

Mascot Search Results

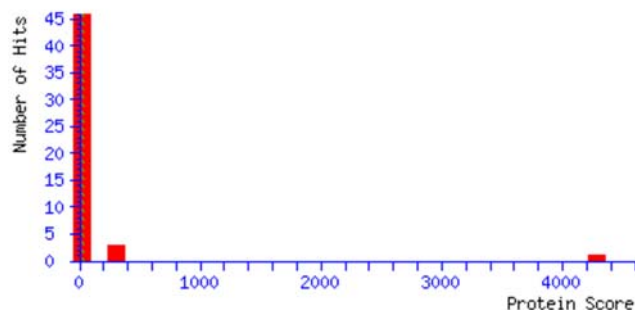
User :
Email :
Search title : Winton_26_8_15_SipDE3_pt1.raw
MS data file : F:\Data\Ling Zhong\velosorbi\26-8-15-winton\Winton_26_8_15_SipDE3_pt1.raw
Database : Sprot 29_1_15 (547357 sequences; 194874700 residues)
Timestamp : 26 Aug 2015 at 22:48:40 GMT
Protein hits :

[SIPD_ECOLI](#) Cell invasion protein SipD OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=sipD PE=1 SV=1
[PHEA_ECOLI](#) P-protein OS=Escherichia coli (strain K12) GN=pheA PE=1 SV=1
[LACI_ECOLI](#) Lactose operon repressor OS=Escherichia coli (strain K12) GN=lacI PE=1 SV=3
[OMPA_ECOLI](#) Outer membrane protein A OS=Escherichia coli (strain K12) GN=ompA PE=1 SV=1
[HIS7_ECO57](#) Histidine biosynthesis bifunctional protein HisB OS=Escherichia coli O157:H7 GN=hisB PE=1 SV=1
[HIS7_SHIFL](#) Histidine biosynthesis bifunctional protein HisB OS=Shigella flexneri GN=hisB PE=3 SV=2
[DNAJ_ECOHS](#) Chaperone protein DnaJ OS=Escherichia coli O9:H4 (strain HS) GN=dnaJ PE=3 SV=1
[RECA_ECOBW](#) Protein RecA OS=Escherichia coli (strain K12 / MC4100 / BW2952) GN=recA PE=3 SV=1
[PGK_ECOHS](#) Phosphoglycerate kinase OS=Escherichia coli O9:H4 (strain HS) GN=pgk PE=3 SV=1
[EFTU_SALAR](#) Elongation factor Tu OS=Salmonella arizonae (strain ATCC BAA-731 / CDC346-86 / RSK2980) GN=tuf1 PE=3 SV=1
[MALE_ECOLI](#) Maltose-binding periplasmic protein OS=Escherichia coli (strain K12) GN=male PE=1 SV=1
[ASTC_ECOWW](#) Succinylornithine transaminase OS=Escherichia coli (strain K12 / MC4100 / BW2952) GN=astC PE=3 SV=1
[FTSZ_ECOLI](#) Cell division protein FtsZ OS=Escherichia coli (strain K12) GN=ftsZ PE=1 SV=1
[YCBX_ECOLI](#) Uncharacterized protein YcbX OS=Escherichia coli (strain K12) GN=ycbX PE=1 SV=1
[HFLC_ECOLI](#) Modulator of FtsH protease HflC OS=Escherichia coli (strain K12) GN=hflC PE=1 SV=1
[TRYF_PIG](#) Trypsin OS=Sus scrofa PE=1 SV=1
[K1C10_CANFA](#) Keratin, type I cytoskeletal 10 OS=Canis familiaris GN=KRT10 PE=2 SV=1
[SUCC_ECOBW](#) Succinyl-CoA ligase [ADP-forming] subunit beta OS=Escherichia coli (strain K12 / MC4100 / BW2952) GN=sucC PE=3 SV=1
[RL28_ECO24](#) 50S ribosomal protein L28 OS=Escherichia coli O139:H28 (strain E24377A / ETEC) GN=rpMB PE=3 SV=1
[G3P1_ECO57](#) Glyceraldehyde-3-phosphate dehydrogenase A OS=Escherichia coli O157:H7 GN=gapA PE=3 SV=2
[MALK_ECOWW](#) Maltose/maltodextrin import ATP-binding protein MalK OS=Escherichia coli (strain K12) GN=malK PE=1 SV=1
[LCRV_YERPE](#) Virulence-associated V antigen OS=Yersinia pestis GN=lcrV PE=1 SV=1
[CDAR_ECOWW](#) Carbohydrate diacid regulator OS=Escherichia coli (strain K12) GN=cdaR PE=1 SV=2
[K2C1_HUMAN](#) Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6
[RL9_CITK8](#) 50S ribosomal protein L9 OS=Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696) GN=rpLI PE=3 SV=1
[RIBD_ECOWW](#) Riboflavin biosynthesis protein RibD OS=Escherichia coli (strain K12) GN=ribD PE=1 SV=1
[SLYD_ECOWW](#) FKBP-type peptidyl-prolyl cis-trans isomerase SlyD OS=Escherichia coli (strain K12) GN=slyD PE=1 SV=1
[ARGE_ECOWW](#) Acetylornithine deacetylase OS=Escherichia coli (strain K12 / MC4100 / BW2952) GN=argE PE=3 SV=1
[H2A1B_HUMAN](#) Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2
[RL5_ACTP2](#) 50S ribosomal protein L5 OS=Actinobacillus pleuropneumoniae serotype 5b (strain L20) GN=rpLE PE=3 SV=1
[YCIW_ECOWW](#) Uncharacterized protein YciW OS=Escherichia coli (strain K12) GN=yCiW PE=4 SV=2
[AHP_C_ECOLI](#) Alkyl hydroperoxide reductase subunit C OS=Escherichia coli (strain K12) GN=ahpC PE=1 SV=2
[MDH_ECOWW](#) Malate dehydrogenase OS=Escherichia coli (strain K12 / MC4100 / BW2952) GN=mdh PE=3 SV=1
[DIEXF_DANRE](#) Digestive organ expansion factor OS=Danio rerio GN=diexf PE=2 SV=2
[RL6_CITK8](#) 50S ribosomal protein L6 OS=Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696) GN=rpLF PE=3 SV=1
[RL1_ACTP2](#) 50S ribosomal protein L1 OS=Actinobacillus pleuropneumoniae serotype 5b (strain L20) GN=rpLA PE=3 SV=1
[RL4_CITK8](#) 50S ribosomal protein L4 OS=Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696) GN=rpLD PE=3 SV=1
[YPT1_YEAST](#) GTP-binding protein YPT1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YPT1 PE=1 SV=2
[REF_HEVBR](#) Rubber elongation factor protein OS=Hevea brasiliensis PE=1 SV=2
[YCEA_ECOBW](#) UPF0176 protein YceA OS=Escherichia coli (strain K12 / MC4100 / BW2952) GN=yceA PE=3 SV=1
[ALF_ECOWW](#) Fructose-bisphosphate aldolase class 2 OS=Escherichia coli (strain K12) GN=fbaA PE=1 SV=2
[GSA2_STRGC](#) Malate dehydrogenase OS=Streptomyces griseus subsp. griseus (strain JCM 4626 / NBRC 13350) GN=mdh PE=3 SV=1
[MDH_STACT](#) Glutamate-1-semialdehyde 2,1-aminomutase 2 OS=Staphylococcus carnosus (strain TM300) GN=hemL2 PE=3 SV=1
[DACA_ECOWW](#) D-alanyl-D-alanine carboxypeptidase DacA OS=Escherichia coli (strain K12) GN=dacA PE=1 SV=1
[MQNA_THET8](#) Chorismate dehydratase OS=Thermus thermophilus (strain HB8 / ATCC 27634 / DSM 579) GN=mqna PE=1 SV=1
[PSD3_HUMAN](#) PH and SEC7 domain-containing protein 3 OS=Homo sapiens GN=PSD3 PE=1 SV=2

RBSA_BACLD	Ribose import ATP-binding protein RbsA OS=Bacillus licheniformis (strain DSM 13 / ATCC 14580) GN=rbsA PE=3 SV=1
GH312_ORYSJ	Probable indole-3-acetic acid-amido synthetase GH3.12 OS=Oryza sativa subsp. japonica GN=GH3.12 PE=2 SV=1
RS12_ALCBS	30S ribosomal protein S12 OS=Alcanivorax borkumensis (strain SK2 / ATCC 700651 / DSM 11573) GN=rpsL PE=3 SV=1
RL24_AERS4	50S ribosomal protein L24 OS=Aeromonas salmonicida (strain A449) GN=rplX PE=3 SV=1
AAT_ECOLI	Aspartate aminotransferase OS=Escherichia coli (strain K12) GN=aspC PE=1 SV=1

Mascot Score Histogram

Ions score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Individual ions scores > 29 indicate identity or extensive homology ($p < 0.05$). Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As [Help](#)

Significance threshold $p <$ Max. number of hits

Standard scoring MudPIT scoring Ions score or expect cut-off Show sub-sets

Show pop-ups Suppress pop-ups Sort unassigned Require bold red

Preferred taxonomy

Error tolerant

- [SIPD_SALTY](#) Mass: 37090 Score: 4284 Matches: 178(144) Sequences: 27(26) emPAI: 16.70
Cell invasion protein SipD OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=sipD PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 34	388.2314	774.4482	774.4487	-0.60	0	(41)	0.0037	1	U	K.LDVTSLK.N
<input checked="" type="checkbox"/> 35	388.2321	774.4496	774.4487	1.20	0	47	0.00099	1	U	K.LDVTSLK.N
<input checked="" type="checkbox"/> 76	410.6969	819.3792	819.3796	-0.46	0	(20)	0.49	1	U	K.LEMDNAK.Y
<input checked="" type="checkbox"/> 77	410.6971	819.3796	819.3796	0.03	0	21	0.33	1	U	K.LEMDNAK.Y
<input checked="" type="checkbox"/> 101	423.7192	845.4238	845.4243	-0.50	0	(39)	0.013	1	U	K.VATEAEAR.Q
<input checked="" type="checkbox"/> 102	423.7193	845.4240	845.4243	-0.26	0	(55)	0.00034	1	U	K.VATEAEAR.Q

<input checked="" type="checkbox"/>	103	423.7193	845.4240	845.4243	-0.26	0	(29)	0.13	1	U	K.VATEAEAR.Q
<input checked="" type="checkbox"/>	104	423.7194	845.4242	845.4243	-0.03	0	(42)	0.0064	1	U	K.VATEAEAR.Q
<input checked="" type="checkbox"/>	105	423.7195	845.4244	845.4243	0.21	0	(30)	0.11	1	U	K.VATEAEAR.Q
<input checked="" type="checkbox"/>	106	423.7196	845.4246	845.4243	0.45	0	(54)	0.00048	1	U	K.VATEAEAR.Q
<input checked="" type="checkbox"/>	107	423.7196	845.4246	845.4243	0.45	0	(54)	0.00042	1	U	K.VATEAEAR.Q
<input checked="" type="checkbox"/>	108	423.7197	845.4248	845.4243	0.68	0	59	0.00014	1	U	K.VATEAEAR.Q
<input checked="" type="checkbox"/>	109	423.7197	845.4248	845.4243	0.68	0	(55)	0.00033	1	U	K.VATEAEAR.Q
<input checked="" type="checkbox"/>	110	423.7197	845.4248	845.4243	0.68	0	(48)	0.0016	1	U	K.VATEAEAR.Q
<input checked="" type="checkbox"/>	111	423.7198	845.4250	845.4243	0.92	0	(54)	0.00048	1	U	K.VATEAEAR.Q
<input checked="" type="checkbox"/>	112	423.7198	845.4250	845.4243	0.92	0	(39)	0.015	1	U	K.VATEAEAR.Q
<input checked="" type="checkbox"/>	224	479.7627	957.5108	957.5106	0.25	0	53	0.00042	1	U	K.MGGWLLPGK.D
<input checked="" type="checkbox"/>	236	487.7598	973.5050	973.5055	-0.49	0	(39)	0.015	1	U	K.MGGWLLPGK.D + Oxidation (M)
<input checked="" type="checkbox"/>	237	487.7601	973.5056	973.5055	0.13	0	(27)	0.23	1	U	K.MGGWLLPGK.D + Oxidation (M)
<input checked="" type="checkbox"/>	238	487.7603	973.5060	973.5055	0.54	0	(32)	0.062	1	U	K.MGGWLLPGK.D + Oxidation (M)
<input checked="" type="checkbox"/>	285	508.7722	1015.5298	1015.5298	0.05	0	(38)	0.017	1	U	K.NDLNSLVNK.Y
<input checked="" type="checkbox"/>	286	508.7724	1015.5302	1015.5298	0.44	0	(46)	0.0028	1	U	K.NDLNSLVNK.Y
<input checked="" type="checkbox"/>	287	508.7725	1015.5304	1015.5298	0.64	0	47	0.002	1	U	K.NDLNSLVNK.Y
<input checked="" type="checkbox"/>	321	517.2981	1032.5816	1032.5815	0.12	0	55	0.00015	1	U	K.TTLQTLTQK.Y
<input checked="" type="checkbox"/>	424	557.7692	1113.5238	1113.5243	-0.44	0	(24)	0.14	1	U	K.YQAWQSGFK.A
<input checked="" type="checkbox"/>	425	557.7692	1113.5238	1113.5243	-0.44	0	(36)	0.01	1	U	K.YQAWQSGFK.A
<input checked="" type="checkbox"/>	426	557.7693	1113.5240	1113.5243	-0.26	0	(24)	0.15	1	U	K.YQAWQSGFK.A
<input checked="" type="checkbox"/>	427	557.7694	1113.5242	1113.5243	-0.08	0	(35)	0.013	1	U	K.YQAWQSGFK.A
<input checked="" type="checkbox"/>	428	557.7694	1113.5242	1113.5243	-0.08	0	(23)	0.21	1	U	K.YQAWQSGFK.A
<input checked="" type="checkbox"/>	430	557.7694	1113.5242	1113.5243	-0.08	0	(21)	0.29	1	U	K.YQAWQSGFK.A
<input checked="" type="checkbox"/>	431	557.7694	1113.5242	1113.5243	-0.08	0	(32)	0.024	1	U	K.YQAWQSGFK.A
<input checked="" type="checkbox"/>	432	557.7694	1113.5242	1113.5243	-0.08	0	(35)	0.011	1	U	K.YQAWQSGFK.A
<input checked="" type="checkbox"/>	433	557.7695	1113.5244	1113.5243	0.10	0	(20)	0.31	1	U	K.YQAWQSGFK.A
<input checked="" type="checkbox"/>	434	557.7695	1113.5244	1113.5243	0.10	0	(33)	0.016	1	U	K.YQAWQSGFK.A
<input checked="" type="checkbox"/>	435	557.7695	1113.5244	1113.5243	0.10	0	(33)	0.018	1	U	K.YQAWQSGFK.A
<input checked="" type="checkbox"/>	436	557.7696	1113.5246	1113.5243	0.28	0	43	0.0016	1	U	K.YQAWQSGFK.A
<input checked="" type="checkbox"/>	437	557.7696	1113.5246	1113.5243	0.28	0	(32)	0.021	1	U	K.YQAWQSGFK.A
<input checked="" type="checkbox"/>	438	557.7696	1113.5246	1113.5243	0.28	0	(26)	0.075	1	U	K.YQAWQSGFK.A
<input checked="" type="checkbox"/>	439	557.7697	1113.5248	1113.5243	0.46	0	(32)	0.018	1	U	K.YQAWQSGFK.A
<input checked="" type="checkbox"/>	440	557.7697	1113.5248	1113.5243	0.46	0	(36)	0.0071	1	U	K.YQAWQSGFK.A
<input checked="" type="checkbox"/>	441	557.7697	1113.5248	1113.5243	0.46	0	(35)	0.0086	1	U	K.YQAWQSGFK.A
<input checked="" type="checkbox"/>	442	557.7697	1113.5248	1113.5243	0.46	0	(28)	0.039	1	U	K.YQAWQSGFK.A
<input checked="" type="checkbox"/>	443	557.7698	1113.5250	1113.5243	0.64	0	(25)	0.079	1	U	K.YQAWQSGFK.A
<input checked="" type="checkbox"/>	444	557.7698	1113.5250	1113.5243	0.64	0	(34)	0.0097	1	U	K.YQAWQSGFK.A
<input checked="" type="checkbox"/>	445	557.7698	1113.5250	1113.5243	0.64	0	(40)	0.0026	1	U	K.YQAWQSGFK.A
<input checked="" type="checkbox"/>	446	557.7698	1113.5250	1113.5243	0.64	0	(33)	0.013	1	U	K.YQAWQSGFK.A
<input checked="" type="checkbox"/>	447	557.7700	1113.5254	1113.5243	1.00	0	(23)	0.14	1	U	K.YQAWQSGFK.A
<input checked="" type="checkbox"/>	448	557.7701	1113.5256	1113.5243	1.18	0	(22)	0.18	1	U	K.YQAWQSGFK.A
<input checked="" type="checkbox"/>	543	583.7713	1165.5280	1165.5285	-0.36	1	(32)	0.017	1	U	K.DSKLEMDNAK.Y + Oxidation (M)
<input checked="" type="checkbox"/>	544	389.5167	1165.5283	1165.5285	-0.17	1	(21)	0.25	1	U	K.DSKLEMDNAK.Y + Oxidation (M)
<input checked="" type="checkbox"/>	545	583.7715	1165.5284	1165.5285	-0.02	1	(23)	0.17	1	U	K.DSKLEMDNAK.Y + Oxidation (M)
<input checked="" type="checkbox"/>	546	583.7717	1165.5288	1165.5285	0.32	1	(40)	0.0036	1	U	K.DSKLEMDNAK.Y + Oxidation (M)

<input checked="" type="checkbox"/>	547	583.7718	1165.5290	1165.5285	0.49	1	(31)	0.027	1	U	K.DSKLEMDNAK.Y + Oxidation (M)
<input checked="" type="checkbox"/>	548	583.7718	1165.5290	1165.5285	0.49	1	(37)	0.0065	1	U	K.DSKLEMDNAK.Y + Oxidation (M)
<input checked="" type="checkbox"/>	549	583.7718	1165.5290	1165.5285	0.49	1	(40)	0.0034	1	U	K.DSKLEMDNAK.Y + Oxidation (M)
<input checked="" type="checkbox"/>	551	583.7719	1165.5292	1165.5285	0.66	1	(46)	0.00088	1	U	K.DSKLEMDNAK.Y + Oxidation (M)
<input checked="" type="checkbox"/>	552	583.7719	1165.5292	1165.5285	0.66	1	51	0.00029	1	U	K.DSKLEMDNAK.Y + Oxidation (M)
<input checked="" type="checkbox"/>	553	583.7721	1165.5296	1165.5285	1.01	1	(38)	0.0061	1	U	K.DSKLEMDNAK.Y + Oxidation (M)
<input checked="" type="checkbox"/>	554	583.7726	1165.5306	1165.5285	1.87	1	(27)	0.067	1	U	K.DSKLEMDNAK.Y + Oxidation (M)
<input checked="" type="checkbox"/>	665	637.3590	1272.7034	1272.7037	-0.23	0	(24)	0.2	1	U	R.QQLTSSLNALAK.S
<input checked="" type="checkbox"/>	666	637.3596	1272.7046	1272.7037	0.72	0	(55)	0.00017	1	U	R.QQLTSSLNALAK.S
<input checked="" type="checkbox"/>	667	637.3599	1272.7052	1272.7037	1.19	0	58	7.7e-005	1	U	R.QQLTSSLNALAK.S
<input checked="" type="checkbox"/>	708	650.8322	1299.6498	1299.6493	0.43	0	(49)	0.00079	1	U	K.MVQDIDGLGAPGK.D
<input checked="" type="checkbox"/>	716	652.8564	1303.6982	1303.6983	-0.07	0	(67)	9.5e-006	1	U	R.GTDIISLSQAATK.I
<input checked="" type="checkbox"/>	717	652.8564	1303.6982	1303.6983	-0.07	0	(63)	2.9e-005	1	U	R.GTDIISLSQAATK.I
<input checked="" type="checkbox"/>	718	652.8565	1303.6984	1303.6983	0.09	0	(50)	0.00058	1	U	R.GTDIISLSQAATK.I
<input checked="" type="checkbox"/>	719	652.8568	1303.6990	1303.6983	0.55	0	(41)	0.0042	1	U	R.GTDIISLSQAATK.I
<input checked="" type="checkbox"/>	720	652.8568	1303.6990	1303.6983	0.55	0	(81)	5.1e-007	1	U	R.GTDIISLSQAATK.I
<input checked="" type="checkbox"/>	721	435.5737	1303.6993	1303.6983	0.72	0	(50)	0.00061	1	U	R.GTDIISLSQAATK.I
<input checked="" type="checkbox"/>	722	652.8570	1303.6994	1303.6983	0.85	0	93	3.2e-008	1	U	R.GTDIISLSQAATK.I
<input checked="" type="checkbox"/>	723	652.8572	1303.6998	1303.6983	1.16	0	(78)	8.3e-007	1	U	R.GTDIISLSQAATK.I
<input checked="" type="checkbox"/>	741	658.8290	1315.6434	1315.6442	-0.58	0	(39)	0.0069	1	U	K.MVQDIDGLGAPGK.D + Oxidation (M)
<input checked="" type="checkbox"/>	742	658.8295	1315.6444	1315.6442	0.18	0	(82)	3.3e-007	1	U	K.MVQDIDGLGAPGK.D + Oxidation (M)
<input checked="" type="checkbox"/>	743	658.8300	1315.6454	1315.6442	0.94	0	94	2.1e-008	1	U	K.MVQDIDGLGAPGK.D + Oxidation (M)
<input checked="" type="checkbox"/>	858	463.9243	1388.7511	1388.7511	-0.03	1	60	5e-005	1	U	K.DGNTVKLDVTSLK.N
<input checked="" type="checkbox"/>	886	711.8878	1421.7610	1421.7613	-0.19	0	(47)	0.0012	1	U	K.VLSSTISSSLETAK.S
<input checked="" type="checkbox"/>	887	711.8879	1421.7612	1421.7613	-0.05	0	(47)	0.0011	1	U	K.VLSSTISSSLETAK.S
<input checked="" type="checkbox"/>	888	711.8879	1421.7612	1421.7613	-0.05	0	(73)	2.9e-006	1	U	K.VLSSTISSSLETAK.S
<input checked="" type="checkbox"/>	889	711.8882	1421.7618	1421.7613	0.37	0	(57)	9.5e-005	1	U	K.VLSSTISSSLETAK.S
<input checked="" type="checkbox"/>	890	474.9279	1421.7619	1421.7613	0.39	0	(46)	0.0012	1	U	K.VLSSTISSSLETAK.S
<input checked="" type="checkbox"/>	891	711.8883	1421.7620	1421.7613	0.51	0	(51)	0.00043	1	U	K.VLSSTISSSLETAK.S
<input checked="" type="checkbox"/>	892	711.8884	1421.7622	1421.7613	0.65	0	(78)	8e-007	1	U	K.VLSSTISSSLETAK.S
<input checked="" type="checkbox"/>	893	711.8884	1421.7622	1421.7613	0.65	0	105	1.6e-009	1	U	K.VLSSTISSSLETAK.S
<input checked="" type="checkbox"/>	894	711.8886	1421.7626	1421.7613	0.93	0	(50)	0.00047	1	U	K.VLSSTISSSLETAK.S
<input checked="" type="checkbox"/>	895	711.8892	1421.7638	1421.7613	1.78	0	(51)	0.00038	1	U	K.VLSSTISSSLETAK.S
<input checked="" type="checkbox"/>	896	711.8892	1421.7638	1421.7613	1.78	0	(39)	0.0061	1	U	K.VLSSTISSSLETAK.S
<input checked="" type="checkbox"/>	897	711.8893	1421.7640	1421.7613	1.92	0	(51)	0.00045	1	U	K.VLSSTISSSLETAK.S
<input checked="" type="checkbox"/>	979	750.8705	1499.7264	1499.7256	0.57	0	79	5.1e-007	1	U	K.YSNANSLYDNLVK.V
<input checked="" type="checkbox"/>	980	750.8707	1499.7268	1499.7256	0.84	0	(69)	6.6e-006	1	U	K.YSNANSLYDNLVK.V
<input checked="" type="checkbox"/>	981	750.8710	1499.7274	1499.7256	1.24	0	(67)	1e-005	1	U	K.YSNANSLYDNLVK.V
<input checked="" type="checkbox"/>	986	752.3730	1502.7314	1502.7325	-0.68	0	(56)	0.00016	1	U	K.SGVSLSAEQNENLR.S
<input checked="" type="checkbox"/>	987	752.3735	1502.7324	1502.7325	-0.01	0	(51)	0.00044	1	U	K.SGVSLSAEQNENLR.S
<input checked="" type="checkbox"/>	988	752.3737	1502.7328	1502.7325	0.25	0	(41)	0.0041	1	U	K.SGVSLSAEQNENLR.S
<input checked="" type="checkbox"/>	989	752.3738	1502.7330	1502.7325	0.39	0	(67)	1e-005	1	U	K.SGVSLSAEQNENLR.S
<input checked="" type="checkbox"/>	990	752.3738	1502.7330	1502.7325	0.39	0	(32)	0.031	1	U	K.SGVSLSAEQNENLR.S
<input checked="" type="checkbox"/>	991	752.3738	1502.7330	1502.7325	0.39	0	(34)	0.021	1	U	K.SGVSLSAEQNENLR.S
<input checked="" type="checkbox"/>	992	752.3738	1502.7330	1502.7325	0.39	0	81	3.8e-007	1	U	K.SGVSLSAEQNENLR.S
<input checked="" type="checkbox"/>	993	752.3739	1502.7332	1502.7325	0.52	0	(34)	0.018	1	U	K.SGVSLSAEQNENLR.S

