.29	-3.6	2	'14/18	3091
676	R.AQYDELARK.N		2	31.680	0.094	365.19	-0.5	3	'11/16	2156
677	R.ALHSLLLR.L		1	24.500	0.059	308.20	-0.3	3	'9/14	4637
678	R.SGGGGGGLGSGGSIR.S		1	84.490	4.1e-007	616.80	-0.6	2	'14/30	2135
679	K.ATDLGGTSQAGTSQR.F		1	83.470	5.3e-007	725.35	0.5	2	'10/28	1266
680	K.YEKDVADYKSK.G		1	33.810	0.054	337.17	1.0	4	'7/20	1971
681	R.SGFSSVSVSR.S		1	70.830	7.8e-006	506.76	-0.6	2	'9/18	2346
682	R.EAVIAAAFAK.L		1	38.630	0.018	495.78	0.3	2	'7/18	3882
683	R.LQAEIEGLK.G		1	35.240	0.044	500.79	-0.6	2	'6/16	3078

684	K.CDEWSVNSVGK.I		2	76.020	9.5e-007	640.78	-0.2	2	'9/20	3003
685	K.SVTEQGAELSNEER.N		2	113.220	3.8e-010	774.86	-0.6	2	'11/26	2017
686	R.AEVNGLAAQGK.Y		2	65.080	3.4e-005	529.29	0.9	2	'8/20	1593
687	K.VVSEQKDTLGNTQIK.Q		1	36.310	0.033	553.97	-0.4	3	'13/28	2419
688	K.IFNLYPR.K		2	41.470	0.0076	461.76	0.7	2	'6/12	4414
689	K.SAAQAAAQTNSNAAGKQLR.K		1	54.530	0.00049	619.99	1.3	3	'12/36	2005
690	M.PEFLEDPSVLTKDK.L		1	20.480	1.4	539.95	-2.4	3	'8/26	4420
691	R.YSLSGGGTSSH.-		1	50.700	0.00042	526.74	-0.7	2	'10/20	1538
692	R.SGVSLAALK.K		1	54.940	0.00048	423.26	0.1	2	'7/16	3264
693	R.DGEEAGAYDGPR.T		3	55.850	3.8e-005	618.76	-0.2	2	'8/22	1751
694	R.ALGQNPTNAEVLK.V		1	46.490	0.003	677.87	-0.1	2	'9/24	2874
695	K.EAALSTALSEKR.T		1	26.980	0.3	425.90	0.6	3	'10/22	2765
696	K.EELQANGSAPAADK.E		1	69.290	1.1e-005	700.84	-1.1	2	'10/26	1416
697	K.SVTGTDVDIVFSK.V		1	54.320	0.00073	684.35	-5.0	2	'10/24	4329
698	R.TYDETYQR.Y		2	30.360	0.032	538.24	-0.9	2	'7/14	1343
699	R.DGRGALQNIIPASTGAAK.A		1	25.970	0.3	580.65	-1.0	3	'17/34	4086
700	K.SEETLDEGPPKYTK.S		1	45.150	0.0042	531.93	0.7	3	'7/26	2395
701	K.DSPSVWAAVPGK.T		1	50.360	0.001	607.31	1.0	2	'8/22	3920
702	K.EAVAPVQEESDLEK.K		1	53.790	0.00048	772.38	2.1	2	'8/26	2680
703	K.GSGTAEVELK.K		1	28.580	0.25	495.76	1.8	2	'6/18	1723
704	K.SADTLWGIQK.E		1	45.640	0.0051	559.80	1.0	2	'13/18	3958
705	K.FENWGACDGGTGTKVR.Q		1	22.630	1.2	585.60	-1.0	3	'16/30	3499
706	R.LELCDER.V		1	34.190	0.036	467.72	-0.7	2	'6/12	2136
707	R.WCAVQGQVDEK.T		1	47.880	0.0011	660.30	-2.0	2	'14/20	2430
708	R.LQQENSILR.D		1	42.020	0.012	550.81	-0.2	2	'7/16	2544
709	R.LGYTPVCR.A		1	33.030	0.065	483.25	-4.0	2	'6/14	2386
710	K.EEDEEPESPPEKK.T		3	45.650	0.00092	771.84	-2.9	2	'7/24	1151
711	K.SQLVYQSR.R		1	27.470	0.25	490.76	0.0	2	'8/14	1806
712	K.THPHFVIPYR.C		1	23.250	0.67	422.90	0.9	3	'7/18	5185
713	K.TDEGIAYR.G		1	40.010	0.008	462.72	-0.9	2	'7/14	1738
714	K.TGGAVDRLTDTSR.Y		1	25.080	0.53	450.23	0.2	3	'9/24	2830
715	R.ALANSLACQGK.Y		1	53.260	0.00077	566.79	-3.6	2	'7/20	2143
716	R.KLLEGEEER.L		3	37.930	0.03	551.79	-0.5	2	'7/16	2672
717	R.SLLEGQEDHYNNLSASKVL.-		1	33.990	0.074	706.35	-1.3	3	'8/36	5058
718	K.DLLFK.D		3	27.850	0.12	318.19	-0.5	2	'4/8	3948
719	K.EEAPDILCLQETK.C		1	62.550	7e-005	773.38	1.4	2	'9/24	4317

720	R.FFSDCKIQNGAQGIR.F		1	43.900	0.0059	580.96	2.0	3	'13/28	3985
721	K.LCFSTAQHAS.-		1	41.420	0.0085	561.26	-0.4	2	'7/18	2420
722	R.IRIDSLSAQLSQLQK.Q		1	23.370	0.28	567.33	-0.4	3	'12/28	5210
723	R.LLIPRWR.E		2	30.100	0.018	477.31	-1.3	2	'4/12	4361
724	K.AEHDQLLLNYAKK.E		1	21.920	1	386.46	0.3	4	'8/24	4199
725	R.YRPGTVALR.E		2	30.440	0.1	344.87	0.5	3	'6/16	3104
726	K.LSSSFSSR.G		1	30.990	0.059	435.72	-0.1	2	'4/14	1599
727	R.EACGVIVELIK.S		1	38.560	0.024	615.84	1.8	2	'6/20	5125
728	R.LAPEYEAAATR.L		3	73.200	8.2e-006	596.30	-0.8	2	'10/20	2259
729	R.TLSDYNIQK.E		2	36.100	0.034	541.28	-0.1	2	'14/16	2401
730	R.AEDGENYDIK.K		1	27.940	0.22	577.25	-0.3	2	'5/18	1718
731	R.FKSHTDQLVLIFAGK.I		1	29.980	0.095	568.66	2.1	3	'7/28	6068
732	K.HQTVPQNTGGKNPDPWAKNLNEK.D		2	24.860	0.44	644.08	-0.3	4	'14/44	3891
733	R.SSASFSTTAVSAR.Y		1	91.020	8.2e-008	636.32	0.4	2	'9/24	2235
734	K.GLGLDESGLAK.Q		1	36.780	0.04	530.29	1.2	2	'5/20	3427
735	K.SAEIDSDDTGGSAAQK.Q		1	93.470	2e-008	776.34	-0.9	2	'12/30	1171
736	R.ADGYVLEGK.E		1	40.870	0.01	476.24	1.6	2	'7/16	2295
737	M.PEPVKSAPVPK.K		1	32.860	0.046	383.56	0.3	3	'8/20	2231
738	R.LTIAEER.D		1	28.320	0.33	416.23	1.0	2	'6/12	1906
739	K.IGGIGTVPVGR.V		2	63.790	1.9e-005	513.31	-0.1	2	'7/20	3173
740	R.SRKESYSIYVYK.V		1	38.530	0.02	508.27	0.7	3	'9/22	4031
741	R.VEIIANDQGNR.I		1	66.110	3.2e-005	614.82	-0.2	2	'8/20	2085
742	R.VLSSIEQK.S		2	35.690	0.047	452.26	0.0	2	'6/14	1791
743	K.ESNGPVKVWGSIK.G		2	43.060	0.0081	700.88	0.6	2	'9/24	4610
744	R.FDSDAASPR.E		4	73.910	1.8e-005	483.22	1.7	2	'8/16	1252
745	K.AINQGGLTSVAVR.G		1	67.820	2.4e-005	643.36	-0.2	2	'9/24	3087
746	K.ADVQSIIGLQR.F		1	28.960	0.23	600.35	7.8	2	'8/20	4245
747	R.AITIASQTNCPLYVTK.V		1	63.280	8.3e-005	890.47	-0.3	2	'10/30	3905
748	R.FDSDAASPR.G		7	73.910	1.8e-005	483.22	1.7	2	'8/16	1252
749	R.VGPSNQPSTSAR.A		1	23.980	0.48	600.80	1.0	2	'7/22	1102
750	R.KLVIIESDLER.A		8	32.440	0.075	438.93	0.0	3	'8/20	4555
751	R.IYVGNLPPDIR.T		2	57.770	0.00023	628.85	1.3	2	'9/20	4114
752	K.EVYFAER.V		1	26.960	0.13	457.22	-0.4	2	'4/12	2674
753	R.AADALEEQQR.C		2	40.680	0.0079	565.77	-3.8	2	'7/18	1378
754	K.QKVDSLLENLEK.I		3	23.760	0.65	472.60	-0.2	3	'7/22	4998
755	K.GAVAEDGDELR.T		1	74.600	2.4e-006	566.27	0.0	2	'9/20	1884
756	R.LKQQSELQSQVR.Y		1	46.170	0.0036	481.94	-0.3	3	'7/22	2472
757	K.IKGEHPGLSIGDVAK.K		2	43.490	0.0051	507.62	-0.4	3	'8/28	4462

