

Proteomic and metagenomic insights into prehistoric Spanish Levantine Rock Art

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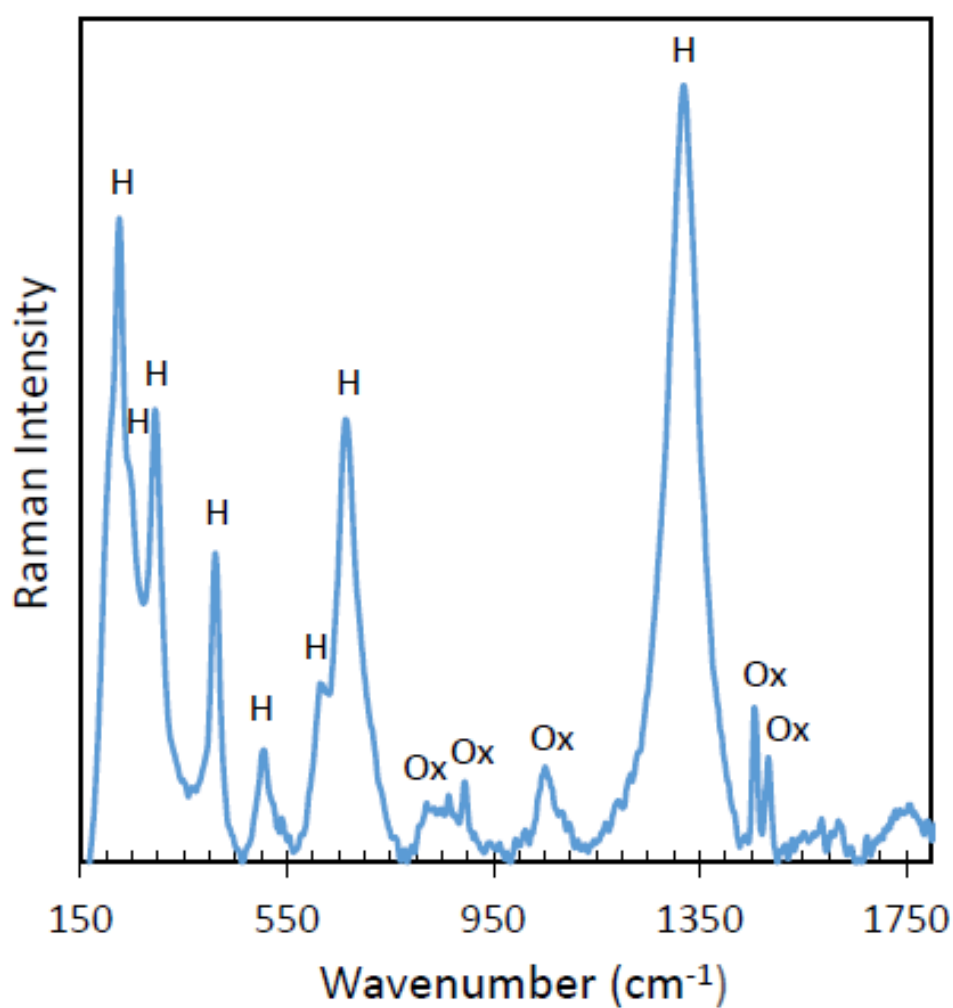
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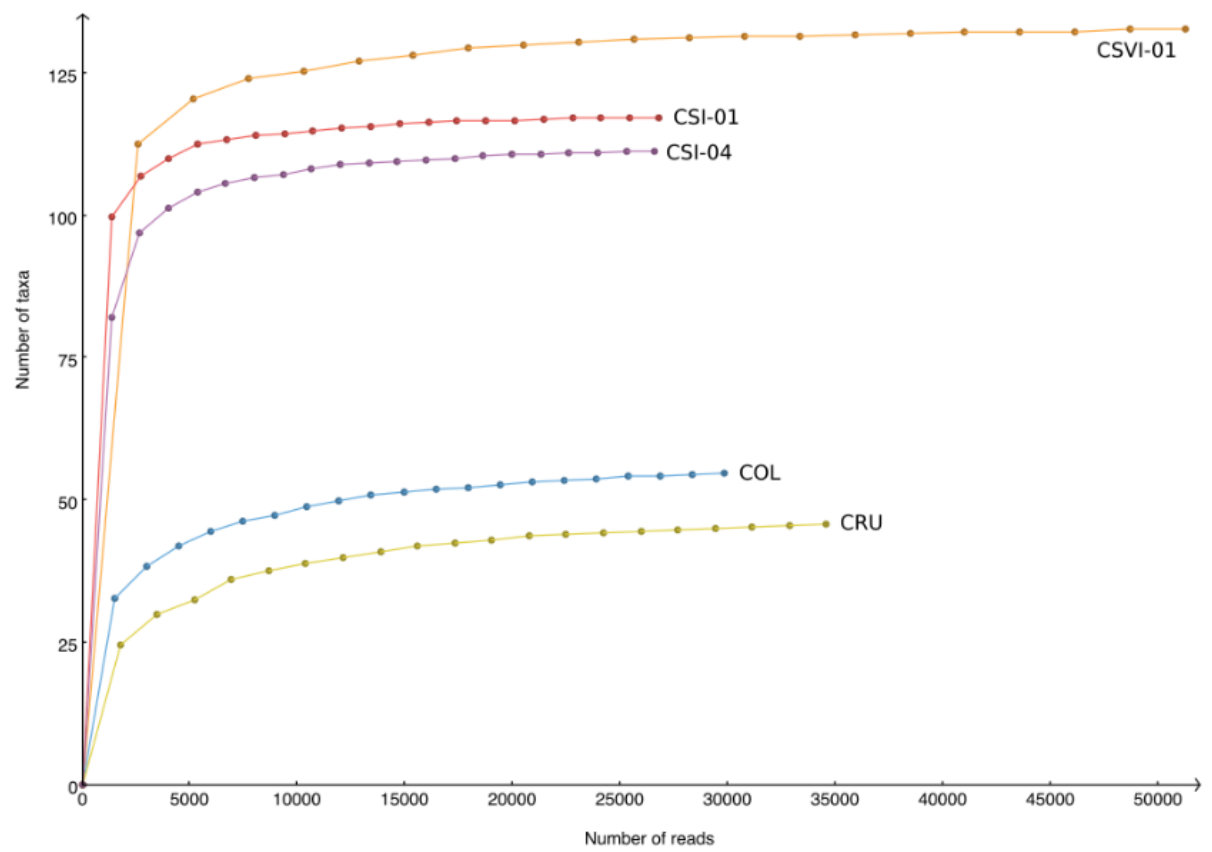
Supplementary tables and figures

Supplementary Table S1 | Summary of sequencing statistics.

Sample	Raw reads				Trimmed reads			
	Num. Seq	Av. Length	Total Mb	Av. Qual	Num. Seq	Av. Length	Total Mb	Av. Qual
CSI-01	51266	457,33	23,45	36,92	50728	433,67	22	37,11
CSI-04	62185	452,38	28,13	35,6	61517	429,1	26,4	37,22
CSVI-01	103839	456,08	47,36	37,02	102928	433,27	44,6	37,22
CRU	75932	442,62	33,61	36,98	75250	419,75	31,59	37,24
COL	75151	446,41	33,55	36,81	74332	423,27	31,46	37,04



Supplementary Figure S1 | Raman spectrum obtained from sample CSV-02. The bands indicated by H, belong to Hematite iron oxide phase (Fe_2O_3) and the bands indicated by Ox, correspond to the whewellite phase (calcium oxalate monohydrate, $\text{CaC}_2\text{O}_4 \cdot \text{H}_2\text{O}$).



Supplementary Figure S2 | Rarefaction analysis of 16S rRNA data.

Supplementary Data S1 | Protein identification in individual searches against SWISSPROT database.

N	CSI_2	Total	%Cov	%Cov(50)	%Cov(95)	Accession	Name	Species	Peptides(95%)
1	80,71	80,71	70,81000209	68,48000288	60,55999994	sp P04264 K2C1_HUMAN	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV	HUMAN	78
2	73,99	73,99	63,35999966	60,44999956	58,89999866	sp P13645 K1C10_HUMAN	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 S	HUMAN	67
3	61,29	70,74	74,18000102	67,91999936	58,06000233	sp P35908 K2E2_HUMAN	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KR	HUMAN	51
4	41,82	42,51	58,10999987	52,81000137	50,72000027	sp P35527 K1C9_HUMAN	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=	HUMAN	29
5	17,59	17,59	64,93999958	48,05000126	48,05000126	sp P00761 TRYP_PIG	Trypsin OS=Sus scrofa PE=1 SV=1	PIG	20
9	10,67	26,62	31,56000078	26,76999867	22,86999971	sp P48668 K2C6C_HUMAN	Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C PE=1	HUMAN	18
9	0	26,62	31,56000078	26,76999867	22,86999971	sp P02538 K2C6A_HUMAN	Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1	HUMAN	18
16	6,11	22,99	37,63000071	26,44000053	21,69000059	sp P13647 K2C5_HUMAN	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV	HUMAN	17
16	0	22,06	34,97000039	23,81999994	19,08999979	sp A5A6M8 K2C5_PANTR	Keratin, type II cytoskeletal 5 OS=Pan troglodytes GN=KRT5 PE=2 S	PANTR	16
6	16,07	22,38	39,10999894	28,74999994	23,68000001	sp P08779 K1C16_HUMAN	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 S	HUMAN	14
17	6,02	22,22	45,12999952	33,68999958	27,12000012	sp P02533 K1C14_HUMAN	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 S	HUMAN	13
13	8,01	15,16	22,14999944	15,21999985	13,49000037	sp Q7Z794 K2C1B_HUMAN	Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=2	HUMAN	12
28	2,01	15,6	21,40000015	16,38000011	14,40999955	sp P13646 K1C13_HUMAN	Keratin, type I cytoskeletal 13 OS=Homo sapiens GN=KRT13 PE=1 S	HUMAN	12
7	12,01	16,96	22,10000008	17,59999999	17,59999999	sp P19013 K2C4_HUMAN	Keratin, type II cytoskeletal 4 OS=Homo sapiens GN=KRT4 PE=1 SV	HUMAN	11
8	11,33	11,33	37,72000074	37,72000074	37,72000074	sp P06702 S10A9_HUMAN	Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1	HUMAN	8
11	9,01	9,01	21,51000053	10,99999994	10,99999994	sp P02768 ALBU_HUMAN	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	HUMAN	6
12	8,66	8,66	100	61,29000187	49,45999998	sp P05109 S10A8_HUMAN	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	HUMAN	6
29	2,01	4,61	15,37999958	5,000000075	5,000000075	sp Q8N1N4 K2C78_HUMAN	Keratin, type II cytoskeletal 78 OS=Homo sapiens GN=KRT78 PE=2	HUMAN	6
54	0,24	10,2	25,45999885	12,72999942	8,332999796	sp Q04695 K1C17_HUMAN	Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 S	HUMAN	6
54	0	10,2	23,61000031	12,72999942	8,332999796	sp A5A6M0 K1C17_PANTR	Keratin, type I cytoskeletal 17 OS=Pan troglodytes GN=KRT17 PE=2	PANTR	6
10	9,87	9,87	69,56999898	62,31999993	55,80000281	sp P15252 REF_HEVBR	Rubber elongation factor protein OS=Hevea brasiliensis PE=1 SV=2	HEVBR	5
14	6,57	6,57	10,10000035	8,293999732	6,196000054	sp Q02413 DSG1_HUMAN	Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	HUMAN	4
15	6,32	6,32	56,36000037	56,36000037	56,36000037	sp P81065 DCD_HUMAN	Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	HUMAN	4
18	5,62	5,62	22,82000035	17,44000018	11,54000014	sp P29508 SPB3_HUMAN	Serpin B3 OS=Homo sapiens GN=SERPINB3 PE=1 SV=2	HUMAN	3
19	5,54	5,54	23,19999933	23,19999933	15,19999951	sp Q912K5 ACTB_SIGHI	Actin, cytoplasmic 1 OS=Sigmodon hispidus GN=ACTB PE=2 SV=1	SIGHI	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp Q8JJ88 ACTG_TRISC	Actin, cytoplasmic 2 OS=Triakis scyllium GN=actg1 PE=2 SV=1	TRISC	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp Q76N69 ACTB_CHLAE	Actin, cytoplasmic 1 OS=Chlorocebus aethiops GN=ACTB PE=2 SV=	CHLAE	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp Q71FK5 ACTB_CAVPO	Actin, cytoplasmic 1 OS=Cavia porcellus GN=ACTB PE=2 SV=1	CAVPO	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp Q711N9 ACTB_MESAU	Actin, cytoplasmic 1 OS=Mesocricetus auratus GN=ACTB PE=1 SV=	MESAU	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp Q6QAQ1 ACTB_PIG	Actin, cytoplasmic 1 OS=Sus scrofa GN=ACTB PE=1 SV=2	PIG	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp Q6P378 ACTG_XENTR	Actin, cytoplasmic 2 OS=Xenopus tropicalis GN=actg1 PE=2 SV=1	XENTR	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp Q5ZMQ2 ACTG_CHICK	Actin, cytoplasmic 2 OS=Gallus gallus GN=ACTG1 PE=1 SV=1	CHICK	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp Q5R6G0 ACTB_PONAB	Actin, cytoplasmic 1 OS=Pongo abelii GN=ACTB PE=2 SV=1	PONAB	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp Q5R1X3 ACTB_PANTR	Actin, cytoplasmic 1 OS=Pan troglodytes GN=ACTB PE=2 SV=1	PANTR	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp Q5JAK2 ACTG_PELLE	Actin, cytoplasmic 2 OS=Pelophylax lessonae GN=actg1 PE=2 SV=1	PELLE	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp Q4R561 ACTB_MACFA	Actin, cytoplasmic 1 OS=Macaca fascicularis GN=ACTB PE=2 SV=1	MACFA	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp Q4LOY2 ACTB_SPECI	Actin, cytoplasmic 1 OS=Spermophilus citellus GN=ACTB PE=2 SV=	SPECI	3
19	0	5,54	24,09999967	24,09999967	15,79000056	sp P84856 ACTB_CHLPG	Actin, cytoplasmic 1 OS=Chlorocebus pygerythrus GN=ACTB PE=1 S	CHLPG	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp P84336 ACTB_CAMDR	Actin, cytoplasmic 1 OS=Camelus dromedarius GN=ACTB PE=1 SV=	CAMDR	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp P63261 ACTG_HUMAN	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1	HUMAN	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp P63260 ACTG_MOUSE	Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1	MOUSE	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp P63259 ACTG_RAT	Actin, cytoplasmic 2 OS=Rattus norvegicus GN=Actg1 PE=1 SV=1	RAT	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp P63258 ACTG_BOVIN	Actin, cytoplasmic 2 OS=Bos taurus GN=ACTG1 PE=1 SV=1	BOVIN	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp P63257 ACTG_TRIVU	Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE=2 SV	TRIVU	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp P63256 ACTG_ANSAN	Actin, cytoplasmic 2 OS=Anser anser anser GN=ACTG1 PE=2 SV=1	ANSAN	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp P60713 ACTB_SHEEP	Actin, cytoplasmic 1 OS=Ovis aries GN=ACTB PE=2 SV=1	SHEEP	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp P60712 ACTB_BOVIN	Actin, cytoplasmic 1 OS=Bos taurus GN=ACTB PE=1 SV=1	BOVIN	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp P60711 ACTB_RAT	Actin, cytoplasmic 1 OS=Rattus norvegicus GN=Actb PE=1 SV=1	RAT	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp P60710 ACTB_MOUSE	Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1	MOUSE	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp P60709 ACTB_HUMAN	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	HUMAN	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp P60708 ACTB_HORSE	Actin, cytoplasmic 1 OS=Equus caballus GN=ACTB PE=2 SV=1	HORSE	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp P60707 ACTB_TRIVU	Actin, cytoplasmic 1 OS=Trichosurus vulpecula GN=ACTB PE=2 SV=	TRIVU	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp P60706 ACTB_CHICK	Actin, cytoplasmic 1 OS=Gallus gallus GN=ACTB PE=1 SV=1	CHICK	3
19	0	5,54	23,19999981	23,19999981	15,16000032	sp P53505 ACT5_XENLA	Actin, cytoplasmic type 5 OS=Xenopus laevis PE=3 SV=1	XENLA	3
19	0	5,54	23,19999981	23,19999981	15,16000032	sp P53478 ACT5_CHICK	Actin, cytoplasmic type 5 OS=Gallus gallus PE=3 SV=1	CHICK	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp P48975 ACTB_CRIGR	Actin, cytoplasmic 1 OS=Cricetulus griseus GN=actb PE=3 SV=1	CRIGR	3
19	0	5,54	23,19999981	23,19999981	15,16000032	sp P15475 ACTB_XENBO	Actin, cytoplasmic 1 OS=Xenopus borealis GN=actb PE=3 SV=1	XENBO	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp O18840 ACTB_CANLF	Actin, cytoplasmic 1 OS=Canis lupus familiaris GN=ACTB PE=2 SV=3	CANLF	3
19	0	5,54	23,19999933	23,19999933	15,19999951	sp A2BDB0 ACTG_XENLA	Actin, cytoplasmic 2 OS=Xenopus laevis GN=actg1 PE=2 SV=1	XENLA	3
19	0	5,15	23,19999981	15,16000032	15,16000032	sp P84185 ACT5C_ANOGA	Actin-5C OS=Anopheles gambiae GN=Act5C PE=2 SV=1	ANOGA	3
19	0	5,15	23,19999981	15,16000032	15,16000032	sp P84184 ACT3B_HELAM	Actin-A3b, cytoplasmic OS=Helicoverpa armigera GN=actA3b PE=2	HELAM	3
19	0	5,15	23,19999981	15,16000032	15,16000032	sp P84183 ACT4_BOMMO	Actin, cytoplasmic A4 OS=Bombyx mori GN=A4 PE=2 SV=1	BOMMO	3
19	0	5,15	23,19999981	15,16000032	15,16000032	sp P10987 ACT1_DROME	Actin-5C OS=Drosophila melanogaster GN=Act5C PE=1 SV=4	DROME	3
19	0	5,15	15,19999951	15,19999951	15,19999951	sp Q93129 ACTB_BRABE	Actin, cytoplasmic OS=Branchiostoma belcheri PE=2 SV=1	BRABE	3
19	0	5,15	21,43000066	21,43000066	21,43000066	sp Q92193 ACT_CRAVI	Actin (Fragment) OS=Crassostrea virginica PE=2 SV=1	CRAVI	3
19	0	5,15	15,19999951	15,19999951	15,19999951	sp Q6NVA9 ACTB_XENTR	Actin, cytoplasmic 1 OS=Xenopus tropicalis GN=actb PE=2 SV=1	XENTR	3
19	0	5,15	15,08000046	15,08000046	15,08000046	sp Q250472 ACT2_MOLOC	Actin, muscle-type OS=Molgula oculata PE=3 SV=1	MOLOC	3
19	0	5,15	15,16000032	15,16000032	15,16000032	sp Q25010 ACT3A_HELAM	Actin, cytoplasmic A3a OS=Helicoverpa armigera GN=actA3a PE=2	HELAM	3
19	0	5,15	18,44999939	18,44999939	18,44999939	sp Q03342 ACT3_ECHGR	Actin-3 (Fragment) OS=Echinococcus granulosus GN=ACTIII PE=2 S	ECHGR	3
19	0	5,15	15,03999978	15,03999978	15,03999978	sp Q00214 ACTM_STYPL	Actin, muscle OS=Styela plicata PE=3 SV=1	STYPL	3
19	0	5,15	15,16000032	15,16000032	15,16000032	sp P90689 ACT_BRUMA	Actin OS=Brugia malayi PE=1 SV=1	BRUMA	3
19	0	5,15	15,16000032	15,16000032	15,16000032	sp P68556 ACT1_DIPDE	Actin-1/4 OS=Diphyllbothrium dendriticum GN=ACT1 PE=2 SV=1	DIPDE	3
19	0	5,15	15,16000032	15,16000032	15,16000032	sp P68555 ACT_TAESO	Actin OS=Taenia solium GN=ACT1 PE=3 SV=1	TAESO	3
19	0	5,15	15,16000032	15,16000032	15,16000032	sp P53471 ACT2_SCHMA	Actin-2 OS=Schistosoma mansoni PE=2 SV=1	SCHMA	3
19	0	5,15	15,16000032	15,16000032	15,16000032	sp P53456 ACT2_DIPDE	Actin-2 OS=Diphyllbothrium dendriticum GN=ACT2 PE=2 SV=1	DIPDE	3
19	0	5,15	15,16000032	15,16000032	15,16000032	sp P04829 ACT3_BOMMO	Actin, cytoplasmic A3 OS=Bombyx mori PE=3 SV=3	BOMMO	3
19	0	5,15	15,16000032	15,16000032	15,16000032	sp P02572 ACT2_DROME	Actin-42A OS=Drosophila melanogaster GN=Act42A PE=1 SV=3	DROME	3
19	0	5,15	15,19999951	15,19999951	15,19999951	sp O93400 ACTB_XENLA	Actin, cytoplasmic 1 OS=Xenopus laevis GN=actb PE=2 SV=1	XENLA	3
19	0	5,15	15,16000032	15,16000032	15,16000032	sp O18500 ACT2_SACKO	Actin-2 OS=Saccoglossus kowalevskii PE=2 SV=1	SACKO	3
19	0	5,15	15,16000032	15,16000032	15,16000032	sp O18499 ACT1_SACKO	Actin-1 OS=Saccoglossus kowalevskii PE=2 SV=1	SACKO	3
20	4,9	4,9	14,03000057	14,03000057	12,83999979	sp Q5RAB4 G3P_PONAB	Glyceraldehyde-3-phosphate dehydrogenase OS=Pongo abelii GN=	PONAB	3
20	0	4,9	14,03000057	14,03000057	12,83999979	sp P04406 G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapiens G	HUMAN	3
24	3,25	3,25	3,596000001	3,596000001	3,596000001	sp Q8VNN2 BGAL_ECOLX	Beta-galactosidase OS=Escherichia coli GN=lacZ PE=3 SV=1	ECOLX	3
24	0	3,25	3,612999991	3,612999991	3,612999991	sp Q3Z583 BGAL_SHISS	Beta-galactosidase OS=Shigella sonnei (strain Ss046) GN=lacZ PE=3	SHISS	3
24	0	3,25	3,612999991	3,612999991	3,612999991	sp P00722 BGAL_ECOLI	Beta-galactosidase OS=Escherichia coli (strain K12) GN=lacZ PE=1 S	ECOLI	3
24	0	3,25	3,612999991	3,612999991	3,612999991	sp B1U0T5 BGAL_ECOLC	Beta-galactosidase OS=Escherichia coli (strain ATCC 8739 / DSM 15	ECOLC	3
24	0	3,25	3,612999991	3,612999991	3,612999991	sp A7ZWZ1 BGAL_ECOHS	Beta-galactosidase OS=Escherichia coli O9:H4 (strain HS) GN=lacZ I	ECOHS	3
24	0	3,25	3,612999991	3,612999991	3,612999991	sp A7Z191 BGAL_ECO24	Beta-galactosidase OS=Escherichia coli O139:H28 (strain E24377A, E	ECO24	3
32	2	3,04	4,887999967	4,887999967	4,887999967	sp Q6IFX1 K1C24_RAT	Keratin, type I cytoskeletal 24 OS=Rattus norvegicus GN=Krt24 PE=	RAT	3
32	0	3,04	4,687999934	4,687999934</					

19	0	3,4	17,06999987	17,06999987	9,066999704	sp Q7ZVF9 ACTB2_DANRE	Actin, cytoplasmic 2 OS=Danio rerio GN=actbb PE=2 SV=2	DANRE	2
19	0	3,4	17,06999987	17,06999987	9,066999704	sp P83751 ACTB_CTEID	Actin, cytoplasmic 1 OS=Ctenopharyngodon idella GN=actb PE=3 S	CTEID	2
19	0	3,4	17,06999987	17,06999987	9,066999704	sp P83750 ACTB_CYPCA	Actin, cytoplasmic 1 OS=Cyprinus carpio GN=actb PE=3 SV=1	CYPCA	2
19	0	3,4	17,02000052	17,02000052	9,042999893	sp P53506 ACT8_XENLA	Actin, cytoplasmic type 8 OS=Xenopus laevis PE=3 SV=1	XENLA	2
19	0	3,4	17,06999987	17,06999987	9,066999704	sp P53485 ACTB2_TAKRU	Actin, cytoplasmic 2 OS=Takifugu rubripes GN=actbb PE=3 SV=1	TAKRU	2
21	4,2	4,2	23,82999957	16,43999964	11,06999964	sp P25311 ZA2G_HUMAN	Zinc-alpha-2-glycoprotein OS=Homo sapiens GN=AZGP1 PE=1 SV=2	HUMAN	2
22	3,61	3,61	13,51000071	8,23699987	5,601000041	sp P02769 ALBU_BOVIN	Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	BOVIN	2
23	3,56	3,56	51,09000206	51,09000206	21,73999995	sp P80511 S10AC_HUMAN	Protein S100-A12 OS=Homo sapiens GN=S100A12 PE=1 SV=2	HUMAN	2
24	0	2	2,147999965	2,147999965	2,147999965	sp Q8X685 BGAL_ECO57	Beta-galactosidase OS=Escherichia coli O157:H7 GN=lacZ PE=3 SV=	ECO57	2
24	0	2	2,147999965	2,147999965	2,147999965	sp Q8FKG6 BGAL_ECOL6	Beta-galactosidase OS=Escherichia coli O6:H1 (strain C7073 / ATC	ECOL6	2
24	0	2	2,147999965	2,147999965	2,147999965	sp Q32JB6 BGAL_SHIDS	Beta-galactosidase OS=Shigella dysenteriae serotype 1 (strain Sd1	SHIDS	2
24	0	2	2,147999965	2,147999965	2,147999965	sp Q1RFJ2 BGAL_ECOUT	Beta-galactosidase OS=Escherichia coli (strain UT89 / UPEC) GN=l	ECOUT	2
24	0	2	2,147999965	2,147999965	2,147999965	sp Q0TKT1 BGAL_ECOL5	Beta-galactosidase OS=Escherichia coli O6:K15:H31 (strain 536 /	UI ECOL5	2
24	0	2	2,147999965	2,147999965	2,147999965	sp B7UJI9 BGAL_ECO27	Beta-galactosidase OS=Escherichia coli O127:H6 (strain E2348/69	/ ECO27	2
24	0	2	2,147999965	2,147999965	2,147999965	sp B7N8Q1 BGAL_ECOLU	Beta-galactosidase OS=Escherichia coli O17:K52:H18 (strain UMN0	ECOLU	2
24	0	2	2,147999965	2,147999965	2,147999965	sp B522P7 BGAL_ECOSE	Beta-galactosidase OS=Escherichia coli O157:H7 (strain EC4115 /	E ECOSE	2
24	0	2	2,147999965	2,147999965	2,147999965	sp B1LIM9 BGAL_ECOSM	Beta-galactosidase OS=Escherichia coli (strain SMS-3-5 / SECEC)	GN ECOSM	2
24	0	2	2,147999965	2,147999965	2,147999965	sp A7KGA5 BGAL2_KLEPN	Beta-galactosidase OS=Klebsiella pneumoniae GN=lacZ PE=3 SV=1	KLEPN	2
24	0	2	2,147999965	2,147999965	2,147999965	sp A6T129 BGAL2_KLEP7	Beta-galactosidase 2 OS=Klebsiella pneumoniae subsp. pneumonia	KLEP7	2
24	0	2	2,147999965	2,147999965	2,147999965	sp A1A831 BGAL_ECOK1	Beta-galactosidase OS=Escherichia coli O1:K1 / APEC GN=lacZ PE=3	ECOK1	2
25	2,86	2,86	65,82000256	65,82000256	65,82000256	sp P02814 SMR3B_HUMAN	Submaxillary gland androgen-regulated protein 3B OS=Homo sapie	HUMAN	2
22	0	1,24	6,095999852	6,095999852	3,460000083	sp P14639 ALBU_SHEEP	Serum albumin OS=Ovis aries GN=ALB PE=1 SV=1	SHEEP	1
26	2,11	2,11	3,892999887	3,892999887	2,415999956	sp Q8WNW3 PLAK_PIG	Junction plakoglobin OS=Sus scrofa GN=Jup PE=2 SV=1	PIG	1
26	0	2,11	3,892999887	3,892999887	2,415999956	sp Q8SPJ1 PLAK_BOVIN	Junction plakoglobin OS=Bos taurus GN=JUP PE=2 SV=1	BOVIN	1
26	0	2,11	3,892999887	3,892999887	2,415999956	sp Q6PK08 PLAK_RAT	Junction plakoglobin OS=Rattus norvegicus GN=Jup PE=1 SV=1	RAT	1
26	0	2,11	3,892999887	3,892999887	2,415999956	sp Q02257 PLAK_MOUSE	Junction plakoglobin OS=Mus musculus GN=Jup PE=1 SV=3	MOUSE	1
26	0	2,11	3,892999887	3,892999887	2,415999956	sp P14923 PLAK_HUMAN	Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	HUMAN	1
27	2,08	2,08	34,90999937	34,90999937	26,4200002	sp Q5R9M3 THIO_PONAB	Thioredoxin OS=Pongo abelii GN=TXN PE=3 SV=3	PONAB	1
27	0	2,08	35,24000049	35,24000049	26,66999996	sp P10599 THIO_HUMAN	Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3	HUMAN	1
30	2,01	2,01	24,75000024	10,89000031	10,89000031	sp P31151 S10A7_HUMAN	Protein S100-A7 OS=Homo sapiens GN=S100A7 PE=1 SV=4	HUMAN	1
31	2,01	2,01	27,54999995	11,21999994	11,21999994	sp Q6B345 S10AB_RAT	Protein S100-A11 OS=Rattus norvegicus GN=S100a11 PE=3 SV=1	RAT	1
31	0	2,01	27,54999995	11,21999994	11,21999994	sp P50543 S10AB_MOUSE	Protein S100-A11 OS=Mus musculus GN=S100a11 PE=1 SV=1	MOUSE	1
31	0	2,01	25,709999861	10,48000008	10,48000008	sp P31949 S10AB_HUMAN	Protein S100-A11 OS=Homo sapiens GN=S100A11 PE=1 SV=2	HUMAN	1
31	0	2,01	26,46999955	10,77999994	10,77999994	sp P24480 S10AB_RABIT	Protein S100-A11 OS=Oryctolagus cuniculus GN=S100A11 PE=1 SV=	RABIT	1
33	2	2	18,37999997	10,58000028	10,58000028	sp P12763 FETUA_BOVIN	Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	BOVIN	1
34	2	2	11,80000007	4,129999876	4,129999876	sp Q6TEQ7 ANXA2_CANLF	Annexin A2 OS=Canis lupus familiaris GN=ANXA2 PE=1 SV=1	CANLF	1
34	0	2	11,80000007	4,129999876	4,129999876	sp Q5R5A0 ANXA2_PONAB	Annexin A2 OS=Pongo abelii GN=ANXA2 PE=2 SV=1	PONAB	1
34	0	2	11,80000007	4,129999876	4,129999876	sp Q2Q1M6 ANXA2_CEREL	Annexin A2 OS=Cervus elaphus GN=ANXA2 PE=2 SV=1	CEREL	1
34	0	2	11,80000007	4,129999876	4,129999876	sp Q07936 ANXA2_RAT	Annexin A2 OS=Rattus norvegicus GN=Anxa2 PE=1 SV=2	RAT	1
34	0	2	11,80000007	4,129999876	4,129999876	sp P19620 ANXA2_PIG	Annexin A2 OS=Sus scrofa GN=ANXA2 PE=1 SV=4	PIG	1
34	0	2	11,80000007	4,129999876	4,129999876	sp P07351 ANXA2_HUMAN	Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2	HUMAN	1
34	0	2	11,80000007	4,129999876	4,129999876	sp P04272 ANXA2_BOVIN	Annexin A2 OS=Bos taurus GN=ANXA2 PE=1 SV=2	BOVIN	1
34	0	2	11,80000007	4,129999876	4,129999876	sp A2SW69 ANXA2_SHEEP	Annexin A2 OS=Ovis aries GN=ANXA2 PE=1 SV=1	SHEEP	1
34	0	2	8,850000054	4,129999876	4,129999876	sp P07356 ANXA2_MOUSE	Annexin A2 OS=Mus musculus GN=Anxa2 PE=1 SV=2	MOUSE	1
34	0	2	15,08000046	7,034999877	7,034999877	sp COHJG9 ANXA2_MESAU	Annexin A2 (Fragments) OS=Mesocricetus auratus PE=1 SV=1	MESAU	1
35	2	2	15,13999999	4,086999968	4,086999968	sp P34955 A1AT_BOVIN	Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE=1 SV=1	BOVIN	1
36	2	2	8,677999675	3,719000146	3,719000146	sp P31944 CASPE_HUMAN	Caspase-14 OS=Homo sapiens GN=CASP14 PE=1 SV=2	HUMAN	1
37	2	2	0,961900037	0,460099988	0,460099988	sp Q5D862 FILA2_HUMAN	Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	HUMAN	1
38	2	2	6,831999868	3,415999934	3,415999934	sp P05089 ARGI1_HUMAN	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2	HUMAN	1
39	2	2	1,345000044	1,345000044	1,345000044	sp Q9Z1P2 ACTN1_RAT	Alpha-actinin-1 OS=Rattus norvegicus GN=Actn1 PE=1 SV=1	RAT	1
39	0	2	1,317000017	1,317000017	1,317000017	sp Q9QXQ0 ACTN4_HUMAN	Alpha-actinin-4 OS=Rattus norvegicus GN=Actn4 PE=1 SV=2	RAT	1
39	0	2	1,341999974	1,341999974	1,341999974	sp Q9JI91 ACTN2_MOUSE	Alpha-actinin-2 OS=Mus musculus GN=Actn2 PE=1 SV=2	MOUSE	1
39	0	2	1,327	1,327	1,327	sp Q90734 ACTN4_CHICK	Alpha-actinin-4 OS=Gallus gallus GN=ACTN4 PE=1 SV=1	CHICK	1
39	0	2	1,345000044	1,345000044	1,345000044	sp Q7TPR4 ACTN1_MOUSE	Alpha-actinin-1 OS=Mus musculus GN=Actn1 PE=1 SV=1	MOUSE	1
39	0	2	1,317000017	1,317000017	1,317000017	sp Q5RCS6 ACTN4_PONAB	Alpha-actinin-4 OS=Pongo abelii GN=ACTN4 PE=2 SV=1	PONAB	1
39	0	2	1,341999974	1,341999974	1,341999974	sp Q3ZC55 ACTN2_BOVIN	Alpha-actinin-2 OS=Bos taurus GN=ACTN2 PE=2 SV=1	BOVIN	1
39	0	2	1,345000044	1,345000044	1,345000044	sp Q3B7N2 ACTN1_BOVIN	Alpha-actinin-1 OS=Bos taurus GN=ACTN1 PE=2 SV=1	BOVIN	1
39	0	2	1,345000044	1,345000044	1,345000044	sp Q2PFV7 ACTN1_MACFA	Alpha-actinin-1 OS=Macaca fascicularis GN=ACTN1 PE=2 SV=1	MACFA	1
39	0	2	1,331999991	1,331999991	1,331999991	sp Q0II9J ACTN3_BOVIN	Alpha-actinin-3 OS=Bos taurus GN=ACTN3 PE=2 SV=1	BOVIN	1
39	0	2	1,331999991	1,331999991	1,331999991	sp Q08043 ACTN3_HUMAN	Alpha-actinin-3 OS=Homo sapiens GN=ACTN3 PE=1 SV=2	HUMAN	1
39	0	2	1,315999962	1,315999962	1,315999962	sp P57780 ACTN4_MOUSE	Alpha-actinin-4 OS=Mus musculus GN=Actn4 PE=1 SV=1	MOUSE	1
39	0	2	1,341999974	1,341999974	1,341999974	sp P35609 ACTN2_HUMAN	Alpha-actinin-2 OS=Homo sapiens GN=ACTN2 PE=1 SV=1	HUMAN	1
39	0	2	1,338000037	1,338000037	1,338000037	sp P20111 ACTN2_CHICK	Alpha-actinin-2 OS=Gallus gallus GN=ACTN2 PE=2 SV=1	CHICK	1
39	0	2	1,345000044	1,345000044	1,345000044	sp P12814 ACTN1_HUMAN	Alpha-actinin-1 OS=Homo sapiens GN=ACTN1 PE=1 SV=2	HUMAN	1
39	0	2	1,343999989	1,343999989	1,343999989	sp P05094 ACTN1_CHICK	Alpha-actinin-1 OS=Gallus gallus GN=ACTN1 PE=1 SV=3	CHICK	1
39	0	2	1,333000045	1,333000045	1,333000045	sp O88990 ACTN3_MOUSE	Alpha-actinin-3 OS=Mus musculus GN=Actn3 PE=2 SV=1	MOUSE	1
39	0	2	1,317000017	1,317000017	1,317000017	sp Q43707 ACTN4_HUMAN	Alpha-actinin-4 OS=Homo sapiens GN=ACTN4 PE=1 SV=2	HUMAN	1
39	0	2	1,317000017	1,317000017	1,317000017	sp A5D7D1 ACTN4_BOVIN	Alpha-actinin-4 OS=Bos taurus GN=ACTN4 PE=2 SV=1	BOVIN	1
40	2	2	1,456999965	1,456999965	1,456999965	sp Q7SIH1 A2MG_BOVIN	Alpha-2-macroglobulin OS=Bos taurus GN=A2M PE=1 SV=2	BOVIN	1
41	2	2	2,051999979	2,051999979	2,051999979	sp Q3SX14 GELS_BOVIN	Gelsolin OS=Bos taurus GN=GSN PE=2 SV=1	BOVIN	1
41	0	2	2,051999979	2,051999979	2,051999979	sp Q28372 GELS_HORSE	Gelsolin OS=Equus caballus GN=GSN PE=1 SV=2	HORSE	1
41	0	2	1,943000033	1,943000033	1,943000033	sp P20305 GELS_PIG	Gelsolin (Fragment) OS=Sus scrofa GN=GSN PE=1 SV=1	PIG	1
41	0	2	1,917999983	1,917999983	1,917999983	sp P06396 GELS_HUMAN	Gelsolin OS=Homo sapiens GN=GSN PE=1 SV=1	HUMAN	1
42	2	2	1,913999952	1,913999952	1,913999952	sp P22758 TGM1_RABIT	Protein-glutamine gamma-glutamyltransferase K OS=Oryctolagus c	RABIT	1
42	0	2	1,957999915	1,957999915	1,957999915	sp P22735 TGM1_HUMAN	Protein-glutamine gamma-glutamyltransferase K OS=Homo sapien	HUMAN	1
43	2	2	9,544999897	9,544999897	9,544999897	sp Q75629 CREG1_HUMAN	Protein CREG1 OS=Homo sapiens GN=CREG1 PE=1 SV=1	HUMAN	1
44	1,68	1,68	32,78999925	20,9800005	20,9800005	sp Q8MKD1 UBB_HORSE	Polyubiquitin-B OS=Equus caballus GN=UBB PE=2 SV=3	HORSE	1
44	0	1,68	32,89000094	21,05000019	21,05000019	sp Q865C5 UBIQ_CAMDR	Ubiquitin OS=Camelus dromedarius PE=3 SV=2	CAMDR	1
44	0	1,68	30,86000085	19,75000054	19,75000054	sp Q63429 UBC_RAT	Polyubiquitin-C OS=Rattus norvegicus GN=Ubc PE=1 SV=1	RAT	1
44	0	1,68	39,68000114	25,40000081	25,40000081	sp P84589 UBIQ_LUMTE	Ubiquitin (Fragment) OS=Lumbricus terrestris PE=1 SV=2	LUMTE	1
44	0	1,68	16,03000015	10,26000008	10,26000008	sp P79781 RS27A_CHICK	Ubiquitin-40S ribosomal protein S27a OS=Gallus gallus GN=RPS27	CHICK	1
44	0	1,68	19,52999979	12,5	12,5	sp P68205 RL40_OPHHA	Ubiquitin-60S ribosomal protein L40 OS=Ophiophagus hannah PE=	OPHHA	1
44	0	1,68	16,03000015	10,26000008	10,26000008	sp P68203 RS27A_SPOFR	Ubiquitin-40S ribosomal protein S27a OS=Spodoptera frugiperda P	SPOFR	1
44	0	1,68	16,13000035	10,32000035	10,32000035	sp P68202 RS27A_PLUXY	Ubiquitin-40S ribosomal protein S27a OS=Plutella xylostella PE=2	S PLUXY	1
44	0	1,68	16,03000015	10,26000008	10,26000008	sp P68200 RS27A_ICTPU	Ubiquitin-40S ribosomal protein S27a OS=Ictalurus punctatus GN=I	ICTPU	1
44	0	1,68	32,89000094	21,05000019	21,05000019	sp P68197 UBIQ_CERCA	Ubiquitin OS=Ceratitis capitata PE=1 SV=1	CERCA	1
44	0	1,68	19,52999979	12,5	12,5	sp P63053 RL40_PIG	Ubiquitin-60S ribosomal protein L40 OS=Sus scrofa GN=UBA52 PE=	PIG	1
44	0	1,68	19,52999979	12,5	12,5	sp P63052 RL40_FELCA	Ubiquitin-60S ribosomal protein L40 OS=Felis catus GN=UBA52 PE=	FELCA	1
44	0	1,68	19,52999979	12,5	12,5	sp P63050 RL40_CANLF	Ubiquitin-60S ribosomal protein L40 OS=Canis lupus familiaris GN=	CANLF	1
44	0	1,68	19,52999979	12,5	12,5	sp P63048 RL40_BOVIN	Ubiquitin-60S ribosomal protein L40 OS=Bos taurus GN=UBA52 PE=	BOVIN	1
44	0	1,68	16,03000015	10,26000008	10,26000008	sp P62992 RS27A_BOVIN	Ubiquitin-40S ribosomal protein S27a OS=Bos taurus GN=RPS27A	F BOVIN	1
44	0	1,68	19,52999979	12,5	12,5	sp P62987 RL40_HUMAN	Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=UBA52	HUMAN	1
44	0	1,68	19,52999979	12,5	12,5	sp P62986 RL40_RAT	Ubiquitin-60S ribosomal protein L40 OS=Rattus norvegicus GN=Ub	RAT	1
44	0	1,68	19,52999979	12,5	12,5	sp P			

44	0	1,68	16,03000015	10,26000008	10,26000008	sp P62982 RS27A_RAT	Ubiquitin-40S ribosomal protein S27a OS=Rattus norvegicus GN=Rt RAT	1
44	0	1,68	16,03000015	10,26000008	10,26000008	sp P62979 RS27A_HUMAN	Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=RP52: HUMAN	1
44	0	1,68	16,03000015	10,26000008	10,26000008	sp P62978 RS27A_CAVPO	Ubiquitin-40S ribosomal protein S27a OS=Cavia porcellus GN=RP52: CAVPO	1
44	0	1,68	30,39999902	19,44999993	19,44999993	sp P62976 UBIQP_CRIGR	Polyubiquitin OS=Cricetulus griseus PE=2 SV=2	1
44	0	1,68	32,89000094	21,05000019	21,05000019	sp P62975 UBIQ_RABIT	Ubiquitin OS=Oryctolagus cuniculus PE=1 SV=1	1
44	0	1,68	35,33000052	19,15999949	19,15999949	sp P62972 UBIQP_XENLA	Polyubiquitin (Fragment) OS=Xenopus laevis PE=1 SV=2	1
44	0	1,68	16,13000035	10,32000035	10,32000035	sp P29504 RS27A_MANSE	Ubiquitin-40S ribosomal protein S27a OS=Manduca sexta PE=2 SV= MANSE	1
44	0	1,68	19,52999979	12,5	12,5	sp P18101 RL40_DROME	Ubiquitin-60S ribosomal protein L40 OS=Drosophila melanogaster DROME	1
44	0	1,68	16,03000015	10,26000008	10,26000008	sp P15357 RS27A_DROME	Ubiquitin-40S ribosomal protein S27a OS=Drosophila melanogaster: DROME	1
44	0	1,68	32,60999918	20,87000012	20,87000012	sp P0CH28 UBC_BOVIN	Polyubiquitin-C OS=Bos taurus GN=UBC PE=1 SV=1	1
44	0	1,68	32,76999891	20,97000033	20,97000033	sp P0CG69 UBIQP_DROME	Polyubiquitin OS=Drosophila melanogaster GN=Ubi-p63E PE=3 SV= DROME	1
44	0	1,68	32,82999992	21,00999951	21,00999951	sp P0CG68 UBC_PIG	Polyubiquitin-C OS=Sus scrofa GN=UBC PE=2 SV=1	1
44	0	1,68	32,74999857	20,96000016	20,96000016	sp P0CG67 UBB_GORGO	Polyubiquitin-B OS=Gorilla gorilla GN=UBB PE=3 SV=1	1
44	0	1,68	32,8399986	21,01999968	21,01999968	sp P0CG66 UBC_GORGO	Polyubiquitin-C OS=Gorilla gorilla GN=UBC PE=3 SV=1	1
44	0	1,68	32,74999857	20,96000016	20,96000016	sp P0CG65 UBB_PANTR	Polyubiquitin-B OS=Pan troglodytes GN=UBB PE=3 SV=1	1
44	0	1,68	32,85000026	21,01999968	21,01999968	sp P0CG64 UBC_PANTR	Polyubiquitin-C OS=Pan troglodytes GN=UBC PE=3 SV=1	1
44	0	1,68	32,78999925	20,98000005	20,98000005	sp P0CG62 UBB_CHICK	Polyubiquitin-B OS=Gallus gallus GN=UBB PE=2 SV=1	1
44	0	1,68	32,85000026	21,01999968	21,01999968	sp P0CG61 UBC_PONPY	Polyubiquitin-C OS=Pongo pygmaeus GN=UBC PE=3 SV=1	1
44	0	1,68	32,74999857	20,96000016	20,96000016	sp P0CG60 UBB_PONPY	Polyubiquitin-B OS=Pongo pygmaeus GN=UBB PE=3 SV=1	1
44	0	1,68	32,78999925	20,98000005	20,98000005	sp P0CG55 UBB_SHEEP	Polyubiquitin-B OS=Ovis aries GN=UBB PE=2 SV=1	1
44	0	1,68	32,15000033	20,57999969	20,57999969	sp P0CG54 UBB_CAVPO	Polyubiquitin-B OS=Cavia porcellus GN=UBB PE=2 SV=1	1
44	0	1,68	32,78999925	20,98000005	20,98000005	sp P0CG53 UBB_BOVIN	Polyubiquitin-B OS=Bos taurus GN=UBB PE=1 SV=1	1
44	0	1,68	32,78999925	20,98000005	20,98000005	sp P0CG51 UBB_RAT	Polyubiquitin-B OS=Rattus norvegicus GN=Ubb PE=1 SV=1	1
44	0	1,68	30,64999878	19,61999983	19,61999983	sp P0CG50 UBC_MOUSE	Polyubiquitin-C OS=Mus musculus GN=Ubc PE=1 SV=2	1
44	0	1,68	32,78999925	20,98000005	20,98000005	sp P0CG49 UBB_MOUSE	Polyubiquitin-B OS=Mus musculus GN=Ubb PE=2 SV=1	1
44	0	1,68	32,85000026	21,01999968	21,01999968	sp P0CG48 UBC_HUMAN	Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=3	1
44	0	1,68	32,74999857	20,96000016	20,96000016	sp P0CG47 UBB_HUMAN	Polyubiquitin-B OS=Homo sapiens GN=UBB PE=1 SV=1	1
44	0	1,68	19,52999979	12,5	12,5	sp P0C276 RL40_SHEEP	Ubiquitin-60S ribosomal protein L40 OS=Ovis aries GN=UBA52 PE= SHEEP	1
44	0	1,68	19,52999979	12,5	12,5	sp P0C275 RL40_PONPY	Ubiquitin-60S ribosomal protein L40 OS=Pongo pygmaeus GN=UBA: PONPY	1
44	0	1,68	19,52999979	12,5	12,5	sp P0C273 RL40_MACFA	Ubiquitin-60S ribosomal protein L40 OS=Macaca fascicularis GN=U MACFA	1
45	1,5	1,5	7,767000049	3,155000135	3,155000135	sp P07339 CATD_HUMAN	Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1	1
46	1,04	1,04	3,403000161	3,403000161	3,403000161	sp Q7YR44 CDSN_PANTR	Corneodesmosin OS=Pan troglodytes GN=CDSN PE=2 SV=1	1
46	0	1,04	3,370999917	3,370999917	3,370999917	sp Q5TM45 CDSN_MACMU	Corneodesmosin OS=Macaca mulatta GN=CDSN PE=3 SV=1	1
46	0	1,04	3,403000161	3,403000161	3,403000161	sp Q15517 CDSN_HUMAN	Corneodesmosin OS=Homo sapiens GN=CDSN PE=1 SV=3	1
47	0,85	0,85	4,02700007	2,907999977	1,678000018	sp Q08554 DSC1_HUMAN	Desmocollin-1 OS=Homo sapiens GN=DSC1 PE=1 SV=2	1
48	0,72	0,72	3,895999864	2,597000077	2,597000077	sp Q08188 TGM3_HUMAN	Protein-glutamine gamma-glutamyltransferase E OS=Homo sapien HUMAN	1
49	0,65	0,65	22,95999974	22,22000062	6,667000055	sp Q01469 FABP5_HUMAN	Fatty acid-binding protein, epidermal OS=Homo sapiens GN=FABP: HUMAN	1
50	0,58	0,58	24,66000021	8,218999952	8,218999952	sp P12273 PIP_HUMAN	Prolactin-inducible protein OS=Homo sapiens GN=PIP PE=1 SV=1	1
50	0	0,55	8,218999952	8,218999952	8,218999952	sp A0A890 PIP_HYLAG	Prolactin-inducible protein homolog OS=Hylobates agilis GN=PIP PI HYLAG	1
50	0	0,55	8,218999952	8,218999952	8,218999952	sp A0A888 PIP_PONPY	Prolactin-inducible protein homolog OS=Pongo pygmaeus GN=PIP PONPY	1
51	0,41	0,41	1,950999908	0,626999978	0,626999978	sp P15924 DESP_HUMAN	Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	1
51	0	0,41	1,248999964	0,624299981	0,624299981	sp E9Q557 DESP_MOUSE	Desmoplakin OS=Mus musculus GN=Dsp PE=1 SV=1	1
52	0,36	0,36	7,512000203	7,512000203	7,512000203	RRRRRsp P13673 SKGR_XENLA	REVERSED Skin granule protein OS=Xenopus laevis GN=sgp PE=2 SV=1 XENLA	1
53	0,3	0,3	7,534000278	7,534000278	7,534000278	sp Q9NZT1 CALL5_HUMAN	Calmodulin-like protein 5 OS=Homo sapiens GN=CALML5 PE=1 SV= HUMAN	1
55	0,21	0,21	1,917999983	1,917999983	0	RRRRRsp Q9SFC7 FB135_ARATH	REVERSED F-box protein At3g07870 OS=Arabidopsis thaliana GN=Ar ARATH	0
56	0,18	0,18	1,28899999	1,28899999	0	sp Q92E69 SECA2_LISIN	Protein translocase subunit SecA 2 OS=Listeria innocua serovar 6a LISIN	0
56	0	0,18	1,28899999	1,28899999	0	sp Q722W7 SECA2_LISMF	Protein translocase subunit SecA 2 OS=Listeria monocytogenes ser LISMF	0
56	0	0,18	1,28899999	1,28899999	0	sp P0DJP3 SECA2_LISMO	Protein translocase subunit SecA 2 OS=Listeria monocytogenes ser LISMO	0
56	0	0,18	1,28899999	1,28899999	0	sp G2K3V6 SECA2_LISM4	Protein translocase subunit SecA 2 OS=Listeria monocytogenes ser LISM4	0
57	0,15	0,15	2,228000015	2,228000015	0	sp Q5NX24 GLGC_AROAE	Glucose-1-phosphate adenylyltransferase OS=Aromatoleum arom: AROAE	0
58	0,09	0,09	2,762999944	1,727000065	0	sp Q5T749 KPRP_HUMAN	Keratinocyte proline-rich protein OS=Homo sapiens GN=KPRP PE=: HUMAN	0
58	0	0,09	1,431000046	1,431000046	0	sp Q7TQM5 KPRP_RAT	Keratinocyte proline-rich protein OS=Rattus norvegicus GN=Krrp P RAT	0
59	0,06	0,06	3,406000137	3,406000137	0	sp Q6LY02 MCH_METMP	Methenyltetrahydromethanopterin cyclohydrolase OS=Methanoccc METMP	0
59	0	0,06	3,406000137	3,406000137	0	sp A6VGD1 MCH_METM7	Methenyltetrahydromethanopterin cyclohydrolase OS=Methanoccc METM7	0
59	0	0,06	3,406000137	3,406000137	0	sp A6UPJ2 MCH_METVS	Methenyltetrahydromethanopterin cyclohydrolase OS=Methanoccc METVS	0
59	0	0,06	3,406000137	3,406000137	0	sp A4FWY5 MCH_METM5	Methenyltetrahydromethanopterin cyclohydrolase OS=Methanoccc METM5	0

N	CSI_3	Total	%Cov	%Cov(50)	%Cov(95)	Accession	Name	Species	Peptides(95%)
1	115,6	115,6	69,0999985	66,6100025	65,9900001	sp P04264 K2C1_HUMAN	Keratin, type II cytoskeletal 1 OS=Homo sapier	HUMAN	113
2	88,01	88,01	60,2699995	58,5600019	57,0200026	sp P13645 K1C10_HUMAN	Keratin, type I cytoskeletal 10 OS=Homo sapie	HUMAN	89
3	74,33	74,37	77,6899993	77,6899993	77,6899993	sp P35527 K1C9_HUMAN	Keratin, type I cytoskeletal 9 OS=Homo sapien	HUMAN	66
4	67,97	80,24	76,9999981	71,9900012	68,8600004	sp P35908 K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal OS=H	HUMAN	51
5	38,34	38,34	65,7999992	59,7400001	59,7400001	sp P00761 TRYP_PIG	Trypsin OS=Sus scrofa PE=1 SV=1	PIG	36
7	24,32	45,67	43,7299997	35,4200006	31,8599999	sp P13647 K2C5_HUMAN	Keratin, type II cytoskeletal 5 OS=Homo sapier	HUMAN	27
7	0	43,67	41,0499999	32,7699989	29,2199999	sp A5A6M8 K2C5_PANTR	Keratin, type II cytoskeletal 5 OS=Pan troglody	PANTR	26
12	11,56	42	44,8599994	32,4499995	30,3200006	sp P48668 K2C6C_HUMAN	Keratin, type II cytoskeletal 6C OS=Homo sapie	HUMAN	26
12	0,02	40,11	44,1500008	30,6699991	28,5499999	sp P02538 K2C6A_HUMAN	Keratin, type II cytoskeletal 6A OS=Homo sapi	HUMAN	25
6	34,05	42,02	67,1599984	50,849998	46,1899996	sp P02533 K1C14_HUMAN	Keratin, type I cytoskeletal 14 OS=Homo sapie	HUMAN	24
9	14,55	38,98	63,6399984	51,8000007	44,8199987	sp P08779 K1C16_HUMAN	Keratin, type I cytoskeletal 16 OS=Homo sapie	HUMAN	20
16	8	21,47	39,8099989	28,0099988	25	sp Q04695 K1C17_HUMAN	Keratin, type I cytoskeletal 17 OS=Homo sapie	HUMAN	11
16	0	21,46	36,8099988	28,0099988	25	sp A5A6M0 K1C17_PANTR	Keratin, type I cytoskeletal 17 OS=Pan troglody	PANTR	11
16	0	19,04	31,1800003	21,9400004	20,5500007	sp Q9QWL7 K1C17_MOUSE	Keratin, type I cytoskeletal 17 OS=Mus muscul	MOUSE	10
16	0	19,04	31,1800003	21,9400004	20,5500007	sp Q6IFU8 K1C17_RAT	Keratin, type I cytoskeletal 17 OS=Rattus norv	RAT	10
8	16,27	16,27	10,52	4,80699986	3,62199992	sp P15924 DESP_HUMAN	Desmoplakin OS=Homo sapiens GN=DSP PE=1	HUMAN	8
10	14	14	37,7200007	37,7200007	37,7200007	sp P06702 S10A9_HUMAN	Protein S100-A9 OS=Homo sapiens GN=S100A	HUMAN	8
13	9,14	9,14	59,1400027	59,1400027	59,1400027	sp P05109 S10A8_HUMAN	Protein S100-A8 OS=Homo sapiens GN=S100A	HUMAN	8
29	2	11,52	8,80099982	8,80099982	8,80099982	sp P19013 K2C4_HUMAN	Keratin, type II cytoskeletal 4 OS=Homo sapier	HUMAN	7
11	12,11	12,11	18,1199998	15,5699998	13,29	sp Q8WNW3 PLAK_PIG	Junction plakoglobin OS=Sus scrofa GN=Jup PE	PIG	6
11	0	12,11	18,1199998	15,5699998	13,29	sp Q8SPJ1 PLAK_BOVIN	Junction plakoglobin OS=Bos taurus GN=JUP P	BOVIN	6
11	0	12,11	18,1199998	15,5699998	13,29	sp Q02257 PLAK_MOUSE	Junction plakoglobin OS=Mus musculus GN=Ju	MOUSE	6
11	0	12,11	18,1199998	15,5699998	13,29	sp P14923 PLAK_HUMAN	Junction plakoglobin OS=Homo sapiens GN=JL	HUMAN	6
11	0	11,81	15,8399999	13,29	13,29	sp Q6P0K8 PLAK_RAT	Junction plakoglobin OS=Rattus norvegicus GN	RAT	6
22	4,03	11,6	15,0000006	6,92299977	6,92299977	sp Q8N1N4 K2C78_HUMAN	Keratin, type II cytoskeletal 78 OS=Homo sapie	HUMAN	6
15	8,06	8,06	60,2800012	46,0999995	46,0999995	sp P01037 CYTN_HUMAN	Cystatin-SN OS=Homo sapiens GN=CST1 PE=1	HUMAN	5
17	8	8	11,3300003	8,86700004	8,86700004	sp P02768 ALBU_HUMAN	Serum albumin OS=Homo sapiens GN=ALB PE=	HUMAN	5
14	8,14	8,14	71,0099995	44,9299991	38,4099999	sp P15252 REF_HEVBR	Rubber elongation factor protein OS=Hevea b	HEVBR	4
17	0	6	10,5099998	6,56799972	6,56799972	sp Q5NVH5 ALBU_PONAB	Serum albumin OS=Pongo abelii GN=ALB PE=2	PONAB	4
18	7,64	7,64	23,1399998	13,82	13,82	sp Q5T749 KPRP_HUMAN	Keratinocyte proline-rich protein OS=Homo sa	HUMAN	4
19	6,33	6,33	55,4799974	35,6200001	23,2899994	sp P12273 PIP_HUMAN	Prolactin-inducible protein OS=Homo sapiens	HUMAN	3
20	6,02	6,02	56,3600004	54,549998	54,549998	sp P81605 DCD_HUMAN	Dermcidin OS=Homo sapiens GN=DCD PE=1 S	HUMAN	3
21	6	6	9,24699977	5,1479999	5,1479999	sp Q02413 DSG1_HUMAN	Desmoglein-1 OS=Homo sapiens GN=DSG1 PE	HUMAN	3
30	2	4,55	6,72099963	4,88799997	4,88799997	sp Q6IFX1 K1C24_RAT	Keratin, type I cytoskeletal 24 OS=Rattus norv	RAT	3
30	0	4,55	6,44500032	4,68799993	4,68799993	sp A1L317 K1C24_MOUSE	Keratin, type I cytoskeletal 24 OS=Mus muscul	MOUSE	3
23	4,02	4,02	65,8200026	63,29	63,29	sp P02814 SMR3B_HUMAN	Submaxillary gland androgen-regulated protei	HUMAN	2
31	2	4,01	34,7499996	21,2799996	21,2799996	sp P09228 CYTT_HUMAN	Cystatin-SA OS=Homo sapiens GN=CST2 PE=1	HUMAN	2
39	1,3	1,3	32,7899992	32,7899992	32,7899992	sp Q8MKD1 UBB_HORSE	Polyubiquitin-B OS=Equus caballus GN=UBB P	HORSE	2
39	0	1,3	32,8900009	32,8900009	32,8900009	sp Q865C5 UBIQ_CAMDR	Ubiquitin OS=Camelus dromedarius PE=3 SV=2	CAMDR	2
39	0	1,3	30,8600008	30,8600008	sp Q63429 UBC_RAT	Polyubiquitin-C OS=Rattus norvegicus GN=Ubc	RAT	2	
39	0	1,3	39,6800011	39,6800011	sp P84589 UBIQ_LUMTE	Ubiquitin (Fragment) OS=Lumbricus terrestris	LUMTE	2	
39	0	1,3	16,0300002	16,0300002	sp P79781 RS27A_CHICK	Ubiquitin-40S ribosomal protein S27a OS=Gall	CHICK	2	
39	0	1,3	19,5299998	19,5299998	sp P68205 RL40_OPHHA	Ubiquitin-60S ribosomal protein L40 OS=Ophic	OPHHA	2	
39	0	1,3	16,0300002	16,0300002	sp P68203 RS27A_SPOFR	Ubiquitin-40S ribosomal protein S27a OS=Spo	SPOFR	2	
39	0	1,3	16,1300004	16,1300004	sp P68202 RS27A_PLUXY	Ubiquitin-40S ribosomal protein S27a OS=Plut	PLUXY	2	
39	0	1,3	16,0300002	16,0300002	sp P68200 RS27A_ICTPU	Ubiquitin-40S ribosomal protein S27a OS=Ict	ICTPU	2	
39	0	1,3	32,8900009	32,8900009	sp P68197 UBIQ_CERCA	Ubiquitin OS=Ceratitiscapitata PE=1 SV=1	CERCA	2	
39	0	1,3	19,5299998	19,5299998	sp P63053 RL40_PIG	Ubiquitin-60S ribosomal protein L40 OS=Sus s	PIG	2	
39	0	1,3	19,5299998	19,5299998	sp P63052 RL40_FELCA	Ubiquitin-60S ribosomal protein L40 OS=Felis	FELCA	2	
39	0	1,3	19,5299998	19,5299998	sp P63050 RL40_CANLF	Ubiquitin-60S ribosomal protein L40 OS=Canis	CANLF	2	
39	0	1,3	19,5299998	19,5299998	sp P63048 RL40_BOVIN	Ubiquitin-60S ribosomal protein L40 OS=Bos t	BOVIN	2	
39	0	1,3	16,0300002	16,0300002	sp P62992 RS27A_BOVIN	Ubiquitin-40S ribosomal protein S27a OS=Bos	BOVIN	2	
39	0	1,3	19,5299998	19,5299998	sp P62987 RL40_HUMAN	Ubiquitin-60S ribosomal protein L40 OS=Hom	HUMAN	2	
39	0	1,3	19,5299998	19,5299998	sp P62986 RL40_RAT	Ubiquitin-60S ribosomal protein L40 OS=Rattu	RAT	2	
39	0	1,3	19,5299998	19,5299998	sp P62984 RL40_MOUSE	Ubiquitin-60S ribosomal protein L40 OS=Mus	r MOUSE	2	
39	0	1,3	16,0300002	16,0300002	sp P62983 RS27A_MOUSE	Ubiquitin-40S ribosomal protein S27a OS=Mus	MOUSE	2	
39	0	1,3	16,0300002	16,0300002	sp P62982 RS27A_RAT	Ubiquitin-40S ribosomal protein S27a OS=Ratt	RAT	2	
39	0	1,3	16,0300002	16,0300002	sp P62979 RS27A_HUMAN	Ubiquitin-40S ribosomal protein S27a OS=Hon	HUMAN	2	
39	0	1,3	16,0300002	16,0300002	sp P62978 RS27A_CAVPO	Ubiquitin-40S ribosomal protein S27a OS=Cavi	CAVPO	2	
39	0	1,3	30,3999999	30,3999999	30,3999999	sp P62976 UBIQP_CRIGR	Polyubiquitin OS=Cricetulus griseus PE=2 SV=2	CRIGR	2
39	0	1,3	32,8900009	32,8900009	sp P62975 UBIQ_RABIT	Ubiquitin OS=Oryctolagus cuniculus PE=1 SV=1	RABIT	2	
39	0	1,3	35,3300005	35,3300005	sp P62972 UBIQP_XENLA	Polyubiquitin (Fragment) OS=Xenopus laevis P	XENLA	2	
39	0	1,3	16,1300004	16,1300004	sp P29504 RS27A_MANSE	Ubiquitin-40S ribosomal protein S27a OS=Mar	MANSE	2	
39	0	1,3	19,5299998	19,5299998	sp P18101 RL40_DROME	Ubiquitin-60S ribosomal protein L40 OS=Drosc	DROME	2	
39	0	1,3	16,0300002	16,0300002	sp P15357 RS27A_DROME	Ubiquitin-40S ribosomal protein S27a OS=Dro	DROME	2	
39	0	1,3	32,6099992	32,6099992	sp POCH28 UBC_BOVIN	Polyubiquitin-C OS=Bos taurus GN=UBC PE=1	BOVIN	2	
39	0	1,3	32,7699989	32,7699989	sp POCG69 UBIQP_DROME	Polyubiquitin OS=Drosophila melanogaster GN	DROME	2	
39	0	1,3	32,8299999	32,8299999	sp POCG68 UBC_PIG	Polyubiquitin-C OS=Sus scrofa GN=UBC PE=2	S PIG	2	
39	0	1,3	32,7499986	32,7499986	sp POCG67 UBB_GORGO	Polyubiquitin-B OS=Gorilla gorilla gorilla GN=U	GORGO	2	
39	0	1,3	32,8399986	32,8399986	sp POCG66 UBC_GORGO	Polyubiquitin-C OS=Gorilla gorilla gorilla GN=U	GORGO	2	
39	0	1,3	32,7499986	32,7499986	sp POCG65 UBB_PANTR	Polyubiquitin-B OS=Pan troglodytes GN=UBB F	PANTR	2	
39	0	1,3	32,8500003	32,8500003	sp POCG64 UBC_PANTR	Polyubiquitin-C OS=Pan troglodytes GN=UBC F	PANTR	2	
39	0	1,3	32,7899992	32,7899992	sp POCG62 UBB_CHICK	Polyubiquitin-B OS=Gallus gallus GN=UBB PE=	CHICK	2	
39	0	1,3	32,8500003	32,8500003	sp POCG61 UBC_PONPY	Polyubiquitin-C OS=Pongo pygmaeus GN=UBC	PONPY	2	
39	0	1,3	32,7499986	32,7499986	sp POCG60 UBB_PONPY	Polyubiquitin-B OS=Pongo pygmaeus GN=UBB	PONPY	2	
39	0	1,3	32,7899992	32,7899992	sp POCG55 UBB_SHEEP	Polyubiquitin-B OS=Ovis aries GN=UBB PE=2	S SHEEP	2	
39	0	1,3	32,1500003	32,1500003	sp POCG54 UBB_CAVPO	Polyubiquitin-B OS=Cavia porcellus GN=UBB P	CAVPO	2	
39	0	1,3	32,7899992	32,7899992	sp POCG53 UBB_BOVIN	Polyubiquitin-B OS=Bos taurus GN=UBB PE=1	BOVIN	2	
39	0	1,3	32,7899992	32,7899992	sp POCG51 UBB_RAT	Polyubiquitin-B OS=Rattus norvegicus GN=U	RAT	2	
39	0	1,3	30,6499988	30,6499988	sp POCG50 UBC_MOUSE	Polyubiquitin-C OS=Mus musculus GN=Ubc PE	MOUSE	2	
39	0	1,3	32,7899992	32,7899992	sp POCG49 UBB_MOUSE	Polyubiquitin-B OS=Mus musculus GN=Ubb PE	MOUSE	2	
39	0	1,3	32,8500003	32,8500003	sp POCG48 UBC_HUMAN	Polyubiquitin-C OS=Homo sapiens GN=UBC PE	HUMAN	2	
39	0	1,3	32,7499986	32,7499986	sp POCG47 UBB_HUMAN	Polyubiquitin-B OS=Homo sapiens GN=UBB PE	HUMAN	2	
39	0	1,3	19,5299998	19,5299998	sp POC276 RL40_SHEEP	Ubiquitin-60S ribosomal protein L40 OS=Ovis	ε SHEEP	2	
39	0	1,3	19,5299998	19,5299998	sp POC275 RL40_PONPY	Ubiquitin-60S ribosomal protein L40 OS=Pong	r PONPY	2	
39	0	1,3	19,5299998	19,5299998	sp POC273 RL40_MACFA	Ubiquitin-60S ribosomal protein L40 OS=Maca	MACFA	2	
24	2,08	2,08	4,14999984	4,14999984	2,14200001	sp Q13835 PKP1_HUMAN	Plakophilin-1 OS=Homo sapiens GN=PKP1 PE=	HUMAN	1
24	0	2,08	4,25800011	4,25800011	2,19800007	sp P97350 PKP1_MOUSE	Plakophilin-1 OS=Mus musculus GN=Pkp1 PE=	MOUSE	1

