

Proteomic Data Tables (Additional File 4)

Metaproteomic analyses of urinary pellets using LC-nESI-ion trap MS/MS instruments (LTQ-XL and Velos Pro, Thermo Fisher Scientific) and the Mascot search engine version 2.3 (Matrix Science) for spectral data interpretation based on a selection of 19 bacterial and a human genome-wide protein sequence database.

There are 11 separate tables (worksheets) each presenting a protein summary report and a peptide summary report. These reports were derived from Mascot v2.3 analysis using the software Proteome Discoverer (Thermo Fisher Scientific). Each of the pairs of reports (11) represents analysis of one urinary sample (from two technical LC-MS/MS replicate analyses). First, we applied the MudPIT scoring approach for our database searches using Mascot v2.3.

A peptide filter with a Mascot significance threshold of $p < 0.05$ was applied. Second, to obtain a more robust false discovery rate on the peptide level, we used the Mascot Percolator option where machine learning is employed to recalculate the false peptide discovery rate. A stringent peptide confidence threshold in the Percolator analysis mode was set with a q-value (the minimal false discovery rate) ≤ 0.01 . On the protein level, we filtered requiring a minimal number of two distinct peptides with the rank 1, or one distinct peptide only, if the peptide was ranked 1 and if the peptide's PEP threshold value (from the Percolator analysis) was $10e-4$ or lower. The protein summary report designates the identified proteins (or protein groups based on Mascot's algorithm to define protein groups with high amino acid sequence similarity). The peptide summary report provides the sequences of all identified peptides (above the PEP threshold of $10e-4$ if a single distinct peptide was identified for a given protein).

The UniRef90 database (<http://www.uniprot.org/>) was comprised of a selection of non-redundant human protein sequences.

Nineteen sequenced bacterial genomes representing species occasionally or frequently associated with bacteriuria UTIs, were also selected for database (downloaded from NCBI).

The total number of protein sequences searched was 283115. Of these, 61395 sequences were from the human UniRef90 dataset.

The bacterial databases are listed below:

- 1) *Lactobacillus delbrueckii* subsp. *bulgaricus* PB2003/044-T3-4 AEAT01000000 (<http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=784613>)
- 2) *Lactobacillus jensenii* JV-V16 ACGQ02000000 (<http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=525329>)
- 3) *Lactobacillus gasseri* JV-V03 ACGQ02000000 (<http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=525326>)
- 4) *Corynebacterium urealyticum* (<http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=504474&lvl=3&lin=f&keep=1&srchmode=1&unlock>)
- 5) *Escherichia coli* UPEC (<http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=199310&lvl=3&lin=f&keep=1&srchmode=1&unlock>)
- 6) *Peptoniphilus asaccharolyticus* (<http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=1258&lvl=3&lin=f&keep=1&srchmode=1&unlock>)
- 7) *Klebsiella pneumoniae* (<http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=507522&lvl=3&lin=f&keep=1&srchmode=1&unlock>)
- 8) *Streptococcus pneumoniae* (<http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=1313&lvl=3&lin=f&keep=1&srchmode=1&unlock>)
- 9) *Prevotella intermedia* (<http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=28131&lvl=3&lin=f&keep=1&srchmode=1&unlock>)
- 10) *Anaerococcus vaginalis* (<http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=33037&lvl=3&lin=f&keep=1&srchmode=1&unlock>)
- 11) *Staphylococcus epidermidis* (<http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=1282&lvl=3&lin=f&keep=1&srchmode=1&unlock>)
- 12) *Proteus mirabilis* (<http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=529507&lvl=3&lin=f&keep=1&srchmode=1&unlock>)
- 13) *Pseudomonas aeruginosa* (<http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=208964&lvl=3&lin=f&keep=1&srchmode=1&unlock>)
- 14) *Finogoldia magna* (<http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=1260&lvl=3&lin=f&keep=1&srchmode=1&unlock>)
- 15) *Enterococcus faecalis* (<http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=1351&lvl=3&lin=f&keep=1&srchmode=1&unlock>)
- 16) *Enterococcus faecium* (<http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=1352&lvl=3&lin=f&keep=1&srchmode=1&unlock>)
- 17) *Morganella morganii* (<http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=582&lvl=3&lin=f&keep=1&srchmode=1&unlock>)
- 18) *Enterobacter hormaechei* (<http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=158836&lvl=3&lin=f&keep=1&srchmode=1&unlock>)
- 19) *Ureaplasma urealyticum* (<http://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?mode=Info&id=2130&lvl=3&lin=f&keep=1&srchmode=1&unlock>)

On the following pages, the number part of the sample identifier (line 1) represents the human subject number (with a peptide summary section following the protein summary section)

Protein Summary Report

Index	indicates the order of the list in which the table was exported from Proteome Discoverer
Prot_hit	indicates protein family grouping; a family member will represent multiple same-set proteins. All proteins in a same-set group are indistinguishable on the basis of the peptide match evidence.
Accession	gi and Ref Seq ID
Description	the name of the protein that appears in the Accession column
Mascot score	Mascot incorporates a probability-based implementation of the Mowse algorithm (see http://www.matrixscience.com/search_form_select.html).
Coverage	the percentage of the protein sequence covered by identified peptides
# peptide	the number of significant distinct peptide sequences in the protein group
# PSM	the total number of identified peptide sequences (peptide spectrum matches) for the protein, including those redundantly identified
# AA	the sequence length of the protein
MW [kDa]	the calculated molecular weight of the protein (without considering PTMs) and isoelectric point of protein
calc. pI	the theoretically calculated isoelectric point, which is the pH at which a particular molecule carries no net electrical charge

Peptide Summary Report

Sequence	the sequence of amino acids that compose the peptide
Protein Descriptions	the proteins associated with the peptide. This description is taken from the FASTA file
# proteins	the number of identified proteins in the protein group of a master protein
# protein group	the number of protein groups in which this peptide is found
Protein Group Accession	the master protein accession that contain the peptide
Modifications	type of modification
q-value	A q-value is the minimal false discovery rate at which the identification is considered correct (a Mascot Percolator analysis value)
PEP	the probability that the observed PSM is incorrect (a Mascot Percolator analysis value)
Charge	the charge state of the peptide
m/z [Da]	the mass-to-charge ratio of the precursor ion, in daltons
MH+ [Da]	the protonated monoisotopic mass of the peptides, in daltons
Delta Mass [Da]	the difference between the theoretical mass of the peptide and the experimental mass of the precursor ion, in daltons

ZDLCSCI_37 Protein Summary

index	Prot_hit	Accession	Description	Mascot Score	Coverage	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pi
1	1	P63261	Actin, cytoplasmic 2 n=1334 RepID=ACTG_HUMAN	430.28	32.53%	7	10	375	41.8	5.48
2	2	P35579	Myosin-9 n=677 Tax=Tetrapoda RepID=MYH9_HUMAN	129.54	1.63%	2	2	1960	226.4	5.6
3	3	P15508	Spectrin beta chain, erythrocyte n=14 Tax=Euarchoptogilres RepID=SPTB1_MOUSE	119.09	1.27%	2	2	2128	245.1	5.33
4	4	P04264	Keratin, type II cytoskeletal 1 n=7 Tax=Eutheria RepID=K2C1_HUMAN	324.61	10.87%	2	3	644	66	8.12
5	5	P13645	Keratin, type I cytoskeletal 10 n=12 Tax=Eutheria RepID=K1C10_HUMAN	111.28	3.25%	1	1	584	58.8	5.21
6	6.1	P08727	Keratin, type I cytoskeletal 19 n=9 Tax=Eutheria RepID=K1C19_HUMAN	248.48	7.25%	2	4	400	44.1	5.14
7	6.2	B4DE59	cDNA FLJ60424, highly similar to Junction plakoglobin n=1 Tax=Homo sapiens RepID=B4DE59_HUMAN	248.48	5.15%	2	4	563	62.6	5.17
8	7	P62937	Peptidyl-prolyl cis-trans isomerase A n=98 Tax=Theria RepID=PP1A_HUMAN	191.2	16.97%	2	4	165	18	7.81
9	8	P11277	Spectrin beta chain, erythrocyte n=18 Tax=Eutheria RepID=SPTB1_HUMAN	207.73	2.99%	4	4	2137	246.3	5.27
10	9.1	E9PFJ3	Uncharacterized protein n=3 Tax=Simiiformes RepID=E9PFJ3_HUMAN	600.81	9.17%	6	15	578	63.3	5.31
11	9.2	P07911	Uromodulin n=2 Tax=Catarrhini RepID=UROM_HUMAN	600.81	8.28%	6	15	640	69.7	5.24
12	10	P68871	Hemoglobin subunit beta n=102 Tax=Primates RepID=HBB_HUMAN	2997.24	14.48%	10	66	147	16	7.28
13	11	E9PFT6	Uncharacterized protein n=2 Tax=Homo sapiens RepID=E9PFT6_HUMAN	657.72	27.66%	3	18	141	15.4	7.91
14	12	P00918	Carbonic anhydrase 2 n=8 Tax=Primates RepID=CAH2_HUMAN	185.59	15.77%	3	6	260	29.2	7.4
15	13	P69905	Hemoglobin subunit alpha n=29 Tax=Primates RepID=HBA_HUMAN	1236.61	39.44%	5	30	142	15.2	8.68
16	14	P02081	Hemoglobin fetal subunit beta n=8 Tax=Eutheria RepID=HBFB_BOVIN	247.92	14.48%	2	13	145	15.8	7.03
17	15	A4FUA1	GUCA1B protein (Fragment) n=1 Tax=Homo sapiens RepID=A4FUA1_HUMAN	336.59	58.67%	3	9	75	8.6	5.41
18	16.1	P62741	Hemoglobin subunit gamma-1 n=6 Tax=Hominidae RepID=HBG1_GORGO	161.29	15.65%	2	11	147	16.1	7.64
19	16.2	P69891	Hemoglobin subunit gamma-1 n=20 Tax=Catarrhini RepID=HBG1_HUMAN	161.29	15.65%	2	11	147	16.1	7.2
20	16.3	Q9G157	Hemoglobin subunit gamma n=39 Tax=Simiiformes RepID=HBG_CALIA	161.29	15.65%	2	11	147	16	6.93
21	17	P13646	Keratin, type I cytoskeletal 13 n=13 Tax=Simiiformes RepID=K1C13_HUMAN	606.2	22.27%	7	16	458	49.6	4.96
22	18.1	B4DRW1	cDNA FLJ55805, highly similar to Keratin, type II cytoskeletal 4 n=2 Tax=Hominidae RepID=B4DRW1_HUMAN	396.82	8.02%	3	11	474	51.7	6.81
23	18.2	P19013	Keratin, type II cytoskeletal 4 n=14 Tax=Simiiformes RepID=K2C4_HUMAN	396.82	7.12%	3	11	534	57.2	6.61
24	19	E7UEE8	Uncharacterized protein n=14 Tax=Eutheria RepID=E7UEE8_HUMAN	93.79	4.62%	2	3	520	55.8	6.27
25	19.1	P02538	Keratin, type II cytoskeletal 6A n=25 Tax=Euarchoptogilres RepID=K2C6A_HUMAN	93.79	4.26%	2	3	564	60	8
26	19.2	F6RMN8	Uncharacterized protein n=4 Tax=Simiiformes RepID=F6RMN8_CALIA	93.79	4.49%	2	3	535	57.8	8.22
27	20.1	E9PF79	Pyruvate kinase n=4 Tax=Simiiformes RepID=E9PF79_HUMAN	82.19	6.33%	2	2	458	50	7.64
28	20.2	P14618	Pyruvate kinase isozymes M1/M2 n=16 Tax=Simiiformes RepID=KPYM_HUMAN	82.19	5.46%	2	2	531	57.9	7.84
29	20.3	B4DRT3	Pyruvate kinase n=2 Tax=Homo sapiens RepID=B4DRT3_HUMAN	82.19	5.68%	2	2	511	55.9	7.5
30	20.4	B4DUU6	Pyruvate kinase n=4 Tax=Simiiformes RepID=B4DUU6_HUMAN	82.19	5.62%	2	2	516	56.2	8.44
31	20.5	P52480	Pyruvate kinase isozymes M1/M2 n=40 Tax=Tetrapoda RepID=KPYM_MOUSE	82.19	5.46%	2	2	531	57.8	7.47
32	21	P05062	Fructose-bisphosphate aldolase B n=20 Tax=Eutheria RepID=ALDOB_HUMAN	90.46	4.12%	1	1	364	39.4	7.87
33	22	P02730	Band 3 anion transport protein n=4 Tax=Simiiformes RepID=SB3AT_HUMAN	416.26	8.78%	6	10	911	101.7	5.19
34	23.1	P16157-15	Isoform Er14 of Ankyrin-1 n=9 Tax=Simiiformes RepID=P16157-15	122.97	1.59%	2	4	1821	200.1	6.92
35	23.2	P16157	Ankyrin-1 n=50 Tax=Mammalia RepID=ANK1_HUMAN	122.97	1.54%	2	4	1881	206.1	6.01
36	24	P02549	Spectrin alpha chain, erythrocyte n=16 Tax=Simiiformes RepID=SPTA1_HUMAN	567.72	3.97%	6	11	2419	279.8	5.05
37	25.1	E7ENH1	Uncharacterized protein n=6 Tax=Coelomata RepID=E7ENH1_HUMAN	103.15	10.70%	2	3	271	30.7	4.96
38	25.2	E7EWR1	Uncharacterized protein n=5 Tax=Simiiformes RepID=E7EWR1_HUMAN	103.15	8.22%	2	3	353	39.7	4.93
39	25.3	F7FYG3	Uncharacterized protein n=3 Tax=Simiiformes RepID=F7FYG3_CALIA	103.15	9.15%	2	3	317	35.9	4.88
40	25.4	Q55T81	Tubulin beta polypeptide n=8 Tax=Eukaryota RepID=Q55T81_HUMAN	103.15	7.80%	2	3	372	41.7	4.91
41	26.1	P06899	Histone H2B type 1-J n=102 Tax=Euteleostomi RepID=H2B1_HUMAN	172.33	11.90%	1	2	126	13.9	10.32
42	26.2	P62807	Histone H2B type 1-C/E/F/G/I n=44 Tax=Euteleostomi RepID=H2B1C_HUMAN	172.33	11.90%	1	2	126	13.9	10.32
43	26.3	B4DR52	Histone H2B n=5 Tax=Euarchoptogilres RepID=B4DR52_HUMAN	172.33	9.04%	1	2	166	18	10.32
44	26.4	P58876	Histone H2B type 1-D n=136 Tax=Coelomata RepID=H2B1D_HUMAN	172.33	11.90%	1	2	126	13.9	10.32
45	27.1	E9PEX0	Uncharacterized protein n=2 Tax=Homo sapiens RepID=E9PEX0_HUMAN	84.53	2.27%	1	1	704	78.4	5.59
46	27.2	E9PEW9	Uncharacterized protein n=3 Tax=Eutheria RepID=E9PEW9_HUMAN	84.53	2.09%	1	1	767	86	5.43
47	27.3	P11171	Protein 4.1 n=17 Tax=Eutheria RepID=41_HUMAN	84.53	1.85%	1	1	864	97	5.58
48	27.4	Q1WWM3	EPB41 protein (Fragment) n=6 Tax=Eutheria RepID=Q1WWM3_HUMAN	84.53	2.16%	1	1	742	83.2	5.72
49	27.5	Q6Q7P4	Protein 4.1 n=15 Tax=Eutheria RepID=41_CANFA	84.53	1.98%	1	1	810	90.6	5.55
50	28.1	UPI000D48568	UPI000D48568 related cluster n=1 Tax=Homo sapiens RepID=UPI000D48568	149.43	8.60%	1	3	186	20.4	9.06
51	28.2	P04792	Heat shock protein beta-1 n=6 Tax=Simiiformes RepID=HSPB1_HUMAN	149.43	7.80%	1	3	205	22.8	6.4
52	29.1	A8MX94	Uncharacterized protein n=1 Tax=Homo sapiens RepID=A8MX94_HUMAN	202.44	9.20%	1	2	174	19.5	5.97
53	29.2	P09211	Glutathione S-transferase P n=4 Tax=Simiiformes RepID=GSTP1_HUMAN	202.44	7.62%	1	2	210	23.3	5.64
54	30.1	B4DUK1	cDNA FLJ51310, moderately similar to Peroxiredoxin-6 (EC 1.11.1.15) n=1 Tax=Homo sapiens RepID=B4DUK1_HUMAN	264.19	20.79%	1	4	101	11.2	5.39
55	30.2	P30041	Peroxiredoxin-6 n=17 Tax=Eutheria RepID=PRDX6_HUMAN	264.19	9.38%	1	4	224	25	6.38
56	31	P00915	Carbonic anhydrase 1 n=8 Tax=Catarrhini RepID=CAH1_HUMAN	353.05	27.97%	5	9	261	28.9	7.12
57	32.1	B4DY56	ATP synthase subunit alpha n=3 Tax=Eutheria RepID=B4DY56_HUMAN	74.41	4.71%	1	1	531	57.5	9.22
58	32.2	P25705	ATP synthase subunit alpha, mitochondrial n=53 Tax=Euteleostomi RepID=ATPA_HUMAN	74.41	4.52%	1	1	553	59.7	9.13
59	33.1	Q5T3N1	Annexin A1 (Fragment) n=3 Tax=Eutheria RepID=Q5T3N1_HUMAN	182.48	19.12%	2	3	204	22.7	5.53
60	33.2	P04083	Annexin A1 n=14 Tax=Eutheria RepID=ANXA1_HUMAN	182.48	11.27%	2	3	346	38.7	7.02
61	34.1	F7GZR9	Uncharacterized protein n=2 Tax=Simiiformes RepID=F7GZR9_CALIA	81.2	16.07%	1	1	112	12.5	6.6
62	34.2	P23528	Cofilin-1 n=29 Tax=Eutheria RepID=COF1_HUMAN	81.2	10.84%	1	1	166	18.5	8.09
63	35	P45974	Ubiquitin carboxyl-terminal hydrolase 5 n=20 Tax=Amniota RepID=UBP5_HUMAN	67.96	3.03%	1	1	858	95.7	5.03

