

# Mascot Search Results

User : r-nakagawa  
Email :  
Search title : SN221365\_deTOP2B\_Erk1ml\_lul\_Node:2  
MS data file : File Name: Z:\SN221365\_deTOP2B\_Erk1ml\_lul.raw; File Path: :File Time: 3/1/2023 3:35:46 PM; File Size: 351320790 [Byte]  
Database 1 : cRAP STRAV\_protein6\_20230313 (118 sequences: 39090 residues)  
Database 2 : Original\_21\_21\_TOP2B\_1-566\_20210618 (1 sequences: 589 residues)  
Database 3 : Uniprot\_Proteome\_E.coli\_K12\_Proteome\_E.coli\_K12\_UP000000625\_2022\_01 (4448 sequences: 1358110 residues)  
Timestamp : 13 Sep 2023 at 00:28:03 GMT  
Enzyme : Trypsin  
Fixed modifications : Acetyl (Protein N-term), Oxidation (M), Phospho (ST), Phospho (Y)  
Variable modifications :  
Mass values : Monoisotopic  
Protein Mass : Unrestricted  
Peptide Mass Tolerance : ± 10 ppm  
Fragment Mass Tolerance : ± 0.8 Da  
Max Missed Cleavages : 3  
Instrument type : Default  
Number of queries : 13219  
Protein hits : 2:::TOP2B\_1-566  
1:::sp|K1C10\_HUMAN|  
1:::sp|K2C1\_HUMAN|  
1:::sp|K22E\_HUMAN|  
1:::sp|K1G9\_HUMAN|  
1:::sp|HBB\_HUMAN|  
1:::sp|K1C15\_SHEEP|  
3:::P0AA25\_THIO\_ECOLI|  
1:::sp|HBA\_HUMAN|  
1:::sp|LRYP\_PIG|  
1:::sp|ALBU\_BOVIN|  
3:::P76298\_FLHA\_ECOLI|  
1:::sp|KRHB4\_HUMAN|  
1:::sp|CAS9\_BOVIN|  
1:::sp|RS27A\_HUMAN|  
3:::P0AD96\_LIVJ\_ECOLI|  
3:::P7721\_CUSC\_ECOLI|  
3:::P75882\_GFCO\_ECOLI|  
3:::006065\_ATOC\_ECOLI|  
3:::P62601\_TREFF\_ECOLI|  
3:::Q0A23761A0A1H2C767\_ECOLI|  
3:::P32191ALSA\_ECOLI|  
3:::P76092\_YNBC\_ECOLI|  
3:::Q46857\_DKGA\_ECOLI|  
3:::P0ARHO\_F TSA\_ECOLI|  
3:::P12996\_BIOR\_ECOLI|  
3:::P39359\_YJHG\_ECOLI|  
3:::P21361\_YEIB\_ECOLI|  
3:::P142008\_ARFB\_ECOLI|  
3:::P12422\_WCAK\_ECOLI|  
3:::P46891\_COF\_ECOLI|  
1:::sp|CYC\_HUMAN|  
3:::P0A759\_NAGB\_ECOLI|  
3:::P0C018\_RL18\_ECOLI|  
3:::P0A1V0\_RSS2\_ECOLI|  
3:::P08333\_GNTR\_ECOLI|  
3:::P32053\_INIA\_ECOLI|  
3:::P06149\_DLD\_ECOLI|  
3:::P0AD18\_YGIM\_ECOLI|  
3:::P63201\_GADW\_ECOLI|  
3:::P22106\_ASNB\_ECOLI|  
3:::P15029\_FECO\_ECOLI|  
3:::P21393\_CASQ\_ECOLI|  
3:::P16104\_RLHA\_ECOLI|  
3:::P21393\_RECJ\_ECOLI|  
3:::P38035\_RTOR\_ECOLI|  
3:::P80645\_SSDU\_ECOLI|  
3:::P0AAJ8\_HYBA\_ECOLI|  
3:::P77380\_BORD\_ECOLI|  
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3:::P0A158\_RL18\_ECOLI|  
3:::P45522\_KEFB\_ECOLI|  
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3:::P0A1E9\_MALE\_ECOLI|  
3:::P33668\_YBBC\_ECOLI|  
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3:::P64822\_YHVD\_ECOLI|  
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3:::P0A996\_SECE\_ECOLI|  
3:::P14900\_MURD\_ECOLI|  
3:::P28249\_ASMA\_ECOLI|  
3:::P0ADF6\_EDD\_ECOLI|  
3:::P0AB65\_MRDA\_ECOLI|  
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3:::P0AFA2\_NARX\_ECOLI|  
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3:::P0A1R9\_RSTI\_ECOLI|  
3:::P25771\_IIGB\_ECOLI|  
1:::sp|UB2E\_HUMAN|  
3:::P75830\_MACA\_ECOLI|  
3:::P17169\_GLMS\_ECOLI|  
3:::P0AAH4\_SAPD\_ECOLI|  
3:::P76015\_DHAQ\_ECOLI|  
3:::P77765\_RNAAM\_ECOLI|  
3:::Q0DFV4\_YMDE\_ECOLI|  
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3:::P0A9M0\_LON\_ECOLI|  
3:::P09831\_GLTR\_ECOLI|  
3:::P0A1V3\_RS3\_ECOLI|  
3:::P02918\_PBPB\_ECOLI|  
3:::P37013\_NORR\_ECOLI|  
3:::P114292\_HYFR\_ECOLI|  
3:::P38134\_ETK\_ECOLI|  
3:::P55140\_YGCG\_ECOLI|  
3:::P00582\_DPOT\_ECOLI|  
3:::P76352\_YFEO\_ECOLI|  
3:::P0AGF6\_TDCB\_ECOLI|  
TOP2B\_1-566  
sp|K1C10\_HUMAN|  
sp|K2C1\_HUMAN|  
sp|K22E\_HUMAN|  
sp|K1G9\_HUMAN|  
sp|HBB\_HUMAN|  
sp|K1C15\_SHEEP|  
Thioredoxin I OS=Escherichia coli (strain K12) OX=83333 GN=trxA PE=1 SV=2  
sp|HBA\_HUMAN|  
sp|LRYP\_PIG|  
sp|ALBU\_BOVIN|  
Flagellar biosynthesis protein FlhA OS=Escherichia coli (strain K12) OX=83333 GN=flhA PE=3 SV=1  
sp|KRHB4\_HUMAN|  
sp|CAS9\_BOVIN|  
sp|RS27A\_HUMAN|  
Leu/Ile/Val-binding protein OS=Escherichia coli (strain K12) OX=83333 GN=livJ PE=1 SV=1  
Cation efflux system protein CusC OS=Escherichia coli (strain K12) OX=83333 GN=cusC PE=1 SV=1  
Uncharacterized lipoprotein GfcD OS=Escherichia coli (strain K12) OX=83333 GN=gfcD PE=3 SV=1  
Regulatory protein AtoC OS=Escherichia coli (strain K12) OX=83333 GN=atoC PE=1 SV=2  
Cytoplasmic trehalase OS=Escherichia coli (strain K12) OX=83333 GN=treF PE=1 SV=1  
Chaperone protein ClpB OS=Escherichia coli (strain K12) OX=83333 GN=clpB PE=3 SV=1  
D-1,6-bisphosphate 3-epimerase OS=Escherichia coli (strain K12) OX=83333 GN=alse PE=1 SV=1  
Uncharacterized protein YnbC OS=Escherichia coli (strain K12) OX=83333 GN=ynbC PE=1 SV=1  
2,5-diketone-D-gluconic acid reductase A OS=Escherichia coli (strain K12) OX=83333 GN=dkgA PE=1 SV=3  
Cell division protein FtsA OS=Escherichia coli (strain K12) OX=83333 GN=ftsA PE=1 SV=1  
Biotin synthase OS=Escherichia coli (strain K12) OX=83333 GN=bioB PE=1 SV=2  
D-xylosate dehydratase YjhG OS=Escherichia coli (strain K12) OX=83333 GN=yjhG PE=1 SV=2  
Uncharacterized protein YeiB OS=Escherichia coli (strain K12) OX=83333 GN=yeiB PE=3 SV=1  
Chromatin synthase OS=Escherichia coli (strain K12) OX=83333 GN=aroc PE=1 SV=4  
Colanic acid biosynthesis protein WcaK OS=Escherichia coli (strain K12) OX=83333 GN=wcaK PE=3 SV=2  
HMP-PP phosphatase OS=Escherichia coli (strain K12) OX=83333 GN=cof PE=1 SV=2  
sp|CYC\_HUMAN|  
Glucosamine-6-phosphate deaminase OS=Escherichia coli (strain K12) OX=83333 GN=nagB PE=1 SV=1  
50S ribosomal protein L18 OS=Escherichia coli (strain K12) OX=83333 GN=rpL18 PE=1 SV=1  
30S ribosomal protein S2 OS=Escherichia coli (strain K12) OX=83333 GN=rpsB PE=1 SV=2  
HTH-type transcriptional regulator GntR OS=Escherichia coli (strain K12) OX=83333 GN=gntR PE=1 SV=1  
Prophage integrase IntA OS=Escherichia coli (strain K12) OX=83333 GN=intA PE=1 SV=2  
Quinone-dependent D-lactate dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=dld PE=1 SV=3  
Uncharacterized protein YgiM OS=Escherichia coli (strain K12) OX=83333 GN=ygiM PE=3 SV=1  
HTH-type transcriptional regulator GadW OS=Escherichia coli (strain K12) OX=83333 GN=gadW PE=1 SV=1  
Asparagine synthetase B [glutamine-hydrolyzing] OS=Escherichia coli (strain K12) OX=83333 GN=asnB PE=1 SV=3  
Fe(3+) dicitrate transport system permease protein FecD OS=Escherichia coli (strain K12) OX=83333 GN=fecD PE=1 SV=2  
Aspartate--RNA ligase OS=Escherichia coli (strain K12) OX=83333 GN=aspS PE=1 SV=1  
23S rRNA guanylyl transferase OS=Escherichia coli (strain K12) OX=83333 GN=rha PE=1 SV=2  
Single-stranded-DNA-specific exonuclease RecJ OS=Escherichia coli (strain K12) OX=83333 GN=recJ PE=1 SV=2  
Transcriptional regulatory protein RtcR OS=Escherichia coli (strain K12) OX=83333 GN=rtcR PE=4 SV=2  
Alkanesulfonate monooxygenase OS=Escherichia coli (strain K12) OX=83333 GN=ssuD PE=1 SV=3  
Hydrogenase-2 operon protein HybA OS=Escherichia coli (strain K12) OX=83333 GN=hybA PE=3 SV=1  
Prophage lipoprotein Bor homolog OS=Escherichia coli (strain K12) OX=83333 GN=borD PE=3 SV=1  
CRISPR system Cascade subunit CasA OS=Escherichia coli (strain K12) OX=83333 GN=casA PE=1 SV=1  
Ribosomal small subunit pseudouridine synthase A OS=Escherichia coli (strain K12) OX=83333 GN=rsaA PE=1 SV=1  
Glutathione-regulated potassium-efflux system protein KefB OS=Escherichia coli (strain K12) OX=83333 GN=kefB PE=3 SV=1  
Probable electron transfer flavoprotein-quinone oxidoreductase YdiS OS=Escherichia coli (strain K12) OX=83333 GN=ydiS PE=3 SV=1  
Maltose/maltodextrin-binding periplasmic protein OS=Escherichia coli (strain K12) OX=83333 GN=malE PE=1 SV=1  
Uncharacterized protein YbbC OS=Escherichia coli (strain K12) OX=83333 GN=ybbC PE=2 SV=1  
Melibiose carrier protein OS=Escherichia coli (strain K12) OX=83333 GN=melB PE=1 SV=2  
Uncharacterized protein YhdV OS=Escherichia coli (strain K12) OX=83333 GN=yhdV PE=3 SV=1  
PTS system fructose-specific ELIB BC component OS=Escherichia coli (strain K12) OX=83333 GN=fraA PE=1 SV=1  
2,3-cyclic-nucleotide 2-phosphodiesterase/3'-nucleotidase OS=Escherichia coli (strain K12) OX=83333 GN=cpdB PE=1 SV=2  
Malonyl-[acyl]-carrier protein D-methyltransferase OS=Escherichia coli (strain K12) OX=83333 GN=bioC PE=1 SV=2  
Protein translocase subunit SecE OS=Escherichia coli (strain K12) OX=83333 GN=secE PE=1 SV=1  
UDP-N-acetylmuramoylalanine--D-glutamate ligase OS=Escherichia coli (strain K12) OX=83333 GN=murD PE=1 SV=3  
Protein AsmA OS=Escherichia coli (strain K12) OX=83333 GN=asma PE=3 SV=2  
Phosphogluconate dehydratase OS=Escherichia coli (strain K12) OX=83333 GN=edd PE=1 SV=1  
Peptidoglycan D,D-transpeptidase MrdA OS=Escherichia coli (strain K12) OX=83333 GN=mrda PE=1 SV=1  
Elongation factor P-like protein SapD OS=Escherichia coli (strain K12) OX=83333 GN=sapD PE=1 SV=1  
ATP-dependent RNA helicase HraA OS=Escherichia coli (strain K12) OX=83333 GN=hraA PE=1 SV=3  
Signal recognition particle protein OS=Escherichia coli (strain K12) OX=83333 GN=ffh PE=1 SV=1  
Nitrate/nitrite sensor protein NarX OS=Escherichia coli (strain K12) OX=83333 GN=narX PE=1 SV=1  
Glycerol-3-phosphate regulon repressor OS=Escherichia coli (strain K12) OX=83333 GN=glpR PE=1 SV=1  
Glucans biosynthesis protein G OS=Escherichia coli (strain K12) OX=83333 GN=mdoG PE=1 SV=1  
30S ribosomal protein S11 OS=Escherichia coli (strain K12) OX=83333 GN=rpsK PE=1 SV=2  
DNA ligase B OS=Escherichia coli (strain K12) OX=83333 GN=ligB PE=1 SV=2  
sp|UB2E\_HUMAN|  
Macrolide export protein MacA OS=Escherichia coli (strain K12) OX=83333 GN=macA PE=1 SV=2  
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] OS=Escherichia coli (strain K12) OX=83333 GN=glmS PE=1 SV=4  
Putrescine export system ATP-binding protein SapD OS=Escherichia coli (strain K12) OX=83333 GN=sapD PE=1 SV=1  
PEP-dependent dihydroxyacetone kinase, dihydroxyacetone-binding subunit DhaK OS=Escherichia coli (strain K12) OX=83333 GN=dhaK PE=5 SV=3  
3-exoribonuclease OS=Escherichia coli (strain K12) OX=83333 GN=ygiV PE=1 SV=1  
Putative uncharacterized protein YmdE OS=Escherichia coli (strain K12) OX=83333 GN=ymdE PE=5 SV=3  
Probable ketamine kinase YniA OS=Escherichia coli (strain K12) OX=83333 GN=yniA PE=3 SV=1  
FhuE receptor OS=Escherichia coli (strain K12) OX=83333 GN=fhuE PE=1 SV=2  
Lon protease OS=Escherichia coli (strain K12) OX=83333 GN=lon PE=1 SV=1  
Glutamate synthase [NADPH] large chain OS=Escherichia coli (strain K12) OX=83333 GN=gltB PE=1 SV=3  
30S ribosomal protein S3 OS=Escherichia coli (strain K12) OX=83333 GN=rpsC PE=1 SV=2  
Penicillin-binding protein 1A OS=Escherichia coli (strain K12) OX=83333 GN=mcrA PE=1 SV=1  
Anaerobic nitric oxide reductase transcription regulator NorR OS=Escherichia coli (strain K12) OX=83333 GN=norR PE=1 SV=2  
DNA-binding transcription activator Hyfr OS=Escherichia coli (strain K12) OX=83333 GN=hyfr PE=1 SV=1  
Tyrosine-protein kinase etk OS=Escherichia coli (strain K12) OX=83333 GN=etk PE=1 SV=2  
UPF0603 protein YgcG OS=Escherichia coli (strain K12) OX=83333 GN=ygcG PE=3 SV=2  
DNA polymerase I OS=Escherichia coli (strain K12) OX=83333 GN=polA PE=1 SV=1  
Probable FMN/FAD exporter YeeO OS=Escherichia coli (strain K12) OX=83333 GN=yeeO PE=1 SV=4  
L-threonine dehydratase catabolic TdcB OS=Escherichia coli (strain K12) OX=83333 GN=tdcB PE=1 SV=1