25	2,05	2,05	9,06499997	4,81600016	4,81600016	sp P20758 IGHA1_GORGO	Ig alpha-1 chain C region OS=Gorilla gorilla gor GORGO	1
25	0	2,05	9,06499997	4,81600016	4,81600016	sp P01876 IGHA1_HUMAN	Ig alpha-1 chain C region OS=Homo sapiens GI HUMAN	1
25	0	2	5,00000007	5,00000007	5,00000007	sp P01877 IGHA2_HUMAN	Ig alpha-2 chain C region OS=Homo sapiens GI HUMAN	1
26	2,01	2,01	12,74999998	4,02700007	4,02700007	sp P25311 ZA2G_HUMAN	Zinc-alpha-2-glycoprotein OS=Homo sapiens G HUMAN	1
27	2,01	2,01	26,42000002	26,42000002	26,42000002	sp Q5R9M3 THIO_PONAB	Thioredoxin OS=Pongo abelii GN=TXN PE=3 SV PONAB	1
27	0	2,01	26,67	26,67	26,67	sp P10599 THIO_HUMAN	Thioredoxin OS=Homo sapiens GN=TXN PE=1 ! HUMAN	1
28	2,01	2,01	5,52899987	4,08699997	4,08699997	sp P34955 A1AT_BOVIN	Alpha-1-antiproteinase OS=Bos taurus GN=SEI BOVIN	1
32	2	2	8,072	2,14200001	2,14200001	sp P02769 ALBU_BOVIN	Serum albumin OS=Bos taurus GN=ALB PE=1 S BOVIN	1
33	2	2	2,44999994	1,45699997	1,45699997	sp Q7SIH1 A2MG_BOVIN	Alpha-2-macroglobulin OS=Bos taurus GN=A2I BOVIN	1
34	2	2	3,16799991	1,18800001	1,18800001	sp P33610 PRI2_MOUSE	DNA primase large subunit OS=Mus musculus MOUSE	1
34	0	2	3,156	1,18300002	1,18300002	sp O89044 PRI2_RAT	DNA primase large subunit OS=Rattus norvegici RAT	1
34	0	2	0,79889996	0,79889996	0,79889996	sp Q9R6X3 PHYB_NOSS1	Cyanobacterial phytochrome B OS=Nostoc sp. NOSS1	1
34	0	2	2,66699996	2,66699996	2,66699996	sp Q5WGU8 KCY_BACSK	Cytidylate kinase OS=Bacillus clausii (strain KSI BACSK	1
34	0	2	1,28499996	1,28499996	1,28499996	sp Q5UN58 YR665_MIMIV	Uncharacterized protein R665 OS=Acanthamo MIMIV	1
34	0	2	0,6904	0,6904	0,6904	sp Q03279 PO21_BRACO	Retrovirus-related Pol polyprotein from type-1 BRACO	1
34	0	2	0,48500001	0,48500001	0,48500001	sp P53254 UTP22_YEAST	U3 small nucleolar RNA-associated protein 22 YEAST	1
34	0	2	1,17899999	1,17899999	1,17899999	sp P49643 PRI2_HUMAN	DNA primase large subunit OS=Homo sapiens HUMAN	1
34	0	2	0,63029998	0,63029998	0,63029998	sp P0CN43 EIF3A_CRYNB	Eukaryotic translation initiation factor 3 subun CRYNB	1
34	0	2	0,63029998	0,63029998	0,63029998	sp P0CN42 EIF3A_CRYNJ	Eukaryotic translation initiation factor 3 subun CRYNJ	1
34	0	2	2,24699993	2,24699993	2,24699993	sp B3QP81 TRPA_CHLP8	Tryptophan synthase alpha chain OS=Chlorobac CHLP8	1
34	0	2	1,91099998	1,91099998	1,91099998	sp A4IHY0 OXND1_XENTR	Oxidoreductase NAD-binding domain-containi XENTR	1
34	0	2	2,128	2,128	2,128	RRRRRsp Q9TLX3 LPXC_CYACA	REVERSED UDP-3-O-[3-hydroxymyristoyl] N-ac CYACA	1
34	0	2	0,96930005	0,96930005	0,96930005	RRRRRsp Q9LTX2 TIR1L_ARATH	REVERSED Transport inhibitor response 1-like ARATH	1
34	0	2	1,143	1,143	1,143	RRRRRsp Q9ESB3 HRG_MOUSE	REVERSED Histidine-rich glycoprotein OS=Mus MOUSE	1
34	0	2	1,143	1,143	1,143	RRRRRsp Q99P58 HRG_RAT	REVERSED Histidine-rich glycoprotein OS=Ratt RAT	1
34	0	2	1,47799999	1,47799999	1,47799999	RRRRRsp Q8FGZ9 ASTC_ECOL6	REVERSED Succinylornithine transaminase OS= ECOL6	1
34	0	2	1,47799999	1,47799999	1,47799999	RRRRRsp Q1RB45 ASTC_ECOUT	REVERSED Succinylornithine transaminase OS= ECOUT	1
34	0	2	1,47799999	1,47799999	1,47799999	RRRRRsp Q0TH82 ASTC_ECOL5	REVERSED Succinylornithine transaminase OS= ECOL5	1
34	0	2	1,04	1,04	1,04	RRRRRsp Q0I3B0 SYR_HAES1	REVERSED Arginine--tRNA ligase OS=Haemophil HAES1	1
34	0	2	0,36859999	0,36859999	0,36859999	RRRRRsp Q09779 THO2_SCHPO	REVERSED THO complex subunit 2 OS=Schizos SCHPO	1
34	0	2	1,81300007	1,81300007	1,81300007	RRRRRsp Q01558 G3PC_LEIME	REVERSED Glyceraldehyde-3-phosphate dehyd LEIME	1
34	0	2	0,84149996	0,84149996	0,84149996	RRRRRsp P53276 UTP8_YEAST	REVERSED U3 small nucleolar RNA-associated YEAST	1
34	0	2	0,48349998	0,48349998	0,48349998	RRRRRsp P23634 AT2B4_HUMAN	REVERSED Plasma membrane calcium-transpo HUMAN	1
34	0	2	1,81300007	1,81300007	1,81300007	RRRRRsp P0A9B5 G3P_SHIFL	REVERSED Glyceraldehyde-3-phosphate dehyd SHIFL	1
34	0	2	1,81300007	1,81300007	1,81300007	RRRRRsp P0A9B4 G3P1_ECO57	REVERSED Glyceraldehyde-3-phosphate dehyd ECO57	1
34	0	2	1,81300007	1,81300007	1,81300007	RRRRRsp P0A9B3 G3P_ECOL6	REVERSED Glyceraldehyde-3-phosphate dehyd ECOL6	1
34	0	2	1,81300007	1,81300007	1,81300007	RRRRRsp P0A9B2 G3P1_ECOLI	REVERSED Glyceraldehyde-3-phosphate dehyd ECOLI	1
34	0	2	1,81300007	1,81300007	1,81300007	RRRRRsp P0A1P1 G3P_SALTI	REVERSED Glyceraldehyde-3-phosphate dehyd SALTI	1
34	0	2	1,81300007	1,81300007	1,81300007	RRRRRsp P0A1P0 G3P_SALTY	REVERSED Glyceraldehyde-3-phosphate dehyd SALTY	1
34	0	2	1,81300007	1,81300007	1,81300007	RRRRRsp I2BA89 G3P_SHIBC	REVERSED Glyceraldehyde-3-phosphate dehyd SHIBC	1
34	0	2	0,49709999	0,49709999	0,49709999	RRRRRsp D3K0R6 AT2B4_BOVIN	REVERSED Plasma membrane calcium-transpo BOVIN	1
34	0	2	1,47799999	1,47799999	1,47799999	RRRRRsp B7USC9 ASTC_ECO27	REVERSED Succinylornithine transaminase OS= ECO27	1
34	0	2	1,47799999	1,47799999	1,47799999	RRRRRsp B7NT29 ASTC_ECO7I	REVERSED Succinylornithine transaminase OS= ECO7I	1
34	0	2	1,47799999	1,47799999	1,47799999	RRRRRsp B7N584 ASTC_ECOLU	REVERSED Succinylornithine transaminase OS= ECOLU	1
34	0	2	1,47799999	1,47799999	1,47799999	RRRRRsp B7MVM7 ASTC_ECO81	REVERSED Succinylornithine transaminase OS= ECO81	1
34	0	2	1,47799999	1,47799999	1,47799999	RRRRRsp B7MAV9 ASTC_ECO45	REVERSED Succinylornithine transaminase OS= ECO45	1
34	0	2	1,47799999	1,47799999	1,47799999	RRRRRsp B7LQ44 ASTC_ESCF3	REVERSED Succinylornithine transaminase OS= ESCF3	1
34	0	2	1,81300007	1,81300007	1,81300007	RRRRRsp B7LQ20 G3P_ESCF3	REVERSED Glyceraldehyde-3-phosphate dehyd ESCF3	1
34	0	2	1,47799999	1,47799999	1,47799999	RRRRRsp B1LDY3 ASTC_ECOSM	REVERSED Succinylornithine transaminase OS= ECOSM	1
34	0	2	1,04	1,04	1,04	RRRRRsp B0UUF1 SYR_HISS2	REVERSED Arginine--tRNA ligase OS=Histophil HISS2	1
34	0	2	1,47799999	1,47799999	1,47799999	RRRRRsp A1A8S9 ASTC_ECOK1	REVERSED Succinylornithine transaminase OS= ECOK1	1
35	2	2	5,9390001	1,76599994	1,76599994	sp P21910 LAML2_XENLA	Lamin-L(II) OS=Xenopus laevis PE=2 SV=1 XENLA	1
36	2	2	26,3500005	8,10799971	8,10799971	sp P17897 LYZ1_MOUSE	Lysozyme C-1 OS=Mus musculus GN=Lyz1 PE= MOUSE	1
36	0	2	8,3920002	8,3920002	8,3920002	sp Q9PU28 LYSC_SCOMX	Lysozyme C OS=Scophthalmus maximus GN=ly SCOMX	1
36	0	2	8,3920002	8,3920002	8,3920002	sp Q9DD65 LYSC_PAROL	Lysozyme C OS=Paralichthys olivaceus PE=2 SV PAROL	1
36	0	2	8,10799971	8,10799971	8,10799971	sp Q6B411 LYSM_BOVIN	Lysozyme C, milk isozyme OS=Bos taurus PE=2 BOVIN	1
36	0	2	8,10799971	8,10799971	8,10799971	sp Q659U5 LYSC_HALGR	Lysozyme C OS=Halichoerus grypus GN=LYZ PE HALGR	1
36	0	2	8,10799971	8,10799971	8,10799971	sp Q659U1 LYSC_PHOVI	Lysozyme C OS=Phoca vitulina GN=LYZ PE=1 S' PHOVI	1
36	0	2	8,10799971	8,10799971	8,10799971	sp Q659U0 LYSC_LEPWE	Lysozyme C OS=Leptonychotes weddellii GN=L LEPWE	1
36	0	2	8,10799971	8,10799971	8,10799971	sp Q05820 LYSC2_RAT	Putative lysozyme C-2 OS=Rattus norvegicus G RAT	1
36	0	2	9,23099965	9,23099965	9,23099965	sp P85345 LYSC_AMYCA	Lysozyme C OS=Amyda cartilaginea GN=LYZ PE AMYCA	1
36	0	2	8,21899995	8,21899995	8,21899995	sp P85045 LYS_BUFGA	Lysozyme C (Fragment) OS=Bufo gargarizans a BUFGA	1
36	0	2	9,23099965	9,23099965	9,23099965	sp P81709 LYSC2_CANLF	Lysozyme C, spleen isozyme OS=Canis lupus fa CANLF	1
36	0	2	8,10799971	8,10799971	8,10799971	sp P79847 LYSC_PYGNE	Lysozyme C OS=Pygathrix nemaeus GN=LYZ PE PYGNE	1
36	0	2	8,10799971	8,10799971	8,10799971	sp P79811 LYSC_NASLA	Lysozyme C OS=Nasalis larvatus GN=LYZ PE=3 NASLA	1
36	0	2	8,10799971	8,10799971	8,10799971	sp P79239 LYSC_PONPY	Lysozyme C OS=Pongo pygmaeus GN=LYZ PE=3 PONPY	1
36	0	2	8,10799971	8,10799971	8,10799971	sp P79180 LYSC_HYLLA	Lysozyme C OS=Hylobates lar GN=LYZ PE=2 SV HYLLA	1
36	0	2	8,10799971	8,10799971	8,10799971	sp P79179 LYSC_GORGO	Lysozyme C OS=Gorilla gorilla gorilla GN=LYZ P GORGO	1
36	0	2	8,10799971	8,10799971	8,10799971	sp P67980 LYSC_TRAFR	Lysozyme C OS=Trachypithecus francoisi GN=L TRAFR	1
36	0	2	8,10799971	8,10799971	8,10799971	sp P67979 LYSC_TRAOB	Lysozyme C OS=Trachypithecus obscurus GN=L TRAOB	1
36	0	2	8,10799971	8,10799971	8,10799971	sp P67978 LYSC_TRAVT	Lysozyme C OS=Trachypithecus vetulus GN=LY TRAVT	1
36	0	2	8,10799971	8,10799971	8,10799971	sp P67977 LYSC_SEMEN	Lysozyme C OS=Semnopithecus entellus GN=L SEMEN	1
36	0	2	8,3920002	8,3920002	8,3920002	sp P61944 LYSC_TAKRU	Lysozyme C OS=Takifugu rubripes PE=2 SV=1 TAKRU	1
36	0	2	8,10799971	8,10799971	8,10799971	sp P61632 LYSC_COLGU	Lysozyme C OS=Colobus guereza GN=LYZ PE=2 COLGU	1
36	0	2	8,10799971	8,10799971	8,10799971	sp P61631 LYSC_COLAN	Lysozyme C OS=Colobus angolensis GN=LYZ PE COLAN	1
36	0	2	8,10799971	8,10799971	8,10799971	sp P61628 LYSC_PANTR	Lysozyme C OS=Pan troglodytes GN=LYZ PE=2 PANTR	1
36	0	2	8,10799971	8,10799971	8,10799971	sp P61627 LYSC_PANPA	Lysozyme C OS=Pan paniscus GN=LYZ PE=3 SV PANPA	1
36	0	2	8,10799971	8,10799971	8,10799971	sp P61626 LYSC_HUMAN	Lysozyme C OS=Homo sapiens GN=LYZ PE=1 S' HUMAN	1
36	0	2	9,23099965	9,23099965	9,23099965	sp P37712 LYSC_CAMDR	Lysozyme C OS=Camelus dromedarius GN=LYZ CAMDR	1
36	0	2	9,23099965	9,23099965	9,23099965	sp P16973 LYSC_RABIT	Lysozyme C OS=Orctolagus cuniculus GN=LYZ RABIT	1
36	0	2	8,10799971	8,10799971	8,10799971	sp P12069 LYSC3_PIG	Lysozyme C-3 OS=Sus scrofa PE=1 SV=2 PIG	1
36	0	2	8,21899995	8,21899995	8,21899995	sp P12068 LYSC2_PIG	Lysozyme C-2 OS=Sus scrofa PE=1 SV=2 PIG	1
36	0	2	9,375	9,375	9,375	sp P12067 LYSC1_PIG	Lysozyme C-1 OS=Sus scrofa PE=1 SV=1 PIG	1
36	0	2	8,3329998	8,3329998	8,3329998	sp P11941 LYSC2_ONCMY	Lysozyme C II OS=Oncorhynchus mykiss PE=1 ! ONCMY	1
36	0	2	8,10799971	8,10799971	8,10799971	sp P08905 LYZ2_MOUSE	Lysozyme C-2 OS=Mus musculus GN=Lyz2 PE= MOUSE	1
36	0	2	8,10799971	8,10799971	8,10799971	sp P00697 LYSC1_RAT	Lysozyme C-1 OS=Rattus norvegicus GN=Lyz1 RAT	1
37	2	2	6,68499991	6,68499991	6,68499991	sp P12763 FETUA_BOVIN	Alpha-2-HS-glycoprotein OS=Bos taurus GN=A BOVIN	1
38	1,58	1,58	7,82999992	3,46800014	1,67800002	sp Q08554 DSC1_HUMAN	Desmocollin-1 OS=Homo sapiens GN=DSC1 PE HUMAN	1
40	0,77	0,77	13,73	5,07499985	5,07499985	sp P04406 G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (HUMAN	1

40	0	0,75	5,09000011	5,09000011	5,09000011	sp Q9UVC0 G3P_WICCF	Glyceraldehyde-3-phosphate dehydrogenase (WICCF	1
40	0	0,75	5,07499985	5,07499985	5,07499985	sp Q9PJN6 G3P_CHLMU	Glyceraldehyde-3-phosphate dehydrogenase (CHLMU	1
40	0	0,75	5,07499985	5,07499985	5,07499985	sp Q92211 G3P_CANAW	Glyceraldehyde-3-phosphate dehydrogenase (CANAW	1
40	0	0,75	5,13599999	5,13599999	5,13599999	sp Q01558 G3PC_LEIME	Glyceraldehyde-3-phosphate dehydrogenase, LEIME	1
40	0	0,75	5,01499996	5,01499996	5,01499996	sp P9WN83 G3P_MYCTU	Glyceraldehyde-3-phosphate dehydrogenase (MYCTU	1
40	0	0,75	5,01499996	5,01499996	5,01499996	sp P9WN82 G3P_MYCTO	Glyceraldehyde-3-phosphate dehydrogenase (MYCTO	1
40	0	0,75	5,01499996	5,01499996	5,01499996	sp P64179 G3P_MYCBO	Glyceraldehyde-3-phosphate dehydrogenase (MYCBO	1
40	0	0,75	4,98499982	4,98499982	4,98499982	sp P49644 G3PC_CHLRE	Glyceraldehyde-3-phosphate dehydrogenase, CHLRE	1
40	0	0,75	5,01499996	5,01499996	5,01499996	sp P48812 G3P_BRUMA	Glyceraldehyde-3-phosphate dehydrogenase (BRUMA	1
40	0	0,75	5,01499996	5,01499996	5,01499996	sp P46713 G3P_MYCLE	Glyceraldehyde-3-phosphate dehydrogenase (MYCLE	1
40	0	0,75	5,02999984	5,02999984	5,02999984	sp P34922 G3PC_PEA	Glyceraldehyde-3-phosphate dehydrogenase, PEA	1
40	0	0,75	4,98499982	4,98499982	4,98499982	sp P32810 G3P3_CAEBR	Glyceraldehyde-3-phosphate dehydrogenase : CAEBR	1
40	0	0,75	4,98499982	4,98499982	4,98499982	sp P32809 G3P2_CAEBR	Glyceraldehyde-3-phosphate dehydrogenase 2 CAEBR	1
40	0	0,75	4,98499982	4,98499982	4,98499982	sp P17330 G3P3_CAEEL	Glyceraldehyde-3-phosphate dehydrogenase : CAEEL	1
40	0	0,75	4,98499982	4,98499982	4,98499982	sp P17329 G3P2_CAEEL	Glyceraldehyde-3-phosphate dehydrogenase 2 CAEEL	1
40	0	0,75	5,09000011	5,09000011	5,09000011	sp P0CE13 G3P_CHLTR	Glyceraldehyde-3-phosphate dehydrogenase (CHLTR	1
40	0	0,75	5,07499985	5,07499985	5,07499985	sp O59841 G3P_OGAPD	Glyceraldehyde-3-phosphate dehydrogenase (OGAPD	1
40	0	0,75	5,01499996	5,01499996	5,01499996	sp O01360 G3P_ONCVO	Glyceraldehyde-3-phosphate dehydrogenase (ONCVO	1
40	0	0,75	5,09000011	5,09000011	5,09000011	sp B0B879 G3P_CHLT2	Glyceraldehyde-3-phosphate dehydrogenase (CHLT2	1
41	0,63	0,63	14,14999996	14,14999996	14,14999996	sp P0CG06 LAC3_HUMAN	Ig lambda-3 chain C regions OS=Homo sapiens HUMAN	1
41	0	0,63	14,14999996	14,14999996	14,14999996	sp P0CG05 LAC2_HUMAN	Ig lambda-2 chain C regions OS=Homo sapiens HUMAN	1
41	0	0,63	14,14999996	14,14999996	14,14999996	sp P0CG04 LAC1_HUMAN	Ig lambda-1 chain C regions OS=Homo sapiens HUMAN	1
41	0	0,63	14,14999996	14,14999996	14,14999996	sp P0CF74 LAC6_HUMAN	Ig lambda-6 chain C region OS=Homo sapiens HUMAN	1
41	0	0,63	7,00900033	7,00900033	7,00900033	sp B9A064 IGLL5_HUMAN	Immunoglobulin lambda-like polypeptide 5 OS HUMAN	1
41	0	0,63	14,14999996	14,14999996	14,14999996	sp A0M8Q6 LAC7_HUMAN	Ig lambda-7 chain C region OS=Homo sapiens HUMAN	1
42	0,56	0,56	3,53399999	1,43999998	1,43999998	sp P01833 PIGR_HUMAN	Polymeric immunoglobulin receptor OS=Homo sapiens HUMAN	1
43	0,3	0,3	6,83199987	3,41599993	0	sp P05089 ARG1_HUMAN	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 HUMAN	0
44	0,28	0,28	1,89399999	1,89399999	0	RRRRRsp P94282 SYFA_BORBU	REVERSED Phenylalanine--tRNA ligase alpha subunit BORBU	0
45	0,19	0,19	2,76800003	2,76800003	0	RRRRRsp P97281 SGCD_MESAU	REVERSED Delta-sarcoglycan OS=Mesocricetus MESAU	0
45	0	0,19	2,76800003	2,76800003	0	RRRRRsp P82347 SGCD_MOUSE	REVERSED Delta-sarcoglycan OS=Mus musculus MOUSE	0
46	0,12	0,12	1,88299995	1,88299995	0	sp Q50339 Y588_MYCPN	Uncharacterized lipoprotein MPN_588 OS=Mytilus MYCPN	0

N	Ctrl	dudoso_CSI_4	Total	%Cov	%Cov(50)	%Cov(95)	Accession	Name	Species	Peptides(95%)
1	109,68	109,68	70,8100021	70,8100021	67,6999986	sp P04264 K2C1_HUMAN	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE= HUMAN	87		
2	91,02	91,02	61,8200004	61,8200004	56,3399971	sp P13645 K1C10_HUMAN	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PI HUMAN	80		
3	57,75	67,12	68,8600004	60,2500021	58,8400006	sp P35908 K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN HUMAN	47		
4	53,23	54,34	64,3700004	62,2799993	59,0699971	sp P35527 K1C9_HUMAN	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE= HUMAN	40		
5	45,59	45,59	65,7999992	65,7999992	59,740001	sp P00761 TRYP_PIG	Trypsin OS=Sus scrofa PE=1 SV=1	39		
8	20,1	32,82	34,7499996	26,7800003	26,7800003	sp P13647 K2C5_HUMAN	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE= HUMAN	21		
26	0	25,24	29,2600006	23,3999997	19,4999993	sp P04259 K2C6B_HUMAN	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6B F HUMAN	21		
8	0	30,82	32,0899993	24,1600007	24,1600007	sp A5A6M8 K2C5_PANTR	Keratin, type II cytoskeletal 5 OS=Pan troglodytes GN=KRT5 PI PANTR	20		
26	4,52	25,25	32,980001	25,3500015	19,3299994	sp P48668 K2C6C_HUMAN	Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C F HUMAN	19		
26	0	25,24	30,8499992	23,2299998	21,0999995	sp P02538 K2C6A_HUMAN	Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A F HUMAN	19		
7	25,71	31,8	50,4199982	45,3399986	37,9200011	sp P02533 K1C14_HUMAN	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PI HUMAN	16		
23	5,9	16,21	20,07	16,6099995	15,05	sp Q7Z794 K2C1B_HUMAN	Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 F HUMAN	15		
6	26,33	26,33	44,0800011	29,58	20,2800006	sp P02788 TRFL_HUMAN	Lactotransferrin OS=Homo sapiens GN=LTF PE=1 SV=6	12		
9	19,85	19,85	29,0600002	23,5599995	21,9899997	sp P01833 PIGR_HUMAN	Polymeric immunoglobulin receptor OS=Homo sapiens GN=PI HUMAN	11		
25	4,92	18,53	26,2199998	25,8800009	20,51	sp P08779 K1C16_HUMAN	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PI HUMAN	10		
37	2,11	14,59	13,6500001	7,88500011	5,38499989	sp Q8N1N4 K2C78_HUMAN	Keratin, type II cytoskeletal 78 OS=Homo sapiens GN=KRT78 F HUMAN	10		
12	15,02	15,02	47,8799999	40,7900006	40,7900006	sp P01876 IGHA1_HUMAN	Ig alpha-1 chain C region OS=Homo sapiens GN=IGHA1 PE=1 S HUMAN	9		
10	15,55	15,55	55,4799974	55,4799974	55,4799974	sp P12273 PIP_HUMAN	Prolactin-inducible protein OS=Homo sapiens GN=PIP PE=1 SV HUMAN	8		
11	15,19	15,19	83,3299994	71,0099995	71,0099995	sp P15252 REF_HEVBR	Rubber elongation factor protein OS=Hevea brasiliensis PE=1 : HEVBR	8		
39	2,01	14,28	21,9899997	18,9799994	16,9	sp Q04695 K1C17_HUMAN	Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PI HUMAN	8		
39	0	14,28	21,9899997	18,9799994	16,9	sp A5A6M0 K1C17_PANTR	Keratin, type I cytoskeletal 17 OS=Pan troglodytes GN=KRT17 PANTR	8		
13	13,81	13,81	43,2900012	31,8800002	28,52	sp P25311 ZA2G_HUMAN	Zinc-alpha-2-glycoprotein OS=Homo sapiens GN=AZGP1 PE=1 HUMAN	7		
14	13,05	13,05	15,4400006	10,87	10,87	sp Q02413 DSG1_HUMAN	Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	7		
40	2,01	11,03	49,7099996	30,0000012	30,0000012	sp P01877 IGHA2_HUMAN	Ig alpha-2 chain C region OS=Homo sapiens GN=IGHA2 PE=1 S HUMAN	7		
16	9,85	9,85	17,08	14,4500002	11,9900003	sp Q5NVH5 ALBU_PONAB	Serum albumin OS=Pongo abelii GN=ALB PE=2 SV=2	6		
16	0	9,85	17,08	14,4500002	11,9900003	sp P02768 ALBU_HUMAN	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	6		
17	8,81	8,81	44,1199988	35,2899998	35,2899998	sp O82803 SRPP_HEVBR	Small rubber particle protein OS=Hevea brasiliensis GN=SRPP HEVBR	6		
15	10	10	70,9699988	70,9699988	sp P05109 S10A8_HUMAN	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	5			
19	8,01	8,01	64,1499996	64,1499996	sp P01834 IGKC_HUMAN	Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1 SV=: HUMAN	5			
21	7,6	7,6	49,12	37,7200007	37,7200007	sp P06702 S10A9_HUMAN	Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1	5		
18	8,58	8,58	31,9499999	15,1999995	13,6399999	sp Q5T749 KPRP_HUMAN	Keratinocyte proline-rich protein OS=Homo sapiens GN=KPRP HUMAN	4		
20	8	56,3600004	56,3600004	56,3600004	sp P81605 DCD_HUMAN	Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	4			
22	6,07	6,07	22,0899999	13,73	13,73	sp P04406 G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapien HUMAN	3		
24	5,35	5,35	39,8600012	39,8600012	31,7600012	sp P79239 LYSC_PONPY	Lysozyme C OS=Pongo pygmaeus GN=LYZ PE=2 SV=1	3		
24	0	5,35	39,8600012	39,8600012	31,7600012	sp P79179 LYSC_GORGO	Lysozyme C OS=Gorilla gorilla GN=LYZ PE=2 SV=1	3		
24	0	5,35	39,8600012	39,8600012	31,7600012	sp P61628 LYSC_PANTR	Lysozyme C OS=Pan troglodytes GN=LYZ PE=2 SV=2	3		
24	0	5,35	39,8600012	39,8600012	31,7600012	sp P61627 LYSC_PANPA	Lysozyme C OS=Pan paniscus GN=LYZ PE=3 SV=1	3		
24	0	5,35	39,8600012	39,8600012	31,7600012	sp P61626 LYSC_HUMAN	Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1	3		
27	0	4,35	22,9300007	17,0699999	sp Q912K5 ACTB_SIGHI	Actin, cytoplasmic 1 OS=Sigmodon hispidus GN=ACTB PE=2 SV SIGHI	3			
27	0	4,35	22,9300007	17,0699999	sp Q8JJB8 ACTG_TRISC	Actin, cytoplasmic 2 OS=Triakis scyllium GN=actg1 PE=2 SV=1 TRISC	3			
27	0	4,35	22,9300007	17,0699999	sp Q7ZV17 ACTB1_DANRE	Actin, cytoplasmic 1 OS=Danio rerio GN=actba PE=2 SV=2 DANRE	3			
27	0	4,35	22,9300007	17,0699999	sp Q7ZVF9 ACTB2_DANRE	Actin, cytoplasmic 2 OS=Danio rerio GN=actbb PE=2 SV=2 DANRE	3			
27	0	4,35	22,9300007	17,0699999	sp Q76N69 ACTB_CHLAE	Actin, cytoplasmic 1 OS=Chlorocebus aethiops GN=ACTB PE=2 CHLAE	3			
27	0	4,35	22,9300007	17,0699999	sp Q71FK5 ACTB_CAVPO	Actin, cytoplasmic 1 OS=Cavia porcellus GN=ACTB PE=2 SV=1 CAVPO	3			
27	0	4,35	22,9300007	17,0699999	sp Q711N9 ACTB_MESAU	Actin, cytoplasmic 1 OS=Mesocricetus auratus GN=ACTB PE=1 MESAU	3			
27	0	4,35	22,9300007	17,0699999	sp Q6QQA1 ACTB_PIG	Actin, cytoplasmic 1 OS=Sus scrofa GN=ACTB PE=1 SV=2 PIG	3			
27	0	4,35	22,9300007	17,0699999	sp Q6P378 ACTG_XENTR	Actin, cytoplasmic 2 OS=Xenopus tropicalis GN=actg1 PE=2 SV XENTR	3			
27	0	4,35	22,9300007	17,0699999	sp Q6NVA9 ACTB_XENTR	Actin, cytoplasmic 1 OS=Xenopus tropicalis GN=actb PE=2 SV= XENTR	3			
27	0	4,35	22,9300007	17,0699999	sp Q5ZMQ2 ACTG_CHICK	Actin, cytoplasmic 2 OS=Gallus gallus GN=ACTG1 PE=1 SV=1 CHICK	3			
27	0	4,35	22,9300007	17,0699999	sp Q5R6G0 ACTB_PONAB	Actin, cytoplasmic 1 OS=Pongo abelii GN=ACTB PE=2 SV=1 PONAB	3			
27	0	4,35	22,9300007	17,0699999	sp Q5R1X3 ACTB_PANTR	Actin, cytoplasmic 1 OS=Pan troglodytes GN=ACTB PE=2 SV=1 PANTR	3			
27	0	4,35	22,9300007	17,0699999	sp Q5JAK2 ACTG_PELLE	Actin, cytoplasmic 2 OS=Peromylax lessonae GN=actg1 PE=2 S PELLE	3			
27	0	4,35	22,9300007	17,0699999	sp Q4R561 ACTB_MACFA	Actin, cytoplasmic 1 OS=Macaca fascicularis GN=ACTB PE=2 SV MACFA	3			
27	0	4,35	22,9300007	17,0699999	sp Q4LOY2 ACTB_SPECI	Actin, cytoplasmic 1 OS=Spermophilus citellus GN=ACTB PE=2 SPECI	3			
27	0	4,35	23,8199994	17,7300006	sp P84856 ACTB_CHLPG	Actin, cytoplasmic 1 OS=Chlorocebus pygerythrus GN=ACTB P CHLPG	3			
27	0	4,35	22,9300007	17,0699999	sp P84336 ACTB_CAMDR	Actin, cytoplasmic 1 OS=Camelus dromedarius GN=ACTB PE=1 CAMDR	3			
27	0	4,35	22,9300007	17,0699999	sp P83751 ACTB_CTEID	Actin, cytoplasmic 1 OS=Ctenopharyngodon idella GN=actb PE CTEID	3			
27	0	4,35	22,9300007	17,0699999	sp P83750 ACTB_CYPCA	Actin, cytoplasmic 1 OS=Cyprinus carpio GN=actb PE=3 SV=1 CYPCA	3			
27	0	4,35	22,9300007	17,0699999	sp P68143 ACTB_OREMO	Actin, cytoplasmic 1 OS=Oreochromis mossambicus GN=actb I OREMO	3			
27	0	4,35	22,9300007	17,0699999	sp P68142 ACTB1_TAKRU	Actin, cytoplasmic 1 OS=Takifugu rubripes GN=actba PE=2 SV- TAKRU	3			
27	0	4,35	22,9300007	17,0699999	sp P63261 ACTG_HUMAN	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1 HUMAN	3			
27	0	4,35	22,9300007	17,0699999	sp P63260 ACTG_MOUSE	Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1 MOUSE	3			
27	0	4,35	22,9300007	17,0699999	sp P63259 ACTG_RAT	Actin, cytoplasmic 2 OS=Rattus norvegicus GN=Actg1 PE=1 SV RAT	3			
27	0	4,35	22,9300007	17,0699999	sp P63258 ACTG_BOVIN	Actin, cytoplasmic 2 OS=Bos taurus GN=ACTG1 PE=1 SV=1 BOVIN	3			
27	0	4,35	22,9300007	17,0699999	sp P63257 ACTG_TRIVU	Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE= TRIVU	3			
27	0	4,35	22,9300007	17,0699999	sp P63256 ACTG_ANSAN	Actin, cytoplasmic 2 OS=Anser anser anser GN=ACTG1 PE=2 SV- ANSAN	3			
27	0	4,35	22,9300007	17,0699999	sp P60713 ACTB_SHEEP	Actin, cytoplasmic 1 OS=Ovis aries GN=ACTB PE=2 SV=1 SHEEP	3			
27	0	4,35	22,9300007	17,0699999	sp P60712 ACTB_BOVIN	Actin, cytoplasmic 1 OS=Bos taurus GN=ACTB PE=1 SV=1 BOVIN	3			
27	0	4,35	22,9300007	17,0699999	sp P60711 ACTB_RAT	Actin, cytoplasmic 1 OS=Rattus norvegicus GN=Actb PE=1 SV= RAT	3			
27	0	4,35	22,9300007	17,0699999	sp P60710 ACTB_MOUSE	Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1 MOUSE	3			
27	0	4,35	22,9300007	17,0699999	sp P60709 ACTB_HUMAN	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1 HUMAN	3			
27	0	4,35	22,9300007	17,0699999	sp P60708 ACTB_HORSE	Actin, cytoplasmic 1 OS=Equus caballus GN=ACTB PE=2 SV=1 HORSE	3			
27	0	4,35	22,9300007	17,0699999	sp P60707 ACTB_TRIVU	Actin, cytoplasmic 1 OS=Trichosurus vulpecula GN=ACTB PE=2 TRIVU	3			
27	0	4,35	22,9300007	17,0699999	sp P60706 ACTB_CHICK	Actin, cytoplasmic 1 OS=Gallus gallus GN=ACTB PE=1 SV=1 CHICK	3			
27	0	4,35	22,8699997	17,0200005	sp P53506 ACT8_XENLA	Actin, cytoplasmic type 8 OS=Xenopus laevis PE=3 SV=1 XENLA	3			
27	0	4,35	22,8699997	17,0200005	sp P53505 ACT5_XENLA	Actin, cytoplasmic type 5 OS=Xenopus laevis PE=3 SV=1 XENLA	3			
27	0	4,35	22,9300007	17,0699999	sp P53486 ACTB3_TAKRU	Actin, cytoplasmic 3 OS=Takifugu rubripes GN=actbc PE=2 SV- TAKRU	3			
27	0	4,35	22,9300007	17,0699999	sp P53485 ACTB2_TAKRU	Actin, cytoplasmic 2 OS=Takifugu rubripes GN=actbb PE=3 SV- TAKRU	3			
27	0	4,35	22,8699997	17,0200005	sp P53478 ACT5_CHICK	Actin, cytoplasmic type 5 OS=Gallus gallus PE=3 SV=1 CHICK	3			
27	0	4,35	22,9300007	17,0699999	sp P48975 ACTB_CRIGR	Actin, cytoplasmic 1 OS=Cricetulus griseus GN=ACTB PE=3 SV= CRIGR	3			
27	0	4,35	22,8699997	17,0200005	sp P15475 ACTB_XENBO	Actin, cytoplasmic 1 OS=Xenopus borealis GN=actb PE=3 SV=1 XENBO	3			
27	0	4,35	22,9300007	17,0699999	sp Q93400 ACTB_XENLA	Actin, cytoplasmic 1 OS=Xenopus laevis GN=actb PE=2 SV=1 XENLA	3			
27	0	4,35	22,9300007	17,0699999	sp Q42161 ACTB_SALSA	Actin, cytoplasmic 1 OS=Salmo salar GN=actb PE=2 SV=1 SALSA	3			
27	0	4,35	22,9300007	17,0699999	sp Q18840 ACTB_CANLF	Actin, cytoplasmic 1 OS=Canis lupus familiaris GN=ACTB PE=2 CANLF	3			

27	0	4,45	22,9300007	17,0699999	9,0669997	sp P02578 ACT1_ACACA	Actin-1 OS=Acanthamoeba castellanii PE=1 SV=1	ACACA	2
27	0	4,45	22,8100002	16,9799998	9,01900008	sp O65316 ACT_MESV1	Actin OS=Mesostigma viride PE=3 SV=1	MESV1	2
27	0	4,45	22,8699997	17,0200005	9,04299989	sp O16808 ACT_MAYDE	Actin OS=Mayetiola destructor PE=2 SV=1	MAYDE	2
27	0	4,45	24,2699996	20,7100004	10,9999999	sp Q03342 ACT3_ECHGR	Actin-3 (Fragment) OS=Echinococcus granulosus GN=ACTIII PE ECHGR		2
27	0	4,45	20,0000003	17,0699999	9,0669997	sp P50138 ACT_PUCGR	Actin OS=Puccinia graminis PE=3 SV=1	PUCGR	2
27	0	4,01	22,9300007	9,0669997	9,0669997	sp P48465 ACT_CRYNH	Actin OS=Cryptococcus neoformans var. grubii serotype A (str CRYNH		2
27	0	4	14,9299994	9,0669997	9,0669997	sp Q9Y707 ACT2_SUIBO	Actin-2 OS=Suillus bovinus GN=ACT2 PE=2 SV=1	SUIBO	2
27	0	4	14,9299994	9,0669997	9,0669997	sp Q9Y702 ACT1_SCHCO	Actin-1 OS=Schizophyllum commune GN=ACT1 PE=2 SV=1	SCHCO	2
27	0	4	14,9299994	9,0669997	9,0669997	sp Q9UVX4 ACT_COPC7	Actin OS=Coprinopsis cinerea (strain Okayama-7 / 130 / ATCC COPC7		2
27	0	4	14,9299994	9,0669997	9,0669997	sp Q9UVV9 ACTG_ACRCH	Actin, gamma OS=Acremonium chrysogenum GN=ACT PE=3 SV=1	ACRCH	2
27	0	4	14,8900002	9,04299989	9,04299989	sp Q964E3 ACTC_BIOAL	Actin, cytoplasmic OS=Biomphalaria alexandrina PE=3 SV=1	BIOAL	2
27	0	4	14,8900002	9,04299989	9,04299989	sp Q964E2 ACTC_BIOPF	Actin, cytoplasmic OS=Biomphalaria pfeifferi PE=3 SV=1	BIOPF	2
27	0	4	14,8900002	9,04299989	9,04299989	sp Q964E1 ACTC_BIOOB	Actin, cytoplasmic OS=Biomphalaria obstructa PE=3 SV=1	BIOOB	2
27	0	4	14,8900002	9,04299989	9,04299989	sp Q964E0 ACTC_BIOTE	Actin, cytoplasmic OS=Biomphalaria tenagophila PE=3 SV=1	BIOTE	2
27	0	4	14,8900002	9,04299989	9,04299989	sp Q964D9 ACTC_PLATR	Actin, cytoplasmic OS=Planorbella trivolvis PE=3 SV=1	PLATR	2
27	0	4	14,9299994	9,0669997	9,0669997	sp Q93131 ACTC_BRAFL	Actin, cytoplasmic OS=Branchiostoma floridae PE=2 SV=1	BRAFL	2
27	0	4	14,9299994	9,0669997	9,0669997	sp Q93129 ACTC_BRABE	Actin, cytoplasmic OS=Branchiostoma belcheri PE=2 SV=1	BRABE	2
27	0	4	14,9299994	9,0669997	9,0669997	sp Q8X119 ACT_EXODE	Actin OS=Exophiala dermatitidis PE=3 SV=1	EXODE	2
27	0	4	14,9299994	9,0669997	9,0669997	sp Q6TFC2 ACT_GAEGA	Actin OS=Gaeumannomyces graminis var. avenae GN=ACT PE= GAEGA		2
27	0	4	14,8900002	9,04299989	9,04299989	sp Q553U6 ACT22_DICDI	Putative actin-22 OS=Dictyostelium discoideum GN=act22 PE= DICDI		2
27	0	4	14,8900002	9,04299989	9,04299989	sp Q54GX7 ACT10_DICDI	Actin-10 OS=Dictyostelium discoideum GN=act10 PE=1 SV=1	DICDI	2
27	0	4	14,8100004	8,99500027	8,99500027	sp Q25472 ACT2_MOLOC	Actin, muscle-type OS=Molgula oculata PE=3 SV=1	MOLOC	2
27	0	4	14,8900002	9,04299989	9,04299989	sp Q25010 ACT3A_HELAM	Actin, cytoplasmic A3a OS=Helicoverpa armigera GN=actA3a F HELAM		2
27	0	4	14,8900002	9,04299989	9,04299989	sp Q07903 ACTC_STRPU	Actin, cytoskeletal 2A OS=Strongylocentrotus purpuratus GN= STRPU		2
27	0	4	14,9299994	9,0669997	9,0669997	sp Q00215 ACTC_STYPL	Actin, cytoplasmic OS=Styela plicata PE=3 SV=1	STYPL	2
27	0	4	14,8900002	9,04299989	9,04299989	sp P92179 ACTC_BIOGL	Actin, cytoplasmic OS=Biomphalaria glabrata PE=2 SV=2	BIOGL	2
27	0	4	14,8900002	9,04299989	9,04299989	sp P84185 ACT5C_ANOGA	Actin-5C OS=Anopheles gambiae GN=Act5C PE=2 SV=1	ANOGA	2
27	0	4	14,8900002	9,04299989	9,04299989	sp P84184 ACT3B_HELAM	Actin-A3b, cytoplasmic OS=Helicoverpa armigera GN=actA3b I HELAM		2
27	0	4	14,8900002	9,04299989	9,04299989	sp P84183 ACT4_BOMMO	Actin, cytoplasmic A4 OS=Bombyx mori GN=A4 PE=2 SV=1	BOMMO	2
27	0	4	14,8900002	9,04299989	9,04299989	sp P83969 ACT1_BACDO	Actin, indirect flight muscle OS=Bactrocera dorsalis PE=3 SV=1 BACDO		2
27	0	4	14,8900002	9,04299989	9,04299989	sp P83968 ACT6_DROSI	Actin, indirect flight muscle OS=Drosophila simulans GN=Act6 DROSI		2
27	0	4	14,8900002	9,04299989	9,04299989	sp P83967 ACT6_DROME	Actin, indirect flight muscle OS=Drosophila melanogaster GN= DROME		2
27	0	4	14,9299994	9,0669997	9,0669997	sp P78711 ACT_NEUCR	Actin OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1 ^a NEUCR		2
27	0	4	14,8900002	9,04299989	9,04299989	sp P69005 ACTD_STRPU	Actin, cytoskeletal 2B OS=Strongylocentrotus purpuratus GN= STRPU		2
27	0	4	14,8900002	9,04299989	9,04299989	sp P69004 ACT2_STRFN	Actin-15B OS=Strongylocentrotus franciscanus PE=2 SV=1	STRFN	2
27	0	4	14,8900002	9,04299989	9,04299989	sp P69003 ACT1_HELTB	Actin Cyl, cytoplasmic OS=Heliocidaris tuberculata PE=3 SV=1	HELTB	2
27	0	4	14,8900002	9,04299989	9,04299989	sp P69002 ACT1_HELER	Actin Cyl, cytoplasmic OS=Heliocidaris erythrogramma PE=3 S' HELER		2
27	0	4	14,8900002	9,04299989	9,04299989	sp P68556 ACT1_DIPDE	Actin-1/4 OS=Diphyllobothrium dendriticum GN=ACT1 PE=2 S DIPDE		2
27	0	4	14,8900002	9,04299989	9,04299989	sp P68555 ACT_TAESO	Actin OS=Taenia solium GN=ACT1 PE=3 SV=1	TAESO	2
27	0	4	14,9299994	9,0669997	9,0669997	sp P53689 ACT_PHARH	Actin OS=Phaffia rhodozyma PE=3 SV=1	PHARH	2
27	0	4	14,8900002	9,04299989	9,04299989	sp P53501 ACT3_DROME	Actin-57B OS=Drosophila melanogaster GN=Act57B PE=1 SV= DROME		2
27	0	4	14,8900002	9,04299989	9,04299989	sp P53474 ACTE_STRPU	Actin, cytoskeletal 3A OS=Strongylocentrotus purpuratus GN= STRPU		2
27	0	4	14,8900002	9,04299989	9,04299989	sp P53473 ACTB_STRPU	Actin, cytoskeletal 1B OS=Strongylocentrotus purpuratus GN= STRPU		2
27	0	4	14,8900002	9,04299989	9,04299989	sp P53472 ACTA_STRPU	Actin, cytoskeletal 1A OS=Strongylocentrotus purpuratus GN= STRPU		2
27	0	4	14,8900002	9,04299989	9,04299989	sp P53466 ACT2_LYTPI	Actin, cytoskeletal 2 OS=Lytechinus pictus PE=2 SV=1	LYTPI	2
27	0	4	14,8900002	9,04299989	9,04299989	sp P53465 ACT1_LYTPI	Actin, cytoskeletal 1 OS=Lytechinus pictus PE=2 SV=1	LYTPI	2
27	0	4	14,8900002	9,04299989	9,04299989	sp P53456 ACT2_DIPDE	Actin-2 OS=Diphyllobothrium dendriticum GN=ACT2 PE=2 SV= DIPDE		2
27	0	4	14,9299994	9,0669997	9,0669997	sp P53455 ACT_AJECG	Actin OS=Ajellomyces capsulatus (strain I6186AR / H82 / ATCC AJECG		2
27	0	4	14,8900002	9,04299989	9,04299989	sp P49871 ACT_MANSE	Actin, muscle OS=Manduca sexta PE=2 SV=1	MANSE	2
27	0	4	14,8900002	9,04299989	9,04299989	sp P49128 ACT1_AEDAE	Actin-1 OS=Aedes aegypti GN=ACT-1 PE=2 SV=2	AEDAE	2
27	0	4	14,8900002	9,04299989	9,04299989	sp P45886 ACT3_BACDO	Actin-3, muscle-specific OS=Bactrocera dorsalis PE=2 SV=1	BACDO	2
27	0	4	14,8900002	9,04299989	9,04299989	sp P45885 ACT2_BACDO	Actin-2, muscle-specific OS=Bactrocera dorsalis PE=2 SV=1	BACDO	2
27	0	4	14,8900002	9,04299989	9,04299989	sp P41341 ACTY_LIMPO	Actin-11 OS=Limulus polyphemus PE=2 SV=1	LIMPO	2
27	0	4	14,8900002	9,04299989	9,04299989	sp P41340 ACT3_LIMPO	Actin-3 OS=Limulus polyphemus PE=1 SV=1	LIMPO	2
27	0	4	14,8900002	9,04299989	9,04299989	sp P41339 ACTA_LIMPO	Actin, acrosomal process isoform OS=Limulus polyphemus PE= LIMPO		2
27	0	4	14,8900002	9,04299989	9,04299989	sp P41113 ACT3_PODCA	Actin-3 OS=Podocoryna carnea GN=ACT3 PE=3 SV=1	PODCA	2
27	0	4	14,8900002	9,04299989	9,04299989	sp P41112 ACT1_PODCA	Actin-1/2 OS=Podocoryna carnea GN=ACTIA PE=2 SV=1	PODCA	2
27	0	4	14,9299994	9,0669997	9,0669997	sp P20359 ACTG_EMENI	Actin, gamma OS=Emericella nidulans (strain FGSC A4 / ATCC EMENI		2
27	0	4	14,8900002	9,04299989	9,04299989	sp P18603 ACT4_ARTSX	Actin, clone 403 OS=Artemia sp. PE=2 SV=1	ARTSX	2
27	0	4	14,8900002	9,04299989	9,04299989	sp P18499 ACTF_STRPU	Actin, cytoskeletal 3B OS=Strongylocentrotus purpuratus GN= STRPU		2
27	0	4	14,8900002	9,04299989	9,04299989	sp P17126 ACT_HYDVU	Actin, non-muscle 6.2 OS=Hydra vulgaris PE=3 SV=1	HYDVU	2
27	0	4	14,8900002	9,04299989	9,04299989	sp P12717 ACTM_PISOC	Actin, muscle OS=Pisaster ochraceus PE=3 SV=1	PISOC	2
27	0	4	14,8900002	9,04299989	9,04299989	sp P12716 ACTC_PISOC	Actin, cytoplasmic OS=Pisaster ochraceus PE=3 SV=1	PISOC	2
27	0	4	14,9700001	9,09100026	9,09100026	sp P12431 ACTM_STRPU	Actin, muscle OS=Strongylocentrotus purpuratus PE=3 SV=1	STRPU	2
27	0	4	14,8900002	9,04299989	9,04299989	sp P10990 ACT1_STRFN	Actin-15A OS=Strongylocentrotus franciscanus PE=3 SV=1	STRFN	2
27	0	4	14,8900002	9,04299989	9,04299989	sp P10987 ACT1_DROME	Actin-5C OS=Drosophila melanogaster GN=Act5C PE=1 SV=4	DROME	2
27	0	4	14,8900002	9,04299989	9,04299989	sp P10981 ACT5_DROME	Actin-87E OS=Drosophila melanogaster GN=Act87E PE=1 SV= DROME		2
27	0	4	14,9299994	9,0669997	9,0669997	sp P10365 ACT_THELA	Actin OS=Thermomyces lanuginosus PE=3 SV=1	THELA	2
27	0	4	14,8900002	9,04299989	9,04299989	sp P07836 ACT1_BOMMO	Actin, muscle-type A1 OS=Bombyx mori PE=3 SV=1	BOMMO	2
27	0	4	14,8900002	9,04299989	9,04299989	sp P07830 ACT1_DICDI	Major actin OS=Dictyostelium discoideum GN=act1 PE=1 SV=2 DICDI		2
27	0	4	14,8900002	9,04299989	9,04299989	sp P07829 ACT3_DICDI	Actin-3 OS=Dictyostelium discoideum GN=act3 PE=3 SV=3	DICDI	2
27	0	4	14,8900002	9,04299989	9,04299989	sp P04829 ACT3_BOMMO	Actin, cytoplasmic A3 OS=Bombyx mori PE=3 SV=3	BOMMO	2
27	0	4	14,8900002	9,04299989	9,04299989	sp P02576 ACTA_PHYPO	Actin, plasmoidal isoform OS=Physarum polycephalum GN=AF PHYPO		2
27	0	4	14,8900002	9,04299989	9,04299989	sp P02572 ACT2_DROME	Actin-42A OS=Drosophila melanogaster GN=Act42A PE=1 SV= DROME		2
27	0	4	14,8900002	9,04299989	9,04299989	sp O18500 ACT2_SACKO	Actin-2 OS=Saccoglossus kowalevskii PE=2 SV=1	SACKO	2
27	0	4	14,8900002	9,04299989	9,04299989	sp O17320 ACT_CRAGI	Actin OS=Crassostrea gigas PE=2 SV=1	CRAGI	2
27	0	4	14,9299994	9,0669997	9,0669997	sp O13419 ACT_BOTFU	Actin OS=Botryotinia fuckeliana GN=actA PE=3 SV=1	BOTFU	2
27	0	4	16,9200003	12,7800003	12,7800003	sp Q92193 ACT_CRAVI	Actin (Fragment) OS=Crassostrea virginica PE=2 SV=1	CRAVI	2
27	0	4	12,5699997	9,49700028	9,49700028	sp Q55E06 ACT23_DICDI	Putative actin-23 OS=Dictyostelium discoideum GN=act23 PE= DICDI		2
27	0	4	11,8699998	8,97099972	8,97099972	sp Q00214 ACTM_STYPL	Actin, muscle OS=Styela plicata PE=3 SV=1	STYPL	2
27	0	4	11,97	9,04299989	9,04299989	sp P45887 ACT5_BACDO	Actin-5, muscle-specific OS=Bactrocera dorsalis PE=2 SV=1	BACDO	2
27	0	4	11,97	9,04299989	9,04299989	sp P02574 ACT4_DROME	Actin, larval muscle OS=Drosophila melanogaster GN=Act79B DROME		2
27	0	4	11,97	9,04299989	9,04299989	sp O18499 ACT1_SACKO	Actin-1 OS=Saccoglossus kowalevskii PE=2 SV=1	SACKO	2
28	4,32	4,32	32,2299987	20,2500001	14,8800001	sp P31944 CASPE_HUMAN	Caspase-14 OS=Homo sapiens GN=CASP14 PE=1 SV=2	HUMAN	2
29	4,18	4,18	30,250001	25,9299994	19,1400006	sp Q5VSP4 LC1L1_HUMAN	Putative lipocalin 1-like protein 1 OS=Homo sapiens GN=LCN1 HUMAN		2
29	0	4,18	27,8400004	23,8600001	17,6100001	sp P31025 LCN1_HUMAN	Lipocalin-1 OS=Homo sapiens GN=LCN1 PE=1 SV=1	HUMAN	2
30	4	4	14,4899994	14,4899994	14,4899994	sp Q9GZZ8 LACRT_HUMAN	Extracellular glycoprotein lacritin OS=Homo sapiens GN=LACR HUMAN		2
31	3,83	3,83	6,42699972	4,34800014	4,34800014	sp Q7YR44 CDSN_PANTR	Corneodesmosin OS=Pan troglodytes GN=CDSN PE=2 SV=1	PANTR	2
31	0	3,83	6,42699972	4,34800014	4,34800014	sp Q15517 CDSN_HUMAN	Corneodesmosin OS=Homo sapiens GN=CDSN PE=1 SV=3	HUMAN	2
32	3,82	4,2	9,22600031	8,072	5,60100004	sp P02769 ALBU_BOVIN	Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	BOVIN	2
33	3,18	3,18	23,2700005	16,9799998	16,9799998	sp P01591 IGJ_HUMAN	Immunoglobulin J chain OS=Homo sapiens GN=JCHAIN PE=1 S HUMAN		2
34	2,67	2,67	44,5499986	32,6700002	32,6700002	sp P31151 S10A7_HUMAN	Protein S100-A7 OS=Homo sapiens GN=S100A7 PE=1 SV=4	HUMAN	2
36	2,5	2,5	50,940001	33,0199987	33,0199987	sp P0CG06 LAC3_HUMAN	Ig lambda-3 chain C regions OS=Homo sapiens GN=IGLC3 PE=1 HUMAN		2
36	0	2,5	50,940001	33,0199987	33,0199987	sp P0CG05 LAC2_HUMAN	Ig lambda-2 chain C regions OS=Homo sapiens GN=IGLC2 PE=1 HUMAN		2
36	0	2,48	20,0900003	16,3599998	16,3599998	sp B9A064 IGLL5_HUMAN	Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens HUMAN		2
36	0	2,48	33,0199987	33,0199987	33,0199987	sp P0CG04 LAC1_HUMAN	Ig lambda-1 chain C regions OS=Homo sapiens GN=IGLC1 PE=1 HUMAN		2
48	1,84	1,84	6,02600016	1,84599999	1,08000003	sp P15924 DESP_HUMAN	Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	HUMAN	2