758	K.LVSESSDVLPK.-		1	64.240	0.00012	587.32	-0.9	2	'7/20	2740
759	K.LLQDFFNGKELNK.S		3	24.030	0.77	522.61	-2.0	3	'11/24	5201
760	R.FDSDAASPR.T		2	73.910	1.8e-005	483.22	1.7	2	'8/16	1252
761	R.KESYSVYVYK.V		4	67.420	2.8e-005	633.32	-1.0	2	'7/18	3096
762	R.CEDVNECEAQR.C		1	71.200	4.1e-007	705.28	2.5	2	'7/20	1116
763	R.FSAVALCK.A		1	33.090	0.057	448.24	0.6	2	'11/14	2914
764	K.FGEVVDCTLK.L		1	56.700	0.00026	584.29	-0.9	2	'6/18	3400
765	R.SAEYGSSLQSSR.S		1	68.590	8.9e-006	636.30	-1.3	2	'9/22	1700
766	K.CLKDGAGDVAFVK.H		6	78.100	3.1e-006	690.35	-2.2	2	'8/24	3839
767	K.SATEYKNEEYQR.S		1	30.950	0.054	506.57	0.7	3	'8/22	1667
768	R.IAEFTTNLTEEEEK.S		1	109.230	1.7e-009	827.40	1.1	2	'12/26	3754
769	K.AVEHINKTIAPALVSK.K		1	30.330	0.04	423.50	0.3	4	'8/30	4024
770	R.KASGPPVSELITK.A		2	56.120	0.00023	663.88	-0.9	2	'9/24	4020
771	K.STAGDTHLGGEDFDNR.M		2	44.360	0.001	564.58	1.2	3	'16/30	2594
772	K.TLFVK.G		1	24.230	0.16	304.19	0.0	2	'4/8	2712
773	K.SVSGTDVQEECR.E		1	63.620	2.5e-005	683.80	0.0	2	'9/22	1334
774	K.ITITNDQNR.L		1	36.430	0.041	537.78	-0.2	2	'7/16	1494
775	K.ERNGLSLAALKK.A		2	43.420	0.0029	433.93	0.1	3	'7/22	4196
776	R.AEDGENYDIKK.Q		2	64.710	3.5e-005	641.30	1.0	2	'9/20	1558
777	K.IIAPPER.K		3	21.970	0.3	398.24	2.5	2	'4/12	1849
778	R.EPTPVLGSGAAAAGR.S		1	52.660	0.00073	677.36	0.5	2	'10/28	2723
779	K.QQYTNQLAK.E		1	33.130	0.068	547.29	1.0	2	'6/16	1647
780	K.KSDVEAIFSK.Y		3	57.870	0.00018	562.30	-0.8	2	'7/18	3559
781	K.SEHPGLSIGDTAK.K		1	24.520	0.5	437.89	0.2	3	'12/24	2790
782	K.KSASDLTWDNLKGK.K		2	32.210	0.12	521.61	-0.3	3	'14/26	3540
783	R.RAAEEAEEAR.V		1	25.920	0.18	566.27	-9.9	2	'4/18	1884
784	R.VTQKSYKVSTSGPR.A		2	35.280	0.035	513.28	1.8	3	'6/26	2263
785	R.LEALDANSR.K		1	49.040	0.0019	494.76	0.5	2	'8/16	1957
786	K.TASEMVLADDNFSTIVAAVEEGR.A	0.00001000000000000000000.0	1	34.730	0.038	814.39	-2.0	3	'15/44	6212
787	K.CSTSSLLEACTFR.R		4	104.860	1.7e-009	766.35	-1.6	2	'10/24	4084
788	R.CLVEKGDVAFVKHQTVPQNTGGK.N		4	22.920	0.61	628.83	0.4	4	'12/44	4540
789	K.TAENATSGETLEENEAGD.-		1	124.400	7.6e-012	919.38	0.6	2	'22/34	2249
790	K.VLAGDKNFITAEELR.R		1	29.470	0.19	559.30	-1.1	3	'14/28	4704
791	K.HSTIFENLANK.A		6	64.760	6.3e-005	637.33	2.0	2	'9/20	4446
792	R.IQLQCQDGSTR.T		1	60.380	0.0001	653.32	2.2	2	'8/20	1778

793	R.ENIVIQCEAK.G		1	42.880	0.0079	602.31	0.5	2	'6/18	2435
794	R.AADPAPEVR.K		1	44.480	0.0039	463.24	-1.1	2	'7/16	1320
795	K.EISDDEAEEEK.G		1	42.720	0.00076	647.27	-2.2	2	'8/20	1208
796	K.LAADDFR.I		1	40.680	0.015	404.20	0.2	2	'6/12	2407
797	K.LGLRQVTGVTR.V		1	27.940	0.12	400.58	-0.5	3	'10/20	4210
798	R.NQGGYGGSSSSSSYGSGRR.F		2	26.390	0.11	617.61	0.4	3	'8/36	1769
799	K.TLETVPLER.K		1	23.480	0.62	529.30	-3.6	2	'9/16	3054
800	-.KAVSGEAR.F		1	32.580	0.13	409.24	19.6	2	'6/14	3760
801	K.VPQVSTPTLVEVSR.N		1	75.230	2.9e-006	756.42	-2.3	2	'12/26	3896
802	K.FLNKLAEER.R		1	23.530	0.72	373.88	0.1	3	'6/16	4791
803	K.DSYVGDEAQSK.R		3	64.040	1.8e-005	599.76	-0.2	2	'9/20	1331
804	K.FLNKLAEERR.Q		1	31.370	0.089	319.68	0.7	4	'6/18	4808
805	K.INHCRFDEFFSEGCAPGSKK.D		4	37.080	0.01	597.27	-3.0	4	'13/38	5474
806	R.NSILAQVLDQSAR.A		1	80.910	1.2e-006	707.89	1.5	2	'16/24	5483
807	K.LAADDFR.T		1	40.680	0.015	404.20	0.2	2	'6/12	2407
808	K.WSLLQQQK.T		1	28.690	0.25	515.79	-0.9	2	'9/14	3847
809	K.VQVSYKGETK.A		2	21.910	0.82	380.21	0.4	3	'8/18	1640
810	R.AEAALEEESR.Q		1	58.590	0.00012	552.76	1.3	2	'7/18	1427
811	R.VLAALQER.L		1	34.980	0.033	450.27	-4.2	2	'10/14	2814
812	K.EEASGSSVTAEEAK.K		1	70.890	5.1e-006	697.82	-1.1	2	'8/26	1127
813	K.SVEEYANCHLAR.A		2	96.510	7.1e-008	724.83	1.4	2	'9/22	2886
814	K.DGAGDVAFVK.H		6	62.350	9e-005	489.75	-0.2	2	'9/18	2873
815	R.WAATEQEEGISLK.V		1	79.890	1.5e-006	731.37	0.5	2	'9/24	3588
816	K.VVSEQKDTLGNTQIKQK.S		2	71.060	8e-006	639.35	0.9	3	'22/32	2442
817	R.CLVEKGDVAFVK.H		4	64.310	8.6e-005	455.58	0.1	3	'8/22	3901
818	R.SITNTTVCTK.C		1	50.980	0.00092	562.78	-0.4	2	'7/18	1503
819	K.ATGPPVSELITK.A		1	51.210	0.00077	606.84	-1.7	2	'9/22	3703
820	K.LSKDPNIVIAK.M		1	32.670	0.025	399.91	0.2	3	'11/20	2839
821	R.ALDFAVGEYNK.A		1	54.760	0.0004	613.80	-2.7	2	'9/20	4042
822	K.VNQIGSVTESLQACK.L		1	97.250	3.1e-008	817.41	0.2	2	'12/28	3524
823	R.INEILSNALKR.G		2	32.790	0.047	424.25	1.2	3	'5/20	4226
824	K.ADDTSAATIEK.K		1	40.720	0.012	561.27	2.1	2	'11/20	1233
825	R.YQEQGGEASPQSR.T		1	60.260	9.7e-005	718.82	0.6	2	'7/24	1100
826	R.FGQGGAGPVGGQGPR.G		1	61.870	8e-005	671.34	0.1	2	'8/28	2862
827	R.LVLDSVKLEA.-		1	53.200	0.00062	543.82	-0.2	2	'14/18	4583
828	R.CKQLEEEQQALQKK.L		2	21.140	1.3	440.73	-0.3	4	'16/26	2905
829	K.VQQLVPK.R		1	43.330	0.0014	406.26	0.7	2	'5/12	1869