Sequence	Protein Descriptions	# Proteins	# Protein Groups	Protein Group Accessions	Modifications	q-Value	PEP	Charge	m/z [Da]	MH+ [Da]	Delta Mass [Da]
FFESFGDLTPDAVmGNPK	Hemoglobin subunit beta n=102 Tax=Primates Ref	1	1	P68871	M15(Oxidation)	0	0.000886	2	1038.41272	2075.81816	0.44
PGGLLGDVAPNFEANTTVGR	cDNA FLJ51310, moderately similar to Peroxiredox	2	1	B4DUK1		0	1.59E-07	2	1049.62878	2098.25029	0.08
PGGLLGDVAPNFEANTTVGR	cDNA FLJ51310, moderately similar to Peroxiredox	2	1	B4DUK1		0	6.52E-08	2	1049.92371	2098.84014	0.37
PGGLLGDVAPNFEANTTVGR	cDNA FLJ51310, moderately similar to Peroxiredox	2	1	B4DUK1		0	9.22E-07	2	1049.94446	2098.88164	0.39
PGGLLGDVAPNFEANTTVGR	cDNA FLJ51310, moderately similar to Peroxiredox	2	1	B4DUK1		0	3.19E-07	2	1049.96448	2098.92168	0.41
EAVEKEFELPLNWMKDK	Endoplasmin n=58 Tax=Amniota RepID=ENPL_HU1	1	1	P14625		0	0.0127	3	703.05579	2107.15281	0.37
GLDAHLEQIFQEAHGMVAR	Spectrin beta chain, erythrocyte n=18 Tax=Eutheri	1	1	P11277		0	1.18E-05	3	708.08832	2122.2504	0.07
aSPDWGYDDKNGPEQWSK	Carbonic anhydrase 1 n=8 Tax=Catarrhini. RepID=C	1	1	P00915	N-Term(Acetyl)	0	3.71E-05	2	1061.82056	2122.63384	0.36
aSPDWGYDDKNGPEQWSK	Carbonic anhydrase 1 n=8 Tax=Catarrhini. RepID=C	1	1	P00915	N-Term(Acetyl)	0	1.23E-05	2	1061.86084	2122.7144	0.4
aSPDWGYDDKNGPEQWSK	Carbonic anhydrase 1 n=8 Tax=Catarrhini. RepID=C	1	1	P00915	N-Term(Acetyl)	0	3.40E-05	2	1061.87134	2122.7354	0.41
aSPDWGYDDKNGPEQWSK	Carbonic anhydrase 1 n=8 Tax=Catarrhini. RepID=C	1	1	P00915	N-Term(Acetyl)	0	3.54E-06	2	1062.09106	2123.17485	0.63
SAVTALWGKVNDEVGGEALGR	Hemoglobin subunit beta n=102 Tax=Primates Ref	1	1	P68871		0	3.72E-08	2	1115.03845	2229.06963	0.45
SAVTALWGKVNDEVGGEALGR	Hemoglobin subunit beta n=102 Tax=Primates Ref	1	1	P68871		0	4.86E-08	2	1115.03894	2229.0706	0.45
VYVELQELVMDEKNQELR	Band 3 anion transport protein n=4 Tax=Simiiform	1	1	P02730		0	0.000814	3	745.88623	2235.64414	0.17
VYVELQELVMDEKNQELR	Band 3 anion transport protein n=4 Tax=Simiiform	1	1	P02730		0	3.69E-06	2	1118.44128	2235.87529	0.37
VYVELQELVMDEKNQELR	Band 3 anion transport protein n=4 Tax=Simiiform	1	1	P02730		0	8.61E-06	2	1118.4801	2235.95293	0.41
EIINVGHSFHVNFEDNDNR	Carbonic anhydrase 1 n=8 Tax=Catarrhini. RepID=C	1	1	P00915		0	6.35E-05	3	752.97333	2256.90543	0.29
FFESFGDLTPDAVmGNPKVK	Hemoglobin subunit beta n=102 Tax=Primates Ref	1	1	P68871		0	7.34E-05	3	763.08923	2287.25315	0.38
GGPGSAVSPYPTFNPSDVAALHK	Annexin A1 (Fragment) n=3 Tax=Eutheria RepID=C	2	1	Q5T3N1		0	6.53E-06	3	786.48773	2357.44864	0.43
GGGGGSGSGSSYSGGGSGSGGGGGGGR	Keratin, type II cytoskeletal 1 n=7 Tax=Eutheria Re	1	1	P04264		0	2.59E-09	2	1192.96936	2384.93144	0.49
ILNNGHAFNVEFDDSDQKAVLK	Carbonic anhydrase 2 n=8 Tax=Primates RepID=CA	1	1	P00918		0	6.70E-06	3	825.69489	2475.0701	0.28
ILNNGHAFNVEFDDSDQKAVLK	Carbonic anhydrase 2 n=8 Tax=Primates RepID=CA	1	1	P00918		0	5.62E-07	3	825.83325	2475.4852	0.42
ILNNGHAFNVEFDDSDQKAVLK	Carbonic anhydrase 2 n=8 Tax=Primates RepID=CA	1	1	P00918		0	3.44E-06	3	825.85559	2475.52222	0.44
HQGVmVGMGKDSVVGDEAQSQR	Actin, cytoplasmic 2 n=1334 RepID=ACTG_HUMA	1	1	P63261	M5(Oxidation)	0	5.67E-08	3	842.12415	2524.35788	0.4
ILGADTSVLEETGRVLSGDGIAR	ATP synthase subunit alpha n=3 Tax=Eutheria Rep	2	1	B4DY56		0	5.79E-06	3	853.54382	2558.61692	0.42
DSTIQVVENGESQGRFSVQMFR	Uncharacterized protein n=3 Tax=Simiiformes Rep	2	1	E9PFJ3		0	0.000505	3	868.14307	2600.54123	0.39
SLSNVGDNVPMQHNRPQPLK	Carbonic anhydrase 1 n=8 Tax=Catarrhini. RepID=C	1	1	P00915		0	0.000696	3	920.85193	2760.54123	0.38
IGVEELKEFSTYKFFDENLTR	Spectrin alpha chain, erythrocyte n=16 Tax=Simiifc	1	1	P02549		0	2.67E-05	3	934.50952	2801.51401	0.38
IGVEELQESVPLKFLGPGYTGR	Ubiquitin carboxyl-terminal hydrolase 5 n=20 Tax=	1	1	P45974		0	5.98E-05	3	953.14478	2857.41977	0.3
SLSNVGDNVPMQHNRPQPLKGR	Carbonic anhydrase 1 n=8 Tax=Catarrhini. RepID=C	1	1	P00915		0	1.08E-07	3	991.93237	2973.78257	0.42
VHLTPEEKSAVTALWGKVNDEVGGEALGR	Hemoglobin subunit beta n=102 Tax=Primates Ref	1	1	P68871		0	5.99E-09	3	1054.90686	3162.70603	0.35
VHLTPEEKSAVTALWGKVNDEVGGEALGR	Hemoglobin subunit beta n=102 Tax=Primates Ref	1	1	P68871		0	2.21E-08	3	1054.91101	3162.71848	0.35
TTGVMDSGDVTHTVPIYEGYALPHAILR	Actin, cytoplasmic 2 n=1334 RepID=ACTG_HUMA	1	1	P63261		0	5.28E-08	3	1062.20667	3184.60544	0.33
GSYGSGSGSGSGSGSGGGGGHGSYSGSSGGYR	Keratin, type II cytoskeletal 1 n=7 Tax=Eutheria Re	1	1	P04264		0	3.36E-08	3	1105.04285	3313.11399	0.27
GSYSGSGSGSGSGSGGGGGHGSYSGSSGGYR	Keratin, type II cytoskeletal 1 n=7 Tax=Eutheria Re	1	1	P04264		0	4.13E-07	3	1105.1947	3313.56955	0.42

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index	Prot_hit	Accession	Description	Mascot Score	Coverage	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pl
1	1.1	334126439	translation elongation factor Tu [Enterobacter hormaechei ATCC 49619]	620.27	25.00%	7	18	376	41.1	5.24
2	1.2	206581075	translation elongation factor Tu [Klebsiella pneumoniae 344]	620.27	23.86%	7	18	394	43.2	5.53
3	2	334125929	elongation factor G [Enterobacter hormaechei ATCC 49162]	219.67	8.81%	4	4	704	77.5	5.34
4	3	334125399	enolase [Enterobacter hormaechei ATCC 49162]	355.04	12.04%	4	6	432	45.6	5.31
5	4	334124376	DNA-binding protein VicH [Enterobacter hormaechei ATCC 49162]	82.49	10.22%	1	1	137	15.6	5.16
6	5	334123809	chaperone GroEL [Enterobacter hormaechei ATCC 49162]	930.79	28.47%	12	21	548	57.1	4.94
7	6	334122625	formate acetyltransferase [Enterobacter hormaechei ATCC 49162]	224.84	7.76%	4	7	760	85	6.09
8	7.1	334122578	outer membrane protein A [Enterobacter hormaechei ATCC 49162]	104.29	3.35%	2	3	358	38.3	5.24
9	7.2	197284675	outer membrane protein A [Proteus mirabilis HI4320]	104.29	3.31%	2	3	362	39	5.85
10	8.1	206579217	ribosomal protein L2 [Klebsiella pneumoniae 342]	210.65	13.19%	3	5	273	29.8	10.93
11	8.2	334125920	50S ribosomal protein L2 [Enterobacter hormaechei ATCC 49162]	210.65	13.19%	3	5	273	29.8	10.93
12	9.1	206578965	ribosomal protein L29 [Klebsiella pneumoniae 342]	61.43	34.92%	1	1	63	7.2	10.27
13	9.2	334125915	50S ribosomal protein L29 [Enterobacter hormaechei ATCC 49162]	61.43	34.92%	1	1	63	7.2	10.59
14	10	206576984	outer membrane protein TolC [Klebsiella pneumoniae 344]	157.23	7.74%	3	4	491	53.3	6.19
15	11.1	206578717	fructose-bisphosphate aldolase [Klebsiella pneumoniae 344]	68.59	11.42%	2	2	359	39.2	5.96
16	11.2	334125530	fructose-bisphosphate aldolase [Enterobacter hormaechei ATCC 49162]	68.59	11.42%	2	2	359	39.2	5.86
17	12	206580560	autonomous glycol radical cofactor [Klebsiella pneumoniae 344]	75.57	31.50%	2	2	127	14.2	5.02
18	13	206576322	colicin I receptor [Klebsiella pneumoniae 342]	134.82	2.44%	1	2	657	73.1	5.41
19	14.1	206580610	aldehyde-alcohol dehydrogenase [Klebsiella pneumoniae 344]	396.76	8.64%	4	6	891	95.9	6.79
20	14.2	26247570	bifunctional acetaldehyde-CoA/alcohol dehydrogenase [Escherichia coli CFT073]	396.76	8.64%	4	6	891	96.1	6.79
21	15	206576961	quinone dehydrogenase (pyrroloquinoline-quinone) [Klebsiella pneumoniae 344]	80.25	2.41%	1	1	790	85	7.09
22	16.1	206577927	NADP-specific glutamate dehydrogenase [Klebsiella pneumoniae 344]	281.24	11.86%	3	5	447	48.5	7.01
23	16.2	334122327	glutamate dehydrogenase [Enterobacter hormaechei ATCC 49162]	281.24	11.86%	3	5	447	48.3	6.62
24	17	206580183	glyceraldehyde-3-phosphate dehydrogenase (phosphorylase) [Klebsiella pneumoniae 344]	185.13	15.11%	3	5	331	35.5	7.11
25	18.1	206577508	outer membrane protein A [Klebsiella pneumoniae 342]	127.72	4.00%	1	2	350	37.4	6.25
26	18.2	26246978	outer membrane protein A [Escherichia coli CFT073]	127.72	3.69%	1	2	379	41	6.71
27	19	206577432	formate acetyltransferase [Klebsiella pneumoniae 342]	338.73	10.00%	5	9	760	85.2	5.85
28	20.1	206576199	alkyl hydroperoxide reductase subunit F [Klebsiella pneumoniae 344]	87.51	4.61%	1	1	521	56	5.59
29	20.2	334122925	alkyl hydroperoxide reductase [Enterobacter hormaechei ATCC 49162]	87.51	4.61%	1	1	521	55.8	5.5
30	21.1	206577586	alkyl hydroperoxide reductase subunit C [Klebsiella pneumoniae 344]	132.91	17.11%	2	3	187	20.8	5.17
31	21.2	334122926	alkyl hydroperoxide reductase C [Enterobacter hormaechei ATCC 49162]	132.91	15.92%	2	3	201	22.4	5.02
32	21.3	26246586	alkyl hydroperoxide reductase subunit C [Escherichia coli CFT073]	132.91	17.11%	2	3	187	20.7	5.17
33	24	206576800	antioxidant, AhpC/TSA family [Klebsiella pneumoniae 342]	118.49	12.50%	2	3	200	22.3	5.29
34	25	206577768	dihydrolypoyllysine-residue acetyltransferase [Klebsiella pneumoniae 344]	161.94	2.70%	1	2	630	65.7	5.31
35	26	206579361	ribosomal protein S6 [Klebsiella pneumoniae 342]	109.96	14.50%	1	1	131	15.1	5.38
36	27.1	206580695	DNA-binding protein HU, alpha subunit [Klebsiella pneumoniae 344]	164.67	16.67%	1	2	90	9.5	9.58
37	27.2	334123929	DNA-binding protein HU-beta [Enterobacter hormaechei ATCC 49162]	164.67	16.67%	1	2	90	9.5	9.58
38	28.1	206578905	DNA-directed RNA polymerase, beta' subunit [Klebsiella pneumoniae 344]	187.86	2.63%	2	3	1407	155.3	6.8
39	28.2	26250759	DNA-directed RNA polymerase subunit beta' [Escherichia coli CFT073]	187.86	2.63%	2	3	1407	155.1	7.08
40	29.1	206579488	DNA-directed RNA polymerase, beta subunit [Klebsiella pneumoniae 344]	214.34	4.25%	3	4	1342	150.4	5.29
41	29.2	334123945	DNA-directed RNA polymerase subunit beta [Enterobacter hormaechei ATCC 49162]	214.34	4.21%	3	4	1353	151.6	5.27
42	29.3	26250758	DNA-directed RNA polymerase subunit beta [Escherichia coli CFT073]	214.34	4.21%	3	4	1353	151.8	5.27
43	30.1	206577086	ribosomal protein L10 [Klebsiella pneumoniae 342]	96.04	17.58%	2	2	165	17.8	8.98
44	30.2	334123947	50S ribosomal protein L10 [Enterobacter hormaechei ATCC 49162]	96.04	17.58%	2	2	165	17.8	8.98
45	30.3	26250755	50S ribosomal protein L10 [Escherichia coli CFT073]	96.04	17.58%	2	2	165	17.7	8.98
46	31.1	206575827	ATP synthase FO, B subunit [Klebsiella pneumoniae 342]	230.53	9.62%	1	4	156	17.4	5.8
47	31.2	334121919	ATP synthase FO sector subunit B [Enterobacter hormaechei ATCC 49162]	230.53	9.62%	1	4	156	17.4	5.8
48	32.1	206577341	ATP synthase F1, beta subunit [Klebsiella pneumoniae 344]	227.21	13.48%	5	6	460	50.2	5.03
49	32.2	334121923	ATP synthase F1 sector beta subunit [Enterobacter hormaechei ATCC 49162]	227.21	13.48%	5	6	460	50.2	5
50	33.1	197285060	NAD(P) transhydrogenase subunit alpha [Proteus mirabilis HI4320]	169.17	3.34%	1	2	509	54.4	6.44
51	33.2	334122109	NAD(P) transhydrogenase subunit alpha [Enterobacter hormaechei ATCC 49162]	169.17	3.19%	1	2	533	56.8	6.28
52	33.3	206576623	NAD(P) transhydrogenase, alpha subunit [Klebsiella pneumoniae 344]	169.17	3.31%	1	2	514	54.6	6.71
53	33.4	26247850	NAD(P) transhydrogenase subunit alpha [Escherichia coli CFT073]	169.17	3.22%	1	2	528	56.4	5.85
54	34	197286390	60 kDa chaperonin [Proteus mirabilis HI4320]	143.37	6.20%	2	4	548	57.6	4.89
55	35.1	197286887	FOF1 ATP synthase subunit alpha [Proteus mirabilis HI4320]	208.79	7.80%	3	4	513	55.5	5.69
56	35.2	206580919	ATP synthase F1, alpha subunit [Klebsiella pneumoniae 344]	208.79	7.80%	3	4	513	55.1	6
57	35.3	26250478	FOF1 ATP synthase subunit alpha [Escherichia coli CFT073]	208.79	7.80%	3	4	513	55.2	6.13
58	36.1	26246451	transcriptional regulator HU subunit beta [Escherichia coli CFT073]	95.57	16.67%	1	1	90	9.2	9.7
59	36.2	334123164	DNA-binding protein HU-beta [Enterobacter hormaechei ATCC 49162]	95.57	16.67%	1	1	90	9.1	9.77
60	37.1	26246936	30S ribosomal protein S1 [Escherichia coli CFT073]	106.29	7.54%	2	3	557	61.1	4.98
61	37.2	334122618	30S ribosomal protein S1 [Enterobacter hormaechei ATCC 49162]	106.29	7.54%	2	3	557	61.2	4.98
62	38.1	26247927	major outer membrane lipoprotein [Escherichia coli CFT073]	176.06	30.77%	2	4	78	8.3	9.25
63	38.2	334122238	major outer membrane lipoprotein [Enterobacter hormaechei ATCC 49162]	176.06	30.77%	2	4	78	8.4	9.31
64	39	26248038	glyceraldehyde-3-phosphate dehydrogenase [Escherichia coli CFT073]	123.37	8.38%	2	3	334	35.9	6.8
65	40	26249182	phosphopyruvate hydratase [Escherichia coli CFT073]	417.5	13.19%	4	8	432	45.6	5.48
66	41.1	26249880	DNA-directed RNA polymerase subunit alpha [Escherichia coli CFT073]	242.37	18.54%	4	6	329	36.5	5.06
67	41.2	334125900	DNA-directed RNA polymerase subunit alpha [Enterobacter hormaechei ATCC 49162]	242.37	18.54%	4	6	329	36.4	5.06

index	Prot_hit	Accession	Description	Mascot Score	Coverage	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pI
68	42.1	161486053	ketol-acid reductoisomerase [Escherichia coli CFT073]	78.13	6.92%	2	3	491	54	5.31
69	42.2	334121775	ketol-acid reductoisomerase [Enterobacter hormaechei A	78.13	6.92%	2	3	491	54.1	5.25
70	42.3	206575721	ketol-acid reductoisomerase [Klebsiella pneumoniae 342]	78.13	6.92%	2	3	491	54	5.38
71	43	26251035	chaperonin GroEL [Escherichia coli CFT073]	574.68	19.53%	9	15	548	57.3	4.94
72	44	P04264	Keratin, type II cytoskeletal 1 n=7 Tax=Eutheria RepID=K2	213.64	7.45%	4	6	644	66	8.12
73	45.1	E9PFJ3	Uncharacterized protein n=3 Tax=Simiiformes RepID=E9P	378.23	5.36%	2	5	578	63.3	5.31
74	45.2	P07911	Uromodulin n=2 Tax=Catarrhini RepID=UROM_HUMAN	378.23	4.84%	2	5	640	69.7	5.24
75	45.3	Q5R5C1	Uromodulin n=8 Tax=Simiiformes RepID=UROM_PONAB	378.23	4.84%	2	5	641	69.8	5.24
76	46.1	B4DW52	Uncharacterized protein n=12 Tax=Coelomata RepID=B4C	129.13	17.29%	3	3	347	38.6	5.35
77	46.2	P63261	Actin, cytoplasmic 2 n=1334 RepID=ACTG_HUMAN	129.13	16.00%	3	3	375	41.8	5.48
78	47.1	P13646	Keratin, type I cytoskeletal 13 n=13 Tax=Simiiformes Repl	857.7	29.91%	8	21	458	49.6	4.96
79	47.2	P08727	Keratin, type I cytoskeletal 19 n=9 Tax=Eutheria RepID=K1	356.14	6.25%	2	6	400	44.1	5.14
80	48.1	B4DRW1	cDNA FLJ55805, highly similar to Keratin, type II cytoskele	647.41	21.73%	9	20	474	51.7	6.81
81	48.2	P19013	Keratin, type II cytoskeletal 4 n=14 Tax=Simiiformes Repl	647.41	19.29%	9	20	534	57.2	6.61
82	49	F6RMN8	Uncharacterized protein n=4 Tax=Simiiformes RepID=F6R	479.04	14.95%	8	17	535	57.8	8.22
83	50	P04792	Heat shock protein beta-1 n=6 Tax=Simiiformes RepID=HS	101.04	16.10%	2	2	205	22.8	6.4
84	51.1	A8MX94	Uncharacterized protein n=1 Tax=Homo sapiens RepID=A	180.75	9.20%	1	2	174	19.5	5.97
85	51.2	P09211	Glutathione S-transferase P n=4 Tax=Simiiformes RepID=C	180.75	7.62%	1	2	210	23.3	5.64
86	52	E7EU87	Uncharacterized protein n=3 Tax=Simiiformes RepID=E7E	265.42	10.99%	6	10	555	58.9	5.97
87	52.2	P13647	Keratin, type II cytoskeletal 5 n=17 Tax=Eutheria RepID=K	265.42	10.34%	6	10	590	62.3	7.74
88	53	P04083	Annexin A1 n=14 Tax=Eutheria RepID=ANXA1_HUMAN	742.81	38.44%	10	17	346	38.7	7.02