48	0	1,84	5,93100004	1,83799993	1,07500004	sp E9Q557 DESP_MOUSE	Desmoplakin OS=Mus musculus GN=Dsp PE=1 SV=1	MOUSE	2
27	0	2,41	18,5699999	12,7299994	4,77499999	sp P53457 ACT3_DIPDE	Actin-3 OS=Diphyllobothrium dendriticum GN=ACT3 PE=2 SV=	DIPDE	1
27	0	2,41	18,1299999	12,2699998	4,26700003	sp P43239 ACT1_PNECA	Actin-1 OS=Pneumocystis carinii PE=2 SV=1	PNECA	1
27	0	2,41	18,6199993	12,7700001	4,7869999	sp P30163 ACT2_ONCVO	Actin-2 OS=Onchocerca volvulus GN=act-2b PE=3 SV=1	ONCVO	1
27	0	2,41	18,6199993	12,7700001	4,7869999	sp P30162 ACT1_ONCVO	Actin-1 OS=Onchocerca volvulus GN=act-1a PE=3 SV=1	ONCVO	1
27	0	2,41	18,0899993	12,2299999	4,25500013	sp P17304 ACTM_APLCA	Actin, muscle OS=Aplysia californica PE=2 SV=1	APLCA	1
27	0	2,41	18,6199993	12,7700001	4,7869999	sp P10984 ACT2_CAEEL	Actin-2 OS=Caenorhabditis elegans GN=act-2 PE=3 SV=3	CAEEL	1
27	0	2,41	18,5699999	12,7299994	4,77499999	sp O65315 ACT_COLSC	Actin OS=Coleochaete scutata PE=2 SV=1	COLSC	1
27	0	2,41	15,6499997	12,7299994	4,77499999	sp P53498 ACT_CHLRE	Actin OS=Chlamydomonas reinhardtii PE=2 SV=1	CHLRE	1
27	0	2,41	15,6499997	12,7299994	4,77499999	sp P20904 ACT_VOLCA	Actin OS=Volvox carteri PE=3 SV=1	VOLCA	1
31	0	2,01	5,43100014	3,37099992	3,37099992	sp Q5TM45 CDSN_MACMU	Corneodesmosin OS=Macaca mulatta GN=CDSN PE=3 SV=1	MACMU	1
32	0	1,7	3,46000008	3,46000008	3,46000008	sp P14639 ALBU_SHEEP	Serum albumin OS=Ovis aries GN=ALB PE=1 SV=1	SHEEP	1
34	0	1,54	12,8700003	12,8700003	12,8700003	sp Q865G5 S1A7A_HUMAN	Protein S100-A7A OS=Homo sapiens GN=S100A7A PE=1 SV=3	HUMAN	1
35	2,58	2,58	30,6100011	30,6100011	18,3699995	sp P01040 CYTA_HUMAN	Cystatin-A OS=Homo sapiens GN=CSTA PE=1 SV=1	HUMAN	1
36	0	1,75	32,0800006	14,1499996	14,1499996	sp P0CF74 LAC6_HUMAN	Ig lambda-6 chain C region OS=Homo sapiens GN=IGLC6 PE=4	HUMAN	1
36	0	1,75	32,0800006	14,1499996	14,1499996	sp A0M8Q6 LAC7_HUMAN	Ig lambda-7 chain C region OS=Homo sapiens GN=IGLC7 PE=4	HUMAN	1
38	2,04	2,04	12,0499998	12,0499998	2,56399997	sp P29508 SPB3_HUMAN	Serpin B3 OS=Homo sapiens GN=SERPINB3 PE=1 SV=2	HUMAN	1
41	2,01	2,01	8,14799964	3,45700011	3,45700011	sp Q96P63 SPB12_HUMAN	Serpin B12 OS=Homo sapiens GN=SERPINB12 PE=1 SV=1	HUMAN	1
42	2	2,47	6,51699975	4,68400009	3,25900018	sp Q6IFX1 K1C24_RAT	Keratin, type I cytoskeletal 24 OS=Rattus norvegicus GN=Krt24	RAT	1
42	0	2,47	6,25	4,49200012	3,125	sp A11317 K1C24_MOUSE	Keratin, type I cytoskeletal 24 OS=Mus musculus GN=Krt24 PE	MOUSE	1
43	2	2	37,2799993	19,7500005	19,7500005	sp Q63429 UBC_RAT	Polyubiquitin-C OS=Rattus norvegicus GN=Ubc PE=1 SV=1	RAT	1
43	0	2	32,7899992	20,9800005	20,9800005	sp Q8MKD1 UBB_HORSE	Polyubiquitin-B OS=Equus caballus GN=UBB PE=2 SV=3	HORSE	1
43	0	2	32,8900009	21,0500002	21,0500002	sp Q865C5 UBIQ_CAMDR	Ubiquitin OS=Camelus dromedarius PE=3 SV=2	CAMDR	1
43	0	2	39,6800011	25,4000008	25,4000008	sp P84589 UBIQ_LUMTE	Ubiquitin (Fragment) OS=Lumbricus terrestris PE=1 SV=2	LUMTE	1
43	0	2	16,0300002	10,2600001	10,2600001	sp P79781 RS27A_CHICK	Ubiquitin-40S ribosomal protein S27a OS=Gallus gallus GN=RP	CHICK	1
43	0	2	19,5299998	12,5	12,5	sp P68205 RL40_OPHHA	Ubiquitin-60S ribosomal protein L40 OS=Ophiophagus hannah	OPHHA	1
43	0	2	16,0300002	10,2600001	10,2600001	sp P68203 RS27A_SPOFR	Ubiquitin-40S ribosomal protein S27a OS=Spodoptera frugiper	SPOFR	1
43	0	2	16,1300004	10,3200004	10,3200004	sp P68202 RS27A_PLUXY	Ubiquitin-40S ribosomal protein S27a OS=Plutella xylostella P	PLUXY	1
43	0	2	16,0300002	10,2600001	10,2600001	sp P68200 RS27A_ICTPU	Ubiquitin-40S ribosomal protein S27a OS=Ictalurus punctatus	ICTPU	1
43	0	2	32,8900009	21,0500002	21,0500002	sp P68197 UBIQ_CERCA	Ubiquitin OS=Ceratitidis capitata PE=1 SV=1	CERCA	1
43	0	2	19,5299998	12,5	12,5	sp P63053 RL40_PIG	Ubiquitin-60S ribosomal protein L40 OS=Sus scrofa GN=UBA5	PIG	1
43	0	2	19,5299998	12,5	12,5	sp P63052 RL40_FELCA	Ubiquitin-60S ribosomal protein L40 OS=Felis catus GN=UBA5	FELCA	1
43	0	2	19,5299998	12,5	12,5	sp P63050 RL40_CANLF	Ubiquitin-60S ribosomal protein L40 OS=Canis lupus familiaris	CANLF	1
43	0	2	19,5299998	12,5	12,5	sp P63048 RL40_BOVIN	Ubiquitin-60S ribosomal protein L40 OS=Bos taurus GN=UBA5	BOVIN	1
43	0	2	16,0300002	10,2600001	10,2600001	sp P62992 RS27A_BOVIN	Ubiquitin-40S ribosomal protein S27a OS=Bos taurus GN=RP	BOVIN	1
43	0	2	19,5299998	12,5	12,5	sp P62987 RL40_HUMAN	Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=U	HUMAN	1
43	0	2	19,5299998	12,5	12,5	sp P62986 RL40_RAT	Ubiquitin-60S ribosomal protein L40 OS=Rattus norvegicus GN	RAT	1
43	0	2	19,5299998	12,5	12,5	sp P62984 RL40_MOUSE	Ubiquitin-60S ribosomal protein L40 OS=Mus musculus GN=U	MOUSE	1
43	0	2	16,0300002	10,2600001	10,2600001	sp P62983 RS27A_MOUSE	Ubiquitin-40S ribosomal protein S27a OS=Mus musculus GN=I	MOUSE	1
43	0	2	16,0300002	10,2600001	10,2600001	sp P62982 RS27A_RAT	Ubiquitin-40S ribosomal protein S27a OS=Rattus norvegicus G	RAT	1
43	0	2	16,0300002	10,2600001	10,2600001	sp P62979 RS27A_HUMAN	Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=f	HUMAN	1
43	0	2	16,0300002	10,2600001	10,2600001	sp P62978 RS27A_CAVPO	Ubiquitin-40S ribosomal protein S27a OS=Cavia porcellus GN=	CAVPO	1
43	0	2	30,3999999	19,4499999	19,4499999	sp P62976 UBIQP_CRIGR	Polyubiquitin OS=Cricetulus griseus PE=2 SV=2	CRIGR	1
43	0	2	32,8900009	21,0500002	21,0500002	sp P62975 UBIQ_RABIT	Ubiquitin OS=Oryctolagus cuniculus PE=1 SV=1	RABIT	1
43	0	2	35,3300005	19,1599995	19,1599995	sp P62972 UBIQP_XENLA	Polyubiquitin (Fragment) OS=Xenopus laevis PE=1 SV=2	XENLA	1
43	0	2	16,1300004	10,3200004	10,3200004	sp P29504 RS27A_MANSE	Ubiquitin-40S ribosomal protein S27a OS=Manduca sexta PE=	MANSE	1
43	0	2	19,5299998	12,5	12,5	sp P18101 RL40_DROME	Ubiquitin-60S ribosomal protein L40 OS=Drosophila melanog	DROME	1
43	0	2	16,0300002	10,2600001	10,2600001	sp P15357 RS27A_DROME	Ubiquitin-40S ribosomal protein S27a OS=Drosophila melan	DROME	1
43	0	2	32,6099992	20,8700001	20,8700001	sp P0CH28 UBC_BOVIN	Polyubiquitin-C OS=Bos taurus GN=UBC PE=1 SV=1	BOVIN	1
43	0	2	32,7699989	20,9700003	20,9700003	sp P0CG69 UBIQP_DROME	Polyubiquitin OS=Drosophila melanogaster GN=Ubi-p63E PE=	DROME	1
43	0	2	32,8299999	21,0099995	21,0099995	sp P0CG68 UBC_PIG	Polyubiquitin-C OS=Sus scrofa GN=UBC PE=2 SV=1	PIG	1
43	0	2	32,7499986	20,9600002	20,9600002	sp P0CG67 UBB_GORGO	Polyubiquitin-B OS=Gorilla gorilla gorilla GN=UBB PE=3 SV=	GORGO	1
43	0	2	32,8399986	21,0199997	21,0199997	sp P0CG66 UBC_GORGO	Polyubiquitin-C OS=Gorilla gorilla gorilla GN=UBC PE=3 SV=	GORGO	1
43	0	2	32,7499986	20,9600002	20,9600002	sp P0CG65 UBB_PANTR	Polyubiquitin-B OS=Pan troglodytes GN=UBB PE=3 SV=1	PANTR	1
43	0	2	32,8500003	21,0199997	21,0199997	sp P0CG64 UBC_PANTR	Polyubiquitin-C OS=Pan troglodytes GN=UBC PE=3 SV=1	PANTR	1
43	0	2	32,7899992	20,9800005	20,9800005	sp P0CG62 UBB_CHICK	Polyubiquitin-B OS=Gallus gallus GN=UBB PE=2 SV=1	CHICK	1
43	0	2	32,8500003	21,0199997	21,0199997	sp P0CG61 UBC_PONPY	Polyubiquitin-C OS=Pongo pygmaeus GN=UBC PE=3 SV=1	PONPY	1
43	0	2	32,7499986	20,9600002	20,9600002	sp P0CG60 UBB_PONPY	Polyubiquitin-B OS=Pongo pygmaeus GN=UBB PE=3 SV=1	PONPY	1
43	0	2	32,7899992	20,9800005	20,9800005	sp P0CG55 UBB_SHEEP	Polyubiquitin-B OS=Ovis aries GN=UBB PE=2 SV=1	SHEEP	1
43	0	2	32,1500003	20,5799997	20,5799997	sp P0CG54 UBB_CAVPO	Polyubiquitin-B OS=Cavia porcellus GN=UBB PE=2 SV=1	CAVPO	1
43	0	2	32,7899992	20,9800005	20,9800005	sp P0CG53 UBB_BOVIN	Polyubiquitin-B OS=Bos taurus GN=UBB PE=1 SV=1	BOVIN	1
43	0	2	32,7899992	20,9800005	20,9800005	sp P0CG51 UBB_RAT	Polyubiquitin-B OS=Rattus norvegicus GN=Ubb PE=1 SV=1	RAT	1
43	0	2	30,6499988	19,6199998	19,6199998	sp P0CG50 UBC_MOUSE	Polyubiquitin-C OS=Mus musculus GN=Ubc PE=1 SV=2	MOUSE	1
43	0	2	32,7899992	20,9800005	20,9800005	sp P0CG49 UBB_MOUSE	Polyubiquitin-B OS=Mus musculus GN=Ubb PE=2 SV=1	MOUSE	1
43	0	2	32,8500003	21,0199997	21,0199997	sp P0CG48 UBC_HUMAN	Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=3	HUMAN	1
43	0	2	32,7499986	20,9600002	20,9600002	sp P0CG47 UBB_HUMAN	Polyubiquitin-B OS=Homo sapiens GN=UBB PE=1 SV=1	HUMAN	1
43	0	2	19,5299998	12,5	12,5	sp P0C276 RL40_SHEEP	Ubiquitin-60S ribosomal protein L40 OS=Ovis aries GN=UBA5	SHEEP	1
43	0	2	19,5299998	12,5	12,5	sp P0C275 RL40_PONPY	Ubiquitin-60S ribosomal protein L40 OS=Pongo pygmaeus GN	PONPY	1
43	0	2	19,5299998	12,5	12,5	sp P0C273 RL40_MACFA	Ubiquitin-60S ribosomal protein L40 OS=Macaca fascicularis	MACFA	1
44	2	2	1,798	0,46009999	0,46009999	sp Q5D862 FILA2_HUMAN	Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	HUMAN	1
45	2	2	6,20499998	2,59700008	2,59700008	sp Q08188 TGM3_HUMAN	Protein-glutamine gamma-glutamyltransferase E OS=Homo sa	HUMAN	1
46	2	2	15,9700006	15,9700006	15,9700006	sp P01777 HV316_HUMAN	Ig heavy chain V-III region TEI OS=Homo sapiens PE=1 SV=1	HUMAN	1
46	0	2	15,8299997	15,8299997	15,8299997	sp P01766 HV305_HUMAN	Ig heavy chain V-III region BRO OS=Homo sapiens PE=1 SV=1	HUMAN	1
46	0	2	16,2400007	16,2400007	16,2400007	sp P01764 HV303_HUMAN	Ig heavy chain V-III region 23 OS=Homo sapiens GN=IGHV3-23	HUMAN	1
47	2	2	7,80100003	7,80100003	7,80100003	sp P01037 CYTN_HUMAN	Cystatin-SN OS=Homo sapiens GN=CST1 PE=1 SV=3	HUMAN	1
47	0	2	7,80100003	7,80100003	7,80100003	sp P01036 CYTS_HUMAN	Cystatin-S OS=Homo sapiens GN=CST4 PE=1 SV=3	HUMAN	1
49	1,65	1,65	11,3600001	3,78599986	3,78599986	sp P10909 CLUS_HUMAN	Clusterin OS=Homo sapiens GN=CLU PE=1 SV=1	HUMAN	1
50	1,51	1,51	31,7499995	12,7000004	6,87799975	sp P05090 APOD_HUMAN	Apolipoprotein D OS=Homo sapiens GN=APOD PE=1 SV=1	HUMAN	1
51	1,42	1,42	4,36200015	1,67800002	1,67800002	sp Q08554 DSC1_HUMAN	Desmocollin-1 OS=Homo sapiens GN=DSC1 PE=1 SV=2	HUMAN	1
52	1,26	1,26	4,29500006	1,47700002	1,47700002	sp Q8WNNW3 PLAK_PIG	Junction plakoglobin OS=Sus scrofa GN=Jup PE=2 SV=1	PIG	1
52	0	1,26	4,29500006	1,47700002	1,47700002	sp Q8SPJ1 PLAK_BOVIN	Junction plakoglobin OS=Bos taurus GN=JUP PE=2 SV=1	BOVIN	1
52	0	1,26	4,29500006	1,47700002	1,47700002	sp Q6P0K8 PLAK_RAT	Junction plakoglobin OS=Rattus norvegicus GN=Jup PE=1 SV=	RAT	1
52	0	1,26	4,29500006	1,47700002	1,47700002	sp Q02257 PLAK_MOUSE	Junction plakoglobin OS=Mus musculus GN=Jup PE=1 SV=3	MOUSE	1
52	0	1,26	4,29500006	1,47700002	1,47700002	sp P14923 PLAK_HUMAN	Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	HUMAN	1
53	1,25	1,26	24,6699996	24,6699996	24,6699996	sp P55000 SLUR1_HUMAN	Secreted Ly-6uPAR-related protein 1 OS=Homo sapiens GN=	HUMAN	1
54	0,98	0,98	11,8000001	2,95000002	2,95000002	sp Q6TEQ7 ANXA2_CANLF	Annexin A2 OS=Canis lupus familiaris GN=ANXA2 PE=1 SV=1	CANLF	1
54	0	0,98	11,8000001	2,95000002	2,95000002	sp Q5R5A0 ANXA2_PONAB	Annexin A2 OS=Pongo abelii GN=ANXA2 PE=2 SV=1	PONAB	1
54	0	0,98	11,8000001	2,95000002	2,95000002	sp Q2Q1M6 ANXA2_CEREL	Annexin A2 OS=Cervus elaphus GN=ANXA2 PE=2 SV=1	CEREL	1
54	0	0,98	11,8000001	2,95000002	2,95000002	sp Q07936 ANXA2_RAT	Annexin A2 OS=Rattus norvegicus GN=Anxa2 PE=1 SV=2	RAT	1
54	0	0,98	11,8000001	2,95000002	2,95000002	sp P19620 ANXA2_PIG	Annexin A2 OS=Sus scrofa GN=ANXA2 PE=1 SV=4	PIG	1
54	0	0,98	11,8000001	2,95000002	2,95000002	sp P07355 ANXA2_HUMAN	Annexin A2 OS=Homo sapiens GN=ANXA2 PE=1 SV=2	HUMAN	1
54	0	0,98	11,8000001	2,95000002	2,95000002	sp P04272 ANXA2_BOVIN	Annexin A2 OS=Bos taurus GN=ANXA2 PE=1 SV=2	BOVIN	1
54	0	0,98	11,8000001	2,95000002	2,95000002	sp A2SW69 ANXA2_SHEEP	Annexin A2 OS=Ovis aries GN=ANXA2 PE=1 SV=1	SHEEP	1
54	0	0,93	7,6700002	2,95000002	2,95000002	sp A6NMY6 AXA2L_HUMAN	Putative annexin A2-like protein OS=Homo sapiens GN=ANXA	HUMAN	1
55	0,92	0,92	3,48399989	3,48399989	3,48399989	sp A6VL73 Y342_ACTSZ	UPF0761 membrane protein Asuc_0342 OS=Actinobacillus su	ACTSZ	1
56	0,86	0,86	100	100	100	sp P84735 PS19_PINST	Putative LRR disease resistance protein/transmembrane rece	PINST	1
56	0	0,86	100	100	100	sp P84732 PS16_PINST	Putative LRR disease resistance protein/transmembrane rece	PINST	1

56	0	0,86	100	100	100	sp P84720 PS4_PINST	Putative LRR disease resistance protein/transmembrane rece	PINST	1
57	0,78	0,78	2,42599994	2,42599994	2,42599994	sp Q0CQH1 NOP58_ASPTN	Nucleolar protein 58 OS=Aspergillus terreus (strain NIH 2624 /	ASPTN	1
58	0,76	0,76	0,87050004	0,87050004	0,87050004	sp Q05884 AMY_STRLI	Alpha-amylase OS=Streptomyces lividans GN=amy PE=1 SV=1	STRLI	1
59	0,67	0,67	3,63599993	3,63599993	3,63599993	sp P01857 IGHG1_HUMAN	Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG1 PE=1	HUMAN	1
60	0,65	0,65	7,76700005	3,15500014	3,15500014	sp P07339 CATD_HUMAN	Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1	HUMAN	1
61	0,58	0,58	20,2099994	5,85100017	5,85100017	sp O75223 GGCT_HUMAN	Gamma-glutamylcyclotransferase OS=Homo sapiens GN=GGC	HUMAN	1
62	0,5	0,5	0,96420003	0,96420003	0,96420003	RRRRRsp Q8Z303 KATG_SALTI	REVERSED Catalase-peroxidase OS=Salmonella typhi GN=k	katG SALTI	1
62	0	0,5	0,96420003	0,96420003	0,96420003	RRRRRsp Q5PK60 KATG_SALPA	REVERSED Catalase-peroxidase OS=Salmonella paratyphi A	(st SALPA	1
62	0	0,5	0,96420003	0,96420003	0,96420003	RRRRRsp Q57HA8 KATG_SALCH	REVERSED Catalase-peroxidase OS=Salmonella choleraesuis	(s SALCH	1
62	0	0,5	1,97199993	1,97199993	1,97199993	RRRRRsp P59487 AROB_BUCBP	REVERSED 3-dehydroquinase synthase OS=Buchnera aphidico	BUCBP	1
62	0	0,5	0,96420003	0,96420003	0,96420003	RRRRRsp P17750 KATG_SALTY	REVERSED Catalase-peroxidase OS=Salmonella typhimurium	(: SALTY	1
62	0	0,5	0,96420003	0,96420003	0,96420003	RRRRRsp B5BJM5 KATG_SALPK	REVERSED Catalase-peroxidase OS=Salmonella paratyphi A	(st SALPK	1
62	0	0,5	0,96420003	0,96420003	0,96420003	RRRRRsp B4TQG7 KATG_SALSV	REVERSED Catalase-peroxidase OS=Salmonella schwarzengru	SALSV	1
62	0	0,5	0,96420003	0,96420003	0,96420003	RRRRRsp B4TCP6 KATG_SALHS	REVERSED Catalase-peroxidase OS=Salmonella heidelberg	(str SALHS	1
62	0	0,5	0,96420003	0,96420003	0,96420003	RRRRRsp B4TOV5 KATG_SALNS	REVERSED Catalase-peroxidase OS=Salmonella newport (stra	strai SALNS	1
62	0	0,5	0,96420003	0,96420003	0,96420003	RRRRRsp A9N0FO KATG_SALPB	REVERSED Catalase-peroxidase OS=Salmonella paratyphi B	(st SALPB	1
62	0	0,5	0,96420003	0,96420003	0,96420003	RRRRRsp A9MI19 KATG_SALAR	REVERSED Catalase-peroxidase OS=Salmonella arizonae (stra	strai SALAR	1
62	0	0,5	0,96420003	0,96420003	0,96420003	RRRRRsp A8AKX8 KATG_CITK8	REVERSED Catalase-peroxidase OS=Citrobacter koseri (strain	/ CITK8	1
62	0	0,5	0,96549997	0,96549997	0,96549997	RRRRRsp A6T9H9 KATG_KLEP7	REVERSED Catalase-peroxidase OS=Klebsiella pneumoniae	sub KLEP7	1
62	0	0,5	0,96420003	0,96420003	0,96420003	RRRRRsp A4WGS7 KATG_ENT38	REVERSED Catalase-peroxidase OS=Enterobacter sp. (strain	6: ENT38	1
66	0,22	0,22	1,76599994	1,76599994	1,76599994	sp P21910 LAML2_XENLA	Lamin-L(II) OS=Xenopus laevis PE=2 SV=1	XENLA	1
63	0,27	0,27	6,96199983	6,96199983	6,96199983	0 sp Q9UGM3 DMBT1_HUMAN	Deleted in malignant brain tumors 1 protein OS=Homo sapien	HUMAN	0
64	0,25	0,25	1,04900002	1,04900002	1,04900002	0 RRRRRsp P48479 NIM1_NEUCR	REVERSED G2-specific protein kinase nim-1 OS=Neurospora	cr NEUCR	0
65	0,24	0,24	4,80000004	4,80000004	4,80000004	0 sp Q5T750 XP32_HUMAN	Skin-specific protein 32 OS=Homo sapiens GN=XP32 PE=1 SV=	HUMAN	0
67	0,21	0,21	0,93649998	0,93649998	0,93649998	0 sp Q9LJX4 PUM5_ARATH	Pumilio homolog 5 OS=Arabidopsis thaliana GN=APUM5 PE=1	ARATH	0
68	0,17	0,17	1,17300004	1,17300004	1,17300004	0 sp Q2KWY3 LEPA_BORA1	Elongation factor 4 OS=Bordetella avium (strain 197N) GN=le	leP BORA1	0
68	0	0,17	1,04	1,04	1,04	0 RRRRRsp Q1LKN9 UVRC_CUPMC	REVERSED UvrABC system protein C OS=Cupriavidus metallid	i CUPMC	0
69	0,16	0,16	1,91799998	1,91799998	1,91799998	0 RRRRRsp Q9SFC7 FB135_ARATH	REVERSED F-box protein At3g07870 OS=Arabidopsis thaliana	/ ARATH	0
70	0,15	0,15	6,68499991	6,68499991	6,68499991	0 sp P12763 FETUA_BOVIN	Alpha-2-HS-glycoprotein OS=Bos taurus GN=AHSG PE=1 SV=2	BOVIN	0
71	0,13	0,13	100	100	100	0 sp P85958 UP02_PSEMZ	Unknown protein 2 (Fragment) OS=Pseudotsuga menziesii PE:	PSEMZ	0
72	0,12	0,12	1,53999999	1,53999999	1,53999999	0 RRRRRsp Q8IX18 DHX40_HUMA	REVERSED Probable ATP-dependent RNA helicase DHX40 OS=	HUMAN	0
72	0	0,12	1,53999999	1,53999999	1,53999999	0 RRRRRsp Q6PE54 DHX40_MOU5	REVERSED Probable ATP-dependent RNA helicase DHX40 OS=	MOUSE	0
72	0	0,12	1,53999999	1,53999999	1,53999999	0 RRRRRsp Q5XI69 DHX40_RAT	REVERSED Probable ATP-dependent RNA helicase DHX40 OS=	RAT	0
72	0	0,12	1,53999999	1,53999999	1,53999999	0 RRRRRsp Q5R864 DHX40_PONA	REVERSED Probable ATP-dependent RNA helicase DHX40 OS=	PONAB	0
73	0,11	0,11	0,76819998	0,76819998	0,76819998	0 sp Q8T9W4 ABCB3_DICDI	ABC transporter B family member 3 OS=Dictyostelium discoi	d: DICDI	0
74	0,11	0,11	12,0899998	12,0899998	12,0899998	0 sp A6LPJ0 SP5G_CLOB8	Putative septation protein SpoVG OS=Clostridium beijerinckii	CLOB8	0
75	0,11	0,11	10,2799997	10,2799997	10,2799997	0 RRRRRsp B9K6M6 Y433_THENN	REVERSED UPF0102 protein CTN_0433 OS=Thermotoga neap	: THENN	0
76	0,1	0,1	2,38099992	2,38099992	2,38099992	0 sp Q7V121 LEU1_PROMP	2-isopropylmalate synthase OS=Prochlorococcus marinus sub:	PROMP	0
76	0	0,1	2,38099992	2,38099992	2,38099992	0 sp A2BX52 LEU1_PROM5	2-isopropylmalate synthase OS=Prochlorococcus marinus (str:	PROM5	0
77	0,08	0,08	7,01799989	7,01799989	7,01799989	0 sp Q03QY4 ATPF_LACBA	ATP synthase subunit b OS=Lactobacillus brevis (strain ATCC	3 LACBA	0
78	0,08	0,08	0,50090002	0,50090002	0,50090002	0 sp O77384 LRR4_PLAF7	Protein PFC0760c OS=Plasmodium falciparum (isolate 3D7) G	I PLAF7	0
79	0,07	0,07	1,77500006	1,33100003	1,33100003	0 sp Q6C186 CLF1_YARLI	Pre-mRNA-splicing factor CLF1 OS=Yarrowia lipolytica (strain	/ YARLI	0
80	0,05	0,05	0,5988	0,5988	0,5988	0 sp Q9LZW9 RTOR2_ARATH	Regulatory-associated protein of TOR 2 OS=Arabidopsis thalia	ARATH	0
81	0,05	0,05	0,24550001	0,24550001	0,24550001	0 sp Q756G2 TOM1_ASHGO	Probable E3 ubiquitin-protein ligase TOM1 OS=Ashbya gossyp	ASHGO	0
82	0,05	0,05	0,60840002	0,60840002	0,60840002	0 RRRRRsp Q9NRP7 STK36_HUMA	REVERSED Serine/threonine-protein kinase 36 OS=Homo sapi	HUMAN	0
82	0	0,05	0,6079	0,6079	0,6079	0 RRRRRsp Q69ZM6 STK36_MOU5	REVERSED Serine/threonine-protein kinase 36 OS=Mus muscu	MOUSE	0
83	0,05	0,05	2,00500004	2,00500004	2,00500004	0 RRRRRsp Q21DC2 RLMN_RHOPB	REVERSED Dual-specificity RNA methyltransferase RlmN OS=R	RHOPB	0
84	0,05	0,05	3,66199985	3,66199985	3,66199985	0 RRRRRsp Q04852 T2C1_CITFR	REVERSED Type-2 restriction enzyme CfrBI OS=Citrobacter fre	CITFR	0

N	CSV_1	Total	%Cov	%Cov(50)	%Cov(95)	Accession	Name	Species	Peptides(95%)
1	74,54	74,54	64,60000277	61,01999879	54,97000217	sp P04264 K2C1_HUMAN	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=	HUMAN	51
2	58,75	58,75	55,98999858	55,98999858	54,44999933	sp P13645 K1C10_HUMAN	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV	HUMAN	37
3	48,86	56,87	62,27999926	56,33999705	53,99000049	sp P35908 K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=KRT	HUMAN	32
4	47,53	47,53	65,96999764	64,37000036	55,22000194	sp P35527 K1C9_HUMAN	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE=1 SV=3	HUMAN	28
5	30,77	35,39	55,39000034	52,21999884	49,47000146	sp P08779 K1C16_HUMAN	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PE=1 SV	HUMAN	19
6	17,15	34,87	37,05999851	32,44999945	30,66999912	sp P02538 K2C6A_HUMAN	Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A PE=1 S	HUMAN	18
6	0	32,87	34,92999971	30,32000065	28,549999	sp P48668 K2C6C_HUMAN	Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C PE=1 S'	HUMAN	17
8	10,23	28,09	49,79000042	41,10000134	34,11000073	sp P02533 K1C14_HUMAN	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PE=1 SV	HUMAN	16
10	9,79	25,1	32,37000108	22,54000008	20,50999999	sp P13647 K2C5_HUMAN	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE=1 SV=	HUMAN	13
20	1,66	21,47	19,39000004		17,67999977	sp P06394 K1C10_BOVIN	Keratin, type I cytoskeletal 10 OS=Bos taurus GN=KRT10 PE=3 SV=1	BOVIN	13
7	14,1	14,1	43,29000115	38,10000122	38,10000122	sp P00761 TRYR_PIG	Trypsin OS=Sus scrofa PE=1 SV=1	PIG	12
10	0	23,1	28,04000008	19,93000068	17,91000068	sp A5A6M8 K2C5_PANTR	Keratin, type II cytoskeletal 5 OS=Pan troglodytes GN=KRT5 PE=2 SV	PANTR	12
19	1,8	11,4	13,28999996	11,36000007	11,36000007	sp Q6IFZ6 K2C1B_MOUSE	Keratin, type II cytoskeletal 1b OS=Mus musculus GN=Krt77 PE=1 SV	MOUSE	10
19	0	9,63	16,9599995	12,52000034	12,52000034	sp Q6IG01 K2C1B_RAT	Keratin, type II cytoskeletal 1b OS=Rattus norvegicus GN=Krt77 PE=	RAT	10
12	3,59	11,57	28,70000005	17,82000065	17,58999974	sp Q04695 K1C17_HUMAN	Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PE=1 SV	HUMAN	7
12	0	11,57	28,70000005	17,82000065	17,58999974	sp A5A6M0 K1C17_PANTR	Keratin, type I cytoskeletal 17 OS=Pan troglodytes GN=KRT17 PE=2 S	PANTR	7
19	0	8,19	12,98000067	7,43900016	7,43900016	sp Q7Z794 K2C1B_HUMAN	Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 PE=2 S'	HUMAN	7
12	0	9,18	22,63000011	15,94000012	13,16000074	sp Q9QWL7 K1C17_MOUSE	Keratin, type I cytoskeletal 17 OS=Mus musculus GN=KRT17 PE=1 SV	MOUSE	6
12	0	9,18	22,63000011	15,94000012	13,16000074	sp Q6IFU8 K1C17_RAT	Keratin, type I cytoskeletal 17 OS=Rattus norvegicus GN=Krt17 PE=1	RAT	6
12	0	9,18	19,49999928	13,15000057	12,92999983	sp A1L595 K1C17_BOVIN	Keratin, type I cytoskeletal 17 OS=Bos taurus GN=KRT17 PE=2 SV=1	BOVIN	6
9	10	10	76,09000206	51,45000219	51,45000219	sp P15252 REF_HEVBR	Rubber elongation factor protein OS=Hevea brasiliensis PE=1 SV=2	HEVBR	5
22	1,14	9,37	11,72999963	7,308000326	7,308000326	sp Q8N1N4 K2C78_HUMAN	Keratin, type II cytoskeletal 78 OS=Homo sapiens GN=KRT78 PE=2 S'	HUMAN	5
13	3,31	3,31	25,45000017	25,45000017	25,45000017	sp P81605 DCD_HUMAN	Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	HUMAN	3
14	3,24	3,24		25	17,64999926	sp O82803 SRPP_HEVBR	Small rubber particle protein OS=Hevea brasiliensis GN=SRPP PE=1	HEVBR	3
11	4	4	35,47999859	23,65999967	23,65999967	sp P05109 S10A8_HUMAN	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	HUMAN	2
15	2	2,82	4,68400009	4,68400009	4,68400009	sp Q6IFX1 K1C24_RAT	Keratin, type I cytoskeletal 24 OS=Rattus norvegicus GN=Krt24 PE=3	RAT	2
15	0	2,82	4,492000118	4,492000118	4,492000118	sp A1L317 K1C24_MOUSE	Keratin, type I cytoskeletal 24 OS=Mus musculus GN=Krt24 PE=2 SV	MOUSE	2
16	2	2	24,56	11,40000001	11,40000001	sp P06702 S10A9_HUMAN	Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1	HUMAN	1
17	2	2	8,392000198	8,392000198	8,392000198	sp Q9PU28 LYSC_SCOMX	Lysozyme C OS=Scophthalmus maximus GN=lys PE=2 SV=1	SCOMX	1
17	0	2	8,392000198	8,392000198	8,392000198	sp Q9DD65 LYSC_PAROL	Lysozyme C OS=Paralichthys olivaceus PE=2 SV=1	PAROL	1
17	0	2	8,107999712	8,107999712	8,107999712	sp Q6B411 LYSM_BOVIN	Lysozyme C, milk isozyme OS=Bos taurus PE=2 SV=1	BOVIN	1
17	0	2	8,107999712	8,107999712	8,107999712	sp Q659U5 LYSC_HALGR	Lysozyme C OS=Halichoerus grypus GN=LYZ PE=2 SV=1	HALGR	1
17	0	2	8,107999712	8,107999712	8,107999712	sp Q659U1 LYSC_PHOVI	Lysozyme C OS=Phoca vitulina GN=LYZ PE=2 SV=1	PHOVI	1
17	0	2	8,107999712	8,107999712	8,107999712	sp Q659U0 LYSC_LEPWE	Lysozyme C OS=Leptonychotes weddellii GN=LYZ PE=2 SV=1	LEPWE	1
17	0	2	8,107999712	8,107999712	8,107999712	sp Q05820 LYSC2_RAT	Putative lysozyme C-2 OS=Rattus norvegicus GN=Ly2z PE=5 SV=1	RAT	1
17	0	2	9,230999649	9,230999649	9,230999649	sp P85345 LYSC_AMYCA	Lysozyme C OS=Amyda cartilaginea GN=LYZ PE=1 SV=1	AMYCA	1
17	0	2	8,218999952	8,218999952	8,218999952	sp P85045 LYS_BUFGA	Lysozyme C (Fragment) OS=Bufo gargarizans andrewsi PE=1 SV=1	BUFGA	1
17	0	2	9,230999649	9,230999649	9,230999649	sp P81709 LYSC2_CANLF	Lysozyme C, spleen isozyme OS=Canis lupus familiaris PE=1 SV=1	CANLF	1
17	0	2	8,107999712	8,107999712	8,107999712	sp P79847 LYSC_PYGNE	Lysozyme C OS=Pygathrix nemaeus GN=LYZ PE=3 SV=1	PYGNE	1
17	0	2	8,107999712	8,107999712	8,107999712	sp P799811 LYSC_NASLA	Lysozyme C OS=Nasalis larvatus GN=LYZ PE=3 SV=1	NASLA	1
17	0	2	8,107999712	8,107999712	8,107999712	sp P79239 LYSC_PONPY	Lysozyme C OS=Pongo pygmaeus GN=LYZ PE=2 SV=1	PONPY	1
17	0	2	8,107999712	8,107999712	8,107999712	sp P79180 LYSC_HYLLA	Lysozyme C OS=Hylobates lar GN=LYZ PE=2 SV=1	HYLLA	1
17	0	2	8,107999712	8,107999712	8,107999712	sp P79179 LYSC_GORGO	Lysozyme C OS=Gorilla gorilla gorilla GN=LYZ PE=2 SV=1	GORGO	1
17	0	2	8,107999712	8,107999712	8,107999712	sp P67980 LYSC_TRAFR	Lysozyme C OS=Trachypithecus francoisi GN=LYZ PE=2 SV=1	TRAFR	1
17	0	2	8,107999712	8,107999712	8,107999712	sp P67979 LYSC_TRAOB	Lysozyme C OS=Trachypithecus obscurus GN=LYZ PE=2 SV=1	TRAOB	1
17	0	2	8,107999712	8,107999712	8,107999712	sp P67978 LYSC_TRAVT	Lysozyme C OS=Trachypithecus vetulus GN=LYZ PE=3 SV=1	TRAVT	1
17	0	2	8,107999712	8,107999712	8,107999712	sp P67977 LYSC_SEMEN	Lysozyme C OS=Semnopithecus entellus GN=LYZ PE=1 SV=1	SEMEN	1
17	0	2	8,392000198	8,392000198	8,392000198	sp P61944 LYSC_TAKRU	Lysozyme C OS=Takifugu rubripes PE=2 SV=1	TAKRU	1
17	0	2	8,107999712	8,107999712	8,107999712	sp P61632 LYSC_COLGU	Lysozyme C OS=Colobus guereza GN=LYZ PE=2 SV=1	COLGU	1
17	0	2	8,107999712	8,107999712	8,107999712	sp P61631 LYSC_COLAN	Lysozyme C OS=Colobus angolensis GN=LYZ PE=3 SV=1	COLAN	1
17	0	2	8,107999712	8,107999712	8,107999712	sp P61628 LYSC_PANTR	Lysozyme C OS=Pan troglodytes GN=LYZ PE=2 SV=1	PANTR	1
17	0	2	8,107999712	8,107999712	8,107999712	sp P61627 LYSC_PANPA	Lysozyme C OS=Pan paniscus GN=LYZ PE=3 SV=1	PANPA	1
17	0	2	8,107999712	8,107999712	8,107999712	sp P61626 LYSC_HUMAN	Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1	HUMAN	1
17	0	2	9,230999649	9,230999649	9,230999649	sp P37712 LYSC_CAMDR	Lysozyme C OS=Camelus dromedarius GN=LYZ PE=1 SV=1	CAMDR	1
17	0	2	8,107999712	8,107999712	8,107999712	sp P17897 LYZ1_MOUSE	Lysozyme C-1 OS=Mus musculus GN=Ly2z1 PE=1 SV=1	MOUSE	1
17	0	2	9,230999649	9,230999649	9,230999649	sp P16973 LYSC_RABIT	Lysozyme C OS=Oryctolagus cuniculus GN=LYZ PE=1 SV=1	RABIT	1
17	0	2	8,107999712	8,107999712	8,107999712	sp P12069 LYSC3_PIG	Lysozyme C-3 OS=Sus scrofa PE=1 SV=2	PIG	1
17	0	2	8,218999952	8,218999952	8,218999952	sp P12068 LYSC2_PIG	Lysozyme C-2 OS=Sus scrofa PE=1 SV=2	PIG	1
17	0	2	9,375	9,375	9,375	sp P12067 LYSC1_PIG	Lysozyme C-1 OS=Sus scrofa PE=1 SV=1	PIG	1
17	0	2	8,332999796	8,332999796	8,332999796	sp P11941 LYSC2_ONCMY	Lysozyme C II OS=Oncorhynchus mykiss PE=1 SV=2	ONCMY	1
17	0	2	8,107999712	8,107999712	8,107999712	sp P08905 LYZ2_MOUSE	Lysozyme C-2 OS=Mus musculus GN=Ly2z2 PE=1 SV=2	MOUSE	1
17	0	2	8,107999712	8,107999712	8,107999712	sp P00697 LYSC1_RAT	Lysozyme C-1 OS=Rattus norvegicus GN=Ly2z1 PE=1 SV=2	RAT	1
18	1,89	1,89	8,696000278	3,415999934	3,415999934	sp P05089 ARG1_HUMAN	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2	HUMAN	1
21	1,36	1,36	8,218999952	8,218999952	8,218999952	sp P12273 PIP_HUMAN	Prolactin-inducible protein OS=Homo sapiens GN=PIP PE=1 SV=1	HUMAN	1
21	0	1,36	8,218999952	8,218999952	8,218999952	sp A0A890 PIP_HYLAG	Prolactin-inducible protein homolog OS=Hylobates agilis GN=PIP PE	HYLAG	1
21	0	1,36	8,218999952	8,218999952	8,218999952	sp A0A888 PIP_PONPY	Prolactin-inducible protein homolog OS=Pongo pygmaeus GN=PIP P	PONPY	1
23	0,9	0,9	2,135000005	2,135000005	2,135000005	sp Q35N005 ALBU_PONAB	Serum albumin OS=Pongo abelii GN=ALB PE=2 SV=2	PONAB	1
23	0	0,9	2,167000063	2,167000063	2,167000063	sp Q28522 ALBU_MACMU	Serum albumin (Fragment) OS=Macaca mulatta GN=ALB PE=2 SV=1	MACMU	1
23	0	0,9	2,135000005	2,135000005	2,135000005	sp P02768 ALBU_HUMAN	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	HUMAN	1
23	0	0,9	2,137999982	2,137999982	2,137999982	sp A2V9Z4 ALBU_MACFA	Serum albumin OS=Macaca fascicularis GN=ALB PE=2 SV=1	MACFA	1
24	0,55	0,55	5,601000041	2,142000012	2,142000012	sp P02769 ALBU_BOVIN	Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	BOVIN	1
25	0,36	0,36	1,765999943	1,765999943	1,765999943	sp P21910 LAML2_XENLA	Lamin-1(LI) OS=Xenopus laevis PE=2 SV=1	XENLA	1
26	0,3	0,3	6,577000022	1,477000024		sp Q8WNW3 PLAK_PIG	Junction plakoglobin OS=Sus scrofa GN=Jup PE=2 SV=1	PIG	0
26	0	0,3	6,577000022	1,477000024		sp Q8SP1 PLAK_BOVIN	Junction plakoglobin OS=Bos taurus GN=JUP PE=2 SV=1	BOVIN	0
26	0	0,3	6,577000022	1,477000024		sp Q6P0K8 PLAK_RAT	Junction plakoglobin OS=Rattus norvegicus GN=Jup PE=1 SV=1	RAT	0
26	0	0,3	6,577000022	1,477000024		sp Q02257 PLAK_MOUSE	Junction plakoglobin OS=Mus musculus GN=Jup PE=1 SV=3	MOUSE	0
26	0	0,3	6,577000022	1,477000024		sp P14923 PLAK_HUMAN	Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	HUMAN	0
27	0,15	0,15	0,359000009	0,359000009		0 RRRRRsp Q19317 NBEA_CAEEI	REVERSED Putative neurobeachin homolog OS=Caenorhabditis eleg	CAEEI	0
27	0	0,15	0,356000007	0,356000007		0 RRRRRsp A8XSV3 NBEA_CAEBI	REVERSED Putative neurobeachin homolog OS=Caenorhabditis brigg	CAEBR	0
28	0,12	0,12	3,908000141	1,81099996		0 sp Q02413 DSG1_HUMAN	Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	HUMAN	0
28	0	0,12	1,817999966	1,817999966		0 sp Q3BD17 DSG1_PIG	Desmoglein-1 OS=Sus scrofa GN=DSG1 PE=2 SV=1	PIG	0
28	0	0,12	1,821999997	1,821999997		0 sp Q03763 DSG1_BOVIN	Desmoglein-1 OS=Bos taurus GN=DSG1 PE=1 SV=1	BOVIN	0
29	0,1	0,1	2,425999939	2,425999939		0 sp Q0CQH1 NOP58_ASPTN	Nucleolar protein 58 OS=Aspergillus terreus (strain NIH 2624 / FGSC	ASPTN	0
30	0,09	0,09	1,631999947	1,631999947		0 sp Q42191 OXA1_ARATH	Mitochondrial inner membrane protein OXA1 OS=Arabidopsis thalia	ARATH	0
31	0,08	0,08	1,917999983	1,917999983		0 RRRRRsp Q9SFC7 FB135_ARAT	REVERSED F-box protein At3g07870 OS=Arabidopsis thaliana GN=At	ARAT	0
32	0,05	0,05	0,245500007	0,245500007		0 sp Q756G2 TOM1_ASHGO	Probable E3 ubiquitin-protein ligase TOM1 OS=Ashbya gossypii (stra	ASHGO	0
33	0,05	0,05	0,241999984	0,241999984		0 sp Q5I0K7 ALG13_RAT	UDP-N-acetylglucosamine transferase subunit ALG13 homolog OS=F	RAT	0
33	0	0,05	3,333000094	3,333000094		0 sp B1XPZ8 HIS1_SYNP2	ATP phosphoribosyltransferase OS=Synecchococcus sp. (strain ATCC	SYNP2	0
34	0,05	0,05	0,608400023	0,608400023		0 RRRRRsp Q9NRP7 STK36_HUM	REVERSED Serine/threonine-protein kinase 36 OS=Homo sapiens GN	HUMAN	0
34	0	0,05	0,607899996	0,607899996		0 RRRRRsp Q69ZM6 STK36_MOI	REVERSED Serine/threonine-protein kinase 36 OS=Mus musculus GN	MOUSE	0
35	0,05	0,05	2,005000004	2,005000004		0 RRRRRsp Q21DC2 RLMN_RHOI	REVERSED Dual-specificity RNA methyltransferase RlmN OS=Rhodosp	RHOPB	0

N	CSV_2	Total	%Cov	%Cov(50)	%Cov(95)	Accession	Name	Species	Peptides(95%)
3	43,27	43,27	58,4399998	58,4399998	58,4399998	sp P00761 TRYP_PIG	Trypsin OS=Sus scrofa PE=1 SV=1	PIG	34
1	54,17	54,17	57,2799981	54,7699988	52,8999984	sp P35908 K22E_HUMAN	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapi	HUMAN	28
4	40,02	48,04	46,9399984	43,7999993	32,9699993	sp A5A6M6 K2C1_PANTR	Keratin, type II cytoskeletal 1 OS=Pan troglodytes GN=K	PANTR	28
4	0	48,02	42,6999986	39,5999998	32,6099992	sp P04264 K2C1_HUMAN	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KR	HUMAN	28
2	46,08	46,08	51,3700008	47,7699995	47,7699995	sp P13645 K1C10_HUMAN	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=Kf	HUMAN	27
5	26	26	41,5699989	32,1000001	32,1000001	sp P35527 K1C9_HUMAN	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KR	HUMAN	14
12	2	18	13,1200001	13,1200001	13,1200001	sp P04259 K2C6B_HUMAN	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=K	HUMAN	9
6	16	16	71,0099995	71,0099995	71,0099995	sp P15252 REF_HEVBR	Rubber elongation factor protein OS=Hevea brasiliensis	HEVBR	8
12	0	16	11,3499999	11,3499999	11,3499999	sp P48668 K2C6C_HUMAN	Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=K	HUMAN	8
12	0	16	11,3499999	11,3499999	11,3499999	sp P02538 K2C6A_HUMAN	Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=K	HUMAN	8
13	2	14	11,1900002	9,15300027	9,15300027	sp P13637 K2C5_HUMAN	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KR	HUMAN	7
13	0	14	11,1500002	9,12199989	9,12199989	sp A5A6M8 K2C5_PANTR	Keratin, type II cytoskeletal 5 OS=Pan troglodytes GN=K	PANTR	7
7	4,01	8,01	16,6999996	9,93700027	9,93700027	sp P08779 K1C16_HUMAN	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=Kf	HUMAN	4
14	2	8,01	19,4900006	9,95799974	9,95799974	sp P02533 K1C14_HUMAN	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=Kf	HUMAN	4
8	4	4	25,4500002	23,6399993	23,6399993	sp P81605 DCD_HUMAN	Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	HUMAN	2
9	4	4	19,1200003	19,1200003	12,7499998	sp O82803 SRPP_HEVBR	Small rubber particle protein OS=Hevea brasiliensis GN=	HEVBR	2
10	4	4	5,58300018	5,58300018	5,58300018	sp Q5NVH5 ALBU_PONAB	Serum albumin OS=Pongo abelii GN=ALB PE=2 SV=2	PONAB	2
10	0	4	5,58300018	5,58300018	5,58300018	sp P02768 ALBU_HUMAN	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	HUMAN	2
11	4	4	24,56	24,56	24,56	sp P06702 S10A9_HUMAN	Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 S	HUMAN	2
10	0	2	2,16700006	2,16700006	2,16700006	sp Q28522 ALBU_MACMU	Serum albumin (Fragment) OS=Macaca mulatta GN=AL	MACMU	1
10	0	2	2,13799998	2,13799998	2,13799998	sp A2V9Z4 ALBU_MACFA	Serum albumin OS=Macaca fascicularis GN=ALB PE=2 S	MACFA	1
15	2	2	34,4099998	22,5799993	22,5799993	sp P05109 S10A8_HUMAN	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 S	HUMAN	1
16	2	2	5,60100004	2,14200001	2,14200001	sp P02769 ALBU_BOVIN	Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	BOVIN	1
17	2	2	4,44400012	4,44400012	4,44400012	sp Q9A1W2 RL5_STRP1	50S ribosomal protein L5 OS=Streptococcus pyogenes s	STRP1	1
17	0	2	4,44400012	4,44400012	4,44400012	sp Q975V1 RL5_STRPN	50S ribosomal protein L5 OS=Streptococcus pneumoniae	STRPN	1
17	0	2	4,44400012	4,44400012	4,44400012	sp Q8E7S9 RL5_STRA3	50S ribosomal protein L5 OS=Streptococcus agalactiae	STRA3	1
17	0	2	4,44400012	4,44400012	4,44400012	sp Q8E2C2 RL5_STRA5	50S ribosomal protein L5 OS=Streptococcus agalactiae	STRA5	1
17	0	2	4,44400012	4,44400012	4,44400012	sp Q8CWW4 RL5_STRR6	50S ribosomal protein L5 OS=Streptococcus pneumoniae	STRR6	1
17	0	2	4,46900018	4,46900018	4,46900018	sp Q81VR8 RL5_BACAN	50S ribosomal protein L5 OS=Bacillus anthracis GN=rplE	BACAN	1
17	0	2	4,46900018	4,46900018	4,46900018	sp Q81J30 RL5_BACCR	50S ribosomal protein L5 OS=Bacillus cereus (strain ATC	BACCR	1
17	0	2	4,44400012	4,44400012	4,44400012	sp Q7CNP5 RL5_STRP8	50S ribosomal protein L5 OS=Streptococcus pyogenes s	STRP8	1
17	0	2	4,46900018	4,46900018	4,46900018	sp Q73F84 RL5_BACC1	50S ribosomal protein L5 OS=Bacillus cereus (strain ATC	BACC1	1
17	0	2	4,46900018	4,46900018	4,46900018	sp Q6HPP6 RL5_BACHK	50S ribosomal protein L5 OS=Bacillus thuringiensis subs	BACHK	1
17	0	2	4,46900018	4,46900018	4,46900018	sp Q63H78 RL5_BACCZ	50S ribosomal protein L5 OS=Bacillus cereus (strain 2K	BACCZ	1
17	0	2	4,44400012	4,44400012	4,44400012	sp Q5XEC3 RL5_STRP6	50S ribosomal protein L5 OS=Streptococcus pyogenes s	STRP6	1
17	0	2	4,46900018	4,46900018	4,46900018	sp Q5WLQ0 RL5_BACSK	50S ribosomal protein L5 OS=Bacillus clausii (strain KSV	BACSK	1
17	0	2	4,44400012	4,44400012	4,44400012	sp Q5M2C5 RL5_STRT2	50S ribosomal protein L5 OS=Streptococcus thermophil	STRT2	1
17	0	2	4,44400012	4,44400012	4,44400012	sp Q5LX53 RL5_STRT1	50S ribosomal protein L5 OS=Streptococcus thermophil	STRT1	1
17	0	2	4,44400012	4,44400012	4,44400012	sp Q48VT7 RL5_STRPM	50S ribosomal protein L5 OS=Streptococcus pyogenes s	STRPM	1
17	0	2	4,44400012	4,44400012	4,44400012	sp Q3K3V7 RL5_STRA1	50S ribosomal protein L5 OS=Streptococcus agalactiae	STRA1	1
17	0	2	4,44400012	4,44400012	4,44400012	sp Q1WSA2 RL5_LACS1	50S ribosomal protein L5 OS=Lactobacillus salivarius (st	LACS1	1
17	0	2	4,44400012	4,44400012	4,44400012	sp Q1JPO5 RL5_STRPC	50S ribosomal protein L5 OS=Streptococcus pyogenes s	STRPC	1
17	0	2	4,44400012	4,44400012	4,44400012	sp Q1JJ50 RL5_STRPD	50S ribosomal protein L5 OS=Streptococcus pyogenes s	STRPD	1
17	0	2	4,44400012	4,44400012	4,44400012	sp Q1JE46 RL5_STRPB	50S ribosomal protein L5 OS=Streptococcus pyogenes s	STRPB	1
17	0	2	4,44400012	4,44400012	4,44400012	sp Q1J901 RL5_STRPF	50S ribosomal protein L5 OS=Streptococcus pyogenes s	STRPF	1
17	0	2	4,44400012	4,44400012	4,44400012	sp Q04MM4 RL5_STRP2	50S ribosomal protein L5 OS=Streptococcus pneumoniae	STRP2	1
17	0	2	4,44400012	4,44400012	4,44400012	sp Q03IG3 RL5_STRTD	50S ribosomal protein L5 OS=Streptococcus thermophil	STRTD	1
17	0	2	4,44400012	4,44400012	4,44400012	sp P0DE57 RL5_STRPQ	50S ribosomal protein L5 OS=Streptococcus pyogenes s	STRPQ	1
17	0	2	4,44400012	4,44400012	4,44400012	sp P0DE56 RL5_STRP3	50S ribosomal protein L5 OS=Streptococcus pyogenes s	STRP3	1
17	0	2	4,46900018	4,46900018	4,46900018	sp C6E4P5 RL5_GEOSM	50S ribosomal protein L5 OS=Geobacter sp. (strain M21	GEOSM	1
17	0	2	4,46900018	4,46900018	4,46900018	sp C3P9R7 RL5_BACAA	50S ribosomal protein L5 OS=Bacillus anthracis (strain F	BACAA	1
17	0	2	4,46900018	4,46900018	4,46900018	sp C3J941 RL5_BACAC	50S ribosomal protein L5 OS=Bacillus anthracis (strain C	BACAC	1
17	0	2	4,46900018	4,46900018	4,46900018	sp C1ET51 RL5_BACC3	50S ribosomal protein L5 OS=Bacillus cereus (strain 03E	BACC3	1
17	0	2	4,44400012	4,44400012	4,44400012	sp C1CPA0 RL5_STRZT	50S ribosomal protein L5 OS=Streptococcus pneumoniae	STRZT	1
17	0	2	4,44400012	4,44400012	4,44400012	sp C1CIA9 RL5_STRZP	50S ribosomal protein L5 OS=Streptococcus pneumoniae	STRZP	1
17	0	2	4,44400012	4,44400012	4,44400012	sp C1CC18 RL5_STRZJ	50S ribosomal protein L5 OS=Streptococcus pneumoniae	STRZJ	1
17	0	2	4,44400012	4,44400012	4,44400012	sp C1CAM4 RL5_STRP7	50S ribosomal protein L5 OS=Streptococcus pneumoniae	STRP7	1
17	0	2	4,44400012	4,44400012	4,44400012	sp C0MCC2 RL5_STRS7	50S ribosomal protein L5 OS=Streptococcus equi subsp	STRS7	1
17	0	2	4,44400012	4,44400012	4,44400012	sp C0M9H3 RL5_STRER	50S ribosomal protein L5 OS=Streptococcus equi subsp	STRER	1
17	0	2	4,46900018	4,46900018	4,46900018	sp B9IZK6 RL5_BACCQ	50S ribosomal protein L5 OS=Bacillus cereus (strain Q1)	BACCQ	1
17	0	2	4,44400012	4,44400012	4,44400012	sp B8ZKG9 RL5_STRPJ	50S ribosomal protein L5 OS=Streptococcus pneumoniae	STRPJ	1
17	0	2	4,46900018	4,46900018	4,46900018	sp B7JKD1 RL5_BACCO	50S ribosomal protein L5 OS=Bacillus cereus (strain AH)	BACCO	1
17	0	2	4,46900018	4,46900018	4,46900018	sp B7IT31 RL5_BACC2	50S ribosomal protein L5 OS=Bacillus cereus (strain G9)	BACC2	1
17	0	2	4,46900018	4,46900018	4,46900018	sp B7HQV6 RL5_BACC7	50S ribosomal protein L5 OS=Bacillus cereus (strain AH)	BACC7	1
17	0	2	4,46900018	4,46900018	4,46900018	sp B7HJ60 RL5_BACC4	50S ribosomal protein L5 OS=Bacillus cereus (strain B4)	BACC4	1
17	0	2	4,46900018	4,46900018	4,46900018	sp B7GJ79 RL5_ANOFW	50S ribosomal protein L5 OS=Anoxybacillus flavithermu	ANOFW	1
17	0	2	4,44400012	4,44400012	4,44400012	sp B5XJ48 RL5_STRPZ	50S ribosomal protein L5 OS=Streptococcus pyogenes s	STRPZ	1
17	0	2	4,46900018	4,46900018	4,46900018	sp B5EFR2 RL5_GEOBB	50S ribosomal protein L5 OS=Geobacter bemidjiensis (s	GEOBB	1
17	0	2	4,44400012	4,44400012	4,44400012	sp B5EG67 RL5_STRP4	50S ribosomal protein L5 OS=Streptococcus pneumoniae	STRP4	1
17	0	2	4,44400012	4,44400012	4,44400012	sp B4U512 RL5_STREM	50S ribosomal protein L5 OS=Streptococcus equi subsp	STREM	1
17	0	2	4,44400012	4,44400012	4,44400012	sp B2IS52 RL5_STRPS	50S ribosomal protein L5 OS=Streptococcus pneumoniae	STRPS	1
17	0	2	4,44400012	4,44400012	4,44400012	sp B1I8L0 RL5_STRPI	50S ribosomal protein L5 OS=Streptococcus pneumoniae	STRPI	1
17	0	2	4,46900018	4,46900018	4,46900018	sp A9VP89 RL5_BACWK	50S ribosomal protein L5 OS=Bacillus weihenstephaner	BACWK	1
17	0	2	4,44400012	4,44400012	4,44400012	sp A8AZL3 RL5_STRGC	50S ribosomal protein L5 OS=Streptococcus gordonii (s)	STRGC	1
17	0	2	4,44400012	4,44400012	4,44400012	sp A3CK75 RL5_STRSV	50S ribosomal protein L5 OS=Streptococcus sanguinis (	STRSV	1
17	0	2	4,44400012	4,44400012	4,44400012	sp A2RC26 RL5_STRPG	50S ribosomal protein L5 OS=Streptococcus pyogenes s	STRPG	1
17	0	2	4,46900018	4,46900018	4,46900018	sp A0R8J2 RL5_BACAH	50S ribosomal protein L5 OS=Bacillus thuringiensis (str	BACAH	1
18	2	2	0,46009999	0,46009999	0,46009999	sp Q5D862 FILA2_HUMAN	Flaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	HUMAN	1
19	2	2	1,63199995	1,63199995	1,63199995	sp Q42191 OXA1_ARATH	Mitochondrial inner membrane protein OXA1 OS=Arabi	ARATH	1
20	2	2	1,89699996	1,89699996	1,89699996	sp Q10CE4 GLO1_ORYSJ	Peroxisomal (S)-2-hydroxy-acid oxidase GLO1 OS=Oryz	ORYSJ	1
20	0	2	1,89699996	1,89699996	1,89699996	sp B8AKX6 GLO1_ORYSI	Peroxisomal (S)-2-hydroxy-acid oxidase GLO1 OS=Oryz	ORYSI	1
21	2	2	0,87050004	0,87050004	0,87050004	sp Q05884 AMY_STRLI	Alpha-amylase OS=Streptomyces lividans GN=amy PE=	STRLI	1
22	2	2	3,78299989	3,78299989	3,78299989	sp P49065 ALBU_RABIT	Serum albumin OS=Oryctolagus cuniculus GN=ALB PE=	RABIT	1
23	0,33	0,33	1,91799998	1,91799998	1,91799998	RRRRRsp Q9SFC7 FB135_ARATH	REVERSED F-box protein At3g07870 OS=Arabidopsis th	ARATH	1
24	0,09	2	100	100	100	sp P84735 PS19_PINST	Putative LRR disease resistance protein/transmembran	PINST	1
24	0	2	100	100	100	sp P84732 PS16_PINST	Putative LRR disease resistance protein/transmembran	PINST	1
24	0	2	100	100	100	sp P84720 PS4_PINST	Putative LRR disease resistance protein/transmembran	PINST	1

N	CSV_3	Total	%Cov	%Cov(50)	%Cov(95)	Accession	Name	Species	Peptides(95%)
1	21,82	21,82	44,9000001	22,29000032	20,56999952	sp A5A6M6 K2C1_PANTR	Keratin, type II cytoskeletal 1 OS=Pan troglodytes	PANTR	11
1	0	19,65	42,39000082	19,41000074	17,70000011	sp P04264 K2C1_HUMAN	Keratin, type II cytoskeletal 1 OS=Homo sapiens	C HUMAN	10
2	15,52	15,52	36,80000007	32,89999962	32,89999962	sp P00761 TRYP_PIG	Trypsin OS=Sus scrofa PE=1 SV=1	PIG	18
3	4,29	4,29	35,04000008	7,041999698	4,930000007	sp Q6EIZ0 K1C10_CANLF	Keratin, type I cytoskeletal 10 OS=Canis lupus farr	CANLF	2
3	0	4,29	32,53000081	6,848999858	4,794999957	sp P13645 K1C10_HUMAN	Keratin, type I cytoskeletal 10 OS=Homo sapiens	I HUMAN	2
4	4,06	4,06	31,61999881	5,9390001	5,9390001	sp P35527 K1C9_HUMAN	Keratin, type I cytoskeletal 9 OS=Homo sapiens	G HUMAN	2
5	3,1	3,1	11,85000017	5,491000041	5,491000041	sp Q72KU3 PYRD_THET2	Dihydroorotate dehydrogenase (quinone) OS=Th	THET2	2
6	0,05	0,05	1,844999939	0	0	RRRRRsp Q7VN62 UBIB_HAEDU	REVERSED Probable protein kinase UbiB OS=Haer	HAEDU	0