## Target Decoy False discovery rate

Peptide matches above identity threshold 574 64 11.15 %  
Peptide matches above homology or identity threshold 581 66 11.36 %

## Select Summary Report

Format As  Select Summary (protein hits)  [Help](#) [Help](#)  
Significance threshold p<  Max. number of hits  Show Percolator scores   
Standard scoring  MudPIT scoring   Display non-significant matches  Show sub-sets   
Show pop-ups  Suppress pop-ups  Require bold red   
Preferred taxonomy

All queries  Unassigned  Below homology threshold  Below identity threshold

1. 2:::TOP2B\_1-566 Mass: 66629 Score: 7506 Matches: 303(303) Sequences: 40(40) emPAI: 20.66

TOP2B\_1-566

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
397	401.7246	801.4346	801.4344	0.17	0	37	0.00029	1	U	K.AQTQLNK.K
473	410.7507	819.4867	819.4854	1.61	0	32	0.00067	1	U	K.IVGLQYK.K 464 471

<a href="#">516</a>	414.7813	827.5480	827.5480	0.01	1	28	0.0016	1	U	K.LIEVVK.K
<a href="#">623</a>	426.2422	850.4698	850.4701	-0.35	0	29	0.0012	1	U	R.YGVFPLR.G <a href="#">624</a> <a href="#">626</a> <a href="#">627</a>
<a href="#">758</a>	439.7584	877.5023	877.5022	0.22	0	34	0.00051	1	U	K.GIPVVEHK.V <a href="#">759</a>
<a href="#">975</a>	459.7572	917.4999	917.5004	-0.59	0	49	2e-005	1	U	K.DIVALMTR.R
<a href="#">1054</a>	465.7721	929.5297	929.5294	0.33	1	27	0.0025	1	U	K.AQTQLNKK.C <a href="#">1053</a>
<a href="#">1085</a>	467.7551	933.4956	933.4953	0.24	0	(40)	0.00015	1	U	K.DIVALMTR.R <a href="#">1082</a> <a href="#">1083</a> <a href="#">1084</a> <a href="#">1086</a>
<a href="#">1149</a>	473.2666	944.5187	944.5179	0.91	0	50	1.5e-005	1	U	K.LDETGVALK.V
<a href="#">1201</a>	478.2316	954.4486	954.4481	0.54	0	26	0.0051	1	U	K.FVTETACK.E
<a href="#">1252</a>	480.7449	959.4752	959.4746	0.64	0	(20)	0.016	1	U	K.ENMTLQPK.S <a href="#">1250</a>
<a href="#">1341</a>	488.2222	974.4299	974.4305	-0.62	0	54	4.3e-006	1	U	K.LDDANDAGG.H <a href="#">1342</a> <a href="#">1343</a>
<a href="#">1348</a>	488.7413	975.4681	975.4695	-1.46	0	22	0.0088	1	U	K.ENMTLQPK.S <a href="#">1352</a> <a href="#">1353</a>
<a href="#">1393</a>	491.7548	981.4951	981.4953	-0.26	0	39	0.00024	1	U	K.LCNIFSTK.F
<a href="#">1412</a>	493.7636	985.5126	985.5120	0.54	0	43	5.7e-005	1	U	R.SYVDLYK.D <a href="#">1410</a> <a href="#">1411</a> <a href="#">1413</a>
<a href="#">1585</a>	505.2440	1008.4735	1008.4732	0.26	1	(20)	0.012	1	U	R.DKNMTCIK.V
<a href="#">1604</a>	506.7296	1011.4446	1011.4444	0.20	0	43	8.1e-005	1	U	R.AYDLAGSCR.G
<a href="#">1704</a>	513.2408	1024.4671	1024.4681	-1.01	1	30	0.002	1	U	R.DKNMTCIK.V
<a href="#">1714</a>	514.2324	1026.4503	1026.4505	-0.23	0	46	2.7e-005	1	U	K.SYDDAESLK.T <a href="#">1716</a> <a href="#">1717</a>
<a href="#">1771</a>	518.2516	1034.4887	1034.4880	0.73	1	38	0.00025	1	U	K.KEESATANK.N
<a href="#">2142</a>	360.8647	1079.5724	1079.5723	0.03	0	(33)	0.00077	1	U	K.VIHELANER.W <a href="#">2132</a> <a href="#">2134</a> <a href="#">2137</a> <a href="#">2140</a> <a href="#">2145</a> <a href="#">2147</a> <a href="#">2150</a> <a href="#">2152</a>
<a href="#">2144</a>	540.7935	1079.5725	1079.5723	0.19	0	57	3.5e-006	1	U	K.VIHELANER.W <a href="#">2131</a> <a href="#">2135</a> <a href="#">2139</a> <a href="#">2143</a> <a href="#">2146</a> <a href="#">2148</a> <a href="#">2149</a>
<a href="#">2492</a>	374.8732	1121.5976	1121.5982	-0.49	1	(20)	0.017	1	U	R.DRYGVFPLR.G
<a href="#">2493</a>	561.8066	1121.5986	1121.5982	0.35	1	28	0.0021	1	U	R.DRYGVFPLR.G
<a href="#">2561</a>	376.8962	1127.6668	1127.6663	0.48	0	(36)	0.00027	1	U	K.SLAVSGLGVIGR.D
<a href="#">2563</a>	564.8409	1127.6672	1127.6663	0.81	0	74	4.4e-008	1	U	K.SLAVSGLGVIGR.D <a href="#">2549</a> <a href="#">2550</a> <a href="#">2551</a> <a href="#">2552</a> <a href="#">2554</a> <a href="#">2555</a> <a href="#">2556</a> <a href="#">2557</a> <a href="#">2558</a> <a href="#">2559</a> <a href="#">2560</a> <a href="#">2562</a> <a href="#">2564</a> <a href="#">2565</a> <a href="#">2566</a>
<a href="#">2786</a>	576.8188	1151.6230	1151.6227	0.32	0	28	0.0021	1	U	R.EVTFVPGLYK.I <a href="#">2774</a> <a href="#">2777</a> <a href="#">2779</a> <a href="#">2783</a> <a href="#">2784</a>
<a href="#">2814</a>	578.2802	1154.5458	1154.5455	0.30	1	34	0.0008	1	U	K.KSYDDAESLK.T <a href="#">2812</a>
<a href="#">2853</a>	387.2326	1158.6760	1158.6761	-0.11	0	(37)	0.00028	1	U	K.AGVSVKPFQVK.N <a href="#">2858</a> <a href="#">2859</a>
<a href="#">2857</a>	580.3454	1158.6762	1158.6761	0.06	0	48	2e-005	1	U	K.AGVSVKPFQVK.N <a href="#">2849</a> <a href="#">2856</a> <a href="#">2861</a> <a href="#">2862</a>
<a href="#">3045</a>	396.8872	1187.6396	1187.6398	-0.11	1	(30)	0.0022	1	U	K.DKLDETGVALK.V <a href="#">3046</a> <a href="#">3052</a>
<a href="#">3050</a>	594.8272	1187.6398	1187.6398	0.04	1	50	2.2e-005	1	U	K.DKLDETGVALK.V <a href="#">3047</a> <a href="#">3049</a> <a href="#">3051</a>
<a href="#">3118</a>	600.2537	1198.4929	1198.4933	-0.33	0	(28)	0.0018	1	U	K.QTWMNNMK.T <a href="#">3120</a>
<a href="#">3121</a>	600.2544	1198.4942	1198.4933	0.72	0	32	0.0009	1	U	K.QTWMNNMK.T <a href="#">3117</a> <a href="#">3119</a> <a href="#">3122</a>
<a href="#">3223</a>	608.2517	1214.4888	1214.4882	0.48	0	(31)	0.00074	1	U	K.QTWMNNMK.T <a href="#">3219</a> <a href="#">3221</a> <a href="#">3225</a>
<a href="#">3224</a>	608.2518	1214.4889	1214.4882	0.60	0	(27)	0.0019	1	U	K.QTWMNNMK.T <a href="#">3222</a>
<a href="#">3226</a>	608.2526	1214.4905	1214.4882	1.92	0	(30)	0.00091	1	U	K.QTWMNNMK.T
<a href="#">3542</a>	625.8076	1249.6007	1249.6013	-0.47	0	44	8.5e-005	1	U	R.WDVCLTSEK.G
<a href="#">3760</a>	637.8605	1273.7065	1273.7064	0.08	1	77	2.7e-008	1	U	K.LDKDIVALMTR.R <a href="#">3750</a> <a href="#">3752</a> <a href="#">3755</a> <a href="#">3759</a> <a href="#">3761</a> <a href="#">3762</a> <a href="#">3764</a> <a href="#">3765</a>
<a href="#">3766</a>	425.5762	1273.7068	1273.7064	0.35	1	(33)	0.00078	1	U	K.LDKDIVALMTR.R <a href="#">3753</a> <a href="#">3768</a>
<a href="#">3890</a>	430.9077	1289.7012	1289.7013	-0.12	1	(33)	0.001	1	U	K.LDKDIVALMTR.R <a href="#">3881</a> <a href="#">3884</a> <a href="#">3886</a> <a href="#">3888</a> <a href="#">3895</a> <a href="#">3896</a>
<a href="#">3894</a>	645.8581	1289.7016	1289.7013	0.26	1	(62)	1.4e-006	1	U	K.LDKDIVALMTR.R <a href="#">3882</a> <a href="#">3883</a> <a href="#">3885</a> <a href="#">3887</a> <a href="#">3889</a> <a href="#">3892</a> <a href="#">3893</a>
<a href="#">4374</a>	453.2417	1356.7032	1356.7038	-0.45	0	(44)	0.00011	1	U	R.HVDYVVDQVVGK.L <a href="#">4380</a> <a href="#">4390</a>