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index	Prot_hit	Accession	Description	Mascot Score	Coverage	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pI
1	1.1	334126439	translation elongation factor Tu [Enteroba	259.21	16.49%	5	8	376	41.1	5.24
2	1.2	206581075	translation elongation factor Tu [Klebsiella	259.21	15.74%	5	8	394	43.2	5.53
3	2.1	334125906	30S ribosomal protein S5 [Enterobacter hc	52.55	8.43%	1	1	166	17.5	10.05
4	2.2	206580716	ribosomal protein S5 [Klebsiella pneumoni	52.55	8.38%	1	1	167	17.6	10.11
5	3	334124376	DNA-binding protein VicH [Enterobacter h	93.41	10.22%	1	1	137	15.6	5.16
6	4	334123949	50S ribosomal protein L11 [Enterobacter h	100.95	9.86%	1	1	142	14.9	9.63
7	5	334123809	chaperone GroEL [Enterobacter hormaech	774.57	30.11%	10	16	548	57.1	4.94
8	6.1	334123523	chaperone DnaK [Enterobacter hormaech	62.89	2.35%	1	1	637	69.1	4.96
9	6.2	206580041	chaperone protein DnaK [Klebsiella pneun	62.89	2.35%	1	1	638	69.1	4.97
10	6.3	26245936	molecular chaperone DnaK [Escherichia cc	62.89	2.35%	1	1	638	69.1	4.97
11	7	334122625	formate acetyltransferase [Enterobacter h	236.46	10.39%	5	6	760	85	6.09
12	8	334122578	outer membrane protein A [Enterobacter	105.67	5.59%	2	3	358	38.3	5.24
13	9	206577432	formate acetyltransferase [Klebsiella pneu	182.41	8.03%	4	5	760	85.2	5.85
14	10.1	206577586	alkyl hydroperoxide reductase subunit C [I	117.43	17.11%	3	3	187	20.8	5.17
15	10.2	334122926	alkyl hydroperoxide reductase C [Enteroba	117.43	15.92%	3	3	201	22.4	5.02
16	10.3	26246586	alkyl hydroperoxide reductase subunit C [I	117.43	17.11%	3	3	187	20.7	5.17
17	11	206576800	antioxidant, AhpC/TSA family [Klebsiella pi	68.79	7.00%	1	1	200	22.3	5.29
18	12.1	206576843	pyruvate dehydrogenase (acetyl-transferri	86.71	1.92%	1	2	887	99.5	5.64
19	12.2	334123432	pyruvate decarboxylase, E1 component of	86.71	1.92%	1	2	887	99.6	5.69
20	12.3	26246055	pyruvate dehydrogenase subunit E1 [Eschi	86.71	1.92%	1	2	887	99.6	5.68
21	13.1	206580695	DNA-binding protein HU, alpha subunit [KI	62.94	16.67%	1	1	90	9.5	9.58
22	13.2	334123929	DNA-binding protein HU-beta [Enterobact	62.94	16.67%	1	1	90	9.5	9.58
23	14.1	197285345	bifunctional acetaldehyde-CoA/alcohol de	87.63	2.14%	1	1	887	96.2	6.38
24	14.2	334124374	aldehyde-alcohol dehydrogenase [Enterob	87.63	2.07%	1	1	920	99.1	6.81
25	14.3	206580610	aldehyde-alcohol dehydrogenase [Klebsiel	87.63	2.13%	1	1	891	95.9	6.79
26	14.4	26247570	bifunctional acetaldehyde-CoA/alcohol de	87.63	2.13%	1	1	891	96.1	6.79
27	15	197286390	60 kDa chaperonin [Proteus mirabilis HI43	158.69	8.39%	2	4	548	57.6	4.89
28	16.1	197286616	50S ribosomal protein L10 [Proteus mirabi	104.53	7.88%	1	2	165	17.6	8.68
29	16.2	334123947	50S ribosomal protein L10 [Enterobacter h	104.53	7.88%	1	2	165	17.8	8.98
30	16.3	206577086	ribosomal protein L10 [Klebsiella pneumoi	104.53	7.88%	1	2	165	17.8	8.98
31	16.4	26250755	50S ribosomal protein L10 [Escherichia col	104.53	7.88%	1	2	165	17.7	8.98
32	17.1	197286887	FOF1 ATP synthase subunit alpha [Proteus	227.1	2.53%	1	3	513	55.5	5.69
33	17.2	334121921	ATP synthase F1 sector alpha subunit [Ent	227.1	2.53%	1	3	513	55.3	6.13
34	17.3	206580919	ATP synthase F1, alpha subunit [Klebsiella	227.1	2.53%	1	3	513	55.1	6
35	17.4	26250478	FOF1 ATP synthase subunit alpha [Escheric	227.1	2.53%	1	3	513	55.2	6.13
36	18.1	197287068	50S ribosomal protein L3 [Proteus mirabili	84.35	9.09%	1	2	209	22.5	9.86
37	18.2	334125923	50S ribosomal protein L3 [Enterobacter hc	84.35	9.09%	1	2	209	22.2	9.82
38	18.3	206576036	ribosomal protein L3 [Klebsiella pneumoni	84.35	9.09%	1	2	209	22.2	9.91
39	18.4	26249915	50S ribosomal protein L3 [Escherichia coli	84.35	9.09%	1	2	209	22.2	9.91
40	19.1	197287127	transcription termination factor Rho [Prot	87.39	5.25%	1	1	419	46.9	7.25
41	19.2	334126167	transcription termination factor Rho [Ente	87.39	5.25%	1	1	419	47	7.25
42	19.3	206576949	transcription termination factor Rho [Kleb	87.39	5.25%	1	1	419	47	7.25
43	19.4	26250521	transcription termination factor Rho [Esch	87.39	4.97%	1	1	443	49.6	7.3
44	20.1	161486147	autonomous glycyl radical cofactor GrcA [I	244.8	16.54%	1	3	127	14.3	5.17
45	20.2	206580560	autonomous glycyl radical cofactor [Klebsi	244.8	16.54%	1	3	127	14.2	5.02
46	21	26249182	phosphopyruvate hydratase [Escherichia c	227.61	13.19%	3	4	432	45.6	5.48
47	22	P35579	Myosin-9 n=67 Tax=Tetrapoda RepID=MYI	185.28	2.45%	3	4	1960	226.4	5.6
48	23	P15924	Desmoplakin n=28 Tax=Mammalia RepID=	76.4	0.45%	1	1	2871	331.6	6.81
49	24	P04264	Keratin, type II cytoskeletal 1 n=7 Tax=Euti	1746.82	28.11%	14	35	644	66	8.12
50	25	P35527	Keratin, type I cytoskeletal 9 n=4 Tax=Cata	96.6	6.42%	2	3	623	62	5.24
51	26	P13645	Keratin, type I cytoskeletal 10 n=12 Tax=Et	240.51	15.41%	6	7	584	58.8	5.21
52	27	P02533	Keratin, type I cytoskeletal 14 n=8 Tax=Eut	317.41	11.23%	5	10	472	51.5	5.16
53	28	Q7RTS7	Keratin, type II cytoskeletal 74 n=7 Tax=Sir	373.36	6.81%	3	14	529	57.8	7.71
54	29	P06702	Protein S100-A9 n=5 Tax=Hominoidea Rep	121.49	24.56%	2	3	114	13.2	6.13
55	30	O60437	Periplakin n=3 Tax=Hominoidea RepID=PE	126.93	1.99%	2	2	1756	204.6	5.6
56	31	P62937	Peptidyl-prolyl cis-trans isomerase A n=98	108.16	9.09%	1	2	165	18	7.81
57	32.1	E9PFJ3	Uncharacterized protein n=3 Tax=Simiiforr	235.29	5.02%	2	4	578	63.3	5.31
58	32.2	P07911	Uromodulin n=2 Tax=Catarrhini RepID=UR	235.29	4.53%	2	4	640	69.7	5.24
59	33	A4FU1	GUCA1B protein (Fragment) n=1 Tax=Hom	1314.14	58.67%	3	24	75	8.6	5.41
60	34	P13646	Keratin, type I cytoskeletal 13 n=13 Tax=Si	2129.98	34.06%	12	55	458	49.6	4.96
61	35.1	B4DRW1	cDNA FLJ55805, highly similar to Keratin, t	1113.26	24.05%	11	33	474	51.7	6.81
62	35.2	P19013	Keratin, type II cytoskeletal 4 n=14 Tax=Sir	1113.26	21.35%	11	33	534	57.2	6.61
63	36	F6RMN8	Uncharacterized protein n=4 Tax=Simiiforr	607.51	13.46%	7	23	535	57.8	8.22

index	Prot_hit	Accession	Description	Score	Coverage	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pI
64	37.1	P06899	Histone H2B type 1-J n=102 Tax=Euteleost	98.7	11.90%	1	1	126	13.9	10.32
65	37.2	P62807	Histone H2B type 1-C/E/F/G/I n=44 Tax=Eu	98.7	11.90%	1	1	126	13.9	10.32
66	37.3	B4DR52	Histone H2B n=5 Tax=Euarchoptoglyres Re	98.7	9.04%	1	1	166	18	10.32
67	37.4	P58876	Histone H2B type 1-D n=136 Tax=Coeloma	98.7	11.90%	1	1	126	13.9	10.32
68	38.1	UPI0000D48568	UPI0000D48568 related cluster n=1 Tax=H	116.71	13.98%	2	3	186	20.4	9.06
69	38.2	P04792	Heat shock protein beta-1 n=6 Tax=Simiifc	116.71	12.68%	2	3	205	22.8	6.4
70	39.1	A8MX94	Uncharacterized protein n=1 Tax=Homo s	132.02	9.20%	1	1	174	19.5	5.97
71	39.2	P09211	Glutathione S-transferase P n=4 Tax=Simii	132.02	7.62%	1	1	210	23.3	5.64
72	40.1	E7EU87	Uncharacterized protein n=3 Tax=Simiifor	422.23	7.03%	4	17	555	58.9	5.97
73	40.2	P13647	Keratin, type II cytoskeletal 5 n=17 Tax=Eu	422.23	6.61%	4	17	590	62.3	7.74
74	41	P04083	Annexin A1 n=14 Tax=Eutheria RepID=AN	939.97	27.75%	8	19	346	38.7	7.02
75	42.1	Q7KZ86	Plakoglobin (Fragment) n=1 Tax=Homo sa	48.53	9.94%	1	1	171	18.8	8.85
76	42.2	P14923	Junction plakoglobin n=31 Tax=Theria Rep	48.53	2.28%	1	1	745	81.7	6.14
77	43.1	B4DVJ0	Glucose-6-phosphate isomerase n=2 Tax=	75.31	3.20%	1	1	531	60	8.65
78	43.2	B4DG39	Glucose-6-phosphate isomerase n=5 Tax=	75.31	2.99%	1	1	569	64.3	8.91
79	43.3	P06744	Glucose-6-phosphate isomerase n=17 Tax	75.31	3.05%	1	1	558	63.1	8.32
80	44	Q9UBG3	Cornulin n=6 Tax=Catarrhini RepID=CRNN	59.98	3.23%	1	1	495	53.5	6.1
81	45.1	Q96GV1	Enolase (Fragment) n=2 Tax=Eutheria Rep	123.98	6.52%	1	3	184	20.4	7.03
82	45.2	P06733	Alpha-enolase n=53 Tax=Euteleostomi Rep	123.98	2.76%	1	3	434	47.1	7.39

Sequence	Protein Descriptions	# Proteins	# Protein Groups	Protein Group Accessions	Modifications	q-Value	PEP	Charge	m/z [Da]	MH+ [Da]	Delta Mass [Da]
RVLEALQQAEEELAR	cDNA FLJ55805, highly similar to Keratin, type II cytoske	2	1	B4DRW1		0	4.09E-13	2	977.91992	1954.83257	0.38
ELLSQYDFPGDDTPIVR	translation elongation factor Tu [Enterobacter hormae	2	1	334126439		0	2.39E-08	2	983.00964	1965.01201	0.03
LDSELKNMQDMVEDYR	Keratin, type II cytoskeletal 1 n=7 Tax=Eutheria RepID=	1	1	P04264		0	2.40E-06	2	993.95605	1986.90483	0.51
THNLEPYFESFINLR	Keratin, type II cytoskeletal 1 n=7 Tax=Eutheria RepID=	1	1	P04264		0	7.73E-07	2	997.97949	1994.95171	0.49
EIELEDKFNMGAAQMVK	chaperone GroEL [Enterobacter hormaechei ATCC 491f	2	2	334123809;197286390		0	2.41E-07	2	1006.45813	2011.90898	0.48
ILINTPASGGGIGDLYNFK	bifunctional acetaldehyde-CoA/alcohol dehydrogenase	4	1	197285345		0	5.75E-14	2	1011.48279	2021.9583	0.44
DWILQIESVREEGVGR	pyruvate dehydrogenase (acetyl-transferring), homodir	3	1	206576843		0	1.92E-06	3	677.44177	2030.31076	0.43
AMAGLQPLQPEELDAMIR	Calmodulin-like protein 5 n=4 Tax=Hominidae RepID=C	1	1	Q9NZ11		0	0.00011	2	1020.89868	2040.79009	0.38
SAELNKEVSTNTAMIQTSK	GUCA1B protein (Fragment) n=1 Tax=Homo sapiens Re	2	2	A4FUAI,P13646		0	2.29E-11	2	1026.96497	2052.92266	0.45
VLDEKLLVLEADAAIAK	Periplakin n=3 Tax=Hominoidea RepID=PEPL_HUMAN	1	1	O60437		0	1.53E-06	2	1031.72595	2062.44463	0.65
GDRSEDFGVNEDLADSDAR	Annexin A1 n=14 Tax=Eutheria RepID=ANXA1_HUMAN	1	1	P04083		0	3.28E-12	2	1034.8761	2068.74492	0.43
SAELNKEVSTNTAMIQTSK	GUCA1B protein (Fragment) n=1 Tax=Homo sapiens Re	2	2	A4FUAI,P13646	M14(Oxidation)	0	2.44E-11	2	1035.03198	2069.05669	0.52
VLGDKIQLVGGDLVFNNTK	phosphopyruvate hydratase [Escherichia coli CFT073]	1	1	26249182		0	2.75E-06	2	1038.73987	2076.47246	0.67
SGETEDATIADLAVGTAAGQIK	phosphopyruvate hydratase [Escherichia coli CFT073]	1	1	26249182		0	1.36E-09	2	1060.07532	2119.14336	0.54
FNNFINDSLEGAVDALER	6,7-dimethyl-8-ribityllumazine synthase [Proteus mirab	1	1	197283995		0	0.0811	3	713.28564	2137.84238	0.26
QAWFIEEEQYVQTVK	Annexin A1 n=14 Tax=Eutheria RepID=ANXA1_HUMAN	1	1	P04083		0	3.17E-10	2	1071.49963	2141.99199	0.49
NKLNDELALQQAEDLAR	Keratin, type II cytoskeletal 1 n=7 Tax=Eutheria RepID=	1	1	P04264		0	5.23E-13	2	1092.97839	2184.94951	0.41
NVTPYEGDESFLAGADATTK	formate acetyltransferase [Enterobacter hormaechei A'	1	1	334122625		0	1.27E-13	2	1126.57434	2252.14141	0.57
NVVLDKSGFAPITTKDGVSVAR	chaperone GroEL [Enterobacter hormaechei ATCC 491f	1	1	334123809		0	4.53E-09	3	759.16864	2275.49137	0.42
AEAESYQSQYEELQITAGR	Keratin, type II cytoskeletal 1 n=7 Tax=Eutheria RepID=	1	1	P04264		0	2.56E-09	2	1144.06421	2287.12114	0.5
TDLEMQIESLNEELAYMKK	Keratin, type I cytoskeletal 13 n=13 Tax=Simiiformes Re	1	1	P13646		0	2.76E-06	3	762.80658	2286.40519	0.43
EMLLDAMENPEKYPQLTIR	formate acetyltransferase [Klebsiella pneumoniae 342]	1	1	206577432		0	2.14E-06	2	1146.54163	2292.07598	0.47
AANDLLNSFWLLEDSEKGEAR	autonomous glycol radical cofactor GrCA [Escherichia ct	2	1	161486147		0	2.27E-11	2	1183.07288	2365.13848	0.5
GGGGGGYSGSGSSYSGGGYSGGGGGGGGR	Keratin, type II cytoskeletal 1 n=7 Tax=Eutheria RepID=	1	1	P04264		0	1.70E-17	2	1192.90918	2384.81108	0.43
SGEDIFGGVLEILQDGFGLR	transcription termination factor Rho [Proteus mirabilis	4	1	197287127		0	1.03E-10	2	1192.9939	2384.98052	0.4
VVINKDITTIIDGVGEEAAIQGR	chaperone GroEL [Enterobacter hormaechei ATCC 491f	1	1	334123809		0	2.75E-12	2	1200.57678	2400.14629	0.43
NLDLSIAEVAQYEEIAQR	Uncharacterized protein n=4 Tax=Simiiformes RepID=Fi	1	1	F6RMN8		0	1.48E-10	2	1210.02209	2419.03691	0.39
RKAEAESLYQSKYELQITAGR	Keratin, type II cytoskeletal 1 n=7 Tax=Eutheria RepID=	1	1	P04264		0	5.86E-11	2	1251.42273	2501.83818	0.29
RVVINKDITTIIDGVGEEAAIQGR	chaperone GroEL [Enterobacter hormaechei ATCC 491f	1	1	334123809		0	4.54E-09	3	852.92786	2556.76902	0.46
VDQLSNDVNmRSDVQAAKDDAAR	major outer membrane lipoprotein [Escherichia coli CF	2	1	26247927	M11(Oxidation)	0	0.000798	3	869.52112	2606.5488	0.44
TLTIADNGIMNRDEVIDHLGTIAK	chaperone HtpG [Enterobacter hormaechei ATCC 491f.	1	1	334123123		0	0.0115	3	890.22485	2668.66001	0.43
NYSPPYNTIDDLQDQIVDLTVGNKK	Keratin, type I cytoskeletal 9 n=4 Tax=Catarrhini RepID=	1	1	P35527		0	5.38E-06	3	968.46912	2903.3928	0.33
NLDLSIAEVAQYEEIAQR	chaperone GroEL [Enterobacter hormaechei ATCC 491f	1	1	334123809		0	3.53E-06	3	973.11487	2917.33005	0.27
AIAQGVGISANSDETGTIAQAmEKVKG	60 Kda chaperonin [Proteus mirabilis HI4320]	1	1	197286390	M24(Oxidation)	0	0.0872	3	973.41028	2918.21628	-0.1
TIDDLKNQILNLTDMANILLQDANAR	Keratin, type I cytoskeletal 10 n=12 Tax=Eutheria RepID	1	1	P13645		0	1.52E-10	3	1018.59094	3053.75827	0.38
VGKGVITVEDGTGLDELDVVEGMQFDR	chaperone GroEL [Enterobacter hormaechei ATCC 491f	1	1	334123809		0	2.19E-10	3	1046.57861	3137.72129	0.41
VLELDSKTDLEmQIESLNEELAYMKK	Keratin, type I cytoskeletal 13 n=13 Tax=Simiiformes Re	1	1	P13646	M14(Oxidation)	0	2.25E-13	3	1101.00439	3300.99863	0.45
AGEGNYNAATEEYGNMIDFGILDPTKVTR	chaperone GroEL [Enterobacter hormaechei ATCC 491f	1	1	334123809		0	1.75E-13	3	1123.30396	3367.89731	0.45