830	R.CTGGEVGATSALAPK.I		1	86.730	2.8e-007	709.85	0.0	2	'13/28	2454
831	R.FSSSSGYGGGSSR.V		1	75.480	8.2e-007	618.27	1.8	2	'11/24	1371
832	R.SVSPCSNVESR.L		1	40.380	0.0079	611.28	2.0	2	'6/20	1393
833	R.SETKDLLFRDDTVCLAK.L		8	37.470	0.025	1006.01	-3.7	2	'7/32	4695
834	R.VFIGNLNTAIVK.K		1	43.730	0.0025	644.89	0.4	2	'14/22	4840
835	R.IVSQPQPAR.R		1	40.870	0.006	498.29	1.0	2	'6/16	1206
836	R.NLPATDPLQR.E		1	26.260	0.29	562.81	-0.4	2	'5/18	3023
837	R.DAEDAVYGR.D		1	49.250	0.0014	498.23	0.4	2	'6/16	1838
838	K.SCCSCCPVGCAK.C		1	56.930	2.9e-006	723.26	0.6	2	'7/22	1336
839	K.VGAHAGEYGAEALER.M		2	49.940	0.00099	510.58	-0.9	3	'9/28	3850
840	K.IESQTQEEVR.D		1	49.230	0.0015	609.80	0.2	2	'8/18	1165
841	R.SHSAHFFEFLTK.E		1	34.980	0.048	484.24	1.2	3	'8/22	6077
842	K.DLLFKDSAHGFLKVPPR.M		6	24.900	0.26	485.77	-1.0	4	'19/32	5779
843	K.NIYSEELR.E		1	36.490	0.025	512.26	-3.3	2	'5/14	2927
844	R.TISETIER.L		1	50.550	0.0017	474.75	0.1	2	'7/14	1943
845	K.ADKDYHFKVDNDENEHQLSLR.T		1	20.550	0.81	515.45	0.5	5	'22/40	4249
846	R.SEVTDLRR.T		1	25.070	0.58	325.85	0.1	3	'8/14	1824
847	R.YQCYCYGR.G		1	21.740	0.075	585.23	0.0	2	'7/14	2079
848	K.ESQSPDTTIQR.T		1	41.250	0.007	631.30	-1.7	2	'7/20	1276
849	K.CETQNPVSAR.R		1	51.690	0.00049	581.27	2.5	2	'9/18	1264
850	K.AQQELEEQTRR.A		1	36.240	0.031	463.24	1.3	3	'8/20	1603
851	R.NTKKEGDLIAAQAR.L		1	39.090	0.015	505.61	-0.3	3	'14/26	3142
852	R.IGAEVYHNLKNVIK.E		2	22.070	0.48	400.23	-0.4	4	'17/26	5334
853	R.YLNFFTK.A		1	29.130	0.24	466.75	0.2	2	'6/12	4986
854	R.TNNLETGPSTR.L		1	56.350	0.00028	595.29	0.1	2	'6/20	1333
855	K.CATITPDEAR.V		1	30.950	0.051	567.26	-3.4	2	'8/18	1665
856	K.YGVNPGPIVGTTR.K		1	43.470	0.008	665.86	0.8	2	'15/24	3279
857	K.SNVSDAVAQSTR.I		6	92.240	9e-008	617.80	0.4	2	'16/22	1895
858	R.ALEAANGELEVK.I		1	66.300	3.5e-005	622.33	-0.4	2	'8/22	2889
859	R.CNNVLYIR.G		1	40.800	0.012	526.27	2.0	2	'6/14	3322
860	K.DCGATWVVLGHSER.R		4	62.530	5.2e-005	793.87	0.8	2	'9/26	4246
861	R.RIHLELR.N		2	42.380	0.0024	312.86	0.5	3	'6/12	4370
862	K.AGLVIGKGGETIKQLQER.A		6	50.590	0.00042	633.03	-1.7	3	'19/34	4882
863	R.EGFINYLTR.E		1	31.270	0.081	556.79	4.7	2	'5/16	5147
864	K.EAGEGGEAEAPAAEGGK.D		1	83.720	1.7e-007	765.34	0.8	2	'25/32	1203
865	K.TYIPPKGETK.K		1	20.190	1.6	378.55	0.2	3	'10/18	1666

866	K.ALFLETEQLK.K		1	34.880	0.071	596.34	1.9	2	'12/18	4609
867	K.LEAALGEAKK.Q		1	24.870	0.54	343.87	0.4	3	'9/18	2253
868	R.VYWKQVAR.N		1	29.680	0.13	350.53	1.1	3	'9/14	3578
869	M.PVDFTGYWK.M		1	33.140	0.051	556.77	-0.2	2	'6/16	4811
870	R.TFNTSTGGLLLPSDTKR.S		1	42.650	0.0079	603.32	-2.4	3	'8/32	4190
871	K.DAFADAVQR.A		2	59.890	0.00013	496.74	0.9	2	'7/16	2730
872	R.LLQAETASNSAR.A		2	74.310	7.3e-006	630.83	0.3	2	'10/22	1829
873	K.CASLQKFGER.A		2	58.320	0.0002	598.30	2.0	2	'8/18	2769
874	R.AVFPSIVGRPR.H		9	24.990	0.28	599.86	-0.5	2	'7/20	4559
875	K.FINYVKNCFR.M		2	57.590	0.00024	680.84	-4.8	2	'7/18	4743
876	R.TVVAGSSDAAQKAVR.M		1	29.180	0.23	487.27	1.0	3	'12/28	2108
877	R.LVSLIGSK.T		1	22.650	0.3	408.76	-0.4	2	'6/14	3233
878	R.TAQEVETYR.R		1	61.380	7.4e-005	548.77	-1.1	2	'8/16	1530
879	R.ALELEQER.K		1	27.660	0.25	494.26	1.1	2	'7/14	2315
880	R.ALINSPEGAVGR.S		1	44.930	0.0032	592.33	0.2	2	'7/22	2980
881	K.QGGGGGGGSVPGIER.M		3	85.100	3.4e-007	642.82	0.1	2	'12/28	2186
882	K.TAEAGGVTGKGQDGIGSK.A		1	35.900	0.046	544.94	-1.0	3	'14/34	1988
883	R.AVFPSIVGRPR.Q		6	24.990	0.28	599.86	-0.5	2	'7/20	4559
884	R.ELGYVEAK.S		1	20.380	1.1	454.74	0.4	2	'7/14	2169
885	R.VNEVNQFAAK.L		1	20.220	1.8	560.29	2.6	2	'8/18	2223
886	R.INEILSNALK.R		2	36.350	0.033	557.83	0.3	2	'5/18	4217
887	R.QTVAVGVIK.A		1	44.870	0.0036	457.79	0.0	2	'8/16	2571
888	K.ILGATIENSR.I		1	57.900	0.0003	537.30	-1.4	2	'9/18	2850
889	R.RHVFGESDELIGQK.V		6	73.990	1e-005	538.95	0.3	3	'10/26	4431
890	R.TGGTQTDLFTCGK.C		1	86.600	1.5e-007	693.32	-0.2	2	'9/24	2936
891	R.IQELEDLLAK.E		1	40.320	0.015	586.33	-3.2	2	'8/18	4860
892	K.KITISDCGQL.-		1	28.190	0.27	567.79	-1.4	2	'6/18	3379
893	K.ELALGQDR.I		1	27.890	0.24	451.24	-0.3	2	'6/14	2257
894	K.ALFLETEQLKK.L		1	20.610	0.84	440.59	0.2	3	'9/20	4424
895	R.KAALKTASDFITK.M		4	38.950	0.0076	465.27	0.3	3	'8/24	4473
896	R.AVEVLPK.A		2	34.130	0.021	378.24	-0.3	2	'4/12	2164
897	K.YICENQDSISSK.L		1	21.830	0.31	722.32	-0.1	2	'12/22	1923
898	K.GDVAFVKHQTVPQNTGGKNPDPWAK.N		4	23.600	0.6	673.60	-0.7	4	'19/48	4463
899	R.LAAEQELIR.L		1	55.600	0.00039	521.80	-1.7	2	'8/16	3070
900	R.NFWVSGLSSTTR.A		1	40.510	0.013	677.84	2.1	2	'7/22	4828
901	K.LSELEAALQR.A		1	59.250	0.00022	565.31	0.1	2	'7/18	3875
902	K.STESLQANVQR.L		1	70.840	1.3e-005	616.81	-1.5	2	'8/20	1688