<a href="#">4388</a>	679.3593	1356.7041	1356.7038	0.24	0	81	2.5e-008	1	U	R.HVDYVVDQVVGK.L <a href="#">4375</a> <a href="#">4376</a> <a href="#">4377</a> <a href="#">4378</a> <a href="#">4381</a> <a href="#">4382</a> <a href="#">4383</a> <a href="#">4384</a> <a href="#">4385</a> <a href="#">4386</a> <a href="#">4387</a> <a href="#">4389</a> <a href="#">4391</a> <a href="#">4392</a> <a href="#">4394</a>
<a href="#">5153</a>	731.3817	1460.7488	1460.7511	-1.58	0	82	1.6e-008	1	U	K.IFDEILVNAADNK.Q <a href="#">5157</a> <a href="#">5158</a> <a href="#">5163</a> <a href="#">5169</a> <a href="#">5170</a> <a href="#">5174</a> <a href="#">5176</a> <a href="#">5180</a> <a href="#">5181</a> <a href="#">5182</a> <a href="#">5183</a> <a href="#">5185</a> <a href="#">5187</a>
<a href="#">5160</a>	487.9241	1460.7505	1460.7511	-0.40	0	(49)	3.2e-005	1	U	K.IFDEILVNAADNK.Q <a href="#">5151</a> <a href="#">5152</a> <a href="#">5155</a> <a href="#">5156</a> <a href="#">5159</a> <a href="#">5161</a> <a href="#">5162</a> <a href="#">5164</a> <a href="#">5165</a> <a href="#">5166</a> <a href="#">5167</a> <a href="#">5168</a> <a href="#">5171</a> <a href="#">5172</a> <a href="#">5173</a> <a href="#">5175</a>
<a href="#">5875</a>	765.4037	1528.7928	1528.7919	0.61	0	96	6e-010	1	U	K.QIMENAEINNIK.I <a href="#">5877</a>
<a href="#">5876</a>	510.6049	1528.7928	1528.7919	0.64	0	(32)	0.0017	1	U	K.QIMENAEINNIK.I
<a href="#">6055</a>	773.4005	1544.7865	1544.7868	-0.18	0	(75)	8e-008	1	U	K.QIMENAEINNIK.I <a href="#">6052</a> <a href="#">6053</a> <a href="#">6054</a> <a href="#">6056</a>
<a href="#">6238</a>	522.9128	1565.7167	1565.7169	-0.11	2	20	0.04	1	U	K.KEESATANKNDSSK.K <a href="#">6239</a>
<a href="#">6773</a>	820.9358	1639.8571	1639.8570	0.10	0	81	1.6e-008	1	U	K.GFQQISFVNSIATTK.G <a href="#">6758</a> <a href="#">6759</a> <a href="#">6761</a> <a href="#">6762</a> <a href="#">6763</a> <a href="#">6764</a> <a href="#">6765</a> <a href="#">6769</a> <a href="#">6770</a> <a href="#">6771</a> <a href="#">6772</a> <a href="#">6775</a> <a href="#">6776</a> <a href="#">6777</a> <a href="#">6778</a> <a href="#">6779</a>
<a href="#">6774</a>	547.6264	1639.8573	1639.8570	0.17	0	(56)	5.1e-006	1	U	K.GFQQISFVNSIATTK.G <a href="#">6756</a> <a href="#">6760</a> <a href="#">6766</a> <a href="#">6767</a> <a href="#">6782</a>
<a href="#">7469</a>	866.4067	1730.7989	1730.7968	1.23	0	(69)	4.4e-007	1	U	K.IMIMTDQDQDGSNIK.A <a href="#">7466</a>
<a href="#">7470</a>	577.9414	1730.8024	1730.7968	3.25	0	(23)	0.02	1	U	K.IMIMTDQDQDGSNIK.A <a href="#">7468</a>
<a href="#">7565</a>	583.2707	1746.7902	1746.7917	-0.84	0	(32)	0.0016	1	U	K.IMIMTDQDQDGSNIK.A <a href="#">7580</a>
<a href="#">7567</a>	874.4030	1746.7915	1746.7917	-0.11	0	(68)	3.8e-007	1	U	K.IMIMTDQDQDGSNIK.A <a href="#">7569</a> <a href="#">7576</a>
<a href="#">7570</a>	874.4031	1746.7916	1746.7917	-0.06	0	77	6.1e-008	1	U	K.IMIMTDQDQDGSNIK.A <a href="#">7575</a>
<a href="#">7578</a>	583.2716	1746.7930	1746.7917	0.78	0	(48)	4.3e-005	1	U	K.IMIMTDQDQDGSNIK.A <a href="#">7564</a> <a href="#">7568</a> <a href="#">7571</a> <a href="#">7572</a> <a href="#">7573</a> <a href="#">7574</a> <a href="#">7579</a>
<a href="#">7688</a>	588.6029	1762.7869	1762.7866	0.18	0	(62)	2.5e-006	1	U	K.IMIMTDQDQDGSNIK.A <a href="#">7679</a> <a href="#">7680</a> <a href="#">7681</a> <a href="#">7682</a> <a href="#">7686</a> <a href="#">7687</a> <a href="#">7689</a> <a href="#">7691</a> <a href="#">7693</a> <a href="#">7694</a> <a href="#">7700</a>
<a href="#">7697</a>	882.4014	1762.7882	1762.7866	0.91	0	(72)	3e-007	1	U	K.IMIMTDQDQDGSNIK.A <a href="#">7678</a> <a href="#">7684</a> <a href="#">7685</a> <a href="#">7692</a> <a href="#">7695</a> <a href="#">7696</a> <a href="#">7698</a> <a href="#">7699</a>
<a href="#">7762</a>	591.9606	1772.8600	1772.8615	-0.82	0	(24)	0.014	1	U	K.HSLECTLILTEGSAK.S
<a href="#">7763</a>	887.4382	1772.8618	1772.8615	0.22	0	93	1.8e-009	1	U	K.HSLECTLILTEGSAK.S
<a href="#">8521</a>	629.3266	1884.9580	1884.9581	-0.04	0	(59)	2.5e-006	1	U	K.VSIDPESNIISWNGK.G
<a href="#">8522</a>	943.4864	1884.9583	1884.9581	0.11	0	77	4.3e-008	1	U	K.VSIDPESNIISWNGK.G
<a href="#">9649</a>	724.9902	2171.9488	2171.9470	0.83	0	40	0.00043	1	U	K.HFDGEDYTCITFQPLSK.F
<a href="#">10285</a>	805.3811	2413.1216	2413.1260	-1.85	1	55	1.5e-005	1	U	K.IKHFQDGEDYTCITFQPLSK.F <a href="#">10286</a>
<a href="#">10546</a>	1244.1186	2486.2226	2486.2217	0.36	0	86	1.3e-008	1	U	K.VYVPALIFGQLLTSSNYDDDEK.K <a href="#">10538</a> <a href="#">10543</a> <a href="#">10548</a> <a href="#">10550</a> <a href="#">10551</a>
<a href="#">10547</a>	829.7482	2486.2227	2486.2217	0.40	0	(54)	2.1e-005	1	U	K.VYVPALIFGQLLTSSNYDDDEK.K <a href="#">10541</a>
<a href="#">10737</a>	859.4251	2575.2534	2575.2529	0.19	0	39	0.00073	1	U	K.NHIWVFINLIENPTFDSOTK.E
<a href="#">10815</a>	872.4458	2614.3155	2614.3166	-0.43	1	(54)	1.9e-005	1	U	K.VYVPALIFGQLLTSSNYDDDEK.V <a href="#">10813</a> <a href="#">10817</a> <a href="#">10818</a> <a href="#">10824</a> <a href="#">10829</a> <a href="#">10830</a>
<a href="#">10819</a>	654.5865	2614.3169	2614.3166	0.10	1	(47)	9.7e-005	1	U	K.VYVPALIFGQLLTSSNYDDDEK.V <a href="#">10820</a>
<a href="#">10827</a>	1308.1665	2614.3185	2614.3166	0.72	1	64	2.1e-006	1	U	K.VYVPALIFGQLLTSSNYDDDEK.V <a href="#">10812</a>

2. [L::sp|K1C10\\_HUMAN|](#) Mass: 59711 Score: 1630 Matches: 47(47) Sequences: 26(26) emPAI: 7.52

sp|K1C10\_HUMAN|

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">419</a>	404.2030	806.3915	806.3923	-0.98	0	42	8.9e-005	1		R.LAADDFR.L
<a href="#">428</a>	405.2240	808.4334	808.4330	0.45	0	30	0.00091	1		R.LASYLDK.V
<a href="#">602</a>	424.2297	846.4449	846.4447	0.30	0	25	0.0049	1	U	K.SEITELR.R
<a href="#">959</a>	458.6957	915.3769	915.3756	1.39	0	25	0.0042	1		K.NHEEEMK.D
<a href="#">1464</a>	497.2533	992.4920	992.4927	-0.71	0	45	4.9e-005	1	U	K.YENEVALR.Q
<a href="#">1476</a>	498.2636	994.5126	994.5123	0.27	1	27	0.0057	1	U	K.IKEWYEK.H
<a href="#">1537</a>	502.2799	1002.5453	1002.5458	-0.47	1	23	0.0079	1	U	K.SEITELRR.N
<a href="#">1751</a>	516.3022	1030.5899	1030.5910	-1.10	0	55	3.4e-006	1		R.VLDELTLTK.A
<a href="#">2223</a>	545.7691	1089.5236	1089.5237	-0.10	0	(46)	3.8e-005	1	U	K.VTQNLNDR.L
<a href="#">2354</a>	553.7668	1105.5191	1105.5186	0.44	0	59	2e-006	1	U	K.VTQNLNDR.L <a href="#">2352</a>
<a href="#">3133</a>	601.3123	1200.6100	1200.6098	0.13	0	62	1.5e-006	1		R.QSVEADINGLR.R