N	CtrIdrodoso_CSVI_1	Total	%Cov	%Cov(50)	%Cov(95)	Accession	Name	Species	Peptides(95%)
1	78,22	78,22	69,24999952	66,61000252	57,60999918	sp P04264 K2C1_HUMAN	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 I HUMAN	HUMAN	61
2	62,37	62,37	62,5	52,2300005	52,05000043	sp P13645 K1C10_HUMAN	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 HUMAN	HUMAN	56
3	49,5	58,27	74,01999831	61,6599977	50,55000186	sp P35908 K2E2_HUMAN	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens HUMAN	HUMAN	37
4	42,41	42,41	69,81999874	63,08000088	57,45999813	sp P35527 K1C9_HUMAN	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 P HUMAN	HUMAN	33
18	2	27,56	32,74999857	30,98999858	29,9999998	sp Q6E1Z0 K1C10_CANLF	Keratin, type I cytoskeletal 10 OS=Canis lupus familiaris GN CANLF	CANLF	25
7	13,59	26,47	36,61000133	27,97000011	24,20000014	sp P13647 K2C5_HUMAN	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 I HUMAN	HUMAN	19
7	0	24,47	33,950001	25,33999979	22,30000049	sp A5A6M8 K2C5_PANTR	Keratin, type II cytoskeletal 5 OS=Pan troglodytes GN=KRT5 PANTR	PANTR	18
11	0	24,61	29,96000051	27,30000019	18,79000068	sp P48668 K2C6C_HUMAN	Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6 HUMAN	HUMAN	17
11	0	24,61	29,96000051	27,30000019	18,79000068	sp P02538 K2C6A_HUMAN	Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6 HUMAN	HUMAN	17
11	4	24,68	29,96000051	24,28999999	18,97000074	sp P04259 K2C6B_HUMAN	Keratin, type II cytoskeletal 6B OS=Homo sapiens GN=KRT6 HUMAN	HUMAN	16
5	19,37	23,82	55,29999733	41,53000116	31,77999854	sp P02533 K1C14_HUMAN	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 HUMAN	HUMAN	14
8	8,82	8,82	41,99000001	38,96000087	32,89999962	sp P00761 TRYP_PIG	Trypsin OS=Sus scrofa PE=1 SV=1	PIG	13
6	18,16	22,65	41,99999869	28,16999853	25,33000112	sp Q9N5B2 KRT84_HUMAN	Keratin, type II cuticular Hb4 OS=Homo sapiens GN=KRT84 HUMAN	HUMAN	12
9	7,03	21,43	54,3299973	33,61999989	31,70999885	sp P08779 K1C16_HUMAN	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 HUMAN	HUMAN	12
12	4	14,16	23,3099997	20,03999949	18,1099996	sp Q6IG01 K2C18_RAT	Keratin, type II cytoskeletal 1b OS=Rattus norvegicus GN=K RAT	RAT	10
12	0	12,09	16,9599995	16,07999951	14,33999985	sp Q6IFZ6 K2C18_MOUSE	Keratin, type II cytoskeletal 1b OS=Mus musculus GN=Krt77 MOUSE	MOUSE	9
19	2	8,93	29,39999998	18,28999966	16,20000005	sp Q04695 K1C17_HUMAN	Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 HUMAN	HUMAN	6
19	0	7,82	25	13,88999969	11,81000024	sp A5A6M0 K1C17_PANTR	Keratin, type I cytoskeletal 17 OS=Pan troglodytes GN=KRT PANTR	PANTR	5
13	3,84	4,69	21,62999958	11,29999998	8,173000067	sp Q15323 K1H1_HUMAN	Keratin, type I cuticular Ha1 OS=Homo sapiens GN=KRT31 I HUMAN	HUMAN	3
13	0	4,69	21,62999958	11,29999998	8,173000067	sp A5A6M5 K1H1_PANTR	Keratin, type I cuticular Ha1 OS=Pan troglodytes GN=KRT31 PANTR	PANTR	3
13	0	4,07	8,252000064	8,252000064	8,252000064	sp P02534 K1M1_SHEEP	Keratin, type I microfibrillar 48 kDa, component 8C-1 OS=C SHEEP	SHEEP	3
14	3,72	4,92	9,670999646	9,670999646	9,670999646	sp Q43790 KRT86_HUMAN	Keratin, type II cuticular Hb6 OS=Homo sapiens GN=KRT86 HUMAN	HUMAN	3
37	1,72	4,55	14,84999955	7,92099825	7,92099825	sp Q14525 K33B_HUMAN	Keratin, type I cuticular Ha3-II OS=Homo sapiens GN=KRT3 HUMAN	HUMAN	3
10	4,45	4,45	53,61999869	40,58000147	18,11999977	sp P15252 REF_HEVBR	Rubber elongation factor protein OS=Hevea brasiliensis PE HEVBR	HEVBR	2
13	0	3,32	13,00999969	10,19999981	6,887999922	sp Q9D646 KRT34_MOUSE	Keratin, type I cuticular Ha4 OS=Mus musculus GN=Krt34 P MOUSE	MOUSE	2
13	0	2,84	7,142999768	7,142999768	4,241000116	sp Q14532 K1H2_HUMAN	Keratin, type I cuticular Ha2 OS=Homo sapiens GN=KRT32 I HUMAN	HUMAN	2
13	0	2,19	8,41299966	8,41299966	5,288000032	sp Q61765 K1H1_MOUSE	Keratin, type I cuticular Ha1 OS=Mus musculus GN=Krt31 P MOUSE	MOUSE	2
14	0	3,09	5,347000062	5,347000062	5,347000062	sp Q14533 KRT81_HUMAN	Keratin, type II cuticular Hb1 OS=Homo sapiens GN=KRT81 HUMAN	HUMAN	2
14	0	3,09	5,477000028	5,477000028	5,477000028	sp P78385 KRT83_HUMAN	Keratin, type II cuticular Hb3 OS=Homo sapiens GN=KRT83 HUMAN	HUMAN	2
15	3,02	3,02	3,657000139	1,183999982	0,801100023	sp P15924 DESP_HUMAN	Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	HUMAN	2
16	2,93	2,93	22,73000032	12,72999942	12,72999942	sp P81605 DCD_HUMAN	Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	HUMAN	2
20	2	2,64	4,68400009	4,68400009	4,68400009	sp Q6IFX1 K1C24_RAT	Keratin, type I cytoskeletal 24 OS=Rattus norvegicus GN=Krt RAT	RAT	2
20	0	2,64	4,492000118	4,492000118	4,492000118	sp A1L317 K1C24_MOUSE	Keratin, type I cytoskeletal 24 OS=Mus musculus GN=Krt24 MOUSE	MOUSE	2
39	1,57	2,44	7,495000213	4,283000156	4,283000156	sp O76013 KRT36_HUMAN	Keratin, type I cuticular Ha6 OS=Homo sapiens GN=KRT36 I HUMAN	HUMAN	2
39	0	2,44	4,22799997	4,22799997	4,22799997	sp B1AQ75 KRT36_MOUSE	Keratin, type I cuticular Ha6 OS=Mus musculus GN=Krt36 P MOUSE	MOUSE	2
13	0	2,2	10,14999971	6,187999994	2,969999984	sp O76009 KRT38_HUMAN	Keratin, type I cuticular Ha3-I OS=Homo sapiens GN=KRT38 HUMAN	HUMAN	1
13	0	2,2	10,14999971	6,187999994	2,969999984	sp A5A6P3 KRT3A_PANTR	Keratin, type I cuticular Ha3-I OS=Pan troglodytes GN=KRT: PANTR	PANTR	1
13	0	1,31	9,652999789	6,931000023	3,712999821	sp Q8K0Y2 KT33A_MOUSE	Keratin, type I cuticular Ha3-I OS=Mus musculus GN=Krt33 MOUSE	MOUSE	1
15	0	2,23	1,665000059	0,832500029	0,450900011	sp E9Q557 DESP_MOUSE	Desmoplakin OS=Mus musculus GN=Dsp PE=1 SV=1	MOUSE	1
17	2,03	2,03	46,23999894	22,57999927	22,57999927	sp P05109 S10A8_HUMAN	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	HUMAN	1
21	2	2	7,323999703	1,465000026	1,465000026	sp A7ZW21 BGAL_ECOHS	Beta-galactosidase OS=Escherichia coli O9:H4 (strain HS) G ECOHS	ECOHS	1
21	0	2	7,323999703	1,465000026	1,465000026	sp A7ZJ91 BGAL_ECO24	Beta-galactosidase OS=Escherichia coli Q139:H28 (strain E2 ECO24	ECO24	1
21	0	2	6,055000052	1,465000026	1,465000026	sp Q3Z583 BGAL_SHISS	Beta-galactosidase OS=Shigella sonnei (strain S046) GN=la SHISS	SHISS	1
21	0	2	4,58999984	1,465000026	1,465000026	sp P00722 BGAL_ECOLI	Beta-galactosidase OS=Escherichia coli (strain K12) GN=la ECOLI	ECOLI	1
21	0	2	4,58999984	1,465000026	1,465000026	sp B1J0T5 BGAL_ECOLC	Beta-galactosidase OS=Escherichia coli (strain ATCC 8739 / ECOLC	ECOLC	1
21	0	2	3,303999826	1,458000019	1,458000019	sp Q8VNN2 BGAL_ECOLX	Beta-galactosidase OS=Escherichia coli GN=la2c PE=3 SV=1	ECOLX	1
22	2	2	8,668000251	4,22799997	4,22799997	RRRRRsp P08779 K1C16_HUMAN	REVERSED Keratin, type I cytoskeletal 16 OS=Homo sapiens HUMAN	HUMAN	1
23	2	2	0,961900037	0,460099988	0,460099988	sp Q5D862 FILA2_HUMAN	Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	HUMAN	1
24	2	2	28,13000083	19,37000006	19,37000006	sp Q3L177 K134_HUMAN	Keratin-associated protein 13-4 OS=Homo sapiens GN=KRT HUMAN	HUMAN	1
25	2	2	16,43999964	10,96000001	10,96000001	sp P12273 PIP_HUMAN	Prolactin-inducible protein OS=Homo sapiens GN=PIP PE=1 HUMAN	HUMAN	1
25	0	2	10,96000001	10,96000001	10,96000001	sp P60989 PIP_PANTR	Prolactin-inducible protein homolog OS=Pan troglodytes G PANTR	PANTR	1
26	2	2	24,56	11,40000001	11,40000001	sp P06702 S10A9_HUMAN	Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1	HUMAN	1
27	2	2	1,511000004	1,511000004	1,511000004	sp Q9FMA3 PEX5_ARATH	Peroxisome biogenesis protein 5 OS=Arabidopsis thaliana c ARATH	ARATH	1
28	2	2	2,096999995	2,096999995	2,096999995	sp Q2KZ15 DXS_BORA1	1-deoxy-D-xylulose-5-phosphate synthase OS=Bordetella a BORA1	BORA1	1
29	2	2	4,072000086	4,072000086	4,072000086	sp P21883 ODP2_BACSU	Dihydrolipoyllysine-residue acetyltransferase component c BACSU	BACSU	1
30	2	2	5,606999993	5,606999993	5,606999993	sp P02662 CASA1_BOVIN	Alpha-S1-casein OS=Bos taurus GN=CSN151 PE=1 SV=2	BOVIN	1
30	0	2	5,606999993	5,606999993	5,606999993	sp O62823 CASA1_BUBBU	Alpha-S1-casein OS=Bubalus bubalis GN=CSN151 PE=2 SV=	BUBBU	1
31	2	2	7,353000343	7,353000343	7,353000343	sp O82803 SRPP_HEVBR	Small rubber particle protein OS=Hevea brasiliensis GN=SR HEVBR	HEVBR	1
32	2	2	2,199999988	2,199999988	2,199999988	sp O64793 Y1675_ARATH	G-type lectin S-receptor-like serine/threonine-protein kina: ARATH	ARATH	1
33	2	2	1,286000013	1,286000013	1,286000013	sp F1MDL2 INTU_BOVIN	Protein intumed OS=Bos taurus GN=INTU PE=3 SV=2	BOVIN	1
34	2	2	1,28899999	1,28899999	1,28899999	sp AGZP10 SEY1_YEAS7	Protein SEY1 OS=Saccharomyces cerevisiae (strain YJM789) YEAS7	YEAS7	1
35	2	2	0,897500012	0,897500012	0,897500012	sp A1A316 RPOC_BIFAA	DNA-directed RNA polymerase subunit beta' OS=Bifidobact BIFAA	BIFAA	1
36	1,89	2	4,478000104	4,478000104	4,478000104	sp Q5RAB4 G3P_PONAB	Glyceraldehyde-3-phosphate dehydrogenase OS=Pongo ab PONAB	PONAB	1
36	0	2	4,478000104	4,478000104	4,478000104	sp P04406 G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sa: HUMAN	HUMAN	1
38	1,64	1,64	13,30000013	4,14500013	4,14500013	sp Q5T749 KPRP_HUMAN	Keratinocyte proline-rich protein OS=Homo sapiens GN=KP HUMAN	HUMAN	1
40	1,15	1,15	10,86999997	3,415999934	3,415999934	sp P05089 ARG1_HUMAN	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2	HUMAN	1
41	0,99	0,99	1,030999981	1,030999981	1,030999981	sp A4J927 SECA_DESRM	Protein translocase subunit SecA OS=Desulfofotomaculum re DESRM	DESRM	1
42	0,95	0,95	1,683999971	1,683999971	1,683999971	sp Q86Y23 HORN_HUMAN	Hornerin OS=Homo sapiens GN=HRRN PE=1 SV=2	HUMAN	1
43	0,86	0,86	1,882999949	1,882999949	1,882999949	sp Q50339 Y588_MYCPN	Uncharacterized lipoprotein MPN_588 OS=Mycoplasma pn MYCPN	MYCPN	1
45	0,65	0,65	3,398999944	3,398999944	3,398999944	sp ASEKG6 PLSX_BRAS8	Phosphate acyltransferase OS=Bradyrhizobium sp. (strain E BRAS8	BRAS8	1
45	0	0,65	3,398999944	3,398999944	3,398999944	sp A4YW85 PLSX_BRASO	Phosphate acyltransferase OS=Bradyrhizobium sp. (strain C BRASO	BRASO	1
46	0,38	0,38	6,25	6,25	6,25	RRRRRsp Q8PM31 3HAO_XANAC	REVERSED 3-hydroxyanthranilate 3,4-dioxygenase OS=Xant XANAC	XANAC	1
52	0,11	0,11	1,765999943	1,765999943	1,765999943	sp P21910 LAML2_XENLA	Lamin-L(II) OS=Xenopus laevis PE=2 SV=1	XENLA	0
44	0,77	0,77	14,22999948	4,966000095	0	sp Q8WNW3 PLAK_PIG	Junction plakoglobin OS=Sus scrofa GN=Jup PE=2 SV=1	PIG	0
44	0	0,77	14,22999948	4,966000095	0	sp Q8SPJ1 PLAK_BOVIN	Junction plakoglobin OS=Bos taurus GN=JUP PE=2 SV=1	BOVIN	0
44	0	0,77	14,22999948	4,966000095	0	sp Q02257 PLAK_MOUSE	Junction plakoglobin OS=Mus musculus GN=Jup PE=1 SV=3	MOUSE	0
44	0	0,77	14,22999948	4,966000095	0	sp P14923 PLAK_HUMAN	Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	HUMAN	0
47	0,36	0,36	2,563999966	2,563999966	0	sp Q67N85 TDH_SYMTH	L-threonine 3-dehydrogenase OS=Symbiobacterium therm SYMTH	SYMTH	0
48	0,2	0,2	1,522000041	1,522000041	0	sp P42357 HUTH_HUMAN	Histidine ammonia-lyase OS=Homo sapiens GN=HAL PE=1 HUMAN	HUMAN	0
48	0	0,2	1,522000041	1,522000041	0	sp P35492 HUTH_MOUSE	Histidine ammonia-lyase OS=Mus musculus GN=Hal PE=1 S MOUSE	MOUSE	0
48	0	0,2	1,522000041	1,522000041	0	sp P21213 HUTH_RAT	Histidine ammonia-lyase OS=Rattus norvegicus GN=Hal PE: RAT	RAT	0
49	0,18	0,18	1,049000025	1,049000025	0	RRRRRsp P48479 NIM1_NEUCR	REVERSED G2-specific protein kinase nim-1 OS=Neurospor: NEUCR	NEUCR	0
50	0,17	0,17	30,61000109	12,24000007	0	sp P01040 CYTA_HUMAN	Cystatin-A OS=Homo sapiens GN=CSTA PE=1 SV=1	HUMAN	0
51	0,13	0,13	1,532999985	1,532999985	0	sp P13894 LT_BFPVY	Large T antigen OS=Budgerigar fledgling disease virus PE=3 BFPVY	BFPVY	0
53	0,06	0,06	10,19999981	1,716000028	0	sp Q02413 DSG1_HUMAN	Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	HUMAN	0
54	0,06	0,06	3,599999845	3,599999845	0	sp Q22328 AGL8_SOLCO	Agamou-like MADS-box protein AGL8 homolog OS=Solana: SOLCO	SOLCO	0
55	0,05	0,05	2,452000044	2,452000044	0	RRRRRsp Q81M67 BUK_BACAN	REVERSED Probable butyrate kinase OS=Bacillus anthracis (str BACAN	BACAN	0
55	0	0,05	2,452000044	2,452000044	0	RRRRRsp Q818T1 BUK_BACCR	REVERSED Probable butyrate kinase OS=Bacillus cereus (str BACCR	BACCR	0
55	0	0,05	2,452000044	2,452000044	0	RRRRRsp Q731D0 BUK_BACC1	REVERSED Probable butyrate kinase OS=Bacillus cereus (str BACC1	BACC1	0
55	0	0,05	2,452000044	2,452000044	0	RRRRRsp Q6HE00 BUK_BACHK	REVERSED Probable butyrate kinase OS=Bacillus thuringiens BACHK	BACHK	0
55	0	0,05	2,452000044	2,452000044	0	RRRRRsp Q635C1 BUK_BACCZ	REVERSED Probable butyrate kinase OS=Bacillus cereus (str BACCZ	BACCZ	0
55	0	0,05	2,452000044	2,452000044	0	RRRRRsp C3P7U3 BUK_BACAA	REVERSED Probable butyrate kinase OS=Bacillus anthracis (BACAA	BACAA	0
55	0	0,05	2,452000044	2,452000044	0	RRRRRsp C3JL78 BUK_BACAC	REVERSED Probable butyrate kinase OS=Bacillus anthracis (BACAC	BACAC	0
55	0	0,05	2,452000044	2,452000044	0	RRRRRsp C1ERN7 BUK_BACC3	REVERSED Probable butyrate kinase OS=Bacillus cereus (str BACC3	BACC3	

N	Ctrl_CSVII_1	Total	%Cov	%Cov(50)	%Cov(95)	Accession	Name	Species	Peptides(95%)
1	89,54	89,54	71,11999989	69,88000274	66,46000147	sp P04264 K2C1_HUMAN	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE= HUMAN	67	
2	71,35	71,35	58,73000026	57,19000011	54,44999933	sp P13645 K1C10_HUMAN	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PI HUMAN	58	
3	55,57	62,35	80,27999997	63,38000298	56,33999705	sp P35908 K2E2_HUMAN	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapiens GN=HUMAN	38	
4	43,8	44,07	72,86999822	68,22000146	57,13999867	sp P35527 K1C9_HUMAN	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT9 PE= HUMAN	30	
6	21,23	21,23	48,91999996	48,91999996	39,82999921	sp P00761 TRYP_PIG	Trypsin OS=Sus scrofa PE=1 SV=1	21	
7	17,48	28,77	49,11000133	40,95999897	30,84999919	sp P02538 K2C6A_HUMAN	Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=KRT6A F HUMAN	16	
5	24,87	27,33	56,56999946	43,22000146	36,23000085	sp P02533 K1C14_HUMAN	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KRT14 PI HUMAN	15	
7	0,01	26,8	46,81000113	41,31000042	29,08000052	sp P48668 K2C6C_HUMAN	Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=KRT6C P HUMAN	15	
12	4,52	21,77	46,09000087	34,67000127	25,15999973	sp P08779 K1C16_HUMAN	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KRT16 PI HUMAN	11	
13	4,18	19,79	39,66000008	25,42000115	16,26999974	sp P13647 K2C5_HUMAN	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KRT5 PE= HUMAN	10	
21	0	9,23	11,89000001	11,89000001	11,36000007	sp Q6IFZ6 K2C1B_MOUSE	Keratin, type II cytoskeletal 1b OS=Mus musculus GN=Krt17 PI MOUSE	10	
21	0	7,97	15,41000009	13,09999973	12,52000034	sp Q6IG01 K2C1B_RAT	Keratin, type II cytoskeletal 1b OS=Rattus norvegicus GN=Krt7 RAT	10	
13	0	17,79	36,98999882	22,80000001	13,6800006	sp A5A6M8 K2C5_PANTR	Keratin, type II cytoskeletal 5 OS=Pan troglodytes GN=KRT5 PE PANTR	9	
16	4	11,21	26,15999987	17,722000033	13,88999969	sp Q04695 K1C17_HUMAN	Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KRT17 PI HUMAN	6	
16	0	11,21	24,31000024	15,51000029	13,88999969	sp A5A6M0 K1C17_PANTR	Keratin, type I cytoskeletal 17 OS=Pan troglodytes GN=KRT17 PANTR	6	
8	10,34	10,34	71,00999951	69,56999898	55,07000089	sp P15252 REF_HEVBR	Rubber elongation factor protein OS=Hevea brasiliensis PE=1 ! HEVBR	5	
9	10	10	70,96999884	70,96999884	sp P05109 S10A8_HUMAN	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV=1	HUMAN	5	
10	7,8	7,8	37,72000074	37,72000074	37,72000074	sp P06702 S10A9_HUMAN	Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV=1	HUMAN	5
16	0	9,19	20,09000033	13,62999976	9,46900025	sp Q9QWL7 K1C17_MOUSE	Keratin, type I cytoskeletal 17 OS=Mus musculus GN=Krt17 PE MOUSE	5	
16	0	9,19	20,09000033	13,62999976	9,46900025	sp Q6IFU8 K1C17_RAT	Keratin, type I cytoskeletal 17 OS=Rattus norvegicus GN=Krt17 RAT	5	
16	0	9,04	25,61999857	14,66999948	10,94999984	sp Q61781 K1C14_MOUSE	Keratin, type I cytoskeletal 14 OS=Mus musculus GN=Krt14 PE MOUSE	5	
21	2,17	6,69	16,77999943	11,06999964	7,43900016	sp Q7Z794 K2C1B_HUMAN	Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=KRT77 P HUMAN	5	
11	5,68	5,68	12,38999963	7,722000033	6,00599818	sp Q02413 DSG1_HUMAN	Desmoglein-1 OS=Homo sapiens GN=DSG1 PE=1 SV=2	HUMAN	5
16	0	5,03	10,50999984	8,276999742	6,711000204	sp Q6IFV3 K1C15_RAT	Keratin, type I cytoskeletal 15 OS=Rattus norvegicus GN=Krt15 RAT	3	
17	3,65	3,65	56,36000037	56,36000037	56,36000037	sp P81605 DCD_HUMAN	Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	HUMAN	3
25	2,01	4,61	16,92000051	5,000000075	4,61499989	sp K8N1N4 K2C78_HUMAN	Keratin, type II cytoskeletal 78 OS=Homo sapiens GN=KRT78 P HUMAN	3	
14	4,17	4,18	17,44000018	6,735999882	5,699000135	sp Q5T749 KPRP_HUMAN	Keratinocyte proline-rich protein OS=Homo sapiens GN=KPRP HUMAN	2	
15	4,05	4,05	9,030999988	3,119999915	3,119999915	sp Q5NVH5 ALBU_PONAB	Serum albumin OS=Pongo abelii GN=ALB PE=2 SV=2	PONAB	2
13	0	9,05	9,030999988	3,119999915	3,119999915	sp P02768 ALBU_HUMAN	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	HUMAN	2
15	0	4,02	7,666999847	3,16700004	3,16700004	sp Q28522 ALBU_MACMU	Serum albumin (Fragment) OS=Macaca mulatta GN=ALB PE=2 MACMU	2	
15	0	4,02	7,565999776	3,125	3,125	sp A2V924 ALBU_MACFA	Serum albumin OS=Macaca fascicularis GN=ALB PE=2 SV=1	MACFA	2
18	3,45	3,45	38,35999966	17,81000048	17,81000048	sp P12313 PIP_HUMAN	Prolactin-inducible protein OS=Homo sapiens GN=PIP PE=1 SV HUMAN	2	
19	2,86	2,86	12,83999979	12,83999979	8,657000214	sp Q5RAB4 G3P_PONAB	Glyceraldehyde-3-phosphate dehydrogenase OS=Pongo abelii PONAB	2	
19	0	2,86	12,83999979	12,83999979	8,657000214	sp P04406 G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo sapien HUMAN	2	
31	1,83	1,86	8,07199997	5,601000041	5,601000041	sp P02769 ALBU_BOVIN	Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	BOVIN	2
18	0	2	23,28999937	10,96000001	10,96000001	sp P60989 PIP_PANTR	Prolactin-inducible protein homolog OS=Pan troglodytes GN=f PANTR	1	
20	2,6	2,6	19,05000061	19,05000061	10,11999995	sp P17314 IAAC3_WHEAT	Alpha-amylase/trypsin inhibitor CM3 OS=Triticum aestivum PE WHEAT	1	
22	2,17	2,17	14,4600004	9,091000259	3,719000146	sp P31944 CASPE_HUMAN	Caspase-14 OS=Homo sapiens GN=CASP14 PE=1 SV=2	HUMAN	1
23	2,05	2,05	32,78999925	20,98000005	20,98000005	sp Q8MKD1 UBB_HORSE	Polyubiquitin-B OS=Equus caballus GN=UBB PE=2 SV=3	HORSE	1
23	0	2,05	32,89000094	21,05000019	21,05000019	sp Q865C5 UBIQ_CAMDR	Ubiquitin OS=Camelus dromedarius PE=3 SV=2	CAMDR	1
23	0	2,05	30,86000085	19,75000054	sp Q63429 UBC_RAT	Polyubiquitin-C OS=Rattus norvegicus GN=Ubc PE=1 SV=1	RAT	1	
23	0	2,05	39,68000114	25,40000081	25,40000081	sp P84589 UBIQ_LUMTE	Ubiquitin (Fragment) OS=Lumbricus terrestris PE=1 SV=2	LUMTE	1
23	0	2,05	16,03000015	10,26000008	10,26000008	sp P79781 RS27A_CHICK	Ubiquitin-40S ribosomal protein S27a OS=Gallus gallus GN=RP CHICK	1	
23	0	2,05	19,52999979	12,5	12,5	sp P68205 RL40_OPHHA	Ubiquitin-60S ribosomal protein L40 OS=Ophiophagus hannah OPHHA	1	
23	0	2,05	16,03000015	10,26000008	10,26000008	sp P68203 RS27A_SPOFR	Ubiquitin-40S ribosomal protein S27a OS=Spodoptera frugiper SPOFR	1	
23	0	2,05	16,13000035	10,32000035	10,32000035	sp P68202 RS27A_PLUXY	Ubiquitin-40S ribosomal protein S27a OS=Plutella xylostella PE LUXY	1	
23	0	2,05	16,03000015	10,26000008	10,26000008	sp P68200 RS27A_ICTPU	Ubiquitin-40S ribosomal protein S27a OS=Ictalurus punctatus ICTPU	1	
23	0	2,05	32,89000094	21,05000019	21,05000019	sp P68197 UBIQ_CERCA	Ubiquitin OS=Ceratitidis capitata PE=1 SV=1	CERCA	1
23	0	2,05	19,52999979	12,5	12,5	sp P63053 RL40_PIG	Ubiquitin-60S ribosomal protein L40 OS=Sus scrofa GN=UBA5; PIG	1	
23	0	2,05	19,52999979	12,5	12,5	sp P63052 RL40_FELCA	Ubiquitin-60S ribosomal protein L40 OS=Felis catus GN=UBA5; FELCA	1	
23	0	2,05	19,52999979	12,5	12,5	sp P63050 RL40_CANLF	Ubiquitin-60S ribosomal protein L40 OS=Canis lupus familiaris CANLF	1	
23	0	2,05	19,52999979	12,5	12,5	sp P63048 RL40_BOVIN	Ubiquitin-60S ribosomal protein L40 OS=Bos taurus GN=UBA5 BOVIN	1	
23	0	2,05	16,03000015	10,26000008	10,26000008	sp P62992 RS27A_BOVIN	Ubiquitin-40S ribosomal protein S27a OS=Bos taurus GN=RP5; BOVIN	1	
23	0	2,05	19,52999979	12,5	12,5	sp P62987 RL40_HUMAN	Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens GN=Uf HUMAN	1	
23	0	2,05	19,52999979	12,5	12,5	sp P62986 RL40_RAT	Ubiquitin-60S ribosomal protein L40 OS=Rattus norvegicus GN RAT	1	
23	0	2,05	19,52999979	12,5	12,5	sp P62984 RL40_MOUSE	Ubiquitin-60S ribosomal protein L40 OS=Mus musculus GN=Uf MOUSE	1	
23	0	2,05	16,03000015	10,26000008	10,26000008	sp P62983 RS27A_MOUSE	Ubiquitin-40S ribosomal protein S27a OS=Mus musculus GN=f MOUSE	1	
23	0	2,05	16,03000015	10,26000008	10,26000008	sp P62982 RS27A_RAT	Ubiquitin-40S ribosomal protein S27a OS=Rattus norvegicus G RAT	1	
23	0	2,05	16,03000015	10,26000008	10,26000008	sp P62979 RS27A_HUMAN	Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens GN=f HUMAN	1	
23	0	2,05	16,03000015	10,26000008	10,26000008	sp P62978 RS27A_CAVPO	Ubiquitin-40S ribosomal protein S27a OS=Cavia porcellus GN= CAVPO	1	
23	0	2,05	30,39999902	19,44999993	sp P62976 UBIQP_CRIGR	Polyubiquitin OS=Cricetulus griseus PE=2 SV=2	CRIGR	1	
23	0	2,05	32,89000094	21,05000019	sp P62975 UBIQ_RABIT	Ubiquitin OS=Oryctolagus cuniculus PE=1 SV=1	RABIT	1	
23	0	2,05	35,33000052	19,15999949	sp P62972 UBIQP_XENLA	Polyubiquitin (Fragment) OS=Xenopus laevis PE=1 SV=2	XENLA	1	
23	0	2,05	16,13000035	10,32000035	sp P29504 RS27A_MANSE	Ubiquitin-40S ribosomal protein S27a OS=Manduca sexta PE= MANSE	1		
23	0	2,05	19,52999979	12,5	12,5	sp P18101 RL40_DROME	Ubiquitin-60S ribosomal protein L40 OS=Drosophila melanog DROME	1	
23	0	2,05	16,03000015	10,26000008	10,26000008	sp P15357 RS27A_DROME	Ubiquitin-40S ribosomal protein S27a OS=Drosophila melanog DROME	1	
23	0	2,05	32,60999918	20,87000012	sp P0CH28 UBC_BOVIN	Polyubiquitin-C OS=Bos taurus GN=UBC PE=1 SV=1	BOVIN	1	
23	0	2,05	32,76999981	20,97000033	sp P0CG69 UBIQP_DROME	Polyubiquitin OS=Drosophila melanogaster GN=Ubi-p63E PE= DROME	1		
23	0	2,05	32,82999992	21,00999951	sp P0CG68 UBC_PIG	Polyubiquitin-C OS=Sus scrofa GN=UBC PE=2 SV=1	PIG	1	
23	0	2,05	32,749999857	20,96000016	sp P0CG67 UBB_GORGO	Polyubiquitin-B OS=Gorilla gorilla gorilla GN=UBB PE=3 SV=1	GORGO	1	
23	0	2,05	32,83999986	21,01999968	sp P0CG66 UBC_GORGO	Polyubiquitin-C OS=Gorilla gorilla gorilla GN=UBC PE=3 SV=1	GORGO	1	
23	0	2,05	32,749999857	20,96000016	sp P0CG65 UBB_PANTR	Polyubiquitin-B OS=Pan troglodytes GN=UBB PE=3 SV=1	PANTR	1	
23	0	2,05	32,85000026	21,01999968	sp P0CG64 UBC_PANTR	Polyubiquitin-C OS=Pan troglodytes GN=UBC PE=3 SV=1	PANTR	1	
23	0	2,05	32,78999925	20,98000005	sp P0CG62 UBB_CHICK	Polyubiquitin-B OS=Gallus gallus GN=UBB PE=2 SV=1	CHICK	1	
23	0	2,05	32,85000026	21,01999968	sp P0CG61 UBC_PONPY	Polyubiquitin-C OS=Pongo pygmaeus GN=UBC PE=3 SV=1	PONPY	1	
23	0	2,05	32,749999857	20,96000016	sp P0CG60 UBB_PONPY	Polyubiquitin-B OS=Pongo pygmaeus GN=UBB PE=3 SV=1	PONPY	1	
23	0	2,05	32,78999925	20,98000005	sp P0CG55 UBB_SHEEP	Polyubiquitin-B OS=Ovis aries GN=UBB PE=2 SV=1	SHEEP	1	
23	0	2,05	32,15000033	20,57999969	sp P0CG54 UBB_CAVPO	Polyubiquitin-B OS=Cavia porcellus GN=UBB PE=2 SV=1	CAVPO	1	
23	0	2,05	32,78999925	20,98000005	sp P0CG53 UBB_BOVIN	Polyubiquitin-B OS=Bos taurus GN=UBB PE=1 SV=1	BOVIN	1	
23	0	2,05	32,78999925	20,98000005	sp P0CG51 UBB_RAT	Polyubiquitin-B OS=Rattus norvegicus GN=Ubb PE=1 SV=1	RAT	1	
23	0	2,05	30,64999878	19,61999983	sp P0CG50 UBC_MOUSE	Polyubiquitin-C OS=Mus musculus GN=Ubc PE=1 SV=2	MOUSE	1	
23	0	2,05	32,78999925	20,98000005	sp P0CG49 UBB_MOUSE	Polyubiquitin-B OS=Mus musculus GN=Ubb PE=2 SV=1	MOUSE	1	
23	0	2,05	32,85000026	21,01999968	sp P0CG48 UBC_HUMAN	Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=3	HUMAN	1	
23	0	2,05	32,749999857	20,96000016	sp P0CG47 UBB_HUMAN	Polyubiquitin-B OS=Homo sapiens GN=UBB PE=1 SV=1	HUMAN	1	
23	0	2,05	19,52999979	12,5	12,5	sp P0C276 RL40_SHEEP	Ubiquitin-60S ribosomal protein L40 OS=Ovis aries GN=UBA52 SHEEP	1	
23	0	2,05	19,52999979	12,5	12,5	sp P0C275 RL40_PONPY	Ubiquitin-60S ribosomal protein L40 OS=Pongo pygmaeus GN=PNPY	1	
23	0	2,05	19,52999979	12,5	12,5	sp P0C273 RL40_MACFA	Ubiquitin-60S ribosomal protein L40 OS=Macaca fascicularis G MACFA	1	
24	2,02	2,02	11,99999973	4,267000034	4,267000034	sp Q9Y707 ACT2_SUIBO	Actin-2 OS=Suillus bovinus GN=ACT2 PE=2 SV=1	SUIBO	1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp Q9Y702 ACT1_SCHCO	Actin-1 OS=Schizophyllum commune GN=ACT1 PE=2 SV=1	SCHCO	1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp Q9UUVX4 ACT_COPC7	Actin OS=Coprinosopsis cinerea (strain Okayama-7 / 130 / ATCC COPC7	1	
24	0	2,02	11,96999997	4,255000129	sp Q964E3 ACTC_BIOAL	Actin, cytoplasmic OS=Biophalaria alexandrina PE=3 SV=1	BIOAL	1	
24	0	2,02	11,96999997	4,255000129	sp Q964E2 ACTC_BIOFP	Actin, cytoplasmic OS=Biophalaria pfeifferi PE=3 SV=1	BIOFP	1	
24	0	2,02	11,96999997	4,255000129	sp Q964E1 ACTC_BIOOB	Actin, cytoplasmic OS=Biophalaria obstructa PE=3 SV=1	BIOOB	1	
24	0	2,02	11,96999997	4,255000129	sp Q964E0 ACTC_BIOTE	Actin, cytoplasmic OS=Biophalaria tenagophila PE=3 SV=1	BIOTE	1	
24	0	2,02	11,96999997	4,255000129	sp Q964D9 ACTC_PLATR	Actin, cytoplasmic OS=Planorbella trivolvis PE=3 SV=1	PLATR	1	
24	0	2,02	11,99999973	4,267000034	sp Q93131 ACTC_BRAFL	Actin, cytoplasmic OS=Branchiostoma floridae PE=2 SV=1	BRAFL	1	
24	0	2,02	11,99999973	4,267000034	sp Q93129 ACTC_BRABE	Actin, cytoplasmic OS=Branchiostoma belcheri PE=2 SV=1	BRABE	1	
24	0	2,02	11,99999973	4,267000034	sp Q912K5 ACTB_SIGHI	Actin, cytoplasmic 1 OS=Sigmodon hispidus GN=ACTB PE=2 SV SIGHI	1	1	
24	0	2,02	11,99999973	4,267000034	sp Q8JJ88 ACTG_TRISC	Actin, cytoplasmic 2 OS=Triakis scyllium GN=actg1 PE=2 SV=1	TRISC	1	
24	0	2,02	11,99999973	4,2					

24	0	2,02	11,99999973	4,267000034	4,267000034	sp Q7ZVF9 ACTB2_DANRE	Actin, cytoplasmic 2 OS=Danio rerio GN=actb2 PE=2 SV=2	DANRE	1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp Q76N69 ACTB_CHLAE	Actin, cytoplasmic 1 OS=Chlorocebus aethiops GN=ACTB PE=2 CHLAE		1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp Q71FK5 ACTB_CAVPO	Actin, cytoplasmic 1 OS=Cavia porcellus GN=ACTB PE=2 SV=1	CAVPO	1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp Q711N9 ACTB_MESAU	Actin, cytoplasmic 1 OS=Mesocricetus auratus GN=ACTB PE=1 MESAU		1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp Q6QAQ1 ACTB_PIG	Actin, cytoplasmic 1 OS=Sus scrofa GN=ACTB PE=1 SV=2	PIG	1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp Q6P378 ACTB_XENTR	Actin, cytoplasmic 2 OS=Xenopus tropicalis GN=actg1 PE=2 SV XENTR		1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp Q6NVA9 ACTB_XENTR	Actin, cytoplasmic 1 OS=Xenopus tropicalis GN=actb PE=2 SV= XENTR		1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp Q5ZMQ2 ACTG_CHICK	Actin, cytoplasmic 2 OS=Gallus gallus GN=ACTG1 PE=1 SV=1	CHICK	1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp Q5R6G0 ACTB_PONAB	Actin, cytoplasmic 1 OS=Pongo abelii GN=ACTB PE=2 SV=1	PONAB	1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp Q5R1X3 ACTB_PANTR	Actin, cytoplasmic 1 OS=Pan troglodytes GN=ACTB PE=2 SV=1	PANTR	1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp Q5JAK2 ACTG_PELLE	Actin, cytoplasmic 2 OS=Pelophylax lessonae GN=actg1 PE=2 S PELLE		1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp Q553U6 ACT2_DICDI	Putative actin-22 OS=Dictyostelium discoideum GN=act22 PE=2 DICDI		1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp Q54GX7 ACT10_DICDI	Actin-10 OS=Dictyostelium discoideum GN=act10 PE=1 SV=1	DICDI	1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp Q4R561 ACTB_MACFA	Actin, cytoplasmic 1 OS=Macaca fascicularis GN=ACTB PE=2 SV MACFA		1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp Q4LOY2 ACTB_SPECI	Actin, cytoplasmic 1 OS=Spermophilus citellus GN=ACTB PE=2 SPECI		1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp Q26065 ACT_PLAMG	Actin, adductor muscle OS=Placopecten magellanicus PE=2 SV PLAMG		1
24	0	2,02	11,90000027	4,233000055	4,233000055	sp Q25472 ACT2_MOLOC	Actin, muscle-type OS=Molgula oculata PE=3 SV=1	MOLOC	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp Q25010 ACT3A_HELAM	Actin, cytoplasmic A3a OS=Helicoverpa armigera GN=actA3a P HELAM		1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp Q07903 ACTC_STRPU	Actin, cytoskeletal 2A OS=Strongylocentrotus purpuratus GN= STRPU		1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp Q00215 ACTC_STYPL	Actin, cytoplasmic OS=Styela plicata PE=3 SV=1	STYPL	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P92182 ACT1_LUMTE	Actin-1 OS=Lumbricus terrestris GN=ACT1 PE=2 SV=1	LUMTE	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P92179 ACTC_BIOGL	Actin, cytoplasmic OS=Biophphalaria glabrata PE=2 SV=2	BIOGL	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P92176 ACT2_LUMTE	Actin-2 OS=Lumbricus terrestris GN=ACT2 PE=2 SV=1	LUMTE	1
24	0	2,02	12,09999993	4,301000014	4,301000014	sp P91754 ACT_LUMRU	Actin (Fragment) OS=Lumbricus rubellus PE=2 SV=1	LUMRU	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P90689 ACT_BRUMA	Actin OS=Brugia malayi PE=1 SV=1	BRUMA	1
24	0	2,02	12,47000024	4,431999847	4,431999847	sp P84856 ACTB_CHLPG	Actin, cytoplasmic 1 OS=Chlorocebus pygerythrus GN=ACTB PI CHLPG		1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp P84336 ACTB_CAMDR	Actin, cytoplasmic 1 OS=Camelus dromedarius GN=ACTB P=1 CAMDR		1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P84185 ACT5C_ANOGA	Actin-5C OS=Anopheles gambiae GN=Act5C PE=2 SV=1	ANOGA	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P84184 ACT3B_HELAM	Actin-A3b, cytoplasmic OS=Helicoverpa armigera GN=actA3b I HELAM		1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P84183 ACTB_BOMMO	Actin, cytoplasmic A4 OS=Bombyx mori GN=A4 PE=2 SV=1	BOMMO	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P83969 ACT1_BACDO	Actin, indirect flight muscle OS=Bactrocera dorsalis PE=3 SV=1	BACDO	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P83968 ACT6_DROSI	Actin, indirect flight muscle OS=Drosophila simulans GN=Act8 DROSI		1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P83967 ACT6_DROME	Actin, indirect flight muscle OS=Drosophila melanogaster GN= DROME		1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp P83751 ACTB_CTEID	Actin, cytoplasmic 1 OS=Ctenopharyngodon idella GN=actb PE CTEID		1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp P83750 ACTB_CYPCA	Actin, cytoplasmic 1 OS=Cyprinus carpio GN=actb PE=3 SV=1	CYPCA	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P69005 ACTC_STRPU	Actin, cytoskeletal 2B OS=Strongylocentrotus purpuratus GN= STRPU		1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P69004 ACT2_STRFN	Actin-15B OS=Strongylocentrotus franciscanus PE=2 SV=1	STRFN	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P69003 ACT1_HELTB	Actin Cyl, cytoplasmic OS=Heliocidaris tuberculata PE=3 SV=1	HELTB	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P69002 ACT1_HELER	Actin Cyl, cytoplasmic OS=Heliocidaris erythrogramma PE=3 S HELER		1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P68556 ACT1_DIPDE	Actin-1/4 OS=Diphyllbothrium dendriticum GN=ACT1 PE=2 S DIPDE		1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P68555 ACT_TAESO	Actin OS=Taenia solium GN=ACT1 PE=3 SV=1	TAESO	1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp P68143 ACTB_OREMO	Actin, cytoplasmic 1 OS=Oreochromis mossambicus GN=actb I OREMO		1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp P68142 ACTB1_TAKRU	Actin, cytoplasmic 1 OS=Takifugu rubripes GN=actba PE=2 SV= TAKRU		1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp P63261 ACTG_HUMAN	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1 SV=1	HUMAN	1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp P63260 ACTG_MOUSE	Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1 SV=1	MOUSE	1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp P63259 ACTG_RAT	Actin, cytoplasmic 2 OS=Rattus norvegicus GN=Actg1 PE=1 SV= RAT		1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp P63258 ACTG_BOVIN	Actin, cytoplasmic 2 OS=Bos taurus GN=ACTG1 PE=1 SV=1	BOVIN	1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp P63257 ACTG_TRIVU	Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACTG1 PE= TRIVU		1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp P63256 ACTG_ANSAN	Actin, cytoplasmic 2 OS=Anser anser anser GN=ACTG1 PE=2 S ANSAN		1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp P60713 ACTB_SHEEP	Actin, cytoplasmic 1 OS=Ovis aries GN=ACTB PE=2 SV=1	SHEEP	1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp P60712 ACTB_BOVIN	Actin, cytoplasmic 1 OS=Bos taurus GN=ACTB PE=1 SV=1	BOVIN	1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp P60711 ACTB_RAT	Actin, cytoplasmic 1 OS=Rattus norvegicus GN=Actb PE=1 SV= RAT		1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp P60710 ACTB_MOUSE	Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 SV=1	MOUSE	1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp P60709 ACTB_HUMAN	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 SV=1	HUMAN	1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp P60708 ACTB_HORSE	Actin, cytoplasmic 1 OS=Equus caballus GN=ACTB PE=2 SV=1	HORSE	1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp P60707 ACTB_TRIVU	Actin, cytoplasmic 1 OS=Trichosurus vulpecula GN=ACTB PE=2 TRIVU		1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp P60706 ACTB_CHICK	Actin, cytoplasmic 1 OS=Gallus gallus GN=ACTB PE=1 SV=1	CHICK	1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp P53689 ACT_PHARH	Actin OS=Phaffia rhodozyma PE=3 SV=1	PHARH	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P53506 ACT8_XENLA	Actin, cytoplasmic type 8 OS=Xenopus laevis PE=3 SV=1	XENLA	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P53505 ACT5_XENLA	Actin, cytoplasmic type 5 OS=Xenopus laevis PE=3 SV=1	XENLA	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P53501 ACT3_DROME	Actin-57B OS=Drosophila melanogaster GN=Act57B PE=1 SV= DROME		1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp P53486 ACTB3_TAKRU	Actin, cytoplasmic 3 OS=Takifugu rubripes GN=actcb PE=2 SV= TAKRU		1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp P53485 ACTB3_TAKRU	Actin, cytoplasmic 2 OS=Takifugu rubripes GN=actcb PE=3 SV= TAKRU		1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P53478 ACT5_CHICK	Actin, cytoplasmic type 5 OS=Gallus gallus PE=3 SV=1	CHICK	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P53474 ACTE_STRPU	Actin, cytoskeletal 3A OS=Strongylocentrotus purpuratus GN= STRPU		1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P53473 ACTB_STRPU	Actin, cytoskeletal 1B OS=Strongylocentrotus purpuratus GN= STRPU		1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P53472 ACTA_STRPU	Actin, cytoskeletal 1A OS=Strongylocentrotus purpuratus GN= STRPU		1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P53471 ACT2_SCHMA	Actin-2 OS=Schistosoma mansoni PE=2 SV=1	SCHMA	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P53470 ACT1_SCHMA	Actin-1 OS=Schistosoma mansoni PE=2 SV=1	SCHMA	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P53466 ACT2_LYTPI	Actin, cytoskeletal 2 OS=Lytechinus pictus PE=2 SV=1	LYTPI	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P53465 ACT1_LYTPI	Actin, cytoskeletal 1 OS=Lytechinus pictus PE=2 SV=1	LYTPI	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P53464 ACTM_HELTB	Actin, cytoskeletal OS=Heliocidaris tuberculata PE=3 SV=1	HELTB	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P53463 ACTM_HELER	Actin, cytoskeletal OS=Heliocidaris erythrogramma PE=3 SV=1	HELER	1
24	0	2,02	12,12999997	4,312999919	4,312999919	sp P53458 ACT5_DIPDE	Actin-5 (Fragment) OS=Diphyllbothrium dendriticum GN=AC DIPDE		1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P53456 ACT2_DIPDE	Actin-2 OS=Diphyllbothrium dendriticum GN=ACT2 PE=2 SV= DIPDE		1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P49871 ACT_MANSE	Actin, muscle OS=Manduca sexta PE=2 SV=1	MANSE	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P49128 ACT1_AEDAE	Actin-1 OS=Aedes aegypti GN=ACT-1 PE=2 SV=2	AEDAE	1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp P48975 ACTB_CRIGR	Actin, cytoplasmic 1 OS=Cricetulus griseus GN=ACTB PE=3 SV= CRIGR		1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp P48465 ACT_CRYNH	Actin OS=Cryptococcus neoformans var. grubii serotype A (str. CRYNH		1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P45887 ACT5_BACDO	Actin-5, muscle-specific OS=Bactrocera dorsalis PE=2 SV=1	BACDO	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P45886 ACT3_BACDO	Actin-3, muscle-specific OS=Bactrocera dorsalis PE=2 SV=1	BACDO	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P45885 ACT2_BACDO	Actin-2, muscle-specific OS=Bactrocera dorsalis PE=2 SV=1	BACDO	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P41341 ACTY_LIMPO	Actin-11 OS=Limulus polyphemus PE=2 SV=1	LIMPO	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P41340 ACT3_LIMPO	Actin-3 OS=Limulus polyphemus PE=1 SV=1	LIMPO	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P41339 ACTA_LIMPO	Actin, acrosomal process isoform OS=Limulus polyphemus PE= LIMPO		1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P41113 ACT3_PODCA	Actin-3 OS=Podocoryna carnea GN=ACT3 PE=3 SV=1	PODCA	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P41112 ACT1_PODCA	Actin-1/2 OS=Podocoryna carnea GN=ACTIA PE=2 SV=1	PODCA	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P18603 ACT4_ARTSX	Actin, clone 403 OS=Artemia sp. PE=2 SV=1	ARTSX	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P18499 ACTF_STRPU	Actin, cytoskeletal 3B OS=Strongylocentrotus purpuratus GN= STRPU		1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P17126 ACT_HYDVU	Actin, non-muscle 6.2 OS=Hydra vulgaris PE=3 SV=1	HYDVU	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P15475 ACTB_XENBO	Actin, cytoplasmic 1 OS=Xenopus borealis GN=actb PE=3 SV=1	XENBO	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P12717 ACTM_PISOC	Actin, muscle OS= Pisaster ochraceus PE=3 SV=1	PISOC	1
24	0	2,02	11,96999997						

24	0	2,02	11,99999973	4,267000034	4,267000034	sp P02578 ACT1_ACACA	Actin-1 OS=Acanthamoeba castellanii PE=1 SV=1	ACACA	1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P02576 ACTA_PHYPO	Actin, plasmodial isoform OS=Phyarsum polycephalum GN=AR PHYPO		1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P02574 ACT2_DROME	Actin, larval muscle OS=Drosophila melanogaster GN=Act79B DROME		1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp P02572 ACT2_DROME	Actin-42A OS=Drosophila melanogaster GN=Act42A PE=1 SV=1 DROME		1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp O93400 ACTB_XENLA	Actin, cytoplasmic 1 OS=Xenopus laevis GN=actb PE=2 SV=1 XENLA		1
24	0	2,02	11,94000021	4,244000092	4,244000092	sp O65316 ACT2_MESVI	Actin OS=Mesostigma viride PE=3 SV=1 MESVI		1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp O42161 ACTB_SALSA	Actin, cytoplasmic 1 OS=Salmo salar GN=actb PE=2 SV=1 SALSA		1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp O18840 ACTB_CANLF	Actin, cytoplasmic 1 OS=Canis lupus familiaris GN=ACTB PE=2 CANLF		1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp O18500 ACT2_SACKO	Actin-2 OS=Saccoglossus kowalevskii PE=2 SV=1 SACKO		1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp O17320 ACT_CRAGI	Actin OS=Crassostrea gigas PE=2 SV=1 CRAGI		1
24	0	2,02	11,96999997	4,255000129	4,255000129	sp O16808 ACT_MAYDE	Actin OS=Mayetiola destructor PE=2 SV=1 MAYDE		1
24	0	2,02	11,99999973	4,267000034	4,267000034	sp A2BDB0 ACTG_XENLA	Actin, cytoplasmic 2 OS=Xenopus laevis GN=actg1 PE=2 SV=1 XENLA		1
24	0	2,02	12,78000027	6,01500012	6,01500012	sp Q92193 ACT_CRAVI	Actin (Fragment) OS=Crassostrea virginica PE=2 SV=1 CRAVI		1
24	0	2,02	9,497000277	4,469000176	4,469000176	sp Q55EU6 ACT23_DICDI	Putative actin-23 OS=Dictyostelium discoideum GN=act23 PE=2 DICDI		1
24	0	2,02	10,99999994	5,178000033	5,178000033	sp Q03342 ACT3_ECHGR	Actin-3 (Fragment) OS=Echinococcus granulosus GN=ACTIII PE ECHGR		1
24	0	2,02	8,970999718	4,222000018	4,222000018	sp Q00214 ACTM_STYPL	Actin, muscle OS=Styela plicata PE=3 SV=1 STYPL		1
24	0	2,02	9,066999704	4,267000034	4,267000034	sp P50138 ACT_PUCGR	Actin OS=Puccinia graminis PE=3 SV=1 PUCGR		1
24	0	2,02	9,042999893	4,255000129	4,255000129	sp O18499 ACT1_SACKO	Actin-1 OS=Saccoglossus kowalevskii PE=2 SV=1 SACKO		1
24	0	2,01	11,99999973	4,267000034	4,267000034	sp Q9UVW9 ACTG_ACRCH	Actin, gamma OS=Acremonium chrysogenum GN=ACT PE=3 SV=1 ACRCH		1
24	0	2,01	11,99999973	4,267000034	4,267000034	sp Q8X119 ACT_EXODE	Actin OS=Exophiala dermatitidis PE=3 SV=1 EXODE		1
24	0	2,01	11,99999973	4,267000034	4,267000034	sp Q6TFC2 ACT_GAEGA	Actin OS=Gaeumannomyces graminis var. avenae GN=ACT PE=3 GAEGA		1
24	0	2,01	11,99999973	4,267000034	4,267000034	sp P78711 ACT_NEUCR	Actin OS=Neurospora crassa (strain ATCC 24698 / 74-OR23-1A NEUCR		1
24	0	2,01	11,99999973	4,267000034	4,267000034	sp P53455 ACT_AJECG	Actin OS=Ajiellomyces capsulatus (strain G186AR / H82 / ATCC AJECG		1
24	0	2,01	11,99999973	4,267000034	4,267000034	sp P20359 ACTG_EMENI	Actin, gamma OS=Emericella nidulans (strain FGSC A4 / ATCC EMENI		1
24	0	2,01	11,99999973	4,267000034	4,267000034	sp P10365 ACT_THELA	Actin OS=Thermomyces lanuginosus PE=3 SV=1 THELA		1
24	0	2,01	11,99999973	4,267000034	4,267000034	sp O13419 ACT_BOTFU	Actin OS=Botryotinia fuckeliana GN=actA PE=3 SV=1 BOTFU		1
24	0	2,01	9,042999893	4,255000129	4,255000129	sp Q8BF73 ACTBL_MOUSE	Beta-actin-like protein 2 OS=Mus musculus GN=Actbl2 PE=1 SV=1 MOUSE		1
24	0	2,01	9,042999893	4,255000129	4,255000129	sp Q562R1 ACTBL_HUMAN	Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 PE=1 SV=1 HUMAN		1
24	0	2	7,180999964	4,255000129	4,255000129	sp Q9UVZ8 ACT_CANDC	Actin OS=Candida dubliniensis (strain CD36 / ATCC MYA-646 / CANDC		1
24	0	2	7,199999969	4,267000034	4,267000034	sp Q9UR50 ACTG_PENCH	Actin, gamma OS=Penicillium chrysogenum GN=ACT PE=3 SV=1 PENCH		1
24	0	2	7,199999969	4,267000034	4,267000034	sp Q9BYX7 ACTBM_HUMAN	Putative beta-actin-like protein 3 OS=Homo sapiens GN=POTE HUMAN		1
24	0	2	7,162000239	4,244000092	4,244000092	sp Q98972 ACTS_ORYLA	Actin, alpha skeletal muscle OS=Oryzias latipes GN=acta1 PE=2 ORYLA		1
24	0	2	7,142999768	4,233000055	4,233000055	sp Q93132 ACTM_BRALF	Actin, muscle OS=Branchiostoma floridae PE=2 SV=1 BRALF		1
24	0	2	7,124000043	4,222000018	4,222000018	sp Q93130 ACTM_BRABE	Actin, muscle OS=Branchiostoma belcheri PE=2 SV=1 BRABE		1
24	0	2	7,162000239	4,244000092	4,244000092	sp Q90X97 ACTS_ATRMM	Actin, alpha skeletal muscle OS=Atractaspis microlepidota mic ATRMM		1
24	0	2	7,180999964	4,255000129	4,255000129	sp Q75D00 ACT_ASHGO	Actin OS=Ashbya gossypii (strain ATCC 10895 / CBS 109.51 / F ASHGO		1
24	0	2	2,511999942	1,487999968	1,487999968	sp Q6S8J3 POTEE_HUMAN	POTE ankyrin domain family member E OS=Homo sapiens GN= HUMAN		1
24	0	2	7,162000239	4,244000092	4,244000092	sp Q6P8G3 ACT3_XENTR	Actin, alpha sarcomeric/skeletal OS=Xenopus tropicalis GN=ac XENTR		1
24	0	2	7,162000239	4,244000092	4,244000092	sp Q6P640 ACTG_XENTR	Actin, alpha cardiac muscle 1 OS=Xenopus tropicalis GN=act1 XENTR		1
24	0	2	7,162000239	4,244000092	4,244000092	sp Q5R9Q5 ACTS_PONAB	Actin, alpha skeletal muscle OS=Pongo abelii GN=ACTA1 PE=2 PONAB		1
24	0	2	7,180999964	4,255000129	4,255000129	sp Q5E9B5 ACTH_BOVIN	Actin, gamma-enteric smooth muscle OS=Bos taurus GN=ACT1 BOVIN		1
24	0	2	7,162000239	4,244000092	4,244000092	sp Q3ZC07 ACTC_BOVIN	Actin, alpha cardiac muscle 1 OS=Bos taurus GN=ACTC1 PE=2 BOVIN		1
24	0	2	7,199999969	4,267000034	4,267000034	sp Q0PGG4 ACTB_BOSMU	Actin, cytoplasmic 1 OS=Bos mutus grunniens GN=ACTB PE=2 BOSMU		1
24	0	2	14,05999959	8,332999796	8,332999796	sp P86700 ACT_CHIOP	Actin, muscle (Fragments) OS=Chionoeetes opilio PE=1 SV=1 CHIOP		1
24	0	2	7,199999969	4,267000034	4,267000034	sp P79818 ACTB_ORYLA	Actin, cytoplasmic 1 OS=Oryzias latipes GN=actb PE=2 SV=1 ORYLA		1
24	0	2	7,162000239	4,244000092	4,244000092	sp P68264 ACTS_OREMO	Actin, alpha skeletal muscle OS=Oreochromis mossambicus GN=OREMO		1
24	0	2	7,162000239	4,244000092	4,244000092	sp P68140 ACTSA_TAKRU	Actin, alpha skeletal muscle A OS=Takifugu rubripes GN=acta1 TAKRU		1
24	0	2	7,162000239	4,244000092	4,244000092	sp P68139 ACTS_CHICK	Actin, alpha skeletal muscle OS=Gallus gallus GN=ACTA1 PE=1 CHICK		1
24	0	2	7,162000239	4,244000092	4,244000092	sp P68138 ACTS_BOVIN	Actin, alpha skeletal muscle OS=Bos taurus GN=ACTA1 PE=1 BOVIN		1
24	0	2	7,162000239	4,244000092	4,244000092	sp P68137 ACTS_PIG	Actin, alpha skeletal muscle OS=Sus scrofa GN=ACTA1 PE=3 SV PIG		1
24	0	2	7,162000239	4,244000092	4,244000092	sp P68136 ACTS_RAT	Actin, alpha skeletal muscle OS=Rattus norvegicus GN=Acta1 RAT		1
24	0	2	7,162000239	4,244000092	4,244000092	sp P68135 ACTS_RABIT	Actin, alpha skeletal muscle OS=Oryctolagus cuniculus GN=AC RABIT		1
24	0	2	7,162000239	4,244000092	4,244000092	sp P68134 ACTS_MOUSE	Actin, alpha skeletal muscle OS=Mus musculus GN=Acta1 PE= MOUSE		1
24	0	2	7,162000239	4,244000092	4,244000092	sp P68133 ACTS_HUMAN	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACTA1 PE= HUMAN		1
24	0	2	7,162000239	4,244000092	4,244000092	sp P68035 ACTC_RAT	Actin, alpha cardiac muscle 1 OS=Rattus norvegicus GN=Actc1 RAT		1
24	0	2	7,162000239	4,244000092	4,244000092	sp P68034 ACTC_CHICK	Actin, alpha cardiac muscle 1 OS=Gallus gallus GN=ACTC1 PE= CHICK		1
24	0	2	7,162000239	4,244000092	4,244000092	sp P68033 ACTC_MOUSE	Actin, alpha cardiac muscle 1 OS=Mus musculus GN=Actc1 PE= MOUSE		1
24	0	2	7,162000239	4,244000092	4,244000092	sp P68032 ACTC_HUMAN	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACTC1 PE HUMAN		1
24	0	2	7,180999964	4,255000129	4,255000129	sp P63270 ACTH_CHICK	Actin, gamma-enteric smooth muscle OS=Gallus gallus GN=AC CHICK		1
24	0	2	7,180999964	4,255000129	4,255000129	sp P63269 ACTH_RAT	Actin, gamma-enteric smooth muscle OS=Rattus norvegicus G RAT		1
24	0	2	7,180999964	4,255000129	4,255000129	sp P63268 ACTH_MOUSE	Actin, gamma-enteric smooth muscle OS=Mus musculus GN= MOUSE		1
24	0	2	7,180999964	4,255000129	4,255000129	sp P63267 ACTH_HUMAN	Actin, gamma-enteric smooth muscle OS=Homo sapiens GN= HUMAN		1
24	0	2	7,162000239	4,244000092	4,244000092	sp P62740 ACTA_RABIT	Actin, aortic smooth muscle OS=Oryctolagus cuniculus GN=AC RABIT		1
24	0	2	7,162000239	4,244000092	4,244000092	sp P62739 ACTA_BOVIN	Actin, aortic smooth muscle OS=Bos taurus GN=ACTA2 PE=1 S BOVIN		1
24	0	2	7,162000239	4,244000092	4,244000092	sp P62738 ACTA_RAT	Actin, aortic smooth muscle OS=Rattus norvegicus GN=Acta2 I RAT		1
24	0	2	7,162000239	4,244000092	4,244000092	sp P62737 ACTA_MOUSE	Actin, aortic smooth muscle OS=Mus musculus GN=Acta2 PE= MOUSE		1
24	0	2	7,162000239	4,244000092	4,244000092	sp P62736 ACTA_HUMAN	Actin, aortic smooth muscle OS=Homo sapiens GN=ACTA2 PE= HUMAN		1
24	0	2	7,199999969	4,267000034	4,267000034	sp P60011 ACT_SACBA	Actin OS=Saccharomyces bayanus GN=ACT1 PE=3 SV=1 SACBA		1
24	0	2	7,199999969	4,267000034	4,267000034	sp P60010 ACT_YEAST	Actin OS=Saccharomyces cerevisiae (strain ATCC 204508 / S28 YEAST		1
24	0	2	7,199999969	4,267000034	4,267000034	sp P60009 ACT_CANGA	Actin OS=Candida glabrata (strain ATCC 2001 / CBS 138 / JCM CANGA		1
24	0	2	7,162000239	4,244000092	4,244000092	sp P53482 ACTSB_TAKRU	Actin, alpha skeletal muscle B OS=Takifugu rubripes GN=acta1 TAKRU		1
24	0	2	7,162000239	4,244000092	4,244000092	sp P53480 ACTC_TAKRU	Actin, alpha cardiac OS=Takifugu rubripes PE=2 SV=1 TAKRU		1
24	0	2	7,162000239	4,244000092	4,244000092	sp P53479 ACTS_CYPCA	Actin, alpha skeletal muscle OS=Cyprinus carpio GN=acta1 PE= CYPCA		1
24	0	2	7,142999768	4,233000055	4,233000055	sp P53475 ACTN_STYCL	Actin, muscle OS=Styela clava GN=TB12 PE=2 SV=1 STYCL		1
24	0	2	7,142999768	4,233000055	4,233000055	sp P53467 ACTM_MOLOC	Actin, larval muscle-type OS=Molgula oculata PE=3 SV=1 MOLOC		1
24	0	2	7,162000239	4,244000092	4,244000092	sp P49055 ACTS_CARAU	Actin, alpha skeletal muscle OS=Carassius auratus GN=acta1 P CARAU		1
24	0	2	7,199999969	4,267000034	4,267000034	sp P43239 ACT1_PNECA	Actin-1 OS=Pneumocystis carinii PE=2 SV=1 PNECA		1
24	0	2	7,199999969	4,267000034	4,267000034	sp P29751 ACTB_RABIT	Actin, cytoplasmic 1 OS=Oryctolagus cuniculus GN=ACTB PE=2 RABIT		1
24	0	2	7,142999768	4,233000055	4,233000055	sp P27130 ACT2_HALRO	Actin, muscle 2/4/4A OS=Halocynthia roretzi GN=MA2 PE=2 S HALRO		1
24	0	2	7,142999768	4,233000055	4,233000055	sp P26198 ACTM_STYCL	Actin, muscle OS=Styela clava PE=2 SV=1 STYCL		1
24	0	2	7,162000239	4,244000092	4,244000092	sp P20399 ACT2_XENTR	Actin, alpha cardiac muscle 2 OS=Xenopus tropicalis PE=2 SV= XENTR		1
24	0	2	7,180999964	4,255000129	4,255000129	sp P18601 ACT2_ARTSX	Actin, clone 211 OS=Artemia sp. PE=2 SV=1 ARTSX		1
24	0	2	7,180999964	4,255000129	4,255000129	sp P18600 ACT1_ARTSX	Actin, clone 205 OS=Artemia sp. PE=2 SV=1 ARTSX		1
24	0	2	7,180999964	4,255000129	4,255000129	sp P17304 ACTM_APLCA	Actin, muscle OS=Aplysia californica PE=2 SV=1 APLCA		1
24	0	2	7,199999969	4,267000034	4,267000034	sp P17128 ACT_KLULA	Actin OS=Kluyveromyces lactis (strain ATCC 8585 / CBS 2359 / KLULA		1
24	0	2	7,180999964	4,255000129	4,255000129	sp P14235 ACT_CANAX	Actin OS=Candida albicans GN=ACT1 PE=3 SV=1 CANAX		1
24	0	2	7,162000239	4,244000092	4,244000092	sp P10995 ACT2_XENLA	Actin, alpha skeletal muscle 2 OS=Xenopus laevis GN=act2 PE= XENLA		1
24	0	2	7,199999969	4,267000034	4,267000034	sp P10989 ACT_SCHPO	Actin OS=Schizosaccharomyces pombe (strain 972 / ATCC 248 SCHPO		1
24	0	2	7,162000239	4,244000092	4,244000092	sp P08023 ACTA_CHICK	Actin, aortic smooth muscle OS=Gallus gallus GN=ACTA2 PE=1 CHICK		1
24	0	2	7,180999964	4,255000129	4,255000129	sp P07837 ACT2_BOMMO	Actin, muscle-type A2 OS=Bombyx mori PE=3 SV=1 BOMMO		1
24	0	2	7,162000239	4,244000092	4,244000092	sp P04752 ACT3_XENLA	Actin, alpha skeletal muscle 3 OS=Xenopus laevis GN=act3 PE= XENLA		1
24	0	2	7,162000239	4,244000092	4,244000092	sp P04751 ACTC_XENLA	Actin, alpha cardiac muscle 1 OS=Xenopus laevis GN=actc1 PE= XENLA		1
24	0	2	7,180999964	4,255000129	4,255000129	sp O74258 ACT_OGAPD	Actin OS=Ogataea parapolyphora (strain DL-1 / ATCC 26012 OGAPD		1
24	0	2	7,199999969	4,267000034	4,267000034	sp O17503 ACTC_BRALA	Actin, cytoplasmic OS=Branchiostoma lanceolatum PE=2 SV=1 BRALA		1
24	0	2	7,105000317	4,210999981	4,210999981	sp O17502 ACTM_BRALA	Actin, muscle OS=Branchiostoma lanceolatum PE=2 SV=1 BRALA		1
24	0	2	7,142999768	4,233000055	4,233000055	sp O15998			