903	R.QCLPCGPGGKGR.C		2	35.680	0.032	429.54	0.5	3	'13/22	2516
904	R.SSTETCYSAIPK.A		1	54.170	0.00021	672.31	-0.4	2	'9/22	2303
905	R.QTVAVGVIK.N		1	44.870	0.0036	457.79	0.0	2	'8/16	2571
906	R.RGDLPFVVPR.R		4	40.970	0.0075	385.89	0.1	3	'6/18	4857
907	K.SLLELAR.M		1	46.390	0.0044	401.25	1.1	2	'6/12	4019
908	R.DLESLR.E		1	21.220	1.8	366.70	1.2	2	'5/10	2444
909	R.ASLEAAIADAEQR.G		2	76.800	2.8e-006	672.84	2.1	2	'9/24	4253
910	R.LVEVDSGR.Q		1	25.170	1	437.74	0.3	2	'6/14	1521
911	R.KPLVIIAEDVDGEALSTLVLNR.L		2	40.160	0.0035	789.12	0.0	3	'7/42	6724
912	R.GFGFILFK.D		1	26.490	0.32	464.77	0.0	2	'5/14	6175
913	R.SQEQEVLER.G		1	55.960	0.00029	559.28	-3.6	2	'6/16	1822
914	R.IGGGIDVPVPR.H		2	62.560	4.1e-005	540.32	2.1	2	'10/20	3725
915	K.EFQLFSSPHGK.D		2	29.920	0.16	426.22	0.4	3	'6/20	4362
916	R.VRFATHAAALSVR.N		1	35.860	0.027	350.45	-1.2	4	'11/24	4673
917	R.TTPSVVAFTADGER.L		1	77.030	3.2e-006	725.86	1.4	2	'9/26	3644
918	K.ASLLHQDSESR.R		2	58.170	0.00016	621.81	-0.2	2	'7/20	2318
919	R.SLDNFFAKR.D		1	22.340	0.67	366.53	0.4	3	'8/16	4456
920	K.TGVTSTSDSEEEGDDQEGEKKR.K		1	57.580	6.7e-005	596.76	-2.1	4	'11/42	1578
921	K.YEELQSLAGKHGDDLR.R		1	32.010	0.088	458.48	-1.3	4	'7/30	3915
922	R.GLQATQLAR.S		1	43.840	0.0057	479.28	-0.3	2	'6/16	2280
923	R.LIDLHSPSEIVK.Q		1	25.920	0.23	450.93	0.2	3	'10/22	4041
924	K.VLTPTQVK.N		1	29.990	0.1	443.27	0.3	2	'6/14	1986
925	R.FLEQQNQVLQTK.W		2	62.170	0.00013	738.40	0.3	2	'8/22	3236
926	K.CGLVPVLAENYK.S		1	36.310	0.045	681.86	-3.9	2	'13/22	4759
927	R.VTEDSEEEEEEEEER.E		1	115.190	1.4e-011	934.36	-0.5	2	'12/28	1497
928	K.SASDLTWDNLKGKK.S		6	54.910	0.00066	781.91	0.1	2	'11/26	3571
929	R.LAKLSDGVAVLK.V		1	31.460	0.042	405.25	-1.0	3	'9/22	4091
930	R.SGAQASSTPLSPTR.I		1	59.020	0.00021	680.35	0.7	2	'7/26	1771
931	K.AEDGATPSPSNETPK.K		1	33.910	0.025	750.85	2.0	2	'6/28	1267
932	K.KQELEEICHDLEAR.V		1	20.950	0.98	590.62	2.3	3	'15/26	4839
933	R.TTPSYVAFTDTER.L		6	62.000	5.7e-005	744.35	-0.3	2	'8/24	3582
934	K.TLDFDALSVGQR.G		1	63.460	7.5e-005	661.34	1.4	2	'7/22	4749
935	K.VAVTEGCQPSR.V		1	50.290	0.001	602.29	-0.5	2	'8/20	1345
936	R.RALDFAVGEYNK.A		1	26.990	0.31	461.57	-0.5	3	'8/22	4123
937	K.EVFEDAAEIR.L		1	55.960	0.00031	589.79	-1.0	2	'8/18	3475
938	R.KGSHGLEIFQR.C		1	42.870	0.0082	424.57	0.2	3	'11/20	5093