<input checked="" type="checkbox"/>	994	752.3740	1502.7334	1502.7325	0.65	0	(76)	1.4e-006	1	U	K.SGVSLSAEQNENLR.S
<input checked="" type="checkbox"/>	995	752.3741	1502.7336	1502.7325	0.79	0	(70)	4.9e-006	1	U	K.SGVSLSAEQNENLR.S
<input checked="" type="checkbox"/>	996	752.3743	1502.7340	1502.7325	1.05	0	(71)	5.8e-006	1	U	K.SGVSLSAEQNENLR.S
<input checked="" type="checkbox"/>	997	752.3743	1502.7340	1502.7325	1.05	0	(75)	2e-006	1	U	K.SGVSLSAEQNENLR.S
<input checked="" type="checkbox"/>	998	752.3743	1502.7340	1502.7325	1.05	0	(48)	0.0011	1	U	K.SGVSLSAEQNENLR.S
<input checked="" type="checkbox"/>	999	752.3744	1502.7342	1502.7325	1.18	0	(75)	2.3e-006	1	U	K.SGVSLSAEQNENLR.S
<input checked="" type="checkbox"/>	1000	752.3745	1502.7344	1502.7325	1.32	0	(37)	0.014	1	U	K.SGVSLSAEQNENLR.S
<input checked="" type="checkbox"/>	1001	752.3747	1502.7348	1502.7325	1.58	0	(53)	0.00033	1	U	K.SGVSLSAEQNENLR.S
<input checked="" type="checkbox"/>	1002	752.3759	1502.7372	1502.7325	3.18	0	(29)	0.076	1	U	K.SGVSLSAEQNENLR.S
<input checked="" type="checkbox"/>	1110	524.9445	1571.8117	1571.8130	-0.85	1	(21)	0.56	1	U	K.MGGWLLPGKDGNTVK.L
<input checked="" type="checkbox"/>	1111	786.9144	1571.8142	1571.8130	0.79	1	(37)	0.015	1	U	K.MGGWLLPGKDGNTVK.L
<input checked="" type="checkbox"/>	1140	530.2764	1587.8074	1587.8079	-0.35	1	(26)	0.16	1	U	K.MGGWLLPGKDGNTVK.L + Oxidation (M)
<input checked="" type="checkbox"/>	1141	530.2766	1587.8080	1587.8079	0.03	1	(25)	0.19	1	U	K.MGGWLLPGKDGNTVK.L + Oxidation (M)
<input checked="" type="checkbox"/>	1143	794.9119	1587.8092	1587.8079	0.84	1	45	0.0019	1	U	K.MGGWLLPGKDGNTVK.L + Oxidation (M)
<input checked="" type="checkbox"/>	1144	530.2771	1587.8095	1587.8079	0.98	1	(25)	0.22	1	U	K.MGGWLLPGKDGNTVK.L + Oxidation (M)
<input checked="" type="checkbox"/>	1219	815.9097	1629.8048	1629.8032	1.00	1	83	2.8e-007	1	U	K.MVQDIDGLGAPGKDSK.L
<input checked="" type="checkbox"/>	1242	549.6064	1645.7974	1645.7981	-0.47	1	(53)	0.00029	1	U	K.MVQDIDGLGAPGKDSK.L + Oxidation (M)
<input checked="" type="checkbox"/>	1243	549.6066	1645.7980	1645.7981	-0.10	1	(45)	0.0018	1	U	K.MVQDIDGLGAPGKDSK.L + Oxidation (M)
<input checked="" type="checkbox"/>	1245	823.9070	1645.7994	1645.7981	0.79	1	(57)	0.00012	1	U	K.MVQDIDGLGAPGKDSK.L + Oxidation (M)
<input checked="" type="checkbox"/>	1246	549.6071	1645.7995	1645.7981	0.81	1	(42)	0.0036	1	U	K.MVQDIDGLGAPGKDSK.L + Oxidation (M)
<input checked="" type="checkbox"/>	1247	549.6071	1645.7995	1645.7981	0.81	1	(32)	0.037	1	U	K.MVQDIDGLGAPGKDSK.L + Oxidation (M)
<input checked="" type="checkbox"/>	1321	567.9594	1700.8564	1700.8556	0.48	0	(22)	0.41	1	U	R.QWLSELNLPNSCLK.S + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1322	851.4355	1700.8564	1700.8556	0.52	0	(37)	0.014	1	U	R.QWLSELNLPNSCLK.S + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1323	851.4357	1700.8568	1700.8556	0.76	0	61	5.4e-005	1	U	R.QWLSELNLPNSCLK.S + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1324	851.4362	1700.8578	1700.8556	1.35	0	(39)	0.0085	1	U	R.QWLSELNLPNSCLK.S + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1326	851.4372	1700.8598	1700.8556	2.52	0	(32)	0.039	1	U	R.QWLSELNLPNSCLK.S + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1327	851.4380	1700.8614	1700.8556	3.46	0	(23)	0.3	1	U	R.QWLSELNLPNSCLK.S + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1432	886.9916	1771.9686	1771.9680	0.39	1	91	3.1e-008	1	U	K.LDVTSLKNDLNSLVNK.Y
<input checked="" type="checkbox"/>	1433	591.6637	1771.9693	1771.9680	0.74	1	(43)	0.0018	1	U	K.LDVTSLKNDLNSLVNK.Y
<input checked="" type="checkbox"/>	1434	591.6641	1771.9705	1771.9680	1.42	1	(42)	0.0029	1	U	K.LDVTSLKNDLNSLVNK.Y
<input checked="" type="checkbox"/>	1466	913.9795	1825.9444	1825.9462	-0.96	0	(52)	0.00028	1	U	K.SYGSGYVVTVDLTPK.M
<input checked="" type="checkbox"/>	1467	913.9799	1825.9452	1825.9462	-0.52	0	(58)	8e-005	1	U	K.SYGSGYVVTVDLTPK.M
<input checked="" type="checkbox"/>	1468	913.9801	1825.9456	1825.9462	-0.30	0	(33)	0.022	1	U	K.SYGSGYVVTVDLTPK.M
<input checked="" type="checkbox"/>	1469	913.9807	1825.9468	1825.9462	0.36	0	(42)	0.0034	1	U	K.SYGSGYVVTVDLTPK.M
<input checked="" type="checkbox"/>	1470	913.9808	1825.9470	1825.9462	0.47	0	69	5.3e-006	1	U	K.SYGSGYVVTVDLTPK.M
<input checked="" type="checkbox"/>	1471	913.9810	1825.9474	1825.9462	0.68	0	(67)	1e-005	1	U	K.SYGSGYVVTVDLTPK.M
<input checked="" type="checkbox"/>	1472	913.9812	1825.9478	1825.9462	0.90	0	(64)	1.9e-005	1	U	K.SYGSGYVVTVDLTPK.M
<input checked="" type="checkbox"/>	1473	609.6567	1825.9483	1825.9462	1.14	0	(62)	3.3e-005	1	U	K.SYGSGYVVTVDLTPK.M
<input checked="" type="checkbox"/>	1474	913.9816	1825.9486	1825.9462	1.34	0	(38)	0.008	1	U	K.SYGSGYVVTVDLTPK.M
<input checked="" type="checkbox"/>	1475	913.9816	1825.9486	1825.9462	1.34	0	(43)	0.0026	1	U	K.SYGSGYVVTVDLTPK.M
<input checked="" type="checkbox"/>	1476	913.9816	1825.9486	1825.9462	1.34	0	(43)	0.0026	1	U	K.SYGSGYVVTVDLTPK.M
<input checked="" type="checkbox"/>	1477	913.9817	1825.9488	1825.9462	1.45	0	(65)	1.5e-005	1	U	K.SYGSGYVVTVDLTPK.M
<input checked="" type="checkbox"/>	1478	913.9821	1825.9496	1825.9462	1.89	0	(54)	0.00019	1	U	K.SYGSGYVVTVDLTPK.M
<input checked="" type="checkbox"/>	1479	913.9824	1825.9502	1825.9462	2.22	0	(37)	0.013	1	U	K.SYGSGYVVTVDLTPK.M
<input checked="" type="checkbox"/>	1480	913.9825	1825.9504	1825.9462	2.33	0	(40)	0.006	1	U	K.SYGSGYVVTVDLTPK.M
<input checked="" type="checkbox"/>	1481	913.9830	1825.9514	1825.9462	2.88	0	(54)	0.00019	1	U	K.SYGSGYVVTVDLTPK.M

<input checked="" type="checkbox"/>	1522	940.4753	1878.9360	1878.9357	0.20	1	75	2.1e-006	1	U	K.AQEENMKTTLTQTLTQK.Y + Oxidation (M)
<input checked="" type="checkbox"/>	1523	627.3198	1878.9376	1878.9357	1.01	1	(38)	0.011	1	U	K.AQEENMKTTLTQTLTQK.Y + Oxidation (M)
<input checked="" type="checkbox"/>	1593	1012.4990	2022.9834	2022.9833	0.08	0	(58)	0.00012	1	U	R.SAFSAPTSALFSASPMAQPR.T
<input checked="" type="checkbox"/>	1594	675.3361	2022.9865	2022.9833	1.57	0	(54)	0.00028	1	U	R.SAFSAPTSALFSASPMAQPR.T
<input checked="" type="checkbox"/>	1601	1020.4960	2038.9774	2038.9782	-0.37	0	(24)	0.26	1	U	R.SAFSAPTSALFSASPMAQPR.T + Oxidation (M)
<input checked="" type="checkbox"/>	1602	1020.4960	2038.9774	2038.9782	-0.37	0	(42)	0.0041	1	U	R.SAFSAPTSALFSASPMAQPR.T + Oxidation (M)
<input checked="" type="checkbox"/>	1605	1020.4970	2038.9794	2038.9782	0.61	0	(31)	0.043	1	U	R.SAFSAPTSALFSASPMAQPR.T + Oxidation (M)
<input checked="" type="checkbox"/>	1606	1020.4970	2038.9794	2038.9782	0.61	0	(53)	0.00025	1	U	R.SAFSAPTSALFSASPMAQPR.T + Oxidation (M)
<input checked="" type="checkbox"/>	1607	1020.4970	2038.9794	2038.9782	0.61	0	(57)	0.0001	1	U	R.SAFSAPTSALFSASPMAQPR.T + Oxidation (M)
<input checked="" type="checkbox"/>	1608	1020.4970	2038.9794	2038.9782	0.61	0	(68)	8.8e-006	1	U	R.SAFSAPTSALFSASPMAQPR.T + Oxidation (M)
<input checked="" type="checkbox"/>	1609	1020.4970	2038.9794	2038.9782	0.61	0	(71)	4.3e-006	1	U	R.SAFSAPTSALFSASPMAQPR.T + Oxidation (M)
<input checked="" type="checkbox"/>	1610	1020.4970	2038.9794	2038.9782	0.61	0	72	3.7e-006	1	U	R.SAFSAPTSALFSASPMAQPR.T + Oxidation (M)
<input checked="" type="checkbox"/>	1611	680.6672	2038.9798	2038.9782	0.77	0	(59)	7.3e-005	1	U	R.SAFSAPTSALFSASPMAQPR.T + Oxidation (M)
<input checked="" type="checkbox"/>	1612	680.6672	2038.9798	2038.9782	0.77	0	(69)	7.9e-006	1	U	R.SAFSAPTSALFSASPMAQPR.T + Oxidation (M)
<input checked="" type="checkbox"/>	1613	680.6673	2038.9801	2038.9782	0.91	0	(35)	0.017	1	U	R.SAFSAPTSALFSASPMAQPR.T + Oxidation (M)
<input checked="" type="checkbox"/>	1614	680.6675	2038.9807	2038.9782	1.21	0	(28)	0.095	1	U	R.SAFSAPTSALFSASPMAQPR.T + Oxidation (M)
<input checked="" type="checkbox"/>	1615	1020.4980	2038.9814	2038.9782	1.59	0	(30)	0.07	1	U	R.SAFSAPTSALFSASPMAQPR.T + Oxidation (M)
<input checked="" type="checkbox"/>	1617	680.6680	2038.9822	2038.9782	1.94	0	(29)	0.084	1	U	R.SAFSAPTSALFSASPMAQPR.T + Oxidation (M)
<input checked="" type="checkbox"/>	1695	1062.5400	2123.0654	2123.0647	0.34	0	(29)	0.082	1	U	K.YNQINSNTVLFPAQSGSGVK.V
<input checked="" type="checkbox"/>	1696	708.6962	2123.0668	2123.0647	0.96	0	(70)	7e-006	1	U	K.YNQINSNTVLFPAQSGSGVK.V
<input checked="" type="checkbox"/>	1697	708.6964	2123.0674	2123.0647	1.25	0	(31)	0.059	1	U	K.YNQINSNTVLFPAQSGSGVK.V
<input checked="" type="checkbox"/>	1698	1062.5410	2123.0674	2123.0647	1.28	0	79	9.4e-007	1	U	K.YNQINSNTVLFPAQSGSGVK.V
<input checked="" type="checkbox"/>	1859	839.1066	2514.2980	2514.2966	0.56	1	38	0.0069	1	U	K.TTLQTLTQKYSNANSLYDNLVK.V
<input checked="" type="checkbox"/>	1872	845.7396	2534.1970	2534.1997	-1.07	0	(35)	0.013	1	U	K.IHQAQQTLSQSTPPISEENNDER.T
<input checked="" type="checkbox"/>	1873	1268.1070	2534.1994	2534.1997	-0.10	0	73	2.3e-006	1	U	K.IHQAQQTLSQSTPPISEENNDER.T
<input checked="" type="checkbox"/>	1874	845.7406	2534.2000	2534.1997	0.11	0	(26)	0.088	1	U	K.IHQAQQTLSQSTPPISEENNDER.T
<input checked="" type="checkbox"/>	1876	845.7409	2534.2009	2534.1997	0.47	0	(34)	0.014	1	U	K.IHQAQQTLSQSTPPISEENNDER.T
<input checked="" type="checkbox"/>	1878	845.7413	2534.2021	2534.1997	0.94	0	(21)	0.32	1	U	K.IHQAQQTLSQSTPPISEENNDER.T
<input checked="" type="checkbox"/>	1879	845.7414	2534.2024	2534.1997	1.06	0	(41)	0.0035	1	U	K.IHQAQQTLSQSTPPISEENNDER.T
<input checked="" type="checkbox"/>	1880	845.7415	2534.2027	2534.1997	1.18	0	(38)	0.0069	1	U	K.IHQAQQTLSQSTPPISEENNDER.T
<input checked="" type="checkbox"/>	1884	845.7420	2534.2042	2534.1997	1.77	0	(30)	0.035	1	U	K.IHQAQQTLSQSTPPISEENNDER.T
<input checked="" type="checkbox"/>	1885	845.7421	2534.2045	2534.1997	1.89	0	(37)	0.0082	1	U	K.IHQAQQTLSQSTPPISEENNDER.T
<input checked="" type="checkbox"/>	1954	992.8314	2975.4724	2975.4697	0.91	1	82	2.9e-007	1	U	K.IHQAQQTLSQSTPPISEENNDERTLAR.Q
<input checked="" type="checkbox"/>	1967	1041.2030	3120.5872	3120.5840	1.03	1	46	0.00084	1	U	K.NDLNSLVNKYNQINSNTVLFPAQSGSGVK.V

2. [PHEA_ECOLI](#) Mass: 43084 Score: 384 Matches: 15(13) Sequences: 14(12) emPAI: 1.83

P-protein OS=Escherichia coli (strain K12) GN=pheA PE=1 SV=1

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide	
<input checked="" type="checkbox"/>	7	352.7264	703.4382	703.4381	0.22	0	32	0.0069	1	U	R.FVVVLAR.K
<input checked="" type="checkbox"/>	17	373.2339	744.4532	744.4534	-0.20	0	37	0.0029	1	U	R.IAFLGPK.G
<input checked="" type="checkbox"/>	72	409.2243	816.4340	816.4341	-0.08	0	20	1.6	1	U	K.ELGEITR.S
<input checked="" type="checkbox"/>	99	422.7426	843.4706	843.4702	0.57	0	26	0.32	2	U	R.ELAVEVGK.A
<input checked="" type="checkbox"/>	144	449.7896	897.5646	897.5647	-0.07	0	53	0.00015	1	U	K.LLALLAER.R

<input checked="" type="checkbox"/>	228	481.2462	960.4778	960.4777	0.15	0	55	0.00033	1		K.GSYSHLAAR.Q
<input checked="" type="checkbox"/>	422	557.3171	1112.6196	1112.6189	0.63	0	87	1.3e-007	1	U	M.TSENPLLALR.E
<input checked="" type="checkbox"/>	471	377.2240	1128.6502	1128.6502	-0.06	1	35	0.022	1	U	K.ALKELGEITR.S
<input checked="" type="checkbox"/>	494	571.3142	1140.6138	1140.6139	-0.02	0	53	0.0003	1	U	K.AINVSDQVPAK.T
<input checked="" type="checkbox"/>	660	635.3622	1268.7098	1268.7088	0.80	1	69	5.2e-006	1	U	R.KAINVSDQVPAK.T
<input checked="" type="checkbox"/>	933	726.8345	1451.6544	1451.6503	2.83	0	61	2.6e-005	1	U	R.HFEQFIESGCAK.F + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	939	730.3345	1458.6544	1458.6548	-0.23	0	(35)	0.0083	1	U	K.IEYTESTSAAMEK.V
<input checked="" type="checkbox"/>	955	738.3325	1474.6504	1474.6497	0.50	0	82	1.4e-007	1	U	K.IEYTESTSAAMEK.V + Oxidation (M)
<input checked="" type="checkbox"/>	1781	762.4346	2284.2820	2284.2824	-0.20	0	34	0.0059	1	U	K.TTLLMATGQAGALVEALLVLR.N + Oxidation (M)
<input checked="" type="checkbox"/>	1793	775.7458	2324.2156	2324.2124	1.34	0	52	0.00026	1	U	K.SPHVAALGSEAGGTTYGLQVLER.I

Proteins matching the same set of peptides:

[PHEA_SHIFL](#) Mass: 43084 Score: 384 Matches: 15(13) Sequences: 14(12)

P-protein OS=Shigella flexneri GN=pheA PE=3 SV=1

[PHEA_ECO57](#) Mass: 43084 Score: 384 Matches: 15(13) Sequences: 14(12)

P-protein OS=Escherichia coli O157:H7 GN=pheA PE=3 SV=1

3. [LACI_ECOLI](#) Mass: 38566 Score: 266 Matches: 9(8) Sequences: 9(8) emPAI: 1.04

Lactose operon repressor OS=Escherichia coli (strain K12) GN=lacI PE=1 SV=3

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide	
<input checked="" type="checkbox"/>	249	494.7747	987.5348	987.5349	-0.06	0	69	1.6e-005	1	U	R.LLGQTSVDR.L
<input checked="" type="checkbox"/>	361	534.7936	1067.5726	1067.5723	0.30	0	41	0.0053	1	U	R.NQIQPIAER.E
<input checked="" type="checkbox"/>	393	546.8171	1091.6196	1091.6199	-0.28	0	35	0.012	1	U	K.AAVHNLLAQR.V
<input checked="" type="checkbox"/>	576	592.8538	1183.6930	1183.6925	0.50	0	60	5.5e-005	1	U	R.LLQLSQGQAVK.G
<input checked="" type="checkbox"/>	596	602.8216	1203.6286	1203.6281	0.43	0	84	3.8e-007	1	U	R.ALADSLMQLAR.Q + Oxidation (M)
<input checked="" type="checkbox"/>	811	679.3577	1356.7008	1356.6997	0.82	0	58	9e-005	1	U	K.TTLAPNTQTASPR.A
<input checked="" type="checkbox"/>	965	495.9394	1484.7964	1484.7947	1.13	1	24	0.27	1	U	R.KTTLAPNTQTASPR.A
<input checked="" type="checkbox"/>	1118	788.9047	1575.7948	1575.7927	1.39	0	76	2.5e-006	1	U	R.ADQLGASVVVSMVER.S + Oxidation (M)
<input checked="" type="checkbox"/>	1507	621.9796	1862.9170	1862.9196	-1.40	1	32	0.042	1	U	R.EKVEAAMAELNYIPNR.V + Oxidation (M)

4. [OMPA_ECOLI](#) Mass: 37178 Score: 240 Matches: 7(6) Sequences: 7(6) emPAI: 0.74

Outer membrane protein A OS=Escherichia coli (strain K12) GN=ompA PE=1 SV=1

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide	
<input checked="" type="checkbox"/>	177	458.2663	914.5180	914.5185	-0.52	0	28	0.3	1	U	K.AQGVTAK.L
<input checked="" type="checkbox"/>	608	607.8143	1213.6140	1213.6125	1.29	0	60	3.8e-005	1	U	R.AALIDCLAPDR.R + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	844	689.8885	1377.7624	1377.7616	0.62	1	44	0.0013	1	U	R.RAQSVVDYLISK.G
<input checked="" type="checkbox"/>	877	705.3359	1408.6572	1408.6582	-0.71	0	87	9.7e-008	1	U	R.IGSDAYNQGLSER.R
<input checked="" type="checkbox"/>	1261	827.9207	1653.8268	1653.8250	1.12	0	56	0.00014	1	U	K.LGYPTDDLDIYTR.L
<input checked="" type="checkbox"/>	1446	898.3837	1794.7528	1794.7513	0.87	0	64	3.8e-006	1	U	R.GMGESNPVTGNTCDNVK.Q + Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/>	1770	1116.5860	2231.1574	2231.1586	-0.53	0	44	0.0021	1	U	R.FGQGEAAPVVAPAPAPEVQTK.H

Proteins matching the same set of peptides:[OMPA_ESCF3](#) Mass: 37679 Score: 240 Matches: 7(6) Sequences: 7(6)

Outer membrane protein A OS=Escherichia fergusonii (strain ATCC 35469 / DSM 13698 / CDC 0568-73) GN=ompA PE=3 SV=2

[OMPA_ECO57](#) Mass: 37178 Score: 240 Matches: 7(6) Sequences: 7(6)

Outer membrane protein A OS=Escherichia coli O157:H7 GN=ompA PE=3 SV=1

5. [HIS7_ECO57](#) Mass: 40264 Score: 123 Matches: 7(6) Sequences: 7(6) emPAI: 0.67

Histidine biosynthesis bifunctional protein HisB OS=Escherichia coli O157:H7 GN=hisB PE=1 SV=1

 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 8	361.7077	721.4008	721.4010	-0.25	0	35	0.03	1		R.VESLFK.A
<input checked="" type="checkbox"/> 84	413.7265	825.4384	825.4385	-0.04	0	22	0.23	1		K.YLFIDR.D
<input checked="" type="checkbox"/> 173	457.7220	913.4294	913.4294	0.09	0	35	0.016	1		K.AEFTYQR.V
<input checked="" type="checkbox"/> 260	497.7512	993.4878	993.4879	-0.10	0	58	0.00011	1		R.ANSYVIGDR.A
<input checked="" type="checkbox"/> 318	516.7640	1031.5134	1031.5135	-0.05	0	47	0.00088	1		R.VEGDTLPSSK.G
<input checked="" type="checkbox"/> 417	556.7559	1111.4972	1111.4968	0.42	0	43	0.0022	1		R.YLAEQAMDR.A + Oxidation (M)
<input checked="" type="checkbox"/> 1374	866.4394	1730.8642	1730.8621	1.24	0	47	0.0013	1		R.ATDIQLAENMGINGLR.Y + Oxidation (M)

Proteins matching the same set of peptides:[HIS7_ECOL6](#) Mass: 40277 Score: 123 Matches: 7(6) Sequences: 7(6)

Histidine biosynthesis bifunctional protein HisB OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) GN=hisB PE=3 SV=2

6. [HIS7_SHIFL](#) Mass: 40138 Score: 121 Matches: 7(6) Sequences: 7(6) emPAI: 0.67

Histidine biosynthesis bifunctional protein HisB OS=Shigella flexneri GN=hisB PE=3 SV=2

 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
8	361.7077	721.4008	721.4010	-0.25	0	35	0.03	1		R.VESLFK.A
84	413.7265	825.4384	825.4385	-0.04	0	22	0.23	1		K.YLFIDR.D
173	457.7220	913.4294	913.4294	0.09	0	35	0.016	1		K.AEFTYQR.V
260	497.7512	993.4878	993.4879	-0.10	0	58	0.00011	1		R.ANSYVIGDR.A
318	516.7640	1031.5134	1031.5135	-0.05	0	47	0.00088	1		R.VEGDTLPSSK.G
<input checked="" type="checkbox"/> 900	713.4216	1424.8286	1424.8279	0.54	0	32	0.013	1		K.LAFEPGVIPELLK.L
1374	866.4394	1730.8642	1730.8621	1.24	0	47	0.0013	1		R.ATDIQLAENMGINGLR.Y + Oxidation (M)

7. [DNAJ_ECOHS](#) Mass: 41018 Score: 117 Matches: 4(4) Sequences: 4(4) emPAI: 0.40

Chaperone protein DnaJ OS=Escherichia coli O9:H4 (strain HS) GN=dnaJ PE=3 SV=1

 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 268	500.7563	999.4980	999.4985	-0.49	0	37	0.007	1	U	K.IPAGVDTGDR.I
<input checked="" type="checkbox"/> 332	523.7565	1045.4984	1045.4975	0.92	0	52	0.00018	1	U	R.GGAQGDLPCR.V + Carbamidomethyl (C)
<input checked="" type="checkbox"/> 683	642.3647	1282.7148	1282.7133	1.23	0	41	0.0025	1	U	R.VVETPVGLNEK.Q

[1791](#) 775.3787 2323.1143 2323.1193 -2.15 0 56 0.00014 1 U K.QLLQELQESFGGPTGEHNSPR.S

Proteins matching the same set of peptides:

[DNAJ_ECOLC](#) Mass: 41018 Score: 117 Matches: 4(4) Sequences: 4(4)
 Chaperone protein DnaJ OS=Escherichia coli (strain ATCC 8739 / DSM 1576 / Crooks) GN=dnaJ PE=3 SV=1

[DNAJ_ECOLU](#) Mass: 41018 Score: 117 Matches: 4(4) Sequences: 4(4)
 Chaperone protein DnaJ OS=Escherichia coli O17:K52:H18 (strain UMN026 / ExPEC) GN=dnaJ PE=3 SV=1

[DNAJ_ECOSE](#) Mass: 41018 Score: 117 Matches: 4(4) Sequences: 4(4)
 Chaperone protein DnaJ OS=Escherichia coli (strain SE11) GN=dnaJ PE=3 SV=1

[DNAJ_ECOSM](#) Mass: 41018 Score: 117 Matches: 4(4) Sequences: 4(4)
 Chaperone protein DnaJ OS=Escherichia coli (strain SMS-3-5 / SECEC) GN=dnaJ PE=3 SV=1

[DNAJ_ECOUT](#) Mass: 41018 Score: 117 Matches: 4(4) Sequences: 4(4)
 Chaperone protein DnaJ OS=Escherichia coli (strain UTI89 / UPEC) GN=dnaJ PE=3 SV=1

[DNAJ_SHIBS](#) Mass: 41017 Score: 117 Matches: 4(4) Sequences: 4(4)
 Chaperone protein DnaJ OS=Shigella boydii serotype 4 (strain Sb227) GN=dnaJ PE=3 SV=1

[DNAJ_SHIDS](#) Mass: 41046 Score: 117 Matches: 4(4) Sequences: 4(4)
 Chaperone protein DnaJ OS=Shigella dysenteriae serotype 1 (strain Sd197) GN=dnaJ PE=3 SV=1

[DNAJ_SHISS](#) Mass: 41018 Score: 117 Matches: 4(4) Sequences: 4(4)
 Chaperone protein DnaJ OS=Shigella sonnei (strain Ss046) GN=dnaJ PE=3 SV=1

[DNAJ_ESCF3](#) Mass: 41018 Score: 117 Matches: 4(4) Sequences: 4(4)
 Chaperone protein DnaJ OS=Escherichia fergusonii (strain ATCC 35469 / DSM 13698 / CDC 0568-73) GN=dnaJ PE=3 SV=1

[DNAJ_SHIB3](#) Mass: 41017 Score: 117 Matches: 4(4) Sequences: 4(4)
 Chaperone protein DnaJ OS=Shigella boydii serotype 18 (strain CDC 3083-94 / BS512) GN=dnaJ PE=3 SV=1

[DNAJ_ECO5E](#) Mass: 41048 Score: 117 Matches: 4(4) Sequences: 4(4)
 Chaperone protein DnaJ OS=Escherichia coli O157:H7 (strain EC4115 / EHEC) GN=dnaJ PE=3 SV=1

[DNAJ_ECOL6](#) Mass: 41018 Score: 117 Matches: 4(4) Sequences: 4(4)
 Chaperone protein DnaJ OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) GN=dnaJ PE=3 SV=3