24	0	2	9,301999956	9,301999956	9,301999956	sp Q25381 ACTM_LYTP1	Actin, muscle (Fragment) OS=Lytechinus pictus PE=3 SV=1	LYTP1	1
24	0	2	9,301999956	9,301999956	9,301999956	sp Q25379 ACT3_LYTP1	Actin, cytoskeletal 3 (Fragment) OS=Lytechinus pictus PE=3 SV LYTP1		1
24	0	2	4,233000055	4,233000055	4,233000055	sp P53460 ACT1_HALRO	Actin, muscle 1A OS=Halocynthia roretzi GN=MA1A PE=3 SV=1 HALRO		1
24	0	2	4,969000071	4,969000071	4,969000071	sp P45521 ACT_PROCL	Actin (Fragment) OS=Procamburus clarkii PE=1 SV=1	PROCL	1
26	2	2	3,370999917	1,765999943	1,765999943	sp P21910 LAML2_XENLA	Lamin-L(II) OS=Xenopus laevis PE=2 SV=1	XENLA	1
27	2	2	8,392000198	8,392000198	8,392000198	sp Q9PU28 LYSC_SCOMX	Lysozyme C OS=Scophthalmus maximus GN=lys PE=2 SV=1	SCOMX	1
27	0	2	8,392000198	8,392000198	8,392000198	sp Q9DD65 LYSC_PAROL	Lysozyme C OS=Paralichthys olivaceus PE=2 SV=1	PAROL	1
27	0	2	8,107999712	8,107999712	8,107999712	sp Q6B411 LYSM_BOVIN	Lysozyme C, milk isozyme OS=Bos taurus PE=2 SV=1	BOVIN	1
27	0	2	8,107999712	8,107999712	8,107999712	sp Q659U5 LYSC_HALGR	Lysozyme C OS=Halichoerus grypus GN=LYZ PE=2 SV=1	HALGR	1
27	0	2	8,107999712	8,107999712	8,107999712	sp Q659U1 LYSC_PHOVI	Lysozyme C OS=Phoca vitulina GN=LYZ PE=2 SV=1	PHOVI	1
27	0	2	8,107999712	8,107999712	8,107999712	sp Q659U0 LYSC_LEPWE	Lysozyme C OS=Leptonychotes weddellii GN=LYZ PE=2 SV=1	LEPWE	1
27	0	2	8,107999712	8,107999712	8,107999712	sp Q05820 LYSC2_RAT	Putative lysozyme C-2 OS=Rattus norvegicus GN=Ly22 PE=5 SV RAT		1
27	0	2	9,230999649	9,230999649	9,230999649	sp P85345 LYSC_AMYCA	Lysozyme C OS=Amyda cartilaginea GN=LYZ PE=1 SV=1	AMYCA	1
27	0	2	8,218999952	8,218999952	8,218999952	sp P85045 LYS_BUFGA	Lysozyme C (Fragment) OS=Bufo gargarizans andrewsi PE=1 SV BUFGA		1
27	0	2	9,230999649	9,230999649	9,230999649	sp P81709 LYSC2_CANLF	Lysozyme C, spleen isozyme OS=Canis lupus familiaris PE=1 SV CANLF		1
27	0	2	8,107999712	8,107999712	8,107999712	sp P79847 LYSC_PYGNE	Lysozyme C OS=Pygathrix nemaeus GN=LYZ PE=3 SV=1	PYGNE	1
27	0	2	8,107999712	8,107999712	8,107999712	sp P79811 LYSC_NASLA	Lysozyme C OS=Nasalis larvatus GN=LYZ PE=3 SV=1	NASLA	1
27	0	2	8,107999712	8,107999712	8,107999712	sp P79239 LYSC_PONPY	Lysozyme C OS=Pongo pygmaeus GN=LYZ PE=2 SV=1	PONPY	1
27	0	2	8,107999712	8,107999712	8,107999712	sp P79180 LYSC_HYLLA	Lysozyme C OS=Hylobates lar GN=LYZ PE=2 SV=1	HYLLA	1
27	0	2	8,107999712	8,107999712	8,107999712	sp P79179 LYSC_GORGO	Lysozyme C OS=Gorilla gorilla gorilla GN=LYZ PE=2 SV=1	GORGO	1
27	0	2	8,107999712	8,107999712	8,107999712	sp P67980 LYSC_TRAFR	Lysozyme C OS=Trachypithecus francoisi GN=LYZ PE=2 SV=1	TRAFR	1
27	0	2	8,107999712	8,107999712	8,107999712	sp P67979 LYSC_TRAOB	Lysozyme C OS=Trachypithecus obscurus GN=LYZ PE=2 SV=1	TRAOB	1
27	0	2	8,107999712	8,107999712	8,107999712	sp P67978 LYSC_TRAVT	Lysozyme C OS=Trachypithecus vetulus GN=LYZ PE=3 SV=1	TRAVT	1
27	0	2	8,107999712	8,107999712	8,107999712	sp P67977 LYSC_SEMEN	Lysozyme C OS=Semnopithecus entellus GN=LYZ PE=1 SV=1	SEMEN	1
27	0	2	8,392000198	8,392000198	8,392000198	sp P61944 LYSC_TAKRU	Lysozyme C OS=Takifugu rubripes PE=2 SV=1	TAKRU	1
27	0	2	8,107999712	8,107999712	8,107999712	sp P61632 LYSC_COLGU	Lysozyme C OS=Colobus guereza GN=LYZ PE=2 SV=1	COLGU	1
27	0	2	8,107999712	8,107999712	8,107999712	sp P61631 LYSC_COLAN	Lysozyme C OS=Colobus angolensis GN=LYZ PE=3 SV=1	COLAN	1
27	0	2	8,107999712	8,107999712	8,107999712	sp P61628 LYSC_PANTR	Lysozyme C OS=Pan troglodytes GN=LYZ PE=2 SV=1	PANTR	1
27	0	2	8,107999712	8,107999712	8,107999712	sp P61627 LYSC_PANPA	Lysozyme C OS=Pan paniscus GN=LYZ PE=3 SV=1	PANPA	1
27	0	2	8,107999712	8,107999712	8,107999712	sp P61626 LYSC_HUMAN	Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1	HUMAN	1
27	0	2	9,230999649	9,230999649	9,230999649	sp P37712 LYSC_CAMDR	Lysozyme C OS=Camelus dromedarius GN=LYZ PE=1 SV=1	CAMDR	1
27	0	2	8,107999712	8,107999712	8,107999712	sp P17897 LYZ1_MOUSE	Lysozyme C-1 OS=Mus musculus GN=Ly21 PE=1 SV=1	MOUSE	1
27	0	2	9,230999649	9,230999649	9,230999649	sp P16973 LYSC_RABIT	Lysozyme C OS=Oryctolagus cuniculus GN=LYZ PE=1 SV=1	RABIT	1
27	0	2	8,107999712	8,107999712	8,107999712	sp P12069 LYSC3_PIG	Lysozyme C-3 OS=Sus scrofa PE=1 SV=2	PIG	1
27	0	2	8,218999952	8,218999952	8,218999952	sp P12068 LYSC2_PIG	Lysozyme C-2 OS=Sus scrofa PE=1 SV=2	PIG	1
27	0	2	9,375	9,375	9,375	sp P12067 LYSC1_PIG	Lysozyme C-1 OS=Sus scrofa PE=1 SV=1	PIG	1
27	0	2	8,332999796	8,332999796	8,332999796	sp P11941 LYSC2_ONCMY	Lysozyme C II OS=Oncorhynchus mykiss PE=1 SV=2	ONCMY	1
27	0	2	8,107999712	8,107999712	8,107999712	sp P08905 LYZ2_MOUSE	Lysozyme C-2 OS=Mus musculus GN=Ly22 PE=1 SV=2	MOUSE	1
27	0	2	8,107999712	8,107999712	8,107999712	sp P00697 LYSC1_RAT	Lysozyme C-1 OS=Rattus norvegicus GN=Ly21 PE=1 SV=2	RAT	1
28	2	2	3,9760001	3,9760001	3,9760001	sp P08453 GDB2_WHEAT	Gamma-gliadin OS=Triticum aestivum PE=3 SV=1	WHEAT	1
29	2	2	7,805000246	7,805000246	7,805000246	sp P04792 HSPB1_HUMAN	Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 PE=1 HUMAN		1
30	1,86	1,86	19,85000074	19,85000074	19,85000074	sp P47929 LEG7_HUMAN	Galectin-7 OS=Homo sapiens GN=LGAL57 PE=1 SV=2	HUMAN	1
32	1,49	1,59	4,887999967	4,887999967	3,259000182	sp Q6IFX1 K1C24_RAT	Keratin, type I cytoskeletal 24 OS=Rattus norvegicus GN=Krt24 RAT		1
32	0	1,59	4,687999934	4,687999934	3,125	sp A1L317 K1C24_MOUSE	Keratin, type I cytoskeletal 24 OS=Mus musculus GN=Krt24 PE MOUSE		1
33	1,4	1,4	2,597000077	2,597000077	2,597000077	sp Q08188 TGM3_HUMAN	Protein-glutamine gamma-glutamyltransferase E OS=Homo sa HUMAN		1
35	0,67	0,67	0,460099988	0,460099988	0,460099988	sp Q5D862 FILA2_HUMAN	Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	HUMAN	1
34	0,7	0,7	11,94999963	5,905999988	0	sp Q8WNW3 PLAK_PIG	Junction plakoglobin OS=Sus scrofa GN=Jup PE=2 SV=1	PIG	0
34	0	0,7	11,94999963	5,905999988	0	sp Q8SPJ1 PLAK_BOVIN	Junction plakoglobin OS=Bos taurus GN=JUP PE=2 SV=1	BOVIN	0
34	0	0,7	11,94999963	5,905999988	0	sp Q6P0K8 PLAK_RAT	Junction plakoglobin OS=Rattus norvegicus GN=Jup PE=1 SV=1 RAT		0
34	0	0,7	11,94999963	5,905999988	0	sp Q02257 PLAK_MOUSE	Junction plakoglobin OS=Mus musculus GN=Jup PE=1 SV=3	MOUSE	0
34	0	0,7	11,94999963	5,905999988	0	sp P14923 PLAK_HUMAN	Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV=3	HUMAN	0
36	0,4	0,4	5,189999938	1,080000028	0	sp P15924 DESP_HUMAN	Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	HUMAN	0
36	0	0,37	4,856000096	0,381499995	0	sp E9Q557 DESP_MOUSE	Desmoplakin OS=Mus musculus GN=Dsp PE=1 SV=1	MOUSE	0
37	0,37	0,37	2,563999966	2,563999966	0	RRRRRsp C4Z5P8 UXAC_EUBE2	REVERSED Uronate isomerase OS=Eubacterium eligens (strain EUBE2		0
38	0,18	0,18	6,263999641	1,118999999	0	sp Q08554 DSC1_HUMAN	Desmocollin-1 OS=Homo sapiens GN=DSC1 PE=1 SV=2	HUMAN	0
39	0,18	0,18	3,759000078	3,759000078	0	sp Q7VB19 ISPT_PROMA	Isoprenyl transferase OS=Prochlorococcus marinus (strain SAR PROMA		0
40	0,18	0,18	1,917999983	1,917999983	0	RRRRRsp Q9SFC7 FB135_ARATH	REVERSED F-box protein At3g07870 OS=Arabidopsis thaliana (ARATH		0
41	0,14	0,14	10,27999967	10,27999967	0	RRRRRsp B9K6M6 Y433_THENN	REVERSED UPF0102 protein CTN_0433 OS=Thermotoga neapc THENN		0
42	0,12	0,12	7,24600032	3,864999861	0	RRRRRsp Q37626 NU6M_PROW	REVERSED NADH-ubiquinone oxidoreductase chain 6 OS=Prot PROWI		0
42	0	0,12	1,013999991	1,013999991	0	RRRRRsp Q0V147 AMPP2_PHAN	REVERSED Probable Xaa-Pro aminopeptidase SNOG_02267 OS=PHANO		0
42	0	0,12	0,863900036	0,863900036	0	RRRRRsp E3RNJ5 AMPP2_PYRTT	REVERSED Probable Xaa-Pro aminopeptidase PTT_10145 OS=PYRTT		0
42	0	0,12	1,212000009	1,212000009	0	RRRRRsp B2WKR4 AMPP2_PYRT	REVERSED Probable Xaa-Pro aminopeptidase PTRG_10574 OS=PYRTT		0
43	0,11	0,11	2,452000044	2,452000044	0	RRRRRsp Q81M67 BUK_BACAN	REVERSED Probable butyrate kinase OS=Bacillus anthracis GN= BACAN		0
43	0	0,11	2,452000044	2,452000044	0	RRRRRsp Q818T1 BUK_BACCR	REVERSED Probable butyrate kinase OS=Bacillus cereus (strain BACCR		0
43	0	0,11	2,452000044	2,452000044	0	RRRRRsp Q731D0 BUK_BACCI	REVERSED Probable butyrate kinase OS=Bacillus cereus (strain BACCI		0
43	0	0,11	2,452000044	2,452000044	0	RRRRRsp Q6HE00 BUK_BACHK	REVERSED Probable butyrate kinase OS=Bacillus thuringiensis BACHK		0
43	0	0,11	2,452000044	2,452000044	0	RRRRRsp Q635C1 BUK_BACCZ	REVERSED Probable butyrate kinase OS=Bacillus cereus (strain BACCZ		0
43	0	0,11	2,452000044	2,452000044	0	RRRRRsp C3P7U3 BUK_BACAA	REVERSED Probable butyrate kinase OS=Bacillus anthracis (str BACAA		0
43	0	0,11	2,452000044	2,452000044	0	RRRRRsp C3LJ78 BUK_BACAC	REVERSED Probable butyrate kinase OS=Bacillus anthracis (str BACAC		0
43	0	0,11	2,452000044	2,452000044	0	RRRRRsp C1ERN7 BUK_BACC3	REVERSED Probable butyrate kinase OS=Bacillus cereus (strain BACC3		0
43	0	0,11	2,452000044	2,452000044	0	RRRRRsp B9IXF8 BUK_BACQC	REVERSED Probable butyrate kinase OS=Bacillus cereus (strain BACQC		0
43	0	0,11	2,452000044	2,452000044	0	RRRRRsp B7JM15 BUK_BACCO	REVERSED Probable butyrate kinase OS=Bacillus cereus (strain BACCO		0
43	0	0,11	2,452000044	2,452000044	0	RRRRRsp B7IXF5 BUK_BACC2	REVERSED Probable butyrate kinase OS=Bacillus cereus (strain BACC2		0
43	0	0,11	2,452000044	2,452000044	0	RRRRRsp B7HNS7 BUK_BACCT	REVERSED Probable butyrate kinase OS=Bacillus cereus (strain BACCT		0
43	0	0,11	2,452000044	2,452000044	0	RRRRRsp B7HB35 BUK_BACC4	REVERSED Probable butyrate kinase OS=Bacillus cereus (strain BACC4		0
43	0	0,11	2,452000044	2,452000044	0	RRRRRsp A7GSI3 BUK_BACCN	REVERSED Probable butyrate kinase OS=Bacillus cytotoxicus (s BACCN		0
43	0	0,01	2,452000044	2,452000044	0	RRRRRsp A9VGB0 BUK_BACWK	REVERSED Probable butyrate kinase OS=Bacillus weihensteph: BACWK		

49	0	0,08	0,964200031	0,964200031	0 RRRRRsp A8AKX8 KATG_CITK8 REVERSED Catalase-peroxidase OS=Citrobacter koseri (strain A CITK8	0
49	0	0,08	0,965499971	0,965499971	0 RRRRRsp A6T9H9 KATG_KLEP7 REVERSED Catalase-peroxidase OS=Klebsiella pneumoniae sut KLEP7	0
49	0	0,08	0,964200031	0,964200031	0 RRRRRsp A4WG57 KATG_ENT38 REVERSED Catalase-peroxidase OS=Enterobacter sp. (strain 63 ENT38	0
50	0,07	0,08	1,855999976	1,855999976	0 RRRRRsp A4SCK8 GCSPB_CHLPM REVERSED Probable glycine dehydrogenase (decarboxylating) CHLPM	0
51	0,07	0,07	3,726999834	3,726999834	0 sp O35003 T1214_ARCFU Probable transposase for insertion sequence element ISA1214 ARCFU	0
52	0,06	0,07	3,57099995	3,57099995	0 sp A6WX58 Y840_OCHA4 UPF0314 protein Oant_0840 OS=Ochrobactrum anthropi (stra OCHA4	0
52	0	0,07	1,243000012	1,243000012	0 RRRRRsp Q5UPJ3 YL116_MIMIV REVERSED Uncharacterized protein L116 OS=Acanthamoeba p MIMIV	0
52	0	0,07	1,620000042	1,620000042	0 RRRRRsp Q39K17 HEM1_BURL3 REVERSED Glutamyl-tRNA reductase OS=Burkholderia lata (str BURL3	0
52	0	0,07	1,620000042	1,620000042	0 RRRRRsp Q1BSB3 HEM1_BURCA REVERSED Glutamyl-tRNA reductase OS=Burkholderia cenocej BURCA	0
52	0	0,07	1,620000042	1,620000042	0 RRRRRsp Q0BIP9 HEM1_BURCM REVERSED Glutamyl-tRNA reductase OS=Burkholderia ambifar BURCM	0
52	0	0,07	1,620000042	1,620000042	0 RRRRRsp B4E6U7 HEM1_BURCJ REVERSED Glutamyl-tRNA reductase OS=Burkholderia cenocej BURCJ	0
52	0	0,07	1,620000042	1,620000042	0 RRRRRsp B1YSD6 HEM1_BURA4 REVERSED Glutamyl-tRNA reductase OS=Burkholderia ambifar BURA4	0
52	0	0,07	1,620000042	1,620000042	0 RRRRRsp B1JU55 HEM1_BURCC REVERSED Glutamyl-tRNA reductase OS=Burkholderia cenocej BURCC	0
52	0	0,07	1,620000042	1,620000042	0 RRRRRsp A9AJ67 HEM1_BURM1 REVERSED Glutamyl-tRNA reductase OS=Burkholderia multivo BURM1	0
52	0	0,07	1,620000042	1,620000042	0 RRRRRsp A4JB51 HEM1_BURVG REVERSED Glutamyl-tRNA reductase OS=Burkholderia vietnan BURVG	0
52	0	0,07	1,620000042	1,620000042	0 RRRRRsp A0K438 HEM1_BURCH REVERSED Glutamyl-tRNA reductase OS=Burkholderia cenocej BURCH	0
53	0,06	0,06	5,104000121	3,403000161	0 sp Q7YR44 CDSN_PANTR Corneodesmosin OS=Pan troglodytes GN=CDSN PE=2 SV=1 PANTR	0
53	0	0,06	5,056000128	3,370999917	0 sp Q5TM45 CDSN_MACMU Corneodesmosin OS=Macaca mulatta GN=CDSN PE=3 SV=1 MACMU	0
53	0	0,06	5,104000121	3,403000161	0 sp Q15517 CDSN_HUMAN Corneodesmosin OS=Homo sapiens GN=CDSN PE=1 SV=3 HUMAN	0
54	0,06	0,06	0,613899995	0,245500007	0 sp Q756G2 TOM1_ASHGO Probable E3 ubiquitin-protein ligase TOM1 OS=Ashbya gossyp ASHGO	0
55	0,06	0,06	0,598799996	0,598799996	0 sp Q9LZW9 RTOR2_ARATH Regulatory-associated protein of TOR 2 OS=Arabidopsis thalia ARATH	0
56	0,06	0,06	8,87100026	8,87100026	0 sp P01085 IAA1_WHEAT Alpha-amylase inhibitor 0.19 OS=Triticum aestivum PE=1 SV=1 WHEAT	0
56	0	0,06	8,87100026	8,87100026	0 sp P01084 IAA5_WHEAT Alpha-amylase inhibitor 0.53 OS=Triticum aestivum PE=1 SV=1 WHEAT	0
57	0,05	0,05	5,404999852	2,078999951	0 RRRRRsp Q1IED4 GATB_PSEE4 REVERSED Aspartyl/glutamyl-tRNA(Asn/Gln) amidotransferase PSEE4	0
58	0,05	0,05	2,219000086	0,986399967	0 RRRRRsp C1CVF4 GYRA_DEIDV REVERSED DNA gyrase subunit A OS=Deinococcus deserti (str: DEIDV	0
59	0,05	0,05	3,430999815	3,430999815	0 sp Q96MC5 CP045_HUMAN Uncharacterized protein C16orf45 OS=Homo sapiens GN=C16i HUMAN	0
59	0	0,05	3,448000178	3,448000178	0 sp Q8R1Y2 CP045_MOUSE Uncharacterized protein C16orf45 homolog OS=Mus musculus MOUSE	0
59	0	0,05	3,430999815	3,430999815	0 sp Q5R562 CP045_PONAB Uncharacterized protein C16orf45 homolog OS=Pongo abelii P PONAB	0
59	0	0,05	3,448000178	3,448000178	0 sp Q5FVJ5 CP045_RAT Uncharacterized protein C16orf45 homolog OS=Rattus norveg RAT	0
59	0	0,05	0,9296	0,9296	0 RRRRRsp Q5XHX2 TPRN_RAT REVERSED Taperin OS=Rattus norvegicus GN=Tprn PE=1 SV=2 RAT	0
59	0	0,05	0,934599992	0,934599992	0 RRRRRsp A2AI08 TPRN_MOUSE REVERSED Taperin OS=Mus musculus GN=Tprn PE=1 SV=1 MOUSE	0
60	0,05	0,05	1,453999989	1,453999989	0 sp Q96K58 ZN668_HUMAN Zinc finger protein 668 OS=Homo sapiens GN=ZNF668 PE=1 SV HUMAN	0
60	0	0,05	1,453999989	1,453999989	0 sp Q8K2R5 ZN668_MOUSE Zinc finger protein 668 OS=Mus musculus GN=Znf668 PE=2 SV MOUSE	0
60	0	0,05	1,453999989	1,453999989	0 sp Q4R3I5 ZN668_MACFA Zinc finger protein 668 OS=Macaca fascicularis GN=ZNF668 PE MACFA	0
60	0	0,05	1,453999989	1,453999989	0 sp Q2TA17 ZN668_BOVIN Zinc finger protein 668 OS=Bos taurus GN=ZNF668 PE=2 SV=2 BOVIN	0
61	0,05	0,05	1,601999998	1,601999998	0 sp Q92Y37 NHAA_RHIME Na(+)/H(+) antiporter NhaA OS=Rhizobium meliloti (strain 102 RHIME	0
62	0,05	0,05	1,631999947	1,631999947	0 sp Q42191 OXA1_ARATH Mitochondrial inner membrane protein OXA1 OS=Arabidopsis ARATH	0
63	0,05	0,05	1,999999955	1,999999955	0 RRRRRsp Q7NNG6 ARGD_GLOVI REVERSED Acetylornithine aminotransferase OS=Gloeobacter GLOVI	0
64	0,05	0,05	3,477999941	3,477999941	0 RRRRRsp Q73GB0 PSD_WOLPM REVERSED Phosphatidylserine decarboxylase proenzyme OS=l WOLPM	0
64	0	0,05	3,477999941	3,477999941	0 RRRRRsp COR4EO PSD_WOLWR REVERSED Phosphatidylserine decarboxylase proenzyme OS=l WOLWR	0

N	Ctrl	Idudoso_CSI_1	Total	%Cov	%Cov(50)	%Cov(95)	Accession	Name	Species	Peptides(95%)
1	89,03	89,03	70,02999783	68,79000068	68,79000068	sp P04264 K2C1_HUMAN	Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KR1 HUMAN	70		
2	69,67	69,67	58,89999866	55,4799974	55,4799974	sp P13645 K1C10_HUMAN	Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KR1 HUMAN	48		
3	67,55	74,99	77,14999914	70,88999748	60,72000265	sp P35908 K2Z2_HUMAN	Keratin, type II cytoskeletal 2 epidermal OS=Homo sapie HUMAN	46		
4	57,29	57,4	78,64999771	75,59999824	69,98000145	sp P35527 K1C9_HUMAN	Keratin, type I cytoskeletal 9 OS=Homo sapiens GN=KRT HUMAN	42		
6	20,26	20,26	64,49999809	64,49999809	64,49999809	sp P00761 TRYP_PIG	Trypsin OS=Sus scrofa PE=1 SV=1	29		
5	32,07	35,44	57,84000158	48,73000085	48,73000085	sp P02533 K1C14_HUMAN	Keratin, type I cytoskeletal 14 OS=Homo sapiens GN=KR HUMAN	21		
7	17,59	30,68	38,80999982	32,37000108	27,45999992	sp P13647 K2C5_HUMAN	Keratin, type II cytoskeletal 5 OS=Homo sapiens GN=KR1 HUMAN	16		
7	0	28,83	36,14999951	29,73000109	24,83000001	sp A5A6M8 K2C5_PANTR	Keratin, type II cytoskeletal 5 OS=Pan troglodytes GN=KI PANTR	15		
9	13,2	29,24	34,92999971	33,16000104	27,84000039	sp P48668 K2C6_HUMAN	Keratin, type II cytoskeletal 6C OS=Homo sapiens GN=Kf HUMAN	15		
9	0	29,2	35,98999977	32,80000091	27,84000039	sp P02538 K2C6A_HUMAN	Keratin, type II cytoskeletal 6A OS=Homo sapiens GN=Ki HUMAN	15		
24	5,47	9,78	12,98000067	11,42000034	11,42000034	sp Q72794 K2C1B_HUMAN	Keratin, type II cytoskeletal 1b OS=Homo sapiens GN=Kf HUMAN	12		
28	4,02	22,86	34,25000012	24,95000064	24,95000064	sp P08779 K1C16_HUMAN	Keratin, type I cytoskeletal 16 OS=Homo sapiens GN=KR HUMAN	12		
24	0	11,04	15,02999961	12,72000074	12,72000074	sp Q6IG01 K2C1B_RAT	Keratin, type II cytoskeletal 1b OS=Rattus norvegicus GN=RAT	10		
24	0	11,04	11,54000014	11,54000014	11,54000014	sp Q6IFZ6 K2C1B_MOUSE	Keratin, type II cytoskeletal 1b OS=Mus musculus GN=Kr MOUSE	10		
29	4	18,72	29,39999998	23,14999998	23,14999998	sp Q04695 K1C17_HUMAN	Keratin, type I cytoskeletal 17 OS=Homo sapiens GN=KR HUMAN	9		
10	12,07	12,07	14,86999989	11,2499997	10,2413	sp DSC11	Desmoglein-1 OS=Homo sapiens GN=DSC1 PE=1 SV=2	9		
29	0	16,67	26,39000118	20,13999969	20,13999969	sp A5A6M0 K1C17_PANTR	Keratin, type I cytoskeletal 17 OS=Pan troglodytes GN=K PANTR	9		
8	14,1	14,1	40,50000012	33,46999884	33,46999884	sp P31944 CASPE_HUMAN	Caspase-14 OS=Homo sapiens GN=CASP14 PE=1 SV=2	8		
12	11,57	11,57	15,88000059	12,74999976	10,5099984	sp Q08554 DSC1_HUMAN	Desmocollin-1 OS=Homo sapiens GN=DSC1 PE=1 SV=2	8		
13	11,54	11,54	20,02999932	15,76000005	15,76000005	sp P02768 ALBU_HUMAN	Serum albumin OS=Homo sapiens GN=ALB PE=1 SV=2	8		
13	0	11,42	15,60000032	14,45000023	14,45000023	sp Q5NVH5 ALBU_PONAB	Serum albumin OS=Pongo abelii GN=ALB PE=2 SV=2	7		
14	11,5	11,5	58,70000124	52,17000246	52,17000246	sp P15252 REF_HEVBR	Rubber elongation factor protein OS=Hevea brasiliensis HEVBR	7		
15	11,29	11,29	31,63999915	25,67000091	25,67000091	sp P04406 G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase OS=Homo HUMAN	7		
16	10,45	10,45	56,36000037	56,36000037	56,36000037	sp P81605 DCD_HUMAN	Dermcidin OS=Homo sapiens GN=DCD PE=1 SV=2	7		
11	11,65	11,65	25,90000033	22,82000035	18,71999949	sp P29508 SPB3_HUMAN	Serpin B3 OS=Homo sapiens GN=SERPINB3 PE=1 SV=2	6		
15	0	9,24	26,57000124	20,60000002	20,60000002	sp Q5RAB4 G3P_PONAB	Glyceraldehyde-3-phosphate dehydrogenase OS=Pongo PONAB	6		
17	10,01	10,01	55,44999838	55,44999838	54,54999864	sp P31151 S10A7_HUMAN	Protein S100-A7 OS=Homo sapiens GN=S100A7 PE=1 SV HUMAN	5		
18	8,55	8,55	20,46999931	20,46999931	17,11000055	sp P25311 ZA2G_HUMAN	Zinc-alpha-2-glycoprotein OS=Homo sapiens GN=AZGP1 HUMAN	4		
19	8	8	14,13999945	7,359000295	7,359000295	sp Q08188 TGM3_HUMAN	Protein-glutamine gamma-glutamyltransferase E OS=Ho HUMAN	4		
20	7,17	7,17	30,91000021	17,88000017	17,88000017	sp P01857 IGHG1_HUMAN	Ig gamma-1 chain C region OS=Homo sapiens GN=IGHG: HUMAN	4		
37	2,01	8,24	10,96000001	7,69200027	7,69200027	sp Q8N1N4 K2C78_HUMAN	Keratin, type II cytoskeletal 78 OS=Homo sapiens GN=Kf HUMAN	4		
21	6,27	6,27	4,492999986	1,881000027	0,940399989	sp P15924 DESP_HUMAN	Desmoplakin OS=Homo sapiens GN=DSP PE=1 SV=3	3		
22	6	6	37,72000074	37,72000074	37,72000074	sp P06702 S10A9_HUMAN	Protein S100-A9 OS=Homo sapiens GN=S100A9 PE=1 SV HUMAN	3		
23	6	6	54,07999754	44,90000001	44,90000001	sp P01040 CYTA_HUMAN	Cystatin-A OS=Homo sapiens GN=CSTA PE=1 SV=1	3		
25	5,24	5,24	59,14000273	35,47999859	35,47999859	sp P05109 S10A8_HUMAN	Protein S100-A8 OS=Homo sapiens GN=S100A8 PE=1 SV HUMAN	3		
27	4,21	4,21	39,03999925	28,76999974	23,28999937	sp P12273 PIP_HUMAN	Prolactin-inducible protein OS=Homo sapiens GN=PIP Pf HUMAN	3		
30	4	6,02	10,86999997	8,071999997	8,071999997	sp P02769 ALBU_BOVIN	Serum albumin OS=Bos taurus GN=ALB PE=1 SV=4	3		
21	0	4,04	3,745999932	1,525999978	0,589699997	sp E9Q557 DESP_MOUSE	Desmoplakin OS=Mus musculus GN=Dsp PE=1 SV=1	2		
26	4,54	4,54	44,58999932	44,58999932	32,78999925	sp Q8MKD1 UBB_HORSE	Polyubiquitin-B OS=Equus caballus GN=UBB PE=2 SV=3	2		
26	0	4,54	44,74000037	44,74000037	32,89000094	sp Q865C5 UBIQ_CAMDR	Ubiquitin OS=Camelus dromedarius PE=3 SV=2	2		
26	0	4,54	41,98000133	41,98000133	30,86000085	sp Q63429 UBC_RAT	Polyubiquitin-C OS=Rattus norvegicus GN=Ubc PE=1 SV= RAT	2		
26	0	4,54	53,96999717	53,96999717	39,68000114	sp P84589 UBIQ_LUMTE	Ubiquitin (Fragment) OS=Lumbricus terrestris PE=1 SV=: LUMTE	2		
26	0	4,54	21,78999931	21,78999931	16,03000015	sp P79781 RS27A_CHICK	Ubiquitin-40S ribosomal protein S27a OS=Gallus gallus C CHICK	2		
26	0	4,54	26,55999959	26,55999959	19,52999979	sp P68205 RL40_OPHHA	Ubiquitin-60S ribosomal protein L40 OS=Ophiophagus h. OPHHA	2		
26	0	4,54	21,78999931	21,78999931	16,03000015	sp P68203 RS27A_SPOFR	Ubiquitin-40S ribosomal protein S27a OS=Spodoptera fr SPOFR	2		
26	0	4,54	21,94000036	21,94000036	16,13000035	sp P68202 RS27A_PLUXY	Ubiquitin-40S ribosomal protein S27a OS=Plutella xylost PLUXY	2		
26	0	4,54	21,78999931	21,78999931	16,03000015	sp P68200 RS27A ICTPU	Ubiquitin-40S ribosomal protein S27a OS=Ictalurus punc ICTPU	2		
26	0	4,54	44,74000037	44,74000037	32,89000094	sp P68197 UBIQ_CERCA	Ubiquitin OS=Ceratitis capitata PE=1 SV=1	2		
26	0	4,54	26,55999959	26,55999959	19,52999979	sp P63053 UBIQ_PIG	Ubiquitin-60S ribosomal protein L40 OS=Sus scrofa GN= PIG	2		
26	0	4,54	26,55999959	26,55999959	19,52999979	sp P63052 RL40_FELCA	Ubiquitin-60S ribosomal protein L40 OS=Felis catus GN= FELCA	2		
26	0	4,54	26,55999959	26,55999959	19,52999979	sp P63050 RL40_CANLF	Ubiquitin-60S ribosomal protein L40 OS=Canis lupus far CANLF	2		
26	0	4,54	26,55999959	26,55999959	19,52999979	sp P63048 RL40_BOVIN	Ubiquitin-60S ribosomal protein L40 OS=Bos taurus GN= BOVIN	2		
26	0	4,54	21,78999931	21,78999931	16,03000015	sp P62992 RS27A_BOVIN	Ubiquitin-40S ribosomal protein S27a OS=Bos taurus GN BOVIN	2		
26	0	4,54	26,55999959	26,55999959	19,52999979	sp P62987 RL40_HUMAN	Ubiquitin-60S ribosomal protein L40 OS=Homo sapiens (HUMAN	2		
26	0	4,54	26,55999959	26,55999959	19,52999979	sp P62986 RL40_RAT	Ubiquitin-60S ribosomal protein L40 OS=Rattus norvegic RAT	2		
26	0	4,54	26,55999959	26,55999959	19,52999979	sp P62984 RL40_MOUSE	Ubiquitin-60S ribosomal protein L40 OS=Mus musculus (MOUSE	2		
26	0	4,54	21,78999931	21,78999931	16,03000015	sp P62983 RS27A_MOUSE	Ubiquitin-40S ribosomal protein S27a OS=Mus musculus MOUSE	2		
26	0	4,54	21,78999931	21,78999931	16,03000015	sp P62982 RS27A_RAT	Ubiquitin-40S ribosomal protein S27a OS=Rattus norveg RAT	2		
26	0	4,54	21,78999931	21,78999931	16,03000015	sp P62979 RS27A_HUMAN	Ubiquitin-40S ribosomal protein S27a OS=Homo sapiens HUMAN	2		
26	0	4,54	21,78999931	21,78999931	16,03000015	sp P62978 RS27A_CAVPO	Ubiquitin-40S ribosomal protein S27a OS=Cavia porcellu CAVPO	2		
26	0	4,54	41,33999944	41,33999944	30,39999902	sp P62976 UBIQP_CRIGR	Polyubiquitin OS=Cricetulus griseus PE=2 SV=2	2		
26	0	4,54	44,74000037	44,74000037	32,89000094	sp P62975 UBIQ_RABIT	Ubiquitin OS=Oryctolagus cuniculus PE=1 SV=1	2		
26	0	4,54	46,11000121	46,11000121	35,33000052	sp P62972 UBIQ_XENLA	Polyubiquitin (Fragment) OS=Xenopus laevis PE=1 SV=2	2		
26	0	4,54	21,94000036	21,94000036	16,13000035	sp P29504 RS27A_MANSE	Ubiquitin-40S ribosomal protein S27a OS=Manduca sext MANSE	2		
26	0	4,54	26,55999959	26,55999959	19,52999979	sp P18101 RL40_DROME	Ubiquitin-60S ribosomal protein L40 OS=Drosophila mel DROME	2		
26	0	4,54	21,78999931	21,78999931	16,03000015	sp P15357 RS27A_DROME	Ubiquitin-40S ribosomal protein S27a OS=Drosophila m DROME	2		
26	0	4,54	44,35000122	44,35000122	32,60999918	sp POCH28 UBC_BOVIN	Polyubiquitin-C OS=Bos taurus GN=UBC PE=1 SV=1	2		
26	0	4,54	44,56000003	44,56000003	32,76999891	sp POCG69 UBIQP_DROME	Polyubiquitin OS=Drosophila melanogaster GN=Ubi-p63 DROME	2		
26	0	4,54	44,65000033	44,65000033	32,82999992	sp POCG68 UBC_PIG	Polyubiquitin-C OS=Sus scrofa GN=UBC PE=2 SV=1	2		
26	0	4,54	44,53999996	44,53999996	32,74999857	sp POCG67 UBB_GORGO	Polyubiquitin-B OS=Gorilla gorilla gorilla GN=UBB PE=3 S GORGO	2		
26	0	4,54	44,65999901	44,65999901	32,83999886	sp POCG66 UBC_GORGO	Polyubiquitin-C OS=Gorilla gorilla gorilla GN=UBC PE=3 S GORGO	2		
26	0	4,54	44,53999996	44,53999996	32,74999857	sp POCG65 UBB_PANTR	Polyubiquitin-B OS=Pan troglodytes GN=UBB PE=3 SV=1 PANTR	2		
26	0	4,54	44,67999935	44,67999935	32,85000026	sp POCG64 UBC_PANTR	Polyubiquitin-C OS=Pan troglodytes GN=UBC PE=3 SV=1 PANTR	2		
26	0	4,54	44,58999932	44,58999932	32,78999925	sp POCG62 UBB_CHICK	Polyubiquitin-B OS=Gallus gallus GN=UBB PE=2 SV=1	2		
26	0	4,54	44,67999935	44,67999935	32,85000026	sp POCG61 UBC_PONPY	Polyubiquitin-C OS=Pongo pygmaeus GN=UBB PE=3 SV= PONPY	2		
26	0	4,54	44,53999996	44,53999996	32,74999857	sp POCG60 UBB_PONPY	Polyubiquitin-B OS=Pongo pygmaeus GN=UBB PE=3 SV= PONPY	2		
26	0	4,54	44,58999932	44,58999932	32,78999925	sp POCG55 UBB_SHEEP	Polyubiquitin-B OS=Ovis aries GN=UBB PE=2 SV=1	2		
26	0	4,54	43,72999966	43,72999966	32,15000033	sp POCG54 UBB_CAVPO	Polyubiquitin-B OS=Cavia porcellus GN=UBB PE=2 SV=1	2		
26	0	4,54	44,58999932	44,58999932	32,78999925	sp POCG53 UBB_BOVIN	Polyubiquitin-B OS=Bos taurus GN=UBB PE=1 SV=1	2		
26	0	4,54	44,58999932	44,58999932	32,78999925	sp POCG51 UBB_RAT	Polyubiquitin-B OS=Rattus norvegicus GN=Ubb PE=1 SV- RAT	2		
26	0	4,54	41,69000089	41,69000089	30,64999878	sp POCG50 UBC_MOUSE	Polyubiquitin-C OS=Mus musculus GN=Ubc PE=1 SV=2	2		
26	0	4,54	44,58999932	44,58999932	32,78999925	sp POCG49 UBB_MOUSE	Polyubiquitin-B OS=Mus musculus GN=Ubb PE=2 SV=1	2		
26	0	4,54	44,67000067	44,67000067	32,85000026	sp POCG48 UBC_HUMAN	Polyubiquitin-C OS=Homo sapiens GN=UBC PE=1 SV=3	2		
26	0	4,54	44,53999996	44,53999996	32,74999857	sp POCG47 UBB_HUMAN	Polyubiquitin-B OS=Homo sapiens GN=UBB PE=1 SV=1	2		
26	0	4,54	26,55999959	26,55999959	19,52999979	sp POC276 RL40_SHEEP	Ubiquitin-60S ribosomal protein L40 OS=Ovis aries GN=l SHEEP	2		
26	0	4,54	26,55999959	26,55999959	19,52999979	sp POC275 RL40_PONPY	Ubiquitin-60S ribosomal protein L40 OS=Pongo pygmae PONPY	2		
26	0	4,54	26,55999959	26,55999959	19,52999979	sp POC273 RL40_MACFA	Ubiquitin-60S ribosomal protein L40 OS=Macaca fascicu MACFA	2		
31	4	4	9,066999704	9,066999704	9,066999704	sp Q9Y707 ACT2_SUIBO	Actin-2 OS=Suillus bovinus GN=ACT2 PE=2 SV=1	2		
31	0	4	9,066999704	9,066999704	9,066999704	sp Q9Y702 ACT1_SCHCO	Actin-1 OS=Schizophyllum commune GN=ACT1 PE=2 SV: SCHCO	2		
31	0	4	9,066999704	9,066999704	9,066999704	sp Q9UVX4 ACT_COPC7	Actin OS=Coprinopsis cinerea (strain Okayama-7 / 130 / COPC7	2		
31	0	4	9,066999704	9,066999704	9,066999704	sp Q9UVW9 ACTG_ACRCH	Actin, gamma OS=Acremonium chrysogenum GN=ACT F ACRCH	2		
31	0	4	9,042999893	9,042999893	9,042999893	sp Q964E3 ACTC_BIOAL	Actin, cytoplasmic OS=Biophalaria alexandrina PE=3 S' BIOAL	2		
31	0	4	9,042999893	9,042999893	9,042999893	sp Q964E2 ACTC_BIOFP	Actin, cytoplasmic OS=Biophalaria pfeifferi PE=3 SV=1 BIOFP	2		
31	0	4	9,042999893	9,042999893	9,042999893	sp Q964E1 ACTC_BIOOB	Actin, cytoplasmic OS=Biophalaria obstructa PE=3 SV= BIOOB	2		
31	0	4	9,042999893	9,042999893	9,042999893	sp Q964E0 ACTC_BIOTE	Actin, cytoplasmic OS=Biophalaria tenagophila PE=3 S' BIOTE	2		
31	0	4	9,042999893	9,042999893	9,042999893	sp Q964D9 ACTC_PLATR	Actin, cytoplasmic OS=Planorbella trivolis PE=3 SV=1	2		
31	0	4	9,066999704	9,066999704	9,066999704	sp Q93131 ACTC_BRAFL	Actin, cytopl			

31	0	4	9,066999704	9,066999704	9,066999704	sp Q7ZV17 ACTB1_DANRE	Actin, cytoplasmic 1 OS=Danio rerio GN=actba PE=2 SV=	DANRE	2
31	0	4	9,066999704	9,066999704	9,066999704	sp Q7ZVF9 ACTB2_DANRE	Actin, cytoplasmic 2 OS=Danio rerio GN=actbb PE=2 SV=	DANRE	2
31	0	4	9,066999704	9,066999704	9,066999704	sp Q76N69 ACTB_CHLAE	Actin, cytoplasmic 1 OS=Chlorocebus aethiops GN=actb CHLAE	2	2
31	0	4	9,066999704	9,066999704	9,066999704	sp Q71FK5 ACTB_CAVPO	Actin, cytoplasmic 1 OS=Cavia porcellus GN=ACTB PE=2	CAVPO	2
31	0	4	9,066999704	9,066999704	9,066999704	sp Q711N9 ACTB_MESAU	Actin, cytoplasmic 1 OS=Mesocricetus auratus GN=ACTE MESAU	2	2
31	0	4	9,066999704	9,066999704	9,066999704	sp Q6TCF2 ACT_GAEGA	Actin OS=Gaeumannomyces graminis var. avenae GN=A GAEGA	2	2
31	0	4	9,066999704	9,066999704	9,066999704	sp Q6QQA1 ACTB_PIG	Actin, cytoplasmic 1 OS=Sus scrofa GN=ACTB PE=1 SV=2	PIG	2
31	0	4	9,066999704	9,066999704	9,066999704	sp Q6P378 ACTG_XENTR	Actin, cytoplasmic 2 OS=Xenopus tropicalis GN=actg1 PE XENTR	2	2
31	0	4	9,066999704	9,066999704	9,066999704	sp Q6NVA9 ACTB_XENTR	Actin, cytoplasmic 1 OS=Xenopus tropicalis GN=actb PE= XENTR	2	2
31	0	4	9,066999704	9,066999704	9,066999704	sp Q5ZMQ2 ACTG_CHICK	Actin, cytoplasmic 2 OS=Gallus gallus GN=ACTG1 PE=1 S	CHICK	2
31	0	4	9,066999704	9,066999704	9,066999704	sp Q5R6G0 ACTB_PONAB	Actin, cytoplasmic 1 OS=Pongo abelii GN=ACTB PE=2 SV	PONAB	2
31	0	4	9,066999704	9,066999704	9,066999704	sp Q5R1X3 ACTB_PANTR	Actin, cytoplasmic 1 OS=Pan troglodytes GN=ACTB PE=2	PANTR	2
31	0	4	9,066999704	9,066999704	9,066999704	sp Q5JAK2 ACTG_PELLE	Actin, cytoplasmic 2 OS=Pelophylax lessonae GN=actg1	PELLE	2
31	0	4	9,497000277	9,497000277	9,497000277	sp Q55EU6 ACT23_DICDI	Putative actin-23 OS=Dictyostelium discoideum GN=act	DICDI	2
31	0	4	9,042999893	9,042999893	9,042999893	sp Q553U6 ACT22_DICDI	Putative actin-22 OS=Dictyostelium discoideum GN=act	DICDI	2
31	0	4	9,042999893	9,042999893	9,042999893	sp Q54G67 ACT10_DICDI	Actin-10 OS=Dictyostelium discoideum GN=act10 PE=1	S DICDI	2
31	0	4	9,066999704	9,066999704	9,066999704	sp Q4R561 ACTB_MACFA	Actin, cytoplasmic 1 OS=Macaca fascicularis GN=ACTB P	MACFA	2
31	0	4	9,066999704	9,066999704	9,066999704	sp Q4L0Y2 ACTB_SPECI	Actin, cytoplasmic 1 OS=Spermophilus citellus GN=ACTB	SPECI	2
31	0	4	9,042999893	9,042999893	9,042999893	sp Q26065 ACT_PLAMG	Actin, adductor muscle OS=Placopecten magellanicus P	PLAMG	2
31	0	4	8,995000273	8,995000273	8,995000273	sp Q25472 ACT2_MOLOC	Actin, muscle-type OS=Molgula oculata PE=3 SV=1	MOLOC	2
31	0	4	9,042999893	9,042999893	9,042999893	sp Q25010 ACT3A_HELAM	Actin, cytoplasmic A3a OS=Helicoverpa armigera GN=ac	HELAM	2
31	0	4	9,042999893	9,042999893	9,042999893	sp Q07903 ACTC_STRPU	Actin, cytoskeletal 2A OS=Strongylocentrotus purpuratu	STRPU	2
31	0	4	10,99999994	10,99999994	10,99999994	sp Q03342 ACT3_ECHGR	Actin-3 (Fragment) OS=Echinococcus granulosus GN=AC	ECHGR	2
31	0	4	9,066999704	9,066999704	9,066999704	sp Q00215 ACTC_STYPL	Actin, cytoplasmic OS=Styela plicata PE=3 SV=1	STYPL	2
31	0	4	8,970999718	8,970999718	8,970999718	sp Q00214 ACTM_STYPL	Actin, muscle OS=Styela plicata PE=3 SV=1	STYPL	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P92182 ACT1_LUMTE	Actin-1 OS=Lumbricus terrestris GN=ACT1 PE=2 SV=1	LUMTE	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P92179 ACTC_BIOGL	Actin, cytoplasmic OS=Biomphalaria glabrata PE=2 SV=2	BIOGL	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P92176 ACT2_LUMTE	Actin-2 OS=Lumbricus terrestris GN=ACT2 PE=2 SV=1	LUMTE	2
31	0	4	9,139999747	9,139999747	9,139999747	sp P91754 ACT_LUMRU	Actin (Fragment) OS=Lumbricus rubellus PE=2 SV=1	LUMRU	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P90689 ACT_BRUMA	Actin OS=Brugia malayi PE=1 SV=1	BRUMA	2
31	0	4	9,418000281	9,418000281	9,418000281	sp P84856 ACTB_CHLPG	Actin, cytoplasmic 1 OS=Chlorocebus pygerythrus GN=A	CHLPG	2
31	0	4	9,066999704	9,066999704	9,066999704	sp P84336 ACTB_CAMDR	Actin, cytoplasmic 1 OS=Camelus dromedarius GN=ACTB	CAMDR	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P84185 ACT5C_ANOGA	Actin-5C OS=Anopheles gambiae GN=Act5C PE=2 SV=1	ANOGA	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P84184 ACT3B_HELAM	Actin-A3b, cytoplasmic OS=Helicoverpa armigera GN=ac	HELAM	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P84183 ACT4_BOMMO	Actin, cytoplasmic A4 OS=Bombyx mori GN=A4 PE=2 SV	BOMMO	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P83969 ACT1_BACDO	Actin, indirect flight muscle OS=Bactrocera dorsalis PE=	3 BACDO	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P83968 ACT6_DROSI	Actin, indirect flight muscle OS=Drosophila simulans GN	DROSI	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P83967 ACT6_DROME	Actin, indirect flight muscle OS=Drosophila melanogaste	DROME	2
31	0	4	9,066999704	9,066999704	9,066999704	sp P83751 ACTB_CTEID	Actin, cytoplasmic 1 OS=Ctenopharyngodon idella GN=a	CTEID	2
31	0	4	9,066999704	9,066999704	9,066999704	sp P83750 ACTB_CYPCA	Actin, cytoplasmic 1 OS=Cyprinus carpio GN=actb PE=3	: CYPCA	2
31	0	4	9,066999704	9,066999704	9,066999704	sp P78711 ACT_NEUCR	Actin OS=Neurospora crassa (strain ATCC 24698 / 74-OR	NEUCR	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P69005 ACTD_STRPU	Actin, cytoskeletal 2B OS=Strongylocentrotus purpuratu	STRPU	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P69004 ACT2_STRFN	Actin-15B OS=Strongylocentrotus franciscanus PE=2 SV=	STRFN	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P69003 ACT1_HELTB	Actin Cyl, cytoplasmic OS=Helicoidaris tuberculata PE=3	HELTB	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P69002 ACT1_HELER	Actin Cyl, cytoplasmic OS=Helicoidaris erythrogramma	F HELER	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P68556 ACT1_DIPDE	Actin-1/4 OS=Diphyllbothrium dendriticum GN=ACT1 P	DIPDE	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P68555 ACT_TAESO	Actin OS=Taenia solium GN=ACT1 PE=3 SV=1	TAESO	2
31	0	4	9,066999704	9,066999704	9,066999704	sp P68143 ACTB_OREMO	Actin, cytoplasmic 1 OS=Oreochromis mossambicus GN=	OREMO	2
31	0	4	9,066999704	9,066999704	9,066999704	sp P68142 ACTB1_TAKRU	Actin, cytoplasmic 1 OS=Takifugu rubripes GN=actba PE=	TAKRU	2
31	0	4	9,066999704	9,066999704	9,066999704	sp P63261 ACTG_HUMAN	Actin, cytoplasmic 2 OS=Homo sapiens GN=ACTG1 PE=1	HUMAN	2
31	0	4	9,066999704	9,066999704	9,066999704	sp P63260 ACTG_MOUSE	Actin, cytoplasmic 2 OS=Mus musculus GN=Actg1 PE=1	: MOUSE	2
31	0	4	9,066999704	9,066999704	9,066999704	sp P63259 ACTG_RAT	Actin, cytoplasmic 2 OS=Rattus norvegicus GN=Actg1 PE	RAT	2
31	0	4	9,066999704	9,066999704	9,066999704	sp P63258 ACTG_BOVIN	Actin, cytoplasmic 2 OS=Bos taurus GN=ACTG1 PE=1 SV=	BOVIN	2
31	0	4	9,066999704	9,066999704	9,066999704	sp P63257 ACTG_TRIVU	Actin, cytoplasmic 2 OS=Trichosurus vulpecula GN=ACT	TRIVU	2
31	0	4	9,066999704	9,066999704	9,066999704	sp P63256 ACTG_ANSAN	Actin, cytoplasmic 2 OS=Anser anser GN=ACTG1 P	ANSAN	2
31	0	4	9,066999704	9,066999704	9,066999704	sp P60713 ACTB_SHEEP	Actin, cytoplasmic 1 OS=Ovis aries GN=ACTB PE=2 SV=1	SHEEP	2
31	0	4	9,066999704	9,066999704	9,066999704	sp P60712 ACTB_BOVIN	Actin, cytoplasmic 1 OS=Bos taurus GN=ACTB PE=1 SV=1	BOVIN	2
31	0	4	9,066999704	9,066999704	9,066999704	sp P60711 ACTB_RAT	Actin, cytoplasmic 1 OS=Rattus norvegicus GN=Actb PE=	RAT	2
31	0	4	9,066999704	9,066999704	9,066999704	sp P60710 ACTB_MOUSE	Actin, cytoplasmic 1 OS=Mus musculus GN=Actb PE=1 S	MOUSE	2
31	0	4	9,066999704	9,066999704	9,066999704	sp P60709 ACTB_HUMAN	Actin, cytoplasmic 1 OS=Homo sapiens GN=ACTB PE=1 S	HUMAN	2
31	0	4	9,066999704	9,066999704	9,066999704	sp P60708 ACTB_HORSE	Actin, cytoplasmic 1 OS=Equus caballus GN=ACTB PE=2	: HORSE	2
31	0	4	9,066999704	9,066999704	9,066999704	sp P60707 ACTB_TRIVU	Actin, cytoplasmic 1 OS=Trichosurus vulpecula GN=ACT	E TRIVU	2
31	0	4	9,066999704	9,066999704	9,066999704	sp P60706 ACTB_CHICK	Actin, cytoplasmic 1 OS=Gallus gallus GN=ACTB PE=1	SV CHICK	2
31	0	4	9,066999704	9,066999704	9,066999704	sp P53689 ACT_PHARH	Actin OS=Phaffia rhodozyma PE=3 SV=1	PHARH	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P53506 ACT8_XENLA	Actin, cytoplasmic type 8 OS=Xenopus laevis PE=3 SV=1	XENLA	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P53505 ACT5_XENLA	Actin, cytoplasmic type 5 OS=Xenopus laevis PE=3 SV=1	XENLA	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P53501 ACT3_DROME	Actin-57B OS=Drosophila melanogaster GN=Act57B PE=	DROME	2
31	0	4	9,066999704	9,066999704	9,066999704	sp P53486 ACTB3_TAKRU	Actin, cytoplasmic 3 OS=Takifugu rubripes GN=actcb PE=	TAKRU	2
31	0	4	9,066999704	9,066999704	9,066999704	sp P53485 ACTB2_TAKRU	Actin, cytoplasmic 2 OS=Takifugu rubripes GN=actbb PE=	TAKRU	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P53478 ACT5_CHICK	Actin, cytoplasmic type 5 OS=Gallus gallus PE=3 SV=1	CHICK	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P53474 ACTE_STRPU	Actin, cytoskeletal 3A OS=Strongylocentrotus purpuratu	STRPU	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P53473 ACTB_STRPU	Actin, cytoskeletal 1B OS=Strongylocentrotus purpuratu	STRPU	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P53472 ACTA_STRPU	Actin, cytoskeletal 1A OS=Strongylocentrotus purpuratu	STRPU	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P53471 ACT2_SCHMA	Actin-2 OS=Schistosoma mansoni PE=2 SV=1	SCHMA	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P53470 ACT1_SCHMA	Actin-1 OS=Schistosoma mansoni PE=2 SV=1	SCHMA	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P53466 ACT2_LYPTI	Actin, cytoskeletal 2 OS=Lytechinus pictus PE=2 SV=1	LYPTI	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P53465 ACT1_LYPTI	Actin, cytoskeletal 1 OS=Lytechinus pictus PE=2 SV=1	LYPTI	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P53464 ACTM_HELTB	Actin, cytoskeletal OS=Helicoidaris tuberculata PE=3	SV- HELTB	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P53463 ACTM_HELER	Actin, cytoskeletal OS=Helicoidaris erythrogramma PE=	3 HELER	2
31	0	4	9,164000303	9,164000303	9,164000303	sp P53458 ACT5_DIPDE	Actin-5 (Fragment) OS=Diphyllbothrium dendriticum	G DIPDE	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P53456 ACT2_DIPDE	Actin-2 OS=Diphyllbothrium dendriticum GN=ACT2 PE=	DIPDE	2
31	0	4	9,066999704	9,066999704	9,066999704	sp P53455 ACT_AIECG	Actin OS=Aejlollomyces capsulatus (strain G186AR / H82	/ AIECG	2
31	0	4	9,066999704	9,066999704	9,066999704	sp P50138 ACT_PUCGR	Actin OS=Puccinia graminis PE=3 SV=1	PUCGR	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P49871 ACT_MANSE	Actin, muscle OS=Manduca sexta PE=2 SV=1	MANSE	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P49128 ACT1_AEDAE	Actin-1 OS=Aedes aegypti GN=ACT-1 PE=2 SV=2	AEDAE	2
31	0	4	9,066999704	9,066999704	9,066999704	sp P48975 ACTB_CRIGR	Actin, cytoplasmic 1 OS=Cricetulus griseus GN=ACTB PE=	CRIGR	2
31	0	4	9,066999704	9,066999704	9,066999704	sp P48465 ACT_CRYNH	Actin OS=Cryptococcus neoformans var. grubii serotype	CRYNH	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P45887 ACT5_BACDO	Actin-5, muscle-specific OS=Bactrocera dorsalis PE=2	SV BACDO	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P45886 ACT3_BACDO	Actin-3, muscle-specific OS=Bactrocera dorsalis PE=2	SV BACDO	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P45885 ACT2_BACDO	Actin-2, muscle-specific OS=Bactrocera dorsalis PE=2	SV BACDO	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P41341 ACTY_LIMPO	Actin-11 OS=Limulus polyphemus PE=2 SV=1	LIMPO	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P41340 ACT3_LIMPO	Actin-3 OS=Limulus polyphemus PE=1 SV=1	LIMPO	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P41339 ACTA_LIMPO	Actin, acrosomal process isoform OS=Limulus polyphem	2	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P41113 ACT3_PODCA	Actin-3 OS=Podocoryna carnea GN=ACT3 PE=3 SV=1	PODCA	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P41112 ACT1_PODCA	Actin-1/2 OS=Podocoryna carnea GN=ACTIA PE=2 SV=1	PODCA	2
31	0	4	9,066999704	9,066999704	9,0669997				