2DLCSCI_39 Protein Summary

index	Prot_hit	Accession	Description	Mascot Score	Coverage	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pI
1	1.1	206579217	ribosomal protein L2 [Klebsiella pneumo	96.33	8.06%	2	2	273	29.8	10.93
2	1.2	334125920	50S ribosomal protein L2 [Enterobacter	96.33	8.06%	2	2	273	29.8	10.93
3	2.1	206578965	ribosomal protein L29 [Klebsiella pneumo	95.74	34.92%	2	2	63	7.2	10.27
4	2.2	334125915	50S ribosomal protein L29 [Enterobacter	95.74	34.92%	2	2	63	7.2	10.59
5	3	206577508	outer membrane protein A [Klebsiella pr	208.59	7.43%	2	5	350	37.4	6.25
6	4.1	206580559	ribosomal protein S1 [Klebsiella pneumo	235.33	10.41%	3	4	557	61.1	4.98
7	4.2	334122618	30S ribosomal protein S1 [Enterobacter	235.33	10.41%	3	4	557	61.2	4.98
8	4.3	26246936	30S ribosomal protein S1 [Escherichia cc	235.33	10.41%	3	4	557	61.1	4.98
9	5.1	206577586	alkyl hydroperoxide reductase subunit C	82.84	8.56%	1	1	187	20.8	5.17
10	5.2	334122926	alkyl hydroperoxide reductase C [Entero	82.84	7.96%	1	1	201	22.4	5.02
11	5.3	26246586	alkyl hydroperoxide reductase subunit C	82.84	8.56%	1	1	187	20.7	5.17
12	6.1	206575727	trigger factor [Klebsiella pneumoniae 34	81.04	6.25%	2	2	432	48	4.89
13	6.2	334123168	trigger factor [Enterobacter hormaechei	81.04	6.25%	2	2	432	48.1	4.87
14	6.3	26246446	trigger factor [Escherichia coli CFT073]	81.04	6.25%	2	2	432	48.2	4.86
15	7	206577504	ribosomal protein L9 [Klebsiella pneumo	117.33	20.13%	2	5	149	15.7	6.58
16	8	206579361	ribosomal protein S6 [Klebsiella pneumo	302.23	35.11%	4	7	131	15.1	5.38
17	9	206581075	translation elongation factor Tu [Klebsie	381.16	16.50%	4	8	394	43.2	5.53
18	10.1	197287068	50S ribosomal protein L3 [Proteus mirab	260.45	9.09%	2	6	209	22.5	9.86
19	10.2	334125923	50S ribosomal protein L3 [Enterobacter	260.45	9.09%	2	6	209	22.2	9.82
20	10.3	206576036	ribosomal protein L3 [Klebsiella pneumo	260.45	9.09%	2	6	209	22.2	9.91
21	10.4	26249915	50S ribosomal protein L3 [Escherichia cc	260.45	9.09%	2	6	209	22.2	9.91
22	11.1	197287073	50S ribosomal protein L22 [Proteus mira	73.54	22.73%	1	1	110	12.1	10.18
23	11.2	334125918	50S ribosomal protein L22 [Enterobacter	73.54	22.73%	1	1	110	12.2	10.18
24	12.1	197287127	transcription termination factor Rho [Pri	98.47	5.25%	1	1	419	46.9	7.25
25	12.2	334126167	transcription termination factor Rho [En	98.47	5.25%	1	1	419	47	7.25
26	12.3	206576949	transcription termination factor Rho [Kle	98.47	5.25%	1	1	419	47	7.25
27	12.4	26250521	transcription termination factor Rho [Esi	98.47	4.97%	1	1	443	49.6	7.3
28	13.1	26247927	major outer membrane lipoprotein [Escl	182.06	30.77%	2	4	78	8.3	9.25
29	13.2	334122238	major outer membrane lipoprotein [Ent	182.06	30.77%	2	4	78	8.4	9.31
30	14	161486111	ATP-dependent RNA helicase DeaD [Escl	89.92	2.70%	1	1	629	70.5	8.72
31	15.1	26249880	DNA-directed RNA polymerase subunit ε	68.74	7.29%	1	1	329	36.5	5.06
32	15.2	334125900	DNA-directed RNA polymerase subunit ε	68.74	7.29%	1	1	329	36.4	5.06
33	16	P04264	Keratin, type II cytoskeletal 1 n=7 Tax=El	108.01	4.81%	1	1	644	66	8.12
34	17.1	P08727	Keratin, type I cytoskeletal 19 n=9 Tax=E	209.23	8.75%	2	3	400	44.1	5.14
35	17.2	B4DE59	cDNA FLJ60424, highly similar to Junctio	209.23	6.22%	2	3	563	62.6	5.17
36	18	O60437	Periplakin n=3 Tax=Hominoidea RepID=I	82.43	0.85%	1	1	1756	204.6	5.6
37	19.1	E9PFJ3	Uncharacterized protein n=3 Tax=Simiifc	101.07	2.77%	1	1	578	63.3	5.31
38	19.2	P07911	Uromodulin n=2 Tax=Catarrhini RepID=L	101.07	2.50%	1	1	640	69.7	5.24
39	19.3	Q5R5C1	Uromodulin n=8 Tax=Simiiformes RepID	101.07	2.50%	1	1	641	69.8	5.24
40	20	A4FUA1	GUCA1B protein (Fragment) n=1 Tax=Hc	475.45	58.67%	3	8	75	8.6	5.41
41	21.1	P13646-3	Isoform 3 of Keratin, type I cytoskeletal	685.04	22.86%	8	21	420	45.8	4.88
42	21.2	P13646	Keratin, type I cytoskeletal 13 n=13 Tax=	685.04	20.96%	8	21	458	49.6	4.96
43	22.1	B4DRW1	cDNA FLJ55805, highly similar to Keratin	570.84	20.46%	8	17	474	51.7	6.81
44	22.2	P19013	Keratin, type II cytoskeletal 4 n=14 Tax=!	570.84	18.16%	8	17	534	57.2	6.61
45	23.1	E7EUE8	Uncharacterized protein n=14 Tax=Euthi	622.1	16.54%	8	20	520	55.8	6.27
46	23.2	P02538	Keratin, type II cytoskeletal 6A n=25 Tax	622.1	15.25%	8	20	564	60	8
47	24.1	C9JZN1	Uncharacterized protein n=5 Tax=Catarr	84.39	11.84%	2	3	152	17	9.13
48	24.2	P62879	Guanine nucleotide-binding protein G(I)	84.39	5.29%	2	3	340	37.3	6
49	25	P04792	Heat shock protein beta-1 n=6 Tax=Simi	92.57	16.10%	2	2	205	22.8	6.4
50	26.1	E7EU87	Uncharacterized protein n=3 Tax=Simiifc	414.57	8.47%	4	11	555	58.9	5.97
51	26.2	P13647	Keratin, type II cytoskeletal 5 n=17 Tax=!	414.57	7.97%	4	11	590	62.3	7.74
52	27	P04083	Annexin A1 n=14 Tax=Eutheria RepID=A	688.06	31.79%	8	13	346	38.7	7.02
53	28.1	Q96KK5	Histone H2A type 1-H n=10 Tax=Mamm	79.38	14.06%	2	2	128	13.9	10.89
54	28.2	P0C0S8	Histone H2A type 1 n=295 Tax=Eukaryot	79.38	13.85%	2	2	130	14.1	10.9
55	28.3	Q16777	Histone H2A type 2-C n=33 Tax=Eumeta.	79.38	13.95%	2	2	129	14	10.9
56	28.4	C9JE22	Histone H2A n=7 Tax=Eutheria RepID=C!	79.38	11.92%	2	2	151	16.1	10.23
57	28.5	Q99878	Histone H2A type 1-J n=4 Tax=Eutheria F	79.38	14.06%	2	2	128	13.9	10.89
58	29	Q9UBG3	Cornulin n=6 Tax=Catarrhini RepID=CRN	125.62	3.23%	1	2	495	53.5	6.1

2DLCSCI_33 Protein Summary

index	Prot_hit	Accession	Description	Mascot Score	Coverage	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pI
1	1	P35579	Myosin-9 n=67 Tax=Tetrapoda	442.23	4.29%	6	9	1960	226.4	5.6
2	2	P06702	Protein S100-A9 n=5 Tax=Homi	233.47	31.58%	2	4	114	13.2	6.13

ZDLCS1_33 Peptide Summary

Sequence	Protein Descriptions	# Proteins	# Protein Groups	Protein Group Accessions	Modifications	q-Value	PEP	Charge	m/z [Da]	MH+ [Da]	Delta Mass [Da]
RDLGEELEALK	Myosin-9 n=67 Tax=Tetrapoda ReplD=MYH9	1	1	P35579		0	0.291	2	637.50842	1274.00957	0.67
DSTIQVVENGESSQGR	Uncharacterized protein n=3 Tax=Simiiforme	3	1	E9PFJ3		0	0.257	2	853.94507	1706.88286	0.54
sELDQLRQEAELK	Guanine nucleotide-binding protein G(I)/G(S)	1	1	P62873	N-Term(Acetyl)	0	0.0768	2	865.35803	1729.70879	0.42
VIEHIMEDLDTNADK	Protein S100-A9 n=5 Tax=Hominoidea ReplD	1	1	P06702		0	0.058	2	872.52966	1744.05205	0.61
TELEDTLDTAAQQLR	Myosin-9 n=67 Tax=Tetrapoda ReplD=MYH9	1	1	P35579		0	0.0111	2	960.93542	1920.86357	0.47
ELESQISELQEDLESER	Myosin-9 n=67 Tax=Tetrapoda ReplD=MYH9	1	1	P35579		0	0.00751	2	1017.77063	2034.53398	0.29
TLEEEAKTHEAQIQEMR	Myosin-9 n=67 Tax=Tetrapoda ReplD=MYH9	1	1	P35579		0	0.0186	2	1022.62573	2044.24419	0.63
GDRSEDFGVNEDLADSDAR	cDNA FLJ51887, highly similar to Annexin A1	2	1	B4DL19		0	0.00602	2	1035.06653	2069.12578	0.62
MHEGDEGPGHHHKPGLGEGTP	Protein S100-A9 n=5 Tax=Hominoidea ReplD	1	1	P06702		0	0.0351	2	1088.93066	2176.85405	0.45
NKLNLEDALQQAKEDLAR	Keratin, type II cytoskeletal 1 n=7 Tax=Euthe	1	1	P04264		0	0.0397	3	728.8902	2184.65604	0.18
MQQNIQELEELEEEESAR	Myosin-9 n=67 Tax=Tetrapoda ReplD=MYH9	1	1	P35579		0	0.0201	2	1167.60022	2334.19316	0.57
KMQQNIQELEELEEEESARQK	Myosin-9 n=67 Tax=Tetrapoda ReplD=MYH9	1	1	P35579		0	0.0304	3	906.82544	2718.46177	0.39

2DLCSCI 51 Protein Summary

index	Prot_hit	Accession	Description	Mascot Score	Coverage	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pI
1	1.1	334126439	translation elongation factor Tu [Enterobacter hormaechei ATCC 49619]	423.76	17.55%	4	10	376	41.1	5.24
2	1.2	161486096	elongation factor Tu [Escherichia coli CFT073]	423.76	16.75%	4	10	394	43.3	5.45
3	1.3	26250749	elongation factor Tu [Escherichia coli CFT073]	423.76	16.75%	4	10	394	43.3	5.45
4	2.1	334125906	30S ribosomal protein S5 [Enterobacter hormaechei ATCC 4916]	354.27	19.88%	2	6	166	17.5	10.05
5	2.2	206580716	ribosomal protein S5 [Klebsiella pneumoniae 342]	354.27	19.76%	2	6	167	17.6	10.11
6	3.1	334124951	phosphate acetyltransferase [Enterobacter hormaechei ATCC 49619]	161.45	4.49%	2	3	713	77	5.48
7	3.2	206580523	phosphate acetyltransferase [Klebsiella pneumoniae 342]	161.45	4.48%	2	3	715	77.2	5.47
8	3.3	26248686	phosphate acetyltransferase [Escherichia coli CFT073]	161.45	4.48%	2	3	714	77.2	5.41
9	4.1	334124672	flagellin [Enterobacter hormaechei ATCC 49162]	561.9	8.44%	3	8	569	58.3	4.92
10	4.2	334125162	bacterial flagellin subfamily protein [Enterobacter hormaechei ATCC 49162]	561.9	7.15%	3	8	671	68.4	4.84
11	5	334123809	chaperone GroEL [Enterobacter hormaechei ATCC 49162]	1441.12	35.95%	11	28	548	57.1	4.94
12	6.1	334123523	chaperone DnaK [Enterobacter hormaechei ATCC 49162]	110.62	4.40%	2	2	637	69.1	4.96
13	6.2	206580041	chaperone protein DnaK [Klebsiella pneumoniae 342]	110.62	4.39%	2	2	638	69.1	4.97
14	6.3	26245936	molecular chaperone DnaK [Escherichia coli CFT073]	110.62	4.39%	2	2	638	69.1	4.97
15	7	334123429	dihydrolypoyl dehydrogenase [Enterobacter hormaechei ATCC 49619]	273.02	13.68%	3	6	475	50.7	6.16
16	8	334122958	ferrienterobactin receptor [Enterobacter hormaechei ATCC 49162]	312.97	10.46%	4	9	746	82.6	5.67
17	9	334122625	formate acetyltransferase [Enterobacter hormaechei ATCC 49162]	194.6	8.95%	4	6	760	85	6.09
18	10.1	206580744	ribosomal protein S3 [Klebsiella pneumoniae 342]	201.74	5.17%	1	3	232	25.8	10.3
19	10.2	334125917	30S ribosomal protein S3 [Enterobacter hormaechei ATCC 49162]	201.74	5.15%	1	3	233	26	10.27
20	10.3	197287074	30S ribosomal protein S3 [Proteus mirabilis HI4320]	201.74	5.15%	1	3	233	25.9	10.21
21	11.1	206579163	ribosomal protein L5 [Klebsiella pneumoniae 342]	84.35	8.38%	1	1	179	20.3	9.39
22	11.2	334125911	50S ribosomal protein L5 [Enterobacter hormaechei ATCC 49162]	84.35	8.38%	1	1	179	20.3	9.39
23	11.3	26249896	50S ribosomal protein L5 [Escherichia coli CFT073]	84.35	8.38%	1	1	179	20.3	9.48
24	12.1	206579040	polyribonucleotide nucleotidyltransferase [Klebsiella pneumoniae 342]	291.6	3.94%	2	4	711	76.8	5.17
25	12.2	334125777	polyribonucleotide nucleotidyltransferase [Enterobacter hormaechei ATCC 49162]	291.6	3.93%	2	4	712	77	5.19
26	12.3	26249747	polynucleotide phosphorylase/polyadenylase [Escherichia coli CFT073]	291.6	3.78%	2	4	740	80.5	5.54
27	13.1	206576322	colicin I receptor [Klebsiella pneumoniae 342]	86	3.35%	2	2	657	73.1	5.41
28	13.2	229106376	colicin I receptor [Escherichia coli CFT073]	86	3.32%	2	2	663	73.8	5.29
29	14.1	206580341	threonyl-tRNA synthetase [Klebsiella pneumoniae 342]	66.54	2.02%	1	1	642	73.9	6.23
30	14.2	26247970	threonyl-tRNA synthetase [Escherichia coli CFT073]	66.54	2.02%	1	1	642	74	6.19
31	15	206577432	formate acetyltransferase [Klebsiella pneumoniae 342]	174.34	7.89%	4	5	760	85.2	5.85
32	16.1	206580931	fimbrillin MatB [Klebsiella pneumoniae 342]	146.23	9.23%	1	2	195	20	4.88
33	16.2	26246302	hypothetical protein c0404 [Escherichia coli CFT073]	146.23	9.23%	1	2	195	20.1	4.88
34	17.1	206577768	dihydrolypoyllysine-residue acetyltransferase [Klebsiella pneumoniae 342]	169.35	8.89%	3	4	630	65.7	5.31
35	17.2	334123431	pyruvate dehydrogenase complex E2, dihydroliipoamide acetyltransferase [Klebsiella pneumoniae 342]	169.35	8.85%	3	4	633	65.9	5.15
36	18.1	206578905	DNA-directed RNA polymerase, beta' subunit [Klebsiella pneumoniae 342]	219.1	4.76%	4	5	1407	155.3	6.8
37	18.2	26250759	DNA-directed RNA polymerase subunit beta' [Escherichia coli CFT073]	219.1	4.76%	4	5	1407	155.1	7.08
38	19.2	206579488	DNA-directed RNA polymerase, beta subunit [Klebsiella pneumoniae 342]	291.18	5.96%	4	6	1342	150.4	5.29
39	19.2	334123945	DNA-directed RNA polymerase subunit beta [Enterobacter hormaechei ATCC 49162]	291.18	5.91%	4	6	1353	151.6	5.27
40	19.3	26250758	DNA-directed RNA polymerase subunit beta [Escherichia coli CFT073]	291.18	5.91%	4	6	1353	151.8	5.27
41	20.1	206577086	ribosomal protein L10 [Klebsiella pneumoniae 342]	215.36	29.09%	3	5	165	17.8	8.98
42	20.2	334123947	50S ribosomal protein L10 [Enterobacter hormaechei ATCC 49162]	215.36	29.09%	3	5	165	17.8	8.98
43	20.3	26250755	50S ribosomal protein L10 [Escherichia coli CFT073]	215.36	29.09%	3	5	165	17.7	8.98
44	21.1	206577888	ribosomal protein L11 [Klebsiella pneumoniae 342]	138.7	9.86%	1	2	142	14.9	9.63
45	21.2	26250753	50S ribosomal protein L11 [Escherichia coli CFT073]	138.7	9.86%	1	2	142	14.9	9.63
46	22.1	206580919	ATP synthase F1, alpha subunit [Klebsiella pneumoniae 342]	229.87	9.16%	3	6	513	55.1	6
47	22.2	26250478	F0F1 ATP synthase subunit alpha [Escherichia coli CFT073]	229.87	9.16%	3	6	513	55.2	6.13
48	23	197286390	60 Kda chaperonin [Proteus mirabilis HI4320]	276.5	12.59%	4	7	548	57.6	4.89
49	24.1	197286835	glutamate dehydrogenase [Proteus mirabilis HI4320]	114.74	4.48%	1	1	446	48.4	7.03
50	24.2	334122327	glutamate dehydrogenase [Enterobacter hormaechei ATCC 49162]	114.74	4.47%	1	1	447	48.3	6.62
51	24.3	206577927	NADP-specific glutamate dehydrogenase [Klebsiella pneumoniae 342]	114.74	4.47%	1	1	447	48.5	7.01
52	24.4	26248016	glutamate dehydrogenase [Escherichia coli CFT073]	114.74	4.47%	1	1	447	48.5	6.4
53	25.1	197287068	50S ribosomal protein L3 [Proteus mirabilis HI4320]	79.69	9.09%	1	1	209	22.5	9.86
54	25.2	334125923	50S ribosomal protein L3 [Enterobacter hormaechei ATCC 49162]	79.69	9.09%	1	1	209	22.2	9.82
55	25.3	206576036	ribosomal protein L3 [Klebsiella pneumoniae 342]	79.69	9.09%	1	1	209	22.2	9.91
56	25.4	26249915	50S ribosomal protein L3 [Escherichia coli CFT073]	79.69	9.09%	1	1	209	22.2	9.91
57	26.1	197287076	50S ribosomal protein L29 [Proteus mirabilis HI4320]	157.97	25.40%	1	2	63	7.3	10.27
58	26.2	26249901	50S ribosomal protein L29 [Escherichia coli CFT073]	157.97	25.40%	1	2	63	7.3	9.99
59	27.1	197287093	DNA-directed RNA polymerase subunit alpha [Proteus mirabilis HI4320]	97	8.21%	2	2	329	36.5	5.11
60	27.2	334125900	DNA-directed RNA polymerase subunit alpha [Enterobacter hormaechei ATCC 49162]	97	8.21%	2	2	329	36.4	5.06
61	27.3	26249880	DNA-directed RNA polymerase subunit alpha [Escherichia coli CFT073]	97	8.21%	2	2	329	36.5	5.06
62	28.1	197287189	50S ribosomal protein L9 [Proteus mirabilis HI4320]	106.9	9.40%	1	2	149	15.8	6.32
63	28.2	334123750	5-methyltetrahydropteroyltryptophan--homocysteine S-methyltransferase [Klebsiella pneumoniae 342]	106.9	9.40%	1	2	149	15.6	7.42
64	28.3	206577504	ribosomal protein L9 [Klebsiella pneumoniae 342]	106.9	9.40%	1	2	149	15.7	6.58
65	28.4	26251101	50S ribosomal protein L9 [Escherichia coli CFT073]	106.9	9.40%	1	2	149	15.8	6.58
66	29.1	197287224	cell division protein [Proteus mirabilis HI4320]	79.43	2.17%	1	1	646	70.9	5.83
67	29.2	334125787	ATP-dependent metalloproteinase HflB [Enterobacter hormaechei ATCC 49162]	79.43	2.16%	1	1	647	71	6.11
68	29.3	206578792	ATP-dependent metalloproteinase HflB [Klebsiella pneumoniae 342]	79.43	2.16%	1	1	647	71.1	6.11
69	30	15596155	porin [Pseudomonas aeruginosa PAO1]	181.37	4.06%	1	4	443	48.3	5.16
70	31	15596170	peptidoglycan associated lipoprotein OprL precursor [Pseudomonas aeruginosa PAO1]	158.98	21.43%	2	2	168	17.9	6.34
71	32	15596289	flagellin type B [Pseudomonas aeruginosa PAO1]	842.98	21.11%	6	13	488	49.2	5.62
72	33	15596783	dihydroliipoamide succinyltransferase [Pseudomonas aeruginosa PAO1]	73.53	4.65%	1	1	409	42.9	5.55