939	R.SSGSPYGGGYGSGGGSGGYGSR.R		1	121.580	9.5e-012	955.90	-1.0	2	'16/42	2400
940	K.KSDVEAIFSKYGK.I		3	40.270	0.013	491.27	1.8	3	'12/24	4412
941	K.IFVGGLSPDTPEEK.I		1	72.210	1e-005	744.88	1.1	2	'11/26	3876
942	R.TKLDELKR.Q		1	32.570	0.063	334.87	-1.4	3	'5/14	2780
943	R.QLYEEEIR.E		1	45.460	0.0039	540.27	-0.4	2	'6/14	2753
944	R.VVIIGAGKPAAVVLQTK.G		1	53.990	2.1e-005	555.35	-1.4	3	'18/32	4851
945	R.LEQEIATYR.R		4	56.310	0.00045	561.79	-0.5	2	'6/16	2507
946	R.LEQEIATYR.S		4	56.310	0.00045	561.79	-0.5	2	'6/16	2507
947	R.FGIVTSSAGTGTTEDTEAK.K		1	56.140	0.00023	936.44	-5.5	2	'11/36	3094
948	R.LQTSSVLVSGLR.G		1	70.500	1e-005	630.37	-5.9	2	'8/22	3953
949	R.AELSEGQVR.Q		4	54.130	0.00058	494.76	1.2	2	'8/16	1493
950	R.SYSCQVTHEGSTVEK.T		1	21.260	0.41	571.26	0.2	3	'14/28	2016
951	K.TFDQLTPEESKER.L		1	22.560	0.79	527.26	-1.8	3	'13/24	2844
952	K.AIEENNNFSK.M		1	39.390	0.012	583.28	0.9	2	'5/18	1610
953	K.YIDQEELNK.T		2	44.540	0.0063	576.28	0.1	2	'7/16	2119
954	R.SSAVDPEPQVK.L		1	40.950	0.0091	578.80	0.0	2	'13/20	1626
955	K.WQNSYSIK.V		1	22.500	0.59	513.26	-0.4	2	'5/14	2718
956	R.AGGPTTPLSPTR.L		1	35.870	0.047	577.81	1.6	2	'6/22	2181
957	R.ASGQAFELILSPR.S		2	74.110	6e-006	694.88	2.0	2	'8/24	5214
958	K.LEATINELV.-		1	55.870	0.00047	501.28	-0.3	2	'7/16	5106
959	K.EESDDEAAVEEEEEEKKPK.T		1	21.720	0.22	555.75	-0.9	4	'11/36	1998
960	R.QRAELEELR.Q		1	19.520	3.1	381.88	-0.2	3	'7/16	2982
961	R.LADALQELR.A		1	76.630	2.6e-006	514.79	-0.4	2	'8/16	3802
962	K.VLQATVVAVGSGSK.G		1	118.810	1.4e-010	658.38	0.1	2	'12/26	3010
963	R.QAGLSYIR.Y		1	38.740	0.018	454.25	-0.1	2	'7/14	2833
964	R.LEEPEEPK.V		1	25.210	0.23	485.74	0.4	2	'6/14	1495
965	R.DAVTYTEHAK.C		2	43.300	0.0056	567.78	0.3	2	'11/18	1596
966	K.LAEIGAPIQGNR.E		1	66.060	2.3e-005	619.85	-0.1	2	'9/22	3036
967	R.NSNLVGAAHEELQQSR.I		2	86.240	3.8e-007	876.94	1.1	2	'13/30	3711
968	R.ELVLDNCK.S		1	31.730	0.097	495.75	1.4	2	'6/14	2374
969	K.YVECSALTQK.G		1	40.830	0.0075	599.79	0.0	2	'7/18	2111
970	R.LQAEIEGLKGQR.A		1	22.490	0.85	447.92	0.6	3	'11/22	3020
971	K.ALDLDSSCKEAADGYQR.C		1	46.590	0.0014	633.62	-0.6	3	'14/32	2988
972	R.IQEAGTEVVKAK.A		1	47.820	0.0021	424.91	1.3	3	'9/22	1999
973	K.IAEVDCTAER.N		1	54.030	0.00028	582.27	0.1	2	'9/18	1601

974	K.EAAGKSSGPTSLFAVTVAPPGAR.Q		1	25.840	0.31	724.39	-1.2	3	'10/44	4866
975	R.LLLPGELAK.H		6	39.570	0.002	477.31	0.1	2	'7/16	4361
976	K.LQQENSILR.N		1	42.020	0.012	550.81	-0.2	2	'7/16	2544
977	K.LLSDKLK.E		2	25.360	0.16	408.76	0.5	2	'5/12	2543
978	K.WAEQYLK.I		1	28.220	0.18	469.24	2.0	2	'6/12	3401
979	K.VGVNGFGR.I		1	46.910	0.0034	403.22	-0.5	2	'6/14	2449
980	R.YQKSTELLIR.K		2	32.980	0.048	417.57	-0.2	3	'8/18	3530
981	R.QLLLTADDR.V		1	55.780	0.00045	522.79	-1.5	2	'8/16	3342
982	K.DLAGSIIGK.G		1	20.920	2	437.26	-1.3	2	'5/16	3824
983	K.AVNEKSCNCLLLK.V		1	23.650	0.79	516.93	-0.9	3	'12/24	3364
984	R.LSQETEALGR.S		1	56.790	0.00037	552.29	-3.4	2	'7/18	1894
985	R.AIMTYVSCFYHAFAGAEQAETAANR.I	0.0010000000000000000000000.0	1	32.740	0.035	932.42	0.1	3	'25/48	6215
986	K.EVTEEEAER.F		1	31.820	0.044	546.25	-0.4	2	'5/16	1310
987	R.SDGSCAWYR.G		2	47.210	0.00026	551.23	0.8	2	'8/16	2696
988	R.DASTLQSQKAEGTGDAK.-		1	27.760	0.21	569.61	0.9	3	'13/32	1317
989	R.LEPKPQPPVAEATPR.S		1	43.110	0.0087	543.97	0.1	3	'7/28	2757
990	R.VIGSGCNLDSAR.F		3	53.180	0.00057	624.80	0.6	2	'9/22	2264
991	R.GLETSLAECTFTK.R		1	90.720	8.1e-008	728.85	-4.1	2	'9/24	4103
992	R.INISEGNCPER.I		2	51.920	0.00042	644.80	0.2	2	'8/20	2012
993	K.CSTSIANQAVR.I		2	29.260	0.16	603.80	0.8	2	'8/20	1767
994	K.ADDLGKGGNEESTKTGNAGSR.L		2	60.980	6.8e-005	688.66	-0.4	3	'21/40	1694
995	K.DTLGNTQIKQK.S		1	21.750	1.2	623.34	-5.5	2	'8/20	1731
996	K.NQLTSNPENTVFDAKR.L		1	32.660	0.082	611.97	-0.7	3	'14/30	3391
997	K.ELESQVSGLEK.E		1	25.180	0.55	609.82	13.1	2	'8/20	2682
998	R.TIGISVDPR.R		1	48.750	0.0016	479.27	-0.1	2	'7/16	3086
999	R.SLLEGQEDHYNNLSASK.V		1	30.160	0.22	635.64	-0.2	3	'21/32	3705
1000	R.AEIQIR.I		1	33.450	0.089	365.22	-1.5	2	'5/10	1874
1001	K.TCVADESAENCDK.S		1	50.390	2.9e-005	749.79	1.2	2	'9/24	1133
1002	R.VFTAGSEER.V		1	47.520	0.0017	498.24	-0.2	2	'7/16	1675
1003	R.ALQASALK.A		1	21.870	1.2	401.24	-2.1	2	'5/14	1881
1004	R.LASYLDK.V		4	22.020	0.64	405.22	2.0	2	'5/12	2293
1005	R.VAQLEQVYIR.G		1	68.490	2.1e-005	609.85	-0.5	2	'9/18	3686
1006	R.VFIGNLNTLVVKK.S		3	20.910	0.12	482.30	0.0	3	'11/24	4895
1007	R.YYCFQGNQFLR.F		1	45.390	0.0021	748.34	-0.5	2	'13/20	4703
1008	K.AEPVEVVAPR.G		1	54.300	0.00038	533.80	0.3	2	'7/18	2512
1009	R.VVVLGLLPR.G		1	59.120	2e-006	483.33	-0.6	2	'7/16	5220