<a href="#">3387</a>	617.8431	1233.6717	1233.6717	-0.00	1	34	0.00052	1	U	R.LKYENEVALR.Q
<a href="#">3388</a>	412.2313	1233.6720	1233.6717	0.24	1	(34)	0.00056	1	U	R.LKYENEVALR.Q
<a href="#">3634</a>	631.8023	1261.5901	1261.5899	0.21	0	65	7e-007	1	U	R.SLLEGGSSGGGR.G
<a href="#">3950</a>	434.2033	1299.5880	1299.5877	0.23	1	34	0.00094	1	U	K.NHEEEMKDLR.N
<a href="#">4452</a>	683.3235	1364.6324	1364.6320	0.30	0	66	4.1e-007	1	U	R.SQYEQLAEQNR.K
<a href="#">4567</a>	691.3281	1380.6417	1380.6408	0.64	0	81	2.3e-008	1	U	R.ALEESNYELEGK.I
<a href="#">4903</a>	717.8887	1433.7628	1433.7626	0.15	1	60	2.1e-006	1	U	K.IRLENEIQTYR.S
<a href="#">5458</a>	747.3708	1492.7269	1492.7270	-0.02	1	49	4e-005	1	U	R.SQYEQLAEQNR.K
<a href="#">5459</a>	498.5832	1492.7278	1492.7270	0.53	1	(31)	0.0023	1	U	R.SQYEQLAEQNR.K
<a href="#">7283</a>	854.3888	1706.7630	1706.7649	-1.10	0	110	2.2e-011	1	U	K.GSLGGFFSGGFSR.G
<a href="#">7969</a>	599.6753	1796.0040	1796.0043	-0.15	0	(90)	1.1e-009	1	U	R.NVQALEIQLSQLALK.Q
<a href="#">7971</a>	899.0096	1796.0047	1796.0043	0.19	0	117	1.8e-012	1	U	R.NVQALEIQLSQLALK.Q <a href="#">7970</a>
<a href="#">9028</a>	666.3284	1995.9634	1995.9636	-0.12	0	(41)	0.00034	1	U	K.ELTTEIDNNEIQISSYK.S
<a href="#">9029</a>	998.9900	1995.9653	1995.9636	0.86	0	81	3.4e-008	1	U	K.ELTTEIDNNEIQISSYK.S
<a href="#">9370</a>	1048.5271	2095.0397	2095.0394	0.12	0	(75)	1.6e-007	1	U	K.ADLEMQIESLTELAYLK.K <a href="#">9369</a> <a href="#">9372</a>
<a href="#">9371</a>	699.3545	2095.0416	2095.0394	1.06	0	(49)	5.1e-005	1	U	K.ADLEMQIESLTELAYLK.K
<a href="#">9458</a>	704.6854	2111.0344	2111.0343	0.03	0	(49)	4.4e-005	1	U	K.ADLEMQIESLTELAYLK.K
<a href="#">9459</a>	1056.5249	2111.0353	2111.0343	0.45	0	77	6.9e-008	1	U	K.ADLEMQIESLTELAYLK.K
<a href="#">9788</a>	738.0386	2211.0940	2211.0906	1.53	1	44	0.0002	1	U	K.SKELTTEIDNNEIQISSYK.S <a href="#">9787</a>
<a href="#">9830</a>	742.0526	2223.1358	2223.1344	0.65	1	21	0.027	1	U	K.ADLEMQIESLTELAYLK.K.N
<a href="#">10190</a>	1184.1328	2366.2509	2366.2553	-1.86	0	61	1.9e-006	1	U	K.NQILNLTDDNANILLQIDNAR.L <a href="#">10191</a>
<a href="#">10192</a>	789.7587	2366.2542	2366.2553	-0.49	0	(60)	2.3e-006	1	U	K.NQILNLTDDNANILLQIDNAR.L <a href="#">10193</a>
<a href="#">11262</a>	958.1358	2871.3856	2871.3855	0.05	0	(45)	0.00023	1	U	R.NVSTGDVNVEMNAAPGVDLTQLLNMR.S
<a href="#">11283</a>	963.4665	2887.3776	2887.3804	-0.99	0	(39)	0.00083	1	U	R.NVSTGDVNVEMNAAPGVDLTQLLNMR.S <a href="#">11282</a>
<a href="#">11285</a>	963.4687	2887.3843	2887.3804	1.34	0	65	2.2e-006	1	U	R.NVSTGDVNVEMNAAPGVDLTQLLNMR.S
<a href="#">11322</a>	968.7992	2903.3757	2903.3753	0.12	0	(48)	9.2e-005	1	U	R.NVSTGDVNVEMNAAPGVDLTQLLNMR.S
<a href="#">11763</a>	1018.2139	3051.6200	3051.6200	-0.00	1	60	2.4e-006	1	U	K.TIDDLKNQILNLTDDNANILLQIDNAR.L <a href="#">11762</a>

3. [1::sp|K2C1\\_HUMAN|](#) Mass: 66018 Score: 1517 Matches: 45(45) Sequences: 29(29) emPAI: 7.43

[sp|K2C1\\_HUMAN|](#)

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">406</a>	402.7085	803.4024	803.4025	-0.12	0	28	0.0015	1	U	R.SEIDNVK.K
<a href="#">742</a>	437.7535	873.4924	873.4920	0.47	0	45	4.4e-005	1	U	R.SLVNLGGSK.S
<a href="#">1069</a>	466.7559	931.4973	931.4974	-0.16	1	37	0.00045	1	U	R.SEIDNVKK.Q
<a href="#">1329</a>	487.2696	972.5246	972.5240	0.67	0	41	8.9e-005	1	U	K.IEISELNR.V
<a href="#">1506</a>	500.2263	998.4381	998.4379	0.23	0	45	5e-005	1	U	K.DVDGAYMTK.V
<a href="#">1624</a>	508.2235	1014.4325	1014.4328	-0.30	0	(41)	7.3e-005	1	U	K.DVDGAYMTK.V
<a href="#">1760</a>	517.2620	1032.5094	1032.5087	0.66	0	35	0.00042	1	U	R.TLLEGEESR.M
<a href="#">2015</a>	533.7621	1065.5097	1065.5090	0.62	1	29	0.0019	1	U	K.YEDEINKR.T
<a href="#">2016</a>	356.1772	1065.5099	1065.5090	0.76	1	(23)	0.0082	1	U	K.YEDEINKR.T
<a href="#">2076</a>	537.3011	1072.5877	1072.5876	0.08	1	35	0.00093	1	U	R.LRSEIDNVK.K
<a href="#">2250</a>	546.7552	1091.4959	1091.4956	0.27	0	59	1.4e-006	1	U	R.GSGGSSGSGSIGGR.G
<a href="#">2523</a>	563.2746	1124.5346	1124.5349	-0.25	0	64	7.4e-007	1	U	K.AEAESLYQSK.Y
<a href="#">2538</a>	564.2737	1126.5329	1126.5329	0.01	1	(31)	0.0016	1	U	K.KVDGAYMTK.V
<a href="#">2692</a>	572.2676	1142.5207	1142.5278	-6.16	1	40	0.00014	1	U	K.KVDGAYMTK.V
<a href="#">2769</a>	576.7801	1151.5457	1151.5458	-0.12	1	27	0.0046	1	U	R.NKYEDEINKR
<a href="#">2825</a>	579.2612	1156.5079	1156.5070	0.79	0	42	0.00012	1	U	R.DYQELMNTK.L
<a href="#">2986</a>	590.3039	1178.5932	1178.5931	0.11	0	67	4.8e-007	1	U	K.YEELQITAGR.H <a href="#">2985</a>
<a href="#">3136</a>	401.2345	1200.6816	1200.6826	-0.85	2	23	0.0062	1	U	R.LRSEIDNVK.K
<a href="#">3137</a>	601.3488	1200.6831	1200.6826	0.44	2	(17)	0.028	1	U	R.LRSEIDNVK.K
<a href="#">3791</a>	639.3587	1276.7029	1276.7027	0.17	0	70	1.7e-007	1	U	K.LALDLEIATYR.T
<a href="#">3947</a>	650.7680	1299.5215	1299.5224	-0.64	0	(58)	2.4e-006	1	U	K.NMQDMVEDYR.N
<a href="#">3986</a>	651.8612	1301.7079	1301.7078	0.08	0	65	6.4e-007	1	U	R.SLDLSIAEVK.A
<a href="#">4028</a>	436.8896	1307.6470	1307.6469	0.08	2	37	0.00052	1	U	R.NKYEDEINKR.T
<a href="#">4029</a>	654.8309	1307.6472	1307.6469	0.23	2	(33)	0.0013	1	U	R.NKYEDEINKR.T
<a href="#">4087</a>	658.7659	1315.5172	1315.5173	-0.03	0	(46)	2.3e-005	1	U	K.NMQDMVEDYR.N
<a href="#">4088</a>	658.7664	1315.5183	1315.5173	0.77	0	61	7.9e-007	1	U	K.NMQDMVEDYR.N
<a href="#">4230</a>	666.7634	1331.5123	1331.5122	0.09	0	(48)	1.5e-005	1	U	K.NMQDMVEDYR.N <a href="#">4231</a> <a href="#">4232</a> <a href="#">4233</a>
<a href="#">4283</a>	670.8385	1339.6625	1339.6619	0.46	1	60	2.1e-006	1	U	K.SKAEAESLYQSK.Y
<a href="#">4373</a>	679.3517	1356.6888	1356.6885	0.27	0	72	1.9e-007	1	U	K.LNLDLALQOAK.E
<a href="#">4587</a>	692.3493	1382.6841	1382.6830	0.76	0	64	7.2e-007	1	U	K.SLNNQFASFDK.V
<a href="#">5311</a>	738.3940	1474.7734	1474.7780	-3.10	0	83	1.1e-008	1	U	R.FLEQQNQVLQK.W
<a href="#">6898</a>	829.4002	1656.7859	1656.7856	0.16	0	74	1.6e-007	1	U	R.SGGFSSGSGAGIINYQR.R <a href="#">6899</a>
<a href="#">6900</a>	553.2700	1656.7882	1656.7856	1.55	0	(20)	0.034	1	U	R.SGGFSSGSGAGIINYQR.R
<a href="#">7358</a>	858.9290	1715.8435	1715.8438	-0.15	0	81	2.7e-008	1	U	K.QISNLQOISDAEQR.G
<a href="#">7359</a>	572.9553	1715.8440	1715.8438	0.08	0	(41)	0.00031	1	U	K.QISNLQOISDAEQR.G
<a href="#">8306</a>	615.6538	1843.9396	1843.9388	0.47	1	18	0.042	1	U	K.QOISNLQOISDAEQR.G
<a href="#">9022</a>	665.3300	1992.9683	1992.9693	-0.53	0	45	0.00013	1	U	R.THNLEPYFESFINLR.R
<a href="#">10213</a>	1192.4786	2382.9426	2382.9447	-0.87	0	103	9e-011	1	U	R.GGGGGYSGSSYSGGGYSGGGGGGR.G
<a href="#">10214</a>	795.3222	2382.9447	2382.9447	0.02	0	(76)	4.6e-008	1	U	R.GGGGGYSGSSYSGGGYSGGGGGGR.G
<a href="#">12365</a>	1104.7747	3311.3023	3311.3009	0.42	0	95	9.9e-010	1	U	R.GSYSGSSYSGGGYSGGGGGHGSYSGSSGGYR.G

4. [1::sp|K22E\\_HUMAN|](#) Mass: 66110 Score: 1232 Matches: 35(35) Sequences: 28(28) emPAI: 5.92

[sp|K22E\\_HUMAN|](#)

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">514</a>	414.2188	826.4230	826.4225	0.61	0	33	0.00055	1	U	K.FASFDK.V
<a href="#">523</a>	416.2506	830.4867	830.4862	0.62	0	30	0.00097	1	U	R.SLVGLGGTK.S
<a href="#">1329</a>	487.2696	972.5246	972.5240	0.67	0	41	8.9e-005	1	U	K.IEISELNR.V
<a href="#">1471</a>	497.7876	993.5607	993.5607	-0.03	0	49	1.4e-005	1	U	R.LQGEIAHVK.K
<a href="#">1776</a>	519.2675	1036.5204	1036.5189	1.41	0	54	8.1e-006	1	U	R.YLDGLTAEK.T
<a href="#">1780</a>	519.7591	1037.5037	1037.5029	0.78	1	35	0.00045	1	U	K.KYEDEINKR
<a href="#">1798</a>	521.2823	1040.5500	1040.5502	-0.22	0	46	2.4e-005	1	U	K.VDPEIQNVK.A
<a href="#">2015</a>	533.7621	1065.5097	1065.5090	0.62	1	29	0.0019	1	U	K.YEDEINKR.T
<a href="#">2016</a>	356.1772	1065.5099	1065.5090	0.76	1	(23)	0.0082	1	U	K.YEDEINKR.T
<a href="#">2180</a>	542.7526	1083.4907	1083.4906	0.04	0	38	0.00022	1	U	K.DVDNAYIK.V