31	0	4	9,042999893	9,042999893	9,042999893	sp P10990 ACT1_STRFN	Actin-15A OS=Strongylocentrotus franciscanus PE=3 SV=	STRFN	2
31	0	4	9,042999893	9,042999893	9,042999893	sp P10987 ACT1_DROME	Actin-5C OS=Drosophila melanogaster GN=Act5C PE=1 S DROME		2
31	0	4	9,042999893	9,042999893	9,042999893	sp P10981 ACT5_DROME	Actin-87E OS=Drosophila melanogaster GN=Act87E PE=: DROME		2
31	0	4	9,066999704	9,066999704	9,066999704	sp P10365 ACT_THELA	Actin OS=Thermomyces lanuginosus PE=3 SV=1 THELA		2
31	0	4	9,042999893	9,042999893	9,042999893	sp P07836 ACT1_BOMMO	Actin, muscle-type A1 OS=Bombyx mori PE=3 SV=1 BOMMO		2
31	0	4	9,042999893	9,042999893	9,042999893	sp P07830 ACT1_DICDI	Major actin OS=Dictyostelium discoideum GN=act1 PE=: DICDI		2
31	0	4	9,042999893	9,042999893	9,042999893	sp P07829 ACT3_DICDI	Actin-3 OS=Dictyostelium discoideum GN=act3 PE=3 SV: DICDI		2
31	0	4	9,042999893	9,042999893	9,042999893	sp P04829 ACT3_BOMMO	Actin, cytoplasmic A3 OS=Bombyx mori PE=3 SV=3 BOMMO		2
31	0	4	9,066999704	9,066999704	9,066999704	sp P02578 ACT1_ACACA	Actin-1 OS=Acanthamoeba castellanii PE=1 SV=1 ACACA		2
31	0	4	9,042999893	9,042999893	9,042999893	sp P02576 ACTA_PHYPO	Actin, plasmodial isoform OS=Physarum polycephalum C PHYPO		2
31	0	4	9,042999893	9,042999893	9,042999893	sp P02574 ACT4_DROME	Actin, larval muscle OS=Drosophila melanogaster GN=Ac DROME		2
31	0	4	9,042999893	9,042999893	9,042999893	sp P02572 ACT2_DROME	Actin-42A OS=Drosophila melanogaster GN=act42A PE=: DROME		2
31	0	4	9,066999704	9,066999704	9,066999704	sp O93400 ACTB_XENLA	Actin, cytoplasmic 1 OS=Xenopus laevis GN=actb PE=2 S XENLA		2
31	0	4	9,019000083	9,019000083	9,019000083	sp O65316 ACT_S_MESVI	Actin OS=Mesostigma viride PE=3 SV=1 MESVI		2
31	0	4	9,066999704	9,066999704	9,066999704	sp O42161 ACTB_SALSA	Actin, cytoplasmic 1 OS=Salmo salar GN=actb PE=2 SV=1 SALSA		2
31	0	4	9,066999704	9,066999704	9,066999704	sp O18840 ACTB_CANLF	Actin, cytoplasmic 1 OS=Canis lupus familiaris GN=ACTB CANLF		2
31	0	4	9,042999893	9,042999893	9,042999893	sp O18500 ACT2_SACKO	Actin-2 OS=Saccoglossus kowalevskii PE=2 SV=1 SACKO		2
31	0	4	9,042999893	9,042999893	9,042999893	sp O18499 ACT1_SACKO	Actin-1 OS=Saccoglossus kowalevskii PE=2 SV=1 SACKO		2
31	0	4	9,042999893	9,042999893	9,042999893	sp O17320 ACT_CRAGI	Actin OS=Crassostrea gigas PE=2 SV=1 CRAGI		2
31	0	4	9,042999893	9,042999893	9,042999893	sp O16808 ACT_MAYDE	Actin OS=Mayetilia destructor PE=2 SV=1 MAYDE		2
31	0	4	9,066999704	9,066999704	9,066999704	sp O13419 ACT_BOTFU	Actin OS=Botryotinia fuckeliana GN=actA PE=3 SV=1 BOTFU		2
31	0	4	9,066999704	9,066999704	9,066999704	sp A2BDB0 ACTG_XENLA	Actin, cytoplasmic 2 OS=Xenopus laevis GN=actg1 PE=2 XENLA		2
32	3,49	3,49	25,49000084	21,0800007	16,17999971	sp O82803 SRPP_HEVBR	Small rubber particle protein OS=Hevea brasiliensis GN= HEVBR		2
33	3,19	3,19	35,85000038	26,4200002	26,4200002	sp Q5R9M3 THIO_PONAB	Thioredoxin OS=Pongo abelii GN=TXN PE=3 SV=3 PONAB		2
33	0	3,19	36,19000018	26,66999996	26,66999996	sp P10599 THIO_HUMAN	Thioredoxin OS=Homo sapiens GN=TXN PE=1 SV=3 HUMAN		2
34	3,08	3,08	9,933000058	2,952999994	2,952999994	sp Q8SP11 PLAK_BOVIN	Junction plakoglobin OS=Bos taurus GN=JUP PE=2 SV=1 BOVIN		2
34	0	3,08	9,933000058	2,952999994	2,952999994	sp Q6P0K8 PLAK_RAT	Junction plakoglobin OS=Rattus norvegicus GN=Jup PE=: RAT		2
34	0	3,08	9,933000058	2,952999994	2,952999994	sp Q02257 PLAK_MOUSE	Junction plakoglobin OS=Mus musculus GN=Jup PE=1 SV MOUSE		2
34	0	3,08	9,933000058	2,952999994	2,952999994	sp P14923 PLAK_HUMAN	Junction plakoglobin OS=Homo sapiens GN=JUP PE=1 SV HUMAN		2
34	0	3,08	7,248000056	2,952999994	2,952999994	sp Q8WNW3 PLAK_PIG	Junction plakoglobin OS=Sus scrofa GN=Jup PE=2 SV=1 PIG		2
39	2	4,03	15,89999944	7,951000333	7,951000333	sp P01861 IGHG4_HUMAN	Ig gamma-4 chain C region OS=Homo sapiens GN=IGHG4 HUMAN		2
39	0	4,03	13,78999949	6,897000223	6,897000223	sp P01860 IGHG3_HUMAN	Ig gamma-3 chain C region OS=Homo sapiens GN=IGHG3 HUMAN		2
39	0	4,01	11,03999987	7,975000143	7,975000143	sp P01859 IGHG2_HUMAN	Ig gamma-2 chain C region OS=Homo sapiens GN=IGHG2 HUMAN		2
40	2	2,78	4,684000009	4,684000009	4,684000009	sp Q6IFX1 K1C24_RAT	Keratin, type I cytoskeletal 24 OS=Rattus norvegicus GN: RAT		2
40	0	2,78	4,492000118	4,492000118	4,492000118	sp A1L317 K1C24_MOUSE	Keratin, type I cytoskeletal 24 OS=Mus musculus GN=Kri MOUSE		2
56	1,44	1,44	16,11000001	16,11000001	16,11000001	sp Q15828 CYTM_HUMAN	Cystatin-M OS=Homo sapiens GN=CST6 PE=1 SV=1 HUMAN		2
26	0	2,47	21,66000009	21,66000009	11,81999967	sp P42740 UBIQ_AGLNE	Polyubiquitin OS=Aglaothamnion neglectum PE=2 SV=2 AGLNE		1
26	0	2,47	23,3799994	23,3799994	11,6899997	sp Q8SWD4 UBIQ_ENCCU	Ubiquitin OS=Encephalitozoon cuniculi (strain GB-M1) G ENCCU		1
26	0	2,47	14,05999959	14,05999959	7,03099966	sp P69201 RL40_LEIMA	Ubiquitin-60S ribosomal protein L40 OS=Leishmania ma LEIMA		1
26	0	2,47	14,05999959	14,05999959	7,03099966	sp P69200 RL40_LEITA	Ubiquitin-60S ribosomal protein L40 OS=Leishmania tar LEITA		1
26	0	2,47	11,99999973	11,99999973	5,99999986	sp P69061 RS27A_KLULA	Ubiquitin-40S ribosomal protein S27a OS=Kluyveromyce KLULA		1
26	0	2,47	21,66000009	21,66000009	9,847000241	sp P59669 UBIQ_GEOCY	Polyubiquitin OS=Geodia cydonium PE=2 SV=2 GEOCY		1
26	0	2,47	14,05999959	14,05999959	7,03099966	sp P49632 RL40_CAEEL	Ubiquitin-60S ribosomal protein L40 OS=Caenorhabditis CAEEL		1
26	0	2,47	13,9500007	13,9500007	6,977000087	sp P46575 RL40_EIMBO	Ubiquitin-60S ribosomal protein L40 OS=Elmeria bovis P EIMBO		1
26	0	2,47	13,9500007	13,9500007	6,977000087	sp P40909 RL40_CRYNJ	Ubiquitin-60S ribosomal protein L40 OS=Cryptococcus n CRYNJ		1
26	0	2,47	13,9500007	13,9500007	6,977000087	sp P33190 RL40_TETPY	Ubiquitin-60S ribosomal protein L40 OS=Tetrahymena p TETPY		1
26	0	2,47	27,07000077	27,07000077	13,52999955	sp P23398 UBIQ_STRPU	Polyubiquitin (Fragment) OS=Strongylocentrotus purpur STRPU		1
26	0	2,47	23,5799998	23,5799998	11,7899999	sp P22589 UBIQ_PHYIN	Polyubiquitin OS=Phytophthora infestans PE=1 SV=2 PHYIN		1
26	0	2,47	23,68000001	23,68000001	11,84	sp P19848 UBIQ_COPCO	Ubiquitin OS=Coprinellus congregatus PE=1 SV=1 COPCO		1
26	0	2,47	11,6899997	11,6899997	5,843999982	sp P14799 RS27A_NEUCR	Ubiquitin-40S ribosomal protein S27a OS=Neurospora cr NEUCR		1
26	0	2,47	11,6899997	11,6899997	5,843999982	sp P14797 RS27A_DICDI	Ubiquitin-40S ribosomal protein S27a OS=Dictyostelium DICDI		1
26	0	2,47	14,05999959	14,05999959	7,03099966	sp P14794 RL40_DICDI	Ubiquitin-60S ribosomal protein L40 OS=Dictyostelium c DICDI		1
26	0	2,47	13,9500007	13,9500007	6,977000087	sp P0DJ25 RL40_TETTS	Ubiquitin-60S ribosomal protein L40 OS=Tetrahymena tl TETTS		1
26	0	2,47	14,05999959	14,05999959	7,03099966	sp POCH09 RL402_YEAST	Ubiquitin-60S ribosomal protein L40 OS=Saccharomyces YEAST		1
26	0	2,47	14,05999959	14,05999959	7,03099966	sp POCH08 RL401_YEAST	Ubiquitin-60S ribosomal protein L40 OS=Saccharomyces YEAST		1
26	0	2,47	14,05999959	14,05999959	7,03099966	sp POCH07 RL402_SCHPO	Ubiquitin-60S ribosomal protein L40 OS=Schizosaccharo SCHPO		1
26	0	2,47	14,05999959	14,05999959	7,03099966	sp POCH06 RL401_SCHPO	Ubiquitin-60S ribosomal protein L40 OS=Schizosaccharo SCHPO		1
26	0	2,47	23,61000031	23,61000031	11,80000007	sp POCG88 UBIQ_DICDI	Polyubiquitin-J OS=Dictyostelium discoideum GN=ubqJ f DICDI		1
26	0	2,47	23,62000048	23,62000048	11,81000024	sp POCG82 UBIQ_TETPY	Polyubiquitin OS=Tetrahymena pyriformis GN=Tu20 PE: TETPY		1
26	0	2,47	23,62000048	23,62000048	11,81000024	sp POCG81 UBIQH_DICDI	Polyubiquitin-H OS=Dictyostelium discoideum GN=ubqH F DICDI		1
26	0	2,47	23,61000031	23,61000031	11,80000007	sp POCG80 UBIQI_DICDI	Polyubiquitin-I OS=Dictyostelium discoideum GN=ubqI F DICDI		1
26	0	2,47	23,62000048	23,62000048	11,81000024	sp POCG79 UBIQG_DICDI	Polyubiquitin-G OS=Dictyostelium discoideum GN=ubqG DICDI		1
26	0	2,47	23,63999933	23,63999933	11,81999967	sp POCG78 UBIQF_DICDI	Polyubiquitin-F OS=Dictyostelium discoideum GN=ubqF DICDI		1
26	0	2,47	23,5799998	23,5799998	11,7899999	sp POCG77 UBIQD_DICDI	Polyubiquitin-D OS=Dictyostelium discoideum GN=ubqD DICDI		1
26	0	2,47	23,62000048	23,62000048	11,81000024	sp POCG76 UBIQA_DICDI	Polyubiquitin-A OS=Dictyostelium discoideum GN=ubqA DICDI		1
26	0	2,47	23,62000048	23,62000048	11,81000024	sp POCG75 UBIAP_KLULA	Polyubiquitin OS=Kluyveromyces lactis (strain ATCC 858 KLULA		1
26	0	2,47	23,61000031	23,61000031	11,80000007	sp POCG74 UBIAP_CANAX	Polyubiquitin OS=Candida albicans GN=UBI4 PE=1 SV=1 CANAX		1
26	0	2,47	23,5799998	23,5799998	11,7899999	sp POCG73 UBIIP_CANAX	Polyubiquitin OS=Candida albicans GN=UBI1 PE=1 SV=1 CANAX		1
26	0	2,47	23,55999947	23,55999947	11,77999973	sp POCG72 UBIAP_SCHPO	Polyubiquitin OS=Schizosaccharomyces pombe (strain 9 SCHPO		1
26	0	2,47	23,63000065	23,63000065	11,81000024	sp POCG71 UBIQI_CAEEL	Polyubiquitin-A OS=Caenorhabditis elegans GN=ubq-1 P CAEEL		1
26	0	2,47	23,61000031	23,61000031	11,80000007	sp POCG70 UBIAP_NEUCR	Polyubiquitin OS=Neurospora crassa (strain ATCC 24698 NEUCR		1
26	0	2,47	23,62000048	23,62000048	11,81000024	sp POCG63 UBIAP_YEAST	Polyubiquitin OS=Saccharomyces cerevisiae (strain ATCY YEAST		1
26	0	2,47	11,99999973	11,99999973	5,99999986	sp POC8R3 RS27B_SCHPO	Ubiquitin-40S ribosomal protein S27b OS=Schizosacchar SCHPO		1
26	0	2,47	14,05999959	14,05999959	7,03099966	sp POC224 RL40_NEUCR	Ubiquitin-60S ribosomal protein L40 OS=Neurospora cra NEUCR		1
26	0	2,47	11,99999973	11,99999973	5,99999986	sp POC016 RS27A_SCHPO	Ubiquitin-40S ribosomal protein S27a OS=Schizosacchar SCHPO		1
26	0	2,47	11,84	11,84	5,92099987	sp P05759 RS27A_YEAST	Ubiquitin-40S ribosomal protein S31 OS=Saccharomyces YEAST		1
30	0	2	3,460000083	3,460000083	3,460000083	sp P14639 ALBU_SHEEP	Serum albumin OS=Ovis aries GN=ALB PE=1 SV=1 SHEEP		1
31	0	2,01	9,042999893	4,255000129	4,255000129	sp Q8BFZ3 ACTBL_MOUSE	Beta-actin-like protein 2 OS=Mus musculus GN=Actbl2 F MOUSE		1
31	0	2,01	9,042999893	4,255000129	4,255000129	sp Q562R1 ACTBL_HUMAN	Beta-actin-like protein 2 OS=Homo sapiens GN=ACTBL2 HUMAN		1
31	0	2	2,697999962	1,487999968	1,487999968	sp Q6S8J3 POTEE_HUMAN	POTE ankyrin domain family member E OS=Homo sapie HUMAN		1
31	0	2	2,697999962	1,487999968	1,487999968	sp A5A3E0 POTEF_HUMAN	POTE ankyrin domain family member F OS=Homo sapie HUMAN		1
31	0	2	4,800000042	4,800000042	4,800000042	sp Q9Y896 ACT2_SCHCO	Actin-2 OS=Schizophyllum commune GN=ACT2 PE=3 SV: SCHCO		1
31	0	2	4,800000042	4,800000042	4,800000042	sp Q9Y701 ACT1_SUIBO	Actin-1 OS=Suillus bovinus GN=ACT1 PE=2 SV=1 SUIBO		1
31	0	2	4,255000129	4,255000129	4,255000129	sp Q9UVZ8 ACT_CANDC	Actin OS=Candida dubliniensis (strain CD36 / ATCC MYA CANDC		1
31	0	2	4,800000042	4,800000042	4,800000042	sp Q9UVF3 ACT_YARLI	Actin OS=Yarrowia lipolytica (strain CLIB 122 / E 150) GA YARLI		1
31	0	2	4,267000034	4,267000034	4,267000034	sp Q9UR50 ACTG_PENCH	Actin, gamma OS=Penicillium chrysogenum GN=ACT PE: PENCH		1
31	0	2	4,255000129	4,255000129	4,255000129	sp Q9P4D1 ACT_PICPG	Actin OS=Komagataella pastoris (strain GS115 / ATCC 20 PICPG		1
31	0	2	4,267000034	4,267000034	4,267000034	sp Q9BYX7 ACTBM_HUMAN	Putative beta-actin-like protein 3 OS=Homo sapiens GN: HUMAN		1
31	0	2	4,786999896	4,786999896	4,786999896	sp Q99023 ACT_HYPJE	Actin OS=Hypocrea jecorina GN=act PE=3 SV=1 HYPJE		1
31	0	2	4,244000092	4,244000092	4,244000092	sp Q98972 ACTS_ORYLA	Actin, alpha skeletal muscle OS=Oryzias latipes GN=acta ORYLA		1
31	0	2	5,356999859	5,356999859	5,356999859	sp Q96483 ACT2_SOLL	Actin-51 (Fragment) OS=Solanum lycopersicum PE=3 SV SOLL		1
31	0	2	5,356999859	5,356999859	5,356999859	sp Q96482 ACT1_SOLL	Actin-41 (Fragment) OS=Solanum lycopersicum PE=3 SV SOLL		1
31	0	2	4,233000055	4,233000055	4,233000055	sp Q93132 ACTM_BRAFL	Actin, muscle OS=Branchiostoma floridae PE=2 SV=1 BRAFL		1
31	0	2	4,222000018	4,222000018	4,222000018	sp Q93130 ACTM_BRABE	Actin, muscle OS=Branchiostoma belcheri PE=2 SV=1 BRABE		1
31	0	2	5,754999816	5,754999816	5,754999816	sp Q92192 ACT_CALFI	Actin (Fragment) OS=Calanus finmarchicus PE=2 SV=1 CALFI		1
31	0	2	4,244000092	4,244000092	4,244000092	sp Q90X97 ACTS_ATRMM	Actin, alpha skeletal muscle OS=Atractaspis microlepidio ATRMM		1
31									

31	0	2	4,244000092	4,244000092	4,244000092	sp Q32C07 ACTC_BOVIN	Actin, alpha cardiac muscle 1 OS=Bos taurus GN=ACTC1 BOVIN	1
31	0	2	4,786999896	4,786999896	4,786999896	sp Q39758 ACT_FUCVE	Actin OS=Fucus vesiculosus PE=2 SV=1 FUCVE	1
31	0	2	21,17999941	21,17999941	21,17999941	sp Q39596 ACT_OXYRB	Actin (Fragment) OS=Oxybasis rubra PE=3 SV=1 OXYRB	1
31	0	2	9,301999956	9,301999956	9,301999956	sp Q25381 ACTM_LYTP1	Actin, muscle (Fragment) OS=Lytechinus pictus PE=3 SV: LYTP1	1
31	0	2	9,301999956	9,301999956	9,301999956	sp Q25379 ACT3_LYTP1	Actin, cytoskeletal 3 (Fragment) OS=Lytechinus pictus PI LYTP1	1
31	0	2	10,98000035	10,98000035	10,98000035	sp Q11212 ACT_SPOLI	Actin (Fragment) OS=Spodoptera littoralis PE=2 SV=1 SPOLI	1
31	0	2	4,774999991	4,774999991	4,774999991	sp Q10DV7 ACT1_ORYSJ	Actin-1 OS=Oryza sativa subsp. japonica GN=ACT1 PE=2 ORYSJ	1
31	0	2	4,267000034	4,267000034	4,267000034	sp Q0PGG4 ACTB_BOSMU	Actin, cytoplasmic 1 OS=Bos mutus grunniens GN=ACTB BOSMU	1
31	0	2	4,774999991	4,774999991	4,774999991	sp Q05214 ACT1_TOBAC	Actin OS=Nicotiana tabacum PE=3 SV=1 TOBAC	1
31	0	2	4,786999896	4,786999896	4,786999896	sp Q03341 ACT2_ECHGR	Actin-2 OS=Echinococcus granulosus GN=ACTII PE=3 SV= ECHGR	1
31	0	2	5,421999842	5,421999842	5,421999842	sp P93587 ACT1_SOLTU	Actin-42 (Fragment) OS=Solanum tuberosum PE=3 SV=1 SOLTU	1
31	0	2	5,356999859	5,356999859	5,356999859	sp P93584 ACT9_SOLTU	Actin-82 (Fragment) OS=Solanum tuberosum PE=3 SV=1 SOLTU	1
31	0	2	5,356999859	5,356999859	5,356999859	sp P93375 ACT7_TOBAC	Actin-104 (Fragment) OS=Nicotiana tabacum PE=3 SV=1 TOBAC	1
31	0	2	5,310000107	5,310000107	5,310000107	sp P93373 ACT3_TOBAC	Actin-54 (Fragment) OS=Nicotiana tabacum PE=3 SV=1 TOBAC	1
31	0	2	8,332999796	8,332999796	8,332999796	sp P86700 ACT_CHIOP	Actin, muscle (Fragments) OS=Chionoeetes opilio PE=1 CHIOP	1
31	0	2	40,0000006	40,0000006	40,0000006	sp P85911 ACT1_PSEMZ	Actin-1 (Fragment) OS=Pseudotsuga menziesii PE=1 SV= PSEMZ	1
31	0	2	5,356999859	5,356999859	5,356999859	sp P81129 ACT8_SOLTU	Actin-79 (Fragment) OS=Solanum tuberosum PE=3 SV=1 SOLTU	1
31	0	2	5,356999859	5,356999859	5,356999859	sp P81228 ACT5_SOLTU	Actin-66 (Fragment) OS=Solanum tuberosum PE=3 SV=1 SOLTU	1
31	0	2	4,267000034	4,267000034	4,267000034	sp P79818 ACTB_ORYLA	Actin, cytoplasmic 1 OS=Oryzias latipes GN=actb PE=2 S' ORYLA	1
31	0	2	4,244000092	4,244000092	4,244000092	sp P68264 ACTS_OREMO	Actin, alpha skeletal muscle OS=Oreochromis mossambai OREMO	1
31	0	2	4,244000092	4,244000092	4,244000092	sp P68140 ACTSA_TAKRU	Actin, alpha skeletal muscle A OS=Takifugu rubripes GN= TAKRU	1
31	0	2	4,244000092	4,244000092	4,244000092	sp P68139 ACTS_CHICK	Actin, alpha skeletal muscle OS=Gallus gallus GN=ACTA1 CHICK	1
31	0	2	4,244000092	4,244000092	4,244000092	sp P68138 ACTS_BOVIN	Actin, alpha skeletal muscle OS=Bos taurus GN=ACTA1 F BOVIN	1
31	0	2	4,244000092	4,244000092	4,244000092	sp P68137 ACTS_PIG	Actin, alpha skeletal muscle OS=Sus scrofa GN=ACTA1 P PIG	1
31	0	2	4,244000092	4,244000092	4,244000092	sp P68136 ACTS_RAT	Actin, alpha skeletal muscle OS=Rattus norvegicus GN=≠ RAT	1
31	0	2	4,244000092	4,244000092	4,244000092	sp P68135 ACTS_RABIT	Actin, alpha skeletal muscle OS=Oryctolagus cuniculus G RABIT	1
31	0	2	4,244000092	4,244000092	4,244000092	sp P68134 ACTS_MOUSE	Actin, alpha skeletal muscle OS=Mus musculus GN=Acta MOUSE	1
31	0	2	4,244000092	4,244000092	4,244000092	sp P68133 ACTS_HUMAN	Actin, alpha skeletal muscle OS=Homo sapiens GN=ACT/ HUMAN	1
31	0	2	4,244000092	4,244000092	4,244000092	sp P68035 ACTC_RAT	Actin, alpha cardiac muscle 1 OS=Rattus norvegicus GN= RAT	1
31	0	2	4,244000092	4,244000092	4,244000092	sp P68034 ACTC_CHICK	Actin, alpha cardiac muscle 1 OS=Gallus gallus GN=ACTC CHICK	1
31	0	2	4,244000092	4,244000092	4,244000092	sp P68033 ACTC_MOUSE	Actin, alpha cardiac muscle 1 OS=Mus musculus GN=Act MOUSE	1
31	0	2	4,244000092	4,244000092	4,244000092	sp P68032 ACTC_HUMAN	Actin, alpha cardiac muscle 1 OS=Homo sapiens GN=ACT HUMAN	1
31	0	2	4,255000129	4,255000129	4,255000129	sp P63270 ACTH_CHICK	Actin, gamma-enteric smooth muscle OS=Gallus gallus C CHICK	1
31	0	2	4,255000129	4,255000129	4,255000129	sp P63269 ACTH_RAT	Actin, gamma-enteric smooth muscle OS=Rattus norveg RAT	1
31	0	2	4,255000129	4,255000129	4,255000129	sp P63268 ACTH_MOUSE	Actin, gamma-enteric smooth muscle OS=Mus musculus MOUSE	1
31	0	2	4,255000129	4,255000129	4,255000129	sp P63267 ACTH_HUMAN	Actin, gamma-enteric smooth muscle OS=Homo sapiens HUMAN	1
31	0	2	4,244000092	4,244000092	4,244000092	sp P62740 ACTA_RABIT	Actin, aortic smooth muscle OS=Oryctolagus cuniculus G RABIT	1
31	0	2	4,244000092	4,244000092	4,244000092	sp P62739 ACTA_BOVIN	Actin, aortic smooth muscle OS=Bos taurus GN=ACTA2 F BOVIN	1
31	0	2	4,244000092	4,244000092	4,244000092	sp P62738 ACTA_RAT	Actin, aortic smooth muscle OS=Rattus norvegicus GN=≠ RAT	1
31	0	2	4,244000092	4,244000092	4,244000092	sp P62737 ACTA_MOUSE	Actin, aortic smooth muscle OS=Mus musculus GN=Acta MOUSE	1
31	0	2	4,244000092	4,244000092	4,244000092	sp P62736 ACTA_HUMAN	Actin, aortic smooth muscle OS=Homo sapiens GN=ACT/ HUMAN	1
31	0	2	4,267000034	4,267000034	4,267000034	sp P60011 ACT_SACBA	Actin OS=Saccharomyces bayanus GN=ACT1 PE=3 SV=1 SACBA	1
31	0	2	4,267000034	4,267000034	4,267000034	sp P60010 ACT_YEAST	Actin OS=Saccharomyces cerevisiae (strain ATCC 20450) YEAST	1
31	0	2	4,267000034	4,267000034	4,267000034	sp P60009 ACT_CANGA	Actin OS=Candida glabrata (strain ATCC 2091 / CBS 138 , CANGA	1
31	0	2	4,774999991	4,774999991	4,774999991	sp P53504 ACT1_SORBI	Actin-1 OS=Sorghum bicolor GN=AC1 PE=2 SV=1 SORBI	1
31	0	2	4,774999991	4,774999991	4,774999991	sp P53498 ACT_CHLRE	Actin OS=Chlamydomonas reinhardtii PE=2 SV=1 CHLRE	1
31	0	2	4,774999991	4,774999991	4,774999991	sp P53497 ACT12_ARATH	Actin-12 OS=Arabidopsis thaliana GN=ACT12 PE=1 SV=1 ARATH	1
31	0	2	4,774999991	4,774999991	4,774999991	sp P53496 ACT11_ARATH	Actin-11 OS=Arabidopsis thaliana GN=ACT11 PE=1 SV=1 ARATH	1
31	0	2	4,774999991	4,774999991	4,774999991	sp P53494 ACT4_ARATH	Actin-4 OS=Arabidopsis thaliana GN=ACT4 PE=1 SV=1 ARATH	1
31	0	2	4,774999991	4,774999991	4,774999991	sp P53492 ACT7_ARATH	Actin-7 OS=Arabidopsis thaliana GN=ACT7 PE=1 SV=1 ARATH	1
31	0	2	4,244000092	4,244000092	4,244000092	sp P53482 ACTSB_TAKRU	Actin, alpha skeletal muscle B OS=Takifugu rubripes GN= TAKRU	1
31	0	2	4,244000092	4,244000092	4,244000092	sp P53480 ACTC_TAKRU	Actin, alpha cardiac OS=Takifugu rubripes PE=2 SV=1 TAKRU	1
31	0	2	4,244000092	4,244000092	4,244000092	sp P53479 ACTS_CYPCA	Actin, alpha skeletal muscle OS=Cyprinus carpio GN=act CYPCA	1
31	0	2	4,786999896	4,786999896	4,786999896	sp P53476 ACT_TOXGO	Actin OS=Toxoplasma gondii GN=ACT1 PE=3 SV=1 TOXGO	1
31	0	2	4,233000055	4,233000055	4,233000055	sp P53475 ACTN_STYCL	Actin, muscle OS=Styela clava GN=TB12 PE=2 SV=1 STYCL	1
31	0	2	4,233000055	4,233000055	4,233000055	sp P53467 ACTM_MOLOC	Actin, larval muscle-type OS=Molgula oculata PE=3 SV=1 MOLOC	1
31	0	2	4,786999896	4,786999896	4,786999896	sp P53461 ACTC_HALRO	Actin, nonmuscle OS=Halocynthia roretzi GN=CA1 PE=3 HALRO	1
31	0	2	4,233000055	4,233000055	4,233000055	sp P53460 ACT1_HALRO	Actin, muscle 1A OS=Halocynthia roretzi GN=MA1A PE= HALRO	1
31	0	2	4,82599996	4,82599996	4,82599996	sp P53459 ACT6_DIPDE	Actin-6 (Fragment) OS=Diphyllbothrium dendriticum G DIPDE	1
31	0	2	4,774999991	4,774999991	4,774999991	sp P53457 ACT3_DIPDE	Actin-3 OS=Diphyllbothrium dendriticum GN=ACT3 PE= DIPDE	1
31	0	2	4,244000092	4,244000092	4,244000092	sp P49055 ACTS_CARAU	Actin, alpha skeletal muscle OS=Carassius auratus GN=a CARAU	1
31	0	2	4,774999991	4,774999991	4,774999991	sp P46258 ACT3_PEA	Actin-3 OS=Pisum sativum PE=2 SV=1 PEA	1
31	0	2	4,969000071	4,969000071	4,969000071	sp P45521 ACT_PROCL	Actin (Fragment) OS=Procambarus clarkii PE=1 SV=1 PROCL	1
31	0	2	4,267000034	4,267000034	4,267000034	sp P43239 ACT1_PNECA	Actin-1 OS=Pneumocystis carinii PE=2 SV=1 PNECA	1
31	0	2	4,800000042	4,800000042	4,800000042	sp P35432 ACT1_ECHGR	Actin-1 OS=Echinococcus granulosus GN=ACTI PE=3 SV= ECHGR	1
31	0	2	4,774999991	4,774999991	4,774999991	sp P30171 ACT11_SOLTU	Actin-97 OS=Solanum tuberosum GN=AC97 PE=3 SV=1 SOLTU	1
31	0	2	9,230999649	9,230999649	9,230999649	sp P30170 ACT10_SOLTU	Actin-85C (Fragment) OS=Solanum tuberosum GN=AC85C SOLTU	1
31	0	2	4,774999991	4,774999991	4,774999991	sp P30169 ACT7_SOLTU	Actin-75 OS=Solanum tuberosum GN=AC75 PE=3 SV=1 SOLTU	1
31	0	2	4,774999991	4,774999991	4,774999991	sp P30168 ACT6_SOLTU	Actin-71 OS=Solanum tuberosum GN=ACT71 PE=3 SV=2 SOLTU	1
31	0	2	4,774999991	4,774999991	4,774999991	sp P30167 ACT3_SOLTU	Actin-58 OS=Solanum tuberosum GN=AC58 PE=3 SV=1 SOLTU	1
31	0	2	4,786999896	4,786999896	4,786999896	sp P30165 ACT2_PEA	Actin-2 OS=Pisum sativum PE=2 SV=1 PEA	1
31	0	2	4,786999896	4,786999896	4,786999896	sp P30164 ACT1_PEA	Actin-1 OS=Pisum sativum PE=2 SV=1 PEA	1
31	0	2	4,786999896	4,786999896	4,786999896	sp P30163 ACT2_ONCVO	Actin-2 OS=Onchocerca volvulus GN=act-2b PE=3 SV=1 ONCVO	1
31	0	2	4,786999896	4,786999896	4,786999896	sp P30162 ACT1_ONCVO	Actin-1 OS=Onchocerca volvulus GN=act-1a PE=3 SV=1 ONCVO	1
31	0	2	5,437999964	5,437999964	5,437999964	sp P30161 ACT_COSCS	Actin (Fragment) OS=Costaria costata PE=3 SV=2 COSCS	1
31	0	2	4,267000034	4,267000034	4,267000034	sp P29751 ACTB_RABIT	Actin, cytoplasmic 1 OS=Oryctolagus cuniculus GN=ACTF RABIT	1
31	0	2	4,851999879	4,851999879	4,851999879	sp P27132 ACT2_NAEFO	Actin-2 (Fragment) OS=Naegleria fowleri PE=2 SV=1 NAEFO	1
31	0	2	4,800000042	4,800000042	4,800000042	sp P27131 ACT1_NAEFO	Actin-1 OS=Naegleria fowleri PE=2 SV=2 NAEFO	1
31	0	2	4,233000055	4,233000055	4,233000055	sp P27130 ACT2_HALRO	Actin, muscle 2/4/4A OS=Halocynthia roretzi GN=MA2 F HALRO	1
31	0	2	4,233000055	4,233000055	4,233000055	sp P26198 ACTM_STYCL	Actin, muscle OS=Styela clava PE=2 SV=1 STYCL	1
31	0	2	4,774999991	4,774999991	4,774999991	sp P26197 ACT2_ABSGL	Actin-2 OS=Absidia glauca GN=ACT2 PE=3 SV=1 ABSGL	1
31	0	2	4,786999896	4,786999896	4,786999896	sp P26182 ACT_ACHBI	Actin OS=Achlya bisexualis PE=3 SV=1 ACHBI	1
31	0	2	4,904999956	4,904999956	4,904999956	sp P24263 ACTD_PHYPO	Actin, spherule isoform OS=Physarum polycephalum GN PHYPO	1
31	0	2	4,724000022	4,724000022	4,724000022	sp P23344 ACT2_DAUCA	Actin-2 OS=Daucus carota PE=2 SV=1 DAUCA	1
31	0	2	4,800000042	4,800000042	4,800000042	sp P22132 ACT2_PHYIN	Actin-2 OS=Phytophthora infestans GN=ACTB PE=2 SV=1 PHYIN	1
31	0	2	4,786999896	4,786999896	4,786999896	sp P22131 ACT1_PHYIN	Actin-1 OS=Phytophthora infestans GN=ACTA PE=2 SV=1 PHYIN	1
31	0	2	4,774999991	4,774999991	4,774999991	sp P20904 ACT_VOLCA	Actin OS=Volvox carteri PE=3 SV=1 VOLCA	1
31	0	2	4,244000092	4,244000092	4,244000092	sp P20399 ACT2_XENTR	Actin, alpha cardiac muscle 2 OS=Xenopus tropicalis PE= XENTR	1
31	0	2	5,505000055	5,505000055	5,505000055	sp P18602 ACT3_ARTSX	Actin, clone 302 (Fragment) OS=Artemia sp. PE=2 SV=1 ARTSX	1
31	0	2	4,255000129	4,255000129	4,255000129	sp P18601 ACT2_ARTSX	Actin, clone 211 OS=Artemia sp. PE=2 SV=1 ARTSX	1
31	0	2	4,255000129	4,255000129	4,255000129	sp P18600 ACT1_ARTSX	Actin, clone 205 OS=Artemia sp. PE=2 SV=1 ARTSX	1
31	0	2	4,255000129	4,255000129	4,255000129	sp P17304 ACTM_APLCA	Actin, muscle OS=Aplysia californica PE=2 SV=1 APLCA	1
31	0	2	4,267000034	4,267000034	4,267000034	sp P17128 ACT_KLULA	Actin OS=Kluyveromyces lactis (strain ATCC 8585 / CBS / KLULA	1
31	0	2	4,255000129	4,255000129	4,255000129	sp P14235 ACT_CANAX	Actin OS=Candida albicans GN=ACT1 PE=3 SV=1 CANAX	1
31	0	2	4,800000042	4,800000042	4,800000042	sp P13363 ACT_PHYME	Actin OS=Phytophthora megasperma PE=3 SV=1 PHYME	1
31	0	2	4,244000092	4,244000092	4,244000092	sp P10995 ACT2_XENLA	Actin, alpha skeletal muscle 2 OS=Xenopus laevis GN=ac XENLA	1
31	0	2	4,267000034	4,267000034	4,267000034	sp P10989 ACT_SCHPO	Actin OS=Schizosaccharomyces pombe (strain 972 / ATC SCHPO	1
31	0	2	4,786999896	4,786999896	4,786999896	sp P10986 ACT4_CAEEL	Actin-4 OS=Caenorhabditis elegans GN=act-4 PE=3 SV=2 CAEEL	1
31	0	2	4,786999896	4,786999896	4,786999896	sp P10984 ACT2_CAEEL	Actin-2 OS=Caenorhabditis elegans GN=act-2 PE=3 SV=3 CAEEL	1
31	0	2	12,86000013	12,86000013	12,86000013	sp P10982 ACT1_ABSGL	Actin-1 (Fragment) OS=Absidia glauca GN=ACT1 PE=3 SV ABSGL	1
31	0	2	4,786999896	4,7869998				

31	0	2	4,255000129	4,255000129	4,255000129	sp P07837 ACT2_BOMMO	Actin, muscle-type A2 OS=Bombyx mori PE=3 SV=1	BOMMO	1
31	0	2	4,244000092	4,244000092	4,244000092	sp P04752 ACT3_XENLA	Actin, alpha skeletal muscle 3 OS=Xenopus laevis GN=ac XENLA		1
31	0	2	4,244000092	4,244000092	4,244000092	sp P04751 ACTC_XENLA	Actin, alpha cardiac muscle 1 OS=Xenopus laevis GN=ac XENLA		1
31	0	2	4,774999991	4,774999991	4,774999991	sp P02581 ACT1_SOYBN	Actin-1 OS=Glycine max GN=SAC1 PE=3 SV=2	SOYBN	1
31	0	2	3,302999958	3,302999958	3,302999958	sp P00544 FGR_FSVGR	Tyrosine-protein kinase transforming protein Fgr OS=Fel FSVGR		1
31	0	2	4,774999991	4,774999991	4,774999991	sp O81221 ACT_GOSHI	Actin OS=Gossypium hirsutum PE=3 SV=1	GOSHI	1
31	0	2	4,255000129	4,255000129	4,255000129	sp O74258 ACT_OGAPD	Actin OS=Ogataea parapolymorpha (strain DL-1 / ATCC : OGAPD		1
31	0	2	4,774999991	4,774999991	4,774999991	sp O65315 ACT_COLSC	Actin OS=Coleochaete scutata PE=2 SV=1	COLSC	1
31	0	2	4,761999846	4,761999846	4,761999846	sp O65314 ACT_SCHDU	Actin OS=Scherffelia dubia PE=2 SV=1	SCHDU	1
31	0	2	4,267000034	4,267000034	4,267000034	sp O17503 ACTC_BRALA	Actin, cytoplasmic OS=Branchiostoma lanceolatum PE=2 BRALA		1
31	0	2	4,210999981	4,210999981	4,210999981	sp O17502 ACTM_BRALA	Actin, muscle OS=Branchiostoma lanceolatum PE=2 SV=	BRALA	1
31	0	2	4,233000055	4,233000055	4,233000055	sp O15998 ACTM_CIOSA	Actin, muscle OS=Ciona savignyi PE=2 SV=1	CIOSA	1
31	0	2	4,444000125	4,444000125	4,444000125	sp A5DQ99 ACT_PICGU	Actin OS=Meyerozyma guilliermondii [strain ATCC 6260	PICGU	1
31	0	2	4,774999991	4,774999991	4,774999991	sp A2XLF2 ACT1_ORYSI	Actin-1 OS=Oryza sativa subsp. indica GN=ATCT1 PE=2 SV	ORYSI	1
35	2,02	2,02	7,767000049	3,155000135	3,155000135	sp P07339 CATD_HUMAN	Cathepsin D OS=Homo sapiens GN=CTSD PE=1 SV=1	HUMAN	1
36	2,02	2,02	6,831999868	3,415999934	3,415999934	sp P05089 ARG1_HUMAN	Arginase-1 OS=Homo sapiens GN=ARG1 PE=1 SV=2	HUMAN	1
36	0	2	5,882000178	3,406000137	3,406000137	sp Q61176 ARG1_MOUSE	Arginase-1 OS=Mus musculus GN=Arg1 PE=1 SV=1	MOUSE	1
36	0	2	3,415999934	3,415999934	3,415999934	sp Q95JC8 ARG1_PIG	Arginase-1 OS=Sus scrofa GN=ARG1 PE=2 SV=1	PIG	1
36	0	2	3,415999934	3,415999934	3,415999934	sp Q2KJ64 ARG1_BOVIN	Arginase-1 OS=Bos taurus GN=ARG1 PE=2 SV=1	BOVIN	1
36	0	2	3,406000137	3,406000137	3,406000137	sp P07824 ARG1_RAT	Arginase-1 OS=Rattus norvegicus GN=Arg1 PE=1 SV=2	RAT	1
38	2,01	2,01	0,590999983	0,590999983	0,39400002	sp P20930 FILA_HUMAN	Filaggrin OS=Homo sapiens GN=FLG PE=1 SV=3	HUMAN	1
41	2	2	8,41299966	4,086999968	4,086999968	sp P34955 A1AT_BOVIN	Alpha-1-antiproteinase OS=Bos taurus GN=SERPINA1 PE	BOVIN	1
42	2	2	4,746000096	2,373000048	2,373000048	sp Q6UWP8 SBSN_HUMAN	Suprabasin OS=Homo sapiens GN=SBSN PE=1 SV=2	HUMAN	1
43	2	2	13,51000071	8,107999712	8,107999712	sp Q659U5 LYSC_HALGR	Lysozyme C OS=Halichoerus grypus GN=LYZ PE=2 SV=1	HALGR	1
43	0	2	13,51000071	8,107999712	8,107999712	sp Q659U1 LYSC_PHOVI	Lysozyme C OS=Phoca vitulina GN=LYZ PE=2 SV=1	PHOVI	1
43	0	2	13,51000071	8,107999712	8,107999712	sp Q659U0 LYSC_LEPWE	Lysozyme C OS=Leptonychotes weddellii GN=LYZ PE=2 S	LEPWE	1
43	0	2	13,51000071	8,107999712	8,107999712	sp P79847 LYSC_PYGNE	Lysozyme C OS=Pygathrix nemaeus GN=LYZ PE=3 SV=1	PYGNE	1
43	0	2	13,51000071	8,107999712	8,107999712	sp P79811 LYSC_NASLA	Lysozyme C OS=Nasalis larvatus GN=LYZ PE=3 SV=1	NASLA	1
43	0	2	13,51000071	8,107999712	8,107999712	sp P67980 LYSC_TRAFR	Lysozyme C OS=Trachypithecus francoisi GN=LYZ PE=2 S	TRAFR	1
43	0	2	13,51000071	8,107999712	8,107999712	sp P67979 LYSC_TRAOB	Lysozyme C OS=Trachypithecus obscurus GN=LYZ PE=2 S	TRAOB	1
43	0	2	13,51000071	8,107999712	8,107999712	sp P67978 LYSC_TRAVT	Lysozyme C OS=Trachypithecus vetulus GN=LYZ PE=3 SV	TRAVT	1
43	0	2	13,51000071	8,107999712	8,107999712	sp P67977 LYSC_SEMEN	Lysozyme C OS=Sennopithecus entellus GN=LYZ PE=1 S	SEMEN	1
43	0	2	13,51000071	8,107999712	8,107999712	sp P61632 LYSC_COLGU	Lysozyme C OS=Colobus guereza GN=LYZ PE=2 SV=1	COLGU	1
43	0	2	13,51000071	8,107999712	8,107999712	sp P61631 LYSC_COLAN	Lysozyme C OS=Colobus angolensis GN=LYZ PE=3 SV=1	COLAN	1
43	0	2	13,51000071	8,107999712	8,107999712	sp P61628 LYSC_PANTR	Lysozyme C OS=Pan troglodytes GN=LYZ PE=2 SV=1	PANTR	1
43	0	2	13,51000071	8,107999712	8,107999712	sp P61627 LYSC_PANPA	Lysozyme C OS=Pan paniscus GN=LYZ PE=3 SV=1	PANPA	1
43	0	2	13,51000071	8,107999712	8,107999712	sp P61626 LYSC_HUMAN	Lysozyme C OS=Homo sapiens GN=LYZ PE=1 SV=1	HUMAN	1
43	0	2	8,392000198	8,392000198	8,392000198	sp Q9PU28 LYSC_SCOMX	Lysozyme C OS=Scophthalmus maximus GN=lys PE=2 SV	SCOMX	1
43	0	2	8,392000198	8,392000198	8,392000198	sp Q9DD65 LYSC_PAROL	Lysozyme C OS=Paralichthys olivaceus PE=2 SV=1	PAROL	1
43	0	2	8,107999712	8,107999712	8,107999712	sp Q6B411 LYSM_BOVIN	Lysozyme C, milk isozyyme OS=Bos taurus PE=2 SV=1	BOVIN	1
43	0	2	8,107999712	8,107999712	8,107999712	sp Q05820 LYSC2_RAT	Putative lysozyme C-2 OS=Rattus norvegicus GN=Ly22 PI	RAT	1
43	0	2	9,230999649	9,230999649	9,230999649	sp P85345 LYSC_AMCYA	Lysozyme C OS=Amyda cartilaginea GN=LYZ PE=1 SV=1	AMCYA	1
43	0	2	8,218999952	8,218999952	8,218999952	sp P85045 LYS_BUFGA	Lysozyme C (Fragment) OS=Bufo gargarizans andrewsi P	BUFGA	1
43	0	2	9,230999649	9,230999649	9,230999649	sp P81709 LYSC2_CANLF	Lysozyme C, spleen isozyyme OS=Canis lupus familiaris P	CANLF	1
43	0	2	8,107999712	8,107999712	8,107999712	sp P79239 LYSC_PONPY	Lysozyme C OS=Pongo pygmaeus GN=LYZ PE=2 SV=1	PONPY	1
43	0	2	8,107999712	8,107999712	8,107999712	sp P79180 LYSC_HYLLA	Lysozyme C OS=Hylobates lar GN=LYZ PE=2 SV=1	HYLLA	1
43	0	2	8,107999712	8,107999712	8,107999712	sp P79179 LYSC_GORGO	Lysozyme C OS=Gorilla gorilla GN=LYZ PE=2 SV=1	GORGO	1
43	0	2	8,392000198	8,392000198	8,392000198	sp P61944 LYSC_TAKRU	Lysozyme C OS=Takifugu rubripes PE=2 SV=1	TAKRU	1
43	0	2	9,230999649	9,230999649	9,230999649	sp P37712 LYSC_CAMDR	Lysozyme C OS=Camelus dromedarius GN=LYZ PE=1 SV=	CAMDR	1
43	0	2	8,107999712	8,107999712	8,107999712	sp P17897 LYZ1_MOUSE	Lysozyme C-1 OS=Mus musculus GN=Ly21 PE=1 SV=1	MOUSE	1
43	0	2	9,230999649	9,230999649	9,230999649	sp P16973 LYSC_RABIT	Lysozyme C OS=Oryctolagus cuniculus GN=LYZ PE=1 SV=	RABIT	1
43	0	2	8,107999712	8,107999712	8,107999712	sp P12069 LYSC3_PIG	Lysozyme C-3 OS=Sus scrofa PE=1 SV=2	PIG	1
43	0	2	8,218999952	8,218999952	8,218999952	sp P12068 LYSC2_PIG	Lysozyme C-2 OS=Sus scrofa PE=1 SV=2	PIG	1
43	0	2	9,375	9,375	9,375	sp P12067 LYSC1_PIG	Lysozyme C-1 OS=Sus scrofa PE=1 SV=1	PIG	1
43	0	2	8,332999796	8,332999796	8,332999796	sp P11941 LYSC2_ONCMY	Lysozyme C II OS=Oncorhynchus mykiss PE=1 SV=2	ONCMY	1
43	0	2	8,107999712	8,107999712	8,107999712	sp P08905 LYZ2_MOUSE	Lysozyme C-2 OS=Mus musculus GN=Ly22 PE=1 SV=2	MOUSE	1
43	0	2	8,107999712	8,107999712	8,107999712	sp P00697 LYSC1_RAT	Lysozyme C-1 OS=Rattus norvegicus GN=Ly21 PE=1 SV=2	RAT	1
44	2	2	3,550000116	1,957999915	1,957999915	sp P22735 TGM1_HUMAN	Protein-glutamine gamma-glutamyltransferase K OS=Hc	HUMAN	1
44	0	2	1,913999952	1,913999952	1,913999952	sp P22758 TGM1_RABIT	Protein-glutamine gamma-glutamyltransferase K OS=Or	RABIT	1
45	2	2	3,325999901	3,325999901	3,325999901	sp Q9ZRR5 TBA3_HORVU	Tubulin alpha-3 chain OS=Hordeum vulgare GN=TUBA3	HORVU	1
45	0	2	3,325999901	3,325999901	3,325999901	sp Q9ZRB7 TBA_WHEAT	Tubulin alpha chain OS=Triticum aestivum GN=TUBA PE=	WHEAT	1
45	0	2	3,341000155	3,341000155	3,341000155	sp Q9BQE3 TBA1C_HUMAN	Tubulin alpha-1C chain OS=Homo sapiens GN=TUBA1C F	HUMAN	1
45	0	2	3,325999901	3,325999901	3,325999901	sp Q96460 TBA2_HORVU	Tubulin alpha-2 chain OS=Hordeum vulgare GN=TUBA2	HORVU	1
45	0	2	3,325999901	3,325999901	3,325999901	sp Q71U36 TBA1A_HUMAN	Tubulin alpha-1A chain OS=Homo sapiens GN=TUBA1A F	HUMAN	1
45	0	2	3,333000094	3,333000094	3,333000094	sp Q6VAG0 TBA2_GOSHI	Tubulin alpha-2 chain OS=Gossypium hirsutum PE=2 SV=	GOSHI	1
45	0	2	3,333000094	3,333000094	3,333000094	sp Q6VAF9 TBA4_GOSHI	Tubulin alpha-4 chain OS=Gossypium hirsutum PE=2 SV=	GOSHI	1
45	0	2	3,325999901	3,325999901	3,325999901	sp Q6P9V9 TBA1B_RAT	Tubulin alpha-1B chain OS=Rattus norvegicus GN=Tuba1	RAT	1
45	0	2	3,341000155	3,341000155	3,341000155	sp Q6AYZ1 TBA1C_RAT	Tubulin alpha-1C chain OS=Rattus norvegicus GN=Tuba1	RAT	1
45	0	2	3,325999901	3,325999901	3,325999901	sp Q5R1W4 TBA1B_PANTR	Tubulin alpha-1B chain OS=Pan troglodytes GN=TUBA1B	PANTR	1
45	0	2	3,333000094	3,333000094	3,333000094	sp Q56WH1 TBA3_ARATH	Tubulin alpha-3 chain OS=Arabidopsis thaliana GN=TUBA	ARATH	1
45	0	2	3,325999901	3,325999901	3,325999901	sp Q53M52 TBA2_ORYSJ	Tubulin alpha-2 chain OS=Oryza sativa subsp. japonica G	ORYSJ	1
45	0	2	3,325999901	3,325999901	3,325999901	sp Q4R538 TBA1B_MACFA	Tubulin alpha-1B chain OS=Macaca fascicularis GN=TUB	MACFA	1
45	0	2	3,341000155	3,341000155	3,341000155	sp Q32CJ7 TBA1C_BOVIN	Tubulin alpha-1C chain OS=Bos taurus GN=TUBA1C PE=1	BOVIN	1
45	0	2	3,325999901	3,325999901	3,325999901	sp Q2XVP4 TBA1B_PIG	Tubulin alpha-1B chain OS=Sus scrofa GN=TUBA1B PE=1	PIG	1
45	0	2	3,31900008	3,31900008	3,31900008	sp Q2HJ86 TBA1D_BOVIN	Tubulin alpha-1D chain OS=Bos taurus GN=TUBA1D PE=	BOVIN	1
45	0	2	3,341000155	3,341000155	3,341000155	sp Q28IX8 TBA_XENTR	Tubulin alpha chain OS=Xenopus tropicalis GN=tuba PE=	XENTR	1
45	0	2	3,333000094	3,333000094	3,333000094	sp Q0WV25 TBA4_ARATH	Tubulin alpha-4 chain OS=Arabidopsis thaliana GN=TUBA	ARATH	1
45	0	2	3,325999901	3,325999901	3,325999901	sp P81947 TBA1B_BOVIN	Tubulin alpha-1B chain OS=Bos taurus PE=1 SV=2	BOVIN	1
45	0	2	3,341000155	3,341000155	3,341000155	sp P68373 TBA1C_MOUSE	Tubulin alpha-1C chain OS=Mus musculus GN=Tuba1c P	MOUSE	1
45	0	2	3,325999901	3,325999901	3,325999901	sp P68370 TBA1A_RAT	Tubulin alpha-1A chain OS=Rattus norvegicus GN=Tuba1	RAT	1
45	0	2	3,325999901	3,325999901	3,325999901	sp P68369 TBA1A_MOUSE	Tubulin alpha-1A chain OS=Mus musculus GN=Tuba1a P	MOUSE	1
45	0	2	3,341000155	3,341000155	3,341000155	sp P68365 TBA1C_CRIGR	Tubulin alpha-1C chain OS=Cricetulus griseus GN=TUBA:	CRIGR	1
45	0	2	3,325999901	3,325999901	3,325999901	sp P68363 TBA1B_HUMAN	Tubulin alpha-1B chain OS=Homo sapiens GN=TUBA1B F	HUMAN	1
45	0	2	3,325999901	3,325999901	3,325999901	sp P68362 TBA1A_CRIGR	Tubulin alpha-1A chain OS=Cricetulus griseus GN=TUBA:	CRIGR	1
45	0	2	3,325999901	3,325999901	3,325999901	sp P68361 TBA1B_CRIGR	Tubulin alpha-1B chain OS=Cricetulus griseus GN=TUBA:	CRIGR	1
45	0	2	3,325999901	3,325999901	3,325999901	sp P68360 TBA1B_MERUN	Tubulin alpha-1B chain OS=Meriones unguiculatus GN=	MERUN	1
45	0	2	3,31900008	3,31900008	3,31900008	sp P46259 TBA1_PEA	Tubulin alpha-1 chain OS=Pisum sativum GN=TUBA1 PE=	PEA	1
45	0	2	3,325999901	3,325999901	3,325999901	sp P36220 TBA_TORMA	Tubulin alpha chain OS=Torpedo marmorata PE=2 SV=1	TORMA	1
45	0	2	3,333000094	3,333000094	3,333000094	sp P33629 TBA_PRUDU	Tubulin alpha chain OS=Prunus dulcis GN=TUBA PE=2 SV	PRUDU	1
45	0	2	13,26999962	13,26999962	13,26999962	sp P33628 TBA_PICAB	Tubulin alpha chain (Fragment) OS=Picea abies GN=TUB	PICAB	1
45	0	2	3,333000094	3,333000094	3,333000094	sp P29511 TBA6_ARATH	Tubulin alpha-6 chain OS=Arabidopsis thaliana GN=TUBA	ARATH	1
45	0	2	3,325999901	3,325999901	3,325999901	sp P14641 TBA2_MAIZE	Tubulin alpha-2 chain OS=Zea mays GN=TUBA2 PE=3 SV	MAIZE	1
45	0	2	3,325999901	3,325999901	3,325999901	sp P14640 TBA1_MAIZE	Tubulin alpha-1 chain OS=Zea mays GN=TUBA1 PE=3 SV	MAIZE	1
45	0	2	3,341000155	3,341000155	3,341000155	sp P08537 TBA_XENLA	Tubulin alpha chain OS=Xenopus laevis GN=tuba PE=2 S	XENLA	1
45	0	2	3,325999901	3,325999901	3,325999901	sp P05213 TBA1B_MOUSE	Tubulin alpha-1B chain OS=Mus musculus GN=Tuba1b P	MOUSE	1
45	0	2	3,641000018	3,641000018	3,641000018	sp P02552 TBA1_CHICK	Tubulin alpha-1 chain (Fragment) OS=Gallus gallus PE=	CHICK	1
45	0	2	3,325999901	3,3					

46	0	2	5,556000024	5,556000024	5,556000024	sp Q8K3U7 PRDX2_CRIGR	Peroxiredoxin-2 OS=Cricetulus griseus GN=PRDX2 PE=2 SV=1	1
46	0	2	5,527999997	5,527999997	5,527999997	sp Q6B4U9 PRDX1_MYOLU	Peroxiredoxin-1 OS=Myotis lucifugus GN=PRDX1 PE=1 SV=1	1
46	0	2	5,556000024	5,556000024	5,556000024	sp Q61171 PRDX2_MOUSE	Peroxiredoxin-2 OS=Mus musculus GN=Prdx2 PE=1 SV=1	1
46	0	2	6,215000153	6,215000153	6,215000153	sp Q5RC63 PRDX2_PONAB	Peroxiredoxin-2 OS=Pongo abelii GN=PRDX2 PE=2 SV=3	1
46	0	2	5,556000024	5,556000024	5,556000024	sp Q2PFZ3 PRDX2_MACFA	Peroxiredoxin-2 OS=Macaca fascicularis GN=PRDX2 PE=1 SV=1	1
46	0	2	5,527999997	5,527999997	5,527999997	sp Q06830 PRDX1_HUMAN	Peroxiredoxin-1 OS=Homo sapiens GN=PRDX1 PE=1 SV=1	1
46	0	2	8,660999686	8,660999686	8,660999686	sp P52552 PRDX2_PIG	Peroxiredoxin-2 (Fragment) OS=Sus scrofa GN=PRDX2 P_PIG	1
46	0	2	5,556000024	5,556000024	5,556000024	sp P35704 PRDX2_RAT	Peroxiredoxin-2 OS=Rattus norvegicus GN=Prdx2 PE=1 SV=1	1
46	0	2	5,556000024	5,556000024	5,556000024	sp P32119 PRDX2_HUMAN	Peroxiredoxin-2 OS=Homo sapiens GN=PRDX2 PE=1 SV=1	1
47	2	2	1,683999971	1,683999971	1,683999971	sp Q86Y23 HORN_HUMAN	Hornerin OS=Homo sapiens GN=HRNR PE=1 SV=2	1
48	2	2	3,403000161	3,403000161	3,403000161	sp Q7YR44 CDSN_PANTR	Corneodesmosin OS=Pan troglodytes GN=CDSN PE=2 SV=1	1
48	0	2	3,370999917	3,370999917	3,370999917	sp Q5TM45 CDSN_MACMU	Corneodesmosin OS=Macaca mulatta GN=CDSN PE=3 SV=1	1
48	0	2	3,403000161	3,403000161	3,403000161	sp Q15517 CDSN_HUMAN	Corneodesmosin OS=Homo sapiens GN=CDSN PE=1 SV=1	1
49	2	2	3,162999824	3,162999824	3,162999824	sp Q5FMCO GLYA_LACAC	Serine hydroxymethyltransferase OS=Lactobacillus acid LACAC	1
50	2	2	7,805000246	7,805000246	7,805000246	sp P04792 HSPB1_HUMAN	Heat shock protein beta-1 OS=Homo sapiens GN=HSPB1 HUMAN	1
51	2	2	9,544999897	9,544999897	9,544999897	sp O75629 CREG1_HUMAN	Protein CREG1 OS=Homo sapiens GN=CREG1 PE=1 SV=1	1
52	1,77	1,77	6,7900002	6,7900002	6,7900002	sp Q5VSP4 LC11_HUMAN	Putative lipocalin 1-like protein 1 OS=Homo sapiens GN=	1
52	0	1,77	6,25	6,25	6,25	sp P31025 LCN1_HUMAN	Lipocalin-1 OS=Homo sapiens GN=LCN1 PE=1 SV=1	1
53	1,56	1,56	7,005000114	5,071999878	2,174000069	sp Q8IW75 SPA12_HUMAN	Serpin A12 OS=Homo sapiens GN=SERPINA12 PE=1 SV=1	1
54	1,54	1,54	4,191999882	4,191999882	4,191999882	sp O60911 CATL2_HUMAN	Cathepsin L2 OS=Homo sapiens GN=CTSV PE=1 SV=2	1
55	1,49	1,49	24,26999956	24,26999956	24,26999956	sp P55000 SLUR1_HUMAN	Secreted Ly-6/uPAR-related protein 1 OS=Homo sapiens HUMAN	1
57	1,41	1,41	19,14999932	5,851000175	5,851000175	sp O75223 GGCT_HUMAN	Gamma-glutamylcylotransferase OS=Homo sapiens GN=HUMAN	1
58	1,38	1,38	10,75000018	7,009000331	7,009000331	sp B9A064 IGLL5_HUMAN	Immunoglobulin lambda-like polypeptide 5 OS=Homo sapiens	1
58	0	1,38	14,14999962	14,14999962	14,14999962	sp POCG06 LAC3_HUMAN	Ig lambda-3 chain C regions OS=Homo sapiens GN=IGLC HUMAN	1
58	0	1,38	14,14999962	14,14999962	14,14999962	sp POCG05 LAC2_HUMAN	Ig lambda-2 chain C regions OS=Homo sapiens GN=IGLC HUMAN	1
58	0	1,38	14,14999962	14,14999962	14,14999962	sp POCG04 LAC1_HUMAN	Ig lambda-1 chain C regions OS=Homo sapiens GN=IGLC HUMAN	1
58	0	1,38	14,14999962	14,14999962	14,14999962	sp POCF74 LAC6_HUMAN	Ig lambda-6 chain C region OS=Homo sapiens GN=IGLC6 HUMAN	1
58	0	1,38	14,14999962	14,14999962	14,14999962	sp A0M8Q6 LAC7_HUMAN	Ig lambda-7 chain C region OS=Homo sapiens GN=IGLC7 HUMAN	1
59	1,23	1,23	3,282000124	3,282000124	1,554000005	sp Q5T749 KPRP_HUMAN	Keratinocyte proline-rich protein OS=Homo sapiens GN=	1
60	1,08	1,08	0,598300016	0,598300016	0,239300006	RRRRRsp Q19317 NBEA_CAEEL	REVERSED Putative neurobeachin homolog OS=Caenorh CAEEL	1
61	0,85	0,85	1,917999983	1,917999983	1,917999983	RRRRRsp Q9SFC7 FB135_ARATH	REVERSED F-box protein At3g07870 OS=Arabidopsis th ARATH	1
62	0,69	0,69	4,988000169	3,088000044	3,088000044	sp Q9UI42 CBPA4_HUMAN	Carboxypeptidase A4 OS=Homo sapiens GN=CPA4 PE=1	1
62	0	0,69	5,000000075	3,095000051	3,095000051	sp Q6P8X8 CBPA4_MOUSE	Carboxypeptidase A4 OS=Mus musculus GN=Cpa4 PE=2	1
63	0,64	0,64	13,33000064	4,69099991	1,975000091	sp Q96P63 SPB12_HUMAN	Serpin B12 OS=Homo sapiens GN=SERPINB12 PE=1 SV=1	1
64	0,63	0,63	0,870500039	0,870500039	0,870500039	sp Q05884 AMY_STRLI	Alpha-amylase OS=Streptomyces lividans GN=amy PE=1	1
65	0,55	0,55	100	100	100	sp P84735 PS19_PINST	Putative LRR disease resistance protein/transmembrane PINST	1
65	0	0,55	100	100	100	sp P84732 PS16_PINST	Putative LRR disease resistance protein/transmembrane PINST	1
65	0	0,55	100	100	100	sp P84720 PS4_PINST	Putative LRR disease resistance protein/transmembrane PINST	1
66	0,27	0,27	65,82000256	26,57999992	0	sp P02814 SMR3B_HUMAN	Submaxillary gland androgen-regulated protein 3B OS=H HUMAN	0
67	0,23	0,23	7,406999916	6,667000055	0	sp Q05816 FABP5_MOUSE	Fatty acid-binding protein, epidermal OS=Mus musculus MOUSE	0
67	0	0,23	7,406999916	6,667000055	0	sp Q01469 FABP5_HUMAN	Fatty acid-binding protein, epidermal OS=Homo sapiens HUMAN	0
67	0	0,23	7,406999916	6,667000055	0	sp P55053 FABP5_RAT	Fatty acid-binding protein, epidermal OS=Rattus norvegi RAT	0
68	0,21	0,26	0,836499967	0,836499967	0	sp Q5D862 FILA2_HUMAN	Filaggrin-2 OS=Homo sapiens GN=FLG2 PE=1 SV=1	0
69	0,15	0,15	1,699000038	1,699000038	0	sp Q9HH00 TRET_PYRFU	Trehalose synthase OS=Pyrococcus furiosus (strain ATCC PYRFU	0
69	0	0,15	0,813999958	0,813999958	0	sp Q7NAR7 SYV_MYCGA	Valine--tRNA ligase OS=Mycoplasma gallisepticum (strai MYCGA	0
69	0	0,15	1,699000038	1,699000038	0	sp Q7LYW5 TRET_THELN	Trehalose synthase OS=Thermococcus litoralis (strain A1 THELN	0
69	0	0,15	2,33299993	2,33299993	0	sp Q5UNV7 YL698_MIMIV	Uncharacterized protein L698 OS=Acanthamoeba polypl MIMIV	0
69	0	0,15	0,944699999	0,944699999	0	RRRRRsp Q6KZR2 PURL_PICTO	REVERSED Phosphoribosylformylglycinamide synthase PICTO	0
69	0	0,15	2,692000009	2,692000009	0	RRRRRsp Q6AX41 MC25A_XENLA	REVERSED MICOS complex subunit mic25-a OS=Xenopus: XENLA	0
69	0	0,15	2,766999975	2,766999975	0	RRRRRsp Q5U509 MC25B_XENLA	REVERSED MICOS complex subunit mic25-b OS=Xenopus: XENLA	0
69	0	0,15	2,766999975	2,766999975	0	RRRRRsp Q5FVV3 MC25_XENTR	REVERSED MICOS complex subunit mic25 OS=Xenopus t XENTR	0
69	0	0,15	0,773499999	0,773499999	0	RRRRRsp O13955 VAM6_SCHPO	REVERSED Vacuolar morphogenesis protein 6 OS=Schizo SCHPO	0
70	0,15	0,15	1,535	1,535	0	sp O28606 SAT_ARCFU	Sulfate adenyllyltransferase OS=Archaeoglobus fulgidus ARCFU	0
71	0,1	0,1	45,28000057	13,2100001	0	sp P01834 IGKC_HUMAN	Ig kappa chain C region OS=Homo sapiens GN=IGKC PE=1	0
72	0,07	0,07	2,291999944	2,291999944	0	RRRRRsp P31755 UCH1_YEAST	REVERSED Initiation-specific alpha-1,6-mannosyltransfer YEAST	0
73	0,07	0,07	7,512000203	7,512000203	0	RRRRRsp P13673 SKGR_XENLA	REVERSED Skin granule protein OS=Xenopus laevis GN= SKGR XENLA	0
74	0,06	0,06	1,737000048	1,737000048	0	sp A7M957 RPOC1_CUSRE	DNA-directed RNA polymerase subunit beta' OS=Cuscut CUSRE	0
75	0,05	0,05	2,754000016	2,754000016	0	sp Q67TB7 ATPB_SYMTM	ATP synthase subunit beta OS=Symbiobacterium therm SYMTM	0
76	0,05	0,05	1,765999943	1,765999943	0	sp P21910 LAML2_XENLA	Lamin-L(II) OS=Xenopus laevis PE=2 SV=1	0
77	0,05	0,05	4,14500013	4,14500013	0	sp P01012 OVAL_CHICK	Ovalbumin OS=Gallus gallus GN=SERPINB14 PE=1 SV=2	0
78	0,05	0,05	2,524000034	2,524000034	0	RRRRRsp Q10310 MUG68_SCHPO	REVERSED Meiotically up-regulated gene 68 protein OS= SCHPO	0