[DNAJ_ECO7I](#) Mass: 41018 Score: 117 Matches: 4(4) Sequences: 4(4)
 Chaperone protein DnaJ OS=Escherichia coli O7:K1 (strain IAI39 / ExPEC) GN=dnaJ PE=3 SV=1

[DNAJ_ECO8A](#) Mass: 41018 Score: 117 Matches: 4(4) Sequences: 4(4)
 Chaperone protein DnaJ OS=Escherichia coli O8 (strain IAI1) GN=dnaJ PE=3 SV=1

[DNAJ_SHIF8](#) Mass: 41046 Score: 117 Matches: 4(4) Sequences: 4(4)
 Chaperone protein DnaJ OS=Shigella flexneri serotype 5b (strain 8401) GN=dnaJ PE=3 SV=1

[DNAJ_ECO24](#) Mass: 41018 Score: 117 Matches: 4(4) Sequences: 4(4)
 Chaperone protein DnaJ OS=Escherichia coli O139:H28 (strain E24377A / ETEC) GN=dnaJ PE=3 SV=1

[DNAJ_ECO27](#) Mass: 41018 Score: 117 Matches: 4(4) Sequences: 4(4)
 Chaperone protein DnaJ OS=Escherichia coli O127:H6 (strain E2348/69 / EPEC) GN=dnaJ PE=3 SV=1

[DNAJ_ECO45](#) Mass: 41018 Score: 117 Matches: 4(4) Sequences: 4(4)
 Chaperone protein DnaJ OS=Escherichia coli O45:K1 (strain S88 / ExPEC) GN=dnaJ PE=3 SV=1

[DNAJ_ECO55](#) Mass: 41018 Score: 117 Matches: 4(4) Sequences: 4(4)
 Chaperone protein DnaJ OS=Escherichia coli (strain 55989 / EAEC) GN=dnaJ PE=3 SV=1

[DNAJ_ECO57](#) Mass: 41018 Score: 117 Matches: 4(4) Sequences: 4(4)
 Chaperone protein DnaJ OS=Escherichia coli O157:H7 GN=dnaJ PE=3 SV=3

[DNAJ_ECO81](#) Mass: 41018 Score: 117 Matches: 4(4) Sequences: 4(4)
 Chaperone protein DnaJ OS=Escherichia coli O81 (strain ED1a) GN=dnaJ PE=3 SV=1

8. [RECA_ECOBW](#) **Mass:** 37950 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3) **emPAI:** 0.31

Protein RecA OS=Escherichia coli (strain K12 / MC4100 / BW2952) GN=recA PE=3 SV=1

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 381	542.8215	1083.6284	1083.6288	-0.30	0	74	2.1e-006	1		K.ALAAALGQIEK.Q
<input checked="" type="checkbox"/> 567	588.7787	1175.5428	1175.5418	0.86	0	43	0.003	1	U	K.EGENVVGSETR.V
673	639.8333	1277.6520	1277.6503	1.36	0	29	0.11	2		R.IVEIYGPESGK.T
<input checked="" type="checkbox"/> 1095	780.4488	1558.8830	1558.8831	-0.03	0	38	0.0042	1	U	K.QSNTLLIFINQIR.M
<input checked="" type="checkbox"/> 1570	654.9846	1961.9320	1961.9305	0.74	0	29	0.069	1	U	K.TCAFIDAEHALDPIYAR.K + Carbamidomethyl (C)

Proteins matching the same set of peptides:

[RECA_ECOHS](#) **Mass:** 37950 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3)

Protein RecA OS=Escherichia coli O9:H4 (strain HS) GN=recA PE=3 SV=1

[RECA_ECOLC](#) **Mass:** 37950 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3)

Protein RecA OS=Escherichia coli (strain ATCC 8739 / DSM 1576 / Crooks) GN=recA PE=3 SV=1

[RECA_ECOLI](#) **Mass:** 37950 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3)

Protein RecA OS=Escherichia coli (strain K12) GN=recA PE=1 SV=2

[RECA_ECOLU](#) **Mass:** 37950 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3)

Protein RecA OS=Escherichia coli O17:K52:H18 (strain UMN026 / ExPEC) GN=recA PE=3 SV=1

[RECA_ECOSE](#) **Mass:** 37950 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3)

Protein RecA OS=Escherichia coli (strain SE11) GN=recA PE=3 SV=1

[RECA_ECOSM](#) **Mass:** 37950 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3)

Protein RecA OS=Escherichia coli (strain SMS-3-5 / SECEC) GN=recA PE=3 SV=1

[RECA_ECOUT](#) **Mass:** 37950 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3)

Protein RecA OS=Escherichia coli (strain UTI89 / UPEC) GN=recA PE=3 SV=1

[RECA_SHIBS](#) **Mass:** 37950 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3)

Protein RecA OS=Shigella boydii serotype 4 (strain Sb227) GN=recA PE=3 SV=1

[RECA_SHIDS](#) **Mass:** 37950 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3)

Protein RecA OS=Shigella dysenteriae serotype 1 (strain Sd197) GN=recA PE=3 SV=1

[RECA_SHIFL](#) **Mass:** 37950 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3)

Protein RecA OS=Shigella flexneri GN=recA PE=3 SV=2

[RECA_SHISO](#) **Mass:** 37907 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3)

Protein RecA OS=Shigella sonnei GN=recA PE=3 SV=3

[RECA_SHISS](#) **Mass:** 37950 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3)

Protein RecA OS=Shigella sonnei (strain Ss046) GN=recA PE=3 SV=1

[RECA_ESCF3](#) **Mass:** 37950 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3)

Protein RecA OS=Escherichia fergusonii (strain ATCC 35469 / DSM 13698 / CDC 0568-73) GN=recA PE=3 SV=1

[RECA_SHIB3](#) **Mass:** 37950 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3)

Protein RecA OS=Shigella boydii serotype 18 (strain CDC 3083-94 / BS512) GN=recA PE=3 SV=1

[RECA_ECO5E](#) **Mass:** 37950 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3)

Protein RecA OS=Escherichia coli O157:H7 (strain EC4115 / EHEC) GN=recA PE=3 SV=1

[RECA_ECOL5](#) **Mass:** 37950 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3)

Protein RecA OS=Escherichia coli O6:K15:H31 (strain 536 / UPEC) GN=recA PE=3 SV=1

[RECA_ECOL6](#) **Mass:** 37950 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3)

Protein RecA OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) GN=recA PE=3 SV=2
[RECA_ECO7I](#) **Mass:** 37950 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3)

Protein RecA OS=Escherichia coli O7:K1 (strain IAI39 / ExPEC) GN=recA PE=3 SV=1
[RECA_CITK8](#) **Mass:** 38065 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3)

Protein RecA OS=Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696) GN=recA PE=3 SV=1
[RECA_ECO8A](#) **Mass:** 37950 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3)

Protein RecA OS=Escherichia coli O8 (strain IAI1) GN=recA PE=3 SV=1
[RECA_SHIF8](#) **Mass:** 37950 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3)

Protein RecA OS=Shigella flexneri serotype 5b (strain 8401) GN=recA PE=3 SV=1
[RECA_ECO24](#) **Mass:** 37950 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3)

Protein RecA OS=Escherichia coli O139:H28 (strain E24377A / ETEC) GN=recA PE=3 SV=1
[RECA_ECO27](#) **Mass:** 37950 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3)

Protein RecA OS=Escherichia coli O127:H6 (strain E2348/69 / EPEC) GN=recA PE=3 SV=1
[RECA_ECO45](#) **Mass:** 37950 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3)

Protein RecA OS=Escherichia coli O45:K1 (strain S88 / ExPEC) GN=recA PE=3 SV=1
[RECA_ECO55](#) **Mass:** 37950 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3)

Protein RecA OS=Escherichia coli (strain 55989 / EAEC) GN=recA PE=3 SV=1
[RECA_ECO57](#) **Mass:** 37950 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3)

Protein RecA OS=Escherichia coli O157:H7 GN=recA PE=3 SV=2
[RECA_ECO81](#) **Mass:** 37950 **Score:** 113 **Matches:** 5(3) **Sequences:** 5(3)

Protein RecA OS=Escherichia coli O81 (strain ED1a) GN=recA PE=3 SV=1

9. [PGK_ECOHS](#) **Mass:** 41079 **Score:** 106 **Matches:** 2(2) **Sequences:** 2(2) **emPAI:** 0.18
 Phosphoglycerate kinase OS=Escherichia coli O9:H4 (strain HS) GN=pgk PE=3 SV=1

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 526	578.3534	1154.6922	1154.6910	1.05	0	62	1.6e-005	1	U	R.ASLPTIELALK.Q
<input checked="" type="checkbox"/> 946	732.8829	1463.7512	1463.7508	0.33	0	72	4.5e-006	1	U	R.VATEFSETAPATLK.S

Proteins matching the same set of peptides:

[PGK_ECOLC](#) **Mass:** 41093 **Score:** 106 **Matches:** 2(2) **Sequences:** 2(2)
 Phosphoglycerate kinase OS=Escherichia coli (strain ATCC 8739 / DSM 1576 / Crooks) GN=pgk PE=3 SV=1

[PGK_ECOLI](#) **Mass:** 41093 **Score:** 106 **Matches:** 2(2) **Sequences:** 2(2)
 Phosphoglycerate kinase OS=Escherichia coli (strain K12) GN=pgk PE=1 SV=2

[PGK_SALAR](#) **Mass:** 41107 **Score:** 106 **Matches:** 2(2) **Sequences:** 2(2)
 Phosphoglycerate kinase OS=Salmonella arizonae (strain ATCC BAA-731 / CDC346-86 / RSK2980) GN=pgk PE=3 SV=1

[PGK_SALCH](#) **Mass:** 41107 **Score:** 106 **Matches:** 2(2) **Sequences:** 2(2)
 Phosphoglycerate kinase OS=Salmonella choleraesuis (strain SC-B67) GN=pgk PE=3 SV=1

[PGK_SALDC](#) **Mass:** 41107 **Score:** 106 **Matches:** 2(2) **Sequences:** 2(2)
 Phosphoglycerate kinase OS=Salmonella dublin (strain CT_02021853) GN=pgk PE=3 SV=1

[PGK_SALEP](#) **Mass:** 41107 **Score:** 106 **Matches:** 2(2) **Sequences:** 2(2)
 Phosphoglycerate kinase OS=Salmonella enteritidis PT4 (strain P125109) GN=pgk PE=3 SV=1

[PGK_SALHS](#) **Mass:** 41107 **Score:** 106 **Matches:** 2(2) **Sequences:** 2(2)
 Phosphoglycerate kinase OS=Salmonella heidelberg (strain SL476) GN=pgk PE=3 SV=1

[PGK_SALNS](#) **Mass:** 41107 **Score:** 106 **Matches:** 2(2) **Sequences:** 2(2)

Phosphoglycerate kinase OS=Salmonella newport (strain SL254) GN=pgk PE=3 SV=1
[PGK_SALPA](#) Mass: 41107 Score: 106 Matches: 2(2) Sequences: 2(2)
 Phosphoglycerate kinase OS=Salmonella paratyphi A (strain ATCC 9150 / SARB42) GN=pgk PE=3 SV=1
[PGK_SALPB](#) Mass: 41107 Score: 106 Matches: 2(2) Sequences: 2(2)
 Phosphoglycerate kinase OS=Salmonella paratyphi B (strain ATCC BAA-1250 / SPB7) GN=pgk PE=3 SV=1
[PGK_SALPK](#) Mass: 41107 Score: 106 Matches: 2(2) Sequences: 2(2)
 Phosphoglycerate kinase OS=Salmonella paratyphi A (strain AKU_12601) GN=pgk PE=3 SV=1
[PGK_SALSV](#) Mass: 41107 Score: 106 Matches: 2(2) Sequences: 2(2)
 Phosphoglycerate kinase OS=Salmonella schwarzengrund (strain CVM19633) GN=pgk PE=3 SV=1
[PGK_SALTI](#) Mass: 41107 Score: 106 Matches: 2(2) Sequences: 2(2)
 Phosphoglycerate kinase OS=Salmonella typhi GN=pgk PE=3 SV=2
[PGK_SALTY](#) Mass: 41107 Score: 106 Matches: 2(2) Sequences: 2(2)
 Phosphoglycerate kinase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=pgk PE=3 SV=2
[PGK_SHIBS](#) Mass: 41093 Score: 106 Matches: 2(2) Sequences: 2(2)
 Phosphoglycerate kinase OS=Shigella boydii serotype 4 (strain Sb227) GN=pgk PE=3 SV=1
[PGK_SHIDS](#) Mass: 41065 Score: 106 Matches: 2(2) Sequences: 2(2)
 Phosphoglycerate kinase OS=Shigella dysenteriae serotype 1 (strain Sd197) GN=pgk PE=3 SV=1
[PGK_SHIFL](#) Mass: 41093 Score: 106 Matches: 2(2) Sequences: 2(2)
 Phosphoglycerate kinase OS=Shigella flexneri GN=pgk PE=3 SV=2
[PGK_ECOK1](#) Mass: 41093 Score: 106 Matches: 2(2) Sequences: 2(2)
 Phosphoglycerate kinase OS=Escherichia coli O1:K1 / APEC GN=pgk PE=3 SV=1
[PGK_SALG2](#) Mass: 41107 Score: 106 Matches: 2(2) Sequences: 2(2)
 Phosphoglycerate kinase OS=Salmonella gallinarum (strain 287/91 / NCTC 13346) GN=pgk PE=3 SV=1
[PGK_SALAA4](#) Mass: 41107 Score: 106 Matches: 2(2) Sequences: 2(2)
 Phosphoglycerate kinase OS=Salmonella agona (strain SL483) GN=pgk PE=3 SV=1
[PGK_ECOL5](#) Mass: 41093 Score: 106 Matches: 2(2) Sequences: 2(2)
 Phosphoglycerate kinase OS=Escherichia coli O6:K15:H31 (strain 536 / UPEC) GN=pgk PE=3 SV=1
[PGK_ECOL6](#) Mass: 41093 Score: 106 Matches: 2(2) Sequences: 2(2)
 Phosphoglycerate kinase OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) GN=pgk PE=3 SV=2
[PGK_CROS8](#) Mass: 41252 Score: 106 Matches: 2(2) Sequences: 2(2)
 Phosphoglycerate kinase OS=Cronobacter sakazakii (strain ATCC BAA-894) GN=pgk PE=3 SV=1
[PGK_SHIF8](#) Mass: 41093 Score: 106 Matches: 2(2) Sequences: 2(2)
 Phosphoglycerate kinase OS=Shigella flexneri serotype 5b (strain 8401) GN=pgk PE=3 SV=1
[PGK_ECO24](#) Mass: 41093 Score: 106 Matches: 2(2) Sequences: 2(2)
 Phosphoglycerate kinase OS=Escherichia coli O139:H28 (strain E24377A / ETEC) GN=pgk PE=3 SV=1
[PGK_ECOS7](#) Mass: 41105 Score: 106 Matches: 2(2) Sequences: 2(2)
 Phosphoglycerate kinase OS=Escherichia coli O157:H7 GN=pgk PE=3 SV=3

10. [EFTU_SALAR](#) Mass: 43256 Score: 105 Matches: 3(3) Sequences: 3(3) emPAI: 0.27
 Elongation factor Tu OS=Salmonella arizonae (strain ATCC BAA-731 / CDC346-86 / RSK2980) GN=tuf1 PE=3 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 561	586.3321	1170.6496	1170.6496	0.04	0	57	0.00015	1		K.VGEEVEIVGIK.E
<input checked="" type="checkbox"/> 838	688.8205	1375.6264	1375.6255	0.65	0	53	0.00016	1		R.AFDQIDNAPEEK.A
<input checked="" type="checkbox"/> 1574	982.9859	1963.9572	1963.9527	2.30	0	44	0.0024	1	U	R.ELLSQYDFPGDDTPIVR.G

Proteins matching the same set of peptides:

[EFTU_SALCH](#) **Mass:** 43256 **Score:** 105 **Matches:** 3(3) **Sequences:** 3(3)
Elongation factor Tu OS=Salmonella choleraesuis (strain SC-B67) GN=tuf1 PE=3 SV=1

[EFTU_SALPA](#) **Mass:** 43256 **Score:** 105 **Matches:** 3(3) **Sequences:** 3(3)
Elongation factor Tu OS=Salmonella paratyphi A (strain ATCC 9150 / SARB42) GN=tuf1 PE=3 SV=1

[EFTU_SALPB](#) **Mass:** 43256 **Score:** 105 **Matches:** 3(3) **Sequences:** 3(3)
Elongation factor Tu OS=Salmonella paratyphi B (strain ATCC BAA-1250 / SPB7) GN=tuf1 PE=3 SV=1

[EFTU_SALTI](#) **Mass:** 43256 **Score:** 105 **Matches:** 3(3) **Sequences:** 3(3)
Elongation factor Tu OS=Salmonella typhi GN=tufA PE=3 SV=2

[EFTU_SALTY](#) **Mass:** 43256 **Score:** 105 **Matches:** 3(3) **Sequences:** 3(3)
Elongation factor Tu OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=tufA PE=3 SV=2

[EFTU_SHIBS](#) **Mass:** 43256 **Score:** 105 **Matches:** 3(3) **Sequences:** 3(3)
Elongation factor Tu OS=Shigella boydii serotype 4 (strain Sb227) GN=tuf1 PE=3 SV=1

[EFTU_SHIDS](#) **Mass:** 43256 **Score:** 105 **Matches:** 3(3) **Sequences:** 3(3)
Elongation factor Tu OS=Shigella dysenteriae serotype 1 (strain Sd197) GN=tuf1 PE=3 SV=1

[EFTU_SHIFL](#) **Mass:** 43256 **Score:** 105 **Matches:** 3(3) **Sequences:** 3(3)
Elongation factor Tu OS=Shigella flexneri GN=tufA PE=3 SV=3

[EFTU1_ECO24](#) **Mass:** 43256 **Score:** 105 **Matches:** 3(3) **Sequences:** 3(3)
Elongation factor Tu 1 OS=Escherichia coli O139:H28 (strain E24377A / ETEC) GN=tuf1 PE=3 SV=1

[EFTU1_ECOHS](#) **Mass:** 43256 **Score:** 105 **Matches:** 3(3) **Sequences:** 3(3)
Elongation factor Tu 1 OS=Escherichia coli O9:H4 (strain HS) GN=tuf1 PE=3 SV=1

[EFTU1_ECOK1](#) **Mass:** 43256 **Score:** 105 **Matches:** 3(3) **Sequences:** 3(3)
Elongation factor Tu 1 OS=Escherichia coli O1:K1 / APEC GN=tuf1 PE=3 SV=2

[EFTU1_ECOL5](#) **Mass:** 43256 **Score:** 105 **Matches:** 3(3) **Sequences:** 3(3)
Elongation factor Tu 1 OS=Escherichia coli O6:K15:H31 (strain 536 / UPEC) GN=tuf1 PE=3 SV=1

[EFTU1_ECOLC](#) **Mass:** 43256 **Score:** 105 **Matches:** 3(3) **Sequences:** 3(3)
Elongation factor Tu 1 OS=Escherichia coli (strain ATCC 8739 / DSM 1576 / Crooks) GN=tuf1 PE=3 SV=1

[EFTU1_ECOLI](#) **Mass:** 43256 **Score:** 105 **Matches:** 3(3) **Sequences:** 3(3)
Elongation factor Tu 1 OS=Escherichia coli (strain K12) GN=tufA PE=1 SV=1

[EFTU1_ECOUT](#) **Mass:** 43256 **Score:** 105 **Matches:** 3(3) **Sequences:** 3(3)
Elongation factor Tu 1 OS=Escherichia coli (strain UTI89 / UPEC) GN=tuf1 PE=1 SV=1

[EFTU1_SHIF8](#) **Mass:** 43255 **Score:** 105 **Matches:** 3(3) **Sequences:** 3(3)
Elongation factor Tu 1 OS=Shigella flexneri serotype 5b (strain 8401) GN=tuf1 PE=3 SV=1

[EFTU1_SHISS](#) **Mass:** 43256 **Score:** 105 **Matches:** 3(3) **Sequences:** 3(3)
Elongation factor Tu 1 OS=Shigella sonnei (strain Ss046) GN=tuf1 PE=3 SV=1

[EFTU2_ECOHS](#) **Mass:** 43286 **Score:** 105 **Matches:** 3(3) **Sequences:** 3(3)
Elongation factor Tu 2 OS=Escherichia coli O9:H4 (strain HS) GN=tuf2 PE=3 SV=1

[EFTU2_ECOK1](#) **Mass:** 43286 **Score:** 105 **Matches:** 3(3) **Sequences:** 3(3)
Elongation factor Tu 2 OS=Escherichia coli O1:K1 / APEC GN=tuf2 PE=3 SV=1

[EFTU2_ECOL5](#) **Mass:** 43286 **Score:** 105 **Matches:** 3(3) **Sequences:** 3(3)
Elongation factor Tu 2 OS=Escherichia coli O6:K15:H31 (strain 536 / UPEC) GN=tuf2 PE=3 SV=1

[EFTU2_ECOLC](#) **Mass:** 43286 **Score:** 105 **Matches:** 3(3) **Sequences:** 3(3)
Elongation factor Tu 2 OS=Escherichia coli (strain ATCC 8739 / DSM 1576 / Crooks) GN=tuf2 PE=3 SV=1

[EFTU2_ECOLI](#) **Mass:** 43286 **Score:** 105 **Matches:** 3(3) **Sequences:** 3(3)

Elongation factor Tu 2 OS=Escherichia coli (strain K12) GN=tufB PE=1 SV=1
[EFTU2_ECOUT](#) Mass: 43286 Score: 105 Matches: 3(3) Sequences: 3(3)
 Elongation factor Tu 2 OS=Escherichia coli (strain UTI89 / UPEC) GN=tuf2 PE=3 SV=2
[EFTU2_SHIF8](#) Mass: 43286 Score: 105 Matches: 3(3) Sequences: 3(3)
 Elongation factor Tu 2 OS=Shigella flexneri serotype 5b (strain 8401) GN=tuf2 PE=3 SV=1
[EFTU2_SHISS](#) Mass: 43286 Score: 105 Matches: 3(3) Sequences: 3(3)
 Elongation factor Tu 2 OS=Shigella sonnei (strain Ss046) GN=tuf2 PE=3 SV=1
[EFTU_EC0L6](#) Mass: 43286 Score: 105 Matches: 3(3) Sequences: 3(3)
 Elongation factor Tu OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) GN=tufA PE=3 SV=2
[EFTU_KLEP7](#) Mass: 43219 Score: 105 Matches: 3(3) Sequences: 3(3)
 Elongation factor Tu OS=Klebsiella pneumoniae subsp. pneumoniae (strain ATCC 700721 / MGH 78578) GN=tufA PE=3 SV=1
[EFTU_CROS8](#) Mass: 43177 Score: 105 Matches: 3(3) Sequences: 3(3)
 Elongation factor Tu OS=Cronobacter sakazakii (strain ATCC BAA-894) GN=tuf1 PE=3 SV=1
[EFTU_EC057](#) Mass: 43286 Score: 105 Matches: 3(3) Sequences: 3(3)
 Elongation factor Tu OS=Escherichia coli O157:H7 GN=tufA PE=1 SV=2

11. [MALE_EC0LI](#) Mass: 43360 Score: 101 Matches: 4(3) Sequences: 4(3) emPAI: 0.27
 Maltose-binding periplasmic protein OS=Escherichia coli (strain K12) GN=male PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 225	480.2664	958.5182	958.5196	-1.39	0	46	0.0025	1	U	R.TAVINAASGR.Q
<input checked="" type="checkbox"/> 777	669.3779	1336.7412	1336.7391	1.60	0	45	0.0013	1	U	K.VNYGVTVLPTFK.G
<input checked="" type="checkbox"/> 1427	883.9525	1765.8904	1765.8887	1.01	0	58	0.0001	1	U	R.FGGYAQSGLLAEITPDK.A
<input checked="" type="checkbox"/> 1714	713.7242	2138.1508	2138.1484	1.11	0	21	0.23	1	U	K.GQPSKPFVGVLSAGINAASPNK.E

Proteins matching the same set of peptides:

[MALE_EC057](#) Mass: 43360 Score: 101 Matches: 4(3) Sequences: 4(3)
 Maltose-binding periplasmic protein OS=Escherichia coli O157:H7 GN=male PE=1 SV=1

12. [ASTC_EC0BW](#) Mass: 43638 Score: 99 Matches: 3(2) Sequences: 3(2) emPAI: 0.17
 Succinylornithine transaminase OS=Escherichia coli (strain K12 / MC4100 / BW2952) GN=astC PE=3 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 1368	864.4063	1726.7980	1726.7984	-0.23	0	23	0.2	1	U	R.VFFCNSGAEANEALK.L + Carbamidomethyl (C)
<input checked="" type="checkbox"/> 1562	974.4874	1946.9602	1946.9585	0.88	0	69	7.3e-006	1	U	R.FAPALNVSEEEVTTGLDR.F
<input checked="" type="checkbox"/> 1757	735.7048	2204.0926	2204.0896	1.35	0	37	0.0097	1	U	R.VMTVGHGTTYGGNPLASAVAGK.V + Oxidation (M)

Proteins matching the same set of peptides:

[ASTC_EC0DH](#) Mass: 43638 Score: 99 Matches: 3(2) Sequences: 3(2)
 Succinylornithine transaminase OS=Escherichia coli (strain K12 / DH10B) GN=astC PE=3 SV=1
[ASTC_EC0HS](#) Mass: 43652 Score: 99 Matches: 3(2) Sequences: 3(2)
 Succinylornithine transaminase OS=Escherichia coli O9:H4 (strain HS) GN=astC PE=3 SV=1
[ASTC_EC0LC](#) Mass: 43638 Score: 99 Matches: 3(2) Sequences: 3(2)

Succinylornithine transaminase OS=Escherichia coli (strain ATCC 8739 / DSM 1576 / Crooks) GN=astC PE=3 SV=1
[ASTC_ECOLI](#) Mass: 43638 Score: 99 Matches: 3(2) Sequences: 3(2)
 Succinylornithine transaminase OS=Escherichia coli (strain K12) GN=astC PE=1 SV=1
[ASTC_ECOSE](#) Mass: 43638 Score: 99 Matches: 3(2) Sequences: 3(2)
 Succinylornithine transaminase OS=Escherichia coli (strain SE11) GN=astC PE=3 SV=1
[ASTC_ECO8A](#) Mass: 43638 Score: 99 Matches: 3(2) Sequences: 3(2)
 Succinylornithine transaminase OS=Escherichia coli O8 (strain IAI1) GN=astC PE=3 SV=1
[ASTC_ECO24](#) Mass: 43638 Score: 99 Matches: 3(2) Sequences: 3(2)
 Succinylornithine transaminase OS=Escherichia coli O139:H28 (strain E24377A / ETEC) GN=astC PE=3 SV=1
[ASTC_ECO55](#) Mass: 43706 Score: 99 Matches: 3(2) Sequences: 3(2)
 Succinylornithine transaminase OS=Escherichia coli (strain 55989 / EAEC) GN=astC PE=3 SV=1

13. [FTSZ_ECOLI](#) Mass: 40299 Score: 94 Matches: 2(2) Sequences: 2(2) emPAI: 0.19
 Cell division protein FtsZ OS=Escherichia coli (strain K12) GN=ftsZ PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 400	549.2889	1096.5632	1096.5625	0.67	0	58	6.1e-005	1	U	K.GLGAGANPEVGR.N
<input checked="" type="checkbox"/> 912	720.8556	1439.6966	1439.6966	0.03	0	65	1.5e-005	1	U	R.MAFAEQGITELSK.H + Oxidation (M)