<a href="#">2359</a>	554.2752	1106.5358	1106.5356	0.21	0	33	0.00056	1	U	K.AGYEEIAQR.S
<a href="#">3077</a>	597.3118	1192.6091	1192.6088	0.28	0	62	1.8e-006	1	U	K.YEELQVTVGR.H
<a href="#">3081</a>	398.8752	1193.6039	1193.6040	-0.12	2	52	1e-005	1	U	K.KYEDENK.R.T
<a href="#">3105</a>	599.2782	1196.5419	1196.5422	-0.25	0	50	2.1e-005	1	U	K.GSGISGGGYSGGGK.H
<a href="#">3179</a>	604.8117	1207.6089	1207.6085	0.37	0	69	1.9e-007	1	U	R.TAAENDFVTLK.K
<a href="#">3574</a>	627.8074	1253.6002	1253.6001	0.12	0	87	4.9e-009	1	U	R.GFSSGSAAVSSGGR.R
<a href="#">3637</a>	632.3506	1262.6865	1262.6870	-0.38	0	70	2.4e-007	1	U	K.LALDVEIATYR.K
<a href="#">4119</a>	660.7949	1319.5752	1319.5756	-0.30	0	66	5e-007	1	U	R.HGGGGGGGGGGFGR.S
<a href="#">4120</a>	440.8659	1319.5760	1319.5756	0.29	0	(37)	0.00038	1	U	R.HGGGGGGGGGGFGR.S
<a href="#">4195</a>	665.3235	1328.6325	1328.6320	0.33	0	75	5.6e-008	1	U	K.NVQDAIADAEQR.G
<a href="#">4196</a>	665.3667	1328.7188	1328.7187	0.05	0	68	4.6e-007	1	U	R.NLDLDSIAEVK.A
<a href="#">4261</a>	668.8601	1335.7057	1335.7034	1.70	1	61	1.5e-006	1	U	R.TAAENDFVTLK.D
<a href="#">4489</a>	686.3592	1370.7037	1370.7041	-0.27	0	77	4.2e-008	1	U	K.LNDLEALQQAQ.E
<a href="#">4631</a>	696.3438	1390.6730	1390.6728	0.13	1	65	5.6e-007	1	U	R.SKEEAALYHSK.Y
<a href="#">4632</a>	464.5649	1390.6730	1390.6728	0.13	1	(34)	0.00074	1	U	R.SKEEAALYHSK.Y
<a href="#">5150</a>	730.9034	1459.7922	1459.7922	-0.01	0	76	4.4e-008	1	U	K.VDLLNQEIFLKV.V
<a href="#">5311</a>	738.3940	1474.7734	1474.7780	-3.10	0	83	1.1e-008	1	U	R.FLEQQNVLTQK.W
<a href="#">8274</a>	919.9613	1837.9080	1837.9072	0.48	0	53	1.8e-005	1	U	K.SISISVAGGGGGFAGGGFGR.G
<a href="#">9947</a>	752.6867	2255.0382	2255.0376	0.29	1	(32)	0.0029	1	U	R.TSQNSELNMQDLVEDYKK.K
<a href="#">9995</a>	758.0187	2271.0343	2271.0325	0.79	1	43	0.00021	1	U	R.TSQNSELNMQDLVEDYKK.K
<a href="#">11747</a>	1016.8360	3047.4860	3047.4870	-0.31	0	56	1.7e-005	1	U	K.VLYDAEISQIHQSVTDTNVLISMDNSR.N <a href="#">11748</a>
<a href="#">11778</a>	1022.1687	3063.4842	3063.4819	0.74	0	(47)	0.00012	1	U	K.VLYDAEISQIHQSVTDTNVLISMDNSR.N
<a href="#">13033</a>	1023.7731	4091.0633	4091.0654	-0.53	0	29	0.0075	1	U	R.FGGGGPGVGGGLGGPGGGYGGIHEVSNQSLLOPLNVK.V <a href="#">13034</a>

5. [!::sp|KIC9\\_HUMAN|](#) Mass: 62320 Score: 1205 Matches: 35(35) Sequences: 20(20) emPAI: 3.83

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">428</a>	405.2240	808.4334	808.4330	0.45	0	30	0.00091	1	U	R.LASLQDK.V
<a href="#">432</a>	406.7533	811.4920	811.4916	0.52	1	57	1.8e-006	1	U	K.KGPAAIQK.N
<a href="#">841</a>	449.2103	896.4061	896.4062	-0.08	0	(19)	0.026	1	U	R.MTLDDFR.I
<a href="#">944</a>	457.2079	912.4012	912.4011	0.12	0	26	0.0029	1	U	R.MTLDDFR.I
<a href="#">1967</a>	530.7857	1059.5568	1059.5560	0.73	0	42	0.00011	1	U	K.TLLDIDNTR.M
<a href="#">2002</a>	533.2535	1064.4924	1064.4920	0.37	0	53	5.9e-006	1	U	K.STMQELNSR.L
<a href="#">2157</a>	541.2513	1080.4881	1080.4870	1.05	0	(20)	0.017	1	U	K.STMQELNSR.L
<a href="#">2276</a>	365.8537	1094.5394	1094.5396	-0.20	1	22	0.014	1	U	K.IDQWYDKK.G
<a href="#">2277</a>	548.2772	1094.5398	1094.5396	0.19	1	(17)	0.043	1	U	K.IDQWYDKK.G
<a href="#">2485</a>	561.2961	1120.5777	1120.5764	1.17	0	35	0.00063	1	U	R.QEYEQLIQK.N
<a href="#">3176</a>	603.8054	1205.5962	1205.5962	-0.01	0	41	0.00017	1	U	R.QVLDNLTMEK.S
<a href="#">3374</a>	616.8026	1231.5907	1231.5906	0.12	0	77	4.4e-008	1	U	R.SGGGGGGGLSGGGIR.S
<a href="#">3395</a>	618.2678	1234.5210	1234.5215	-0.36	0	63	9.9e-007	1	U	R.FSSSSGGGGSSR.V
<a href="#">4018</a>	436.5639	1306.6697	1306.6703	-0.46	1	(26)	0.0065	1	U	R.IKFEMEQLR.Q
<a href="#">4148</a>	662.3401	1322.6656	1322.6652	0.27	1	41	0.00022	1	U	R.IKFEMEQLR.Q
<a href="#">4149</a>	441.8960	1322.6661	1322.6652	0.64	1	(32)	0.002	1	U	R.IKFEMEQLR.Q <a href="#">4150</a>
<a href="#">6440</a>	529.5936	1585.7589	1585.7583	0.33	0	(35)	0.00099	1	U	K.VQALEEANNLENK.I
<a href="#">6441</a>	793.8869	1585.7592	1585.7583	0.57	0	80	2.9e-008	1	U	K.VQALEEANNLENK.I
<a href="#">7877</a>	896.3674	1790.7203	1790.7205	-0.08	0	97	3.7e-010	1	U	R.GSGSGSGGGGGGGGGSSR.G <a href="#">7875</a>
<a href="#">8272</a>	613.3267	1836.9582	1836.9581	0.07	0	39	0.00024	1	U	R.HGVQLEIEILOSLSK.K <a href="#">8273</a>
<a href="#">9752</a>	1102.0074	2202.0002	2202.0072	-3.14	0	99	5.8e-010	1	U	K.SDLEMQYETLQELMALK.K <a href="#">9753</a>
<a href="#">9754</a>	735.0093	2202.0060	2202.0072	-0.51	0	(28)	0.0068	1	U	K.SDLEMQYETLQELMALK.K <a href="#">9755</a>
<a href="#">10589</a>	837.3814	2509.1223	2509.1245	-0.88	0	74	2.2e-007	1	U	K.EIETYHNLLEGGQEDFESSGAGK.I <a href="#">10590</a>
<a href="#">11296</a>	965.8013	2894.3820	2894.3828	-0.30	1	55	1.8e-005	1	U	K.NHKEEMSQLTGQNSGDVNVINVPAGK.D
<a href="#">11315</a>	726.3582	2901.4039	2901.4032	0.22	1	(22)	0.049	1	U	K.NYSPYYNTIDDLKQIVDLTVGNK.T
<a href="#">11316</a>	968.1420	2901.4042	2901.4032	0.35	1	40	0.00075	1	U	K.NYSPYYNTIDDLKQIVDLTVGNK.T
<a href="#">12188</a>	1075.0977	3222.2712	3222.2744	-0.99	0	89	4.3e-009	1	U	R.GSGSGSHGGSGFSGSGSGSGGEEASGSGGGYGGGSK.S <a href="#">12189</a>
<a href="#">12291</a>	1088.8422	3263.5047	3263.5066	-0.58	0	92	5.2e-009	1	U	K.DIENQYETQITQIEHEVSSSGEYQSSAK.E

6. [!::sp|HBB\\_HUMAN|](#) Mass: 15971 Score: 317 Matches: 10(10) Sequences: 7(7) emPAI: 7.10

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">1070</a>	466.7639	931.5132	931.5127	0.49	0	31	0.00097	1	U	K.SAVTALWGK.V
<a href="#">1187</a>	476.7583	951.5021	951.5025	-0.45	0	22	0.0085	1	U	-.VHLTPEEK.S
<a href="#">2532</a>	563.7859	1125.5572	1125.5567	0.47	0	29	0.0025	1	U	K.LHVDPENFR.L
<a href="#">2534</a>	376.1931	1125.5576	1125.5567	0.76	0	(21)	0.016	1	U	K.LHVDPENFR.L
<a href="#">2745</a>	383.8961	1148.6664	1148.6666	-0.15	0	(35)	0.00029	1	U	K.VVAGVANALAHK.Y
<a href="#">2746</a>	575.3408	1148.6671	1148.6666	0.48	0	72	6.3e-008	1	U	K.VVAGVANALAHK.Y
<a href="#">3769</a>	637.8674	1273.7202	1273.7183	1.52	0	40	0.00011	1	U	R.LLVVYPWTQR.F
<a href="#">4552</a>	689.8543	1377.6941	1377.6929	0.91	0	25	0.0065	1	U	K.EFTPPVQAAQK.V
<a href="#">9218</a>	1029.9782	2057.9418	2057.9405	0.65	0	95	1.6e-009	1	U	R.FFESFGDLSTPDVAVMGNPK.V
<a href="#">9282</a>	1037.9748	2073.9350	2073.9354	-0.20	0	(82)	3e-008	1	U	R.FFESFGDLSTPDVAVMGNPK.V

7. [!::sp|KIC15\\_SHEEP|](#) Mass: 48740 Score: 203 Matches: 6(6) Sequences: 6(6) emPAI: 0.69

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">419</a>	404.2030	806.3915	806.3923	-0.98	0	42	8.9e-005	1	U	R.LAADDR.L
<a href="#">959</a>	458.6957	915.3769	915.3756	1.39	0	25	0.0042	1	U	K.NHEEMK.E
<a href="#">1436</a>	495.2725	988.5305	988.5301	0.34	1	23	0.0093	1	U	K.SEITDLRR.T
<a href="#">1751</a>	516.3022	1030.5899	1030.5910	-1.10	0	55	3.4e-006	1	U	R.VLDELTLTK.T
<a href="#">3133</a>	601.3123	1200.6100	1200.6098	0.13	0	62	1.5e-006	1	U	R.QSVEADINGLR.R
<a href="#">3974</a>	651.3328	1300.6511	1300.6510	0.09	0	68	3.3e-007	1	U	R.ALEEANADLEVK.I

8. [3::POAA25|THIO\\_ECOLI|](#) Mass: 11913 Score: 181 Matches: 3(3) Sequences: 2(2) emPAI: 1.01

Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">3688</a>	634.3356	1266.6566	1266.6568	-0.15	0	82	1.3e-008	1	U	K.LNIDQNPATAP.Y
<a href="#">8057</a>	903.4532	1804.8919	1804.8917	0.14	0	70	3.1e-007	1	U	K.MIAPILDEIAEYQK.L <a href="#">8056</a>