Supplementary Data S2 | Peptide quantification according to a joint search performed as described in the Methods section

Row	Index	Peak Name	m/z	Ret. Time	Group	CSI_02	CSI_03	CSVII_01	CSI_01	CSI_04	CSVI_01	CSV_01	CSV_02	CSV_03
1	1	GPYESGSGHSSGLGHR	792,862	10,6	sp Q86Y23 HORN_HUMAN	1806,59897	2113,14565	2695,48013	2326,16195	1339,40981	1669,25312	2091,20831	553,932097	971,354705
2	2	KYDEINIKR	597,808	11,18	sp P48668 K2C6C_HUMAN	15140,4977	13227,4831	1497,43565	280,103924	10380,5855	17767,6335	399,889136	1484,32559	4121,44175
3	3	KYDEINIKR	597,808	11,18	sp Q72794 K2C1B_HUMAN	15140,4977	13227,4831	1497,43565	280,103924	10380,5855	17767,6335	399,889136	1484,32559	4121,44175
4	4	KYDEINIKR	597,808	11,18	sp P02538 K2C6A_HUMAN	15140,4977	13227,4831	1497,43565	280,103924	10380,5855	17767,6335	399,889136	1484,32559	4121,44175
5	5	KYDEINIKR	597,808	11,18	sp P13647 K2C5_HUMAN	15140,4977	13227,4831	1497,43565	280,103924	10380,5855	17767,6335	399,889136	1484,32559	4121,44175
6	6	LRSEIDNVKK	401,235	11,45	sp P04264 K2C1_HUMAN	308,783749	81014,2591	65938,0397	34101,769	55260,407	48764,3461	222,786472	129,062916	312,534794
7	7	FSSSSYGGGGSSR	618,268	12	sp P35527 K1C9_HUMAN	9118,99572	19884,996	23478,3809	15894,3071	11076,238	16637,0865	194,98317	1984,03063	140,673244
8	8	VQDQDLNPTPHSK	739,866	12,61	sp Q08554 DSC1_HUMAN	2396,59886	1394,32417	1686,20498	3838,7937	2480,90235	4290,29711	825,894615	383,923514	4254,07182
9	9	SKEEAEALYHSK	696,344	12,79	sp P35908 K22E_HUMAN	36693,7011	25504,8327	6393,88923	931,369682	16689,022	3265,43497	205,176338	161,37934	1324,35237
10	10	NKYDEINIKR	654,831	13,09	sp P48668 K2C6C_HUMAN	50111,3703	82158,8256	6435,73931	579,647855	55130,5901	2795,17713	2185,22721	660,326581	1541,39492
11	11	NKYDEINIKR	654,831	13,09	sp P02538 K2C6A_HUMAN	50111,3703	82158,8256	6435,73931	579,647855	55130,5901	2795,17713	2185,22721	660,326581	1541,39492
12	12	NKYDEINIKR	654,831	13,09	sp P13647 K2C5_HUMAN	50111,3703	82158,8256	6435,73931	579,647855	55130,5901	2795,17713	2185,22721	660,326581	1541,39492
13	13	NKYDEINIKR	654,831	13,09	sp P04264 K2C1_HUMAN	50111,3703	82158,8256	6435,73931	579,647855	55130,5901	2795,17713	2185,22721	660,326581	1541,39492
14	14	LQGEIAHVK	497,787	13,23	sp P35908 K22E_HUMAN	36913,2955	27108,8673	1025,57406	262,555838	15615,4895	313,47883	284,563243	260,35855	522,840394
15	15	LLEGEEC[CAM]JR	503,238	13,57	sp P48668 K2C6C_HUMAN	10385,1853	12939,9576	11650,6205	7490,71475	5743,3509	8036,51915	216,048261	190,281571	263,469593
16	16	LLEGEEC[CAM]JR	503,238	13,57	sp Q8N1N4 K2C78_HUMAN	10385,1853	12939,9576	11650,6205	7490,71475	5743,3509	8036,51915	216,048261	190,281571	263,469593
17	17	LLEGEEC[CAM]JR	503,238	13,57	sp P02538 K2C6A_HUMAN	10385,1853	12939,9576	11650,6205	7490,71475	5743,3509	8036,51915	216,048261	190,281571	263,469593
18	18	LLEGEEC[CAM]JR	503,238	13,57	sp P13647 K2C5_HUMAN	10385,1853	12939,9576	11650,6205	7490,71475	5743,3509	8036,51915	216,048261	190,281571	263,469593
19	19	SKAEAEALYQSK	670,838	13,7	sp P04264 K2C1_HUMAN	121144,581	155355,557	67936,6146	112499,155	1030,12411	672,24795	190,125157	1386,30093	
20	20	YEELQQTAGR	597,791	14,17	sp P13647 K2C5_HUMAN	10021,693	10312,2514	10099,0396	6827,02115	7024,38312	541,316427	222,766018	299,261711	854,270726
21	21	SQYQLEAQENQRK	747,371	14,21	sp P13645 K1C10_HUMAN	205283,5	156023,225	138756,137	67818,4392	158300,007	224172,015	317,57083	250,740568	2620,21659
22	22	AQYDIAEQ	533,264	14,38	sp P04264 K2C1_HUMAN	97358,6963	132847,255	95362,6969	51405,1248	81028,7436	81107,7708	153,428091	7703,8882	4764,38261
23	23	YDPEAASAPGSGNPG[CAM]HEASAAQK	772,339	14,51	sp P81605 DCD_HUMAN	5219,77037	3869,09451	6635,00737	5664,79584	7790,44948	1093,34105	277,974153	622,314053	2511,81092
24	24	SEITELRR	502,279	14,54	sp Q61FW6 K1C10_RAT	228795,808	133698,814	154942,983	83566,3784	110065,08	190,973073	148,413202	281,146641	264,147465
25	25	SEITELRR	502,279	14,54	sp P13645 K1C10_HUMAN	228795,808	133698,814	154942,983	83566,3784	110065,08	190,973073	148,413202	281,146641	264,147465
26	26	IKFEM[DTM]EQNLR	420,563	14,62	sp P35527 K1C9_HUMAN	7065,84367	28132,7516	4208,7821	575,957996	15894,6421	219,183804	14741,1601	301,316805	156,586343
27	27	EVATNSLVSQSK	681,349	14,74	sp Q04695 K1C17_HUMAN	11553,4852	20266,8657	14909,5548	8320,79639	9511,1323	1596,3177	1359,97552	287,458674	784,900933
28	28	EVATNSLVSQSK	681,349	14,74	sp P02533 K1C14_HUMAN	11553,4852	20266,8657	14909,5548	8320,79639	9511,1323	1596,3177	1359,97552	287,458674	784,900933
29	29	GSC[CAM]GIGGGIGGGSSR	639,796	14,79	sp P08779 K1C16_HUMAN	6578,25238	14453,7176	963,475909	144,704224	3436,95641	1731,88596	411,987913	131,037547	1123,24739
30	30	GSC[CAM]GIGGGIGGGSSR	639,796	14,79	sp P02533 K1C14_HUMAN	6578,25238	14453,7176	963,475909	144,704224	3436,95641	1731,88596	411,987913	131,037547	1123,24739
31	31	GRLDSLR	473,259	14,82	sp P48668 K2C6C_HUMAN	729,715624	731,279804	582,676947	146,984893	841,436001	1292,3036	13569,8405	138,407699	1128,74177
32	32	GRLDSLR	473,259	14,82	sp P02538 K2C6A_HUMAN	729,715624	731,279804	582,676947	146,984893	841,436001	1292,3036	13569,8405	138,407699	1128,74177
33	33	GRLDSLR	473,259	14,82	sp P13647 K2C5_HUMAN	729,715624	731,279804	582,676947	146,984893	841,436001	1292,3036	13569,8405	138,407699	1128,74177
34	34	AQYEEIAQR	547,268	14,95	sp P13647 K2C5_HUMAN	9819,15869	12643,0874	8433,09529	6971,16573	7165,96483	151,636962	420,777686	408,939772	1705,4547
35	35	VDNALQSGNSQESVTEQDKS	1068,49	15,06	sp P01834 IGKC_HUMAN	131,685849	367,295024	507,401181	834,202448	2742,58814	256,943055	120,54331	123,721944	230,180499
36	36	NTKQIEAIEINR	658,352	15,15	sp P48668 K2C6C_HUMAN	1606,87748	5118,41389	3724,56962	1797,30537	2750,87653	676,302332	7995,9169	453,282227	611,770133
37	37	NTKQIEAIEINR	658,352	15,15	sp P02538 K2C6A_HUMAN	1606,87748	5118,41389	3724,56962	1797,30537	2750,87653	676,302332	7995,9169	453,282227	611,770133
38	38	SKDEAEALYQTK	691,844	15,57	sp Q72794 K2C1B_HUMAN	5489,98512	1178,96942	958,697725	3319,09687	9561,59625	3126,54184	1842,40303	494,365365	1393,50994
39	39	GGSGGSGGGGSGFGGSGYGGGEEASGSG	1075,1	15,59	sp P35527 K1C9_HUMAN	3732,82425	9637,01111	448,258064	8235,03939	7416,611	8257,96084	151,859191	258,065763	513,500123
40	40	SEDPNDHVG	695,311	15,62	sp P01591 IGI_HUMAN	2011,45187	1582,11823	772,348342	498,995676	7107,76029	1628,6038	1029,1971	235,06162	907,176294
41	41	LLEGGESGGGGGR	631,801	15,62	sp P13645 K1C10_HUMAN	59336,6569	97625,3743	59548,6525	41924,0706	48749,2982	3227,06106	902,96855	665,262665	5029,19297
42	42	AQYEEIAQR	554,276	15,62	sp P48668 K2C6C_HUMAN	803,867173	507,604945	593,938004	492,050444	135,938031	36003,9714	24969,5514	140,496802	1567,57013
43	43	AQYEEIAQR	554,276	15,62	sp P19013 K2C4_HUMAN	803,867173	507,604945	593,938004	492,050444	135,938031	36003,9714	24969,5514	140,496802	1567,57013
44	44	AQYEEIAQR	554,276	15,62	sp P02538 K2C6A_HUMAN	803,867173	507,604945	593,938004	492,050444	135,938031	36003,9714	24969,5514	140,496802	1567,57013
45	45	AQYEEIAQR	554,276	15,62	sp P35908 K22E_HUMAN	803,867173	507,604945	593,938004	492,050444	135,938031	36003,9714	24969,5514	140,496802	1567,57013
46	46	GFGSGVVGVSGSR	627,806	15,7	sp P35908 K22E_HUMAN	80519,3037	47411,5289	51826,3134	27340,041	43572,1117	281,64728	470,769312	179,91871	1516,67006
47	47	HGGGATFGGGGFGFSR	660,795	15,71	sp P35908 K22E_HUMAN	53595,2995	1225,59876	42170,4256	18804,2624	36656,9449	486,995252	3277,45583	537,74677	944,526448
48	48	AAR,ATIMQNLNDR	545,768	15,72	sp Q04695 K1C17_HUMAN	6817,13995	19750,6929	1323,23596	7041,9581	5466,02885	766,106987	170,864958	169,843104	1643,82261
49	49	VPDIEQNVK	521,282	15,88	sp P35908 K22E_HUMAN	1442,83852	443,909882	145,92624	236,903695	227,153069	49298,3215	23919,4745	7793,64062	1365,54682
50	50	TKYHEALR	630,339	15,97	sp P08779 K1C16_HUMAN	1522,1957	17657,8792	2957,00872	196,708613	1392,48271	3262,06837	338,760171	164,723377	1546,62614
51	51	TLLGEESR	517,262	15,97	sp P04264 K2C1_HUMAN	193474,705	210613,915	217100,441	132047,865	161166,769	328,111534	267,786054	214,285175	13354,462
52	52	ISSVLAGGSC[CAM]R	553,784	16,2	sp P08779 K1C16_HUMAN	12950,0866	27644,2531	12855,876	6946,16245	7235,85951	287,866428	924,370537	224,732424	766,012603
53	53	ISSVLAGGSC[CAM]R	553,784	16,2	sp P02533 K1C14_HUMAN	12950,0866	27644,2531	12855,876	6946,16245	7235,85951	287,866428	924,370537	224,732424	766,012603
54	54	YENEVALR	497,254	16,44	sp Q61FW6 K1C10_RAT	36265,8466	24336,6114	24329,3583	12811,4495	19544,4335	19832,249	191,934235	150,121001	174,84755
55	55	LASYLDK	405,223	16,47	sp Q04695 K1C17_HUMAN	66327,8332	66896,226	68654,4532	36070,3236	51609,3425	36531,8035	827,363583	357,294425	1788,70821
56	56	LASYLDK	405,223	16,47	sp P08779 K1C16_HUMAN	66327,8332	66896,226	68654,4532	36070,3236	51609,3425	36531,8035	827,363583	357,294425	1788,70821
57	57	LASYLDK	405,223	16,47	sp P02533 K1C14_HUMAN	66327,8332	66896,226	68654,4532	36070,3236	51609,3425	36531,8035	827,363583	357,294425	1788,70821
58	58	AGEVQPELR	564,29	16,51	sp P25311 ZAG2_HUMAN	3953,5347	2187,86963	5912,70238	5390,53492	8907,98879	490,532903	168,280777	126,050224	2372,43972
59	59	NVKVDPEIQNVK	691,884	16,98	sp P35908 K22E_HUMAN	10393,3617	20126,8822	18424,2962	9053,96308	12255,2854	1996,46701	2699,78399	480,177998	4650,77727
60	60	RQLDSIVGR	586,826	17,08	sp P48668 K2C6C_HUMAN	8592,39771	8319,89751	15667,8419	7100,873					

111	111	LASYLDKVR	532,808	18,47	sp P13645 K1C10_HUMAN	314464,315	380853,45	313837,639	150326,128	384256,528	322,897841	751,220916	240,401455	2535,49268
112	112	TAESWVWQTK	621,787	18,5	sp P13647 K2C5_HUMAN	3097,79212	11875,5073	4703,50259	3036,88754	4524,21441	898,582489	679,943935	787,384376	349,239184
113	113	ALEE[XXX]SYNELEGK	710,301	18,58	sp P13645 K1C10_HUMAN	118648,22	62345,9247	60522,7517	8407,08203	48005,1722	971,564298	390,087003	623,215632	1616,94643
114	114	SISISVAR	416,748	18,61	sp P04264 K2C1_HUMAN	307106,908	380255,589	344433,085	194676,764	34088,134	15412,6729	9600,82254	3290,01623	184,019461
115	115	SLVNLGGSK	437,753	18,66	sp P04264 K2C1_HUMAN	270951,275	249110,24	256503,124	21088,526	21764,874	323,008677	315,414993	933,715494	12438,2412
116	116	YEEQLQVTAGR	583,297	18,74	sp P48668 K2C6C_HUMAN	2745,5897	2573,85006	5763,02422	2800,07053	12858,4484	5926,85067	14205,6419	791,59507	6352,46255
117	117	YEEQLQVTAGR	583,297	18,74	sp P02538 K2C6A_HUMAN	2745,5897	2573,85006	5763,02422	2800,07053	12858,4484	5926,85067	14205,6419	791,59507	6352,46255
118	118	TAANEVFVTLTK	765,868	18,82	sp P48668 K2C6C_HUMAN	28691,1297	56102,0895	38535,9048	18467,7705	10095,555	1378,85049	2504,86529	2400,12216	1772,87922
119	119	TAANEVFVTLTK	765,868	18,82	sp P02538 K2C6A_HUMAN	28691,1297	56102,0895	38535,9048	18467,7705	10095,555	1378,85049	2504,86529	2400,12216	1772,87922
120	120	CAM.VATVSLPR	450,268	18,88	sp P00761 TRYP_PIG	120143,83	66833,7311	179927,47	290987,416	152737,138	110219,192	19,098997	199786,708	137340,223
121	121	M[Oxi]SGE[Dhy][C]CAM APNVSVSVSTSHTTIS	855,057	18,91	sp P04264 K2C1_HUMAN	6401,69805	83880,592	15112,2232	19066,221	23718,7112	952,600539	423,699096	2148,97618	1137,31409
122	122	M[Oxi]S[Dhy]GEC[C]CAM APNVSVSVSTSHTTIS	855,057	18,91	sp P04264 K2C1_HUMAN	6401,69805	83880,592	15112,2232	19066,221	23718,7112	952,600539	423,699096	2148,97618	1137,31409
123	123	VTVTPAPR	421,758	18,92	sp Q05884 AMY_STRU	7522,88062	759629,591	1026370,09	13152993,5	1276963,63	5179833,42	8713097,36	9024869,26	582618,88
124	124	W[2Ox]TTLQEQGTK	618,326	18,95	sp P48668 K2C6C_HUMAN	23083,8264	39106,2732	12657,1146	6700,74219	19549,9841	537519,25	240272,14	70069,5496	6199,17491
125	125	CRM.TAANEVFVTLTK	697,369	18,95	sp P48668 K2C6C_HUMAN	21915,5103	39795,0045	27694,2272	2276,60273	15571,763	899113,623	489457,903	1088,16197	7303,09661
126	126	W[2Ox]TTLQEQGTK	618,326	18,95	sp P02538 K2C6A_HUMAN	23083,8264	39106,2732	12657,1146	6700,74219	19549,9841	537519,25	240272,14	70069,5496	6199,17491
127	127	CRM.TAANEVFVTLTK	697,369	18,95	sp P02538 K2C6A_HUMAN	21915,5103	39795,0045	27694,2272	2276,60273	15571,763	899113,623	489457,903	1088,16197	7303,09661
128	128	W[2Ox]TTLQEQGTK	618,326	18,95	sp P13647 K2C5_HUMAN	23083,8264	39106,2732	12657,1146	6700,74219	19549,9841	537519,25	240272,14	70069,5496	6199,17491
129	129	TNETYKLEAVQIK	822,421	18,98	sp P01040 CYTA_HUMAN	6363,81641	5717,62547	6238,75393	17552,3523	9587,99027	1176,68074	1558,37419	755,238284	2869,8085
130	130	QGTGGDVNVE[CAM]MDAAPGVDSL	1073	19,01	sp P08779 K1C16_HUMAN	31615,5149	15658,7858	9299,51066	2207,4618	1468,19199	300,45538	284,81868	805,056312	891,899138
131	131	CAM.QGTGGDVNVMDEAAPGVDSL	715,669	19,01	sp P08779 K1C16_HUMAN	10990,7414	22079,0866	7981,06758	5011,33887	3244,23279	9852,79178	2434,53994	2137,12749	1882,16787
132	132	W[2Ox]LQSQELPR	623,315	19,04	sp P01877 IGHA2_HUMAN	1603,76966	4976,55103	2646,53609	2275,7618	36238,943	2507,2199	875,339482	895,963228	3137,18021
133	133	W[2Ox]LQSQELPR	623,315	19,04	sp P01876 IGHA1_HUMAN	1603,76966	4976,55103	2646,53609	2275,7618	36238,943	2507,2199	875,339482	895,963228	3137,18021
134	134	QLDSIVGER	508,772	19,08	sp P48668 K2C6C_HUMAN	1545,02698	911,188908	1871,40519	441,747587	1251,7653	33191,0774	45174,7417	9016,96341	3582,64785
135	135	QLDSIVGER	508,772	19,08	sp P02538 K2C6A_HUMAN	1545,02698	911,188908	1871,40519	441,747587	1251,7653	33191,0774	45174,7417	9016,96341	3582,64785
136	136	QLDSIVGER	508,772	19,08	sp P13647 K2C5_HUMAN	1545,02698	911,188908	1871,40519	441,747587	1251,7653	33191,0774	45174,7417	9016,96341	3582,64785
137	137	TGSNDVFPVLK	668,858	19,13	sp Q72794 K2C18_HUMAN	7150,57615	6488,74834	16229,4368	4082,64157	14251,8016	3344,90555	145659,103	1822,2646	7997,24168
138	138	RLLEGDAHLSSQSSGSSQSSR	822,394	19,14	sp P02533 K1C14_HUMAN	5667,53526	6206,37209	1611,1186	293,067193	897,195511	1062,8887	982,345637	886,821056	2523,72712
139	139	TRLEQEIATYRR	512,614	19,17	sp Q04695 K1C17_HUMAN	10869,8488	39138,0597	16260,5793	13698,1202	13338,0262	781,026486	573,375643	382,840602	848,407848
140	140	TRLEQEIATYRR	512,614	19,17	sp P08779 K1C16_HUMAN	10869,8488	39138,0597	16260,5793	13698,1202	13338,0262	781,026486	573,375643	382,840602	848,407848
141	141	TRLEQEIATYRR	512,614	19,17	sp P02533 K1C14_HUMAN	10869,8488	39138,0597	16260,5793	13698,1202	13338,0262	781,026486	573,375643	382,840602	848,407848
142	142	ALAEANAD[NaX]LEVK	662,323	19,26	sp P13646 K1C13_HUMAN	11600,4505	18779,4649	6701,33701	1664,59678	4454,48726	697,559484	1012,97982	384,764085	6976,69475
143	143	ALAEANAD[NaX]LEVK	662,323	19,26	sp P08779 K1C16_HUMAN	11600,4505	18779,4649	6701,33701	1664,59678	4454,48726	697,559484	1012,97982	384,764085	6976,69475
144	144	ALAEANAD[NaX]LEVK	662,323	19,26	sp P02533 K1C14_HUMAN	11600,4505	18779,4649	6701,33701	1664,59678	4454,48726	697,559484	1012,97982	384,764085	6976,69475
145	145	ALAEANADLEVK	651,333	19,3	sp P13646 K1C13_HUMAN	58963,8493	111236,489	63061,0871	42042,2036	33404,9851	2033,47423	3266,74599	874,487739	7424,63992
146	146	ALAEANADLEVK	651,333	19,3	sp P08779 K1C16_HUMAN	58963,8493	111236,489	63061,0871	42042,2036	33404,9851	2033,47423	3266,74599	874,487739	7424,63992
147	147	ALAEANADLEVK	651,333	19,3	sp P02533 K1C14_HUMAN	58963,8493	111236,489	63061,0871	42042,2036	33404,9851	2033,47423	3266,74599	874,487739	7424,63992
148	148	RQSVADINGLR	679,362	19,33	sp P13646 K1C13_HUMAN	32690,4784	40645,7976	33063,6762	2267,32739	1652,40927	467,128205	170,077596	955,634178	
149	149	RQSVADINGLR	679,362	19,33	sp Q61FW6 K1C10_RAT	32690,4784	40645,7976	33063,6762	2267,32739	1652,40927	467,128205	170,077596	955,634178	
150	150	RQSVADINGLR	679,362	19,33	sp P13645 K1C10_HUMAN	32690,4784	40645,7976	33063,6762	2267,32739	1652,40927	467,128205	170,077596	955,634178	
151	151	VQALEANNDLENK	793,885	19,34	sp P35527 K1C9_HUMAN	40327,3643	138268,639	143393,741	80369,0869	73810,8018	11254,229	3340,98106	3454,24334	16598,6923
152	152	TEELNKVEANSVSELVQSSR	707,354	19,38	sp P08779 K1C16_HUMAN	13962,0415	27747,0496	1490,36641	3982,41692	2516,70332	1696,06404	581,122083	1635,2864	7596,18663
153	153	AAR.VATVSLPR	435,774	19,4	sp P00761 TRYP_PIG	593785,197	7592202,94	3330928,33	9301064,01	551244,39	14670,5702	5105,51435	4360231,44	
154	154	QVLDNLMT[Oxi]EK	603,805	19,4	sp P35527 K1C9_HUMAN	29424,4629	59550,8976	77015,774	56245,1601	44310,2221	681,275945	3939,03843	4470,48987	13303,5279
155	155	TKYTELNL	633,838	19,43	sp P02533 K1C14_HUMAN	832,650657	2665,17166	759,264784	3463,60606	1260,70008	1125,82929	51841,3244	14361,2797	1923,35284
156	156	ASLNSLEETK	610,803	19,46	sp P08779 K1C16_HUMAN	19638,8783	27761,1092	828,15346	11028,574	10484,0393	2460,83568	31005,048	10982,3922	5716,0875
157	157	ASLNSLEETK	610,803	19,46	sp P02533 K1C14_HUMAN	19638,8783	27761,1092	828,15346	11028,574	10484,0393	2460,83568	31005,048	10982,3922	5716,0875
158	158	M[Oxi]T[Dhy]LDDFR	448,202	19,46	sp P35527 K1C9_HUMAN	13973,4859	87125,3762	20614,6798	18434,2085	20827,5742	97731,6654	116808,753	1456,04452	4552,50904
159	159	ALAEANELEVK	673,347	19,53	sp Q04695 K1C17_HUMAN	6636,9002	15124,1744	11329,9213	3942,60023	7083,21376	1844,0764	2220,39904	2058,58586	5950,13834
160	160	W[Oxi]TTLQEQGTK	610,32	19,59	sp P48668 K2C6C_HUMAN	16685,8878	36207,404	12189,4901	12222,7108	10748,4697	15678,4971	2378,8358	156,778183	3955,40653
161	161	W[Oxi]TTLQEQGTK	610,32	19,59	sp P02538 K2C6A_HUMAN	16685,8878	36207,404	12189,4901	12222,7108	10748,4697	15678,4971	2378,8358	156,778183	3955,40653
162	162	W[Oxi]TTLQEQGTK	610,32	19,59	sp P13647 K2C5_HUMAN	16685,8878	36207,404	12189,4901	12222,7108	10748,4697	15678,4971	2378,8358	156,778183	3955,40653
163	163	VDHLPR	425,251	19,61	sp P29508 SPB3_HUMAN	14117,1891	1163,94675	6755,70657	14249,7075	308,620564	386,620564	1210,73124	311,386806	3316,3107
164	164	NFDPIK	733,387	19,65	sp P12253 TRYP_HUMAN	9590,69781	10368,7585	10626,891	9663,58916	19012,9664	4826,09132	2207,22612	424,613384	3644,58487
165	165	QEYEQLIQK	561,295	19,69	sp P35527 K1C9_HUMAN	46523,0453	102582,7	78357,4599	44928,9585	55174,3074	68353,9503	956,346405	830,822991	10553,465
166	166	GAVHVDKDVLD	627,82	19,72	sp P81605 DCD_HUMAN	18024,8942	13433,818	26011,7116	1655,98570	36656,9798	4747,76215	847,29627	841,075013	3974,77027
167	167	TEELNREVATNSVSELVQSGK	702,026	19,76	sp Q04695 K1C17_HUMAN	805,983657	2172,82815	379,437423	1053,64084	552,832902	4612,4391	1993,59234	123,363332	2882,71631
168	168	TEELNREVATNSVSELVQSGK	702,026	19,76	sp P02533 K1C14_HUMAN	805,983657	2172,82815	379,437423	1053,64084	552,832902	4612,4391	1993,59234	123,363332	2882,71631
169	169	FLEQQNQVLQTK	738,396	19,84	sp Q72794 K2C18_HUMAN	1099172,48	1578916,84	1335444,87	681892,482	104959,596	2765,51668	1261,99897	320,333495	94976,5368
170	170	FLEQQNQVLQTK	738,396	19,84	sp P35908 K2E2_HUMAN	1099172,								

222	222	FLEQQN[Dea]QVLQTK	738,887	20,7	sp P35908 K22E_HUMAN	43081,5398	70963,8626	54388,9197	25136,0634	40438,8527	24647,3144	511792,523	4029,9685	3684,8987
223	222	FLEQQN[Dea]QVLQTK	738,887	20,7	sp P04264 K2C1_HUMAN	43081,5398	70963,8626	54388,9197	25136,0634	40438,8527	24647,3144	511792,523	4029,9685	3684,8987
224	224	QSVEADINGLRL	679,363	20,74	sp P13646 K1C13_HUMAN	11252,1757	1923,08143	15606,0354	527,581883	18253,3889	795824,896	309287,118	94835,5731	7207,15499
225	225	QSVEADINGLRL	679,363	20,74	sp Q61FW6 K1C10_RAT	11252,1757	1923,08143	15606,0354	527,581883	18253,3889	795824,896	309287,118	94835,5731	7207,15499
226	226	QSVEADINGLRL	679,363	20,74	sp P13645 K1C10_HUMAN	11252,1757	1923,08143	15606,0354	527,581883	18253,3889	795824,896	309287,118	94835,5731	7207,15499
227	227	YEEQLQVTVGR	597,311	20,74	sp P35908 K22E_HUMAN	245161,167	202832,568	171538,034	106445,777	105320,259	810,405926	830,537991	1172,66429	6587,85303
228	228	NLC DPSIQR	592,326	20,76	sp P13647 K2C5_HUMAN	2338,67783	4960,53034	4072,82033	1093,66525	3781,94873	16928,2699	813,308891	504,526039	1697,03251
229	229	ITAVCI[CAM]KVPDESEVVVER	644,004	20,76	sp Q08188 TGM3_HUMAN	5256,38948	5788,5594	1085,0397	2944,29253	7603,6887	2222,02763	1108,58838	377,731786	375,956461
230	230	ILLDVK	350,735	20,77	sp Q04695 K1C17_HUMAN	8732,37541	46546,5939	20475,8894	14809,8982	15081,9782	179,29423	10351,2719	629,63033	959,211934
231	231	ILLDVK	350,735	20,77	sp P08779 K1C16_HUMAN	8732,37541	46546,5939	20475,8894	14809,8982	15081,9782	179,29423	10351,2719	629,63033	959,211934
232	232	ILLDVK	350,735	20,77	sp P02533 K1C14_HUMAN	8732,37541	46546,5939	20475,8894	14809,8982	15081,9782	179,29423	10351,2719	629,63033	959,211934
233	233	ISIGGSC[CAM]AISGGYGS	799,882	20,81	sp P48668 K2C6C_HUMAN	31632,585	65888,7324	1934,74733	448,539143	210,039312	5983,79409	609,89463	2236,22608	4560,61518
234	234	ISIGGSC[CAM]AISGGYGS	799,882	20,81	sp P35908 K2C6A_HUMAN	31632,585	65888,7324	1934,74733	448,539143	210,039312	5983,79409	609,89463	2236,22608	4560,61518
235	235	QRPAEIKDYSPIFK	871,449	20,93	sp P02533 K1C14_HUMAN	1179,543	13618,3101	14866,7759	1676,624	5742,19407	1717,21811	124,835292	581,141749	4436,68824
236	236	YQ[Dea]ELQITAGR	590,303	20,94	sp Q72794 K2C18_HUMAN	690267,392	931229,168	745514,738	5637,5556	787821,111	819523,321	368295,876	68914,4161	1580,3207
237	237	NVAVPLYNR	523,294	20,94	sp P15252 REF_HEVBR	10470,7431	1981,68188	1326,72882	2972,69664	558,58589	29158,6312	49541,8108	18785,0792	5995,43778
238	238	FLEQQ[Dea]NQVLQTK	738,887	21,04	sp Q72794 K2C18_HUMAN	16134,9811	35909,0735	23560,6714	670,860653	16089,1798	46308,2311	14757,4048	2981,7518	2301,5109
239	239	FLEQQ[Dea]NQVLQTK	738,887	21,04	sp P35908 K2C18_HUMAN	16134,9811	35909,0735	23560,6714	670,860653	16089,1798	46308,2311	14757,4048	2981,7518	2301,5109
240	240	ALDPEISSGGLR	672,344	21,08	sp Q08554 DSC1_HUMAN	12060,4325	8035,42592	9305,51255	17323,2427	11047,5545	7592,87461	1474,45118	546,720912	3219,26908
241	241	FLEQQN[Dea]VLQTK	738,889	21,1	sp Q72794 K2C18_HUMAN	16152,1064	35669,8776	23678,2602	13276,2098	16082,8613	46324,5387	14761,5475	2980,86293	6344,5761
242	242	DTGDIFC[CAM]TR	542,741	21,11	sp Q08554 DSC1_HUMAN	356,138921	1327,10138	905,090674	5047,54098	2425,95202	507,3493	4456,02428	200,016421	9254,6831
243	243	WNLDSEPPVVTK	617,362	21,11	sp Q8WNW3 PLAK_PIG	17931,3956	35417,0008	20573,6863	17531,9962	14607,8346	2780,26067	5248,32803	460,186336	8678,71836
244	244	QVLDLASEQM[Oxi]R	653,328	21,11	sp Q72794 K2C18_HUMAN	11949,3156	2579,15087	8242,28675	1050,44973	10713,636	959,300347	1665,58517	402,036013	8333,6102
245	245	AYLEEE[CAM]PATLR	726,346	21,11	sp P25311 ZAG2_HUMAN	400,304295	2556,60302	3884,88274	309,659466	11066,6112	3084,75075	3188,82129	196,64516	1894,86622
246	246	YIEKDTGDIFC[CAM]TR	539,925	21,17	sp Q08554 DSC1_HUMAN	1893,0398	4968,0856	1565,39781	10188,9549	3668,06168	3160,39959	4861,12791	300,288617	9653,11941
247	247	QGTGGDGVNVEIM[Oxi]DAAPGVDLR	1052,48	21,21	sp P08779 K1C16_HUMAN	3921,39794	2114,30638	7386,84704	4230,47268	1914,95531	10052,6856	978,821382	242,10666	3182,2077
248	248	FLEQ[Dea]QNQVLQTK	738,887	21,27	sp Q72794 K2C18_HUMAN	822,816387	36081,8264	23500,9086	13296,1806	16107,1808	21778,3708	25803,0795	5349,14474	3964,86032
249	249	FLEQ[Dea]QNQVLQTK	738,887	21,27	sp P35908 K2C18_HUMAN	822,816387	36081,8264	23500,9086	13296,1806	16107,1808	21778,3708	25803,0795	5349,14474	3964,86032
250	250	CRM.TAAENEFVTLK	633,322	21,27	sp P48668 K2C6C_HUMAN	162282,804	214588,755	423,080776	148912,359	193069,607	1146,98718	1310,43706	683,624009	13419,8811
251	251	CRM.TAAENEFVTLK	633,322	21,27	sp P02538 K2C6A_HUMAN	162282,804	214588,755	423,080776	148912,359	193069,607	1146,98718	1310,43706	683,624009	13419,8811
252	252	CRM.TAAENEFVTLK	633,322	21,27	sp P04264 K2C1_HUMAN	162282,804	214588,755	423,080776	148912,359	193069,607	1146,98718	1310,43706	683,624009	13419,8811
253	253	NLDIPAIQR	584,329	21,3	sp P48668 K2C6C_HUMAN	882,469191	2363,05247	1448,38191	10592,5069	5181,39046	905,189555	492,150848	175,456602	1026,0265
254	254	CRM.TAAENE[NaX]FVTLK	644,314	21,31	sp P48668 K2C6C_HUMAN	18607,2875	397,088496	13843,0022	6636,52446	1601,28714	1639,28648	1446,81126	897,285675	3338,44295
255	255	CRM.TAAENE[NaX]FVTLK	644,314	21,31	sp P02538 K2C6A_HUMAN	18607,2875	397,088496	13843,0022	6636,52446	1601,28714	1639,28648	1446,81126	897,285675	3338,44295
256	256	SC[CAM]AAGTEC[CAM]LUSGW[2ox]GNTK[A	971,933	21,33	sp P00761 TRYP_PIG	3775,58349	5295,04748	886,229941	725,74897	9129,98563	1828,05371	740,596719	172,750487	1476,8765
257	257	YLTWASR	448,735	21,41	sp P01877 IGHA2_HUMAN	291,931775	2108,63971	683,394329	416,084117	23006,09361	339,205713	506,97554	178,962516	1051,08508
258	258	YLTWASR	448,735	21,41	sp P01876 IGHA1_HUMAN	291,931775	2108,63971	683,394329	416,084117	23006,09361	339,205713	506,97554	178,962516	1051,08508
259	259	CAM.FLEQQNQVLQTK	766,906	21,43	sp Q72794 K2C18_HUMAN	1035,95151	3431,92014	1657,8603	909,415218	3389,11299	2954,7693	14201,2567	2619,69301	2087,1081
260	260	CAM.FLEQQNQVLQTK	766,906	21,43	sp P35908 K22E_HUMAN	1035,95151	3431,92014	1657,8603	909,415218	3389,11299	2954,7693	14201,2567	2619,69301	2087,1081
261	261	LLETET[CAM]PQYIR	711,359	21,48	sp P05109 S10AB_HUMAN	417,733821	3391,06974	8615,07276	6688,50211	9467,54925	1237,21341	4920,21688	531,854539	4292,39829
262	262	PRADTAEOGFQEEEL	573,944	21,54	sp P31944 CASPE_HUMAN	2468,29086	6219,19074	5845,99874	18469,3739	10278,4509	4856,1648	4174,92399	673,81816	1492,53877
263	263	QLQNIQIATSR	636,357	21,56	sp P15924 DESP_HUMAN	2073,1871	9517,04281	7349,21523	1670,61564	6853,64675	1075,91281	1404,65802	699,784124	1811,29771
264	264	AELEQLQIR	614,337	21,61	sp Q61FW6 K1C10_RAT	1131,55825	778,592569	6404,0739	5141,39365	9440,79029	1987,59868	930,436247	3089,89095	1744,80654
265	265	CAM.QGVGGEINVEMDAAPGVDLR	1086,03	21,63	sp Q04695 K1C17_HUMAN	159,19244	3650,2427	1904,89381	343,16161	155,831984	292,940805	389,01376	238,805066	388,584568
266	266	ESTHLVLRL	534,314	21,64	sp P68202 RS27A_PLUXY	14539,4812	6027,76232	10729,95	24503,5818	20070,4807	3525,05256	5466,53026	6406,2009	5951,59415
267	267	SISGPGDKEPFF	616,812	21,82	sp Q08554 DSC1_HUMAN	4290,2776	11177,9973	8814,18576	30666,0006	7977,49804	6360,26587	12011,7169	1157,30673	7571,08177
268	268	DAEAW[2ox]FNEK	571,243	21,87	sp Q61FW6 K1C10_RAT	3683,95706	13914,6069	4471,72781	5484,46976	14747,231	484,96815	1817,03467	1212,37599	9982,24914
269	269	STSGGTAALGC[CAM]LVK	661,342	21,88	sp P01857 IGHG1_HUMAN	1126,05096	3183,17967	5114,73796	9658,76562	4223,72718	3653,05891	612,973506	1260,47452	5464,50435
270	270	VIAPSSSLPTSLTHHPR	638,359	21,89	sp Q02413 DSG1_HUMAN	1037,67258	7312,18723	6984,49365	1221,75693	3561,68605	1012,1367	302,029764	2075,06349	6800,30225
271	271	KVPQVSTPTLVEVSR	547,318	21,92	sp P02769 ALBU_BOVIN	15368,2302	151,939711	17767,5708	15334,0628	19776,3841	612,352719	754,64729	283,833109	11989,2889
272	272	KVPQVSTPTLVEVSR	547,318	21,92	sp P02768 ALBU_BOVIN	15368,2302	151,939711	17767,5708	15334,0628	19776,3841	612,352719	754,64729	283,833109	11989,2889
273	273	IISNAS[CAM]TTNC[CAM]LAPLAK	917,463	22,02	sp P04046 G3P_HUMAN	2304,25849	4075,90972	5430,29649	4748,78013	5835,22064	950,092795	1473,47614	181,875373	875,195625
274	274	GLTGFGFSHSV[CAM]GGFR	798,371	22,05	sp Q43790 KRT86_HUMAN	1085,51529	951,959431	2813,39136	959,618317	363,134742	3723,20758	3533,19212	486,545808	6044,11439
275	275	LVNVEFEAK	575,313	22,05	sp P02768 ALBU_HUMAN	8957,63573	11363,643	18280,8389	12160,9761	18190,5488	1050,19796	115,06034	551,297408	7277,16109
276	276	QSLASLAETEGR	695,845	22,07	sp Q61FW6 K1C10_RAT	255305,064	329759,065	274765,004	160053,327	279686,821	2500,42627	5197,01221	2338,96627	27626,361
277	277	QSLASLAETEGR	695,845	22,07	sp P13645 K1C10_HUMAN	255305,064	329759,065	274765,004	160053,327	279686,821	2500,42627	5197,01221	2338,96627	27626,361
278	278	FQNALLVR	480,786	22,12	sp P49065 ALBU_RABIT	3835,41107	1842,47262	1810,6606	7801,66178	9490,17055	364,883361	471,380667	198,118692	24594,4626
279	279	FQNALLVR	480,786	22,12	sp P02768 ALBU_HUMAN	3835,41107	1842,47262	1810,6606	7801,66178	9490,17055	364,883361	471,380667	198,118692	24594,4626
280	280	SNL[CAM]ALC[CAM]IGDEOGENK	904,402	22,14	sp P02788 TRFL_HUMAN	808,918775	1564,51642	751,494176	630,839025	8144,80171	1002,33908	3189,74805	274,337183	7488,04661
281	281	DGAGDVAFIR												

333	333	LAELEALQK	572,318	22,74	sp P13647 K2C5_HUMAN	16293,9461	26358,7407	33280,5281	33510,6522	17254,8655	4212,35986	1307,44402	606,171146	19712,2915
334	334	LGEHNIDVLEGN	719,844	22,75	sp P00761 TRYP_PIG	4313,76412	6014,26911	716,46292	5446,03181	4285,60712	3701,85488	4388,10393	1086,96484	9931,5561
335	335	Q1TYNDLPVGR	606,342	22,76	sp Q8K3U7 PRDX2_CRIGR	6442,25225	10871,4974	14936,3931	7709,38905	6772,31912	896,001586	1801,37654	724,81518	4465,32438
336	336	LKGDAVEDELSVGK	730,386	22,81	sp P81605 DCD_HUMAN	51445,4002	64003,1911	81682,091	89000,5568	98955,3643	2816,27563	4541,47735	1137,97538	16886,3054
337	337	LGEHNIDVLEGN	598,301	22,84	sp P00761 TRYP_PIG	22844,477	30348,6775	33572,3272	28320,7033	33562,4963	1092,98519	1064,14933	1317,08291	23321,4272
338	338	DSASQVVSVAIR	579,828	22,94	sp P15252 REF_HEVBR	54099,7497	54106,302	61441,6053	60705,048	118456,308	2323,87098	3794,23596	748,054432	6798,262
339	339	CRM.LKYENEVALR	639,347	22,95	sp Q61FW6 K1C10_RAT	25511,1361	25086,5363	23818,5466	9356,68179	18748,0358	7219,86512	9406,72529	9237,62776	2210,57811
340	340	YYDGDQDIEFKN	573,265	22,99	sp P25311 ZAG2_HUMAN	9525,03233	7147,36095	6963,35475	7128,32224	16125,9952	6790,9956	1015,48367	560,15654	10673,5137
341	341	ALFEQLQRIAE	714,38	23,02	sp Q61FW6 K1C10_RAT	1356,21232	1374,84427	6551,19694	12312,8781	6332,0035	4868,98171	5095,52624	1054,67006	6301,10415
342	342	DAVEDELSVGK	581,285	23,05	sp P81605 DCD_HUMAN	37728,1008	45014,2303	4106,8118	59228,257	6382,0635	2922,83276	712,40085	526,876006	12249,7048
343	343	VLDLTLTK	516,303	23,07	sp P13645 K1C10_HUMAN	828037,74	822115,195	612958,062	402639,586	652046,112	268,543933	993,432369	1867,72398	83283,5305
344	344	LLRDYQELMNTK	508,602	23,1	sp P04264 K2C1_HUMAN	657,768631	51723,6539	7167,32359	9008,0526	15932,1085	98,876311	142,112943	124,764784	1013,21043
345	345	KAAEAFESLYSKYEELQTAGR	834,422	23,11	sp P04264 K2C1_HUMAN	28176,8482	31757,6002	34793,1424	2340,19657	36679,934	2350,48923	1793,68472	177,646947	2724,98139
346	346	AELIVQPELK	570,336	23,18	sp P15924 DESP_HUMAN	626329,925	314333,981	110986,131	3356542,601	123408,298	92060,502	1173,80463	85014,3511	108795,869
347	347	DASGATFTWTPSSGK	756,853	23,25	sp P01877 IGHA2_HUMAN	704,131986	4311,67315	1207,40514	2732,70974	28392,9118	3819,43347	2375,27706	2104,38946	7453,63469
348	348	AELIVQ[Dea]PELK	570,838	23,3	sp P15924 DESP_HUMAN	1262,46713	10405,626	8198,86853	2171,26206	8903,1065	1331,65803	7276,85868	3393,4396	3416,52558
349	349	ANSVSC[CAM]WSGPGFR	712,823	23,31	sp Q9NSB2 KRT84_HUMAN	981,509239	1748,76071	2588,15656	302,842152	1239,3054	15917,8697	4262,33536	846,973161	2668,47309
350	350	ENPVKSGPVGPFSAAGPISEK	741,39	23,38	sp Q15517 CDN_HUMAN	1201,8412	3160,04447	4806,21083	1048,24583	1509,33307	1647,38246	1852,78828	4078,89876	5613,8806
351	351	PGQ.QS[CAM]VEADINGLRR	699,361	23,38	sp P13646 K1C13_HUMAN	6824,84322	718,87339	15953,001	4641,49751	3326,93672	206,8235	996,384671	1948,02779	14993,7989
352	352	PGQ.QRPAEIKDYSPYFK	862,936	23,43	sp P02533 K1C14_HUMAN	6105,55394	14849,1989	10278,1911	567,999896	5418,65852	2985,9487	4208,84596	972,546746	1592,70151
353	353	ALNSIIDVYHK	636,849	23,47	sp P05109 S10A8_HUMAN	10468,7705	9695,2672	18211,9391	7015,2914	16176,717	3459,21307	5556,33784	1902,79827	7038,21036
354	354	NNFLDRQGVQGY	773,85	23,48	sp Q02413 DSG1_HUMAN	2577,35623	1715,67471	2799,91165	11016,149	1216,18553	7285,91348	6080,90017	1883,59356	5183,68873
355	355	PGQ.QGVGDADINLGR	570,787	23,51	sp P35527 K1C9_HUMAN	53377,4149	214383,673	194020,286	147388,319	115683,2	620,674008	351,474074	2037,15451	50467,5403
356	356	PGQ.QGVGDADIN[Dea]GLR	571,287	23,55	sp P35527 K1C9_HUMAN	104698,009	138718,999	123361,067	159923,082	85548,1103	44297,9408	25518,9446	19323,7728	45762,8547
357	357	ALYAN[Dea]LEPKAEQY	755,877	23,56	sp Q82803 SRPP_HEVBR	2003,64981	3045,94671	10327,2147	3263,61294	6879,22559	2149,91404	54,60967	1004,73236	3142,2944
358	358	ALDEVALTK	536,775	23,58	sp Q72KU3 PYRD_THET2	1458,8925	255,125754	1055,125754	911,120514	1231,67579	2109,34521	438,929975	665,522032	779715,798
359	359	IIIEGQYDADLNDER	846,908	23,58	sp P09228 CYTT_HUMAN	1365,0584	9053,23401	2669,93868	492,362318	2070,09326	4493,65127	1714,34382	1483,24925	2941,20334
360	360	AIGGGLSVGGSGSTIKY	805,923	23,62	sp P48668 K2C6C_HUMAN	8771,26832	14064,0803	11735,384	2952,68219	9430,4608	3821,81685	2240,43506	1677,54757	1853,72326
361	361	AIGGGLSVGGSGSGSTIKY	805,923	23,62	sp P02538 K2C6A_HUMAN	8771,26832	14064,0803	11735,384	2952,68219	9430,4608	3821,81685	2240,43506	1677,54757	1853,72326
362	362	PGQ.QSVEADINGLRR	670,85	23,63	sp P13646 K1C13_HUMAN	694878,079	826580,895	649004,163	382776,361	553478,392	2819,97669	2503,49037	3570,01674	58041,4088
363	363	PGQ.QSVEADINGLRR	670,85	23,63	sp Q61FW6 K1C10_RAT	694878,079	826580,895	649004,163	382776,361	553478,392	2819,97669	2503,49037	3570,01674	58041,4088
364	364	PGQ.QSVEADINGLRR	670,85	23,63	sp P13645 K1C10_HUMAN	694878,079	826580,895	649004,163	382776,361	553478,392	2819,97669	2503,49037	3570,01674	58041,4088
365	365	IGFIEEVK	467,766	23,67	sp Q96P63 SPB12_HUMAN	7348,22632	5824,44666	15061,19458	10566,9334	8515,45808	424,330239	408,633926	140,680819	2488,34121
366	366	LC[CAM]IEGVGPVNISVSSSR	830,92	23,68	sp Q9NSB2 KRT84_HUMAN	1302,25002	2245,16619	2172,05356	1042,86059	2323,55099	42769,7029	189,807718	632,696603	4546,85127
367	367	NGSDC[CAM]PKDFC[CAM]LFQSETK	678,298	23,68	sp P02788 TRFL_HUMAN	1776,60173	3646,90003	2999,0753	1883,6483	9195,08145	881,665109	3324,64505	471,696517	11580,2814
368	368	VLDLTLTK	515,301	23,76	sp Q04693 K1C17_HUMAN	88885,7477	217667,114	120544,949	96153,1877	75346,6843	815,685766	2721,13933	1652,30939	10538,0605
369	369	GALQNIIPASTGAAK	706,399	23,76	sp P04406 G3P_HUMAN	21019,4513	18557,0924	27456,0136	30394,5562	34425,2343	3009,07928	234,053852	1454,47732	19972,0867
370	370	VLDLTLTK	515,301	23,76	sp P08779 K1C16_HUMAN	88885,7477	217667,114	120544,949	96153,1877	75346,6843	815,685766	2721,13933	1652,30939	10538,0605
371	371	VLDLTLTK	515,301	23,76	sp P02533 K1C14_HUMAN	88885,7477	217667,114	120544,949	96153,1877	75346,6843	815,685766	2721,13933	1652,30939	10538,0605
372	372	DAEAWFNEK	555,249	23,78	sp Q61FW6 K1C10_RAT	526157,124	407601,877	315352,68	179635,7	457128,332	687,074831	408,03622	1928,93203	27914,6067
373	373	Yl[odQ][Dea]ELQITAGR	634,252	23,78	sp Q72794 K2C18_HUMAN	6920,52385	5534,33791	5079,64448	2255,72137	3860,92132	2119,63782	2295,34661	3729,79843	3502,34384
374	374	DAEAWFNEK	555,249	23,78	sp P13645 K1C10_HUMAN	526157,124	407601,877	315352,68	179635,7	457128,332	687,074831	408,03622	1928,93203	27914,6067
375	375	VAPEEHFVLLTEAPLNPK	652,028	23,86	sp Q52MQ2 ACTG_CHICK	12517,2125	6708,25088	3094,32357	8193,94492	44122,0359	2804,98919	3594,82176	1474,0222	1541,3985
376	376	VLDLTLT[-2HJK]	515,3	23,88	sp P13645 K1C10_HUMAN	88924,2771	217663,429	120571,607	96319,2629	75386,2425	1186,76351	2757,45965	1851,54394	7188,93916
377	377	QC[CAM]ANLNOAIADAQR	851,4	23,91	sp P13647 K2C5_HUMAN	2170,79263	7375,75393	7012,88262	1213,87111	3128,91262	461,354709	5877,06682	1136,35743	33776,0495
378	378	PGQ.QRPEIKDYSPYFK	870,935	23,97	sp P08779 K1C16_HUMAN	2174,96633	3144,82323	1703,18315	979,824016	1261,98335	2148,51781	10400,4345	927,59707	7360,58293
379	379	PGQ.QRP[Oxi]AEIKDYSPYFK	870,935	23,97	sp P02533 K1C14_HUMAN	2724,96633	3144,82323	1703,18315	979,824016	1261,98335	2148,51781	10400,4345	927,59707	7360,58293
380	380	GMQD[2CM]LVDFKNNKYDEINKR	647,065	24,01	sp P02538 K2C6A_HUMAN	6600,40565	7264,92599	9740,92874	1692,55962	9888,30886	1359,64262	724,3056	456,345201	1736,23503
381	381	CRM.MNQDLVEDFKNNKYDEINKR	647,065	24,01	sp P13647 K2C5_HUMAN	6600,40565	7264,92599	9740,92874	1692,55962	9888,30886	1359,64262	724,3056	456,345201	1736,23503
382	382	GSVPFPLAPSSK	593,828	24,03	sp P01857 IGHG1_HUMAN	6473,39605	4649,80912	5849,2279	21152,1122	7718,68147	3047,10102	1884,96164	3524,8553	9077,93621
383	383	FSYIPNALK	555,303	24,03	sp P15252 REF_HEVBR	270696,976	58851,3502	62068,1509	48974,6666	113294,133	3224,63134	2382,76123	45739,041	1053,6248
384	384	GALQ[Dea]NIIPASTGAAK	706,891	24,16	sp P04406 G3P_HUMAN	5115,52182	2276,08658	7290,18979	18085,1071	3602,40193	26268,0883	2527,04962	3302,45494	8296,32023
385	385	SC[CAM]AAAGTEC[CAM]LISGW[Oxi]GNTK[A	963,936	24,18	sp P00761 TRYP_PIG	5350,9393	10192,204	1678,877	513,155447	13815,2383	1222,04978	1068,56084	909,78635	981,939882
386	386	M[Oxi]S[Dhy]GLDSSNVTVSTSTSSNVASK	819,398	24,18	sp P35908 K22E_HUMAN	4077,00542	12100,7707	7246,60314	4931,67011	6161,60623	2300,38991	196,778769	1729,20522	5604,17284
387	387	DALNIETAE	544,304	24,18	sp Q6TEQ7 ANXA2_CANLF	411,162017	4961,29962	6515,65934	9224,3553	6154,7318	1545,34939	535,88231	513,976447	10136,5248
388	388	GSVPGPFSAAGPISEK	827,926	24,19	sp Q15517 CDN_HUMAN	10400,2304	13981,1858	8619,18443	17914,3243	10790,0532	1887,18145	1963,06575	416,374599	5595,9696
389	389	TAFAQEALDAAGDK	668,825	24,19	sp Q5R9M3 THIO_PONAB	14752,9488	22748,8312	14575,778	18944,594	24273,7673	7641,46557	3614,68505	642,455894	7745,97827
390	390	TLLNKFASFIDK	466,585	24,21	sp P48668 K2C6C_HUMAN	2502,89753	5009,80475	929,094459	534,230589	2624,62158	521,186337	725,561407	211,749074	1737,90103
391	391	TLLNKFASFIDK	466,585	24,21	sp Q9NSB2 KRT84_HUMAN	2502,89753	5009,80475	929,094459	534,230589	2624,62158	521,186337	725,561407	211,749074	1737,90103
392	392	TLLNKFASFIDK	466,585	24,21										

444	444	VDNALQSGNSQESVTEQDSKDSYTSLSLTLSK	1207,24	25,42	sp P01834 IGKC_HUMAN	518,54571	2064,54702	1266,58667	1784,89642	12088,8595	1394,52166	240,605315	217,363282	1513,59486
445	445	DASGVITFTWTPSSGK	770,869	25,42	sp P01876 IGHA1_HUMAN	2059,32625	13839,6016	7958,72964	4639,83937	37036,8759	3209,11419	2258,18991	621,824027	11127,241
446	446	NVQDAIAAEQGEHALK	655,665	25,43	sp P35908 K22E_HUMAN	56888,1216	56289,8339	43365,2662	29976,0611	29422,2756	4246,43998	1138,60236	1289,11039	4931,29665
447	447	VGGVGVPAAPSIAVTNVK	869	25,44	sp Q09NSB2 KRT84_HUMAN	1532,70064	573,11048	1562,55768	1716,44915	2541,12469	72419,3294	120,175315	170,738039	5273,63953
448	448	AEQYAVITWR	618,825	25,52	sp Q08203 SRPP_HEVBR	10720,776	1637,08359	8527,00276	2236,0828	9871,2561	10792,6426	4671,38925	3600,57377	10402,7894
449	449	CAM.HGTTTGHQTGDTT	635,312	25,54	sp Q50862 FLA2_HUMAN	36111,2709	36393,8633	39452,4285	81120,8197	36737,7473	39405,6058	22958,167	47284,1228	33707,7827
450	450	EIETYHNLLGGGQ[XX]DFESSGAGK	850,033	25,61	sp P35527 K1C9_HUMAN	16382,6081	47799,1245	39965,6089	14541,4444	21366,1443	972,37618	712,561785	613,630089	373,227936
451	451	EIETYHNLLGGGQ[XX]DFESSGAGK	844,71	25,62	sp P35527 K1C9_HUMAN	10281,4682	23905,3818	3965,65706	9707,07258	8344,87024	4672,41871	2355,5797	482,441589	3643,96474
452	452	EIETYHNLL[XXX]GGQEDFESSGAGK	850,032	25,62	sp P35527 K1C9_HUMAN	16362,4302	47435,0774	39933,9333	14541,8427	21362,2135	982,81153	705,141093	614,579289	352,289461
453	453	EIETYHN[Dea]LLGGGQ[Dea]JEDFESSGAGK	838,051	25,62	sp P35527 K1C9_HUMAN	79357,2691	303843,585	251238,817	228521,22	15097,027	968,910872	690,506733	745,953458	2961,32674
454	454	YVM[Oxi]GNPNPADLLAVDSR	875,929	25,67	sp Q02413 DSG1_HUMAN	10910,1064	15789,6649	19921,382	12713,0472	13920,3516	6099,69606	606,951558	2138,57736	9926,08357
455	455	SLDGVPPVPVK	562,342	25,68	sp Q08203 SRPP_HEVBR	24273,682	29584,9208	73678,7033	17918,9188	47237,4204	21069,282	15911,8506	29150,7746	6730,13702
456	456	W[2xi]ELLLQVDVSTR	754,372	25,69	sp P04264 K2C1_HUMAN	34414,4315	58083,5724	13939,542	40598,0713	529078,728	235554,37	48542,7451	8925,56189	
457	457	NKLNLELD[XXX]ALQQAQ	813,395	25,69	sp P04264 K2C1_HUMAN	20219,0469	46012,7368	40880,2243	2790,72296	22552,4044	5758,97537	6606,24113	4089,32343	13481,1701
458	458	EIETYHNLLGGGQEDFESSGAGK	837,383	25,73	sp P35527 K1C9_HUMAN	98318,5426	368309,211	296922,559	734,846047	183244,569	2357,38816	1474,6446	525,729253	41878,726
459	459	NKLNLEDAALQQAQ	800,419	25,76	sp P04264 K2C1_HUMAN	252446,033	642572,787	472694,14	261521,586	286325,72	595,732459	1043,39371	1505,36538	19558,6911
460	460	LNLEEAALQQAQ	686,359	25,82	sp P35908 K22E_HUMAN	21778,5786	21698,4222	31174,9935	21543,7509	16011,1783	3088,80562	2523,15196	2044,09932	9704,48797
461	461	NKLALEALQQAQ	639,385	25,85	sp P13647 K2C5_HUMAN	27644,6914	87352,0219	36101,728	41169,197	35197,907	3257,18758	4698,93212	1618,49367	7945,70257
462	462	TLNNKFASFDIKR	551,642	25,89	sp P48668 K2C6_HUMAN	20680,8608	21229,4506	8720,13903	886,201873	1471,49632	759,909929	274,466443	382,42534	2551,24743
463	463	TLNNKFASFDIKR	551,642	25,89	sp Q09NSB2 KRT84_HUMAN	20680,8608	21229,4506	8720,13903	886,201873	1471,49632	759,909929	274,466443	382,42534	2551,24743
464	464	TLNNKFASFDIKR	551,642	25,89	sp P02538 K2C6A_HUMAN	20680,8608	21229,4506	8720,13903	886,201873	1471,49632	759,909929	274,466443	382,42534	2551,24743
465	465	TLNNKFASFDIKR	551,642	25,89	sp P13647 K2C5_HUMAN	20680,8608	21229,4506	8720,13903	886,201873	1471,49632	759,909929	274,466443	382,42534	2551,24743
466	466	TLNNKFASFDIKR	551,642	25,89	sp P35908 K22E_HUMAN	20680,8608	21229,4506	8720,13903	886,201873	1471,49632	759,909929	274,466443	382,42534	2551,24743
467	467	PGQ.QSL[NaX]ASLAETGR	698,322	25,92	sp Q61FW6 K1C10_RAT	32148,4872	33625,3418	13572,37	7684,15599	15018,298	7583,98613	1909,24229	1177,65337	10367,7985
468	468	PGQ.QSVEADINGLR	592,799	25,93	sp P13646 K1C13_HUMAN	46174,2129	48814,3467	45859,0904	29366,8315	35551,0673	1222,73452	793,822954	881,152543	18425,5066
469	469	PGQ.QSVEADINGLR	592,799	25,93	sp Q61FW6 K1C10_RAT	46174,2129	48814,3467	45859,0904	29366,8315	35551,0673	1222,73452	793,822954	881,152543	18425,5066
470	470	GAHVDDVLDVDSV	677,353	25,93	sp P81605 DCD_HUMAN	44790,3362	80745,1462	70052,637	125459,911	74584,0854	3428,18694	3903,37701	710,387365	7788,81276
471	471	PGQ.QSVEADINGLR	592,799	25,93	sp P13645 K1C10_HUMAN	46174,2129	48814,3467	45859,0904	29366,8315	35551,0673	1222,73452	793,822954	881,152543	18425,5066
472	472	PGQ.QSLASLAETGR	687,331	25,96	sp Q61FW6 K1C10_RAT	144668,253	189493,26	131308,634	97380,0308	169742,488	4303,1787	2143,82057	2349,9473	207220,594
473	473	TM[Oxi]NNFLDREQYGYALAVR	769,039	25,96	sp Q02413 DSG1_HUMAN	9603,70553	5299,18601	7932,92988	7933,42974	10771,1371	6433,99693	1434,77892	475,62787	6221,64511
474	474	PGQ.QSLASLAETGR	687,331	25,96	sp P13645 K1C10_HUMAN	144668,253	189493,26	131308,634	97380,0308	169742,488	4303,1787	2143,82057	2349,9473	207220,594
475	475	TITLEVPSDITIENVK	894,648	25,97	sp P68202 RS27A_PLUXY	17489,6583	10030,6245	16404,801	41325,1971	21926,9215	6780,13735	1149,07498	1560,31228	6423,38096
476	476	SAIIVHLYNQDDAEALTR	677,354	25,98	sp Q8WNW3 PLAK_PIG	44672,5366	80719,4314	69904,6049	125349,957	74552,7213	3438,46002	1186,59696	713,109551	8117,5483
477	477	TM[Oxi]NN[Dea]FLDREQYGYALAVR	769,375	26	sp Q02413 DSG1_HUMAN	24537,2115	28440,0477	4638,91497	18373,0015	23083,8695	4968,11882	3136,27365	1667,12464	6734,01522
478	478	GLSTESILPR	395,899	26,01	sp Q5VSP4 LC1L1_HUMAN	191,090492	2653,64127	1931,9448	388,960653	8705,52704	2446,40472	592,468199	1661,58739	954,983381
479	479	DKSGPLPGVDIEGVPVK	617,007	26,04	sp P15252 REF_HEVBR	993,294744	1571,81104	2738,16257	1452,74423	985,743482	16256,9444	20764,1925	9821,73938	1282,80492
480	480	NNLEALEDFEK	661,32	26,06	sp Q5VSP4 LC1L1_HUMAN	5830,28594	8678,44262	5464,30071	10630,1099	88541,5217	1673,00587	358,66372	484,45084	5904,34052
481	481	SC[CAM]AAAGTEC[XXX][C]CAM]USGWGNTK[A	560,279	26,08	sp P00761 TRYP_PIG	45366,667	72181,707	23035,0353	15785,0353	101483,269	401,2167	381,24708	3014,23119	8779,82954
482	482	SC[CAM]AAAGTEC[CAM]USGWGNTK[AAR]	955,939	26,08	sp P00761 TRYP_PIG	231714,037	659748,156	221634,889	184833,948	776113,765	3719,06798	942,182005	1982,99309	47187,7586
483	483	CAM.V[C]CAM]GR[AGA]GGGSGFSGVGGSG	1064,47	26,08	sp P35527 K1C9_HUMAN	3545,39126	14090,3829	11739,3221	8788,91163	8787,53473	2692,60594	1163,99065	780,744106	5012,84543
484	484	Frm.ELLOQVDSTR	659,335	26,11	sp P04264 K2C1_HUMAN	47978,9973	142364,943	76530,1362	63145,018	85639,6037	96355,4285	6063,7671	3731,71646	10157,5882
485	485	GTNYLVLLVR	692,861	26,13	sp P31151 S10A7_HUMAN	2209,46052	5308,45508	4201,98619	14071,3232	16727,4131	1078,39291	4852,52162	1332,45286	733,145118
486	486	RHPDYSVLLLR	489,953	26,14	sp P49065 ALBU_RABIT	21022,2053	2492,03241	3149,16982	17815,3725	17784,3454	2405,39125	715,838522	2389,73171	1134,69281
487	487	RHPDYSVLLLR	489,953	26,14	sp P02768 ALBU_HUMAN	21022,2053	2492,03241	3149,16982	17815,3725	17784,3454	2405,39125	715,838522	2389,73171	1134,69281
488	488	CRM.VQ[Dea]ELQITAGR	611,807	26,18	sp Q072794 K2C1B_HUMAN	2841,64848	22013,7696	4971,25186	8264,92251	12550,3619	22157,3871	3017,91554	2751,87929	9826,43278
489	489	NLFNDNPD[CAM]LAR	790,38	26,23	sp P02768 TRFL_HUMAN	3314,85903	733,141027	5219,6589	1484,69924	26483,8227	3321,53946	2879,71514	974,83841	16113,5387
490	490	CAM.SC[CAM]AAAGTEC[CAM]USGWGNTK[A	984,451	26,24	sp P00761 TRYP_PIG	5484,7633	14955,2065	4522,48464	5442,00019	19016,1724	2079,62899	6044,62476	2748,59061	14011,4038
491	491	LGHEMIDVLEGNEQ[Dea]FINAAK	738,043	26,29	sp P00761 TRYP_PIG	75050,3902	109490,455	115323,935	147925,046	134367,166	2302,73655	1926,24682	1136,35534	60805,3799
492	492	GGLVLC[CAM]GPEPLVAGSTLSR	885,464	26,32	sp Q09NSB2 KRT84_HUMAN	813,845067	3377,70798	1326,0161	3098,58479	275,644832	58997,7441	566,853307	2297,64379	3562,85331
493	493	YGQTILSIDDNLQR	818,42	26,34	sp Q02413 DSG1_HUMAN	13272,4443	18400,8489	14480,909	28051,2053	22857,2162	2668,1309	5146,83194	992,221339	961,151788
494	494	SLPGQNELDLVLTGYQDVK	988,505	26,35	sp P01040 CYTA_HUMAN	9751,5171	9900,226	6758,65445	19097,0666	18486,4159	1290,35884	2127,81421	1843,25638	17826,591
495	495	LGHEMIDVLEGNEQFINAAK	737,706	26,41	sp P00761 TRYP_PIG	66077,7318	91748,41	90475,7151	134191,305	113301,688	2091,17059	1945,64083	769,550819	6083,17811
496	496	STDYGIQFINSR	700,843	26,43	sp P61628 LYSC_PANTR	161253,3795	15641,1792	32554,9736	17828,4847	134345,523	4294,82385	8577,30929	5904,28223	9388,7473
497	497	W[Oxi]ELLLQVNM[Dea]VGTR	746,375	26,44	sp P35908 K22E_HUMAN	21623,324	19800,5444	28696,8087	11423,0289	15702,5624	1865,51472	2980,60364	3576,08875	6438,21642
498	498	TM[Oxi]QSPSGVLQEAADVHAR	713,701	26,5	sp P15924 DESP_HUMAN	3499,19996	15423,397	12482,8798	4960,66091	7429,50079	1377,48321	471,431521	1386,51348	7170,24384
499	499	SC[CAM]AAAGTEC[CAM]USGWGNTK[A]TK[A	956,432	26,5	sp P00761 TRYP_PIG	6174,04356	20891,9474	17950,3354	5763,5696	16980,4353	11945,6763	3478,24832	157054,04	11696,2002
500	500	NKLNLEEAALQQAQ	807,429	26,55	sp P35908 K22E_HUMAN	133405,693	171757,595	164371,462	96072,142	85430,3686	40330,9603	20651,9475	35228,4445	3823,78173
501	501	RFPEC[CAM]SSSYLPLRPSGEGFPNYC[CAM]TPPI	779,369	26,6	sp Q5T749 KPPR_HUMAN	3698,61316	12690,9804	2384,16785	10685,1449	22969,0772	9886,16801	3027,8458	1789,6522	1364,96017
502	502	C[CAM]YAVVPLVYGGTK	828,917	26,62	sp P01591 IGU_HUMAN	3291,43638	2895,21461	2664,32165	380,866047	8050,243				