Proteins matching the same set of peptides:

[FTSZ_SHIFL](#) Mass: 40063 Score: 94 Matches: 2(2) Sequences: 2(2)
 Cell division protein FtsZ OS=Shigella flexneri GN=ftsZ PE=3 SV=2
[FTSZ_EC0L6](#) Mass: 40299 Score: 94 Matches: 2(2) Sequences: 2(2)
 Cell division protein FtsZ OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) GN=ftsZ PE=3 SV=1
[FTSZ_ECO57](#) Mass: 40299 Score: 94 Matches: 2(2) Sequences: 2(2)
 Cell division protein FtsZ OS=Escherichia coli O157:H7 GN=ftsZ PE=3 SV=1

14. [YCBX_ECOLI](#) Mass: 40619 Score: 93 Matches: 3(2) Sequences: 3(2) emPAI: 0.18
 Uncharacterized protein YcbX OS=Escherichia coli (strain K12) GN=ycbX PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 935	485.2928	1452.8566	1452.8552	0.97	1	29	0.016	1	U	R.VQLLEGEVTPCLK.S
<input checked="" type="checkbox"/> 1488	917.4399	1832.8652	1832.8653	-0.03	0	77	7.9e-007	1	U	R.TAQDNGDVDFGQNLIR.N
<input checked="" type="checkbox"/> 1565	977.0133	1952.0120	1952.0075	2.32	0	24	0.2	1	U	R.GNNQQVLLLEQLENQIR.I

15. [HFLC_ECOLI](#) Mass: 37626 Score: 88 Matches: 3(2) Sequences: 3(2) emPAI: 0.20
 Modulator of FtsH protease HflC OS=Escherichia coli (strain K12) GN=hflC PE=1 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide	
<input checked="" type="checkbox"/> 13	365.7265	729.4384	729.4385	-0.04	0	24		1	1	U	R.LTLEVR.D
<input checked="" type="checkbox"/> 308	513.2487	1024.4828	1024.4825	0.31	0	50	0.00047	1	U	R.ATADYEVTR.T	
<input checked="" type="checkbox"/> 1537	949.5021	1896.9896	1896.9833	3.36	0	63	2.3e-005	1	U	R.YYLATGGDISQAEVLLK.R	

Proteins matching the same set of peptides:

[HFLC_SHIFL](#) Mass: 37626 Score: 88 Matches: 3(2) Sequences: 3(2)
 Modulator of FtsH protease HflC OS=Shigella flexneri GN=hflC PE=3 SV=1

[HFLC_ECOL6](#) Mass: 37626 Score: 88 Matches: 3(2) Sequences: 3(2)
 Modulator of FtsH protease HflC OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) GN=hflC PE=3 SV=1

[HFLC_ECO57](#) Mass: 37626 Score: 88 Matches: 3(2) Sequences: 3(2)
 Modulator of FtsH protease HflC OS=Escherichia coli O157:H7 GN=hflC PE=3 SV=1

16. [TRYP_PIG](#) Mass: 24394 Score: 84 Matches: 3(3) Sequences: 3(3) emPAI: 0.52

Trypsin OS=Sus scrofa PE=1 SV=1

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 98	421.7586	841.5026	841.5022	0.59	0	55	0.00033	1	U	R.VATVSLPR.S
<input checked="" type="checkbox"/> 327	523.2856	1044.5566	1044.5564	0.28	0	44	0.0042	1	U	K.LSSPATLNSR.V
<input checked="" type="checkbox"/> 1760	737.7060	2210.0962	2210.0967	-0.25	0	48	0.0009	1	U	R.LGEHNIDVLEGNEQFINAAK.I

17. [K1C10_CANFA](#) Mass: 57676 Score: 77 Matches: 2(2) Sequences: 2(2) emPAI: 0.13

Keratin, type I cytoskeletal 10 OS=Canis familiaris GN=KRT10 PE=2 SV=1

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 62	404.2029	806.3912	806.3923	-1.25	0	37	0.016	1	U	R.LAADDFR.L
<input checked="" type="checkbox"/> 845	691.3277	1380.6408	1380.6408	0.01	0	71	4.6e-006	1	U	R.ALEESNYELEGK.I

Proteins matching the same set of peptides:

[K1C10_HUMAN](#) Mass: 58792 Score: 77 Matches: 2(2) Sequences: 2(2)
 Keratin, type I cytoskeletal 10 OS=Homo sapiens GN=KRT10 PE=1 SV=6

[K1C10_MOUSE](#) Mass: 57735 Score: 77 Matches: 2(2) Sequences: 2(2)
 Keratin, type I cytoskeletal 10 OS=Mus musculus GN=Krt10 PE=1 SV=3

18. [SUCC_ECOBW](#) Mass: 41367 Score: 69 Matches: 3(3) Sequences: 3(3) emPAI: 0.28

Succinyl-CoA ligase [ADP-forming] subunit beta OS=Escherichia coli (strain K12 / MC4100 / BW2952) GN=sucC PE=3 SV=1

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 452	558.2885	1114.5624	1114.5618	0.57	0	47	0.0016	1	U	R.LEGNNALGAK.K
<input checked="" type="checkbox"/> 736	438.5981	1312.7725	1312.7714	0.81	1	35	0.011	1	U	K.KLADSGLNIIAAK.G
<input checked="" type="checkbox"/> 1087	778.9180	1555.8214	1555.8206	0.55	0	37	0.0086	1	U	K.GLTDAQQVVAAVEGK.-

Proteins matching the same set of peptides:

[SUCC_ECODH](#) Mass: 41367 Score: 69 Matches: 3(3) Sequences: 3(3)

Succinyl-CoA ligase [ADP-forming] subunit beta OS=Escherichia coli (strain K12 / DH10B) GN=sucC PE=3 SV=1
[SUCC_ECOHS](#) **Mass:** 41367 **Score:** 69 **Matches:** 3(3) **Sequences:** 3(3)

Succinyl-CoA ligase [ADP-forming] subunit beta OS=Escherichia coli O9:H4 (strain HS) GN=sucC PE=3 SV=1
[SUCC_ECOLC](#) **Mass:** 41367 **Score:** 69 **Matches:** 3(3) **Sequences:** 3(3)

Succinyl-CoA ligase [ADP-forming] subunit beta OS=Escherichia coli (strain ATCC 8739 / DSM 1576 / Crooks) GN=sucC PE=3 SV=1
[SUCC_ECOLI](#) **Mass:** 41367 **Score:** 69 **Matches:** 3(3) **Sequences:** 3(3)

Succinyl-CoA ligase [ADP-forming] subunit beta OS=Escherichia coli (strain K12) GN=sucC PE=1 SV=1
[SUCC_ECOLU](#) **Mass:** 41367 **Score:** 69 **Matches:** 3(3) **Sequences:** 3(3)

Succinyl-CoA ligase [ADP-forming] subunit beta OS=Escherichia coli O17:K52:H18 (strain UMN026 / ExPEC) GN=sucC PE=3 SV=1
[SUCC_ECOSE](#) **Mass:** 41367 **Score:** 69 **Matches:** 3(3) **Sequences:** 3(3)

Succinyl-CoA ligase [ADP-forming] subunit beta OS=Escherichia coli (strain SE11) GN=sucC PE=3 SV=1
[SUCC_ECOSM](#) **Mass:** 41367 **Score:** 69 **Matches:** 3(3) **Sequences:** 3(3)

Succinyl-CoA ligase [ADP-forming] subunit beta OS=Escherichia coli (strain SMS-3-5 / SECEC) GN=sucC PE=3 SV=1
[SUCC_SHIBS](#) **Mass:** 41402 **Score:** 69 **Matches:** 3(3) **Sequences:** 3(3)

Succinyl-CoA ligase [ADP-forming] subunit beta OS=Shigella boydii serotype 4 (strain Sb227) GN=sucC PE=3 SV=1
[SUCC_SHIDS](#) **Mass:** 41325 **Score:** 69 **Matches:** 3(3) **Sequences:** 3(3)

Succinyl-CoA ligase [ADP-forming] subunit beta OS=Shigella dysenteriae serotype 1 (strain Sd197) GN=sucC PE=3 SV=1
[SUCC_SHIFL](#) **Mass:** 41367 **Score:** 69 **Matches:** 3(3) **Sequences:** 3(3)

Succinyl-CoA ligase [ADP-forming] subunit beta OS=Shigella flexneri GN=sucC PE=3 SV=1
[SUCC_SHISS](#) **Mass:** 41367 **Score:** 69 **Matches:** 3(3) **Sequences:** 3(3)

Succinyl-CoA ligase [ADP-forming] subunit beta OS=Shigella sonnei (strain Ss046) GN=sucC PE=3 SV=1
[SUCC_SHIB3](#) **Mass:** 41402 **Score:** 69 **Matches:** 3(3) **Sequences:** 3(3)

Succinyl-CoA ligase [ADP-forming] subunit beta OS=Shigella boydii serotype 18 (strain CDC 3083-94 / BS512) GN=sucC PE=3 SV=1
[SUCC_ECO5E](#) **Mass:** 41367 **Score:** 69 **Matches:** 3(3) **Sequences:** 3(3)

Succinyl-CoA ligase [ADP-forming] subunit beta OS=Escherichia coli O157:H7 (strain EC4115 / EHEC) GN=sucC PE=3 SV=1
[SUCC_ECOL6](#) **Mass:** 41367 **Score:** 69 **Matches:** 3(3) **Sequences:** 3(3)

Succinyl-CoA ligase [ADP-forming] subunit beta OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) GN=sucC PE=3 SV=1
[SUCC_ECO7I](#) **Mass:** 41367 **Score:** 69 **Matches:** 3(3) **Sequences:** 3(3)

Succinyl-CoA ligase [ADP-forming] subunit beta OS=Escherichia coli O7:K1 (strain IAI39 / ExPEC) GN=sucC PE=3 SV=1
[SUCC_SHIF8](#) **Mass:** 41309 **Score:** 69 **Matches:** 3(3) **Sequences:** 3(3)

Succinyl-CoA ligase [ADP-forming] subunit beta OS=Shigella flexneri serotype 5b (strain 8401) GN=sucC PE=3 SV=1
[SUCC_ECO24](#) **Mass:** 41367 **Score:** 69 **Matches:** 3(3) **Sequences:** 3(3)

Succinyl-CoA ligase [ADP-forming] subunit beta OS=Escherichia coli O139:H28 (strain E24377A / ETEC) GN=sucC PE=3 SV=1
[SUCC_ECO55](#) **Mass:** 41367 **Score:** 69 **Matches:** 3(3) **Sequences:** 3(3)

Succinyl-CoA ligase [ADP-forming] subunit beta OS=Escherichia coli (strain 55989 / EAEC) GN=sucC PE=3 SV=1
[SUCC_ECO57](#) **Mass:** 41367 **Score:** 69 **Matches:** 3(3) **Sequences:** 3(3)

Succinyl-CoA ligase [ADP-forming] subunit beta OS=Escherichia coli O157:H7 GN=sucC PE=3 SV=1

19. [RL28_ECO24](#) **Mass:** 9001 **Score:** 68 **Matches:** 1(1) **Sequences:** 1(1) **emPAI:** 0.43
 50S ribosomal protein L28 OS=Escherichia coli O139:H28 (strain E24377A / ETEC) GN=rpMB PE=3 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 383	543.8116	1085.6086	1085.6081	0.54	0	68	1.5e-005	1	U	K.GIDTVLAELR.A

Proteins matching the same set of peptides:

[RL28_ECO27](#) Mass: 9001 Score: 68 Matches: 1(1) Sequences: 1(1)
50S ribosomal protein L28 OS=Escherichia coli O127:H6 (strain E2348/69 / EPEC) GN=rpmb PE=3 SV=1

[RL28_ECO45](#) Mass: 9001 Score: 68 Matches: 1(1) Sequences: 1(1)
50S ribosomal protein L28 OS=Escherichia coli O45:K1 (strain S88 / ExPEC) GN=rpmb PE=3 SV=1

[RL28_ECO55](#) Mass: 9001 Score: 68 Matches: 1(1) Sequences: 1(1)
50S ribosomal protein L28 OS=Escherichia coli (strain 55989 / EAEC) GN=rpmb PE=3 SV=1

[RL28_ECO57](#) Mass: 9001 Score: 68 Matches: 1(1) Sequences: 1(1)
50S ribosomal protein L28 OS=Escherichia coli O157:H7 GN=rpmb PE=3 SV=2

[RL28_ECO5E](#) Mass: 9001 Score: 68 Matches: 1(1) Sequences: 1(1)
50S ribosomal protein L28 OS=Escherichia coli O157:H7 (strain EC4115 / EHEC) GN=rpmb PE=3 SV=1

[RL28_ECO7I](#) Mass: 9001 Score: 68 Matches: 1(1) Sequences: 1(1)
50S ribosomal protein L28 OS=Escherichia coli O7:K1 (strain IAI39 / ExPEC) GN=rpmb PE=3 SV=1

[RL28_ECO81](#) Mass: 9001 Score: 68 Matches: 1(1) Sequences: 1(1)
50S ribosomal protein L28 OS=Escherichia coli O81 (strain ED1a) GN=rpmb PE=3 SV=1

[RL28_ECO8A](#) Mass: 9001 Score: 68 Matches: 1(1) Sequences: 1(1)
50S ribosomal protein L28 OS=Escherichia coli O8 (strain IAI1) GN=rpmb PE=3 SV=1

[RL28_ECOBW](#) Mass: 9001 Score: 68 Matches: 1(1) Sequences: 1(1)
50S ribosomal protein L28 OS=Escherichia coli (strain K12 / MC4100 / BW2952) GN=rpmb PE=3 SV=1

[RL28_ECODH](#) Mass: 9001 Score: 68 Matches: 1(1) Sequences: 1(1)
50S ribosomal protein L28 OS=Escherichia coli (strain K12 / DH10B) GN=rpmb PE=3 SV=1

[RL28_ECOHS](#) Mass: 9001 Score: 68 Matches: 1(1) Sequences: 1(1)
50S ribosomal protein L28 OS=Escherichia coli O9:H4 (strain HS) GN=rpmb PE=3 SV=1

[RL28_ECOL5](#) Mass: 9001 Score: 68 Matches: 1(1) Sequences: 1(1)
50S ribosomal protein L28 OS=Escherichia coli O6:K15:H31 (strain 536 / UPEC) GN=rpmb PE=3 SV=1

[RL28_ECOL6](#) Mass: 9001 Score: 68 Matches: 1(1) Sequences: 1(1)
50S ribosomal protein L28 OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) GN=rpmb PE=3 SV=2

[RL28_ECOLC](#) Mass: 9001 Score: 68 Matches: 1(1) Sequences: 1(1)
50S ribosomal protein L28 OS=Escherichia coli (strain ATCC 8739 / DSM 1576 / Crooks) GN=rpmb PE=3 SV=1

[RL28_ECOLI](#) Mass: 9001 Score: 68 Matches: 1(1) Sequences: 1(1)
50S ribosomal protein L28 OS=Escherichia coli (strain K12) GN=rpmb PE=1 SV=2

[RL28_ECOLU](#) Mass: 9001 Score: 68 Matches: 1(1) Sequences: 1(1)
50S ribosomal protein L28 OS=Escherichia coli O17:K52:H18 (strain UMN026 / ExPEC) GN=rpmb PE=3 SV=1

[RL28_ECOSE](#) Mass: 9001 Score: 68 Matches: 1(1) Sequences: 1(1)
50S ribosomal protein L28 OS=Escherichia coli (strain SE11) GN=rpmb PE=3 SV=1

[RL28_ECOSM](#) Mass: 9001 Score: 68 Matches: 1(1) Sequences: 1(1)
50S ribosomal protein L28 OS=Escherichia coli (strain SMS-3-5 / SECEC) GN=rpmb PE=3 SV=1

[RL28_ECOUT](#) Mass: 9001 Score: 68 Matches: 1(1) Sequences: 1(1)
50S ribosomal protein L28 OS=Escherichia coli (strain UTI89 / UPEC) GN=rpmb PE=3 SV=1

[RL28_ESCF3](#) Mass: 9001 Score: 68 Matches: 1(1) Sequences: 1(1)
50S ribosomal protein L28 OS=Escherichia fergusonii (strain ATCC 35469 / DSM 13698 / CDC 0568-73) GN=rpmb PE=3 SV=1

[RL28_KLEP7](#) Mass: 9001 Score: 68 Matches: 1(1) Sequences: 1(1)
50S ribosomal protein L28 OS=Klebsiella pneumoniae subsp. pneumoniae (strain ATCC 700721 / MGH 78578) GN=rpmb PE=3 SV=1

[RL28_SACD2](#) Mass: 9025 Score: 68 Matches: 1(1) Sequences: 1(1)
50S ribosomal protein L28 OS=Saccharophagus degradans (strain 2-40 / ATCC 43961 / DSM 17024) GN=rpmb PE=3 SV=1

[RL28_SHIB3](#) Mass: 9001 Score: 68 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L28 OS=Shigella boydii serotype 18 (strain CDC 3083-94 / BS512) GN=rpmB PE=3 SV=1
[RL28_SHIBS](#) Mass: 9031 Score: 68 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L28 OS=Shigella boydii serotype 4 (strain Sb227) GN=rpmB PE=3 SV=1
[RL28_SHIDS](#) Mass: 9001 Score: 68 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L28 OS=Shigella dysenteriae serotype 1 (strain Sd197) GN=rpmB PE=3 SV=1
[RL28_SHIFL](#) Mass: 9001 Score: 68 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L28 OS=Shigella flexneri GN=rpmB PE=3 SV=2
[RL28_SHISS](#) Mass: 9001 Score: 68 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L28 OS=Shigella sonnei (strain Ss046) GN=rpmB PE=3 SV=1

20. [G3P1_ECO57](#) Mass: 35510 Score: 68 Matches: 3(2) Sequences: 3(2) emPAI: 0.21

Glyceraldehyde-3-phosphate dehydrogenase A OS=Escherichia coli O157:H7 GN=gapA PE=3 SV=2

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 64	406.2099	810.4052	810.4058	-0.69	0	26	0.17	1	U	K.LTGMAFR.V + Oxidation (M)
<input checked="" type="checkbox"/> 414	554.8414	1107.6682	1107.6652	2.77	0	37	0.0019	1	U	K.VLDLIAHISK.-
<input checked="" type="checkbox"/> 1289	838.3849	1674.7552	1674.7525	1.61	0	49	0.00041	1	U	K.LVSWYDNETGYSNK.V

Proteins matching the same set of peptides:

[G3P1_ECOL6](#) Mass: 35510 Score: 68 Matches: 3(2) Sequences: 3(2)
 Glyceraldehyde-3-phosphate dehydrogenase A OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) GN=gapA PE=3 SV=2
[G3P1_ECOLI](#) Mass: 35510 Score: 68 Matches: 3(2) Sequences: 3(2)
 Glyceraldehyde-3-phosphate dehydrogenase A OS=Escherichia coli (strain K12) GN=gapA PE=1 SV=2
[G3P1_ESCF3](#) Mass: 35518 Score: 68 Matches: 3(2) Sequences: 3(2)
 Glyceraldehyde-3-phosphate dehydrogenase A OS=Escherichia fergusonii (strain ATCC 35469 / DSM 13698 / CDC 0568-73) GN=gapA PE=3 SV=1
[G3P1_SALTI](#) Mass: 35564 Score: 68 Matches: 3(2) Sequences: 3(2)
 Glyceraldehyde-3-phosphate dehydrogenase OS=Salmonella typhi GN=gapA PE=3 SV=2
[G3P1_SALTY](#) Mass: 35564 Score: 68 Matches: 3(2) Sequences: 3(2)
 Glyceraldehyde-3-phosphate dehydrogenase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=gapA PE=3 SV=2
[G3P1_SHIFL](#) Mass: 35510 Score: 68 Matches: 3(2) Sequences: 3(2)
 Glyceraldehyde-3-phosphate dehydrogenase A OS=Shigella flexneri GN=gapA PE=3 SV=2

21. [MALK_ECOLI](#) Mass: 40965 Score: 65 Matches: 2(2) Sequences: 2(2) emPAI: 0.18

Maltose/maltodextrin import ATP-binding protein MalK OS=Escherichia coli (strain K12) GN=malk PE=1 SV=1

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 307	511.7867	1021.5588	1021.5597	-0.81	0	52	0.00048	1	U	R.FVAGFIGSPK.M
<input checked="" type="checkbox"/> 384	544.3085	1086.6024	1086.6033	-0.80	0	43	0.0041	1	U	M.ASVQLQNVTK.A

Proteins matching the same set of peptides:

[MALK_ECOU](#) Mass: 40965 Score: 65 Matches: 2(2) Sequences: 2(2)
 Maltose/maltodextrin import ATP-binding protein MalK OS=Escherichia coli (strain UTI89 / UPEC) GN=malk PE=1 SV=2
[MALK_SHIFL](#) Mass: 40991 Score: 65 Matches: 2(2) Sequences: 2(2)

Maltose/maltodextrin import ATP-binding protein MalK OS=Shigella flexneri GN=malK PE=3 SV=1
[MALK_SHISS](#) Mass: 40965 Score: 65 Matches: 2(2) Sequences: 2(2)
 Maltose/maltodextrin import ATP-binding protein MalK OS=Shigella sonnei (strain Ss046) GN=malK PE=3 SV=1
[MALK_EC05](#) Mass: 40937 Score: 65 Matches: 2(2) Sequences: 2(2)
 Maltose/maltodextrin import ATP-binding protein MalK OS=Escherichia coli O6:K15:H31 (strain 536 / UPEC) GN=malK PE=3 SV=1
[MALK_EC06](#) Mass: 40981 Score: 65 Matches: 2(2) Sequences: 2(2)
 Maltose/maltodextrin import ATP-binding protein MalK OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) GN=malK PE=3 SV=2
[MALK_SHIF8](#) Mass: 41019 Score: 65 Matches: 2(2) Sequences: 2(2)
 Maltose/maltodextrin import ATP-binding protein MalK OS=Shigella flexneri serotype 5b (strain 8401) GN=malK PE=3 SV=1
[MALK_EC057](#) Mass: 40965 Score: 65 Matches: 2(2) Sequences: 2(2)
 Maltose/maltodextrin import ATP-binding protein MalK OS=Escherichia coli O157:H7 GN=malK PE=3 SV=1

22. [LCRV_YERPE](#) Mass: 37217 Score: 65 Matches: 3(1) Sequences: 3(1) emPAI: 0.10

Virulence-associated V antigen OS=Yersinia pestis GN=lcrV PE=1 SV=1

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 484	567.7983	1133.5820	1133.5829	-0.74	0	65	2.8e-005	1	U	R.FNSAIEALNR.F
<input checked="" type="checkbox"/> 1505	620.9635	1859.8687	1859.8690	-0.15	0	22	0.23	1	U	R.AYEQNPOHFIEDLEK.V
<input checked="" type="checkbox"/> 1571	655.0024	1961.9854	1961.9847	0.36	1	24	0.25	1	U	R.VKEFLESSPNTQWELR.A

Proteins matching the same set of peptides:

[LCRV_YERPP](#) Mass: 37101 Score: 65 Matches: 3(1) Sequences: 3(1)

Virulence-associated V antigen OS=Yersinia pestis (strain Pestoides F) GN=lcrV PE=3 SV=1

[LCRV_YERPS](#) Mass: 37313 Score: 65 Matches: 3(1) Sequences: 3(1)

Virulence-associated V antigen OS=Yersinia pseudotuberculosis serotype I (strain IP32953) GN=lcrV PE=4 SV=1

23. [CDAR_EC01](#) Mass: 43660 Score: 60 Matches: 2(2) Sequences: 2(2) emPAI: 0.17

Carbohydrate diacid regulator OS=Escherichia coli (strain K12) GN=cdar PE=1 SV=2

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 1056	769.9017	1537.7888	1537.7889	-0.03	0	33	0.021	1	U	R.VSLGNYFTGPGSIAR.S
<input checked="" type="checkbox"/> 1276	832.9117	1663.8088	1663.8053	2.12	0	44	0.002	1	U	R.ISELTGLDLGNFDDR.L

24. [K2C1_HUMAN](#) Mass: 65999 Score: 60 Matches: 1(1) Sequences: 1(1) emPAI: 0.05

Keratin, type II cytoskeletal 1 OS=Homo sapiens GN=KRT1 PE=1 SV=6

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 715	651.8612	1301.7078	1301.7078	0.02	0	60	7.9e-005	1	U	R.SLDLDSIIAEVK.A

Proteins matching the same set of peptides:

[K2C1_PANTR](#) Mass: 65450 Score: 60 Matches: 1(1) Sequences: 1(1)

Keratin, type II cytoskeletal 1 OS=Pan troglodytes GN=KRT1 PE=2 SV=1
[K2C5_BOVIN](#) Mass: 62898 Score: 60 Matches: 1(1) Sequences: 1(1)
 Keratin, type II cytoskeletal 5 OS=Bos taurus GN=KRT5 PE=1 SV=1
[K2C5_MOUSE](#) Mass: 61729 Score: 60 Matches: 1(1) Sequences: 1(1)
 Keratin, type II cytoskeletal 5 OS=Mus musculus GN=Krt5 PE=1 SV=1
[K2C5_RAT](#) Mass: 61788 Score: 60 Matches: 1(1) Sequences: 1(1)
 Keratin, type II cytoskeletal 5 OS=Rattus norvegicus GN=Krt5 PE=1 SV=1
[K2C6A_MOUSE](#) Mass: 59299 Score: 60 Matches: 1(1) Sequences: 1(1)
 Keratin, type II cytoskeletal 6A OS=Mus musculus GN=Krt6a PE=2 SV=3
[K2C6A_RAT](#) Mass: 59213 Score: 60 Matches: 1(1) Sequences: 1(1)
 Keratin, type II cytoskeletal 6A OS=Rattus norvegicus GN=Krt6a PE=1 SV=1
[K2C6B_MOUSE](#) Mass: 60285 Score: 60 Matches: 1(1) Sequences: 1(1)
 Keratin, type II cytoskeletal 6B OS=Mus musculus GN=Krt6b PE=2 SV=3
[K2C75_BOVIN](#) Mass: 59000 Score: 60 Matches: 1(1) Sequences: 1(1)
 Keratin, type II cytoskeletal 75 OS=Bos taurus GN=KRT75 PE=2 SV=1
[K2C75_MOUSE](#) Mass: 59704 Score: 60 Matches: 1(1) Sequences: 1(1)
 Keratin, type II cytoskeletal 75 OS=Mus musculus GN=Krt75 PE=1 SV=1
[K2C75_RAT](#) Mass: 58991 Score: 60 Matches: 1(1) Sequences: 1(1)
 Keratin, type II cytoskeletal 75 OS=Rattus norvegicus GN=Krt75 PE=3 SV=2
[K2C7_BOVIN](#) Mass: 51546 Score: 60 Matches: 1(1) Sequences: 1(1)
 Keratin, type II cytoskeletal 7 OS=Bos taurus GN=KRT7 PE=2 SV=1

25. [RL9_CITK8](#) Mass: 15760 Score: 59 Matches: 1(1) Sequences: 1(1) emPAI: 0.24
 50S ribosomal protein L9 OS=Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696) GN=rplI PE=3 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 903	715.3809	1428.7472	1428.7460	0.86	0	59	9e-005	1	U	R.DIADAVTAAGVEVAK.S