index	Prot_hit	Accession	Description	Mascot Score	Coverage	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pI
73	34	15596974	porin [Pseudomonas aeruginosa PAO1]	621.64	21.43%	5	13	350	37.6	5.14
74	35	15597001	DNA-binding protein HU [Pseudomonas aeruginosa PAO1]	102.46	25.56%	2	2	90	9.1	9.99
75	36	15598162	acyl carrier protein [Pseudomonas aeruginosa PAO1]	105.24	20.51%	1	2	78	8.7	4.12
76	37	15598965	inosine 5'-monophosphate dehydrogenase [Pseudomonas aeruginosa PAO1]	201.18	4.09%	1	3	489	51.7	6.68
77	38.1	15599445	30S ribosomal protein S8 [Pseudomonas aeruginosa PAO1]	145.76	9.23%	1	4	130	14.2	9.57
78	38.2	334125909	30S ribosomal protein S8 [Enterobacter hormaechei ATCC 4916]	145.76	9.23%	1	4	130	14.1	9.39
79	38.3	206580677	ribosomal protein S8 [Klebsiella pneumoniae 342]	145.76	9.23%	1	4	130	14.1	9.42
80	38.4	197287082	30S ribosomal protein S8 [Proteus mirabilis HI4320]	145.76	9.23%	1	4	130	14.2	9.23
81	38.5	26249894	30S ribosomal protein S8 [Escherichia coli CFT073]	145.76	9.23%	1	4	130	14.1	9.42
82	39	15599581	chaperonin GroEL [Pseudomonas aeruginosa PAO1]	972.87	35.83%	11	21	547	57	5.14
83	40	15599888	ketol-acid reductoisomerase [Pseudomonas aeruginosa PAO1]	239	5.62%	1	4	338	36.4	5.85
84	41	15600562	phosphate ABC transporter periplasmic phosphate-binding prot	182.81	8.98%	1	3	323	34.5	9.09
85	42	15600747	F0F1 ATP synthase subunit beta [Pseudomonas aeruginosa PAO1]	501.51	17.69%	5	10	458	49.5	5.11
86	43	15600748	F0F1 ATP synthase subunit gamma [Pseudomonas aeruginosa PAO1]	47.49	6.64%	1	1	286	31.5	7.87
87	44.1	116516768	eno gene product [Streptococcus pneumoniae D39]	105.34	5.76%	2	3	434	47.1	4.81
88	44.2	225858936	phosphopyruvate hydratase [Streptococcus pneumoniae 70S85]	105.34	5.76%	2	3	434	47.1	4.81
89	44.3	149003747	phosphopyruvate hydratase [Streptococcus pneumoniae SP14-I]	105.34	5.73%	2	3	436	47.3	4.83
90	45.1	116516621	rplL gene product [Streptococcus pneumoniae D39]	182.24	19.67%	3	5	122	12.4	4.49
91	45.2	303254509	50S ribosomal protein L7/L12 [Streptococcus pneumoniae BS45]	182.24	19.67%	3	5	122	12.5	4.49
92	46.1	116516442	gap gene product [Streptococcus pneumoniae D39]	392.14	18.21%	4	9	335	35.8	5.47
93	46.2	225859769	glyceraldehyde-3-phosphate dehydrogenase, type I [Streptococcus pneumoniae D39]	392.14	18.21%	4	9	335	35.8	5.59
94	46.3	182684949	glyceraldehyde-3-phosphate dehydrogenase [Streptococcus pneumoniae D39]	392.14	16.99%	4	9	359	38.7	6.34
95	46.4	169832817	glyceraldehyde-3-phosphate dehydrogenase, type I [Streptococcus pneumoniae D39]	392.14	18.21%	4	9	335	35.8	5.47
96	46.5	298501510	glyceraldehyde-3-phosphate dehydrogenase [Streptococcus pneumoniae D39]	392.14	17.73%	4	9	344	37	5.96
97	46.6	15903867	glyceraldehyde-3-phosphate dehydrogenase [Streptococcus pneumoniae D39]	392.14	16.99%	4	9	359	38.7	6.13
98	46.7	183603733	glyceraldehyde-3-phosphate dehydrogenase, type I [Streptococcus pneumoniae D39]	392.14	17.73%	4	9	344	37	5.96
99	47.1	116515886	unnamed protein product [Streptococcus pneumoniae D39]	100.04	1.47%	1	2	883	97.2	6.55
100	47.2	15903879	bifunctional acetaldehyde-CoA/alcohol dehydrogenase [Streptococcus pneumoniae D39]	100.04	1.46%	1	2	890	98.1	6.48
101	48.1	116515871	rplR gene product [Streptococcus pneumoniae D39]	77.98	25.42%	1	1	118	12.9	10.4
102	48.2	182683204	50S ribosomal protein L18 [Streptococcus pneumoniae CGSP14]	77.98	22.90%	1	1	131	14.4	10.49
103	48.3	111658785	hypothetical protein SpneT_02000082 [Streptococcus pneumoniae D39]	77.98	24.79%	1	1	121	13.2	10.43
104	49.1	116515356	tuf gene product [Streptococcus pneumoniae D39]	336	4.27%	2	5	398	43.9	4.97
105	49.2	182684444	elongation factor Tu [Streptococcus pneumoniae CGSP14]	336	4.21%	2	5	404	44.7	4.94
106	50	169834089	50S ribosomal protein L11 [Streptococcus pneumoniae Hungary]	79.78	17.02%	1	1	141	14.8	9.7
107	51.1	26246055	pyruvate dehydrogenase subunit E1 [Escherichia coli CFT073]	942.61	21.20%	13	27	887	99.6	5.68
108	51.2	206576843	pyruvate dehydrogenase (acetyl-transferring), homodimeric type I [Escherichia coli CFT073]	564.21	14.43%	8	16	887	99.5	5.64
109	52	161486328	dihydroliipoamide dehydrogenase [Escherichia coli CFT073]	426.07	14.14%	4	9	474	50.7	6.15
110	53.1	26246108	serine endoprotease [Escherichia coli CFT073]	122.8	4.22%	1	2	474	49.3	8.56
111	53.1	334123382	protease do [Enterobacter hormaechei ATCC 49162]	122.8	4.19%	1	2	477	49.4	8.56
112	54	26246124	periplasmic chaperone [Escherichia coli CFT073]	83.19	9.94%	1	1	161	17.7	9.7
113	55	26246476	acriflavin resistance protein A [Escherichia coli CFT073]	98.08	5.13%	1	2	409	43.5	8.43
114	56	26246561	outer membrane receptor FepA [Escherichia coli CFT073]	989.75	23.32%	10	22	746	82	5.45
115	57.1	161486279	succinate dehydrogenase flavoprotein subunit [Escherichia coli CFT073]	149.4	2.38%	1	2	588	64.4	6.27
116	57.2	334122842	succinate dehydrogenase [Enterobacter hormaechei ATCC 49162]	149.4	2.38%	1	2	588	64.4	6.02
117	57.3	206580158	succinate dehydrogenase, flavoprotein subunit [Klebsiella pneumoniae 342]	149.4	2.38%	1	2	588	64.5	6.23
118	57.4	197284464	succinate dehydrogenase flavoprotein subunit [Proteus mirabilis HI4320]	149.4	2.38%	1	2	588	64.7	6.02
119	57.5	15596780	succinate dehydrogenase flavoprotein subunit [Pseudomonas aeruginosa PAO1]	149.4	2.37%	1	2	590	63.5	6.49
120	58	26246711	peptidoglycan-associated outer membrane lipoprotein [Escherichia coli CFT073]	197.32	8.29%	1	4	181	19.7	6.8
121	59	26246790	outer membrane protein X [Escherichia coli CFT073]	118.93	8.67%	1	2	173	18.8	7.17
122	60.1	26246936	30S ribosomal protein S1 [Escherichia coli CFT073]	323.59	16.88%	5	7	557	61.1	4.98
123	60.2	334122618	30S ribosomal protein S1 [Enterobacter hormaechei ATCC 49162]	323.59	16.88%	5	7	557	61.2	4.98
124	61	26246978	outer membrane protein A [Escherichia coli CFT073]	234.25	15.83%	5	10	379	41	6.71
125	62	26247566	global DNA-binding transcriptional dual regulator H-NS [Escherichia coli CFT073]	85.19	10.22%	1	1	137	15.5	5.47
126	63	26247570	bifunctional acetaldehyde-CoA/alcohol dehydrogenase [Escherichia coli CFT073]	1498.61	25.25%	17	36	891	96.1	6.79
127	64	26247735	hypothetical protein c1877 [Escherichia coli CFT073]	62.51	5.10%	1	1	353	38.7	9.31
128	65.1	26247927	major outer membrane lipoprotein [Escherichia coli CFT073]	197.29	15.38%	1	4	78	8.3	9.25
129	65.2	334122238	major outer membrane lipoprotein [Enterobacter hormaechei ATCC 49162]	197.29	15.38%	1	4	78	8.4	9.31
130	66	26248038	glyceraldehyde-3-phosphate dehydrogenase [Escherichia coli CFT073]	488.47	19.76%	5	13	334	35.9	6.8
131	67	26248190	flagellin [Escherichia coli CFT073]	577.89	9.24%	3	7	595	60.9	4.91
132	68	26248274	putative inner membrane ABC-transporter [Escherichia coli CFT073]	64.1	2.67%	1	1	600	66.2	9.03
133	69	26248288	putative pesticin receptor [Escherichia coli CFT073]	991.03	32.10%	11	23	673	73.6	5.73
134	70	26248619	DNA gyrase subunit A [Escherichia coli CFT073]	180.81	2.17%	1	2	875	96.9	5.2
135	71.1	26248830	malic enzyme [Escherichia coli CFT073]	98.86	2.64%	1	2	759	82.4	5.5
136	71.2	334125040	NADP-dependent malate dehydrogenase (oxaloacetate-decarboxylating) [Escherichia coli CFT073]	98.86	2.64%	1	2	759	82.3	5.35
137	73	26248869	inosine 5'-monophosphate dehydrogenase [Escherichia coli CFT073]	315.86	7.24%	2	5	511	54.6	6.42
138	74.1	161486147	autonomous glycol radical cofactor GrcA [Escherichia coli CFT073]	91.92	26.77%	2	2	127	14.3	5.17
139	74.2	206580560	autonomous glycol radical cofactor [Klebsiella pneumoniae 342]	91.92	26.77%	2	2	127	14.2	5.02
140	75	26249182	phosphopyruvate hydratase [Escherichia coli CFT073]	550.99	23.84%	5	10	432	45.6	5.48
141	76	26249208	L-fucose isomerase [Escherichia coli CFT073]	122.44	6.26%	2	3	591	65	6.07
142	77	161486121	outer membrane channel protein [Escherichia coli CFT073]	102.75	5.48%	2	3	493	53.7	6.09
143	78	161486111	ATP-dependent RNA helicase DeaD [Escherichia coli CFT073]	162.95	6.84%	2	2	629	70.5	8.72
144	79	26249906	50S ribosomal protein L22 [Escherichia coli CFT073]	80.73	21.82%	1	1	110	12.2	10.23
145	80	26249916	30S ribosomal protein S10 [Escherichia coli CFT073]	92.47	14.56%	1	2	103	11.7	9.69

index	Prot_hit	Accession	Description	Mascot Score	Coverage	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pl
146	81	26249938	30S ribosomal protein S7 [Escherichia coli CFT073]	283.4	11.54%	2	5	156	17.6	10.3
147	82	26250130	outer membrane heme/hemoglobin receptor [Escherichia coli C	559.72	17.28%	6	12	648	71.1	5.22
148	83.1	26250476	F0F1 ATP synthase subunit beta [Escherichia coli CFT073]	580.81	25.43%	6	11	460	50.3	5.01
149	83.2	334121923	ATP synthase F1 sector beta subunit [Enterobacter hormaechei	580.81	25.43%	6	11	460	50.2	5
150	84	26250714	peroxidase/catalase HPI [Escherichia coli CFT073]	118.35	2.17%	1	1	739	81.4	5.31
151	85.1	161486036	glycerol dehydrogenase [Escherichia coli CFT073]	210.67	4.63%	1	3	367	38.7	4.88
152	85.2	334121800	glycerol dehydrogenase [Enterobacter hormaechei ATCC 49162	210.67	4.63%	1	3	367	38.9	5.1
153	85.3	206579133	glycerol dehydrogenase [Klebsiella pneumoniae 342]	210.67	4.63%	1	3	367	38.6	5.1
154	84	26251030	aspartate ammonia-lyase [Escherichia coli CFT073]	58.34	4.67%	1	1	493	54	5.76
155	85	26251035	chaperonin GroEL [Escherichia coli CFT073]	1528.99	36.13%	12	31	548	57.3	4.94
156	86	P62805	Histone H4 n=219 Tax=Eukaryota RepID=H4_HUMAN	111.98	30.10%	2	3	103	11.4	11.36
157	87	P04264	Keratin, type II cytoskeletal 1 n=7 Tax=Eutheria RepID=K2C1_HL	428.67	9.94%	3	5	644	66	8.12
158	88	P13645	Keratin, type I cytoskeletal 10 n=12 Tax=Eutheria RepID=K1C10_	98.17	4.62%	1	2	584	58.8	5.21
159	89	P05109	Protein S100-A8 n=5 Tax=Hominoidea RepID=S10A8_HUMAN	134.52	24.73%	3	5	93	10.8	7.03
160	90	P06702	Protein S100-A9 n=5 Tax=Hominoidea RepID=S10A9_HUMAN	1398.2	78.07%	7	37	114	13.2	6.13
161	91.1	E9PFJ3	Uncharacterized protein n=3 Tax=Simiiformes RepID=E9PFJ3_H	3325.36	14.88%	10	78	578	63.3	5.31
162	91.2	P07911	Uromodulin n=2 Tax=Catarrhini RepID=UROM_HUMAN	3325.36	13.44%	10	78	640	69.7	5.24
163	92.1	Q9UP81	Mutant beta-globin n=1 Tax=Homo sapiens RepID=Q9UP81_HU	181.63	35.96%	2	3	89	9.7	8.19
164	92.2	B3VL86	Mutant beta-globin n=4 Tax=Homo sapiens RepID=B3VL86_HUI	181.63	23.02%	2	3	139	14.9	6.77
165	92.3	P68871	Hemoglobin subunit beta n=102 Tax=Primates RepID=HBB_HUM	181.63	21.77%	2	3	147	16	7.28
166	92.4	Q14473	Beta-globin gene from a thalassemia patient, n=1 Tax=Homo sa	181.63	18.29%	2	3	175	18.9	6.79
167	93.1	B4DW52	Uncharacterized protein n=12 Tax=Coelomata RepID=B4DW52_	257.3	25.65%	5	8	347	38.6	5.35
168	93.2	P63261	Actin, cytoplasmic 2 n=1334 RepID=ACTG_HUMAN	257.3	23.73%	5	8	375	41.8	5.48
169	94.1	P06899	Histone H2B type 1-J n=102 Tax=Euteleostomi RepID=H2B1J_HL	179.87	11.90%	1	2	126	13.9	10.32
170	94.2	P62807	Histone H2B type 1-C/E/F/G/I n=44 Tax=Euteleostomi RepID=H:	179.87	11.90%	1	2	126	13.9	10.32
171	94.3	B4DR52	Histone H2B n=5 Tax=Euarchopterygii RepID=B4DR52_HUMAN	179.87	9.04%	1	2	166	18	10.32
172	94.4	P58876	Histone H2B type 1-D n=136 Tax=Coelomata RepID=H2B1D_HU	179.87	11.90%	1	2	126	13.9	10.32
173	95.1	P01834	Ig kappa chain C region n=2 Tax=Homo sapiens RepID=IGKC_HL	121.21	35.85%	2	2	106	11.6	5.87
174	95.2	UPI000011049E	IGG CTM01 FAB (LIGHT CHAIN) n=2 Tax=Homo sapiens RepID=l	121.21	17.35%	2	2	219	24.1	7.74
175	95.3	Q0KKI6	Immunoglobulin light chain (Fragment) n=3 Tax=Homo sapiens	121.21	17.35%	2	2	219	24	8.06
176	95.4	Q5EFE6	Anti-RhD monoclonal T125 kappa light chain n=1 Tax=Homo sa	121.21	16.24%	2	2	234	25.7	8.43
177	95.5	Q6GMX0	Putative uncharacterized protein n=14 Tax=Euarchopterygii Re	121.21	16.10%	2	2	236	25.8	7.97
178	95.6	Q6P5S8	IGK@ protein n=6 Tax=Homo sapiens RepID=Q6P5S8_HUMAN	121.21	16.10%	2	2	236	25.8	6.33
179	95.7	Q723Y4	Putative uncharacterized protein n=3 Tax=Hominoidea RepID=Q:	121.21	16.10%	2	2	236	25.7	7.59
180	95.8	UPI000011049S	ANTIBODY A5B7 (LIGHT CHAIN) n=1 Tax=Homo sapiens RepID=l	121.21	17.84%	2	2	213	23.1	8.06
181	95.9	UPI0000110769	ANTIBODY n=1 Tax=Homo sapiens RepID=UPI0000110769	121.21	17.76%	2	2	214	23.6	6.33
182	95.10	UPI000014CDC4	OMALIZUMAB LIGHT CHAIN n=2 Tax=Homo sapiens RepID=UPI	121.21	17.43%	2	2	218	23.9	5.39
183	95.11	UPI00003CEBF2	HU35193 Fab fragment, light chain n=3 Tax=Euarchopterygii Re	121.21	17.35%	2	2	219	24	8.06
184	95.12	UPI0001A7C522	HUMAN IGG ABT-325 n=1 Tax=Homo sapiens RepID=UPI0001A	121.21	17.76%	2	2	214	23.5	6.55
185	95.13	UPI0001A7C54C	Fab 213e1 n=3 Tax=Euarchopterygii RepID=UPI0001A7C54C	121.21	17.92%	2	2	212	23.1	7.71
186	95.14	UPI0001C591D8	Humanized recombinant Fab fragment of a murin n=5 Tax=Eu	121.21	16.59%	2	2	229	25.1	5.62
187	95.15	UPI0001D3410B	Immunoglobulin light chain n=1 Tax=Homo sapiens RepID=UPI0	121.21	17.43%	2	2	218	23.3	8.05
188	95.16	UPI0001F2FE82	Fab 2G12, light chain n=2 Tax=Homo sapiens RepID=UPI0001F2	121.21	17.84%	2	2	213	23.2	8.13
189	95.17	UPI0002003CF0	IMMUNOGLOBULIN A1 LIGHT CHAIN n=1 Tax=Homo sapiens Re	121.21	17.35%	2	2	219	24	6.77
190	95.18	UPI000211B3C2	B3 (IGKV4-1) light chain n=1 Tax=Homo sapiens RepID=UPI0002	121.21	17.27%	2	2	220	24.2	6.55
191	95.19	UPI0002177BCC	S4 FAB LIGHT CHAIN n=1 Tax=Homo sapiens RepID=UPI000217:	121.21	18.01%	2	2	211	22.7	7.77
192	96	P01833	Polymeric immunoglobulin receptor n=5 Tax=Hominoidea Repl	91.81	2.62%	1	1	764	83.2	5.74
193	97	Q6MZU6	Putative uncharacterized protein DKFZp686C15213 n=1 Tax=Ho	147.18	8.41%	2	3	464	51.1	7.71
194	98.1	P01876	Ig alpha-1 chain C region n=2 Tax=Homo sapiens RepID=IGHA1_	556.05	14.73%	4	12	353	37.6	6.51
195	98.2	Q96DK0	cDNA FLJ25298 fis, clone STM07683, highly similar to Protein Tr	556.05	10.48%	4	12	496	53.5	6.65
196	98.3	Q6N090	Putative uncharacterized protein DKFZp686G21220 (Fragment)	556.05	10.28%	4	12	506	54.4	6.6
197	98.4	Q6ZW64	cDNA FLJ41552 fis, clone COLON2004478, highly similar to Prot	556.05	10.53%	4	12	494	53.3	6.52
198	98.5	Q8WY24	SNC66 protein n=1 Tax=Homo sapiens RepID=Q8WY24_HUMAN	556.05	10.46%	4	12	497	53.6	6.67
199	99.1	A11195	TUBB2B protein (Fragment) n=16 Tax=Fungi/Metazoa group Re	109.49	23.94%	2	2	188	20.6	5.05
200	99.2	Q13885	Tubulin beta-2A chain n=339 RepID=TBB2A_HUMAN	109.49	10.11%	2	2	445	49.9	4.89
201	99.3	Q5ST81	Tubulin beta polypeptide n=8 Tax=Eukaryota RepID=Q5ST81_HL	109.49	12.10%	2	2	372	41.7	4.91
202	99.4	E9PBJ4	Uncharacterized protein n=2 Tax=Homo sapiens RepID=E9PBJ4_	109.49	18.52%	2	2	243	27.4	4.49
203	100.1	P01857	Ig gamma-1 chain C region n=3 Tax=Homo sapiens RepID=IGHG	372.33	19.70%	4	14	330	36.1	8.19
204	100.2	A8K008	cDNA FLJ78387 n=2 Tax=Homo sapiens RepID=A8K008_HUMAN	372.33	13.77%	4	14	472	51.6	8.16
205	100.3	Q6GMX6	IGH@ protein n=2 Tax=Homo sapiens RepID=Q6GMX6_HUMAN	372.33	13.98%	4	14	465	51.1	8.69
206	100.4	Q6N094	Putative uncharacterized protein DKFZp686O01196 n=3 Tax=Hc	372.33	13.54%	4	14	480	52.6	8.18
207	100.5	Q6N097	Putative uncharacterized protein DKFZp686H20196 n=1 Tax=Ho	372.33	13.51%	4	14	481	52.7	8.48
208	101	P11678	Eosinophil peroxidase n=6 Tax=Simiiformes RepID=PERE_HUM/	104.06	3.50%	3	4	715	81	10.29
209	102	P05164	Myeloperoxidase n=6 Tax=Catarrhini RepID=PERM_HUMAN	190.57	12.35%	6	6	745	83.8	8.97
210	103.1	D6RHJ6	Uncharacterized protein n=1 Tax=Homo sapiens RepID=D6RHJ6	85.85	7.64%	1	1	157	17.7	6.32
211	103.2	P01591	Immunoglobulin J chain n=12 Tax=Simiiformes RepID=IGJ_HUM	85.85	7.55%	1	1	159	18.1	5.24
212	104	P01871	Ig mu chain C region n=4 Tax=Homo sapiens RepID=IGHM_HUM	80.73	3.54%	1	1	452	49.3	6.77
213	105.1	P0CG05	Ig lambda-2 chain C regions n=4 Tax=Homo sapiens RepID=LAC:	474.26	34.91%	3	11	106	11.3	7.24
214	105.2	A0ASE4	Putative uncharacterized protein n=1 Tax=Homo sapiens RepID	474.26	15.74%	3	11	235	24.7	5.94
215	105.3	A2NUT2	Lambda-chain (AA -20 to 215) n=5 Tax=Euarchopterygii RepID	474.26	15.74%	3	11	235	24.6	7.62
216	105.4	C6KXN3	Lambda light chain of human immunoglobulin surface antigen-r	474.26	15.95%	3	11	232	24.7	5.54
217	105.5	Q567P1	IGL@ protein n=3 Tax=Homo sapiens RepID=Q567P1_HUMAN	474.26	15.74%	3	11	235	24.8	7.3
218	105.6	Q6GMW3	IGL@ protein n=7 Tax=Hominoidea RepID=Q6GMW3_HUMAN	474.26	15.81%	3	11	234	24.6	6.37