9.	<a href="#">1::sp HBA_HUMAN </a>	Mass: 15174	Score: 172	Matches: 7(7)	Sequences: 5(5)	emPAI: 4.19						
	sp HBA_HUMAN											
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide	
	<a href="#">107</a>	365.2106	728.4067	728.4068	-0.16	0	24	0.0037	1	U	- . VLSPADK. T	
	<a href="#">2067</a>	536.2806	1070.5466	1070.5471	-0.42	0	27	0.0026	1	U	R. MFLSFPTTK. T	
	<a href="#">2206</a>	544.2784	1086.5422	1086.5420	0.18	0	(16)	0.031	1	U	R. MFLSFPTTK. T	
	<a href="#">3564</a>	626.8609	1251.7073	1251.7075	-0.12	0	57	2.3e-006	1	U	K. FLASVSTVLTSK. Y	
	<a href="#">5872</a>	765.3710	1528.7274	1528.7270	0.29	0	61	2.5e-006	1	U	K. VGAHAGEYGAEALER. M	
	<a href="#">5873</a>	510.5832	1528.7277	1528.7270	0.45	0	(54)	1.1e-005	1	U	K. VGAHAGEYGAEALER. M	
	<a href="#">11687</a>	603.3031	3011.4789	3011.4771	0.62	0	25	0.018	1	U	K. VADALTNAVAHVDDMPNALSALSDLHAHK. L	
10.	<a href="#">1::sp TRYP_PIG </a>	Mass: 25078	Score: 169	Matches: 7(7)	Sequences: 2(2)	emPAI: 0.40						
	sp TRYP_PIG											
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide	
	<a href="#">585</a>	421.7587	841.5029	841.5022	0.92	0	49	1.3e-005	1	U	R. VATVSLPR. S <a href="#">582</a> <a href="#">583</a> <a href="#">584</a> <a href="#">586</a> <a href="#">587</a>	
	<a href="#">1838</a>	523.2856	1044.5567	1044.5564	0.30	0	40	0.00019	1	U	K. LSSPATLSNR. V	
11.	<a href="#">1::sp ALBU_BOVIN </a>	Mass: 71244	Score: 91	Matches: 6(6)	Sequences: 4(4)	emPAI: 0.27						
	sp ALBU_BOVIN											
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide	
	<a href="#">357</a>	395.2398	788.4649	788.4644	0.73	0	16	0.024	1	U	K. LVTDLTK. V	
	<a href="#">454</a>	409.7165	817.4184	817.4181	0.30	0	24	0.0041	1	U	K. ATEEQLK. T	
	<a href="#">991</a>	461.7480	921.4815	921.4807	0.87	0	28	0.0021	1	U	K. AEFVEVTK. L <a href="#">990</a>	
	<a href="#">6751</a>	547.3176	1638.9311	1638.9305	0.35	1	33	0.00049	1	U	R. KVPQVSTPTLVEYSR. S <a href="#">6750</a>	
12.	<a href="#">3::P76298 FLHA_ECOLI</a>	Mass: 74795	Score: 61	Matches: 8(8)	Sequences: 1(1)	emPAI: 0.06						
	Flagellar biosynthesis protein FlhA OS=Escherichia coli (strain K12) OX=83333 GN=flhA PE=3 SV=1											
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide	
	<a href="#">3650</a>	632.8196	1263.6245	1263.6159	6.86	1	(17)	0.038	1	U	R. HIRMTAIGGK. - <a href="#">3645</a>	
	<a href="#">3666</a>	632.8199	1263.6253	1263.6159	7.43	1	25	0.0052	1	U	R. HIRMTAIGGK. - <a href="#">3653</a> <a href="#">3658</a> <a href="#">3660</a> <a href="#">3662</a> <a href="#">3668</a>	
13.	<a href="#">1::sp KRHB4_HUMAN </a>	Mass: 65938	Score: 44	Matches: 2(2)	Sequences: 2(2)	emPAI: 0.14						
	sp KRHB4_HUMAN											
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide	
	<a href="#">514</a>	414.2188	826.4230	826.4225	0.61	0	33	0.00055	1	U	K. FASFIDK. V	
	<a href="#">3637</a>	632.3506	1262.6865	1262.6870	-0.38	0	26	0.0059	2	U	K. LGLDIEIATYR. R	
14.	<a href="#">1::sp CASB_BOVIN </a>	Mass: 25148	Score: 34	Matches: 2(2)	Sequences: 1(1)	emPAI: 0.18						
	sp CASB_BOVIN											
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide	
	<a href="#">9749</a>	734.7257	2201.1552	2201.1555	-0.11	0	26	0.0079	1	U	R. DMPIQAFLLYQEPVLGPVR. G <a href="#">9750</a>	
15.	<a href="#">1::sp RS27A_HUMAN </a>	Mass: 18296	Score: 33	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.26						
	sp RS27A_HUMAN											
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide	
	<a href="#">7847</a>	894.4674	1786.9203	1786.9200	0.18	0	33	0.0017	1	U	K. TITLEVEPSDTIENVK. A	
16.	<a href="#">3::POAD96 LIVJ_ECOLI</a>	Mass: 39223	Score: 31	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.11						
	Leu/Ile/Val-binding protein OS=Escherichia coli (strain K12) OX=83333 GN=livJ PE=1 SV=1											
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide	
	<a href="#">389</a>	400.7350	799.4555	799.4552	0.38	0	31	0.00082	1	U	K. QAVAVANK. V	
	Proteins matching the same set of peptides:											
	<a href="#">3::P04816 LIVK_ECOLI</a>	Mass: 39468	Score: 31	Matches: 1(1)	Sequences: 1(1)							
	Leucine-specific-binding protein OS=Escherichia coli (strain K12) OX=83333 GN=livK PE=1 SV=2											
17.	<a href="#">3::P77211 CUSC_ECOLI</a>	Mass: 50410	Score: 29	Matches: 2(2)	Sequences: 1(1)	emPAI: 0.09						
	Cation efflux system protein CusC OS=Escherichia coli (strain K12) OX=83333 GN=cusc PE=1 SV=1											
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide	
	<a href="#">10192</a>	789.7587	2366.2542	2366.2706	-6.93	1	25	0.0067	2	U	K. IEIPIFNAGRNOALDIAEIR. Q <a href="#">10193</a>	
18.	<a href="#">3::P75882 GFCD_ECOLI</a>	Mass: 78923	Score: 28	Matches: 2(2)	Sequences: 1(1)	emPAI: 0.06						
	Uncharacterized lipoprotein Gfcd OS=Escherichia coli (strain K12) OX=83333 GN=gfcd PE=3 SV=1											
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide	
	<a href="#">1654</a>	509.2822	1016.5498	1016.5502	-0.42	1	21	0.012	1	U	K. DKGATIDVAK. R <a href="#">1657</a>	
19.	<a href="#">3::Q06065 ATOC_ECOLI</a>	Mass: 52428	Score: 25	Matches: 2(2)	Sequences: 1(1)	emPAI: 0.08						
	Regulatory protein AtoC OS=Escherichia coli (strain K12) OX=83333 GN=atoC PE=1 SV=2											
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide	
	<a href="#">3665</a>	422.2156	1263.6251	1263.6203	3.84	1	22	0.011	1	U	R. MPMDG1KALK. E <a href="#">3640</a>	
20.	<a href="#">3::P62601 TREF_ECOLI</a>	Mass: 63828	Score: 24	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.07						
	Cytoplasmic trehalase OS=Escherichia coli (strain K12) OX=83333 GN=tref PE=1 SV=1											
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide	
	<a href="#">6667</a>	812.4225	1622.8304	1622.8280	1.49	1	24	0.0088	1	U	K. LESAIANI\$ALKGK. E	
21.	<a href="#">3::AOA7H2C767 AOA7H2C767_ECOLI</a>	Mass: 79935	Score: 24	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.05						
	Chaperone protein ClpB OS=Escherichia coli (strain K12) OX=83333 GN=clpB PE=3 SV=1											
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide	
	<a href="#">349</a>	394.7112	787.4078	787.4075	0.28	0	24	0.0038	1	U	K. AELEQAK. I	
	Proteins matching the same set of peptides:											
	<a href="#">3::P63284 CLPB_ECOLI</a>	Mass: 95697	Score: 24	Matches: 1(1)	Sequences: 1(1)							
	Chaperone protein ClpB OS=Escherichia coli (strain K12) OX=83333 GN=clpB PE=1 SV=1											
22.	<a href="#">3::P32719 ALSE_ECOLI</a>	Mass: 26263	Score: 24	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.17						

D-allulose-6-phosphate 3-epimerase OS=Escherichia coli (strain K12) OX=83333 GN=alsE PE=1 SV=1										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	6102	776.3944	1550.7743	1550.7870	-8.22	1	24	0.011	1	U M.KI <del>S</del> PSLMC <del>M</del> DLK.F
<hr/>										
23.	3::P76092 YNBC_ECOLI Mass: 65529 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.07									
Uncharacterized protein YnbC OS=Escherichia coli (strain K12) OX=83333 GN=ybcC PE=1 SV=1										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1025	464.2502	926.4859	926.4830	3.20	2	23	0.0053	1	U R.FMRK <del>A</del> MK.L
<hr/>										
24.	3::Q46857 DKGA_ECOLI Mass: 31147 Score: 23 Matches: 1(1) Sequences: 1(1) emPAI: 0.15									
2,5-diketo-D-gluconic acid reductase A OS=Escherichia coli (strain K12) OX=83333 GN=dkgA PE=1 SV=3										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1058	466.2459	930.4771	930.4844	-7.83	0	23	0.0056	1	U - <del>M</del> ANPTVIK.L
<hr/>										
25.	3::POABH0 FTSA_ECOLI Mass: 45815 Score: 22 Matches: 1(1) Sequences: 1(1) emPAI: 0.10									
Cell division protein FtsA OS=Escherichia coli (strain K12) OX=83333 GN=ftsA PE=1 SV=1										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	6076	774.3977	1546.7808	1546.7661	9.51	1	22	0.014	1	U R.GMDKGGVNDLESVVK.C
<hr/>										
26.	3::P12996 BIOB_ECOLI Mass: 39079 Score: 22 Matches: 1(1) Sequences: 1(1) emPAI: 0.11									
Biotin synthase OS=Escherichia coli (strain K12) OX=83333 GN=bioB PE=1 SV=2										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	221	379.7297	757.4448	757.4446	0.21	1	22	0.0074	1	U K.VRDAGIK.V
<hr/>										
27.	3::P39358 YJHG_ECOLI Mass: 70486 Score: 22 Matches: 1(1) Sequences: 1(1) emPAI: 0.06									
D-xylonate dehydratase YjhG OS=Escherichia coli (strain K12) OX=83333 GN=yjhG PE=1 SV=2										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	155	372.7219	743.4292	743.4290	0.30	0	22	0.0063	1	U K.VQTIGAR.F
<hr/>										
Proteins matching the same set of peptides:										
3::P77596 YAGF_ECOLI Mass: 69926 Score: 22 Matches: 1(1) Sequences: 1(1)										
D-xylonate dehydratase YagF OS=Escherichia coli (strain K12) OX=83333 GN=yagF PE=1 SV=1										
<hr/>										
28.	3::P21361 YCI6_ECOLI Mass: 5999 Score: 21 Matches: 1(1) Sequences: 1(1) emPAI: 0.95									
Uncharacterized protein Yci6 OS=Escherichia coli (strain K12) OX=83333 GN=yci6 PE=3 SV=1										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1251	480.7448	959.4751	959.4785	-3.53	1	21	0.013	1	U K.KGGQSGGNK.S
<hr/>										
29.	3::P12008 AROC_ECOLI Mass: 39341 Score: 20 Matches: 1(1) Sequences: 1(1) emPAI: 0.11									
Chorismate synthase OS=Escherichia coli (strain K12) OX=83333 GN=aroC PE=1 SV=4										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	726	436.2313	870.4480	870.4559	-9.06	1	20	0.0094	1	U R.REPDQVK.I
<hr/>										
30.	3::P71242 WCAK_ECOLI Mass: 47598 Score: 20 Matches: 1(1) Sequences: 1(1) emPAI: 0.09									
Colanic acid biosynthesis protein WcaK OS=Escherichia coli (strain K12) OX=83333 GN=wcaK PE=3 SV=2										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	813	445.7563	889.4980	889.4981	-0.07	1	20	0.02	1	U K.RSNITTAK.V
<hr/>										
31.	3::P46891 COF_ECOLI Mass: 30750 Score: 20 Matches: 1(1) Sequences: 1(1) emPAI: 0.15									
HMP-PP phosphatase OS=Escherichia coli (strain K12) OX=83333 GN=cof PE=1 SV=2										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	1234	479.7369	957.4593	957.4572	2.21	0	20	0.024	1	U R.YQI <del>I</del> DVK.K
<hr/>										
32.	1::sp CYC_HUMAN  Mass: 11724 Score: 19 Matches: 1(1) Sequences: 1(1) emPAI: 0.42									
sp CYC_HUMAN										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	5865	764.8877	1527.7609	1527.7697	-5.76	2	19	0.026	1	U K.EERADLIA <del>Y</del> LKK.A
<hr/>										
33.	3::POA759 NAGR_ECOLI Mass: 29983 Score: 19 Matches: 1(1) Sequences: 1(1) emPAI: 0.15									
Glucosamine-6-phosphate deaminase OS=Escherichia coli (strain K12) OX=83333 GN=nagB PE=1 SV=1										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	6044	386.9645	1543.8290	1543.8181	7.09	1	19	0.031	1	U K.ALVEMHKAGOV <del>S</del> FK.H
<hr/>										
34.	3::POC018 RL18_ECOLI Score: 19 Matches: 1(1) Sequences: 1(1)									
50S ribosomal protein L18 OS=Escherichia coli (strain K12) OX=83333 GN=rp18 PE=1 SV=1										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	2276	365.8537	1094.5394	1094.5485	-8.29	1	19	0.029	2	U R.KLOELGATR.L
<hr/>										
35.	3::POA7V0 RS2_ECOLI Mass: 26784 Score: 19 Matches: 1(1) Sequences: 1(1) emPAI: 0.17									
30S ribosomal protein S2 OS=Escherichia coli (strain K12) OX=83333 GN=rpsB PE=1 SV=2										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	3937	649.8182	1297.6219	1297.6192	2.08	1	19	0.025	1	U - <del>M</del> ATVSMRD <del>M</del> LK.A
<hr/>										
36.	3::POACP5 GNTR_ECOLI Mass: 36570 Score: 19 Matches: 1(1) Sequences: 1(1) emPAI: 0.12									
HTH-type transcriptional regulator GntR OS=Escherichia coli (strain K12) OX=83333 GN=gntR PE=1 SV=1										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	647	428.7662	855.5179	855.5178	0.09	0	19	0.014	1	U R.LASVLT <del>P</del> R.E
<hr/>										
37.	3::P32053 INTA_ECOLI Mass: 46736 Score: 19 Matches: 1(1) Sequences: 1(1) emPAI: 0.10									
Prophage integrase IntA OS=Escherichia coli (strain K12) OX=83333 GN=intA PE=1 SV=2										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
	705	434.7535	867.4924	867.4926	-0.32	0	19	0.014	1	U K.AVQP <del>V</del> QAR.G
<hr/>										
38.	3::P06149 DLD_ECOLI Mass: 64914 Score: 18 Matches: 1(1) Sequences: 1(1) emPAI: 0.07									
Quinone-dependent D-lactate dehydrogenase OS=Escherichia coli (strain K12) OX=83333 GN=dld PE=1 SV=3										
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide

39.	<a href="#">3::POADT8 YGIW_ECOLI</a>	Mass: 23062	Score: 18	Matches: 2(2)	Sequences: 2(2)	emPAI: 0.44					
	Uncharacterized protein YgiM OS=Escherichia coli (strain K12) OX=83333 GN=ygiM PE=3 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
		1798	521.2823	1040.5500	1040.5502	-0.22	0	15	0.03	2	U R.VPDLNQVK.T
		2864	580.7947	1159.5748	1159.5721	2.38	0	16	0.03	2	U K.VDAASVQLDDK.Q
40.	<a href="#">3::P63201 GADW_ECOLI</a>	Mass: 28353	Score: 18	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.16					
	HTH-type transcriptional regulator GadW OS=Escherichia coli (strain K12) OX=83333 GN=gadW PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
		2909	389.8357	1166.4852	1166.4930	-6.66	0	18	0.03	1	U R.MYTSLSLIK.K
41.	<a href="#">3::P22106 ASN8_ECOLI</a>	Mass: 63075	Score: 18	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.07					
	Asparagine synthetase B [glutamine-hydrolyzing] OS=Escherichia coli (strain K12) OX=83333 GN=asnB PE=1 SV=3										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
		5635	753.8779	1505.7413	1505.7483	-4.62	1	18	0.04	1	U R.KLLALHMYDCAR.A
42.	<a href="#">3::P15029 FECO_ECOLI</a>	Mass: 34337	Score: 18	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.13					
	Fe(3+) dicitrate transport system permease protein FecD OS=Escherichia coli (strain K12) OX=83333 GN=fecD PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
		3234	406.2104	1215.6092	1215.6104	-0.95	1	18	0.036	1	U K.MLAKTHQPMK.L
43.	<a href="#">3::P21889 SYD_ECOLI</a>	Mass: 66157	Score: 18	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.07					
	Aspartate-tRNA ligase OS=Escherichia coli (strain K12) OX=83333 GN=aspS PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
		5028	724.3921	1446.7696	1446.7708	-0.84	1	18	0.024	1	U R.VAALRVPGGASLR.K
44.	<a href="#">3::P76104 RLHA_ECOLI</a>	Mass: 73170	Score: 17	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.06					
	23S rRNA 5-hydroxycytidine C2501 synthase OS=Escherichia coli (strain K12) OX=83333 GN=rhA PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
		221	379.7297	757.4448	757.4446	0.23	1	17	0.021	2	U K.QAKGNIK.S
45.	<a href="#">3::P21893 REJG_ECOLI</a>	Mass: 63634	Score: 17	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.07					
	Single-stranded-DNA-specific exonuclease RecJ OS=Escherichia coli (strain K12) OX=83333 GN=recJ PE=1 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
		2198	543.8047	1085.5947	1085.6015	-6.24	1	17	0.034	1	U R.MKQIQLR.R
46.	<a href="#">3::P38035 RTCR_ECOLI</a>	Mass: 60604	Score: 17	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.07					
	Transcriptional regulatory protein RtcR OS=Escherichia coli (strain K12) OX=83333 GN=rtcR PE=4 SV=2										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
		2864	580.7947	1159.5748	1159.5638	9.52	1	17	0.024	1	U R.SRSLFELK.R
47.	<a href="#">3::P80645 SSUD_ECOLI</a>	Mass: 41768	Score: 17	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.11					
	Alkanesulfonate monooxygenase OS=Escherichia coli (strain K12) OX=83333 GN=ssuD PE=1 SV=3										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
		292	387.7093	773.4040	773.4032	1.16	0	17	0.02	1	U R.QAATLDR.L
48.	<a href="#">3::POAAJ8 HYBA_ECOLI</a>	Mass: 36949	Score: 17	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.12					
	Hydrogenase-2 operon protein HybA OS=Escherichia coli (strain K12) OX=83333 GN=hybA PE=3 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
		1068	466.7434	931.4723	931.4763	-4.37	0	17	0.028	1	U K.TGIVHYDK.D
49.	<a href="#">3::P77330 BORD_ECOLI</a>	Mass: 10612	Score: 17	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.47					
	Prophage lipoprotein Bor homolog OS=Escherichia coli (strain K12) OX=83333 GN=borD PE=3 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
		128	366.7161	731.4177	731.4177	-0.10	1	17	0.022	1	U K.KTVDAAK.I
50.	<a href="#">3::Q46901 CSEI_ECOLI</a>	Mass: 56493	Score: 17	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.08					
	CRISPR system Cascade subunit CasA OS=Escherichia coli (strain K12) OX=83333 GN=casA PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
		8915	654.0380	1959.0921	1959.0918	0.16	1	17	0.023	1	U R.GIDLRSTVLLNVLILPR.L
51.	<a href="#">3::POAA43 RSUA_ECOLI</a>	Mass: 25963	Score: 17	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.18					
	Ribosomal small subunit pseudouridine synthase A OS=Escherichia coli (strain K12) OX=83333 GN=rsuA PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
		295	388.2185	774.4225	774.4236	-1.35	0	17	0.022	1	U R.LTISEGR.Y
52.	<a href="#">3::P45522 KEFB_ECOLI</a>	Mass: 66482	Score: 17	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.07					
	Glutathione-regulated potassium-efflux system protein KefB OS=Escherichia coli (strain K12) OX=83333 GN=kefB PE=3 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
		2418	557.2803	1112.5461	1112.5413	4.32	1	17	0.049	1	U K.MRIIVLER.D
53.	<a href="#">3::P77337 YDIS_ECOLI</a>	Score: 16	Matches: 1(1)	Sequences: 1(1)							
	Probable electron transfer flavoprotein-quinone oxidoreductase YdiS OS=Escherichia coli (strain K12) OX=83333 GN=ydiS PE=3 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
		1058	466.2459	930.4771	930.4779	-0.81	1	16	0.023	2	U K.MIMGHAKK.I
54.	<a href="#">3::POAEX9 MALE_ECOLI</a>	Mass: 43360	Score: 16	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.10					
	Maltose/maltodextrin-binding periplasmic protein OS=Escherichia coli (strain K12) OX=83333 GN=male PE=1 SV=1										
	Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
		879	452.2427	902.4709	902.4709	-0.01	0	16	0.045	1	U R.OTVDEALK.D
55.	<a href="#">3::P33668 YBBC_ECOLI</a>	Mass: 14257	Score: 16	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.34					
	Uncharacterized protein YbcC OS=Escherichia coli (strain K12) OX=83333 GN=ybcC PE=2 SV=1										

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1662	509.7492	1017.4839	1017.4896	-5.57	1	16	0.035	1	U	K.YSVKIVK.T
<hr/>										
56.	3::P02921 MF1B_ECOLI Mass: 52830 Score: 16 Matches: 1(1) Sequences: 1(1) emPAI: 0.08 Melibiose carrier protein OS=Escherichia coli (strain K12) OX=83333 GN=me1B PE=1 SV=2									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1207	478.7239	955.4331	955.4354	-2.40	0	16	0.035	1	U	-_MSISITTK.L
<hr/>										
57.	3::P64622 YHDV_ECOLI Score: 16 Matches: 1(1) Sequences: 1(1) Uncharacterized protein YhdV OS=Escherichia coli (strain K12) OX=83333 GN=yhdV PE=3 SV=1									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3121	600.2544	1198.4942	1198.4876	5.50	0	16	0.037	4	U	R.LVHINTCK.G
<hr/>										
58.	3::P20966 PTFBC_ECOLI Mass: 57824 Score: 16 Matches: 1(1) Sequences: 1(1) emPAI: 0.08 PTS system fructose-specific E11B'BC component OS=Escherichia coli (strain K12) OX=83333 GN=fruA PE=1 SV=1									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
407	402.7088	803.4029	803.4025	0.58	0	16	0.025	1	U	K.TAQELDK.A
<hr/>										
59.	3::P08331 CPDB_ECOLI Mass: 70902 Score: 16 Matches: 1(1) Sequences: 1(1) emPAI: 0.06 2',3'-cyclic-nucleotide 2'-phosphodiesterase/3'-nucleotidase OS=Escherichia coli (strain K12) OX=83333 GN=cpdB PE=1 SV=2									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
3570	627.3347	1252.6548	1252.6526	1.82	0	16	0.038	1	U	K.QPWFPTPYLIK.D
<hr/>										
60.	3::P12999 B10C_ECOLI Mass: 28373 Score: 16 Matches: 1(1) Sequences: 1(1) emPAI: 0.16 Malonyl-[acyl-carrier protein] O-methyltransferase OS=Escherichia coli (strain K12) OX=83333 GN=bioC PE=1 SV=2									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
6002	514.6168	1540.8286	1540.8395	-7.10	1	16	0.041	1	U	R.QSADALLAMLPRK.Y
<hr/>										
61.	3::P0A696 SECE_ECOLI Mass: 13635 Score: 16 Matches: 1(1) Sequences: 1(1) emPAI: 0.36 Protein translocase subunit SecE OS=Escherichia coli (strain K12) OX=83333 GN=secE PE=1 SV=1									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1550	503.3085	1004.6024	1004.6019	0.56	0	16	0.026	1	U	R.LVSFITGLR.F
<hr/>										
62.	3::P14900 MURD_ECOLI Mass: 47343 Score: 16 Matches: 1(1) Sequences: 1(1) emPAI: 0.09 UDP-N-acetylmuramylalanine--D-glutamate ligase OS=Escherichia coli (strain K12) OX=83333 GN=murD PE=1 SV=3									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2584	566.3040	1130.5934	1130.5866	5.95	1	16	0.042	1	U	R.GVTPRVMDTR.M
<hr/>										
63.	3::P28249 ASMA_ECOLI Mass: 68977 Score: 16 Matches: 1(1) Sequences: 1(1) emPAI: 0.06 Protein AsmA OS=Escherichia coli (strain K12) OX=83333 GN=asmA PE=3 SV=2									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
4032	654.8453	1307.6760	1307.6738	1.71	0	16	0.05	1	U	R.LENVEIGILK.A
<hr/>										
64.	3::P0ADF6 EDD_ECOLI Mass: 65054 Score: 16 Matches: 1(1) Sequences: 1(1) emPAI: 0.07 Phosphogluconate dehydratase OS=Escherichia coli (strain K12) OX=83333 GN=edd PE=1 SV=1									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2	350.1560	698.2974	698.3000	-3.72	0	16	0.027	1	U	R.LSGASGK.V
<hr/>										
65.	3::P0AD65 MRDA_ECOLI Mass: 70812 Score: 16 Matches: 2(2) Sequences: 1(1) emPAI: 0.06 Peptidoglycan D,D-transpeptidase MrdA OS=Escherichia coli (strain K12) OX=83333 GN=mrda PE=1 SV=1									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
296	388.2198	774.4250	774.4276	-3.29	0	14	0.037	1	U	R.FPGVEVK.G 295
<hr/>										
66.	3::P0A6N8 EPLP_ECOLI Mass: 21519 Score: 16 Matches: 1(1) Sequences: 1(1) emPAI: 0.22 Elongation factor P-like protein OS=Escherichia coli (strain K12) OX=83333 GN=yeiP PE=1 SV=1									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2199	362.8725	1085.5957	1085.6015	-5.34	2	16	0.048	1	U	-_MPRANEIKK.G
<hr/>										
67.	3::P43329 HRPA_ECOLI Mass: 149448 Score: 16 Matches: 1(1) Sequences: 1(1) emPAI: 0.03 ATP-dependent RNA helicase HrpA OS=Escherichia coli (strain K12) OX=83333 GN=hrpA PE=1 SV=3									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
2485	561.2961	1120.5777	1120.5798	-1.84	1	16	0.05	2	U	K.SMLIKEGAEK.I
<hr/>										
68.	3::P0AGD7 SRP54_ECOLI Mass: 49812 Score: 16 Matches: 1(1) Sequences: 1(1) emPAI: 0.09 Signal recognition particle protein OS=Escherichia coli (strain K12) OX=83333 GN=ffh PE=1 SV=1									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
1595	505.7787	1009.5428	1009.5412	1.58	3	16	0.032	1	U	K.KMKGGMAK.M
<hr/>										
69.	3::P0AFA2 NARX_ECOLI Mass: 67669 Score: 15 Matches: 1(1) Sequences: 1(1) emPAI: 0.07 Nitrate/nitrite sensor protein NarX OS=Escherichia coli (strain K12) OX=83333 GN=narX PE=1 SV=1									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
202	378.2058	754.3971	754.3973	-0.36	0	15	0.029	1	U	K.TAGLEHK.N
<hr/>										
70.	3::P0ACL0 GLPR_ECOLI Mass: 28087 Score: 15 Matches: 1(1) Sequences: 1(1) emPAI: 0.16 Glycerol-3-phosphate regulon repressor OS=Escherichia coli (strain K12) OX=83333 GN=g1pR PE=1 SV=1									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
416	403.7019	805.3892	805.3817	9.29	0	15	0.03	1	U	K.ATQTEEK.E
<hr/>										
Proteins matching the same set of peptides:										
3::P23840 DIND_ECOLI	Mass: 31173	Score: 15	Matches: 1(1)	Sequences: 1(1)						
DNA damage-inducible protein D OS=Escherichia coli (strain K12) OX=83333 GN=dinD PE=4 SV=1										
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71.	3::P33136 OPGG_ECOLI Mass: 57876 Score: 15 Matches: 1(1) Sequences: 1(1) emPAI: 0.08 Glucans biosynthesis protein G OS=Escherichia coli (strain K12) OX=83333 GN=mDoG PE=1 SV=1									
Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
399	401.7250	801.4355	801.4344	1.27	0	15	0.042	1	U	K.QAOSLAGK.G