Proteins matching the same set of peptides:

[RL9_ECO24](#) Mass: 15759 Score: 59 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L9 OS=Escherichia coli O139:H28 (strain E24377A / ETEC) GN=rplI PE=3 SV=1
[RL9_ECO27](#) Mass: 15759 Score: 59 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L9 OS=Escherichia coli O127:H6 (strain E2348/69 / EPEC) GN=rplI PE=3 SV=1
[RL9_ECO45](#) Mass: 15759 Score: 59 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L9 OS=Escherichia coli O45:K1 (strain S88 / ExPEC) GN=rplI PE=3 SV=1
[RL9_ECO55](#) Mass: 15759 Score: 59 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L9 OS=Escherichia coli (strain 55989 / EAEC) GN=rplI PE=3 SV=1
[RL9_ECO57](#) Mass: 15759 Score: 59 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L9 OS=Escherichia coli O157:H7 GN=rplI PE=3 SV=1
[RL9_ECO5E](#) Mass: 15759 Score: 59 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L9 OS=Escherichia coli O157:H7 (strain EC4115 / EHEC) GN=rplI PE=3 SV=1
[RL9_ECO7I](#) Mass: 15759 Score: 59 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L9 OS=Escherichia coli O7:K1 (strain IAI39 / ExPEC) GN=rplI PE=3 SV=1
[RL9_ECO81](#) Mass: 15759 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Escherichia coli O81 (strain ED1a) GN=rplI PE=3 SV=1
[RL9_EC08A](#) Mass: 15759 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Escherichia coli O8 (strain IAI1) GN=rplI PE=3 SV=1
[RL9_ECOBW](#) Mass: 15759 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Escherichia coli (strain K12 / MC4100 / BW2952) GN=rplI PE=3 SV=1
[RL9_EC0DH](#) Mass: 15759 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Escherichia coli (strain K12 / DH10B) GN=rplI PE=3 SV=1
[RL9_ECOHS](#) Mass: 15759 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Escherichia coli O9:H4 (strain HS) GN=rplI PE=3 SV=1
[RL9_ECOK1](#) Mass: 15759 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Escherichia coli O1:K1 / APEC GN=rplI PE=3 SV=1
[RL9_EC0L5](#) Mass: 15759 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Escherichia coli O6:K15:H31 (strain 536 / UPEC) GN=rplI PE=3 SV=1
[RL9_EC0L6](#) Mass: 15759 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) GN=rplI PE=3 SV=1
[RL9_EC0LC](#) Mass: 15759 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Escherichia coli (strain ATCC 8739 / DSM 1576 / Crooks) GN=rplI PE=3 SV=1
[RL9_EC0LI](#) Mass: 15759 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Escherichia coli (strain K12) GN=rplI PE=1 SV=1
[RL9_EC0LU](#) Mass: 15759 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Escherichia coli O17:K52:H18 (strain UMN026 / ExPEC) GN=rplI PE=3 SV=1
[RL9_EC0SE](#) Mass: 15759 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Escherichia coli (strain SE11) GN=rplI PE=3 SV=1
[RL9_EC0SM](#) Mass: 15759 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Escherichia coli (strain SMS-3-5 / SECEC) GN=rplI PE=3 SV=1
[RL9_EC0UT](#) Mass: 15759 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Escherichia coli (strain UTI89 / UPEC) GN=rplI PE=3 SV=1
[RL9_ERWT9](#) Mass: 15829 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Erwinia tasmaniensis (strain DSM 17950 / Et1/99) GN=rplI PE=3 SV=1
[RL9_ESCF3](#) Mass: 15759 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Escherichia fergusonii (strain ATCC 35469 / DSM 13698 / CDC 0568-73) GN=rplI PE=3 SV=1
[RL9_SERP5](#) Mass: 15890 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Serratia proteamaculans (strain 568) GN=rplI PE=3 SV=1
[RL9_SHIB3](#) Mass: 15759 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Shigella boydii serotype 18 (strain CDC 3083-94 / BS512) GN=rplI PE=3 SV=1
[RL9_SHIB5](#) Mass: 15759 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Shigella boydii serotype 4 (strain Sb227) GN=rplI PE=3 SV=1
[RL9_SHIDS](#) Mass: 15760 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Shigella dysenteriae serotype 1 (strain Sd197) GN=rplI PE=3 SV=1
[RL9_SHIF8](#) Mass: 15759 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Shigella flexneri serotype 5b (strain 8401) GN=rplI PE=3 SV=1
[RL9_SHIFL](#) Mass: 15759 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Shigella flexneri GN=rplI PE=3 SV=1
[RL9_SHISS](#) Mass: 15759 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Shigella sonnei (strain Ss046) GN=rplI PE=3 SV=1
[RL9_YERE8](#) Mass: 15808 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Yersinia enterocolitica serotype O:8 / biotype 1B (strain NCTC 13174 / 8081) GN=rplI PE=3 SV=1
[RL9_YERP3](#) Mass: 15852 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Yersinia pseudotuberculosis serotype O:1b (strain IP 31758) GN=rplI PE=3 SV=1
[RL9_YERPA](#) Mass: 15852 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Yersinia pestis bv. Antiqua (strain Antiqua) GN=rplI PE=3 SV=1
[RL9_YERPB](#) Mass: 15852 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Yersinia pseudotuberculosis serotype 1B (strain PB1/+) GN=rplI PE=3 SV=1
[RL9_YERPE](#) Mass: 15852 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Yersinia pestis GN=rplI PE=3 SV=1
[RL9_YERPG](#) Mass: 15852 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Yersinia pestis bv. Antiqua (strain Angola) GN=rplI PE=3 SV=1
[RL9_YERPQ](#) Mass: 15852 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Yersinia pestis bv. Antiqua (strain Nepal516) GN=rplI PE=3 SV=1
[RL9_YERPP](#) Mass: 15852 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Yersinia pestis (strain Pestoides F) GN=rplI PE=3 SV=1
[RL9_YERPS](#) Mass: 15852 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Yersinia pseudotuberculosis serotype I (strain IP32953) GN=rplI PE=3 SV=1
[RL9_YERPZ](#) Mass: 15852 Score: 59 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L9 OS=Yersinia pseudotuberculosis serotype O:3 (strain YPIII) GN=rplI PE=3 SV=1

26. [RIBD_ECOLI](#) Mass: 40313 Score: 55 Matches: 2(2) Sequences: 2(2) emPAI: 0.19
 Riboflavin biosynthesis protein RibD OS=Escherichia coli (strain K12) GN=ribD PE=1 SV=1

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 47	394.7167	787.4188	787.4188	0.05	0	45	0.0058	1	U	K.LGASLDGR.T
<input checked="" type="checkbox"/> 1133	792.8950	1583.7754	1583.7726	1.80	0	35	0.016	1	U	R.VVASM Q DPNPQVAGR.G + Oxidation (M)

27. [SLYD_ECOLI](#) Mass: 20840 Score: 55 Matches: 1(1) Sequences: 1(1) emPAI: 0.18
 FKBP-type peptidyl-prolyl cis-trans isomerase SlyD OS=Escherichia coli (strain K12) GN=slyD PE=1 SV=1

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 333	523.8033	1045.5920	1045.5920	0.02	0	55	0.00027	1	U	K.FNVEVVAIR.E

Proteins matching the same set of peptides:

[SLYD_SHIFL](#) Mass: 20840 Score: 55 Matches: 1(1) Sequences: 1(1)

FKBP-type peptidyl-prolyl cis-trans isomerase SlyD OS=Shigella flexneri GN=slyD PE=3 SV=1

[SLYD_ECOL6](#) Mass: 20840 Score: 55 Matches: 1(1) Sequences: 1(1)

FKBP-type peptidyl-prolyl cis-trans isomerase SlyD OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) GN=slyD PE=3 SV=1

[SLYD_ECO57](#) Mass: 20840 Score: 55 Matches: 1(1) Sequences: 1(1)

FKBP-type peptidyl-prolyl cis-trans isomerase SlyD OS=Escherichia coli O157:H7 GN=slyD PE=3 SV=1

28. [ARGE_ECOBW](#) Mass: 42320 Score: 54 Matches: 2(2) Sequences: 2(2) emPAI: 0.18
 Acetylornithine deacetylase OS=Escherichia coli (strain K12 / MC4100 / BW2952) GN=argE PE=3 SV=1

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 511	574.3296	1146.6446	1146.6437	0.82	0	26	0.06	1	U	K.LPPFIEIYR.A
<input checked="" type="checkbox"/> 1947	935.8134	2804.4184	2804.4167	0.60	0	46	0.0011	1	U	R.YFAETTLALRPDCAIIGEPTSLQPVR.A + Carbamidomethyl (C)

Proteins matching the same set of peptides:

- [ARGE_ECODH](#) Mass: 42320 Score: 54 Matches: 2(2) Sequences: 2(2)
Acetylnithine deacetylase OS=Escherichia coli (strain K12 / DH10B) GN=argE PE=3 SV=1
- [ARGE_ECOHS](#) Mass: 42333 Score: 54 Matches: 2(2) Sequences: 2(2)
Acetylnithine deacetylase OS=Escherichia coli O9:H4 (strain HS) GN=argE PE=3 SV=1
- [ARGE_ECOLC](#) Mass: 42320 Score: 54 Matches: 2(2) Sequences: 2(2)
Acetylnithine deacetylase OS=Escherichia coli (strain ATCC 8739 / DSM 1576 / Crooks) GN=argE PE=3 SV=1
- [ARGE_ECOLI](#) Mass: 42320 Score: 54 Matches: 2(2) Sequences: 2(2)
Acetylnithine deacetylase OS=Escherichia coli (strain K12) GN=argE PE=1 SV=2
- [ARGE_ECOLU](#) Mass: 42296 Score: 54 Matches: 2(2) Sequences: 2(2)
Acetylnithine deacetylase OS=Escherichia coli O17:K52:H18 (strain UMN026 / ExPEC) GN=argE PE=3 SV=1
- [ARGE_ECOSE](#) Mass: 42310 Score: 54 Matches: 2(2) Sequences: 2(2)
Acetylnithine deacetylase OS=Escherichia coli (strain SE11) GN=argE PE=3 SV=1
- [ARGE_ECOSM](#) Mass: 42265 Score: 54 Matches: 2(2) Sequences: 2(2)
Acetylnithine deacetylase OS=Escherichia coli (strain SMS-3-5 / SECEC) GN=argE PE=3 SV=1
- [ARGE_SHIBS](#) Mass: 42373 Score: 54 Matches: 2(2) Sequences: 2(2)
Acetylnithine deacetylase OS=Shigella boydii serotype 4 (strain Sb227) GN=argE PE=3 SV=1
- [ARGE_SHIDS](#) Mass: 42280 Score: 54 Matches: 2(2) Sequences: 2(2)
Acetylnithine deacetylase OS=Shigella dysenteriae serotype 1 (strain Sd197) GN=argE PE=3 SV=1
- [ARGE_SHIFL](#) Mass: 42411 Score: 54 Matches: 2(2) Sequences: 2(2)
Acetylnithine deacetylase OS=Shigella flexneri GN=argE PE=3 SV=1
- [ARGE_SHISS](#) Mass: 42393 Score: 54 Matches: 2(2) Sequences: 2(2)
Acetylnithine deacetylase OS=Shigella sonnei (strain Ss046) GN=argE PE=3 SV=1
- [ARGE_SHIB3](#) Mass: 42366 Score: 54 Matches: 2(2) Sequences: 2(2)
Acetylnithine deacetylase OS=Shigella boydii serotype 18 (strain CDC 3083-94 / BS512) GN=argE PE=3 SV=1
- [ARGE_ECO5E](#) Mass: 42392 Score: 54 Matches: 2(2) Sequences: 2(2)
Acetylnithine deacetylase OS=Escherichia coli O157:H7 (strain EC4115 / EHEC) GN=argE PE=3 SV=1
- [ARGE_ECOL5](#) Mass: 42239 Score: 54 Matches: 2(2) Sequences: 2(2)
Acetylnithine deacetylase OS=Escherichia coli O6:K15:H31 (strain 536 / UPEC) GN=argE PE=3 SV=1
- [ARGE_ECOL6](#) Mass: 42239 Score: 54 Matches: 2(2) Sequences: 2(2)
Acetylnithine deacetylase OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) GN=argE PE=3 SV=2
- [ARGE_ECO7I](#) Mass: 42251 Score: 54 Matches: 2(2) Sequences: 2(2)
Acetylnithine deacetylase OS=Escherichia coli O7:K1 (strain IAI39 / ExPEC) GN=argE PE=3 SV=1
- [ARGE_ECO8A](#) Mass: 42310 Score: 54 Matches: 2(2) Sequences: 2(2)
Acetylnithine deacetylase OS=Escherichia coli O8 (strain IAI1) GN=argE PE=3 SV=1
- [ARGE_SHIF8](#) Mass: 42397 Score: 54 Matches: 2(2) Sequences: 2(2)
Acetylnithine deacetylase OS=Shigella flexneri serotype 5b (strain 8401) GN=argE PE=3 SV=1
- [ARGE_ECO24](#) Mass: 42337 Score: 54 Matches: 2(2) Sequences: 2(2)
Acetylnithine deacetylase OS=Escherichia coli O139:H28 (strain E24377A / ETEC) GN=argE PE=3 SV=1
- [ARGE_ECO27](#) Mass: 42239 Score: 54 Matches: 2(2) Sequences: 2(2)

Acetylnornithine deacetylase OS=Escherichia coli O127:H6 (strain E2348/69 / EPEC) GN=argE PE=3 SV=1
[ARGE_ECO45](#) **Mass:** 42239 **Score:** 54 **Matches:** 2(2) **Sequences:** 2(2)

Acetylnornithine deacetylase OS=Escherichia coli O45:K1 (strain S88 / ExPEC) GN=argE PE=3 SV=1
[ARGE_ECO55](#) **Mass:** 42320 **Score:** 54 **Matches:** 2(2) **Sequences:** 2(2)

Acetylnornithine deacetylase OS=Escherichia coli (strain 55989 / EAEC) GN=argE PE=3 SV=1
[ARGE_ECO57](#) **Mass:** 42392 **Score:** 54 **Matches:** 2(2) **Sequences:** 2(2)

Acetylnornithine deacetylase OS=Escherichia coli O157:H7 GN=argE PE=3 SV=1
[ARGE_ECO81](#) **Mass:** 42239 **Score:** 54 **Matches:** 2(2) **Sequences:** 2(2)

Acetylnornithine deacetylase OS=Escherichia coli O81 (strain ED1a) GN=argE PE=3 SV=1

29. [H2A1B_HUMAN](#) **Mass:** 14127 **Score:** 54 **Matches:** 1(1) **Sequences:** 1(1) **emPAI:** 0.27

Histone H2A type 1-B/E OS=Homo sapiens GN=HIST1H2AB PE=1 SV=2

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 1949	972.5358	2914.5856	2914.5804	1.79	0	54	6.6e-005	1	U	R.VGAGAPVYLAAVLEYLTAEILELAGNAAR.D

Proteins matching the same set of peptides:

[H2A1C_HUMAN](#) **Mass:** 14097 **Score:** 54 **Matches:** 1(1) **Sequences:** 1(1)
 Histone H2A type 1-C OS=Homo sapiens GN=HIST1H2AC PE=1 SV=3

[H2A1C_RAT](#) **Mass:** 14097 **Score:** 54 **Matches:** 1(1) **Sequences:** 1(1)
 Histone H2A type 1-C OS=Rattus norvegicus PE=1 SV=2

[H2A1D_HUMAN](#) **Mass:** 14099 **Score:** 54 **Matches:** 1(1) **Sequences:** 1(1)
 Histone H2A type 1-D OS=Homo sapiens GN=HIST1H2AD PE=1 SV=2

[H2A1E_RAT](#) **Mass:** 14111 **Score:** 54 **Matches:** 1(1) **Sequences:** 1(1)
 Histone H2A type 1-E OS=Rattus norvegicus PE=1 SV=2

[H2A1F_MOUSE](#) **Mass:** 14153 **Score:** 54 **Matches:** 1(1) **Sequences:** 1(1)
 Histone H2A type 1-F OS=Mus musculus GN=Hist1h2af PE=1 SV=3

[H2A1H_HUMAN](#) **Mass:** 13898 **Score:** 54 **Matches:** 1(1) **Sequences:** 1(1)
 Histone H2A type 1-H OS=Homo sapiens GN=HIST1H2AH PE=1 SV=3

[H2A1H_MOUSE](#) **Mass:** 13942 **Score:** 54 **Matches:** 1(1) **Sequences:** 1(1)
 Histone H2A type 1-H OS=Mus musculus GN=Hist1h2ah PE=1 SV=3

[H2A1J_HUMAN](#) **Mass:** 13928 **Score:** 54 **Matches:** 1(1) **Sequences:** 1(1)
 Histone H2A type 1-J OS=Homo sapiens GN=HIST1H2AJ PE=1 SV=3

[H2A1K_MOUSE](#) **Mass:** 14141 **Score:** 54 **Matches:** 1(1) **Sequences:** 1(1)
 Histone H2A type 1-K OS=Mus musculus GN=Hist1h2ak PE=1 SV=3

[H2A1_BOVIN](#) **Mass:** 14083 **Score:** 54 **Matches:** 1(1) **Sequences:** 1(1)
 Histone H2A type 1 OS=Bos taurus PE=1 SV=2

[H2A1_HUMAN](#) **Mass:** 14083 **Score:** 54 **Matches:** 1(1) **Sequences:** 1(1)
 Histone H2A type 1 OS=Homo sapiens GN=HIST1H2AG PE=1 SV=2

[H2A1_MOUSE](#) **Mass:** 14127 **Score:** 54 **Matches:** 1(1) **Sequences:** 1(1)
 Histone H2A type 1 OS=Mus musculus GN=Hist1h2ab PE=1 SV=3

[H2A1_PSAMI](#) **Mass:** 13306 **Score:** 54 **Matches:** 1(1) **Sequences:** 1(1)
 Late histone H2A.1 OS=Psammecinus miliaris PE=2 SV=2

[H2A1_RAT](#) **Mass:** 14069 **Score:** 54 **Matches:** 1(1) **Sequences:** 1(1)

Histone H2A type 1 OS=Rattus norvegicus PE=1 SV=2
[H2A1_XENLA](#) Mass: 13958 Score: 54 Matches: 1(1) Sequences: 1(1)
 Histone H2A type 1 OS=Xenopus laevis PE=1 SV=2
[H2A2B_HUMAN](#) Mass: 13987 Score: 54 Matches: 1(1) Sequences: 1(1)
 Histone H2A type 2-B OS=Homo sapiens GN=HIST2H2AB PE=1 SV=3
[H2A2_PSAMI](#) Mass: 13191 Score: 54 Matches: 1(1) Sequences: 1(1)
 Late histone H2A.2.1 OS=Psammechinus miliaris PE=2 SV=2
[H2A3_HUMAN](#) Mass: 14113 Score: 54 Matches: 1(1) Sequences: 1(1)
 Histone H2A type 3 OS=Homo sapiens GN=HIST3H2A PE=1 SV=3
[H2A3_MOUSE](#) Mass: 14113 Score: 54 Matches: 1(1) Sequences: 1(1)
 Histone H2A type 3 OS=Mus musculus GN=Hist3h2a PE=1 SV=3
[H2A3_RAT](#) Mass: 14113 Score: 54 Matches: 1(1) Sequences: 1(1)
 Histone H2A type 3 OS=Rattus norvegicus PE=2 SV=3
[H2A4_CHICK](#) Mass: 13932 Score: 54 Matches: 1(1) Sequences: 1(1)
 Histone H2A-IV OS=Gallus gallus PE=1 SV=2
[H2A4_PSAMI](#) Mass: 12903 Score: 54 Matches: 1(1) Sequences: 1(1)
 Late histone H2A.2.2 OS=Psammechinus miliaris PE=3 SV=2
[H2AJ_BOVIN](#) Mass: 14011 Score: 54 Matches: 1(1) Sequences: 1(1)
 Histone H2A.J OS=Bos taurus GN=H2AFJ PE=2 SV=1
[H2AJ_HUMAN](#) Mass: 14011 Score: 54 Matches: 1(1) Sequences: 1(1)
 Histone H2A.J OS=Homo sapiens GN=H2AFJ PE=1 SV=1
[H2AJ_MACFA](#) Mass: 13981 Score: 54 Matches: 1(1) Sequences: 1(1)
 Histone H2A.J OS=Macaca fascicularis GN=H2AFJ PE=2 SV=1
[H2AJ_MOUSE](#) Mass: 14037 Score: 54 Matches: 1(1) Sequences: 1(1)
 Histone H2A.J OS=Mus musculus GN=H2afj PE=1 SV=1
[H2AJ_RAT](#) Mass: 14037 Score: 54 Matches: 1(1) Sequences: 1(1)
 Histone H2A.J OS=Rattus norvegicus GN=H2afj PE=2 SV=1
[H2AX_DANRE](#) Mass: 14992 Score: 54 Matches: 1(1) Sequences: 1(1)
 Histone H2AX OS=Danio rerio GN=h2afx PE=2 SV=3
[H2AX_HUMAN](#) Mass: 15135 Score: 54 Matches: 1(1) Sequences: 1(1)
 Histone H2AX OS=Homo sapiens GN=H2AFX PE=1 SV=2
[H2AX_MOUSE](#) Mass: 15133 Score: 54 Matches: 1(1) Sequences: 1(1)
 Histone H2AX OS=Mus musculus GN=H2afx PE=1 SV=2
[H2AX_XENLA](#) Mass: 14846 Score: 54 Matches: 1(1) Sequences: 1(1)
 Histone H2AX OS=Xenopus laevis GN=h2afx PE=1 SV=3
[H2A_CAIMO](#) Mass: 13948 Score: 54 Matches: 1(1) Sequences: 1(1)
 Histone H2A OS=Cairina moschata PE=3 SV=2
[H2A_ONCMY](#) Mass: 13723 Score: 54 Matches: 1(1) Sequences: 1(1)
 Histone H2A OS=Oncorhynchus mykiss PE=1 SV=2

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30. [RL5_ACTP2](#) Mass: 20342 Score: 49 Matches: 1(1) Sequences: 1(1) emPAI: 0.18
 50S ribosomal protein L5 OS=Actinobacillus pleuropneumoniae serotype 5b (strain L20) GN=rplE PE=3 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 137	441.7924	881.5702	881.5698	0.48	0	49	0.00034	1	U	R.LITIAVPR.I

Proteins matching the same set of peptides:

[RL5_ACTP7](#) **Mass:** 20342 **Score:** 49 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L5 OS=Actinobacillus pleuropneumoniae serotype 7 (strain AP76) GN=rplE PE=3 SV=1

[RL5_ACTPJ](#) **Mass:** 20342 **Score:** 49 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L5 OS=Actinobacillus pleuropneumoniae serotype 3 (strain JL03) GN=rplE PE=3 SV=1

[RL5_ACTSZ](#) **Mass:** 20326 **Score:** 49 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L5 OS=Actinobacillus succinogenes (strain ATCC 55618 / 130Z) GN=rplE PE=3 SV=1

[RL5_CITK8](#) **Mass:** 20275 **Score:** 49 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L5 OS=Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696) GN=rplE PE=3 SV=1

[RL5_CROS8](#) **Mass:** 20288 **Score:** 49 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L5 OS=Cronobacter sakazakii (strain ATCC BAA-894) GN=rplE PE=3 SV=1

[RL5_ECO24](#) **Mass:** 20289 **Score:** 49 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L5 OS=Escherichia coli O139:H28 (strain E24377A / ETEC) GN=rplE PE=3 SV=1

[RL5_ECO27](#) **Mass:** 20289 **Score:** 49 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L5 OS=Escherichia coli O127:H6 (strain E2348/69 / EPEC) GN=rplE PE=3 SV=1

[RL5_ECO45](#) **Mass:** 20289 **Score:** 49 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L5 OS=Escherichia coli O45:K1 (strain S88 / ExPEC) GN=rplE PE=3 SV=1

[RL5_ECO55](#) **Mass:** 20289 **Score:** 49 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L5 OS=Escherichia coli (strain 55989 / EAEC) GN=rplE PE=3 SV=1

[RL5_ECO57](#) **Mass:** 20289 **Score:** 49 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L5 OS=Escherichia coli O157:H7 GN=rplE PE=3 SV=2

[RL5_ECO5E](#) **Mass:** 20289 **Score:** 49 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L5 OS=Escherichia coli O157:H7 (strain EC4115 / EHEC) GN=rplE PE=3 SV=1

[RL5_ECO7I](#) **Mass:** 20289 **Score:** 49 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L5 OS=Escherichia coli O7:K1 (strain IAI39 / ExPEC) GN=rplE PE=3 SV=1

[RL5_ECO81](#) **Mass:** 20289 **Score:** 49 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L5 OS=Escherichia coli O81 (strain ED1a) GN=rplE PE=3 SV=1

[RL5_ECO8A](#) **Mass:** 20289 **Score:** 49 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L5 OS=Escherichia coli O8 (strain IAI1) GN=rplE PE=3 SV=1

[RL5_ECOBW](#) **Mass:** 20289 **Score:** 49 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L5 OS=Escherichia coli (strain K12 / MC4100 / BW2952) GN=rplE PE=3 SV=1

[RL5_ECODH](#) **Mass:** 20289 **Score:** 49 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L5 OS=Escherichia coli (strain K12 / DH10B) GN=rplE PE=3 SV=1

[RL5_ECOHS](#) **Mass:** 20289 **Score:** 49 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L5 OS=Escherichia coli O9:H4 (strain HS) GN=rplE PE=3 SV=1

[RL5_ECOK1](#) **Mass:** 20289 **Score:** 49 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L5 OS=Escherichia coli O1:K1 / APEC GN=rplE PE=3 SV=1

[RL5_ECOL5](#) **Mass:** 20289 **Score:** 49 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L5 OS=Escherichia coli O6:K15:H31 (strain 536 / UPEC) GN=rplE PE=3 SV=1

[RL5_ECOL6](#) **Mass:** 20289 **Score:** 49 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L5 OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) GN=rplE PE=3 SV=2

[RL5_ECOLC](#) **Mass:** 20289 **Score:** 49 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L5 OS=Escherichia coli (strain ATCC 8739 / DSM 1576 / Crooks) GN=rplE PE=3 SV=1

[RL5_ECOLI](#) **Mass:** 20289 **Score:** 49 **Matches:** 1(1) **Sequences:** 1(1)