index	Prot_hit	Accession	Description	Mascot Score	Coverage	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pI
219	105.7	Q6GMX3	IGL@ protein n=3 Tax=Homo sapiens RepID=Q6GMX3_HUMAN	474.26	15.68%	3	11	236	24.7	6.89
220	105.8	Q6IPQ0	IGL@ protein n=6 Tax=Homo sapiens RepID=Q6IPQ0_HUMAN	474.26	15.68%	3	11	236	24.8	6.76
221	105.9	Q7Z2U7	Putative uncharacterized protein n=1 Tax=Homo sapiens RepID=	474.26	15.81%	3	11	234	25	6.38
222	105.10	Q8N5F4	IGL@ protein n=4 Tax=Hominoidea RepID=Q8N5F4_HUMAN	474.26	15.88%	3	11	233	24.9	5.34
223	105.11	UPI000158A17D	Bence Jones KWR Protein - Immunoglobulin Ligh n=1 Tax=Homc	474.26	17.05%	3	11	217	22.7	6.16
224	105.12	UPI0001BEF2DB	Fab 537-10D, light chain n=1 Tax=Homo sapiens RepID=UPI000:	474.26	17.05%	3	11	217	22.9	7.25
225	105.13	UPI0001D63C09	Antibody PG16 Light Chain n=3 Tax=Homo sapiens RepID=UPI00	474.26	17.13%	3	11	216	22.7	6.99
226	105.14	UPI0001D63C0B	Antibody PG9 light chain n=1 Tax=Homo sapiens RepID=UPI000	474.26	17.13%	3	11	216	22.8	8.5
227	106.1	Q9UL88	Myosin-reactive immunoglobulin heavy chain variable region (F	154.17	14.50%	1	2	131	14.1	9.63
228	106.2	UPI0001BEF2D9	Fab 447-52D, heavy chain n=1 Tax=Homo sapiens RepID=UPI00	154.17	8.09%	1	2	235	25.2	8.5
229	107	P01619	Ig kappa chain V-III region B6 n=1 Tax=Homo sapiens RepID=KV	72.47	16.67%	1	1	108	11.6	9.25
230	108.1	B1N7B8	Cryocrystalglobulin CC1 kappa light chain variable region (Frag	88.02	16.82%	1	1	107	11.8	7.99
231	108.2	A0N5G5	Rheumatoid factor D5 light chain (Fragment) n=1 Tax=Homo saj	88.02	15.25%	1	1	118	12.8	8.97
232	109	P02788	Lactotransferrin n=24 Tax=Hominoidea RepID=TRFL_HUMAN	190.97	6.06%	2	3	710	78.1	8.12
233	110.1	B1AM77	Stomatin n=5 Tax=Mammalia RepID=B1AM77_HUMAN	68.29	16.26%	1	1	123	13.5	8.02
234	110.2	E7EQ93	Uncharacterized protein n=3 Tax=Simiiformes RepID=E7EQ93_t	68.29	10.70%	1	1	187	20.8	8.87
235	110.3	P27105	Erythrocyte band 7 integral membrane protein n=13 Tax=Euthe	68.29	6.94%	1	1	288	31.7	7.88

2DLCSCI_36 Protein Summary

index	Prot_hit	Accession	Description	Mascot Score	Coverage	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pI
1	1	334124896	outer membrane protein N [Enterobacter hormaechei ATCC 49	165.28	11.02%	2	3	363	40	4.61
2	2	26246561	outer membrane receptor FepA [Escherichia coli CFT073]	172.29	2.28%	1	2	746	82	5.45
3	3	26248604	outer membrane porin protein C [Escherichia coli CFT073]	266.82	10.67%	2	5	375	41.2	4.83
4	4	26249182	phosphopyruvate hydratase [Escherichia coli CFT073]	166.14	3.70%	1	3	432	45.6	5.48
5	5	P05109	Protein S100-A8 n=5 Tax=Hominoidea RepID=S10A8_HUMAN	326.4	37.63%	5	10	93	10.8	7.03
6	6.1	P06702	Protein S100-A9 n=5 Tax=Hominoidea RepID=S10A9_HUMAN	2872.03	84.21%	10	60	114	13.2	6.13
7	6.2	116517025	unnamed protein product [Streptococcus pneumoniae D39]	48.18	3.13%	1	1	192	22	8.94
8	6.3	225858457	uracil DNA glycosylase family protein [Streptococcus pneumon	48.18	3.13%	1	1	192	22.1	8.69
9	6.4	15900532	hypothetical protein SP_0624 [Streptococcus pneumoniae TIGI	48.18	3.13%	1	1	192	22.1	8.69
10	6.5	182683555	hypothetical protein SPCG_0585 [Streptococcus pneumoniae C	48.18	3.13%	1	1	192	22.1	8.69
11	6.6	307067239	hypothetical protein SPAP_0610 [Streptococcus pneumoniae A	48.18	3.13%	1	1	192	22.1	8.69
12	6.7	168485735	uracil DNA glycosylase family protein [Streptococcus pneumon	48.18	3.13%	1	1	192	22.1	8.69
13	6.8	149002306	hypothetical protein CGSSp14BS69_01654 [Streptococcus pneu	48.18	3.09%	1	1	194	22.3	7.55
14	6.9	148984004	hypothetical protein CGSSp3BS71_07719 [Streptococcus pneur	48.18	3.09%	1	1	194	22.3	8.66
15	7	P80511	Protein S100-A12 n=4 Tax=Hominoidea RepID=S10AC_HUMAN	625.58	36.96%	4	14	92	10.6	6.25
16	8.1	E9PFJ3	Uncharacterized protein n=3 Tax=Simiiformes RepID=E9PFJ3_H	374.35	5.71%	3	8	578	63.3	5.31
17	8.2	P07911	Uromodulin n=2 Tax=Catarrhini RepID=UROM_HUMAN	374.35	5.16%	3	8	640	69.7	5.24
18	9.1	E9PG30	Uncharacterized protein n=21 Tax=Coelomata RepID=E9PG30_	104.41	9.01%	2	2	333	37.1	5.54
19	9.2	P62736	Actin, aortic smooth muscle n=27 Tax=Eukaryota RepID=ACTA_	104.41	7.96%	2	2	377	42	5.39
20	9.3	P63261	Actin, cytoplasmic 2 n=1334 RepID=ACTG_HUMAN	104.41	8.00%	2	2	375	41.8	5.48
21	9.4	B4DW52	Uncharacterized protein n=12 Tax=Coelomata RepID=B4DW52	104.41	8.65%	2	2	347	38.6	5.35
22	9.5	B4E335	Uncharacterized protein n=3 Tax=Coelomata RepID=B4E335_H	104.41	8.55%	2	2	351	39.2	5.59
23	9.6	F5H0N0	Uncharacterized protein n=11 Tax=Simiiformes RepID=F5H0N0	104.41	9.01%	2	2	333	37.4	5.58
24	9.7	Q5T8M7	Actin, alpha 1, skeletal muscle n=5 Tax=Simiiformes RepID=Q5T	104.41	8.77%	2	2	342	37.8	5.58
25	10.1	F6PJX6	Uncharacterized protein n=6 Tax=Eutheria RepID=F6PJX6_HOR	97.83	9.09%	1	1	308	35.6	4.72
26	10.2	P13646	Keratin, type I cytoskeletal 13 n=13 Tax=Simiiformes RepID=K1I	97.83	6.11%	1	1	458	49.6	4.96
27	10.3	P13646-3	Isoform 3 of Keratin, type I cytoskeletal 13 n=7 Tax=Eutheria Re	97.83	6.67%	1	1	420	45.8	4.88
28	11.1	P06899	Histone H2B type 1-J n=102 Tax=Euteleostomi RepID=H2B1J_H	112.51	11.90%	1	1	126	13.9	10.32
29	11.2	P62807	Histone H2B type 1-C/E/F/G/I n=44 Tax=Euteleostomi RepID=H	112.51	11.90%	1	1	126	13.9	10.32
30	11.3	B4DR52	Histone H2B n=5 Tax=Euarchontoglires RepID=B4DR52_HUMAI	112.51	9.04%	1	1	166	18	10.32
31	11.4	P58876	Histone H2B type 1-D n=136 Tax=Coelomata RepID=H2B1D_HL	112.51	11.90%	1	1	126	13.9	10.32
32	12	P05164	Myeloperoxidase n=6 Tax=Catarrhini RepID=PERM_HUMAN	661.02	10.87%	5	13	745	83.8	8.97
33	13	P02788	Lactotransferrin n=24 Tax=Hominoidea RepID=TRFL_HUMAN	334.66	5.35%	3	6	710	78.1	8.12

ZDLCS1_36 Peptide Summary

Sequence	Protein Descriptions	# Proteins	# Protein Groups	Protein Group Accessions	Modifications	q-Value	PEP	Charge	m/z [Da]	MH+ [Da]	Delta Mass [Da]
mSQIER	Protein S100-A9 n=5 Tax=Hominoidea RepID=S10A	9	1	P06702		0.00761	0.0502	2	390.44839	779.88951	0.26
mLTELK	Protein S100-A8 n=5 Tax=Hominoidea RepID=S10A	1	1	P05109	M1(Oxidation)	0.00761	0.0764	2	440.44702	879.88677	0.22
KDLQNLFK	Protein S100-A9 n=5 Tax=Hominoidea RepID=S10A	1	1	P06702		0.00589	0.0137	2	567.62634	1134.24541	0.29
GHFDTLSKGELK	Protein S100-A12 n=4 Tax=Hominoidea RepID=S10	1	1	P80511		0.00761	0.0315	2	666.58105	1332.15483	0.23
IGLDLPAIINMQR	Myeloperoxidase n=6 Tax=Catarrhini RepID=PERM	1	1	P05164		0.00761	0.0246	2	671.40002	1341.79277	0.53
TALQPMVSALNIR	Uncharacterized protein n=3 Tax=Simiiformes Repl	2	1	E9PFJ3		0	5.76E-05	2	707.58606	1414.16484	0.19
GNFHAVYRDDLK	Protein S100-A8 n=5 Tax=Hominoidea RepID=S10A	1	1	P05109		0	0.00263	2	718.06683	1435.12639	0.21
LGHFDTLNGQEFK	Protein S100-A9 n=5 Tax=Hominoidea RepID=S10A	1	1	P06702		0	5.25E-06	1	1455.74548	1455.74548	0.02
YGHTLIQPFMFH	Myeloperoxidase n=6 Tax=Catarrhini RepID=PERM	1	1	P05164		0	0.00853	2	755.56805	1510.12883	0.18
SRDHGLPGYNAWR	Myeloperoxidase n=6 Tax=Catarrhini RepID=PERM	1	1	P05164	0.00761	0.0314	2	765.04639	1529.0855	0.17	
ILLAELEQLKGGQK	Vimentin n=45 Tax=Amniota RepID=VIME_HUMAN	1	1	P08670		0	0.000154	2	770.6803	1540.35332	0.22
SVNGKDAIWNLLR	Lactotransferrin n=24 Tax=Hominoidea RepID=TRFI	1	1	P02788		0	1.30E-05	2	808.16284	1615.31841	0.23
QLSFEFIMLMAR	Protein S100-A9 n=5 Tax=Hominoidea RepID=S10A	1	1	P06702		0	0.000135	2	808.49487	1615.98247	0.59
LDLAGRDLTYLKM	Uncharacterized protein n=21 Tax=Coelomata Repl	7	1	E9PG30		0	0.000165	2	812.8728	1624.73833	0.45
DSTIQVLENGESSQGR	Uncharacterized protein n=3 Tax=Simiiformes Repl	2	1	E9PFJ3		0	1.23E-06	2	853.78229	1706.5573	0.38
VEIHIMEDLDTNADK	Protein S100-A9 n=5 Tax=Hominoidea RepID=S10A	1	1	P06702		0	2.65E-06	2	872.3988	1743.79033	0.48
AMGIMNSFVNDIFER	Histone H2B type 1-J n=102 Tax=Euteleostomi Repl	4	1	P06899		0	5.75E-07	2	872.91675	1744.82622	0.5
SYELPDGQVITIGNER	Uncharacterized protein n=21 Tax=Coelomata Repl	7	1	E9PG30		0	2.00E-06	2	896.35254	1791.6978	0.4
NIETIINTFHQYSVK	Protein S100-A9 n=5 Tax=Hominoidea RepID=S10A	1	1	P06702		0	0.000185	2	904.62744	1808.24761	0.65
FQLFGSPGQKDLFFK	Lactotransferrin n=24 Tax=Hominoidea RepID=TRFI	1	1	P02788		0	3.02E-07	2	906.67505	1812.34282	0.19
VSLKTALQPMVSALNIR	Uncharacterized protein n=3 Tax=Simiiformes Repl	2	1	E9PFJ3		0	7.56E-07	2	921.43396	1841.86064	0.4
ALNSIIDVYHKYSLK	Protein S100-A8 n=5 Tax=Hominoidea RepID=S10A	1	1	P05109		0	3.27E-06	2	939.49988	1877.99248	0.47
AFTSEFTHFLEELTK	phosphopyruvate hydratase [Escherichia coli CFT01	1	1	26249182		0	5.93E-06	2	965.27869	1929.5501	0.31
LGHFDTLNGQEFKELVR	Protein S100-A9 n=5 Tax=Hominoidea RepID=S10A	1	1	P06702		0	0.00226	2	977.44202	1953.87676	0.43
IIELAGFLDSYIPEPER	translation elongation factor Tu [Enterobacter horr	3	1	334126439		0	0.000835	2	981.95593	1962.90459	0.44
WDFAPLQSLLEAGYSR	outer membrane receptor FepA [Escherichia coli CF	1	1	26246561		0	1.88E-07	2	992.0614	1983.11553	0.58
LGHFDTLNGQEFKELVRK	Protein S100-A9 n=5 Tax=Hominoidea RepID=S10A	1	1	P06702		0	1.12E-05	2	1041.49731	2081.98735	0.44
MLTELEKALNSIIDVYHK	Protein S100-A8 n=5 Tax=Hominoidea RepID=S10A	1	1	P05109		0	0.00079	3	706.68909	2118.05271	0.31
mLLELEKALNSIIDVYHK	Protein S100-A8 n=5 Tax=Hominoidea RepID=S10A	1	1	P05109	M1(Oxidation)	0	9.29E-08	2	1067.60022	2134.19316	0.53
MHEGDEGPGHHHKPLGEGTPT	Protein S100-A9 n=5 Tax=Hominoidea RepID=S10A	1	1	P06702		0	1.86E-05	2	1088.92346	2176.83965	0.44
mHEGDEGPGHHHKPLGEGTPT	Protein S100-A9 n=5 Tax=Hominoidea RepID=S10A	1	1	P06702	M1(Oxidation)	0	0.000121	2	1096.91199	2192.8167	0.43
AVSNEIVRFPTDQLTPDQER	Myeloperoxidase n=6 Tax=Catarrhini RepID=PERM	1	1	P05164		0	0.0104	2	1158.47742	2315.94756	0.39
YDANNIYLAAQYQTYNATR	outer membrane protein N [Enterobacter horma	2	2	334124896;26248604		0	9.03E-08	2	1177.8136	2354.61992	-0.26
TKLEEHLGIVNIFHQYSVR	Protein S100-A12 n=4 Tax=Hominoidea RepID=S10	1	1	P80511		0	2.25E-06	2	1206.62073	2412.23418	-0.02
NMSTYVDYKINLLDNDQFTR	outer membrane porin protein C [Escherichia coli C	1	1	26248604		0	5.39E-06	2	1225.9967	2450.98613	0.41
NMSTYVDYKINLLDNDQFTR	outer membrane protein N [Enterobacter horma	1	1	334124896	0.00761	0.0229	3	818.0011	2451.98874	0.28	
TKLEEHLGIVNIFHQYSVR	Protein S100-A12 n=4 Tax=Hominoidea RepID=S10	1	1	P80511	N-Term(Acetyl)	0	4.97E-08	3	819.11005	2455.31559	0.35
TKLEEHLGIVNIFHQYSVRK	Protein S100-A12 n=4 Tax=Hominoidea RepID=S10	1	1	P80511		0	1.04E-06	2	1271.0553	2541.10332	0.37
MTKLEHLGIVNIFHQYSVR	Protein S100-A12 n=4 Tax=Hominoidea RepID=S10	1	1	P80511		0	0.00186	3	848.33832	2543.0004	-0.1
SQVEQLAEQNRKDAEAWFNEK	Keratin, type I cytoskeletal 10 n=12 Tax=Eutheria R	1	1	P13645		0	0.00205	3	862.19165	2584.5604	0.12
FQLFGSPGQKDLFFKDSAIGFSR	Lactotransferrin n=24 Tax=Hominoidea RepID=TRFI	1	1	P02788		0	1.75E-07	2	1323.60083	2646.19438	0.41
mLLELEKALNSIIDVYHKYSLK	Protein S100-A8 n=5 Tax=Hominoidea RepID=S10A	1	1	P05109	M1(Oxidation)	0	6.35E-07	3	913.58215	2738.73191	0.42
SLMFMQWGLLDHLDFTPEPAAR	Myeloperoxidase n=6 Tax=Catarrhini RepID=PERM	1	1	P05164		0	2.80E-06	2	1410.09778	2819.18828	0.43
DLGELEALKTELEDLTDSTAAQQLR	Myosin-9 n=67 Tax=Tetrapoda RepID=MYH9_HUM	1	1	P35579	0.00761	0.101	3	1006.88245	3018.63279	0.38	
VLDELTSKTDLEMQIESLNEELAYMKK	Uncharacterized protein n=6 Tax=Eutheria RepID=F	3	1	F6PJX6		0	1.70E-06	3	1095.61755	3284.83811	0.39
VEIHIMEDLDTNADKLSFEFIMLMAR	Protein S100-A9 n=5 Tax=Hominoidea RepID=S10A	1	1	P06702		0	1.88E-06	2	1670.20459	3339.4019	0.4
VEIHIMEDLDTNADKLSFEFIMLMAR	Protein S100-A9 n=5 Tax=Hominoidea RepID=S10A	1	1	P06702	M24(Oxidation)	0	0.00594	2	1678.2832	3355.55913	0.48