555	555	CRM.TLNNQFASFDIK	720,859	28,38	sp Q8N1N4 K2C78_HUMAN	18367,707	18446,3304	24038,8791	13965,4208	15014,2828	7940,9459	3100,66289	3973,7492	11111,2672
556	556	LGEHNIDVLEGNQFINA	1006,48	28,39	sp P00761 TRYP_PIG	727,009511	9501,21874	2607,94745	10875,5746	8298,98905	1013,36816	775,51085	3661,45705	96029,7752
557	557	ELGIC[CAM]PDDAAVPIK	805,924	28,42	sp P12273 TRYP_HUMAN	2908,51947	10024,7617	2892,9781	12941,4612	17914,482	2544,04988	151,05684	2196,67785	9656,50415
558	558	KSPIFGPEEVNSVEGNSVITC[CAM]YPPTSVN	1143,22	28,45	sp P01833 PIGR_HUMAN	244,450723	354,506425	1390,20147	351,084377	5855,3027	1694,08635	457,488235	444,965772	171,662845
559	559	NVSTGDEVNVE[CAM]MNAAPGVDLTQLLNNM	982,474	28,46	sp Q6IFW6 K1C10_RAT	57169,8546	34149,8275	31825,8079	14681,5433	54303,8977	1113,00439	4160,17478	1585,49692	20263,7695
560	560	NVSTGDEVNVE[CAM]MNAAPGVDLTQLLNNM	982,474	28,46	sp P13645 K1C10_HUMAN	57169,8546	34149,8275	31825,8079	14681,5433	54303,8977	1113,00439	4160,17478	1585,49692	20263,7695
561	561	+1R.TVAAVSVFFPPSDEQLK	701,38	28,55	sp P01834 IGKC_HUMAN	1976,84212	10325,8084	8393,78512	2482,03595	17719,8959	7333,91202	143,984866	8129,41355	17344,9096
562	562	CRM.FLEQQNQVLQTK	759,899	28,59	sp Q27294 K2C1B_HUMAN	22505,4975	45272,1193	2934,7593	14981,775	30983,1044	4833,44145	302,244278	1651,63335	8717,72386
563	563	CRM.FLEQQNQVLQTK	759,899	28,59	sp P35908 K2Z2_HUMAN	22505,4975	45272,1193	2934,7593	14981,775	30983,1044	4833,44145	302,244278	1651,63335	8717,72386
564	564	IITHPNFNGNTLNDNIM[Oxi]LIK	767,063	28,61	sp P00761 TRYP_PIG	13057,5716	19940,761	18966,3029	1836,05065	1179,54815	1019,88553	901,740606	484,253777	5840,30311
565	565	LGEHNIDVLEGNQFINAA	1042,01	28,66	sp P00761 TRYP_PIG	5334,93856	23288,6031	58321,5558	15996,0028	26325,8105	2502,90782	1665,8717	854,862781	205323,297
566	566	SKELTTEIDN[Dea]NIEQISSYK	738,366	28,68	sp P13645 K1C10_HUMAN	50710,1108	36587,6169	62127,9645	17640,4044	27283,0158	6253,15267	97927,1461	429,639077	33283,1065
567	567	FYTIELIK	513,797	28,71	sp P12273 PIIP_HUMAN	339,061378	29441,2753	625,394463	16486,6417	41525,9984	5257,61368	4806,80829	4102,65329	
568	568	GTNYLADVFEK	628,81	28,78	sp P31151 S10AT7_HUMAN	6665,03498	5097,7125	7899,87055	21017,6019	13533,389	4975,2775	1432,73591	1428,83942	381,82495
569	569	NKIIAATENAQPILQIDNAR	769,434	28,78	sp P08779 K1C16_HUMAN	10031,3217	48532,0258	17501,477	14883,7581	18272,2958	17681,6788	567,29896	17712,4517	12249,9666
570	570	YWC[CAM]NDGKTPGAVNAC[CAM]HLSC[CAM]	963,442	28,78	sp P61628 LYSC_PANTR	2586,92653	1238,512	6693,16398	2805,2242	15836,9696	11651,9564	2233,65935	2756,59684	17029,0238
571	571	NKIIAATEN[Dea]AQPILQIDNAR	769,765	28,81	sp P08779 K1C16_HUMAN	4485,50531	20426,9691	4270,24291	896,071181	4446,09964	459,746351	2873,86303	150,01058	10029,0006
572	572	QVILQGVINEAQSK	887	28,82	sp Q08554 DSC1_HUMAN	3078,11278	3818,08059	652,134566	5400,63316	4590,04894	531,309851	1603,25519	4161,61597	2427,61569
573	573	EDRIIPRGGIYNALDNDEWQVR	868,091	28,85	sp P01037 CYTN_HUMAN	329,204988	4389,19625	9248,24858	351,180785	1606,30017	3608,30751	1600,36573	508,296802	2594,05739
574	574	NEGATYAANAALFR	742,38	28,85	sp Q8WNW3 PLAK_PIG	5915,31703	16059,4435	3217,71615	3057,73315	11476,3966	5494,84106	1397,37431	3204,38498	2856,33382
575	575	TPGAVERNAC[CAM]HLSC[CAM]SALLQDNIDAA	976,465	28,88	sp P61628 LYSC_PANTR	1209,24411	6733,68586	3118,2142	715,037005	31274,359	2599,60378	1496,86428	1526,68381	6380,97133
576	576	QEPSQGGTTTFAVTSILR	918,479	28,94	sp P01877 IGHA2_HUMAN	3236,28522	11942,7041	3691,56033	1591,18294	100541,569	1285,98032	1099,55276	972,921742	1203,27054
577	577	QEPSQGGTTTFAVTSILR	918,479	28,94	sp P01876 IGHA1_HUMAN	3236,28522	11942,7041	3691,56033	1591,18294	100541,569	1285,98032	1099,55276	972,921742	1203,27054
578	578	HGVQLEIEI[NaX]LQSQLSK	620,654	28,95	sp P35527 K1C9_HUMAN	3155,1775	37153,1073	13998,1734	12868,915	12698,8751	774,937184	589,663197	548,4807	7636,03239
579	579	YSLTYVETGLSK	704,871	28,97	sp P25311 ZA2G_HUMAN	24253,4169	12951,7912	14730,7717	21120,6921	37032,7662	2277,80004	3328,32171	1429,63129	9128,63703
580	580	HGVQLEIEIQLSQLSK	613,327	29,01	sp P35527 K1C9_HUMAN	20547,1181	608576,477	466663,06	386059,352	368460,431	551,231713	5132,59294	971,921176	18754,8673
581	581	VDSLNDENFLK	703,86	29,04	sp P19013 K2C4_HUMAN	16867,2627	6189,15941	4239,42388	1742,54689	3081,99234	2511,56339	201,54419	196,086313	24031,7777
582	582	NRKDIENQYETQITQIEHEVSSSGQEVQSSAK	916,444	29,05	sp P35527 K1C9_HUMAN	10609,7744	16546,6528	14297,8922	3472,99834	5185,15326	2932,70823	3889,28426	1572,32997	2413,24189
583	583	HGVQLEIEIQLSQ[Dea]LSK	613,662	29,05	sp P35527 K1C9_HUMAN	18122,117	557893,357	408310,566	348569,65	316074,506	1303,94306	2789,96767	418,657378	12856,7688
584	584	IIAATENAQPILQIDNAR	688,719	29,11	sp P08779 K1C16_HUMAN	40624,6282	80530,2002	24718,4336	17963,8129	10549,3604	2323,79025	1273,07007	654,633786	15225,1871
585	585	LTEETVC[CAM]LQDLKVEAYR	1092,03	29,15	sp P15924 DESP_HUMAN	687,01301	6701,31925	2226,4577	410,361675	292,339062	860,863704	2237,83731	202,305912	4943,27823
586	586	YAASSYSLTPEQWVK	872,433	29,3	sp B9A064 IGLS_HUMAN	4142,0684	11850,7766	10991,0752	9359,72979	39618,2953	6798,51766	2220,70611	548,588162	9315,60638
587	587	LISWYDNEFGYSNR	882,405	29,31	sp P04066 G3P_HUMAN	57288,0408	58626,8785	26190,5152	13024,056	20646,89	5494,58095	442,08914	2153,1414	6022,02214
588	588	ELTTEIDNIEQISSYK	998,986	29,34	sp P13645 K1C10_HUMAN	17657,689	170026,509	161997,284	89782,866	107317,259	2761,50995	654,438915	764,290802	17263,6926
589	589	QISNLQQSISDAEQRGENALKDAK	661,589	29,34	sp P04264 K2C1_HUMAN	153141,104	306700,464	124239,2	2677,95451	2990,80782	511,639734	191,722104	196,436399	1465,80929
590	590	FVDSTVVSATVIDR	811,441	29,37	sp P15252 TRYP_HEVBR	21293,4148	30728,9221	41388,5837	32835,989	59768,5055	1855,68603	346,870193	1140,62037	13003,255
591	591	FASFDIKVQLELQNK	648,008	29,41	sp P19013 K2C4_HUMAN	11717,432	22723,8057	2012,82589	5460,13739	121,60534	2660,85438	2610,02822	1431,71018	5992,6399
592	592	RTVQ[Dea]T[Dhy]LEILQSQALAK	977,06	29,48	sp Q6IFX1 K1C24_RAT	5470,4561	8524,17587	2897,41938	1308,67348	945,786143	1879,46511	1000,3582	291,051851	1976,55094
593	593	AAS.RTVQ[Dea]GLEIELQSQALAK	977,06	29,48	sp Q6IFW6 K1C10_RAT	5430,4561	8524,17587	2897,41938	1308,67348	945,786143	1879,46511	1000,3582	291,051851	1976,55094
594	594	IVLVDASSVFN[Dea]TRVQEGAK	968,006	29,53	sp Q08280 SRPP_HEVBR	1306,39028	2394,05788	1771,30157	3517,91649	6639,26711	446,178465	3542,93384	3559,23936	7535,35656
595	595	NADLQVQKPELVEYDRL	747,731	29,53	sp P01833 PIGR_HUMAN	1319,77056	7190,44028	392,385019	2508,42111	26704,4521	1008,75489	204,511812	802,118538	5049,55901
596	596	RISGVDGQDPYGFIVFNQK	734,409	29,57	sp Q02413 DSG1_HUMAN	1540,89666	1598,20702	2143,46828	17025,2261	2687,89505	1012,31406	3038,05407	257,629679	5190,39448
597	597	NNQFASFDIKVR	719,875	29,63	sp Q8N1N4 K2C78_HUMAN	3195,68563	680,879854	500,7736	3102,74661	7699,01879	411,6533	3477,05496	859,98885	7094,56896
598	598	CRM.SC[CAM]AAAGTEC[CAM]LISGWGNTK[A	977,444	29,63	sp P00761 TRYP_PIG	4664,13916	11708,4678	4663,30067	5074,89859	16559,8862	3148,74818	3703,46663	3210,03642	8033,03962
599	599	LALDIEIATY[CAM]R[AGA]	646,348	29,66	sp P19013 K2C4_HUMAN	27087,8319	53943,3154	29880,7028	35297,7869	35711,5703	1284,5719	1272,0202	1064,21147	8735,46312
600	600	LALDLEIN[Dea]AYR	646,35	29,71	sp P21910 LAML2_XENLA	26970,1469	53807,7435	29699,2732	35268,6272	35696,0219	1243,28656	1276,70186	1291,59984	11099,9356
601	601	PGQ.QYTSFHFASLEDVQAK	927,439	29,76	sp P29508 SPB3_HUMAN	11825,5004	4902,18153	6773,76729	9287,41847	5960,77055	6044,44567	1771,31511	4607,87762	7799,41575
602	602	LVSILTNLVTR	614,886	29,77	sp P01833 PIGR_HUMAN	2991,51498	14334,6223	1815,99082	3645,67419	53783,6915	6142,94729	5821,28499	1403,3965	3497,45705
603	603	VNWIQQTIAAN	629,333	29,77	sp P00761 TRYP_PIG	164610,039	203149,909	296404,999	167447,727	327809,61	293,209375	2874,61989	1175,07552	86956,997
604	604	VLYDAEISQIHQSVTDTNVLMS[Oxi]DNDR	1022,17	29,8	sp P35908 K2Z2_HUMAN	37524,35	1273,07857	1078,97724	22823,525	14301,8923	2470,30177	1833,18522	431,934506	2501,42099
605	605	TVQIAAVDVDIR	642,386	29,84	sp P12273 PIIP_HUMAN	31012,081	57894,3701	81824,6125	59408,0341	81319,01929	2427,83259	2653,35057	4706,38162	8607,33989
606	606	KDIENQYETQITQIEHEVSSSGQEVQSSAK	848,909	29,87	sp P35527 K1C9_HUMAN	7622,25805	27728,8803	22916,5453	4012,0043	17845,5547	6529,81827	4838,41921	456,950682	10463,9719
607	607	LNNQ[Dea]FASFDIKVR	547,292	29,87	sp P04264 K2C1_HUMAN	794008,557	1418709,83	598989,283	526048,953	1036923,73	12073,6556	7467,09503	10176,9788	10529,0168
608	608	LGLDIEIATYR	632,351	29,91	sp Q43790 KRT86_HUMAN	20954,9326	32410,3663	39214,5311	29633,0405	17646,0808	36881,2778	26755,5194	13673,6466	39185,9245
609	609	LGLDIEIATYR	632,351	29,91	sp Q9NSB2 KRT84_HUMAN	20954,9326	32410,3663	39214,5311	29633,0405	17646,0808	36881,2778	26755,5194	13673,6466	39185,9245
610	610	SLNSQFASFDIKVR	546,958	29,96	sp P04264 K2C1_HUMAN	917037,7	1645562,05	679291,285	2501,41384	12130,0576	3490,83457	2902,53981	3734,46084	14259,9441
611	611	EFNAETFTFHADIC[CAM]	851,369	30,04	sp P49065 ALBU_RABIT	12719,8376	11125,9473	8625,78726	1193,67236	4541,04698	5738,15973	859,33064	2436,62528	11660,7777
612	612	EFNAETFTFHADIC[CAM]	851,369	30,04	sp P02768 ALBU_HUMAN	12719,8376	11125,9473	8625,78726	1193,67236	4541,04698	5738,15973	859,33064	2436,62528	11660,7777
613	613	VQALEAENNENLKNIQDWYDK	845,739	30,04	sp P35527 K1C9_HUMAN	14124,8255	49834,7009	29007,1417						

666	666	ELTDEIDNNIEQISSYKSEITLRR	746,132	31,27	sp P13645 K1C10_HUMAN	3021,12783	2068,08067	3345,59443	734,592811	883,857415	85442,4626	1927,98717	3022,1236	2418,79807
667	667	TVAAPSVFIFPDSDEQLK	973,515	31,37	sp P01834 IGKC_HUMAN	4383,999	9164,58282	6130,88541	11031,4922	65235,4992	3545,58555	4707,974729	1215,95637	10318,574
668	668	APFASIVAGIGGQ	594,324	31,53	sp P08453 GDB2_WHEAT	65330,5196	20744,0356	62078,8937	69104,0353	17392,4846	41114,6575	12007,3225	11991,9742	6564,92384
669	669	LSGQTIETVSEYLR	871,95	31,53	sp A7ZW21 BGAL_ECOHS	1322,84847	2343,31978	1289,80551	443,294302	327,787896	17662,1625	805,823495	1122,05646	11501,0777
670	670	LIVINGNIPITIFCR	807,452	31,58	sp P04066 G3P_HUMAN	2209,03447	2691,11829	3189,63142	14644,08	1451,02464	8628,7744	765,374341	1641,49485	10285,2438
671	671	VLOGLEKFSQSLSM[Oxi]K	916,495	31,6	sp P08779 K1C16_HUMAN	1297,55556	3133,09629	2047,81274	5913,7261	1257,86411	1522,75085	22141,978	1010,71841	4689,30068
672	672	FSLLKPWA	481,278	31,6	sp Q9GZZ8 LACRT_HUMAN	1543,12648	6654,61722	280,14435	2147,72972	36654,4623	8230,59952	7447,85882	10016,0814	12045,5068
673	673	LEELHGFVNIHFQYSVR	728,38	31,7	sp P80511 S10AC_HUMAN	16957,5866	3061,19123	4765,69629	5718,18203	49819,6988	955,229395	3373,10878	2490,581	12211,3866
674	674	VLYDAEISQIHQSVDTNVLVLSMDNSR	1016,84	31,71	sp P35908 K22E_HUMAN	793,845669	22497,4692	2192,05056	4951,35929	4493,13199	2589,56098	1716,76335	702,80465	2662,66604
675	675	AVFDLEPTEVIDEVR	851,457	31,74	sp Q9ZRB7 TBA_WHEAT	2611,86924	1111,19691	5337,77064	11440,0851	7449,99845	6748,1807	2101,95439	10278,6626	
676	676	FYTIELKVE	627,852	31,76	sp P12273 PIP_HUMAN	33921,3071	35328,9399	28519,6947	310684,386	52960,3717	3418,98423	1774,06937	1517,83616	2447,34721
677	677	ISGVGQPPYGFVINQK	682,371	31,77	sp Q02413 DSG1_HUMAN	2307,87117	20360,6616	5668,42351	16476,5832	28009,7536	6424,35112	2637,52562	6331,14945	32412,8046
678	678	QQTGVGVVYFDVEVGR	957,97	31,81	sp P01037 CYTN_HUMAN	947,481576	8043,77647	5855,18921	1479,36722	2719,87368	4710,3249	567,74288	4308,87322	
679	679	ILTATVDNANILQIDNAR	1034,57	31,84	sp Q04695 K1C17_HUMAN	8089,33081	27784,3223	738,154271	7348,39751	8754,36672	2163,79165	334,476098	1015,07764	1175,12043
680	680	NKLN[Dea]DLEDALQK[Dea]AKEDLAR	729,383	31,84	sp P04264 K2C1_HUMAN	1869,79645	571261,07	5017,3988	259674,55	3506679,24	21398,5349	3711,88772	29614,8493	9614,12571
681	681	NKLNLEDALQK[Dea]AKEDLAR	729,048	31,84	sp P04264 K2C1_HUMAN	6374,6136	876196,448	2747,80483	395324,643	556713,915	422,853876	1154,14557	239,447703	6002,0037
682	682	NELTIINTFHQYSVK	903,971	32,03	sp P06702 S10A9_HUMAN	50692,3565	685,901741	30520,7638	1779,39593	1134,41346	3728,90182	1909,76521	428,889591	8252,68003
683	683	TINQSLLFPHNVDEIPDK	764,753	32,04	sp P04264 K2C1_HUMAN	19339,1158	35207,8092	2483,40821	82273,536	1760,53691	988,293123	595,025099	6300,83723	
684	684	VYNNVQQITIAAN	710,863	32,2	sp P00761 TRYP_PIG	27037,5357	25682,2892	49928,0581	68342,154	31787,8989	3381,58305	136,67816	1834,62461	34998,5476
685	685	PGQ.QISNLQKSSIDAQRGENALK	771,388	32,2	sp P04264 K2C1_HUMAN	25858,0962	40246,0101	1717,7755	24240,0351	30479,1121	7925,4116	2327,9817	1897,74895	22043,5976
686	686	LNDLEDALQQAQEDLAR	648,001	32,22	sp P04264 K2C1_HUMAN	53799,2771	97046,5454	70338,5578	1298,53745	1573,55299	56769,4229	607,128385	455,162798	2714,73318
687	687	IDSGVLGSGGYTAIQLNRL	739,395	32,25	sp P02788 TRFL_HUMAN	1731,1655	1459,89828	14476,9604	3356,76773	12677,2211	722,98997	4399,6441	2229,38508	27197,2427
688	688	SLLTPILNEDIPNAQR	897,489	32,26	sp Q9NS82 KRT84_HUMAN	465,86338	5826,93416	1492,86767	3121,61869	8253,58633	68528,6624	2029,71165	1235,39728	3948,74315
689	689	Frm.TLNN[Dea]QJFASFDK	713,85	32,3	sp Q8N1N4 K2C78_HUMAN	17326,3374	30562,4453	20385,7047	7386,32797	18334,8272	4173,43354	6714,13234	1388,46956	10473,4182
690	690	GAHVDDKVDLDSVL	733,894	32,33	sp P81605 DCD_HUMAN	5697,23032	4543,05516	6428,82812	4449,72765	3532,18325	49605,6748	1469,31599	38360,1473	10710,1816
691	691	Frm.TLN[Dea]NQFASFDK	713,85	32,39	sp Q8N1N4 K2C78_HUMAN	17550,683	30858,6162	20380,09	7327,25934	18403,2584	4175,32038	1856,76037	1396,51745	10401,4425
692	692	FGFGGGPGGVGGGLGGPGGPGGGYGGIHEV	891,095	32,41	sp P35908 K22E_HUMAN	1181,25287	5625,93292	1196,95126	11014,7763	13429,3057	2409,15722	1034,55153	543,954078	941,024094
693	693	QLC[Cam]DAELKAK	588,316	32,46	sp A62P10 SEY1_YEAS7	3677,02318	3069,78126	4783,49259	3094,08913	526,756	3733,22958	12180,6283	5083,55353	16219,1698
694	694	NKLN[Dea]DLEDALQKAKEDLAR	729,046	32,46	sp P04264 K2C1_HUMAN	447004,759	53154,2928	513276,101	9330,35272	27554,1773	530571,131	489,442226	19463,8713	1019,15491
695	695	PGQ.QEPQSGQTTTFAVTSILR	909,963	32,47	sp P01877 IGHA2_HUMAN	1521,92989	9566,08563	2238,36606	2481,12119	59533,3412	6253,6042	2823,49412	738,966678	4493,35752
696	696	PGQ.QEPQSGQTTTFAVTSILR	909,963	32,47	sp P01876 IGHA1_HUMAN	1521,92989	9566,08563	2238,36606	2481,12119	59533,3412	6253,6042	2823,49412	738,966678	4493,35752
697	697	DIENQYETQITQIEHE[KXX]VSSSGQEVQSSAK	661,3	32,5	sp P35527 K1C9_HUMAN	5567,27106	14839,4083	11735,0485	5279,13097	9106,828	4510,23306	3449,72268	4079,89944	12424,9987
698	698	DIENQYETQITQIEHE[NaX]VSSSGQEVQSSAK	822,38	32,5	sp P35527 K1C9_HUMAN	6166,2698	11276,492	2328,89564	1721,3789	2589,36638	2242,47809	3321,2949	1389,58557	17160,3981
699	699	DIENQYETQITQIE[NaX]HEVSSSGQEVQSSAK	1096,17	32,5	sp P35527 K1C9_HUMAN	748,641742	24444,2254	10426,0702	5819,40951	4387,71867	1422,16017	1464,16662	395,971091	605,317198
700	700	DIENQYETQITQIE[KXX]HEVSSSGQEVQSSAK	826,372	32,5	sp P35527 K1C9_HUMAN	14656,7446	41884,1782	29395,9199	11728,4661	19243,5173	11667,374	2209,65328	2173,74047	11518,8442
701	701	QLC[Cam]SFEIYVPMWEN[Dea]R	985,949	32,63	sp P01037 CYTN_HUMAN	922,97725	12751,2034	667,38742	714,703855	927,04339	2911,24127	127,392484	6769,80978	
702	702	SDLEM[Oxi]QYETLQLEEL[Oxi]ALKK	777,709	32,63	sp P35527 K1C9_HUMAN	39519,6079	56515,5834	66820,3566	50756,0619	46071,2157	13701,1842	652,642632	308,332576	11546,491
703	703	KLEELHGFVNIHFQYSVR	603,822	32,68	sp P80511 S10AC_HUMAN	2718,7332	3238,41304	5458,45331	4412,55531	3878,97258	2472,93662	389,43441	3365,76428	
704	704	DIENQYETQITQIEHEVSSSGQEVQSSAK	1088,84	32,68	sp P35527 K1C9_HUMAN	125598,521	480667,326	320201,416	1687,88701	196557,935	397325,753	535,552331	338,96899	5516,73289
705	705	NKLNLEDALQQAQEDLAR	733,386	32,72	sp P35908 K22E_HUMAN	177947,894	195746,911	140900,55	22061,7823	8218,7199	8226,95903	4678,99328	5869,8917	8084,53102
706	706	NVSTDGVNVE[Cam]MNAAPGVDLTQLNNM	977,144	32,73	sp Q61FW6 K1C10_RAT	42671,8927	108238,793	553,398544	14428,2235	4080,646	710,672178	1109,71329	411,739156	1925,17246
707	707	NVSTDGVNVE[Cam]MNAAPGVDLTQLNNM	977,144	32,73	sp P13645 K1C10_HUMAN	42671,8927	108238,793	553,398544	14428,2235	4080,646	710,672178	1109,71329	411,739156	1925,17246
708	708	PGQ.QISNLQKSSIDAQRGENALKDAK	786,107	32,75	sp P04264 K2C1_HUMAN	107133,269	209474,439	113440,072	1655,33681	161910,329	152690,561	1606,01626	797,181272	1263,5945
709	709	CRM.FASFIDKVR	563,307	32,77	sp P48668 K2C6C_HUMAN	3227,38994	2659,11272	5038,13038	8968,35577	8241,65112	4515,29836	11007,8083	16912,3313	8362,70685
710	710	SVVTIVDFVYK	635,358	32,77	sp Q05D862 FILA2_HUMAN	37520,1688	68255,2812	2009,29765	131547,841	106524,95	6307,83893	2062,40205	6364,12284	7356,1358
711	711	CRM.FASFIDKVR	563,307	32,77	sp Q8N1N4 K2C78_HUMAN	3227,38994	2659,11272	5038,13038	8968,35577	8241,65112	4515,29836	11007,8083	16912,3313	8362,70685
712	712	CRM.FASFIDKVR	563,307	32,77	sp Q72794 K2C1B_HUMAN	3227,38994	2659,11272	5038,13038	8968,35577	8241,65112	4515,29836	11007,8083	16912,3313	8362,70685
713	713	CRM.FASFIDKVR	563,307	32,77	sp Q9NS82 KRT84_HUMAN	3227,38994	2659,11272	5038,13038	8968,35577	8241,65112	4515,29836	11007,8083	16912,3313	8362,70685
714	714	CRM.FASFIDKVR	563,307	32,77	sp P02538 K2C6A_HUMAN	3227,38994	2659,11272	5038,13038	8968,35577	8241,65112	4515,29836	11007,8083	16912,3313	8362,70685
715	715	CRM.FASFIDKVR	563,307	32,77	sp P13647 K2C5_HUMAN	3227,38994	2659,11272	5038,13038	8968,35577	8241,65112	4515,29836	11007,8083	16912,3313	8362,70685
716	716	LGEHNDIVLGENEQFINAAK[Frm]JIITHPNFNGN	837,427	32,8	sp P00761 TRYP_PIG	19186,1349	22151,1141	2723,95242	34805,2152	14131,2865	11224,6205	3059,6041	1917,34795	32272,6119
717	717	F[C[Cam]FDLFQIEIKDOR	597,28	32,81	sp Q9P663 SPB12_HUMAN	4476,53679	5424,92291	3141,27196	12748,0728	15421,152	11364,8255	9018,62023	4274,63605	15051,6776
718	718	YPPGLAPPQK[Dea]PFGPGFVPPPPPPYGGPR	983,518	32,83	sp P02814 SMR3B_HUMAN	1092,58776	8352,36214	1153,9634	1114,90669	810,928472	3221,71782	3271,30584	1074,45807	7171,23087
719	719	LALDIEIATYR[Io]dR	702,305	32,86	sp P19013 K2C4_HUMAN	9739,75699	13636,117	14599,8887	11166,2077	7105,955	3738,38413	3493,50394	6691,82394	21901,9825
720	720	TYLSSIPLQGFANFYK	907,987	32,89	sp P12273 PIP_HUMAN	8497,52436	33086,8927	17365,8002	18678,702	30016,5130	4776,21442	1641,37714	377,088458	2723,65908
721	721	C[Cam]IESUAIYK	654,36	32,91	sp Q6B835 S10AB_RAT	11399,1632	13773,5948	2041,053	4597,81836	1458,5618	648,862769	2731,16466	2037,39906	21122,7967
722	722	YNTIDLDKQJVDLTVGNNK	760,058	32,96	sp P35527 K1C9_HUMAN	4763,87623	15440,7733	12002,4185	8047,27806	8273,8046	1068,92722	4443,12042	1963,07958	498,103259
723	723	QEFILVIK	551,846	32,98	sp P05109 S10AB_HUMAN	10597,5774	9472,96075	3484,19618	3786,68883	4706,60237	1068,64835	1334,92103	1868,46369	2704,97562
724	724	GPYPYGGPLAPPQFPGGFVPPSSPPYGGPR	1034,54	33,01	sp P02814 SMR3B_HUMAN	15199,0433	2935,49563	7028,5122	1751,60313					

777	777	N[Dea]LDLDSIIAEVK	665,868	34,26	sp P02538 K2C6A_HUMAN	35515,9371	51627,6801	45930,3905	46582,6894	27474,426	1046832,22	448949,111	149979,036	8903,72582
778	778	NLDL[KXX]SIIAEVK	456,563	34,26	sp P13647 K2C5_HUMAN	1201,13531	1379,17168	2316,02327	3365,08721	1017,45801	44085,4129	794,861259	2888,8419	1190,2013
779	779	NLDLLDLSIIAEVK	665,868	34,26	sp P13647 K2C5_HUMAN	35515,9371	51627,6801	45930,3905	46582,6894	27474,426	1046832,22	448949,111	149979,036	8903,72582
780	780	NLDLLDLSIIAEVK	665,868	34,26	sp P35908 K2Z2_HUMAN	35515,9371	51627,6801	45930,3905	46582,6894	27474,426	1046832,22	448949,111	149979,036	8903,72582
781	781	FGGFGGGPGGVGGLGGPGGGPGGGVGGIHEVS	1024,03	34,32	sp P35908 K2Z2_HUMAN	172739,946	119943,579	98328,4834	67456,4862	96709,7111	31761,8833	1540,9076	1489,16282	28117,5205
782	782	FGGFGGGPGGVGGLGGPGGGPGGGVGGIHEVS	1023,78	34,32	sp P35908 K2Z2_HUMAN	68714,7814	54960,741	42188,2017	29188,855	43737,8547	2419,30501	1149,12276	968,865371	2462,46957
783	783	NQLNLTTD[NaX]NANILQLIDNAR	797,087	34,37	sp P13645 K1C10_HUMAN	25914,0604	26940,1124	8316,78412	6986,00727	11555,0233	902,797746	1121,90094	678,010197	1943,50623
784	784	Frm.TVGLGLEISQSLALK	600,011	34,37	sp Q61FW6 K1C10_RAT	14027,6658	6648,09473	2399,8715	8562,97038	6219,89833	1272,9493	161864,284	5333,76233	1736,86862
785	785	TYLFLQEYLDIAKK	672,982	34,37	sp P29508 SPB3_HUMAN	514,316633	1292,61622	534,013718	7803,80003	2161,4605	3184,43252	2172,55533	1081,56367	3042,00005
786	786	CAM.NLDLDSIIAEVK	693,874	34,38	sp P48668 K2C6C_HUMAN	17142,991	15264,4314	14914,5368	137,925059	5800,75883	9344,24666	1434,29502	2745,33476	10384,7592
787	787	CAM.NLDLDSIIAEVK	693,874	34,38	sp P02538 K2C6A_HUMAN	17142,991	15264,4314	14914,5368	137,925059	5800,75883	9344,24666	1434,29502	2745,33476	10384,7592
788	788	CAM.NLDLDSIIAEVK	693,874	34,38	sp P13647 K2C5_HUMAN	17142,991	15264,4314	14914,5368	137,925059	5800,75883	9344,24666	1434,29502	2745,33476	10384,7592
789	789	YLDFFSIITEVR	721,882	34,38	sp Q8N1N4 K2C7H_HUMAN	16464,5879	17646,7609	1595,30609	10390,9361	11894,619	12135,054	846,618679	2192,18967	13543,06631
790	790	NAGLNLTNDNANILLQIDNAR	789,76	34,45	sp P13645 K1C10_HUMAN	309726,881	306641,527	216914,637	150579,211	230716,292	1353,3849	134,06151	892,88934	17921,3242
791	791	LQGEKATMQNLNDRLAS	1026,52	34,46	sp Q04695 K1C17_HUMAN	26588,0145	42134,6534	4997,24556	38240,7631	55771,4233	96400,4856	1509,15099	130278,104	7444,91635
792	792	FVTHVSDWGALATISTLEAVR	758,402	34,5	sp O75629 CREG1_HUMAN	3048,96218	3539,95907	6756,48996	9862,18197	16798,2019	6760,80483	7637,09362	9664,50032	7952,3978
793	793	AAS.TVQ[Dea]GLEIELQSIALK	899,007	34,63	sp Q61FW6 K1C10_RAT	7131,10897	13898,6737	3418,83279	1203,00132	3179,0042	11965,8295	338920,539	1172,61354	5214,31316
794	794	KDSPQTIPPTYDALHYVSTVEGYIAR	727,888	34,65	sp P31944 CASPE_HUMAN	1624,07568	1153,84165	727,134839	8190,65733	5381,65991	2814,69596	1952,24286	1622,70554	5190,087
795	795	GFGGAGGGGYSSGGFGGGGGGGGGGGGG	1225,77	34,66	sp P35527 K1C9_HUMAN	1035,9646	16615,1008	12393,8412	2482,53827	2045,67076	1293,02262	397,029477	189,730615	1175,83431
796	796	GFGGAGGGGYSSGGFGGGGGGGGGGGGG	1216,28	34,68	sp P35527 K1C9_HUMAN	4503,28905	17727,2217	26693,7407	22357,7599	25950,45179	873,606031	1385,10191	198,500342	5855,01798
797	797	LVDQNIFFSYLNR	801,419	34,8	sp P07339 CATD_HUMAN	2470,56374	1259,99182	3126,89543	21757,8814	15774,2158	9331,57964	3457,34259	1885,68743	23652,2362
798	798	THN[Dea]LEPYFESFINN[Dea]LR	998,493	34,86	sp P04264 K2C1_HUMAN	118309,888	322270,319	2195,6344	94584,15113	130625,178	3781,41188	2907,23157	1435,47206	13548,6058
799	799	THNLE[KXX]PYFESFINN[Dea]LR	977,979	34,86	sp P04264 K2C1_HUMAN	56423,9019	90531,6038	2337,85063	1664,50113	44418,7597	921,002336	1297,3698	1238,81257	2059,55619
800	800	THNLEPYFESFINN[Dea]NLR	665,665	34,86	sp P04264 K2C1_HUMAN	677988,942	1312911,78	1074,05777	568186,3	832301,992	49,168529	201,45832	250,075939	11042,0403
801	801	ADLEM.QMIESLTELAYLKK	761,06	34,93	sp Q04695 K1C17_HUMAN	1267,20688	187,83152	2012,76022	140639,862	272714,229	3196,37964	2793,81418	899,603337	10525,295
802	802	MIETIINTFHQYSV	839,92	34,96	sp P06702 S10A9_HUMAN	19549,9389	9851,9455	1555,91465	455,923104	7549,29242	6377,54339	376,194519	815,849835	2101,1205
803	803	SLDLSIIDYVR	658,856	35,01	sp Q72794 K2C1B_HUMAN	49017,4262	8990,52324	17791,4334	13052,096	596,769934	13721,1565	307,60268	1762,58927	1380,88179
804	804	SFGVGLIYPGSPVSSLYSTALC[CAM]SPST[C	1161,21	35,02	sp Q3U177 KR13A_HUMAN	505,333022	1496,56667	958,52906	1256,70732	541,36686	3910,26776	294,782198	257,172186	3797,915894
805	805	ASASIVTVLVNIEGVPVFRPGSK	747,758	35,02	sp Q02413 DSG1_HUMAN	11345,0554	14471,4444	1357,4768	2797,06844	11349,4542	1564,61157	1847,49103	2586,27239	1036,9646
806	806	SGTASVVC[CAM]LLNNFYR	899,451	35,04	sp P01834 IGKC_HUMAN	6567,45398	24099,792	10125,9224	20581,2932	86653,8608	10203,8716	7352,90032	6371,99375	7677,75014
807	807	IDSGLVGSGYFTAIQNL	1044,54	35,04	sp P02788 TRFL_HUMAN	8769,24301	2689,68692	1062,53201	2959,34041	18443,5824	1276,0035	1229,14239	528,694945	1148,15882
808	808	NNKFASFIDKVRFL	566,972	35,07	sp P48668 K2C6C_HUMAN	3566,04972	1983,59509	504,002003	10409,4848	15402,5399	368,070068	353,797737	556,589115	1142,08777
809	809	NNKFASFIDKVRFL	566,972	35,07	sp Q8N1N4 K2C7H_HUMAN	3566,04972	1983,59509	504,002003	10409,4848	15402,5399	368,070068	353,797737	556,589115	1142,08777
810	810	NNKFASFIDKVRFL	566,972	35,07	sp Q72794 K2C1B_HUMAN	3566,04972	1983,59509	504,002003	10409,4848	15402,5399	368,070068	353,797737	556,589115	1142,08777
811	811	NNKFASFIDKVRFL	566,972	35,07	sp Q9NSB2 KRT84_HUMAN	3566,04972	1983,59509	504,002003	10409,4848	15402,5399	368,070068	353,797737	556,589115	1142,08777
812	812	NNKFASFIDKVRFL	566,972	35,07	sp P02538 K2C6A_HUMAN	3566,04972	1983,59509	504,002003	10409,4848	15402,5399	368,070068	353,797737	556,589115	1142,08777
813	813	NNKFASFIDKVRFL	566,972	35,07	sp P13647 K2C1_HUMAN	3566,04972	1983,59509	504,002003	10409,4848	15402,5399	368,070068	353,797737	556,589115	1142,08777
814	814	ADLEM[DTM]QIESLTELAYLKK	726,055	35,12	sp Q61FW6 K1C10_RAT	2829,5201	2762,39963	1052,55222	1672,16284	1644,33027	1433,25547	907,808189	1345,12686	1543,52697
815	815	CAM.ADLEM.QMIESLTELAYLKK	761,059	35,15	sp Q61FW6 K1C10_RAT	362701,067	505260,353	1098,62658	140553,438	272696,768	558,080713	2750,21165	890,809885	9437,95651
816	816	CAM.ADLEM.QMIESLTELAYLKK	761,059	35,15	sp P13645 K1C10_HUMAN	362701,067	505260,353	1098,62658	140553,438	272696,768	558,080713	2750,21165	890,809885	9437,95651
817	817	NVSTDGYNVEM[Oxi]NAAPGVOLDQLLNNMR	963,467	35,21	sp Q61FW6 K1C10_RAT	2126,69123	11644,8351	3358,90291	3630,50871	7259,95675	1249,01367	1585,87174	2949,68088	5820,33541
818	818	DAGFLSGFLYEYSR	784,373	35,22	sp P02769 ALBU_BOVIN	28058,8519	28872,7818	3098,26584	23585,7863	20604,3433	3515,25627	1562,14752	1301,79361	10858,554
819	819	VIHIEMDLTDNADKQLSFEEFI	912,774	35,29	sp P06702 S10A9_HUMAN	38033,6096	23845,3545	861,374394	18448,9707	476,167966	2820,10896	927,131223	849,393446	2627,95318
820	820	LC[CAM]YVALDFEQEMATASSSSLEK	850,733	35,47	sp Q5ZMQ2 ACTG_CHICK	10933,9692	14385,9573	9841,61341	679,383883	814,915426	4045,7323	1249,97829	226,416612	6792,03583
821	821	LGEHNIDVLEGNQFINAAKIITHPNFNGNTLDN	803,136	35,48	sp P00761 TRYP_PIG	320235,732	13699,2919	256100,535	11132,6258	11506,0379	7864,90756	2625,84394	11304,0278	47556,7077
822	822	THN[Dea]LEPYFESFINN[Dea]LR	665,664	35,49	sp P04264 K2C1_HUMAN	3275,53047	1312865,12	744642,691	3623,92754	3567,66951	1043506,75	903,342001	83211,205	3190,5672
823	823	ADLEM.QMIE[CAM]SLTELAYLKK	761,059	35,51	sp Q61FW6 K1C10_RAT	362736,351	505265,129	272080,249	7247,1999	10806,8167	369987,304	3082,90016	3416,9707	4722,61554
824	824	SFLTDDVVAEKDLFHC[CAM]VSFTLPR	861,11	35,56	sp Q75IH1 A2MG_BOVIN	15706,1249	10524,8156	6557,32022	520,664241	1074,6858	1885,30962	2562,88217	2326,76329	3821,71512
825	825	ADLE[CAM]QMIESLTELAYLKK	761,06	35,75	sp Q61FW6 K1C10_RAT	361012,091	36946,4599	686042,519	6913,6522	10806,8345	369964,341	2543,0304	50322,4122	1116,34866
826	826	DAGFYWC[CAM]LTNGDTLWR	987,942	35,9	sp P01833 PIGR_HUMAN	184,923096	721,630646	1219,40815	593,739117	9078,42886	1270,51909	873,456072	234,867625	490,903161
827	827	FFVAPFVPEVFGK	692,867	35,92	sp P02662 CASA1_BOVIN	683,877938	1686,96207	26809,881	160,604896	15422,3535	9943,60702	369,06917	493,569597	704,43939
828	828	SNLEPFSFYTNLNR	898,458	36,25	sp Q9NSB2 KRT84_HUMAN	14347,0372	29288,0367	4340,89787	21548,9296	24834,6792	14950,2277	491,628618	967,900591	8980,6741
829	829	YC[CAM]GQLQMIQIE[CAM]Q[Dea]ISNLEAQIT	932,454	36,3	sp P35527 K1C9_HUMAN	23114,1312	72799,374	1846,92569	19122,3688	19279,4966	2336,22486	1157,37011	451,753669	8530,17849
830	830	YC[CAM]GQLQMIQIE[CAM]QISNLEAQITDVR	932,122	36,3	sp P35527 K1C9_HUMAN	13686,011	46323,7145	2473,92775	7333,88208	11923,4382	379,814905	478,96314	3355,95491	
831	831	QNLEPFLFEQYNNLR	630,996	36,36	sp P48668 K2C6C_HUMAN	13549,4577	16961,2613	3020,57594	2223,03215	237,131712	680,711228	212,471904	4967,22255	702,037811
832	832	QNLEPFLFEQYNNLR	630,996	36,36	sp P02538 K2C6A_HUMAN	13549,4577	16961,2613	3020,57594	2223,03215	237,131712	680,711228	212,471904	4967,22255	702,037811
833	833	QNLEPFLFEQYNNLR	630,996	36,36	sp P13647 K2C5_HUMAN	13549,4577	16961,2613	3020,57594	2223,03215	237,131712	680,711228	212,471904	4967,22255	702,037811
834	834	VC[CAM]NYVNWVQQTAAN	897,435	36,36	sp P00761 TRYP_PIG	21810,3236	42074,7557	6358,46557	31530,9134	38454,5547	5360,88431	4442,58337	21625,8429	11710,8375
835	835	TAQFAGDLDAAGKLVVDFSAWTC[CAM]GJPC	1019,49	36,39	sp Q5R									

888	888	LDNLQOEIDFLTALYQAELSQMOTQISETNVLSI	1161,07	39,19	sp	P04264	K2C1_HUMAN	62109,818	66610,4346	39184,4378	41586,3315	72054,9836	3526,29633	263,784377	485,397737	3815,30317
889	889	ALVLIAFQAQYLQQC[CAM]PFEDHVK	830,767	39,22	sp	P02768	ALBU_HUMAN	28913,113	13822,2623	362,283311	13882,5502	4355,78012	1820,23121	1535,10502	440,355305	6572,0107
890	890	FTKIEDLRNKIIAATENAQAQPIQLQDNAR	1103,61	39,28	sp	P08779	K1C16_HUMAN	8048,87398	8136,15389	580,908417	705,64792	5281,25267	1778,9273	171,343473	226,02379	4546,07888
891	891	TIDD[KXX]LKNQNLNLTDDNANILLQIDNAR	1030,86	39,28	sp	P13645	K1C10_HUMAN	16617,7039	26363,4962	737,629924	2412,60474	4006,83573	1173,83422	393,816696	755,519752	2095,81851
892	892	TIDDLKNQNLNLTDD[KXX]NANILLQIDNAR	1030,86	39,28	sp	P13645	K1C10_HUMAN	16617,7039	26363,4962	737,629924	2412,60474	4006,83573	1173,83422	393,816696	755,519752	2095,81851
893	893	TIDDLKNQNLNLTDD[NaX]NANILLQIDNAR	1025,54	39,28	sp	P13645	K1C10_HUMAN	28150,0849	33858,6135	1263,73168	10240,3323	16206,3758	3823,86344	445,757277	459,089091	296,893101
894	894	NFOEFILVVK	682,405	39,31	sp	P05109	S10A8_HUMAN	11155,1597	645,135444	1953,58038	3234,58761	3904,5472	14120,5489	1077,13292	1380,04813	8370,78622
895	895	Frm.TIEELQNKILTATVDN[Dea]ANILLQIDNAR	1018,21	39,38	sp	Q04695	K1C17_HUMAN	609951,251	724513,646	387925,407	249089,294	504764,767	2815,42291	1373,72535	619,450712	27315,0915
896	896	SGNTRFRPEVHLPPPSSEELALNELVTLTC[CAM]L	894,224	39,52	sp	P01877	IGHA2_HUMAN	1576,16252	2679,83227	1756,21741	2552,03155	21242,5775	3528,84132	1440,958	1386,67799	1846,97347
897	897	SGNTRFRPEVHLPPPSSEELALNELVTLTC[CAM]L	894,224	39,52	sp	P01876	IGHA1_HUMAN	1576,16252	2679,83227	1756,21741	2552,03155	21242,5775	3528,84132	1440,958	1386,67799	1846,97347
898	898	TIDDLKNQNLNLTDDNANILLQIDNAR	1018,22	39,63	sp	P13645	K1C10_HUMAN	610479,551	724945,749	388092,702	249199,942	505123,611	886793,471	1367,95744	67907,0705	27544,2657
899	899	LGEHNIDVLEGNEQFINAAKIITHPNFNGNTLDN	1124,19	39,66	sp	P00761	TRYP_PIG	146,560751	9027,10186	2970,31818	26720,3894	6301,17317	17370,7915	6461,33417	12131,2238	1895,53144
900	900	NLEPLFETYLSVL	847,461	39,77	sp	P19013	K2C4_HUMAN	12775,6271	2791,21467	1784,61324	5150,5027	791,323842	508,945826	241,21837	1079,81095	3662,4217
901	901	TIDDLKNQNLN[Dea]LTTDDNANILLQIDNAR	1018,55	39,82	sp	P13645	K1C10_HUMAN	946430,288	46463,4932	634976,121	390353,687	5816,58036	1355075,29	327818,753	1047828,309	8454,15155
902	902	DVFLGMFLYEYAR	812,399	39,9	sp	P02768	ALBU_HUMAN	61745,6417	42969,2862	3049,98104	29838,9862	37549,7253	4615,50218	774,366152	2793,02664	13860,5695
903	903	VLEDELTLARADLE[M]2oX]QIESLKEELAYLKK	824,191	40,04	sp	P02533	K1C14_HUMAN	2568,07248	12638,5992	2685,13013	1336,24118	1153,31148	5303,70581	531,38669	2316,45373	3613,21726
904	904	GADVWFKELDINTDGAVNFQEFULIVIKMGVAA	996,917	40,82	sp	P05109	S10A8_HUMAN	12218,9876	477,934734	968,555964	914,699844	1679,08205	1928,17453	319,534018	2014,87584	9856,64432
905	905	ATLVC[CAM]LISDFYPGAVTVVAWK	1106,08	41,3	sp	B9A064	IGLL5_HUMAN	817,050658	1139,90975	721,251775	392,440244	10971,3267	1331,54989	530,392899	812,850831	1915,50841
906	906	PGQ.QNLEPLFEQYINN[Dea]JLR	937,976	41,34	sp	P48668	K2C6C_HUMAN	13456,9879	45388,8949	27796,8161	24441,6277	6484,50012	28906,9552	1512,51435	5616,41731	4297,72651
907	907	PGQ.QNLEPLFEQYINN[Dea]JLR	937,976	41,34	sp	P48668	K2C6C_HUMAN	13456,9879	45388,8949	27796,8161	24441,6277	6484,50012	28906,9552	1512,51435	5616,41731	4297,72651
908	908	PGQ.QNLEPLFEQYINN[Dea]JLR	937,976	41,34	sp	P13647	K2C5_HUMAN	13456,9879	45388,8949	27796,8161	24441,6277	6484,50012	28906,9552	1512,51435	5616,41731	4297,72651
909	909	LGEHNIDVLEGNEQFINAAK[Frm]IITHPNFNGN	927,151	41,41	sp	P00761	TRYP_PIG	1344,69874	1670,15013	1377,26524	1305,01213	1405,69653	2624,24998	1392,52838	2664,88724	4431,53499
910	910	LDNLQOEIDFLTALYQAE[CAM]LSQMOTQISET	1146,81	41,81	sp	P13645	K1C10_HUMAN	182,395231	21156,4398	1577,13073	2181,83276	3484,576324	1157,63924	265,053996	1032,34329	8428,92118
911	911	QLSFEFIMLMAR	807,905	41,84	sp	P06702	S10A9_HUMAN	231197,76	126176,278	60260,3055	90483,5595	53860,6488	3008,60385	989,845537	2814,25561	6270,8897
912	912	YC[CAM]VQLSQIQAQISALEEQLQQIR	916,146	41,85	sp	P13645	K1C10_HUMAN	142908,207	391847,412	2377,17003	112360,005	342527,864	2812,79552	312,759825	789,735934	3592,62346
913	913	YC[CAM]MQLAQIQ[Dea]E[Dhy]MIGSVSEEQLA	907,796	41,94	sp	P02533	K1C14_HUMAN	1147,09867	25650,4641	2174,0591	429,15064	729,524067	1179,93843	579,901932	953,19621	583,230623
914	914	YC[CAM]VQLSQIQSQISALE[NaX]EQLQQIR	696,847	41,97	sp	Q6iFW6	K1C10_RAT	9689,39711	24466,1056	1866,83794	2909,38332	17394,7348	1235,29225	430,125604	615,176919	1848,81275
915	915	YC[CAM]VQLSQIQAQ[Dea]S[Dea]JLR	696,847	41,97	sp	P13645	K1C10_HUMAN	9689,39711	24466,1056	1866,83794	2909,38332	17394,7348	1235,29225	430,125604	615,176919	1848,81275
916	916	YC[CAM]VQLSQIQSQ[Dea]S[Dea]EQLQQIR	921,818	42,01	sp	Q6iFW6	K1C10_RAT	149,339605	9677,24001	1493,45444	1474,80139	3566,23673	11083,753	581,139399	1000,23216	731,109504
917	917	KELDINTDGAVNFQEFULVVK	840,46	42,07	sp	P05109	S10A8_HUMAN	605,692767	1989,95982	5363,55562	2444,66596	3736,00694	13838,5603	2765,15182	5233,64246	8186,03444
918	918	VIHIMEDLDTNADKQLSFEFIMLMAR	1061,51	42,07	sp	P06702	S10A9_HUMAN	876,830114	15717,6639	2466,02486	1290,64492	1823,42449	4340,5306	1706,91634	785,442589	4328,0069
919	919	CAM.YC[CAM]MQLSQIQGLGIVSEEQLAQLR	907,794	42,07	sp	P08779	K1C16_HUMAN	1153,06142	25525,4109	2199,19022	456,64069	739,036943	1091,97842	393,757282	939,634615	1058,4471
920	920	YC[CAM]VQLSQIQSQISALEEQLQQIR	687,36	42,09	sp	Q6iFW6	K1C10_RAT	3814,30327	31336,493	17233,4839	3607,76245	34202,3423	47758,3026	1135,95275	3057,9587	18208,8218
921	921	NLDLDSIAEVKAQEYEEIAQR	806,758	42,22	sp	P48668	K2C6C_HUMAN	679,45713	154,321908	1729,36964	396,754317	1110,18045	16031,5608	737,193271	685,401909	666,527935
922	922	NLDLDSIAEVKAQEYEEIAQR	806,758	42,22	sp	P02538	K2C6A_HUMAN	679,45713	154,321908	1729,36964	396,754317	1110,18045	16031,5608	737,193271	685,401909	666,527935
923	923	NLDLDSIAEVKAQEYEEIAQR	806,758	42,22	sp	P35908	K2E2_HUMAN	679,45713	154,321908	1729,36964	396,754317	1110,18045	16031,5608	737,193271	685,401909	666,527935
924	924	YC[CAM]VQLSQIQSQISALE[XXX]EQLQQIR	700,841	42,23	sp	Q6iFW6	K1C10_RAT	21574,1727	43703,441	12424,6948	1121,99929	48631,0908	30636,5682	319,886801	1784,92287	9343,07262
925	925	YC[CAM]VQLSQIQSQISALEEQLQQIR	921,482	42,25	sp	Q6iFW6	K1C10_RAT	2991,04355	4402,61607	2049,48027	642,354677	1598,80411	3249,23602	1603,98539	1280,88105	5854,13037
926	926	LGEHNIDVLEGNEQFINAAKIITH[AAR]PNFNGB	927,153	42,27	sp	P00761	TRYP_PIG	748,826482	393,548061	2103,98912	1561,42516	510,390253	5317,6595	464,170217	215,07529	3257,18323
927	927	KQSLASLAETEGR[AGA]YC[CAM]VQLSQIQSC	1055,54	42,28	sp	Q6iFW6	K1C10_RAT	6168,58007	1309,36402	4088,51125	3286,51651	5324,14024	9327,18602	1897,23607	594,067908	6023,1982
928	928	CAM.YC[CAM]VQLSQIQ[Dea]S[Dhy]Q[Dea]S	935,152	42,34	sp	Q6iFW6	K1C10_RAT	734,312983	5424,64349	2476,98518	3885,20487	3965,88625	20419,3604	1019,51827	1646,42058	1993,36529
929	929	ADLE[M]Oxi]QIESLTEEALYK	704,686	42,7	sp	Q6iFW6	K1C10_RAT	18980,4262	28388,7707	18965,8894	10742,9153	11195,7797	2110,42018	274,819778	2335,01956	2128,08908
930	930	VLDPNMTFVFNINYSFK	647,355	42,81	sp	P34955	A1AT_BOVIN	4364,26097	8108,41095	8260,57856	3920,83497	6343,97098	5521,8781	1593,1393	3576,04561	8655,22119
931	931	YC[CAM]VQLSQIQ[Dea]S[Dhy]Q[Dea]S[Dea]E	916,477	42,9	sp	Q6iFW6	K1C10_RAT	4373,57893	27153,5409	12772,9797	7245,28892	14347,8377	5719,05901	2492,13816	1336,78629	994,185645
932	932	YC[CAM]VQLSQIQ[Dea]JLR	916,474	42,99	sp	Q6iFW6	K1C10_RAT	4363,8934	27085,6718	4603,07698	7295,76926	14343,0443	8121,49563	2587,85258	1387,01761	1024,31687
933	933	LDNLQOEIDFLTALYQAELSQMOTQISE[CAM]T	1150,81	43	sp	P04264	K2C1_HUMAN	14985,2793	19141,9024	5453,19487	7582,89453	16439,87	1496,02119	946,805357	308,763426	153,230522
934	934	GADVWFKELDINT[Dhy]DGAVNF[Dea]FQEFULI	712,227	43,03	sp	P05109	S10A8_HUMAN	1139,17253	2545,44331	3787,7275	3497,21902	3462,6373	1230,98607	3579,28885	4126,6895	6287,83331
935	935	CAM.RRKGAADVWFKELDINTDGAVNF[Dea]FQI	779,702	43,04	sp	P05109	S10A8_HUMAN	3608,47174	990,94337	402,176242	527,553616	272,520745	522,3537	1010,64745	411,115873	1128,75532
936	936	GADVWFKELDINTDGAVNF[Dea]FQEFULIVIKM	831,099	43,13	sp	P05109	S10A8_HUMAN	4834,85732	15783,2132	392,148758	5433,66689	3777,29617	355,759775	1295,11895	1384,40998	1830,12733
937	937	KIDFSELSLGLDIATDYHK	771,401	43,49	sp	P31151	S10A7_HUMAN	2617,09369	1474,67132	3447,68394	13780,7295	13970,4314	6873,35984	2498,78319	2781,07353	2477,91005
938	938	AQFVPLPVSVSVEFAVAATDC[CAM]IAK	840,446	43,74	sp	P12763	FETUA_BOVIN	6770,63399	7807,75301	8002,57684	7059,12988	2280,77217	2136,96088	342,697626	1356,46106	9227,73591
939	939	LDIQGTGQLFSVIVNQLR	705,407	44,46	sp	P01833	PIGR_HUMAN	3840,48247	5487,70356	9856,4104	17673,4198	6943,33438	3699,56143	11471,6742	3272,04225	19417,7112
940	940	ELDINTDGAVNFQEFULVVK	797,765	44,69	sp	P05109	S10A8_HUMAN	77772,2475	50399,8748	2603,20589	12153,6613	39245,7304	463,903895	1468,43954	12468,4322	6850,8213
941	941	CRM.GADVWFKELDIN[Dea]TDGAVNFQEFULI	838,256	46,17	sp	P05109	S10A8_HUMAN	2216,74023	3955,0395	3724,94518	6370,12425	2266,31242	3532,30482	1118,4445	1932,95559	733,875286
942	942	GADVWFKELDINTDGAVNFQEFULVVK	1065,56	46,31	sp	P05109	S10A8_HUMAN	2263,49127	2958,97162	2453,12248	769,846901	1108,73529	4538,18506	1052,96769	1001,13027	6619,03209
943	943	YLGFLVQDAATYAVTTFSNVYLF	897,125	46,												