50S ribosomal protein L5 OS=Escherichia coli (strain K12) GN=rplE PE=1 SV=2
[RL5_ECOLU](#) Mass: 20289 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Escherichia coli O17:K52:H18 (strain UMN026 / ExPEC) GN=rplE PE=3 SV=1
[RL5_ECOSE](#) Mass: 20289 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Escherichia coli (strain SE11) GN=rplE PE=3 SV=1
[RL5_ECOSM](#) Mass: 20289 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Escherichia coli (strain SMS-3-5 / SECEC) GN=rplE PE=3 SV=1
[RL5_ECOUT](#) Mass: 20289 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Escherichia coli (strain UTI89 / UPEC) GN=rplE PE=3 SV=1
[RL5_ESCF3](#) Mass: 20289 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Escherichia fergusonii (strain ATCC 35469 / DSM 13698 / CDC 0568-73) GN=rplE PE=3 SV=1
[RL5_HAEDU](#) Mass: 20373 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Haemophilus ducreyi (strain 35000HP / ATCC 700724) GN=rplE PE=3 SV=1
[RL5_HAEI8](#) Mass: 20298 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Haemophilus influenzae (strain 86-028NP) GN=rplE PE=3 SV=1
[RL5_HAEIE](#) Mass: 20298 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Haemophilus influenzae (strain PittEE) GN=rplE PE=3 SV=1
[RL5_HAEIG](#) Mass: 20298 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Haemophilus influenzae (strain PittGG) GN=rplE PE=3 SV=1
[RL5_HAEIN](#) Mass: 20298 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd) GN=rplE PE=3 SV=2
[RL5_HAEPS](#) Mass: 20329 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Haemophilus parasuis serovar 5 (strain SH0165) GN=rplE PE=3 SV=1
[RL5_HISS1](#) Mass: 20301 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Histophilus somni (strain 129Pt) GN=rplE PE=3 SV=1
[RL5_HISS2](#) Mass: 20301 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Histophilus somni (strain 2336) GN=rplE PE=3 SV=1
[RL5_KLEP3](#) Mass: 20262 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Klebsiella pneumoniae (strain 342) GN=rplE PE=3 SV=1
[RL5_KLEP7](#) Mass: 20289 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Klebsiella pneumoniae subsp. pneumoniae (strain ATCC 700721 / MGH 78578) GN=rplE PE=3 SV=1
[RL5_MANSM](#) Mass: 20295 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Mannheimia succiniciproducens (strain MBEL55E) GN=rplE PE=3 SV=1
[RL5_PASMU](#) Mass: 20370 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Pasteurella multocida (strain Pm70) GN=rplE PE=3 SV=1
[RL5_SALAA](#) Mass: 20305 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Salmonella agona (strain SL483) GN=rplE PE=3 SV=1
[RL5_SALAR](#) Mass: 20319 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Salmonella arizonae (strain ATCC BAA-731 / CDC346-86 / RSK2980) GN=rplE PE=3 SV=1
[RL5_SALCH](#) Mass: 20305 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Salmonella choleraesuis (strain SC-B67) GN=rplE PE=3 SV=1
[RL5_SALDC](#) Mass: 20305 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Salmonella dublin (strain CT_02021853) GN=rplE PE=3 SV=1
[RL5_SALEP](#) Mass: 20305 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Salmonella enteritidis PT4 (strain P125109) GN=rplE PE=3 SV=1
[RL5_SALG2](#) Mass: 20305 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Salmonella gallinarum (strain 287/91 / NCTC 13346) GN=rplE PE=3 SV=1
[RL5_SALHS](#) Mass: 20305 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Salmonella heidelberg (strain SL476) GN=rplE PE=3 SV=1
[RL5_SALNS](#) Mass: 20305 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Salmonella newport (strain SL254) GN=rplE PE=3 SV=1
[RL5_SALPA](#) Mass: 20305 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Salmonella paratyphi A (strain ATCC 9150 / SARB42) GN=rplE PE=3 SV=1
[RL5_SALPB](#) Mass: 20305 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Salmonella paratyphi B (strain ATCC BAA-1250 / SPB7) GN=rplE PE=3 SV=1
[RL5_SALPC](#) Mass: 20305 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Salmonella paratyphi C (strain RKS4594) GN=rplE PE=3 SV=1
[RL5_SALPK](#) Mass: 20305 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Salmonella paratyphi A (strain AKU_12601) GN=rplE PE=3 SV=1
[RL5_SALSV](#) Mass: 20305 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Salmonella schwarzengrund (strain CVM19633) GN=rplE PE=3 SV=1
[RL5_SALTI](#) Mass: 20305 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Salmonella typhi GN=rplE PE=3 SV=2
[RL5_SALTY](#) Mass: 20305 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=rplE PE=3 SV=2
[RL5_SHIB3](#) Mass: 20289 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Shigella boydii serotype 18 (strain CDC 3083-94 / BS512) GN=rplE PE=3 SV=1
[RL5_SHIBS](#) Mass: 20289 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Shigella boydii serotype 4 (strain Sb227) GN=rplE PE=3 SV=1
[RL5_SHIDS](#) Mass: 20289 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Shigella dysenteriae serotype 1 (strain Sd197) GN=rplE PE=3 SV=1
[RL5_SHIF8](#) Mass: 20289 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Shigella flexneri serotype 5b (strain 8401) GN=rplE PE=3 SV=1
[RL5_SHIFL](#) Mass: 20502 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Shigella flexneri GN=rplE PE=3 SV=3
[RL5_SHISS](#) Mass: 20289 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Shigella sonnei (strain Ss046) GN=rplE PE=3 SV=1
[RL5_YERE8](#) Mass: 20274 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Yersinia enterocolitica serotype O:8 / biotype 1B (strain NCTC 13174 / 8081) GN=rplE PE=3 SV=1
[RL5_YERP3](#) Mass: 20251 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Yersinia pseudotuberculosis serotype O:1b (strain IP 31758) GN=rplE PE=3 SV=1
[RL5_YERPA](#) Mass: 20251 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Yersinia pestis bv. Antiqua (strain Antiqua) GN=rplE PE=3 SV=1
[RL5_YERPB](#) Mass: 20251 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Yersinia pseudotuberculosis serotype IB (strain PB1/+) GN=rplE PE=3 SV=1
[RL5_YERPE](#) Mass: 20251 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Yersinia pestis GN=rplE PE=3 SV=1
[RL5_YERPG](#) Mass: 20251 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Yersinia pestis bv. Antiqua (strain Angola) GN=rplE PE=3 SV=1
[RL5_YERPQ](#) Mass: 20251 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Yersinia pestis bv. Antiqua (strain Nepal516) GN=rplE PE=3 SV=1
[RL5_YERPP](#) Mass: 20251 Score: 49 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L5 OS=Yersinia pestis (strain Pestoides F) GN=rplE PE=3 SV=1
[RL5_YERPS](#) Mass: 20251 Score: 49 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L5 OS=Yersinia pseudotuberculosis serotype I (strain IP32953) GN=rplE PE=3 SV=1
[RL5_YERP](#) Mass: 20251 Score: 49 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L5 OS=Yersinia pseudotuberculosis serotype O:3 (strain YPIII) GN=rplE PE=3 SV=1

31. [YCIW_ECOLI](#) Mass: 42194 Score: 49 Matches: 1(1) Sequences: 1(1) emPAI: 0.09
 Uncharacterized protein YciW OS=Escherichia coli (strain K12) GN=yCiW PE=4 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 356	532.2989	1062.5832	1062.5822	1.02	0	49	0.0012	1	U	R.LAQITQYAR.Q

32. [AHPC_ECOLI](#) Mass: 20748 Score: 45 Matches: 1(1) Sequences: 1(1) emPAI: 0.18
 Alkyl hydroperoxide reductase subunit C OS=Escherichia coli (strain K12) GN=ahpC PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 846	691.3443	1380.6740	1380.6707	2.39	0	45	0.002	1	U	K.YAMIGDPTGALTR.N + Oxidation (M)

Proteins matching the same set of peptides:

[AHPC_SALTI](#) Mass: 20734 Score: 45 Matches: 1(1) Sequences: 1(1)
 Alkyl hydroperoxide reductase subunit C OS=Salmonella typhi GN=ahpC PE=3 SV=2
[AHPC_SALTY](#) Mass: 20734 Score: 45 Matches: 1(1) Sequences: 1(1)
 Alkyl hydroperoxide reductase subunit C OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=ahpC PE=1 SV=2
[AHPC_SHIFL](#) Mass: 20748 Score: 45 Matches: 1(1) Sequences: 1(1)
 Alkyl hydroperoxide reductase subunit C OS=Shigella flexneri GN=ahpC PE=3 SV=2
[AHPC_ECOL6](#) Mass: 20748 Score: 45 Matches: 1(1) Sequences: 1(1)
 Alkyl hydroperoxide reductase subunit C OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) GN=ahpC PE=3 SV=2
[AHPC_ECO57](#) Mass: 20748 Score: 45 Matches: 1(1) Sequences: 1(1)
 Alkyl hydroperoxide reductase subunit C OS=Escherichia coli O157:H7 GN=ahpC PE=3 SV=2

33. [MDH_ECOBW](#) Mass: 32317 Score: 42 Matches: 2(2) Sequences: 2(2) emPAI: 0.24
 Malate dehydrogenase OS=Escherichia coli (strain K12 / MC4100 / BW2952) GN=mdh PE=3 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 515	575.3374	1148.6602	1148.6594	0.76	0	28	0.02	1	U	R.FFSQPLLLGK.N
<input checked="" type="checkbox"/> 672	638.8495	1275.6844	1275.6823	1.69	0	36	0.02	1	U	R.SDLFNVNAGIVK.N

Proteins matching the same set of peptides:

[MDH_ECODH](#) Mass: 32317 Score: 42 Matches: 2(2) Sequences: 2(2)
 Malate dehydrogenase OS=Escherichia coli (strain K12 / DH10B) GN=mdh PE=3 SV=1
[MDH_ECOHS](#) Mass: 32317 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Escherichia coli O9:H4 (strain HS) GN=mdh PE=3 SV=1
[MDH_ECOLC](#) Mass: 32307 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Escherichia coli (strain ATCC 8739 / DSM 1576 / Crooks) GN=mdh PE=3 SV=1
[MDH_ECOLI](#) Mass: 32317 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Escherichia coli (strain K12) GN=mdh PE=1 SV=1
[MDH_ECOLU](#) Mass: 32316 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Escherichia coli O17:K52:H18 (strain UMN026 / ExPEC) GN=mdh PE=3 SV=1
[MDH_ECOSE](#) Mass: 32333 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Escherichia coli (strain SE11) GN=mdh PE=3 SV=1
[MDH_ECOSM](#) Mass: 32317 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Escherichia coli (strain SMS-3-5 / SECEC) GN=mdh PE=3 SV=1
[MDH_ECOUT](#) Mass: 32317 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Escherichia coli (strain UTI89 / UPEC) GN=mdh PE=3 SV=2
[MDH_SALAR](#) Mass: 32393 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Salmonella arizonae (strain ATCC BAA-731 / CDC346-86 / RSK2980) GN=mdh PE=3 SV=1
[MDH_SALCH](#) Mass: 32471 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Salmonella choleraesuis (strain SC-B67) GN=mdh PE=3 SV=1
[MDH_SALDC](#) Mass: 32483 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Salmonella dublin (strain CT_02021853) GN=mdh PE=3 SV=1
[MDH_SALEP](#) Mass: 32455 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Salmonella enteritidis PT4 (strain P125109) GN=mdh PE=3 SV=1
[MDH_SALHS](#) Mass: 32455 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Salmonella heidelberg (strain SL476) GN=mdh PE=3 SV=1
[MDH_SALMU](#) Mass: 29485 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase (Fragment) OS=Salmonella muenchen GN=mdh PE=3 SV=1
[MDH_SALNS](#) Mass: 32498 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Salmonella newport (strain SL254) GN=mdh PE=3 SV=1
[MDH_SALPA](#) Mass: 32455 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Salmonella paratyphi A (strain ATCC 9150 / SARB42) GN=mdh PE=3 SV=2
[MDH_SALPB](#) Mass: 32455 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Salmonella paratyphi B (strain ATCC BAA-1250 / SPB7) GN=mdh PE=3 SV=1
[MDH_SALPC](#) Mass: 32455 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Salmonella paratyphi C (strain RKS4594) GN=mdh PE=3 SV=1
[MDH_SALPK](#) Mass: 32455 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Salmonella paratyphi A (strain AKU_12601) GN=mdh PE=3 SV=1
[MDH_SALSV](#) Mass: 32455 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Salmonella schwarzengrund (strain CVM19633) GN=mdh PE=3 SV=1
[MDH_SALTI](#) Mass: 32485 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Salmonella typhi GN=mdh PE=3 SV=1
[MDH_SALTY](#) Mass: 32455 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=mdh PE=3 SV=2
[MDH_SHIBS](#) Mass: 32317 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Shigella boydii serotype 4 (strain Sb227) GN=mdh PE=3 SV=1
[MDH_SHIDS](#) Mass: 32306 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Shigella dysenteriae serotype 1 (strain Sd197) GN=mdh PE=3 SV=1
[MDH_SHIFL](#) Mass: 32329 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Shigella flexneri GN=mdh PE=3 SV=2
[MDH_SHISS](#) Mass: 32317 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Shigella sonnei (strain Ss046) GN=mdh PE=3 SV=1
[MDH_ECOK1](#) Mass: 32317 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Escherichia coli O1:K1 / APEC GN=mdh PE=3 SV=1
[MDH_SALG2](#) Mass: 32503 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Salmonella gallinarum (strain 287/91 / NCTC 13346) GN=mdh PE=3 SV=1
[MDH_ESCF3](#) Mass: 32400 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Escherichia fergusonii (strain ATCC 35469 / DSM 13698 / CDC 0568-73) GN=mdh PE=3 SV=1
[MDH_KLEP3](#) Mass: 32378 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Klebsiella pneumoniae (strain 342) GN=mdh PE=3 SV=1
[MDH_SHIB3](#) Mass: 32317 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Shigella boydii serotype 18 (strain CDC 3083-94 / BS512) GN=mdh PE=3 SV=1
[MDH_SALA4](#) Mass: 32455 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Salmonella agona (strain SL483) GN=mdh PE=3 SV=1
[MDH_ECO5E](#) Mass: 32317 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Escherichia coli O157:H7 (strain EC4115 / EHEC) GN=mdh PE=3 SV=1
[MDH_ECOL5](#) Mass: 32331 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Escherichia coli O6:K15:H31 (strain 536 / UPEC) GN=mdh PE=3 SV=1
[MDH_ECOL6](#) Mass: 32317 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) GN=mdh PE=3 SV=1
[MDH_ECOT1](#) Mass: 32317 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Escherichia coli O7:K1 (strain IAI39 / ExPEC) GN=mdh PE=3 SV=1
[MDH_KLEP7](#) Mass: 32406 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Klebsiella pneumoniae subsp. pneumoniae (strain ATCC 700721 / MGH 78578) GN=mdh PE=3 SV=1
[MDH_CITK8](#) Mass: 32404 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696) GN=mdh PE=3 SV=1
[MDH_CROS8](#) Mass: 32471 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Cronobacter sakazakii (strain ATCC BAA-894) GN=mdh PE=3 SV=1
[MDH_ECO8A](#) Mass: 32290 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Escherichia coli O8 (strain IAI1) GN=mdh PE=3 SV=1
[MDH_SHIF8](#) Mass: 32329 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Shigella flexneri serotype 5b (strain 8401) GN=mdh PE=3 SV=1
[MDH_ECO24](#) Mass: 32317 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Escherichia coli O139:H28 (strain E24377A / ETEC) GN=mdh PE=3 SV=1
[MDH_ECO27](#) Mass: 32317 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Escherichia coli O127:H6 (strain E2348/69 / EPEC) GN=mdh PE=3 SV=1
[MDH_ENT38](#) Mass: 32412 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Enterobacter sp. (strain 638) GN=mdh PE=3 SV=1
[MDH_ECO45](#) Mass: 32317 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Escherichia coli O45:K1 (strain S88 / ExPEC) GN=mdh PE=3 SV=1
[MDH_ECO55](#) Mass: 32290 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Escherichia coli (strain 55989 / EAEC) GN=mdh PE=3 SV=1
[MDH_ECO57](#) Mass: 32317 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Escherichia coli O157:H7 GN=mdh PE=3 SV=1
[MDH_ECO81](#) Mass: 32317 Score: 42 Matches: 2(2) Sequences: 2(2)

Malate dehydrogenase OS=Escherichia coli O81 (strain ED1a) GN=mdh PE=3 SV=1

34. [DIEXF_DANRE](#) **Mass:** 86748 **Score:** 40 **Matches:** 1(1) **Sequences:** 1(1) **emPAI:** 0.04

Digestive organ expansion factor OS=Danio rerio GN=diexf PE=2 SV=2

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 387	544.8009	1087.5872	1087.5873	-0.06	1	40	0.01	1	U	K.QEIDNLTKK.Q

35. [RL6_CITK8](#) **Mass:** 18876 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1) **emPAI:** 0.20

50S ribosomal protein L6 OS=Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696) GN=rplF PE=3 SV=1

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 521	575.8453	1149.6760	1149.6758	0.23	0	39	0.0025	1	U	K.APVVVPAGVDVK.I

Proteins matching the same set of peptides:

[RL6_ECO24](#) **Mass:** 18892 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Escherichia coli O139:H28 (strain E24377A / ETEC) GN=rplF PE=3 SV=1

[RL6_ECO27](#) **Mass:** 18892 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Escherichia coli O127:H6 (strain E2348/69 / EPEC) GN=rplF PE=3 SV=1

[RL6_ECO45](#) **Mass:** 18892 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Escherichia coli O45:K1 (strain S88 / ExPEC) GN=rplF PE=3 SV=1

[RL6_ECO55](#) **Mass:** 18892 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Escherichia coli (strain 55989 / EAEC) GN=rplF PE=3 SV=1

[RL6_ECO57](#) **Mass:** 18892 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Escherichia coli O157:H7 GN=rplF PE=1 SV=2

[RL6_ECO5E](#) **Mass:** 18892 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Escherichia coli O157:H7 (strain EC4115 / EHEC) GN=rplF PE=3 SV=1

[RL6_ECO7I](#) **Mass:** 18892 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Escherichia coli O7:K1 (strain IAI39 / ExPEC) GN=rplF PE=3 SV=1

[RL6_ECO81](#) **Mass:** 18892 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Escherichia coli O81 (strain ED1a) GN=rplF PE=3 SV=1

[RL6_ECO8A](#) **Mass:** 18892 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Escherichia coli O8 (strain IAI1) GN=rplF PE=3 SV=1

[RL6_ECOBW](#) **Mass:** 18892 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Escherichia coli (strain K12 / MC4100 / BW2952) GN=rplF PE=3 SV=1

[RL6_ECODH](#) **Mass:** 18892 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Escherichia coli (strain K12 / DH10B) GN=rplF PE=3 SV=1

[RL6_ECOHS](#) **Mass:** 18892 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Escherichia coli O9:H4 (strain HS) GN=rplF PE=3 SV=1

[RL6_ECOK1](#) **Mass:** 18892 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Escherichia coli O1:K1 / APEC GN=rplF PE=3 SV=1

[RL6_ECOL5](#) **Mass:** 18892 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Escherichia coli O6:K15:H31 (strain 536 / UPEC) GN=rplF PE=3 SV=1

[RL6_ECOL6](#) **Mass:** 18892 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) GN=rplF PE=3 SV=2

[RL6_ECOLC](#) **Mass:** 18892 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Escherichia coli (strain ATCC 8739 / DSM 1576 / Crooks) GN=rplF PE=3 SV=1

[RL6_ECOLI](#) **Mass:** 18892 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Escherichia coli (strain K12) GN=rplF PE=1 SV=2

[RL6_ECOLU](#) **Mass:** 18892 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Escherichia coli O17:K52:H18 (strain UMN026 / ExPEC) GN=rplF PE=3 SV=1

[RL6_ECOSE](#) **Mass:** 18892 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Escherichia coli (strain SE11) GN=rplF PE=3 SV=1

[RL6_ECOSM](#) **Mass:** 18892 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Escherichia coli (strain SMS-3-5 / SECEC) GN=rplF PE=3 SV=1

[RL6_ECOUT](#) **Mass:** 18892 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Escherichia coli (strain UTI89 / UPEC) GN=rplF PE=3 SV=1

[RL6_ESCF3](#) **Mass:** 18878 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Escherichia fergusonii (strain ATCC 35469 / DSM 13698 / CDC 0568-73) GN=rplF PE=3 SV=1

[RL6_KLEP3](#) **Mass:** 18861 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Klebsiella pneumoniae (strain 342) GN=rplF PE=3 SV=1

[RL6_KLEP7](#) **Mass:** 18832 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Klebsiella pneumoniae subsp. pneumoniae (strain ATCC 700721 / MGH 78578) GN=rplF PE=3 SV=1

[RL6_SALAA4](#) **Mass:** 18848 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Salmonella agona (strain SL483) GN=rplF PE=3 SV=1

[RL6_SALAR](#) **Mass:** 18876 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Salmonella arizonae (strain ATCC BAA-731 / CDC346-86 / RSK2980) GN=rplF PE=3 SV=1

[RL6_SALCH](#) **Mass:** 18848 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Salmonella choleraesuis (strain SC-B67) GN=rplF PE=3 SV=1

[RL6_SALDC](#) **Mass:** 18818 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Salmonella dublin (strain CT_02021853) GN=rplF PE=3 SV=1

[RL6_SALEP](#) **Mass:** 18848 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Salmonella enteritidis PT4 (strain P125109) GN=rplF PE=3 SV=1

[RL6_SALG2](#) **Mass:** 18848 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Salmonella gallinarum (strain 287/91 / NCTC 13346) GN=rplF PE=3 SV=1

[RL6_SALHS](#) **Mass:** 18848 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Salmonella heidelberg (strain SL476) GN=rplF PE=3 SV=1

[RL6_SALNS](#) **Mass:** 18848 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Salmonella newport (strain SL254) GN=rplF PE=3 SV=1

[RL6_SALPA](#) **Mass:** 18848 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Salmonella paratyphi A (strain ATCC 9150 / SARB42) GN=rplF PE=3 SV=1

[RL6_SALPB](#) **Mass:** 18848 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Salmonella paratyphi B (strain ATCC BAA-1250 / SPB7) GN=rplF PE=3 SV=1

[RL6_SALPC](#) **Mass:** 18848 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Salmonella paratyphi C (strain RKS4594) GN=rplF PE=3 SV=1

[RL6_SALPK](#) **Mass:** 18848 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Salmonella paratyphi A (strain AKU_12601) GN=rplF PE=3 SV=1

[RL6_SALSV](#) **Mass:** 18848 **Score:** 39 **Matches:** 1(1) **Sequences:** 1(1)
50S ribosomal protein L6 OS=Salmonella schwarzengrund (strain CVM19633) GN=rplF PE=3 SV=1

[RL6_SALTI](#) Mass: 18848 Score: 39 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L6 OS=Salmonella typhi GN=rp1F PE=3 SV=2
[RL6_SALTY](#) Mass: 18848 Score: 39 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L6 OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=rp1F PE=3 SV=2
[RL6_SHIB3](#) Mass: 18892 Score: 39 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L6 OS=Shigella boydii serotype 18 (strain CDC 3083-94 / BS512) GN=rp1F PE=3 SV=1
[RL6_SHIBS](#) Mass: 18892 Score: 39 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L6 OS=Shigella boydii serotype 4 (strain Sb227) GN=rp1F PE=3 SV=1
[RL6_SHIDS](#) Mass: 18892 Score: 39 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L6 OS=Shigella dysenteriae serotype 1 (strain Sd197) GN=rp1F PE=3 SV=1
[RL6_SHIF8](#) Mass: 18892 Score: 39 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L6 OS=Shigella flexneri serotype 5b (strain 8401) GN=rp1F PE=3 SV=1
[RL6_SHIFL](#) Mass: 18892 Score: 39 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L6 OS=Shigella flexneri GN=rp1F PE=3 SV=2
[RL6_SHISS](#) Mass: 18920 Score: 39 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L6 OS=Shigella sonnei (strain Ss046) GN=rp1F PE=3 SV=1

36. [RL1_ACTP2](#) Mass: 23932 Score: 38 Matches: 2(1) Sequences: 2(1) emPAI: 0.15
 50S ribosomal protein L1 OS=Actinobacillus pleuropneumoniae serotype 5b (strain L20) GN=rplA PE=3 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 613	611.8674	1221.7202	1221.7194	0.71	0	38	0.0037	1	U	R.VVGQLGQVLGPR.G
<input checked="" type="checkbox"/> 685	642.8627	1283.7108	1283.7085	1.81	0	23	0.3	1	U	K.VGTVTPNVAEAVK.N

Proteins matching the same set of peptides:

[RL1_ACTP7](#) Mass: 23932 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Actinobacillus pleuropneumoniae serotype 7 (strain AP76) GN=rplA PE=3 SV=1
[RL1_CITK8](#) Mass: 24859 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696) GN=rplA PE=3 SV=1
[RL1_CROS8](#) Mass: 24687 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Cronobacter sakazakii (strain ATCC BAA-894) GN=rplA PE=3 SV=1
[RL1_ECO24](#) Mass: 24714 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Escherichia coli O139:H28 (strain E24377A / ETEC) GN=rplA PE=3 SV=1
[RL1_ECO27](#) Mass: 24728 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Escherichia coli O127:H6 (strain E2348/69 / EPEC) GN=rplA PE=3 SV=1
[RL1_ECO45](#) Mass: 24714 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Escherichia coli O45:K1 (strain S88 / ExPEC) GN=rplA PE=3 SV=1
[RL1_ECO55](#) Mass: 24714 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Escherichia coli (strain 55989 / EAEC) GN=rplA PE=3 SV=1
[RL1_ECO57](#) Mass: 24714 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Escherichia coli O157:H7 GN=rplA PE=3 SV=2
[RL1_ECO5E](#) Mass: 24714 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Escherichia coli O157:H7 (strain EC4115 / EHEC) GN=rplA PE=3 SV=1
[RL1_ECO7I](#) Mass: 24714 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Escherichia coli O7:K1 (strain IAI39 / ExPEC) GN=rplA PE=3 SV=1

[RL1_ECO81](#) Mass: 24714 Score: 38 Matches: 2(1) Sequences: 2(1)
50S ribosomal protein L1 OS=Escherichia coli O81 (strain ED1a) GN=rplA PE=3 SV=1

[RL1_ECO8A](#) Mass: 24714 Score: 38 Matches: 2(1) Sequences: 2(1)
50S ribosomal protein L1 OS=Escherichia coli O8 (strain IAI1) GN=rplA PE=3 SV=1

[RL1_ECOBW](#) Mass: 24714 Score: 38 Matches: 2(1) Sequences: 2(1)
50S ribosomal protein L1 OS=Escherichia coli (strain K12 / MC4100 / BW2952) GN=rplA PE=3 SV=1

[RL1_ECODH](#) Mass: 24714 Score: 38 Matches: 2(1) Sequences: 2(1)
50S ribosomal protein L1 OS=Escherichia coli (strain K12 / DH10B) GN=rplA PE=3 SV=1

[RL1_ECOHS](#) Mass: 24714 Score: 38 Matches: 2(1) Sequences: 2(1)
50S ribosomal protein L1 OS=Escherichia coli O9:H4 (strain HS) GN=rplA PE=3 SV=1

[RL1_ECOL5](#) Mass: 24714 Score: 38 Matches: 2(1) Sequences: 2(1)
50S ribosomal protein L1 OS=Escherichia coli O6:K15:H31 (strain 536 / UPEC) GN=rplA PE=3 SV=1

[RL1_ECOL6](#) Mass: 24714 Score: 38 Matches: 2(1) Sequences: 2(1)
50S ribosomal protein L1 OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) GN=rplA PE=3 SV=2

[RL1_ECOLC](#) Mass: 24714 Score: 38 Matches: 2(1) Sequences: 2(1)
50S ribosomal protein L1 OS=Escherichia coli (strain ATCC 8739 / DSM 1576 / Crooks) GN=rplA PE=3 SV=1