2DLCSCI 1 Protein Summary

index	Prot_hit	Accession	Description	Mascot Score	Coverage	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pI
1	1	P62805	Histone H4 n=219 Tax=Eukaryota RepID=H4_HUMAN	114.77	39.81%	3	3	103	11.4	11.36
2	2	P35579	Myosin-9 n=67 Tax=Tetrapoda RepID=MYH9_HUMAN	128.95	1.58%	2	2	1960	226.4	5.6
3	3.1	Q3BDU5	Rhabdomyosarcoma antigen MU-RMS-40.12 n=10 Tax=Theria R	102.03	3.08%	1	1	487	55.6	6.65
4	3.2	P02545	Prelamin-A/C n=44 Tax=Eutheria RepID=LMNA_HUMAN	102.03	2.26%	1	1	664	74.1	7.02
5	3.3	Q5TCI9	Lamin A/C (Fragment) n=3 Tax=Catarrhini RepID=Q5TCI9_HUM	102.03	2.92%	1	1	513	57.8	6.18
6	4	P15924	Desmoplakin n=28 Tax=Mammalia RepID=DESP_HUMAN	152.25	1.60%	3	4	2871	331.6	6.81
7	5	P04264	Keratin, type II cytoskeletal 1 n=7 Tax=Eutheria RepID=K2C1_HU	3443.04	36.49%	26	79	644	66	8.12
8	6	P35527	Keratin, type I cytoskeletal 9 n=4 Tax=Catarrhini RepID=K1C9_H	383.7	7.54%	2	5	623	62	5.24
9	7	P13645	Keratin, type I cytoskeletal 10 n=12 Tax=Eutheria RepID=K1C10_	552.7	20.03%	10	19	584	58.8	5.21
10	8	P02533	Keratin, type I cytoskeletal 14 n=8 Tax=Eutheria RepID=K1C14_	493.74	14.41%	7	23	472	51.5	5.16
11	9	P05109	Protein S100-A8 n=5 Tax=Hominoidea RepID=S10A8_HUMAN	109.15	17.20%	2	3	93	10.8	7.03
12	10	P35908	Keratin, type II cytoskeletal 2 epidermal n=7 Tax=Simiiformes Re	1112.85	15.81%	10	34	639	65.4	8
13	11	P12035	Keratin, type II cytoskeletal 3 n=7 Tax=Catarrhini RepID=K2C3_	696.4	13.69%	9	31	628	64.4	6.48
14	12	P02538	Keratin, type II cytoskeletal 6A n=25 Tax=Euarchontoglires Repl	1957.39	30.85%	22	74	564	60	8
15	13	Q8N1N4	Keratin, type II cytoskeletal 78 n=7 Tax=Hominoidea RepID=K2C	371.67	7.31%	4	13	520	56.8	6.02
16	14	P06702	Protein S100-A9 n=5 Tax=Hominoidea RepID=S10A9_HUMAN	261.19	28.95%	3	7	114	13.2	6.13
17	15	O60437	Periplakin n=3 Tax=Hominoidea RepID=PEPL_HUMAN	542.53	9.00%	10	15	1756	204.6	5.6
18	16	P62937	Peptidyl-prolyl cis-trans isomerase A n=98 Tax=Theria RepID=PF	219.98	24.24%	3	7	165	18	7.81
19	17.1	E9PFJ3	Uncharacterized protein n=3 Tax=Simiiformes RepID=E9PFJ3_H	694.38	7.96%	4	20	578	63.3	5.31
20	17.2	P07911	Uromodulin n=2 Tax=Catarrhini RepID=UROM_HUMAN	694.38	7.19%	4	20	640	69.7	5.24
21	18.1	F5H0N0	Uncharacterized protein n=11 Tax=Simiiformes RepID=F5H0N0_	652.16	23.12%	8	21	333	37.4	5.58
22	18.2	P63261	Actin, cytoplasmic 2 n=1334 RepID=ACTG_HUMAN	652.16	20.53%	8	21	375	41.8	5.48
23	18.3	B4DW52	Uncharacterized protein n=12 Tax=Coelomata RepID=B4DW52_	652.16	22.19%	8	21	347	38.6	5.35
24	18.4	B4E335	Uncharacterized protein n=3 Tax=Coelomata RepID=B4E335_HU	652.16	21.94%	8	21	351	39.2	5.59
25	19	A4FUUA1	GUCA1B protein (Fragment) n=1 Tax=Homo sapiens RepID=A4F	1207.45	68.00%	4	23	75	8.6	5.41
26	20	P13646	Keratin, type I cytoskeletal 13 n=13 Tax=Simiiformes RepID=K1C	2872.19	50.00%	22	96	458	49.6	4.96
27	21.1	B4DRW1	cDNA FLJ55805, highly similar to Keratin, type II cytoskeletal 4 n	3272.98	54.01%	27	94	474	51.7	6.81
28	21.2	P19013	Keratin, type II cytoskeletal 4 n=14 Tax=Simiiformes RepID=K2C	3272.98	47.94%	27	94	534	57.2	6.61
29	22.1	P06899	Histone H2B type 1-J n=102 Tax=Euteleostomi RepID=H2B1J_HU	111.17	11.11%	1	2	126	13.9	10.32
30	22.2	P62807	Histone H2B type 1-C/E/F/G/I n=44 Tax=Euteleostomi RepID=H;	111.17	11.11%	1	2	126	13.9	10.32
31	22.3	Q96A08	Histone H2B type 1-A n=22 Tax=Eutheria RepID=H2B1A_HUMAI	111.17	11.02%	1	2	127	14.2	10.32
32	22.4	B4DR52	Histone H2B n=5 Tax=Euarchontoglires RepID=B4DR52_HUMAN	111.17	8.43%	1	2	166	18	10.32
33	22.5	P58876	Histone H2B type 1-D n=136 Tax=Coelomata RepID=H2B1D_HU	111.17	11.11%	1	2	126	13.9	10.32
34	23	P04792	Heat shock protein beta-1 n=6 Tax=Simiiformes RepID=HSPB1_I	344.37	33.17%	5	9	205	22.8	6.4
35	24.1	E7EUJ4	Pyruvate kinase n=4 Tax=Simiiformes RepID=E7EUJ4_HUMAN	70.53	4.37%	1	1	366	40.2	8.03
36	24.2	P14618	Pyruvate kinase isozymes M1/M2 n=16 Tax=Simiiformes RepID-	70.53	3.01%	1	1	531	57.9	7.84
37	24.3	B4DRT3	Pyruvate kinase n=2 Tax=Homo sapiens RepID=B4DRT3_HUMAI	70.53	3.13%	1	1	511	55.9	7.5
38	24.4	B4DUU6	Pyruvate kinase n=4 Tax=Simiiformes RepID=B4DUU6_HUMAN	70.53	3.10%	1	1	516	56.2	8.44
39	24.5	E9PF79	Pyruvate kinase n=4 Tax=Simiiformes RepID=E9PF79_HUMAN	70.53	3.49%	1	1	458	50	7.64
40	24.6	P52480	Pyruvate kinase isozymes M1/M2 n=40 Tax=Tetrapoda RepID=k	70.53	3.01%	1	1	531	57.8	7.47
41	25.1	E7EU87	Uncharacterized protein n=3 Tax=Simiiformes RepID=E7EU87_	1071.16	21.44%	13	38	555	58.9	5.97
42	25.2	P13647	Keratin, type II cytoskeletal 5 n=17 Tax=Eutheria RepID=K2C5_H	1071.16	20.17%	13	38	590	62.3	7.74
43	26	P04083	Annexin A1 n=14 Tax=Eutheria RepID=ANXA1_HUMAN	1646.95	45.66%	14	35	346	38.7	7.02
44	27	UPI00020CE287	UPI00020CE287 related cluster n=1 Tax=Homo sapiens RepID=L	715.14	47.76%	8	53	201	23.1	4.97
45	28	P14923	Junction plakoglobin n=31 Tax=Theria RepID=PLAK_HUMAN	158.88	7.79%	4	4	745	81.7	6.14
46	29	Q9UBG3	Cornulin n=6 Tax=Catarrhini RepID=CRNN_HUMAN	344.14	13.74%	4	5	495	53.5	6.1
47	30	P04080	Cystatin-B n=14 Tax=Simiiformes RepID=CYTB_HUMAN	326.21	45.92%	3	8	98	11.1	7.56
48	31.1	A4K467	Actinin alpha4 isoform n=3 Tax=Simiiformes RepID=A4K467_HU	131.07	5.37%	2	2	521	59.5	4.94
49	31.2	O43707	Alpha-actinin-4 n=40 Tax=Tetrapoda RepID=ACTN4_HUMAN	131.07	3.07%	2	2	911	104.8	5.44
50	31.3	D6PKK4	Alpha actinin 4 short isoform n=8 Tax=Eutheria RepID=D6PKK4_	131.07	4.05%	2	2	692	79.9	5.17
51	32	P27482	Calmodulin-like protein 3 n=5 Tax=Euarchontoglires RepID=CAL	83.59	11.41%	1	1	149	16.9	4.42
52	33	Q01469	Fatty acid-binding protein, epidermal n=10 Tax=Simiiformes Ref	63.04	11.85%	1	1	135	15.2	7.01
53	34.1	Q92817	Envoplakin n=5 Tax=Simiiformes RepID=EVPL_HUMAN	194.38	1.67%	2	4	2033	231.5	6.96
54	34.2	B7ZLH8	EVPL protein n=4 Tax=Simiiformes RepID=B7ZLH8_HUMAN	194.38	1.65%	2	4	2055	233.7	7.25
55	35.1	F5H651	Uncharacterized protein n=5 Tax=Catarrhini RepID=F5H651_HU	66.21	2.01%	1	1	646	72.8	9.26
56	35.2	O95171	Sciellin n=6 Tax=Catarrhini RepID=SCEL_HUMAN	66.21	1.89%	1	1	688	77.5	9.38
57	36	P18054	Arachidonate 12-lipoxygenase, 12S-type n=5 Tax=Eutheria Repl	130.93	4.22%	2	3	663	75.6	6.21
58	37.1	Q0QET7	Glyceraldehyde-3-phosphate dehydrogenase (Fragment) n=4 Te	159.78	16.96%	2	4	230	24.6	8.51
59	37.2	E7EUT5	Glyceraldehyde-3-phosphate dehydrogenase n=3 Tax=Eutheria	159.78	15.00%	2	4	260	27.9	6.95
60	37.3	P04406	Glyceraldehyde-3-phosphate dehydrogenase n=42 Tax=Eutheria	159.78	11.64%	2	4	335	36	8.46
61	38.1	P01834	Ig kappa chain C region n=2 Tax=Homo sapiens RepID=IGKC_HU	378.25	57.55%	4	6	106	11.6	5.87
62	38.2	UPI000011049E	IGG CTPM01 FAB (LIGHT CHAIN) n=2 Tax=Homo sapiens RepID=L	378.25	27.85%	4	6	219	24.1	7.74
63	38.3	Q0KK16	Immunoglobulin light chain (Fragment) n=3 Tax=Homo sapiens	378.25	27.85%	4	6	219	24	8.06
64	38.4	Q5EFE6	Anti-RhD monoclonal T125 kappa light chain n=1 Tax=Homo sap	378.25	26.07%	4	6	234	25.7	8.43
65	38.5	Q6GMX0	Putative uncharacterized protein n=14 Tax=Euarchontoglires Re	378.25	25.85%	4	6	236	25.8	7.97
66	38.6	Q6P5S8	IGK@ protein n=6 Tax=Homo sapiens RepID=Q6P5S8_HUMAN	378.25	25.85%	4	6	236	25.8	6.33
67	38.7	Q7Z3Y4	Putative uncharacterized protein n=3 Tax=Hominae RepID=Q7	378.25	25.85%	4	6	236	25.7	7.59
68	38.8	UPI0000110495	ANTIBODY A5B7 (LIGHT CHAIN) n=1 Tax=Homo sapiens RepID=l	378.25	28.64%	4	6	213	23.1	8.06
69	38.9	UPI0000110769	ANTIBODY n=1 Tax=Homo sapiens RepID=UPI0000110769	378.25	28.50%	4	6	214	23.6	6.33
70	38.10	UPI000014CDC4	OMALIZUMAB LIGHT CHAIN n=2 Tax=Homo sapiens RepID=UPI	378.25	27.98%	4	6	218	23.9	5.39
71	38.11	UPI00003CEBF2	HU3S193 Fab fragment, light chain n=3 Tax=Euarchontoglires Re	378.25	27.85%	4	6	219	24	8.06
72	38.12	UPI0001A7C522	HUMAN IGG ABT-325 n=1 Tax=Homo sapiens RepID=UPI0001A	378.25	28.50%	4	6	214	23.5	6.55

index	Prot_hit	Accession	Description	Mascot Score	Coverage	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pI
73	38.13	UPI0001A7C54C	Fab Z13e1 n=3 Tax=Euarcontoglires RepID=UPI0001A7C54C	378.25	28.77%	4	6	212	23.1	7.71
74	38.14	UPI0001C591D8	Humanized recombinant Fab fragment of a murin n=5 Tax=Euar	378.25	26.64%	4	6	229	25.1	5.62
75	38.15	UPI0001D3410B	Immunoglobulin light chain n=1 Tax=Homo sapiens RepID=UPI0	378.25	27.98%	4	6	218	23.3	8.05
76	38.16	UPI0001F2FE82	Fab 2G12, light chain n=2 Tax=Homo sapiens RepID=UPI0001F2	378.25	28.64%	4	6	213	23.2	8.13
77	38.17	UPI0002003CF0	IMMUNOGLOBULIN A1 LIGHT CHAIN n=1 Tax=Homo sapiens Re	378.25	27.85%	4	6	219	24	6.77
78	38.18	UPI000211B3C2	B3 (IGKV4-1) light chain n=1 Tax=Homo sapiens RepID=UPI0002	378.25	27.73%	4	6	220	24.2	6.55
79	38.19	UPI0002177BCC	S4 FAB LIGHT CHAIN n=1 Tax=Homo sapiens RepID=UPI000217:	378.25	28.91%	4	6	211	22.7	7.77
80	39.1	C7DJS1	Glutathione S-transferase pi (Fragment) n=3 Tax=Homo sapiens	190.28	13.25%	1	3	151	16.7	5.1
81	39.2	P09211	Glutathione S-transferase P n=4 Tax=Simiiformes RepID=GSTP1	190.28	9.52%	1	3	210	23.3	5.64
82	40.1	E5RGE1	Uncharacterized protein n=6 Tax=Tetrapoda RepID=E5RGE1_HU	107.25	26.92%	1	1	52	5.9	4.78
83	40.2	E7ESK7	Uncharacterized protein n=7 Tax=Eutheria RepID=E7ESK7_HUM	107.25	10.22%	1	1	137	15.7	5.27
84	40.3	P63104	14-3-3 protein zeta/delta n=26 Tax=Amniota RepID=1433Z_HUI	107.25	5.71%	1	1	245	27.7	4.79
85	41.1	B4DWQ3	Phosphoglycerate kinase n=7 Tax=Theria RepID=B4DWQ3_HUM	74.97	10.56%	1	1	161	17	5.6
86	41.2	B4E1H9	Phosphoglycerate kinase n=6 Tax=Amniota RepID=B4E1H9_HUI	74.97	5.20%	1	1	327	35	8.32
87	41.3	P00558	Phosphoglycerate kinase 1 n=36 Tax=Theria RepID=PGK1_HUM	74.97	4.08%	1	1	417	44.6	8.1
88	42	P07737	Profilin-1 n=21 Tax=Theria RepID=PROF1_HUMAN	88.6	12.86%	1	1	140	15	8.27
89	43.1	A1L195	TUBB2B protein (Fragment) n=16 Tax=Fungi/Metazoa group Re	168.82	23.94%	2	3	188	20.6	5.05
90	43.2	Q13885	Tubulin beta-2A chain n=339 RepID=TBB2A_HUMAN	168.82	10.11%	2	3	445	49.9	4.89
91	43.3	Q5ST81	Tubulin beta polypeptide n=8 Tax=Eukaryota RepID=Q5ST81_HI	168.82	12.10%	2	3	372	41.7	4.91
92	43.4	E9PBJ4	Uncharacterized protein n=2 Tax=Homo sapiens RepID=E9PBJ4_	168.82	18.52%	2	3	243	27.4	4.49
93	44.1	Q05CF8	KNG1 protein n=1 Tax=Homo sapiens RepID=Q05CF8_HUMAN	83.94	6.53%	1	1	291	33	6.67
94	44.2	C9JEX1	Uncharacterized protein n=3 Tax=Hominoidea RepID=C9JEX1_H	83.94	4.86%	1	1	391	43.8	6.43
95	44.3	P01042	Kininogen-1 n=11 Tax=Catarrhini RepID=KNG1_HUMAN	83.94	2.95%	1	1	644	71.9	6.81
96	45.1	C9K0S6	Uncharacterized protein n=2 Tax=Simiiformes RepID=C9K0S6_H	82.13	44.68%	1	1	47	5.3	5.21
97	45.2	C9JEV8	Uncharacterized protein n=10 Tax=Coelomata RepID=C9JEV8_H	82.13	13.73%	1	1	153	16.9	5.53
98	45.3	Q13748	Tubulin alpha-3C/D chain n=18 Tax=Theria RepID=TBA3C_HUM.	82.13	4.67%	1	1	450	49.9	5.1
99	45.4	Q71U36	Tubulin alpha-1A chain n=597 RepID=TBA1A_HUMAN	82.13	4.66%	1	1	451	50.1	5.06
100	45.5	A8MUB1	Tubulin, alpha 1 (Testis specific), isoform CRA_a n=3 Tax=Simiifc	82.13	4.85%	1	1	433	48.3	5.01
101	45.6	B3KPW9	Tubulin, alpha 8, isoform CRA_b n=17 Tax=Amniota RepID=B3KI	82.13	5.48%	1	1	383	42.9	5.08
102	45.7	F5H5D3	Uncharacterized protein n=5 Tax=Simiiformes RepID=F5H5D3_1	82.13	4.05%	1	1	519	57.7	5.07
103	45.8	E9PGK3	Uncharacterized protein n=4 Tax=Catarrhini RepID=E9PGK3_HU	82.13	6.44%	1	1	326	36.7	8.44
104	45.9	Q8WU19	TUBA1B protein n=2 Tax=Homininae RepID=Q8WU19_HUMAN	82.13	6.27%	1	1	335	37.2	4.98
105	45.10	C9JJQ8	Uncharacterized protein n=1 Tax=Homo sapiens RepID=C9JJQ8_	82.13	10.61%	1	1	198	21.7	6.28
106	45.11	Q29196	Tubulin alpha-1 chain (Fragment) n=15 Tax=Eukaryota RepID=Q	82.13	17.65%	1	1	119	13.1	5.2
107	45.12	Q6QMJ5	Tubulin alpha-1 (Fragment) n=1 Tax=Homo sapiens RepID=Q6Q	82.13	21.43%	1	1	98	10.8	7.52