1010	K.TVTAMDVVYALK.R	0.000010000000.0	1	48.540	0.0018	663.85	-0.8	2	'9/22	4520
1011	K.RKASGPPVSELITK.A		2	54.970	0.00018	494.96	-0.5	3	'22/26	5073
1012	K.QAEILQESR.M		1	27.400	0.29	537.28	-3.4	2	'6/16	2151
1013	R.QITVNDLPVGR.S		2	45.930	0.0028	606.34	1.7	2	'9/20	3671
1014	K.NAGAVIGKGGKNIK.A		1	33.100	0.034	442.93	-0.3	3	'12/26	2998
1015	R.SGLLEVLVR.D		1	40.910	0.0084	493.31	0.5	2	'5/16	5578
1016	K.ESYSVYVYK.V		2	23.640	0.52	569.27	-3.3	2	'6/16	3165
1017	R.FLQDYFDGNLKR.Y		2	29.740	0.15	505.92	-2.8	3	'12/22	4999
1018	R.IALDFQR.G		1	26.050	0.44	431.74	-0.3	2	'4/12	3606
1019	K.VAVNDAHLLQYNHR.V		1	26.380	0.4	413.22	0.1	4	'12/26	3814
1020	R.VLIAAHGNSLR.G		1	20.700	0.68	384.23	0.3	3	'7/20	3352
1021	K.ASAAFSSVGSVITKK.L		1	20.040	0.97	484.94	-0.6	3	'10/28	3694
1022	K.STGGAPTFNVTVTKTDK.T		2	86.620	5.3e-007	862.45	0.6	2	'12/32	2910
1023	R.KLVILEGELER.A		4	37.090	0.015	433.59	0.2	3	'9/20	5009
1024	R.LFQVR.A		2	25.600	0.28	331.70	0.3	2	'4/8	2761
1025	K.DLLFRDDTVCLAK.L		6	69.780	4e-005	783.40	-0.4	2	'11/24	4917
1026	R.VLNTNIDGR.R		1	51.350	0.0013	501.27	1.3	2	'7/16	2101
1027	R.CGETGHVAINCSK.T		1	37.630	0.0053	478.21	-1.0	3	'12/24	2120
1028	R.AIEASNAYSR.I		1	62.230	5.1e-005	541.26	-13.6	2	'7/18	1559
1029	R.IQLVEEELDR.A		15	62.480	8.1e-005	622.33	0.2	2	'8/18	3934
1030	R.DSAQTSVTQAQR.E		2	71.390	8.4e-006	646.32	0.9	2	'10/22	1082
1031	R.ALELENDR.L		1	32.160	0.071	480.24	-1.1	2	'6/14	2168
1032	R.EADVDQDGRVNYEEFAR.M		1	38.210	0.0068	671.64	-0.7	3	'14/32	3491
1033	K.AEAESLYQSK.Y		1	66.540	2.1e-005	563.27	-1.8	2	'10/18	1795
1034	K.EGVVECSFVK.S		1	27.620	0.21	577.28	0.4	2	'6/18	3177
1035	R.SLETENAGLRLR.I		1	35.660	0.044	453.58	-0.1	3	'6/22	3562
1036	K.NLPYKVTQDELK.E		2	49.900	0.0018	724.39	-0.5	2	'7/22	3853
1037	R.SGTDVDAANLR.E		1	76.350	3e-006	559.78	-0.4	2	'9/20	1967
1038	R.VFSGLVSTGLKVR.I		1	20.020	0.41	454.94	0.1	3	'8/24	4880
1039	R.YLAADKDGNVTCER.E		1	31.520	0.058	537.92	0.4	3	'15/26	2469
1040	K.LTVDSAIAR.D		1	34.920	0.064	473.27	-3.5	2	'8/16	2689
1041	K.LLSISGKR.S		2	30.170	0.069	437.28	0.7	2	'4/14	2911
1042	K.VIADNVKDWSK.V		3	19.830	2	425.56	0.4	3	'10/20	3195
1043	K.SDNCEDTPEAGYFAVAVVKK.S		2	59.060	0.00011	734.01	2.6	3	'20/38	4311
1044	R.QGANINEIR.Q		1	57.420	0.00023	507.77	-0.5	2	'8/16	2057
1045	R.KLVILEGELER.S		4	37.090	0.015	433.59	0.2	3	'9/20	5009
1046	K.DLSLEEIQKK.L		4	47.710	0.0027	601.84	1.1	2	'7/18	3153

1047	K.LTMQNLNDR.L	0.001000000.0	1	34.940	0.043	560.77	-0.5	2	'8/16	1450
1048	R.LDIDSPPITAR.N		1	50.150	0.0012	599.33	-0.9	2	'10/20	3585
1049	R.IEDVTPIPSDSTRR.K		1	22.190	0.84	529.28	-2.8	3	'16/26	2676
1050	R.TVIIEQSWGSPK.V		1	59.410	0.00018	672.86	-0.8	2	'10/22	3762
1051	R.RAPQTGIVDECCFR.S		1	35.990	0.021	570.27	0.8	3	'9/26	3610
1052	K.LIELQAGKK.S		1	24.200	0.36	333.88	-1.8	3	'5/16	2733
1053	R.LVSSDPEINTK.K		1	39.060	0.02	601.82	0.7	2	'8/20	1939
1054	R.LSKEEIER.M		2	28.960	0.24	335.19	0.5	3	'6/14	1684
1055	R.NQGGYGGSSSSSSYGSGR.R		2	114.040	6.2e-011	847.85	-0.1	2	'15/34	1332
1056	K.DQVANSAFVER.L		1	66.680	2.7e-005	618.30	-0.1	2	'8/20	2563
1057	R.LSSEMNTSTVNSAR.E	0.00001000000000.0	1	59.510	8.5e-005	756.85	0.3	2	'8/26	1216
1058	R.LGTTPSVYGGAGGR.G		1	46.110	0.0046	646.83	-0.1	2	'8/26	2498
1059	R.DSVLTSKNQIER.L		1	35.010	0.053	463.92	-1.7	3	'12/22	2323
1060	R.SPHSGMTTPMSR.G	0.000001000100.0	1	32.620	0.027	660.79	9.8	2	'6/22	2452
1061	K.KLEENEVIPK.R		1	40.490	0.011	599.84	-0.4	2	'6/18	2878
1062	R.ITESEEVVSR.E		1	83.050	7.9e-007	574.79	0.4	2	'8/18	1703
1063	K.SLVSKGTLVQTK.G		6	53.570	0.0002	630.88	-1.6	2	'8/22	3131
1064	K.KTIERR.Y		1	23.970	0.9	401.74	-15.2	2	'4/10	3563
1065	R.VLQSFTVDSSK.A		1	54.350	0.0006	605.82	0.4	2	'8/20	3001
1066	R.VGLKAPGIIPR.I		2	47.200	0.00011	374.25	0.9	3	'11/20	4341
1067	K.QGCDCECLGGGR.T		1	85.730	4.4e-009	684.76	-0.5	2	'10/22	1504
1068	K.STGGAPTFNVTVTK.T		1	71.390	1.2e-005	690.36	0.9	2	'10/26	3164
1069	R.NTGIICTIGPASR.S		1	61.230	0.00014	680.36	-0.2	2	'7/24	3532
1070	R.HLQLAIRNDEELNK.L		1	23.060	0.66	564.97	-1.0	3	'14/26	4441
1071	R.SGGYGGSRDYYSSR.S		2	37.130	0.0071	504.56	0.5	3	'9/26	2378
1072	R.FATHAAALSVR.N		1	43.760	0.013	381.88	-0.3	3	'8/20	3542
1073	K.KAQQELEEQTRR.A		1	21.560	1.2	505.93	0.3	3	'9/22	2178
1074	K.CCTESLVNR.R		1	49.100	0.00052	569.75	0.7	2	'8/16	1873
1075	R.AGRGFSLEELR.V		1	29.580	0.19	412.22	0.7	3	'12/20	4510
1076	R.GFFYTPK.T		2	26.920	0.27	430.22	0.0	2	'5/12	3945
1077	R.GALQNIIPASTGAAK.A		1	42.940	0.0055	706.40	0.9	2	'9/28	3939
1078	R.IGCIITAR.K		1	48.470	0.0027	452.26	-0.7	2	'7/14	2945
1079	R.VGLKAPGIIPR.T		1	47.200	0.00011	374.25	0.9	3	'11/20	4341
1080	R.NYQQNYQNSESGEK.N		1	57.740	3.7e-005	844.86	-0.4	2	'9/26	1346
1081	R.KIQVLQQQADDAEER.A		3	57.290	0.00031	590.97	0.1	3	'16/28	3186
1082	R.AVVIVDDRGR.S		1	28.290	0.19	367.21	-0.2	3	'5/18	2270
1083	R.CESQSTLDPGAGEAR.A		1	78.790	4.2e-007	789.35	0.2	2	'12/28	1851
1084	R.EAGEQGDIEPR.R		1	69.770	1.4e-005	600.78	0.4	2	'10/20	1433
1085	R.TVIDYNGER.T		2	52.560	0.00068	533.76	-1.9	2	'13/16	2171