[RL1_ECOLI](#) Mass: 24714 Score: 38 Matches: 2(1) Sequences: 2(1)
50S ribosomal protein L1 OS=Escherichia coli (strain K12) GN=rplA PE=1 SV=2

[RL1_ECOLU](#) Mass: 24714 Score: 38 Matches: 2(1) Sequences: 2(1)
50S ribosomal protein L1 OS=Escherichia coli O17:K52:H18 (strain UMN026 / ExPEC) GN=rplA PE=3 SV=1

[RL1_ECOSE](#) Mass: 24714 Score: 38 Matches: 2(1) Sequences: 2(1)
50S ribosomal protein L1 OS=Escherichia coli (strain SE11) GN=rplA PE=3 SV=1

[RL1_ECOSM](#) Mass: 24714 Score: 38 Matches: 2(1) Sequences: 2(1)
50S ribosomal protein L1 OS=Escherichia coli (strain SMS-3-5 / SECEC) GN=rplA PE=3 SV=1

[RL1_ECOUT](#) Mass: 24714 Score: 38 Matches: 2(1) Sequences: 2(1)
50S ribosomal protein L1 OS=Escherichia coli (strain UTI89 / UPEC) GN=rplA PE=3 SV=1

[RL1_ENT38](#) Mass: 24637 Score: 38 Matches: 2(1) Sequences: 2(1)
50S ribosomal protein L1 OS=Enterobacter sp. (strain 638) GN=rplA PE=3 SV=1

[RL1_ERWT9](#) Mass: 24644 Score: 38 Matches: 2(1) Sequences: 2(1)
50S ribosomal protein L1 OS=Erwinia tasmaniensis (strain DSM 17950 / Et1/99) GN=rplA PE=3 SV=1

[RL1_ESCF3](#) Mass: 24714 Score: 38 Matches: 2(1) Sequences: 2(1)
50S ribosomal protein L1 OS=Escherichia fergusonii (strain ATCC 35469 / DSM 13698 / CDC 0568-73) GN=rplA PE=3 SV=1

[RL1_HAEI8](#) Mass: 24092 Score: 38 Matches: 2(1) Sequences: 2(1)
50S ribosomal protein L1 OS=Haemophilus influenzae (strain 86-028NP) GN=rplA PE=3 SV=1

[RL1_HAEIE](#) Mass: 24120 Score: 38 Matches: 2(1) Sequences: 2(1)
50S ribosomal protein L1 OS=Haemophilus influenzae (strain PittEE) GN=rplA PE=3 SV=1

[RL1_HAEIG](#) Mass: 24092 Score: 38 Matches: 2(1) Sequences: 2(1)
50S ribosomal protein L1 OS=Haemophilus influenzae (strain PittGG) GN=rplA PE=3 SV=1

[RL1_HAEIN](#) Mass: 24092 Score: 38 Matches: 2(1) Sequences: 2(1)
50S ribosomal protein L1 OS=Haemophilus influenzae (strain ATCC 51907 / DSM 11121 / KW20 / Rd) GN=rplA PE=3 SV=2

[RL1_HAEPS](#) Mass: 23962 Score: 38 Matches: 2(1) Sequences: 2(1)
50S ribosomal protein L1 OS=Haemophilus parausis serovar 5 (strain SH0165) GN=rplA PE=3 SV=1

[RL1_KLEP3](#) Mass: 24616 Score: 38 Matches: 2(1) Sequences: 2(1)
50S ribosomal protein L1 OS=Klebsiella pneumoniae (strain 342) GN=rplA PE=3 SV=1

[RL1_KLEP7](#) Mass: 24729 Score: 38 Matches: 2(1) Sequences: 2(1)
50S ribosomal protein L1 OS=Klebsiella pneumoniae subsp. pneumoniae (strain ATCC 700721 / MGH 78578) GN=rplA PE=3 SV=1

[RL1_SALA4](#) Mass: 24713 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Salmonella agona (strain SL483) GN=rplA PE=3 SV=1
[RL1_SALAR](#) Mass: 24702 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Salmonella arizonae (strain ATCC BAA-731 / CDC346-86 / RSK2980) GN=rplA PE=3 SV=1
[RL1_SALCH](#) Mass: 24713 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Salmonella choleraesuis (strain SC-B67) GN=rplA PE=3 SV=1
[RL1_SALDC](#) Mass: 24713 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Salmonella dublin (strain CT_02021853) GN=rplA PE=3 SV=1
[RL1_SALEP](#) Mass: 24713 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Salmonella enteritidis PT4 (strain P125109) GN=rplA PE=3 SV=1
[RL1_SALHS](#) Mass: 24713 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Salmonella heidelberg (strain SL476) GN=rplA PE=3 SV=1
[RL1_SALNS](#) Mass: 24713 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Salmonella newport (strain SL254) GN=rplA PE=3 SV=1
[RL1_SALPA](#) Mass: 24713 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Salmonella paratyphi A (strain ATCC 9150 / SARB42) GN=rplA PE=3 SV=1
[RL1_SALPB](#) Mass: 24713 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Salmonella paratyphi B (strain ATCC BAA-1250 / SPB7) GN=rplA PE=3 SV=1
[RL1_SALPC](#) Mass: 24713 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Salmonella paratyphi C (strain RKS4594) GN=rplA PE=3 SV=1
[RL1_SALPK](#) Mass: 24713 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Salmonella paratyphi A (strain AKU_12601) GN=rplA PE=3 SV=1
[RL1_SALSV](#) Mass: 24713 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Salmonella schwarzengrund (strain CVM19633) GN=rplA PE=3 SV=1
[RL1_SALTI](#) Mass: 24713 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Salmonella typhi GN=rplA PE=3 SV=1
[RL1_SALTY](#) Mass: 24713 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=rplA PE=3 SV=1
[RL1_SHIB3](#) Mass: 24714 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Shigella boydii serotype 18 (strain CDC 3083-94 / BS512) GN=rplA PE=3 SV=1
[RL1_SHIB5](#) Mass: 24714 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Shigella boydii serotype 4 (strain Sb227) GN=rplA PE=3 SV=1
[RL1_SHIDS](#) Mass: 24714 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Shigella dysenteriae serotype 1 (strain Sd197) GN=rplA PE=3 SV=1
[RL1_SHIF8](#) Mass: 24714 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Shigella flexneri serotype 5b (strain 8401) GN=rplA PE=3 SV=1
[RL1_SHIFL](#) Mass: 24714 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Shigella flexneri GN=rplA PE=3 SV=2
[RL1_SHISS](#) Mass: 24714 Score: 38 Matches: 2(1) Sequences: 2(1)
 50S ribosomal protein L1 OS=Shigella sonnei (strain Ss046) GN=rplA PE=3 SV=1

37. [RL4_CITK8](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1) emPAI: 0.17
 50S ribosomal protein L4 OS=Citrobacter koseri (strain ATCC BAA-895 / CDC 4225-83 / SGSC4696) GN=rplD PE=3 SV=1

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
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[1100](#) 781.4105 1560.8064 1560.8035 1.86 0 37 0.017 1 U R.DATGIDPVSLIAFDK.V

Proteins matching the same set of peptides:

[RL4_CROS8](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L4 OS=Cronobacter sakazakii (strain ATCC BAA-894) GN=rplD PE=3 SV=1

[RL4_ECO24](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L4 OS=Escherichia coli O139:H28 (strain E24377A / ETEC) GN=rplD PE=3 SV=1

[RL4_ECO27](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L4 OS=Escherichia coli O127:H6 (strain E2348/69 / EPEC) GN=rplD PE=3 SV=1

[RL4_ECO45](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L4 OS=Escherichia coli O45:K1 (strain S88 / ExPEC) GN=rplD PE=3 SV=1

[RL4_ECO55](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L4 OS=Escherichia coli (strain 55989 / EAEC) GN=rplD PE=3 SV=1

[RL4_ECO57](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L4 OS=Escherichia coli O157:H7 GN=rplD PE=3 SV=1

[RL4_ECO5E](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L4 OS=Escherichia coli O157:H7 (strain EC4115 / EHEC) GN=rplD PE=3 SV=1

[RL4_ECO7I](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L4 OS=Escherichia coli O7:K1 (strain IAI39 / ExPEC) GN=rplD PE=3 SV=1

[RL4_ECO81](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L4 OS=Escherichia coli O81 (strain ED1a) GN=rplD PE=3 SV=1

[RL4_ECO8A](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L4 OS=Escherichia coli O8 (strain IAI1) GN=rplD PE=3 SV=1

[RL4_ECOBW](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L4 OS=Escherichia coli (strain K12 / MC4100 / BW2952) GN=rplD PE=3 SV=1

[RL4_ECODH](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L4 OS=Escherichia coli (strain K12 / DH10B) GN=rplD PE=3 SV=1

[RL4_ECOHS](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L4 OS=Escherichia coli O9:H4 (strain HS) GN=rplD PE=3 SV=1

[RL4_ECOK1](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L4 OS=Escherichia coli O1:K1 / APEC GN=rplD PE=3 SV=1

[RL4_ECOL5](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L4 OS=Escherichia coli O6:K15:H31 (strain 536 / UPEC) GN=rplD PE=3 SV=1

[RL4_ECOL6](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L4 OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) GN=rplD PE=3 SV=1

[RL4_ECOLC](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L4 OS=Escherichia coli (strain ATCC 8739 / DSM 1576 / Crooks) GN=rplD PE=3 SV=1

[RL4_ECOLI](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L4 OS=Escherichia coli (strain K12) GN=rplD PE=1 SV=1

[RL4_ECOLU](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L4 OS=Escherichia coli O17:K52:H18 (strain UMN026 / ExPEC) GN=rplD PE=3 SV=1

[RL4_ECOSE](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L4 OS=Escherichia coli (strain SE11) GN=rplD PE=3 SV=1

[RL4_ECOSM](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L4 OS=Escherichia coli (strain SMS-3-5 / SECEC) GN=rplD PE=3 SV=1

[RL4_ECOUT](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L4 OS=Escherichia coli (strain UTI89 / UPEC) GN=rplD PE=3 SV=1
[RL4_ENT38](#) Mass: 22046 Score: 37 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L4 OS=Enterobacter sp. (strain 638) GN=rplD PE=3 SV=1
[RL4_ESCF3](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L4 OS=Escherichia fergusonii (strain ATCC 35469 / DSM 13698 / CDC 0568-73) GN=rplD PE=3 SV=1
[RL4_SALA4](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L4 OS=Salmonella agona (strain SL483) GN=rplD PE=3 SV=1
[RL4_SALAR](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L4 OS=Salmonella arizonae (strain ATCC BAA-731 / CDC346-86 / RSK2980) GN=rplD PE=3 SV=1
[RL4_SALCH](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L4 OS=Salmonella choleraesuis (strain SC-B67) GN=rplD PE=3 SV=1
[RL4_SALDC](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L4 OS=Salmonella dublin (strain CT_02021853) GN=rplD PE=3 SV=1
[RL4_SALEP](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L4 OS=Salmonella enteritidis PT4 (strain P125109) GN=rplD PE=3 SV=1
[RL4_SALG2](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L4 OS=Salmonella gallinarum (strain 287/91 / NCTC 13346) GN=rplD PE=3 SV=1
[RL4_SALHS](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L4 OS=Salmonella heidelberg (strain SL476) GN=rplD PE=3 SV=1
[RL4_SALNS](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L4 OS=Salmonella newport (strain SL254) GN=rplD PE=3 SV=1
[RL4_SALPA](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L4 OS=Salmonella paratyphi A (strain ATCC 9150 / SARB42) GN=rplD PE=3 SV=1
[RL4_SALPC](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L4 OS=Salmonella paratyphi C (strain RKS4594) GN=rplD PE=3 SV=1
[RL4_SALPK](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L4 OS=Salmonella paratyphi A (strain AKU_12601) GN=rplD PE=3 SV=1
[RL4_SALSV](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L4 OS=Salmonella schwarzengrund (strain CVM19633) GN=rplD PE=3 SV=1
[RL4_SALTI](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L4 OS=Salmonella typhi GN=rplD PE=3 SV=1
[RL4_SALTY](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L4 OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=rplD PE=1 SV=1
[RL4_SHIB3](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L4 OS=Shigella boydii serotype 18 (strain CDC 3083-94 / BS512) GN=rplD PE=3 SV=1
[RL4_SHIB5](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L4 OS=Shigella boydii serotype 4 (strain Sb227) GN=rplD PE=3 SV=1
[RL4_SHIDS](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L4 OS=Shigella dysenteriae serotype 1 (strain Sd197) GN=rplD PE=3 SV=1
[RL4_SHIF8](#) Mass: 22064 Score: 37 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L4 OS=Shigella flexneri serotype 5b (strain 8401) GN=rplD PE=3 SV=1
[RL4_SHIFL](#) Mass: 22064 Score: 37 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L4 OS=Shigella flexneri GN=rplD PE=3 SV=1
[RL4_SHISS](#) Mass: 22073 Score: 37 Matches: 1(1) Sequences: 1(1)

50S ribosomal protein L4 OS=Shigella sonnei (strain Ss046) GN=rplD PE=3 SV=1

38. [YPT1_YEAST](#) Mass: 23200 Score: 35 Matches: 1(1) Sequences: 1(1) emPAI: 0.16
 GTP-binding protein YPT1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=YPT1 PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 136	441.7505	881.4864	881.4858	0.71	0	35	0.0081	1	U	R.YATSTVLK.L

39. [REF_HEVBR](#) Mass: 14713 Score: 33 Matches: 2(1) Sequences: 2(1) emPAI: 0.25
 Rubber elongation factor protein OS=Hevea brasiliensis PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 328	523.2936	1044.5726	1044.5716	0.99	0	23	0.47	1	U	K.NVAVPLYNR.F
<input checked="" type="checkbox"/> 1172	803.4460	1604.8774	1604.8774	0.04	0	33	0.02	1	U	K.SGPLQPGVDIIEGPK.N

40. [YCEA_ECOBW](#) Mass: 39756 Score: 33 Matches: 1(1) Sequences: 1(1) emPAI: 0.09
 UPF0176 protein YceA OS=Escherichia coli (strain K12 / MC4100 / BW2952) GN=yceA PE=3 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 1103	782.4138	1562.8130	1562.8093	2.42	0	33	0.034	1	U	R.AQLYAFDPALEGLR.L

Proteins matching the same set of peptides:

[YCEA_ECODH](#) Mass: 39756 Score: 33 Matches: 1(1) Sequences: 1(1)
 UPF0176 protein YceA OS=Escherichia coli (strain K12 / DH10B) GN=yceA PE=3 SV=1

[YCEA_ECOLI](#) Mass: 39756 Score: 33 Matches: 1(1) Sequences: 1(1)
 UPF0176 protein YceA OS=Escherichia coli (strain K12) GN=yceA PE=2 SV=2

[YCEA_ECOLU](#) Mass: 39711 Score: 33 Matches: 1(1) Sequences: 1(1)
 UPF0176 protein YceA OS=Escherichia coli O17:K52:H18 (strain UMN026 / ExPEC) GN=yceA PE=3 SV=1

[YCEA_ECOSM](#) Mass: 39724 Score: 33 Matches: 1(1) Sequences: 1(1)
 UPF0176 protein YceA OS=Escherichia coli (strain SMS-3-5 / SECEC) GN=yceA PE=3 SV=1

[YCEA_SHIDS](#) Mass: 39726 Score: 33 Matches: 1(1) Sequences: 1(1)
 UPF0176 protein YceA OS=Shigella dysenteriae serotype 1 (strain Sd197) GN=yceA PE=3 SV=1

[YCEA_SHIFL](#) Mass: 39710 Score: 33 Matches: 1(1) Sequences: 1(1)
 UPF0176 protein YceA OS=Shigella flexneri GN=yceA PE=3 SV=4

[YCEA_SHISS](#) Mass: 39738 Score: 33 Matches: 1(1) Sequences: 1(1)
 UPF0176 protein YceA OS=Shigella sonnei (strain Ss046) GN=yceA PE=3 SV=1

[YCEA_ECOK1](#) Mass: 39710 Score: 33 Matches: 1(1) Sequences: 1(1)
 UPF0176 protein YceA OS=Escherichia coli O1:K1 / APEC GN=yceA PE=3 SV=1

[YCEA_ECOL5](#) Mass: 39710 Score: 33 Matches: 1(1) Sequences: 1(1)
 UPF0176 protein YceA OS=Escherichia coli O6:K15:H31 (strain 536 / UPEC) GN=yceA PE=3 SV=1

[YCEA_ECOL6](#) Mass: 39710 Score: 33 Matches: 1(1) Sequences: 1(1)
 UPF0176 protein YceA OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) GN=yceA PE=3 SV=2

[YCEA_ECO7I](#) Mass: 39710 Score: 33 Matches: 1(1) Sequences: 1(1)

UPF0176 protein YceA OS=Escherichia coli O7:K1 (strain IAI39 / ExPEC) GN=yceA PE=3 SV=1
[YCEA_ECO8A](#) Mass: 39710 Score: 33 Matches: 1(1) Sequences: 1(1)
 UPF0176 protein YceA OS=Escherichia coli O8 (strain IAI1) GN=yceA PE=3 SV=1
[YCEA_SHIF8](#) Mass: 39710 Score: 33 Matches: 1(1) Sequences: 1(1)
 UPF0176 protein YceA OS=Shigella flexneri serotype 5b (strain 8401) GN=yceA PE=3 SV=1
[YCEA_ECO24](#) Mass: 39710 Score: 33 Matches: 1(1) Sequences: 1(1)
 UPF0176 protein YceA OS=Escherichia coli O139:H28 (strain E24377A / ETEC) GN=yceA PE=3 SV=1
[YCEA_ECO27](#) Mass: 39769 Score: 33 Matches: 1(1) Sequences: 1(1)
 UPF0176 protein YceA OS=Escherichia coli O127:H6 (strain E2348/69 / EPEC) GN=yceA PE=3 SV=1
[YCEA_ECO45](#) Mass: 39710 Score: 33 Matches: 1(1) Sequences: 1(1)
 UPF0176 protein YceA OS=Escherichia coli O45:K1 (strain S88 / ExPEC) GN=yceA PE=3 SV=1
[YCEA_ECO55](#) Mass: 39710 Score: 33 Matches: 1(1) Sequences: 1(1)
 UPF0176 protein YceA OS=Escherichia coli (strain 55989 / EAEC) GN=yceA PE=3 SV=1
[YCEA_ECO81](#) Mass: 39728 Score: 33 Matches: 1(1) Sequences: 1(1)
 UPF0176 protein YceA OS=Escherichia coli O81 (strain ED1a) GN=yceA PE=3 SV=1

41. [ALF_ECOLI](#) Mass: 39123 Score: 33 Matches: 1(1) Sequences: 1(1) emPAI: 0.09
 Fructose-bisphosphate aldolase class 2 OS=Escherichia coli (strain K12) GN=fbaA PE=1 SV=2
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 619	616.8295	1231.6444	1231.6448	-0.32	0	33	0.048	1	U	K.AFQELNAIDVL.-

Proteins matching the same set of peptides:

[ALF_SHIFL](#) Mass: 39123 Score: 33 Matches: 1(1) Sequences: 1(1)
 Fructose-bisphosphate aldolase class 2 OS=Shigella flexneri GN=fbaA PE=3 SV=2
[ALF_ECO57](#) Mass: 39123 Score: 33 Matches: 1(1) Sequences: 1(1)
 Fructose-bisphosphate aldolase class 2 OS=Escherichia coli O157:H7 GN=fbaA PE=3 SV=2

42. [MDH_STRGG](#) Mass: 34541 Score: 32 Matches: 1(1) Sequences: 1(1) emPAI: 0.10
 Malate dehydrogenase OS=Streptomyces griseus subsp. griseus (strain JCM 4626 / NBRC 13350) GN=mdh PE=3 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 252	495.2850	988.5554	988.5553	0.15	1	32	0.039	1	U	K.TGAAVSDIKK.L

43. [GSA2_STACT](#) Mass: 46849 Score: 32 Matches: 1(1) Sequences: 1(1) emPAI: 0.08
 Glutamate-1-semialdehyde 2,1-aminomutase 2 OS=Staphylococcus carnosus (strain TM300) GN=hemL2 PE=3 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 22	379.2278	756.4410	756.4381	3.86	0	32	0.028	1	U	R.EAIPSLK.K

44. [DACA_ECOLI](#) Mass: 44416 Score: 32 Matches: 1(1) Sequences: 1(1) emPAI: 0.08

D-alanyl-D-alanine carboxypeptidase DacA OS=Escherichia coli (strain K12) GN=dacA PE=1 SV=1

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 398	547.7979	1093.5812	1093.5808	0.41	0	32	0.021	1	U	R.FFETVNPLK.V

Proteins matching the same set of peptides:

[DACA_ECOL6](#) Mass: 44416 Score: 32 Matches: 1(1) Sequences: 1(1)

D-alanyl-D-alanine carboxypeptidase DacA OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) GN=dacA PE=3 SV=1

[DACA_ECO57](#) Mass: 44416 Score: 32 Matches: 1(1) Sequences: 1(1)

D-alanyl-D-alanine carboxypeptidase DacA OS=Escherichia coli O157:H7 GN=dacA PE=3 SV=1

45. [MQNA_THET8](#) Mass: 30434 Score: 31 Matches: 1(1) Sequences: 1(1) emPAI: 0.12

Chorismate dehydratase OS=Thermus thermophilus (strain HB8 / ATCC 27634 / DSM 579) GN=mqna PE=1 SV=1

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 129	437.7165	873.4184	873.4192	-0.83	0	31	0.041	1	U	R.EVAEAEAR.R

46. [PSD3_HUMAN](#) Mass: 115962 Score: 30 Matches: 1(1) Sequences: 1(1) emPAI: 0.03

PH and SEC7 domain-containing protein 3 OS=Homo sapiens GN=PSD3 PE=1 SV=2

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 315	516.3093	1030.6040	1030.6022	1.75	0	30	0.039	1	U	R.IISGTLQATK.V

47. [RBSA_BACLD](#) Mass: 54523 Score: 29 Matches: 1(1) Sequences: 1(1) emPAI: 0.07

Ribose import ATP-binding protein RbsA OS=Bacillus licheniformis (strain DSM 13 / ATCC 14580) GN=rbsA PE=3 SV=1

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 31	385.7314	769.4482	769.4487	-0.53	0	29	0.011	1	U	K.WIGIGPK.V

Proteins matching the same set of peptides:

[RBSA_BACSU](#) Mass: 54498 Score: 29 Matches: 1(1) Sequences: 1(1)

Ribose import ATP-binding protein RbsA OS=Bacillus subtilis (strain 168) GN=rbsA PE=3 SV=2

48. [GH312_ORYSJ](#) Mass: 66618 Score: 29 Matches: 1(1) Sequences: 1(1) emPAI: 0.05

Probable indole-3-acetic acid-amido synthetase GH3.12 OS=Oryza sativa subsp. japonica GN=GH3.12 PE=2 SV=1

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 605	607.2849	1212.5552	1212.5523	2.40	0	29	0.051	1	U	R.AFGADAGYAQSR.K

49. [RS12_ALCBS](#) Mass: 13764 Score: 26 Matches: 1(0) Sequences: 1(0)
 30S ribosomal protein S12 OS=Alcanivorax borkumensis (strain SK2 / ATCC 700651 / DSM 11573) GN=rpsL PE=3 SV=1
 Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide	
<input checked="" type="checkbox"/>	147	450.7668	899.5190	899.5189	0.21	0	26	0.34	1	U	M.ATVNQLVR.K

Proteins matching the same set of peptides:

[RS12_BUCA5](#) Mass: 13793 Score: 26 Matches: 1(0) Sequences: 1(0)
 30S ribosomal protein S12 OS=Buchnera aphidicola subsp. Acyrthosiphon pisum (strain 5A) GN=rpsL PE=3 SV=1

[RS12_BUCAI](#) Mass: 13793 Score: 26 Matches: 1(0) Sequences: 1(0)
 30S ribosomal protein S12 OS=Buchnera aphidicola subsp. Acyrthosiphon pisum (strain APS) GN=rpsL PE=3 SV=1

[RS12_BUCAP](#) Mass: 13767 Score: 26 Matches: 1(0) Sequences: 1(0)
 30S ribosomal protein S12 OS=Buchnera aphidicola subsp. Schizaphis graminum (strain Sg) GN=rpsL PE=3 SV=1

[RS12_BUCAT](#) Mass: 13793 Score: 26 Matches: 1(0) Sequences: 1(0)
 30S ribosomal protein S12 OS=Buchnera aphidicola subsp. Acyrthosiphon pisum (strain Tuc7) GN=rpsL PE=3 SV=1

[RS12_BUCBP](#) Mass: 13733 Score: 26 Matches: 1(0) Sequences: 1(0)
 30S ribosomal protein S12 OS=Buchnera aphidicola subsp. Baizongia pistaciae (strain Bp) GN=rpsL PE=3 SV=1

[RS12_ECO24](#) Mass: 13728 Score: 26 Matches: 1(0) Sequences: 1(0)
 30S ribosomal protein S12 OS=Escherichia coli O139:H28 (strain E24377A / ETEC) GN=rpsL PE=3 SV=1

[RS12_ECO27](#) Mass: 13728 Score: 26 Matches: 1(0) Sequences: 1(0)
 30S ribosomal protein S12 OS=Escherichia coli O127:H6 (strain E2348/69 / EPEC) GN=rpsL PE=3 SV=1

[RS12_ECO45](#) Mass: 13728 Score: 26 Matches: 1(0) Sequences: 1(0)
 30S ribosomal protein S12 OS=Escherichia coli O45:K1 (strain S88 / ExPEC) GN=rpsL PE=3 SV=1

[RS12_ECO55](#) Mass: 13728 Score: 26 Matches: 1(0) Sequences: 1(0)
 30S ribosomal protein S12 OS=Escherichia coli (strain 55989 / EAEC) GN=rpsL PE=3 SV=1

[RS12_ECO57](#) Mass: 13728 Score: 26 Matches: 1(0) Sequences: 1(0)
 30S ribosomal protein S12 OS=Escherichia coli O157:H7 GN=rpsL PE=3 SV=2

[RS12_ECO5E](#) Mass: 13728 Score: 26 Matches: 1(0) Sequences: 1(0)
 30S ribosomal protein S12 OS=Escherichia coli O157:H7 (strain EC4115 / EHEC) GN=rpsL PE=3 SV=1

[RS12_ECO7I](#) Mass: 13728 Score: 26 Matches: 1(0) Sequences: 1(0)
 30S ribosomal protein S12 OS=Escherichia coli O7:K1 (strain IAI39 / ExPEC) GN=rpsL PE=3 SV=1

[RS12_ECO81](#) Mass: 13728 Score: 26 Matches: 1(0) Sequences: 1(0)
 30S ribosomal protein S12 OS=Escherichia coli O81 (strain ED1a) GN=rpsL PE=3 SV=1

[RS12_ECO8A](#) Mass: 13728 Score: 26 Matches: 1(0) Sequences: 1(0)
 30S ribosomal protein S12 OS=Escherichia coli O8 (strain IAI1) GN=rpsL PE=3 SV=1

[RS12_ECOBW](#) Mass: 13757 Score: 26 Matches: 1(0) Sequences: 1(0)
 30S ribosomal protein S12 OS=Escherichia coli (strain K12 / MC4100 / BW2952) GN=rpsL PE=3 SV=1