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index	Prot_hit	Accession	Description	Mascot Score	Coverage	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pl
1	1.1	297206263	phosphoglycerate kinase [Lactobacillus jensenii JV-V16]	58.12	2.98%	1	1	403	43	5.4
2	1.2	300361304	phosphoglycerate kinase [Lactobacillus gasserii JV-V03]	58.12	2.98%	1	1	403	43	5.78
3	2.1	297206261	enolase [Lactobacillus jensenii JV-V16]	53.42	3.94%	1	1	432	47	4.84
4	2.2	300361306	enolase [Lactobacillus gasserii JV-V03]	53.42	3.94%	1	1	432	46.9	4.81
5	3.1	297205850	elongation factor EF1A [Lactobacillus jensenii JV-V16]	86.52	4.04%	1	1	396	43.6	5.01
6	3.2	300811976	translation elongation factor Tu [Lactobacillus delbrueckii subsp	86.52	4.04%	1	1	396	43.3	5.01
7	3.3	300361496	elongation factor Tu [Lactobacillus gasserii JV-V03]	86.52	4.04%	1	1	396	43.7	4.98
8	4	297205326	D-lactate dehydrogenase [Lactobacillus jensenii JV-V16]	49.62	5.41%	1	1	333	37.1	5.1
9	5	297205124	50S ribosomal protein L31 [Lactobacillus jensenii JV-V16]	100.8	21.18%	1	1	85	9.5	8.94
10	6	P16401	Histone H1.5 n=15 Tax=Eutheria ReplID=H15_HUMAN	143.52	9.73%	2	4	226	22.6	10.92
11	7.1	Q71U36	Tubulin alpha-1A chain n=597 ReplID=TBA1A_HUMAN	136.77	6.43%	2	3	451	50.1	5.06
12	7.2	F5H5D3	Uncharacterized protein n=5 Tax=Simiiformes ReplID=F5H5D3_H	136.77	5.59%	2	3	519	57.7	5.07
13	8	P11021	78 kDa glucose-regulated protein n=68 Tax=Coelomata ReplID=C	65.18	2.14%	1	1	654	72.3	5.16
14	9	P15924	Desmoplakin n=28 Tax=Mammalia ReplID=DESP_HUMAN	89.64	1.08%	2	3	2871	331.6	6.81
15	10	P04264	Keratin, type II cytoskeletal 1 n=7 Tax=Eutheria ReplID=K2C1_HL	2597.2	45.34%	24	60	644	66	8.12
16	11	P13645	Keratin, type I cytoskeletal 10 n=12 Tax=Eutheria ReplID=K1C10_	363.47	10.27%	5	9	584	58.8	5.21
17	12	P02538	Keratin, type II cytoskeletal 6A n=25 Tax=Euarchothoglyres ReplI	1091.85	26.42%	18	42	564	60	8
18	13	Q8N1N4	Keratin, type II cytoskeletal 78 n=7 Tax=Hominoidea ReplID=K2C	210.64	11.54%	5	7	520	56.8	6.02
19	14	P06702	Protein S100-A9 n=5 Tax=Hominoidea ReplID=S10A9_HUMAN	464.92	28.95%	4	12	114	13.2	6.13
20	15	P98160	Basement membrane-specific heparan sulfate proteoglycan cor	95.09	0.41%	1	1	4391	468.5	6.51
21	16	P13647	Keratin, type II cytoskeletal 5 n=17 Tax=Eutheria ReplID=K2C5_H	514.09	20.17%	11	23	590	62.3	7.74
22	17	O60437	Periplakin n=3 Tax=Hominoidea ReplID=PEPL_HUMAN	331.08	5.47%	7	10	1756	204.6	5.6
23	18	P62937	Peptidyl-prolyl cis-trans isomerase A n=98 Tax=Theria ReplID=PF	156.65	24.24%	3	4	165	18	7.81
24	19.1	E9PFJ3	Uncharacterized protein n=3 Tax=Simiiformes ReplID=E9PFJ3_H	502.43	11.25%	6	12	578	63.3	5.31
25	19.2	P07911	Uromodulin n=2 Tax=Catarrhini ReplID=UROM_HUMAN	502.43	10.16%	6	12	640	69.7	5.24
26	20.1	F5H0N0	Uncharacterized protein n=11 Tax=Simiiformes ReplID=F5H0N0_	342.51	23.42%	7	13	333	37.4	5.58
27	20.2	P63261	Actin, cytoplasmic 2 n=1334 ReplID=ACTG_HUMAN	342.51	20.80%	7	13	375	41.8	5.48
28	20.3	B4E335	Uncharacterized protein n=3 Tax=Coelomata ReplID=B4E335_HI	342.51	22.22%	7	13	351	39.2	5.59
29	21	P69905	Hemoglobin subunit alpha n=29 Tax=Primates ReplID=HBA_HUN	139.96	10.56%	1	2	142	15.2	8.68
30	22	A4FUA1	GUCA1B protein (Fragment) n=1 Tax=Homo sapiens ReplID=A4F	929.78	68.00%	4	19	75	8.6	5.41
31	23.1	P60524	Hemoglobin subunit beta n=66 Tax=Eutheria ReplID=HBB_CANF.	57.37	9.59%	1	1	146	16	8.05
32	23.2	P68871	Hemoglobin subunit beta n=102 Tax=Primates ReplID=HBB_HUN	57.37	9.52%	1	1	147	16	7.28
33	24	P13646	Keratin, type I cytoskeletal 13 n=13 Tax=Simiiformes ReplID=K1C	2444.24	43.45%	23	77	458	49.6	4.96
34	25.1	E7EUT5	Glyceraldehyde-3-phosphate dehydrogenase n=3 Tax=Eutheria	136.15	10.38%	2	3	260	27.9	6.95
35	25.2	P04406	Glyceraldehyde-3-phosphate dehydrogenase n=42 Tax=Eutheri	136.15	8.06%	2	3	335	36	8.46
36	26.1	B4DRW1	cDNA FLJ55805, highly similar to Keratin, type II cytoskeletal 4 n	2441.99	48.10%	26	70	474	51.7	6.81
37	26.2	P19013	Keratin, type II cytoskeletal 4 n=14 Tax=Simiiformes ReplID=K2C	2441.99	42.70%	26	70	534	57.2	6.61
38	27	F6RMN8	Uncharacterized protein n=4 Tax=Simiiformes ReplID=F6RMN8_	1046.42	27.85%	17	41	535	57.8	8.22
39	28.1	E9PF79	Pyruvate kinase n=4 Tax=Simiiformes ReplID=E9PF79_HUMAN	162.84	7.42%	2	3	458	50	7.64
40	28.2	P14618	Pyruvate kinase isozymes M1/M2 n=16 Tax=Simiiformes ReplID=	162.84	6.40%	2	3	531	57.9	7.84
41	28.3	B4DRT3	Pyruvate kinase n=2 Tax=Homo sapiens ReplID=B4DRT3_HUMAN	162.84	6.65%	2	3	511	55.9	7.5
42	28.4	B4DUU6	Pyruvate kinase n=4 Tax=Simiiformes ReplID=B4DUU6_HUMAN	162.84	6.59%	2	3	516	56.2	8.44
43	28.5	P52480	Pyruvate kinase isozymes M1/M2 n=40 Tax=Tetrapoda ReplID=K	162.84	6.40%	2	3	531	57.8	7.47
44	29.1	P06899	Histone H2B type 1-J n=102 Tax=Euteleostomi ReplID=H2B1J_HL	168.71	30.16%	3	4	126	13.9	10.32
45	29.2	P62807	Histone H2B type 1-C/E/F/G/I n=44 Tax=Euteleostomi ReplID=H:	168.71	30.16%	3	4	126	13.9	10.32
46	29.3	B4DR52	Histone H2B n=5 Tax=Euarchothoglyres ReplID=B4DR52_HUMAN	168.71	22.89%	3	4	166	18	10.32
47	29.4	P58876	Histone H2B type 1-D n=136 Tax=Coelomata ReplID=H2B1D_HU	168.71	30.16%	3	4	126	13.9	10.32
48	30	P04792	Heat shock protein beta-1 n=6 Tax=Simiiformes ReplID=HSPB1_I	824.76	56.59%	9	20	205	22.8	6.4
49	31	P09211	Glutathione S-transferase P n=4 Tax=Simiiformes ReplID=GSTP1_	150.3	14.76%	2	3	210	23.3	5.64
50	32	P04083	Annexin A1 n=14 Tax=Eutheria ReplID=ANXA1_HUMAN	1262.15	54.91%	17	28	346	38.7	7.02
51	33	UPI00020CE287	UPI00020CE287 related cluster n=1 Tax=Homo sapiens ReplID=L	359.9	51.74%	6	27	201	23.1	4.97
52	34.1	Q06830	Peroxisome oxidin-1 n=31 Tax=Mammalia ReplID=PRDX1_HUMAN	73.38	6.03%	1	1	199	22.1	8.13
53	34.2	E9PEN3	Uncharacterized protein n=4 Tax=Eutheria ReplID=E9PEN3_HUM	73.38	4.67%	1	1	257	29.3	5.69
54	34.3	Q13162	Peroxisome oxidin-4 n=11 Tax=Eutheria ReplID=PRDX4_HUMAN	73.38	4.43%	1	1	271	30.5	6.29
55	35.1	A9X7H1	Eukaryotic translation elongation factor 1 alpha (Fragment) n=2	100.31	7.34%	1	2	177	19.4	7.28
56	35.2	P68104	Elongation factor 1-alpha 1 n=117 Tax=Euteleostomi ReplID=EF1	100.31	2.81%	1	2	462	50.1	9.01
57	35.3	Q6IQ15	EEF1A1 protein n=17 Tax=Theria ReplID=Q6IQ15_HUMAN	100.31	2.95%	1	2	441	47.8	9.03
58	36.1	F2Z257	Uncharacterized protein n=10 Tax=Catarrhini ReplID=F2Z257_HI	81.19	1.08%	1	1	1478	167.9	6.62
59	36.2	P35579	Myosin-9 n=67 Tax=Tetrapoda ReplID=MYH9_HUMAN	81.19	0.82%	1	1	1960	226.4	5.6
60	36.3	P35749	Myosin-11 n=82 Tax=Amniota ReplID=MYH11_HUMAN	81.19	0.81%	1	1	1972	227.2	5.5
61	36.4	F2Z2U9	Uncharacterized protein n=4 Tax=Catarrhini ReplID=F2Z2U9_HU	81.19	0.90%	1	1	1779	203	6.27
62	36.5	Q7Z406	Myosin-14 n=13 Tax=Eutheria ReplID=MYH14_HUMAN	81.19	0.80%	1	1	1995	227.7	5.6
63	37	P14923	Junction plakoglobin n=31 Tax=Theria ReplID=PLAK_HUMAN	103.46	2.42%	1	1	745	81.7	6.14
64	38	P07355	Annexin A2 n=28 Tax=Eutheria ReplID=ANXA2_HUMAN	256.22	21.83%	4	8	339	38.6	7.75
65	39	Q9UBG3	Cornulin n=6 Tax=Catarrhini ReplID=CRNN_HUMAN	661.89	24.04%	6	10	495	53.5	6.1
66	40	P04080	Cystatin-B n=14 Tax=Simiiformes ReplID=CYTB_HUMAN	311.22	45.92%	3	8	98	11.1	7.56
67	41.1	P62784	Histone H4 n=232 Tax=Eukaryota ReplID=H4_CAEL	80.56	11.65%	1	3	103	11.4	11.19
68	41.2	P62805	Histone H4 n=219 Tax=Eukaryota ReplID=H4_HUMAN	80.56	11.65%	1	3	103	11.4	11.36
69	42	P31947	14-3-3 protein sigma n=20 Tax=Eutheria ReplID=1433S_HUMAN	148.8	17.34%	3	5	248	27.8	4.74
70	43	P06733	Alpha-enolase n=53 Tax=Euteleostomi ReplID=ENOA_HUMAN	102.42	9.45%	2	2	434	47.1	7.39
71	44.1	A4K467	Actinin alpha4 isoform n=3 Tax=Simiiformes ReplID=A4K467_HU	82.19	3.26%	1	1	521	59.5	4.94
72	44.2	O43707	Alpha-actinin-4 n=40 Tax=Tetrapoda ReplID=ACTN4_HUMAN	82.19	1.87%	1	1	911	104.8	5.44

index	Prot_hit	Accession	Description	Mascot Score	Coverage	# Peptides	# PSMs	# AAs	MW [kDa]	calc. pl
73	44.3	D6PXX4	Alpha actinin 4 short isoform n=8 Tax=Eutheria RepID=D6PXX4_	82.19	2.46%	1	1	692	79.9	5.17
74	45	P29508	Serpin B3 n=14 Tax=Hominoidea RepID=SPB3_HUMAN	301.43	14.36%	5	7	390	44.5	6.81
75	46	Q01469	Fatty acid-binding protein, epidermal n=10 Tax=Simiiformes Ref	92.98	11.85%	1	2	135	15.2	7.01
76	47.1	C9J0D1	Histone H2A n=1 Tax=Homo sapiens RepID=C9J0D1_HUMAN	118.31	7.38%	1	3	122	13.2	9.99
77	47.2	P0C0S5	Histone H2A.Z n=78 Tax=Metazoa RepID=H2AZ_HUMAN	118.31	7.03%	1	3	128	13.5	10.58
78	47.3	P0C0S8	Histone H2A type 1 n=295 Tax=Eukaryota RepID=H2A1_HUMAN	118.31	6.92%	1	3	130	14.1	10.9
79	47.4	P16104	Histone H2A.x n=16 Tax=Coelomata RepID=H2AX_HUMAN	118.31	6.29%	1	3	143	15.1	10.74
80	47.5	Q16777	Histone H2A type 2-C n=33 Tax=Eumetazoa RepID=H2A2C_HUN	118.31	6.98%	1	3	129	14	10.9
81	47.6	Q71U99	Histone H2A.V n=25 Tax=Bilateria RepID=H2AV_HUMAN	118.31	7.03%	1	3	128	13.5	10.58
82	47.7	C9JE22	Histone H2A n=7 Tax=Eutheria RepID=C9JE22_HUMAN	118.31	5.96%	1	3	151	16.1	10.23
83	47.8	Q96KK5	Histone H2A type 1-H n=10 Tax=Mammalia RepID=H2A1H_HUN	118.31	7.03%	1	3	128	13.9	10.89
84	47.9	Q99878	Histone H2A type 1-J n=4 Tax=Eutheria RepID=H2A1J_HUMAN	118.31	7.03%	1	3	128	13.9	10.89
85	47.10	Q8IU66	Histone H2A type 2-B n=5 Tax=Eutheria RepID=H2A2B_HUMAN	118.31	6.92%	1	3	130	14	10.89
86	48.1	Q92817	Envoplakin n=5 Tax=Simiiformes RepID=EVPL_HUMAN	125.85	1.48%	2	2	2033	231.5	6.96
87	48.2	B7ZLH8	EVPL protein n=4 Tax=Simiiformes RepID=B7ZLH8_HUMAN	125.85	1.46%	2	2	2055	233.7	7.25
88	49.1	P16403	Histone H1.2 n=12 Tax=Eutheria RepID=H12_HUMAN	162.98	12.68%	2	3	213	21.4	10.93
89	49.2	P10412	Histone H1.4 n=20 Tax=Eutheria RepID=H14_HUMAN	162.98	12.33%	2	3	219	21.9	11.03
90	49.3	P16402	Histone H1.3 n=6 Tax=Simiiformes RepID=H13_HUMAN	162.98	12.22%	2	3	221	22.3	11.02
91	49.4	Q02539	Histone H1.1 n=5 Tax=Catarrhini RepID=H11_HUMAN	162.98	12.56%	2	3	215	21.8	10.99
92	50.1	F5H651	Uncharacterized protein n=5 Tax=Catarrhini RepID=F5H651_HU	72.82	2.01%	1	1	646	72.8	9.26
93	50.2	O95171	Sciellin n=6 Tax=Catarrhini RepID=SCEL_HUMAN	72.82	1.89%	1	1	688	77.5	9.38
94	51	P18054	Arachidonate 12-lipoxygenase, 12S-type n=5 Tax=Eutheria Repl	51.74	1.81%	1	1	663	75.6	6.21
95	52.1	P07476	Involucrin n=2 Tax=Homo sapiens RepID=INVO_HUMAN	96.11	4.79%	2	2	585	68.4	4.61
96	52.2	B4DU44	Involucrin n=2 Tax=Homininae RepID=B4DU44_HUMAN	96.11	4.71%	2	2	595	69.6	4.6
97	52.3	Q28423	Involucrin n=2 Tax=Homininae RepID=Q28423_9PRIM	96.11	4.41%	2	2	635	74	4.61
98	53.1	E9PI65	Uncharacterized protein n=1 Tax=Homo sapiens RepID=E9PI65_	125.61	10.12%	1	2	168	17.9	5.29
99	53.2	P11142	Heat shock cognate 71 kDa protein n=167 Tax=Metazoa RepID=	125.61	2.63%	1	2	646	70.9	5.52
100	53.3	P54652	Heat shock-related 70 kDa protein 2 n=38 Tax=Amniota RepID=	125.61	2.66%	1	2	639	70	5.74
101	53.4	B3KTV0	cDNA FLJ38781 fis, clone LIVER2000216, highly similar to HEAT !	125.61	2.74%	1	2	621	67.9	5.45
102	54.1	F6Y193	Uncharacterized protein n=3 Tax=Simiiformes RepID=F6Y193_C	51.74	3.12%	1	1	417	45.1	5.73
103	54.2	P08107	Heat shock 70 kDa protein 1A/1B n=76 Tax=Gnathostomata Ref	51.74	2.03%	1	1	641	70	5.66
104	54.3	E7EQL7	Uncharacterized protein n=2 Tax=Homo sapiens RepID=E7EQL7	51.74	2.31%	1	1	563	61.4	5.69
105	55	P63104	14-3-3 protein zeta/delta n=26 Tax=Amniota RepID=1433Z_HUF	131.68	13.06%	2	2	245	27.7	4.79
106	56	Q09666	Neuroblast differentiation-associated protein AHNK n=14 Tax=	110.96	1.66%	1	4	5890	628.7	6.15
107	57	C9JZ65	Uncharacterized protein n=1 Tax=Homo sapiens RepID=C9JZ65_	201.68	19.91%	3	4	211	24.4	6.61
108	58	P01040	Cystatin-A n=6 Tax=Catarrhini RepID=CYTA_HUMAN	124.73	14.29%	1	2	98	11	5.5
109	59	Q9UBC9	Small proline-rich protein 3 n=4 Tax=Homininae RepID=SPRR3_I	251.16	27.81%	3	7	169	18.1	8.57
110	60.1	B4DFK7	Carbonyl reductase 1, isoform CRA_c n=2 Tax=Simiiformes Repl	94.3	9.83%	1	2	173	18.7	8.02
111	60.2	A8MTM1	Uncharacterized protein n=1 Tax=Homo sapiens RepID=A8MTM	94.3	7.66%	1	2	222	24.5	8.76
112	60.3	E9PQ63	Uncharacterized protein n=1 Tax=Homo sapiens RepID=E9PQ63	94.3	9.55%	1	2	178	19	6.3
113	60.4	P16152	Carbonyl reductase [NADPH] 1 n=7 Tax=Simiiformes RepID=CBF	94.3	6.14%	1	2	277	30.4	8.32
114	61	P18510	Interleukin-1 receptor antagonist protein n=4 Tax=Catarrhini Re	86.27	9.04%	1	2	177	20	6.19
115	62.1	P01834	Ig kappa chain C region n=2 Tax=Homo sapiens RepID=IGKC_HU	57.53	16.98%	1	1	106	11.6	5.87
116	62.2	UPI000011049E	IGG CTM01 FAB (LIGHT CHAIN) n=2 Tax=Homo sapiens RepID=L	57.53	8.22%	1	1	219	24.1	7.74
117	62.3	Q0KKI6	Immunoglobulin light chain (Fragment) n=3 Tax=Homo sapiens	57.53	8.22%	1	1	219	24	8.06
118	62.4	Q569I7	Putative uncharacterized protein n=1 Tax=Homo sapiens RepID=	57.53	9.52%	1	1	189	20.7	5.27
119	62.5	Q5EFE6	Anti-RhD monoclonal T125 kappa light chain n=1 Tax=Homo saq	57.53	7.69%	1	1	234	25.7	8.43
120	62.6	Q6GMX0	Putative uncharacterized protein n=14 Tax=Euarchontoglires Re	57.53	7.63%	1	1	236	25.8	7.97
121	62.7	Q6P5S8	IGK@ protein n=6 Tax=Homo sapiens RepID=Q6P5S8_HUMAN	57.53	7.63%	1	1	236	25.8	6.33
122	62.8	Q7Z3Y4	Putative uncharacterized protein n=3 Tax=Homininae RepID=Q7	57.53	7.63%	1	1	236	25.7	7.59
123	62.9	UPI000011049S	ANTIBODY A5B7 (LIGHT CHAIN) n=1 Tax=Homo sapiens RepID=I	57.53	8.45%	1	1	213	23.1	8.06
124	62.10	UPI0000110769	ANTIBODY n=1 Tax=Homo sapiens RepID=UPI0000110769	57.53	8.41%	1	1	214	23.6	6.33
125	62.11	UPI000014CD4C	OMALIZUMAB LIGHT CHAIN n=2 Tax=Homo sapiens RepID=UPI	57.53	8.26%	1	1	218	23.9	5.39
126	62.12	UPI00003CEBF2	HU3S193 Fab fragment, light chain n=3 Tax=Euarchontoglires Re	57.53	8.22%	1	1	219	24	8.06
127	62.13	UPI00006EB13F	Fab m18, Light Chain n=1 Tax=Homo sapiens RepID=UPI00006E	57.53	8.45%	1	1	213	23.4	7.27
128	62.14	UPI0001A7C522	HUMAN IGG ABT-325 n=1 Tax=Homo sapiens RepID=UPI0001A7	57.53	8.41%	1	1	214	23.5	6.55
129	62.15	UPI0001A7C54C	Fab Z13e1 n=3 Tax=Euarchontoglires RepID=UPI0001A7C54C	57.53	8.49%	1	1	212	23.1	7.71
130	62.16	UPI0001C591D8	Humanized recombinant Fab fragment of a murin n=5 Tax=Euar	57.53	7.86%	1	1	229	25.1	5.62
131	62.17	UPI0001D3410B	Immunoglobulin light chain n=1 Tax=Homo sapiens RepID=UPI0	57.53	8.26%	1	1	218	23.3	8.05
132	62.18	UPI0001F2FE82	Fab 2G12, light chain n=2 Tax=Homo sapiens RepID=UPI0001F2	57.53	8.45%	1	1	213	23.2	8.13
133	62.19	UPI0002003CF0	IMMUNOGLOBULIN A1 LIGHT CHAIN n=1 Tax=Homo sapiens Re	57.53	8.22%	1	1	219	24	6.77
134	62.20	UPI000211B3C2	B3 (IGKV4-1) light chain n=1 Tax=Homo sapiens RepID=UPI0002	57.53	8.18%	1	1	220	24.2	6.55
135	62.21	UPI0002177BCC	S4 FAB LIGHT CHAIN n=1 Tax=Homo sapiens RepID=UPI0002177	57.53	8.53%	1	1	211	22.7	7.77
136	63	P37802	Transgelin-2 n=14 Tax=Theria RepID=TAGL2_HUMAN	96.81	9.05%	1	1	199	22.4	8.25
137	64.1	B4E1Q0	Uncharacterized protein n=2 Tax=Theria RepID=B4E1Q0_HUMA	50.38	12.82%	1	1	156	17.3	5.55
138	64.2	B3KQV6	cDNA FLJ33169 fis, clone ADRGL2000384, highly similar to Serin	50.38	4.88%	1	1	410	45.6	5.36
139	64.3	B4DQY1	cDNA FLJ56133, highly similar to Serine/threonine-protein phos	50.38	3.60%	1	1	555	61.5	5.12
140	64.4	E9PH38	Uncharacterized protein n=2 Tax=Homo sapiens RepID=E9PH38	50.38	3.93%	1	1	509	56.8	5.69
141	64.5	P30153	Serine/threonine-protein phosphatase 2A 65 kDa regulatory sul	50.38	3.40%	1	1	589	65.3	5.11