72.	<a href="#">3::POA7R9 RS11_ECOLI</a>	Mass: 13950	Score: 15	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.35
30S ribosomal protein S11 OS=Escherichia coli (strain K12) OX=83333 GN=rpsK PE=1 SV=2						
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<a href="#">340</a>	393.7397	785.4648	785.4581	8.53	1 15 0.032 1 U -.MAKAPIR.A
73.	<a href="#">3::P25772 LIGB_ECOLI</a>	Mass: 63425	Score: 15	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.07
DNA ligase B OS=Escherichia coli (strain K12) OX=83333 GN=ligB PE=1 SV=2						
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<a href="#">155</a>	372.7219	743.4292	743.4290	0.30	0 15 0.034 2 U R.VNIGSVR.R
74.	<a href="#">1::sp UB2E1_HUMAN </a>	Mass: 21676	Score: 15	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.21
sp UB2E1_HUMAN						
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<a href="#">1202</a>	478.2539	954.4932	954.4899	3.47	1 15 0.034 1 U K.LLSTSAKR.I
75.	<a href="#">3::P75830 MACA_ECOLI</a>	Mass: 40599	Score: 15	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.11
Macrolide export protein MacA OS=Escherichia coli (strain K12) OX=83333 GN=macA PE=1 SV=2						
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<a href="#">161</a>	373.2138	744.4129	744.4130	-0.06	0 15 0.035 1 U R.EVTIGAR.N
76.	<a href="#">3::P17169 GLMS_ECOLI</a>	Mass: 67081	Score: 14	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.07
Glutamine--fructose-6-phosphate aminotransferase [isomerizing] OS=Escherichia coli (strain K12) OX=83333 GN=gImS PE=1 SV=4						
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<a href="#">3029</a>	594.2587	1186.5028	1186.4941	7.37	0 14 0.042 1 U R.IEQLSQDK.R
77.	<a href="#">3::POAAH4 SAPD_ECOLI</a>	Mass: 38093	Score: 14	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.12
Putrescine export system ATP-binding protein SapD OS=Escherichia coli (strain K12) OX=83333 GN=sapD PE=1 SV=1						
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<a href="#">653</a>	429.2455	856.4765	856.4840	-8.75	0 14 0.048 1 U -.MPLLDIR.N
78.	<a href="#">3::P76015 DHAK_ECOLI</a>	Mass: 38590	Score: 14	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.12
PEP-dependent dihydroxyacetone kinase, dihydroxyacetone-binding subunit DhaK OS=Escherichia coli (strain K12) OX=83333 GN=dhaK PE=1 SV=2						
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<a href="#">103</a>	364.7007	727.3867	727.3864	0.42	0 14 0.038 1 U R.ADAPVAGK.V
79.	<a href="#">3::P77766 RNAAM_ECOLI</a>	Mass: 32902	Score: 14	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.14
5'-3' exoribonuclease OS=Escherichia coli (strain K12) OX=83333 GN=yciV PE=1 SV=1						
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<a href="#">389</a>	400.7350	799.4555	799.4552	0.40	0 14 0.043 2 U R.AQLIAER.L
80.	<a href="#">3::Q7DFV4 YME_ECOLI</a>	Mass: 12057	Score: 14	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.41
Putative uncharacterized protein YmdE OS=Escherichia coli (strain K12) OX=83333 GN=yndE PE=5 SV=3						
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<a href="#">2265</a>	547.7330	1093.4515	1093.4532	-1.54	0 14 0.04 1 U -.MEDGVQAMR.D
81.	<a href="#">3::P77739 KT3K_ECOLI</a>	Mass: 32666	Score: 14	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.14
Probable ketoamine kinase YniA OS=Escherichia coli (strain K12) OX=83333 GN=yniA PE=3 SV=1						
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<a href="#">1076</a>	467.2353	932.4560	932.4538	2.39	0 14 0.041 1 U -.MWOAISR.L
82.	<a href="#">3::P16869 FHUE_ECOLI</a>	Mass: 81239	Score: 14	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.05
FhuE receptor OS=Escherichia coli (strain K12) OX=83333 GN=fhuE PE=1 SV=2						
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<a href="#">3771</a>	638.2576	1274.5006	1274.5114	-8.43	0 14 0.043 1 U R.LITLAIIFR.I
83.	<a href="#">3::POA9M0 LON_ECOLI</a>	Mass: 87725	Score: 14	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.05
Lon protease OS=Escherichia coli (strain K12) OX=83333 GN=lon PE=1 SV=1						
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<a href="#">349</a>	394.7112	787.4078	787.4075	0.28	0 14 0.041 2 U K.AEAELOK.L
84.	<a href="#">3::P09831 GLTB_ECOLI</a>	Mass: 164335	Score: 14	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.03
Glutamate synthase [NADPH] large chain OS=Escherichia coli (strain K12) OX=83333 GN=gltB PE=1 SV=3						
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<a href="#">1158</a>	473.7351	945.4556	945.4572	-1.69	1 14 0.044 1 U R.YVITKDK.L
85.	<a href="#">3::POA7V3 RS3_ECOLI</a>	Mass: 25967	Score: 14	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.18
30S ribosomal protein S3 OS=Escherichia coli (strain K12) OX=83333 GN=rpsC PE=1 SV=2						
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<a href="#">411</a>	403.2065	804.3985	804.3912	9.08	0 14 0.043 1 U R.AVONAMR.L
86.	<a href="#">3::P02918 PBPA_ECOLI</a>	Mass: 93806	Score: 14	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.05
Penicillin-binding protein 1A OS=Escherichia coli (strain K12) OX=83333 GN=mrca PE=1 SV=1						
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<a href="#">2305</a>	549.8038	1097.5930	1097.5941	-1.00	0 14 0.043 1 U K.VQAAQQAQR.N
87.	<a href="#">3::P37013 NORR_ECOLI</a>	Mass: 55601	Score: 14	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.08
Anaerobic nitric oxide reductase transcription regulator NorR OS=Escherichia coli (strain K12) OX=83333 GN=norR PE=1 SV=2						
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<a href="#">155</a>	372.7219	743.4292	743.4290	0.32	0 14 0.043 3 U R.VLAATNR.D
88.	<a href="#">3::P71229 HYFR_ECOLI</a>	Mass: 75771	Score: 14	Matches: 1(1)	Sequences: 1(1)	emPAI: 0.06
DNA-binding transcriptional activator HyfR OS=Escherichia coli (strain K12) OX=83333 GN=hyfr PE=1 SV=1						
Query	Observed	Mr (expt)	Mr (calc)	ppm	Miss	Score Expect Rank Unique Peptide
	<a href="#">155</a>	372.7219	743.4292	743.4290	0.32	0 14 0.043 3 U R.VIAATNR.D

89. [3::P38134|ETK\\_ECOLI](#) Mass: 81191 Score: 14 Matches: 1(1) Sequences: 1(1) emPAI: 0.05

Tyrosine-protein kinase etk OS=Escherichia coli (strain K12) OX=83333 GN=etk PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2384</a>	555.2137	1108.4128	1108.4025	9.34	0	14	0.044	1	U	K.EVSLSMQR.L

90. [3::P55140|YGC6\\_ECOLI](#) Mass: 32527 Score: 13 Matches: 1(1) Sequences: 1(1) emPAI: 0.14

UPF0603 protein Ygc6 OS=Escherichia coli (strain K12) OX=83333 GN=ygc6 PE=3 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">12831</a>	914.3105	3653.2130	3653.2305	-4.81	2	13	0.045	1	U	R.ASGRSYHSDNSGSAGGSDSGGFSGGGGS <del>S</del> GGGGASGRW.-

91. [3::P00582|DPO1\\_ECOLI](#) Mass: 103168 Score: 13 Matches: 1(1) Sequences: 1(1) emPAI: 0.04

DNA polymerase I OS=Escherichia coli (strain K12) OX=83333 GN=polA PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">718</a>	435.7561	869.4976	869.4971	0.59	1	13	0.046	1	U	R.NGVKIDPK.V

92. [3::P76352|YEE0\\_ECOLI](#) Mass: 60477 Score: 13 Matches: 1(1) Sequences: 1(1) emPAI: 0.07

Probable FMN/FAD exporter Yee0 OS=Escherichia coli (strain K12) OX=83333 GN=yee0 PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">13155</a>	1157.1393	4624.5282	4624.5243	0.86	0	13	0.049	1	U	K.IPLLINGSLNINLNIISGILYGLFVWPLGFGVAGLGLTISR.Y

93. [3::POAGF6|TDCB\\_ECOLI](#) Mass: 35552 Score: 13 Matches: 1(1) Sequences: 1(1) emPAI: 0.13

L-threonine dehydratase catabolic TdcB OS=Escherichia coli (strain K12) OX=83333 GN=tdcB PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<a href="#">2500</a>	562.2236	1122.4327	1122.4247	7.13	0	13	0.05	1	U	K.LSSLIDAEK.R