1086	K.LYEQLSGK.-		1	41.960	0.0076	469.25	-0.3	2	'7/14	2195
1087	K.ALAAAGYDVEKNNSR.I		4	79.390	1.9e-006	789.90	3.2	2	'11/28	2608
1088	R.GYSFTTTAER.E		2	46.970	0.0014	566.76	-6.5	2	'8/18	2564
1089	K.FEDENFILK.H		2	50.780	0.0011	577.79	-0.6	2	'13/16	4406
1090	K.DSAHGFLKVPPR.M		6	30.990	0.098	441.91	-0.2	3	'7/22	3761
1091	K.AADIDQEVKER.A		1	29.080	0.19	425.22	2.4	3	'5/20	1897
1092	R.EESREPAPASPAPAGVEIR.S		1	40.750	0.013	655.00	2.5	3	'26/36	2801
1093	R.LASYLDR.V		2	27.760	0.2	419.23	-0.2	2	'5/12	2515
1094	R.AMSDLELR.Q	0.01000000.0	1	47.900	0.0024	475.73	-0.3	2	'7/14	2245
1095	R.LGQGIGPIHLNEIQCTGNEK.S		1	52.730	0.00079	726.70	-1.5	3	'17/38	5068
1096	K.YLGEEYVKAVGNLRK.C		4	19.380	1.3	435.49	-0.6	4	'16/28	5307
1097	K.ITIADCGQLE.-		1	43.170	0.0048	560.27	-1.2	2	'7/18	3739
1098	K.AGLVIGK.G		3	38.660	0.016	329.22	1.1	2	'9/12	2281
1099	K.GGEIQPVSVK.V		1	45.790	0.0023	507.28	0.0	2	'6/18	2089
1100	K.QLEAIDQLHLEYAKR.A		1	19.760	1.4	457.50	0.1	4	'17/28	4802
1101	K.DCVGPEVEK.A		1	44.430	0.0016	516.74	-0.5	2	'10/16	1526
1102	K.VTLTSEEEAR.L		1	47.910	0.0027	567.79	0.5	2	'7/18	1807
1103	K.DANNGNLQLR.N		1	44.910	0.0035	557.78	-0.7	2	'6/18	2099
1104	K.TGGTQTDLFTCGK.C		1	86.600	1.5e-007	693.32	-0.2	2	'9/24	2936
1105	R.EVEGELER.K		1	36.230	0.028	480.73	-1.4	2	'5/14	1572
1106	R.EVCSEQAETGPCR.A		2	63.330	5.7e-006	761.82	0.4	2	'9/24	1305
1107	K.SVEAAAELSAK.D		2	60.900	0.00014	538.29	0.1	2	'13/20	2197
1108	K.SNFSNSADDIKSK.K		2	46.760	0.0019	471.56	-0.5	3	'8/24	1930
1109	R.EDITQSAQHALR.L		1	21.910	1.6	456.90	1.5	3	'6/22	2819
1110	K.AVAGNISDPGLQK.S		1	54.950	0.00035	635.34	1.3	2	'8/24	2394
1111	R.VEVTEFEDIK.S		1	60.510	0.00014	604.81	-0.2	2	'8/18	3916
1112	R.TPITVVK.Q		2	42.090	0.0088	379.24	-0.4	2	'6/12	2055
1113	R.LLAQDQGQGAPLLEPAP.-		1	42.730	0.0083	859.46	1.6	2	'8/32	4817
1114	R.LLEGEESR.L		1	47.490	0.0028	466.74	-0.4	2	'5/14	1588
1115	K.NQVALNPQNTVFDAK.R		1	84.010	5.7e-007	829.93	-1.1	2	'17/28	3796
1116	K.VGGTSDVEVNEK.K		1	67.040	2.4e-005	617.30	-1.2	2	'9/22	1411
1117	R.LQAEEVAQQK.S		1	36.660	0.056	572.31	2.6	2	'7/18	1539
1118	K.NNTQVLINCR.N		1	48.290	0.0024	616.32	1.5	2	'7/18	2382
1119	K.EELEQASQAHGAR.L		1	28.130	0.26	475.90	-0.6	3	'10/24	1685
1120	K.AAFDIFVLGAEDGCISTK.E		1	42.420	0.0073	957.47	-0.5	2	'12/34	6111
1121	K.EGYYGYTGAFR.C		2	48.310	0.00071	642.29	-0.1	2	'8/20	3924

1122	K.EEQKSNTAGSQSQVETEA.-		1	31.970	0.038	961.93	2.1	2	'9/34	1368
1123	R.LAADDFR.L		2	40.680	0.015	404.20	0.2	2	'6/12	2407
1124	R.EGELTVAQGR.V		1	48.690	0.0017	530.28	0.6	2	'6/18	1926
1125	K.SVIPSDGPSVACVKK.A		8	78.210	2.5e-006	772.41	-0.6	2	'12/28	2991
1126	R.IIIEELPK.-		1	34.770	0.014	477.80	0.1	2	'5/14	3949
1127	R.IELYQILK.S		1	31.020	0.045	510.31	0.9	2	'4/14	5177
1128	R.EGGLFPR.G		1	24.700	0.69	388.21	0.6	2	'5/12	3151
1129	K.LLEGEEER.L		3	42.770	0.0059	487.74	-0.7	2	'7/14	1711
1130	K.YHTINGHNAEVR.K		1	25.930	0.28	470.90	-0.1	3	'6/22	2858
1131	M.KSVIPSDGPSVACVK.K		1	25.770	0.44	515.28	-0.3	3	'13/28	3100
1132	R.AAPTAASDQPDSAATTEK.A		1	69.470	1.1e-005	866.41	0.2	2	'21/34	1290
1133	R.LAADDFR.T		2	40.680	0.015	404.20	0.2	2	'6/12	2407
1134	R.VLGLVLLR.G		1	54.440	1.2e-005	441.81	-0.8	2	'7/14	5812
1135	K.CQSFR.D		3	20.850	0.39	349.16	0.4	2	'4/8	1093
1136	R.NFSDNQLQEGK.N		1	56.650	0.00018	640.30	0.6	2	'9/20	2149
1137	R.VIAVNEVGR.S		1	50.800	0.00091	478.78	1.4	2	'7/16	2362
1138	R.AAVLLEQER.Q		1	63.860	5e-005	514.79	0.1	2	'8/16	2729
1139	R.LAADDFR.V		2	40.680	0.015	404.20	0.2	2	'6/12	2407
1140	R.AALQELLSK.G		1	59.080	0.00027	486.79	-0.4	2	'7/16	4321
1141	R.SAGVPSRVIHIR.K		1	25.650	0.15	323.70	1.0	4	'12/22	4059
1142	R.VSFELFADKVPK.T		4	63.140	5.5e-005	690.38	-0.1	2	'10/22	5179
1143	R.VEILANDQGNR.T		1	66.110	3.2e-005	614.82	-0.2	2	'8/20	2085
1144	K.ELEKVCNPIITK.L		2	20.010	1.5	481.93	-0.3	3	'9/22	3332
1145	K.SKEFQLFSSPHGK.D		6	54.990	0.00068	746.38	-1.5	2	'9/24	4562
1146	K.HIAEDADRKYEEVAR.K		8	23.180	0.59	451.23	-0.3	4	'14/28	3277
1147	R.EWEEAER.Q		1	24.620	0.082	474.71	0.8	2	'5/12	1643
1148	R.FGPGVAFR.A		1	35.730	0.043	425.73	1.4	2	'7/14	3956
1149	R.RGFCFITFK.E		1	35.310	0.049	588.31	0.1	2	'5/16	5633
1150	R.YYGYTGAFR.C		1	37.610	0.012	549.26	-1.9	2	'7/16	3673
1151	R.TDYNASVSVPDSSGPER.I		1	56.340	0.00019	890.90	-0.3	2	'10/32	2688
1152	R.DQYELLCLDNTR.K		3	75.280	2.4e-006	770.36	-1.4	2	'18/22	4774
1153	R.CSCASGFLLAADGKR.C		1	29.190	0.12	538.26	2.4	3	'17/28	4011
1154	R.GFCFITFK.E		1	22.480	0.78	510.25	0.2	2	'5/14	5401
1155	K.EKYEKDIAAYR.A		4	25.500	0.42	462.57	-0.4	3	'8/20	3287
1156	R.VLEEGSVEAR.T		1	52.820	0.00095	544.78	-0.8	2	'9/18	1887
1157	M.PYQYPALTPEQKK.E		2	50.090	0.002	781.92	2.2	2	'19/24	3278
1158	K.SAADLISQAR.K		1	76.740	3.8e-006	516.28	-0.1	2	'14/18	2964

1159	K.TQLAVCQQR.I		1	46.370	0.0042	552.28	-0.2	2	'7/16	1715
1160	K.NFGIGQDIQPK.R		1	46.570	0.0039	608.82	-2.5	2	'8/20	3612
1161	K.VALLDVFR.E		1	37.460	0.014	466.78	-2.1	2	'12/14	5667
1162	R.LSLNIDPDAK.V		1	45.220	0.0036	543.30	1.2	2	'6/18	3750
1163	R.KLLASLVK.R		1	23.580	0.071	436.30	-0.9	2	'6/14	4951
1164	K.KHLEINPDHSIIETLR.Q		1	41.660	0.0071	479.52	0.5	4	'8/30	5581
1165	K.GKGGEIQPVSVK.V		2	48.060	0.0017	599.84	-1.3	2	'7/22	2365
1166	K.KGGVASGFKHVVPNEVVVQR.L		2	29.980	0.058	527.55	0.6	4	'19/38	5131
1167	R.NLLSVAYK.N		6	38.320	0.013	454.27	0.2	2	'6/14	3866
1168	K.TANKDHLVTAYNHLFETKR.F		1	43.240	0.0069	452.44	-1.2	5	'10/36	5522
1169	K.IIIPEIQK.V		2	30.100	0.018	477.31	0.1	2	'4/14	4361
1170	R.FDEFFSEGCAPGSK.K		2	85.610	5e-008	789.34	3.9	2	'11/26	4243
1171	K.SQGGEPTYNVAVGR.A		1	91.860	8.8e-008	717.85	0.8	2	'11/26	2490
1172	R.EGTCPEAPTDECKPVK.W		4	68.260	7.3e-006	909.41	0.3	2	'8/30	1819
1173	K.NLNEKDYELLCLDGTRK.S		2	33.400	0.063	694.35	0.5	3	'15/32	4487
1174	K.SLESTTLTEK.E		1	53.200	0.00074	554.79	0.9	2	'6/18	2240
1175	K.LRQPFFQKR.S		2	21.180	0.67	407.24	-3.4	3	'6/16	4656
1176	R.EYNEDEDPAAR.R		1	36.730	0.0034	654.77	3.7	2	'7/20	1421
1177	R.AFKAWAVAR.L		2	39.630	0.015	510.29	-3.8	2	'5/16	4422
1178	K.IDIIPNPQER.T		1	24.210	0.48	597.83	5.0	2	'5/18	3712
1179	R.LLIHQSLAGGIIGVK.G		1	32.000	0.0071	506.98	0.2	3	'9/28	5489
1180	K.EETQPPVALKK.E		1	31.400	0.064	413.90	-0.2	3	'14/20	2107
1181	K.IGPLGLSPK.K		1	38.090	0.0046	441.28	-1.0	2	'10/16	3885
1182	K.ILDILGETCK.S		3	56.540	0.00041	581.31	0.8	2	'6/18	4624
1183	R.DAQDVQASQAEADQQQTR.L		2	78.250	8.4e-007	994.95	-1.3	2	'9/34	1540
1184	R.QAFQIGSPWR.T		1	52.550	0.00099	595.31	-0.1	2	'8/18	4622
1185	R.GDLGIEIPAEK.V		2	34.490	0.041	571.31	-4.9	2	'11/20	3897
1186	R.VLDELTLAR.A		1	61.030	0.00013	515.30	-0.3	2	'8/16	4038
1187	R.KYAVLYQPLFDKR.F		1	29.150	0.1	547.65	4.5	3	'9/24	5434
1188	R.ADLAKYICENQDSISSK.L		1	22.680	0.76	647.98	-3.3	3	'15/32	4017
1189	K.AGAVEKGVPLYR.H		1	21.290	1	420.57	-0.3	3	'11/22	3269
1190	R.IVAPGKGILAADESTGSIAK.R		1	67.310	1.5e-005	633.36	-1.3	3	'12/38	4706
1191	R.IEDVTPIPSDSTR.R		1	55.400	0.00041	715.36	-1.8	2	'11/24	2900
1192	R.VFIGNLNTLVVK.K		3	68.310	4.3e-006	658.90	3.5	2	'10/22	5204

1193	K.WKDSDEADLVLAK.E		1	65.190	4.6e-005	497.26	0.0	3	'8/24	3937
1194	R.ETQSQLETER.S		1	35.000	0.031	610.79	-0.8	2	'7/18	1231
1195	M.PFSNSHNALKLR.F		1	24.020	0.51	346.69	-1.3	4	'12/22	4409
1196	K.ESEFDDEPK.F		1	65.900	5.4e-006	548.23	0.7	2	'7/16	1680
1197	R.VSLASPNR.G		2	33.750	0.052	422.24	-0.1	2	'6/14	1977
1198	K.SQGAALDKYAK.K		1	29.230	0.16	384.54	0.7	3	'7/20	2441
1199	K.CCSGAIIVLTK.S		1	36.250	0.13	611.32	1.6	2	'9/20	3763
1200	R.SLDADEFR.Q		1	29.720	0.083	476.72	-0.3	2	'7/14	2827
1201	K.LAPEFAKR.N		1	20.230	1.6	311.18	-1.4	3	'5/14	2802
1202	K.AKHDELTYF.-		1	24.620	0.62	562.27	-0.3	2	'6/16	4385
1203	K.AALEDTLAETEAR.F		1	89.900	1.7e-007	695.35	-0.4	2	'10/24	3534
1204	K.LLEGEESR.I		3	47.490	0.0028	466.74	-0.4	2	'5/14	1588
1205	R.RGFVFITFK.E		1	23.500	0.73	557.82	1.0	2	'4/16	5890
1206	R.SQSAAVTPSSTTSSTR.A		1	53.270	0.00053	784.38	0.2	2	'9/30	1154
1207	K.LLEGEESR.L		2	47.490	0.0028	466.74	-0.4	2	'5/14	1588
1208	K.IQQLVKEFFNGK.E		1	25.300	0.31	484.27	-0.3	3	'5/22	6006
1209	R.GSAVWCQNVK.T		1	42.410	0.0071	574.78	-1.3	2	'7/18	2678
1210	R.VNHVTLSQPK.I		1	30.720	0.085	374.88	-0.4	3	'9/18	2087
1211	R.VLDELTLAR.T		2	61.030	0.00013	515.30	-0.3	2	'8/16	4038
1212	R.SKVDEAVAVLQAHQAK.E		3	54.560	0.00044	565.31	-4.2	3	'14/30	4296
1213	R.ISSSSFSR.V		1	33.030	0.037	435.72	-0.1	2	'7/14	1599
1214	R.SSFYVNGLTLGGQK.C		3	92.100	8.9e-008	735.88	0.1	2	'19/26	4495
1215	K.DKEACVHK.I		2	29.130	0.069	329.50	-0.5	3	'6/14	1028
1216	K.LQDAEIAR.L		1	53.430	0.00065	458.25	0.2	2	'7/14	1662
1217	K.ELVSSSSSGSDSDSEVDKK.L		2	81.060	3.8e-007	971.94	-0.6	2	'14/36	1529
1218	K.EVANSTANLVK.T		1	53.000	0.00086	573.31	-0.7	2	'9/20	2072
1219	R.IINEPTAAAIAYGLDKK.G		1	26.130	0.23	596.67	-0.7	3	'12/32	4557
1220	K.GEFVTTVQQR.G		1	49.000	0.0019	582.80	-0.1	2	'8/18	2519
1221	K.SEEEQSSSSVKKDETNVK.M		2	31.910	0.06	670.99	-1.5	3	'17/34	1511

#

Serial (sequential) number for peptide.
Sequence

Assigned peptide sequence. Periods (".") delimit the sequence for internal peptides.
PTM Site

Location of the post-translational modification (PTM) in the peptide.

Modification codes: [1] Oxidation (M)
Nr. Scans

The number of MS/MS scans that were matched to this peptide.
Mascot Score

Score given to this peptide/spectrum match by Mascot.
Expectation

The number of matches with equal or better scores that are expected to occur by chance alone.
Isolated Mass

"Mass" in the Orbitrap analyzer.
Delta Mass

Difference between the observed and theoretical masses, in ppm.
Charge State

Inferred ionic state of the peptide.
Matched Ions

Number of matched MS/MS ions, as reported by Mascot.
Scan Nr.

MS/MS scan number in the original Xcalibur RAW file.