[RS12_ECOHS](#) Mass: 13728 Score: 26 Matches: 1(0) Sequences: 1(0)
 30S ribosomal protein S12 OS=Escherichia coli O9:H4 (strain HS) GN=rpsL PE=3 SV=1

[RS12_ECOK1](#) Mass: 13728 Score: 26 Matches: 1(0) Sequences: 1(0)
 30S ribosomal protein S12 OS=Escherichia coli O1:K1 / APEC GN=rpsL PE=3 SV=1

[RS12_ECOL5](#) Mass: 13757 Score: 26 Matches: 1(0) Sequences: 1(0)
 30S ribosomal protein S12 OS=Escherichia coli O6:K15:H31 (strain 536 / UPEC) GN=rpsL PE=3 SV=1

[RS12_EC0L6](#) **Mass:** 13728 **Score:** 26 **Matches:** 1(0) **Sequences:** 1(0)
30S ribosomal protein S12 OS=Escherichia coli O6:H1 (strain CFT073 / ATCC 700928 / UPEC) GN=rpsL PE=3 SV=2

[RS12_EC0LC](#) **Mass:** 13728 **Score:** 26 **Matches:** 1(0) **Sequences:** 1(0)
30S ribosomal protein S12 OS=Escherichia coli (strain ATCC 8739 / DSM 1576 / Crooks) GN=rpsL PE=3 SV=1

[RS12_EC0LI](#) **Mass:** 13728 **Score:** 26 **Matches:** 1(0) **Sequences:** 1(0)
30S ribosomal protein S12 OS=Escherichia coli (strain K12) GN=rpsL PE=1 SV=2

[RS12_EC0LU](#) **Mass:** 13728 **Score:** 26 **Matches:** 1(0) **Sequences:** 1(0)
30S ribosomal protein S12 OS=Escherichia coli O17:K52:H18 (strain UMN026 / ExPEC) GN=rpsL PE=3 SV=1

[RS12_EC0SE](#) **Mass:** 13728 **Score:** 26 **Matches:** 1(0) **Sequences:** 1(0)
30S ribosomal protein S12 OS=Escherichia coli (strain SE11) GN=rpsL PE=3 SV=1

[RS12_EC0SM](#) **Mass:** 13728 **Score:** 26 **Matches:** 1(0) **Sequences:** 1(0)
30S ribosomal protein S12 OS=Escherichia coli (strain SMS-3-5 / SECEC) GN=rpsL PE=3 SV=1

[RS12_EC0UT](#) **Mass:** 13728 **Score:** 26 **Matches:** 1(0) **Sequences:** 1(0)
30S ribosomal protein S12 OS=Escherichia coli (strain UTI89 / UPEC) GN=rpsL PE=3 SV=2

[RS12_ENT38](#) **Mass:** 13728 **Score:** 26 **Matches:** 1(0) **Sequences:** 1(0)
30S ribosomal protein S12 OS=Enterobacter sp. (strain 638) GN=rpsL PE=3 SV=1

[RS12_ERWAM](#) **Mass:** 13688 **Score:** 26 **Matches:** 1(0) **Sequences:** 1(0)
30S ribosomal protein S12 OS=Erwinia amylovora GN=rpsL PE=3 SV=1

[RS12_ERWT9](#) **Mass:** 13729 **Score:** 26 **Matches:** 1(0) **Sequences:** 1(0)
30S ribosomal protein S12 OS=Erwinia tasmaniensis (strain DSM 17950 / Et1/99) GN=rpsL PE=3 SV=1

[RS12_ESCF3](#) **Mass:** 13728 **Score:** 26 **Matches:** 1(0) **Sequences:** 1(0)
30S ribosomal protein S12 OS=Escherichia fergusonii (strain ATCC 35469 / DSM 13698 / CDC 0568-73) GN=rpsL PE=3 SV=1

[RS12_HALHL](#) **Mass:** 13773 **Score:** 26 **Matches:** 1(0) **Sequences:** 1(0)
30S ribosomal protein S12 OS=Halorhodospira halophila (strain DSM 244 / SL1) GN=rpsL PE=3 SV=1

[RS12_IDILO](#) **Mass:** 13708 **Score:** 26 **Matches:** 1(0) **Sequences:** 1(0)
30S ribosomal protein S12 OS=Idiomarina loihiensis (strain ATCC BAA-735 / DSM 15497 / L2-TR) GN=rpsL PE=3 SV=1

[RS12_MARMS](#) **Mass:** 13858 **Score:** 26 **Matches:** 1(0) **Sequences:** 1(0)
30S ribosomal protein S12 OS=Marinomonas sp. (strain MWYL1) GN=rpsL PE=3 SV=1

[RS12_PSEA6](#) **Mass:** 13648 **Score:** 26 **Matches:** 1(0) **Sequences:** 1(0)
30S ribosomal protein S12 OS=Pseudoalteromonas atlantica (strain T6c / ATCC BAA-1087) GN=rpsL PE=3 SV=1

[RS12_SALA4](#) **Mass:** 13728 **Score:** 26 **Matches:** 1(0) **Sequences:** 1(0)
30S ribosomal protein S12 OS=Salmonella agona (strain SL483) GN=rpsL PE=3 SV=1

[RS12_SALCH](#) **Mass:** 13728 **Score:** 26 **Matches:** 1(0) **Sequences:** 1(0)
30S ribosomal protein S12 OS=Salmonella choleraesuis (strain SC-B67) GN=rpsL PE=3 SV=2

[RS12_SALDC](#) **Mass:** 13728 **Score:** 26 **Matches:** 1(0) **Sequences:** 1(0)
30S ribosomal protein S12 OS=Salmonella dublin (strain CT_02021853) GN=rpsL PE=3 SV=1

[RS12_SALEP](#) **Mass:** 13728 **Score:** 26 **Matches:** 1(0) **Sequences:** 1(0)
30S ribosomal protein S12 OS=Salmonella enteritidis PT4 (strain P125109) GN=rpsL PE=3 SV=1

[RS12_SALG2](#) **Mass:** 13728 **Score:** 26 **Matches:** 1(0) **Sequences:** 1(0)
30S ribosomal protein S12 OS=Salmonella gallinarum (strain 287/91 / NCTC 13346) GN=rpsL PE=3 SV=1

[RS12_SALHS](#) **Mass:** 13728 **Score:** 26 **Matches:** 1(0) **Sequences:** 1(0)
30S ribosomal protein S12 OS=Salmonella heidelberg (strain SL476) GN=rpsL PE=3 SV=1

[RS12_SALNS](#) **Mass:** 13728 **Score:** 26 **Matches:** 1(0) **Sequences:** 1(0)
30S ribosomal protein S12 OS=Salmonella newport (strain SL254) GN=rpsL PE=3 SV=1

[RS12_SALPA](#) **Mass:** 13728 **Score:** 26 **Matches:** 1(0) **Sequences:** 1(0)
30S ribosomal protein S12 OS=Salmonella paratyphi A (strain ATCC 9150 / SARB42) GN=rpsL PE=3 SV=3

RS12_SALPC	Mass: 13728	Score: 26	Matches: 1(0)	Sequences: 1(0)
30S ribosomal protein S12 OS=Salmonella paratyphi C (strain RKS4594) GN=rpsL PE=3 SV=1				
RS12_SALPK	Mass: 13728	Score: 26	Matches: 1(0)	Sequences: 1(0)
30S ribosomal protein S12 OS=Salmonella paratyphi A (strain AKU_12601) GN=rpsL PE=3 SV=1				
RS12_SALSV	Mass: 13728	Score: 26	Matches: 1(0)	Sequences: 1(0)
30S ribosomal protein S12 OS=Salmonella schwarzengrund (strain CVM19633) GN=rpsL PE=3 SV=1				
RS12_SALTI	Mass: 13728	Score: 26	Matches: 1(0)	Sequences: 1(0)
30S ribosomal protein S12 OS=Salmonella typhi GN=rpsL PE=3 SV=2				
RS12_SALTY	Mass: 13728	Score: 26	Matches: 1(0)	Sequences: 1(0)
30S ribosomal protein S12 OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=rpsL PE=3 SV=2				
RS12_SHEAM	Mass: 13621	Score: 26	Matches: 1(0)	Sequences: 1(0)
30S ribosomal protein S12 OS=Shewanella amazonensis (strain ATCC BAA-1098 / SB2B) GN=rpsL PE=3 SV=1				
RS12_SHEB2	Mass: 13655	Score: 26	Matches: 1(0)	Sequences: 1(0)
30S ribosomal protein S12 OS=Shewanella baltica (strain OS223) GN=rpsL PE=3 SV=1				
RS12_SHEB8	Mass: 13655	Score: 26	Matches: 1(0)	Sequences: 1(0)
30S ribosomal protein S12 OS=Shewanella baltica (strain OS185) GN=rpsL PE=3 SV=1				
RS12_SHEB9	Mass: 13655	Score: 26	Matches: 1(0)	Sequences: 1(0)
30S ribosomal protein S12 OS=Shewanella baltica (strain OS195) GN=rpsL PE=3 SV=1				
RS12_SHEDO	Mass: 13652	Score: 26	Matches: 1(0)	Sequences: 1(0)
30S ribosomal protein S12 OS=Shewanella denitrificans (strain OS217 / ATCC BAA-1090 / DSM 15013) GN=rpsL PE=3 SV=1				
RS12_SHEFN	Mass: 13655	Score: 26	Matches: 1(0)	Sequences: 1(0)
30S ribosomal protein S12 OS=Shewanella frigidimarina (strain NCIMB 400) GN=rpsL PE=3 SV=1				
RS12_SHEHH	Mass: 13596	Score: 26	Matches: 1(0)	Sequences: 1(0)
30S ribosomal protein S12 OS=Shewanella halifaxensis (strain HAW-EB4) GN=rpsL PE=3 SV=1				
RS12_SHELP	Mass: 13653	Score: 26	Matches: 1(0)	Sequences: 1(0)
30S ribosomal protein S12 OS=Shewanella loihica (strain ATCC BAA-1088 / PV-4) GN=rpsL PE=3 SV=1				
RS12_SHEON	Mass: 13641	Score: 26	Matches: 1(0)	Sequences: 1(0)
30S ribosomal protein S12 OS=Shewanella oneidensis (strain MR-1) GN=rpsL PE=3 SV=1				
RS12_SHEPA	Mass: 13596	Score: 26	Matches: 1(0)	Sequences: 1(0)
30S ribosomal protein S12 OS=Shewanella pealeana (strain ATCC 700345 / ANG-SQ1) GN=rpsL PE=3 SV=1				
RS12_SHEPC	Mass: 13597	Score: 26	Matches: 1(0)	Sequences: 1(0)
30S ribosomal protein S12 OS=Shewanella putrefaciens (strain CN-32 / ATCC BAA-453) GN=rpsL PE=3 SV=1				
RS12_SHEPW	Mass: 13639	Score: 26	Matches: 1(0)	Sequences: 1(0)
30S ribosomal protein S12 OS=Shewanella piezotolerans (strain WP3 / JCM 13877) GN=rpsL PE=3 SV=1				
RS12_SHESA	Mass: 13638	Score: 26	Matches: 1(0)	Sequences: 1(0)
30S ribosomal protein S12 OS=Shewanella sp. (strain ANA-3) GN=rpsL PE=3 SV=1				
RS12_SHESH	Mass: 13640	Score: 26	Matches: 1(0)	Sequences: 1(0)
30S ribosomal protein S12 OS=Shewanella sediminis (strain HAW-EB3) GN=rpsL PE=3 SV=1				
RS12_SHESM	Mass: 13641	Score: 26	Matches: 1(0)	Sequences: 1(0)
30S ribosomal protein S12 OS=Shewanella sp. (strain MR-4) GN=rpsL PE=3 SV=1				
RS12_SHESR	Mass: 13641	Score: 26	Matches: 1(0)	Sequences: 1(0)
30S ribosomal protein S12 OS=Shewanella sp. (strain MR-7) GN=rpsL PE=3 SV=1				
RS12_SHESW	Mass: 13597	Score: 26	Matches: 1(0)	Sequences: 1(0)
30S ribosomal protein S12 OS=Shewanella sp. (strain W3-18-1) GN=rpsL PE=3 SV=1				
RS12_SHEWM	Mass: 13639	Score: 26	Matches: 1(0)	Sequences: 1(0)
30S ribosomal protein S12 OS=Shewanella woodyi (strain ATCC 51908 / MS32) GN=rpsL PE=3 SV=1				

[RS12_SHIB3](#) Mass: 13728 Score: 26 Matches: 1(0) Sequences: 1(0)
 30S ribosomal protein S12 OS=Shigella boydii serotype 18 (strain CDC 3083-94 / BS512) GN=rpsL PE=3 SV=1

[RS12_SHIBS](#) Mass: 13728 Score: 26 Matches: 1(0) Sequences: 1(0)
 30S ribosomal protein S12 OS=Shigella boydii serotype 4 (strain Sb227) GN=rpsL PE=3 SV=1

[RS12_SHIDS](#) Mass: 13728 Score: 26 Matches: 1(0) Sequences: 1(0)
 30S ribosomal protein S12 OS=Shigella dysenteriae serotype 1 (strain Sd197) GN=rpsL PE=3 SV=1

[RS12_SHIF8](#) Mass: 13728 Score: 26 Matches: 1(0) Sequences: 1(0)
 30S ribosomal protein S12 OS=Shigella flexneri serotype 5b (strain 8401) GN=rpsL PE=3 SV=1

[RS12_SHIFL](#) Mass: 13728 Score: 26 Matches: 1(0) Sequences: 1(0)
 30S ribosomal protein S12 OS=Shigella flexneri GN=rpsL PE=3 SV=2

[RS12_SHISS](#) Mass: 13728 Score: 26 Matches: 1(0) Sequences: 1(0)
 30S ribosomal protein S12 OS=Shigella sonnei (strain Ss046) GN=rpsL PE=3 SV=1

50. [RL24_AERS4](#) Mass: 11292 Score: 25 Matches: 1(1) Sequences: 1(1) emPAI: 0.34
 50S ribosomal protein L24 OS=Aeromonas salmonicida (strain A449) GN=rplX PE=3 SV=1

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 379	542.3429	1082.6712	1082.6699	1.21	0	25	0.058	1	U	K.VLVEGINLVK.K

Proteins matching the same set of peptides:

[RL24_BACP2](#) Mass: 11098 Score: 25 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L24 OS=Bacillus pumilus (strain SAFR-032) GN=rplX PE=3 SV=1

[RL24_BREEN](#) Mass: 11235 Score: 25 Matches: 1(1) Sequences: 1(1)
 50S ribosomal protein L24 OS=Brevibacillus brevis (strain 47 / JCM 6285 / NBRC 100599) GN=rplX PE=3 SV=1

51. [AAT_ECOLI](#) Mass: 43546 Score: 25 Matches: 1(0) Sequences: 1(0)
 Aspartate aminotransferase OS=Escherichia coli (strain K12) GN=aspC PE=1 SV=1

Check to include this hit in error tolerant search or archive report

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 469	565.3024	1128.5902	1128.5887	1.33	0	25	0.21	1	U	R.TAQTGGTGALR.V

Proteins matching the same set of peptides:

[AAT_SALTI](#) Mass: 43480 Score: 25 Matches: 1(0) Sequences: 1(0)
 Aspartate aminotransferase OS=Salmonella typhi GN=aspC PE=3 SV=2

[AAT_SALTY](#) Mass: 43494 Score: 25 Matches: 1(0) Sequences: 1(0)
 Aspartate aminotransferase OS=Salmonella typhimurium (strain LT2 / SGSC1412 / ATCC 700720) GN=aspC PE=3 SV=1

Peptide matches not assigned to protein hits: (no details means no match)

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Unique	Peptide
<input checked="" type="checkbox"/> 46	394.2369	786.4592	786.4599	-0.87	0	36	0.071	1		NISLVNK
<input checked="" type="checkbox"/> 150	451.2581	900.5016	900.5029	-1.36	0	33	0.1	1		AVVESIQR
<input checked="" type="checkbox"/> 99	422.7426	843.4706	843.4702	0.57	0	32	0.073	1		LAEVEVGK

<input checked="" type="checkbox"/>	673	639.8333	1277.6520	1277.6503	1.36	0	30	0.088	1	VIEIYGPRESSGK
<input checked="" type="checkbox"/>	360	533.7856	1065.5566	1065.5529	3.56	0	29	0.098	1	QMTLDAPLK
<input checked="" type="checkbox"/>	312	516.2708	1030.5270	1030.5295	-2.35	1	29	0.15	1	ESDASKIPGK
<input checked="" type="checkbox"/>	199	468.2638	934.5130	934.5124	0.72	0	28	0.17	1	YAGVGDIIK
<input checked="" type="checkbox"/>	155	452.2300	902.4454	902.4458	-0.34	0	26	0.22	1	VGASDDLAR
<input checked="" type="checkbox"/>	773	666.8542	1331.6938	1331.6933	0.44	0	25	0.21	1	DLADLQGSVSVTK
<input checked="" type="checkbox"/>	220	479.2471	956.4796	956.4815	-1.90	0	25	0.099	1	EGEEVIPGK
<input checked="" type="checkbox"/>	90	416.2506	830.4866	830.4861	0.61	1	25	0.47	1	LKTDNLK
<input checked="" type="checkbox"/>	1044	766.3898	1530.7650	1530.7613	2.45	1	24	0.22	1	SSLSYFGGVCSRIR
<input checked="" type="checkbox"/>	10	362.7029	723.3912	723.3915	-0.38	0	24	0.15	1	VSISYR
<input checked="" type="checkbox"/>	116	425.7177	849.4208	849.4201	0.89	0	24	0.32	1	VVIGMCGR + Oxidation (M)
<input checked="" type="checkbox"/>	1236	821.9264	1641.8382	1641.8396	-0.81	1	24	0.22	1	ECNIPDERIIDVVK
<input checked="" type="checkbox"/>	1336	853.4332	1704.8518	1704.8570	-3.01	0	24	0.3	1	FNEQEINLSLEELK
<input checked="" type="checkbox"/>	922	723.8563	1445.6980	1445.6998	-1.20	1	24	0.25	1	DISDIEGKDGIR
<input checked="" type="checkbox"/>	59	402.2350	802.4554	802.4548	0.75	0	23	0.61	1	SSVEILR
<input checked="" type="checkbox"/>	269	500.7676	999.5206	999.5237	-3.02	1	23	0.24	1	EDDKVLP GK
<input checked="" type="checkbox"/>	1063	771.8762	1541.7378	1541.7371	0.51	0	22	0.29	1	ECVAQGICFAFIK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	831	686.8762	1371.7378	1371.7432	-3.88	0	22	0.4	1	ILNQTLPEVMAK + Oxidation (M)
<input checked="" type="checkbox"/>	178	458.7709	915.5272	915.5277	-0.49	0	22	0.34	1	ITDVEVLK
<input checked="" type="checkbox"/>	119	428.7664	855.5182	855.5178	0.55	0	22	0.5	1	IALSPSIR
<input checked="" type="checkbox"/>	815	681.3652	1360.7158	1360.7198	-2.90	1	22	0.46	1	AETVRDSIELTK
<input checked="" type="checkbox"/>	154	452.2298	902.4450	902.4457	-0.73	1	22	0.66	1	AEAE EKAR
<input checked="" type="checkbox"/>	274	503.7543	1005.4940	1005.4978	-3.78	0	22	0.69	1	SLTLADSDGK
<input checked="" type="checkbox"/>	48	395.2206	788.4266	788.4280	-1.69	0	22	0.59	1	IDVSDIK
<input checked="" type="checkbox"/>	126	436.7272	871.4398	871.4399	-0.09	0	21	0.23	1	APEITDAR
<input checked="" type="checkbox"/>	255	495.7577	989.5008	989.5038	-2.98	0	21	0.46	1	QMGMLLGPK + Oxidation (M)
<input checked="" type="checkbox"/>	565	587.2969	1172.5792	1172.5785	0.61	1	21	0.48	1	EASKGEDGKPR
<input checked="" type="checkbox"/>	1178	805.9313	1609.8480	1609.8464	1.05	1	21	0.38	1	SYATGPYARELAAIK
<input checked="" type="checkbox"/>	91	416.7422	831.4698	831.4702	-0.40	0	21	0.99	1	IDVTGISK
<input checked="" type="checkbox"/>	92	416.7425	831.4704	831.4702	0.32	0	21	1	1	IDVTGISK
<input checked="" type="checkbox"/>	49	395.2344	788.4542	788.4545	-0.30	0	21	0.44	1	IFGPVTR
<input checked="" type="checkbox"/>	277	503.7555	1005.4964	1005.4978	-1.39	0	21	0.48	1	SLTLADSDGK
<input checked="" type="checkbox"/>	1071	773.3795	1544.7444	1544.7430	0.92	1	21	0.48	1	NEEISQQKADDIR
<input checked="" type="checkbox"/>	113	423.7325	845.4504	845.4494	1.20	0	21	1	1	IDGIETAK
<input checked="" type="checkbox"/>	304	511.7526	1021.4906	1021.4936	-2.91	1	21	0.5	1	GKDLSMPMK + Oxidation (M)
<input checked="" type="checkbox"/>	646	629.3385	1256.6624	1256.6587	2.97	1	21	0.61	1	GCIIFFKSSAK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	873	702.3737	1402.7328	1402.7377	-3.49	0	20	0.62	1	VILCIGETLEEK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	791	673.8619	1345.7092	1345.7064	2.13	0	20	0.59	1	MIAILTEHYAGK
<input checked="" type="checkbox"/>	276	503.7553	1005.4960	1005.4987	-2.64	1	20	0.53	1	GKDLSMPMK
<input checked="" type="checkbox"/>	322	517.7905	1033.5664	1033.5655	0.88	0	20	0.67	1	TLTTLTQTK
<input checked="" type="checkbox"/>	1355	859.4330	1716.8514	1716.8577	-3.64	1	20	0.63	1	VIDSRPAEDGMSIRR + Oxidation (M)
<input checked="" type="checkbox"/>	340	525.2955	1048.5764	1048.5804	-3.81	0	20	0.47	1	ALETFDLISK
<input checked="" type="checkbox"/>	385	544.3214	1086.6282	1086.6285	-0.20	0	20	0.51	1	QTALVDLISK
<input checked="" type="checkbox"/>	184	464.2301	926.4456	926.4466	-1.04	0	20	0.22	1	ACAPLPCPR
<input checked="" type="checkbox"/>	257	495.7578	989.5010	989.5038	-2.78	0	20	0.59	1	QMGMLLGPK + Oxidation (M)
<input checked="" type="checkbox"/>	593	600.8530	1199.6914	1199.6914	0.01	0	20	0.79	1	IGVFPVDGGVIK

<input checked="" type="checkbox"/>	157	452.2786	902.5426	902.5437	-1.12	1	20	0.31	1	LSVELSKK
<input checked="" type="checkbox"/>	1440	888.4266	1774.8386	1774.8374	0.72	0	20	0.5	1	DGTLISEPPSDFQVDR
<input checked="" type="checkbox"/>	689	643.8527	1285.6908	1285.6878	2.40	0	20	0.76	1	QETELEGLLVR
<input checked="" type="checkbox"/>	301	511.7520	1021.4894	1021.4862	3.14	1	20	0.63	1	<u>M</u> GKNSSTPGK + Oxidation (M)
<input checked="" type="checkbox"/>	1536	949.4642	1896.9138	1896.9172	-1.79	1	20	0.57	1	ESVSLEMMEKAGITTTQK + Oxidation (M)
<input checked="" type="checkbox"/>	1006	756.8527	1511.6908	1511.6856	3.47	0	19	0.46	1	<u>M</u> DPVAMAGMLVAMK + 3 Oxidation (M)
<input checked="" type="checkbox"/>	1034	763.8786	1525.7426	1525.7412	0.92	1	19	0.77	1	EFLAFAGKSEEGNK
<input checked="" type="checkbox"/>	734	657.2844	1312.5542	1312.5531	0.86	1	19	0.15	1	RFNDSSEEDK
<input checked="" type="checkbox"/>	1459	907.9985	1813.9824	1813.9794	1.69	1	19	0.46	1	DGLLKPTCGMKISLPNK
<input checked="" type="checkbox"/>	449	557.7706	1113.5266	1113.5243	2.07	0	19	0.51	1	YQAWQSGFK
<input checked="" type="checkbox"/>	819	681.8600	1361.7054	1361.7013	3.05	0	19	0.7	1	<u>M</u> IAILLTEHYAGK + Oxidation (M)
<input checked="" type="checkbox"/>	313	516.2709	1030.5272	1030.5295	-2.15	0	19	1	1	VNSLLDENK
<input checked="" type="checkbox"/>	33	385.7603	769.5060	769.5062	-0.15	0	19	0.34	1	LGVLLQK
<input checked="" type="checkbox"/>	240	488.7495	975.4844	975.4848	-0.33	0	19	1.3	1	NGEIMWVK
<input checked="" type="checkbox"/>	486	568.8008	1135.5870	1135.5907	-3.20	1	19	0.93	1	NASIEKVMTK + Oxidation (M)
<input checked="" type="checkbox"/>	1693	708.4074	2122.2004	2122.1997	0.31	0	19	0.16	1	LLDNAAADLAAISGQKPLITK
<input checked="" type="checkbox"/>	1039	764.3777	1526.7408	1526.7398	0.66	1	19	0.59	1	YLMALAESENSRK + Oxidation (M)
<input checked="" type="checkbox"/>	89	416.2233	830.4320	830.4320	0.05	0	19	0.56	1	LSSMHK + Oxidation (M)
<input checked="" type="checkbox"/>	58	402.2310	802.4474	802.4483	-1.08	1	19	0.98	1	IDRMLR
<input checked="" type="checkbox"/>	1300	562.2757	1683.8053	1683.8039	0.83	0	19	0.63	1	AAQYVASHPGEVCPAK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	744	658.8564	1315.6982	1315.7023	-3.12	0	19	0.89	1	IVDALWELTEK
<input checked="" type="checkbox"/>	208	472.7614	943.5082	943.5087	-0.46	0	19	1.7	1	IVIDSQNR
<input checked="" type="checkbox"/>	235	487.7598	973.5050	973.5055	-0.49	0	19	1.8	1	<u>M</u> GGWLLPGK + Oxidation (M)
<input checked="" type="checkbox"/>	162	454.7396	907.4646	907.4651	-0.48	1	19	1.2	1	GKSVVEIF
<input checked="" type="checkbox"/>	772	666.8271	1331.6396	1331.6364	2.44	1	19	0.72	1	<u>M</u> RSNNNNPLTR + Oxidation (M)
<input checked="" type="checkbox"/>	1616	1020.4980	2038.9814	2038.9782	1.59	0	19	0.9	1	SAFSAPTSALFSASPMAQPR + Oxidation (M)
<input checked="" type="checkbox"/>	603	606.8226	1211.6306	1211.6332	-2.13	0	18	0.72	1	MPINQPSGQIK
<input checked="" type="checkbox"/>	346	529.2780	1056.5414	1056.5451	-3.49	0	18	0.71	1	DGQELTLGPK
<input checked="" type="checkbox"/>	253	495.7574	989.5002	989.4964	3.89	1	18	1.7	1	DKGIICER + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	305	511.7529	1021.4912	1021.4902	0.98	0	18	0.8	1	<u>M</u> GIPNEFAK + Oxidation (M)
<input checked="" type="checkbox"/>	517	575.7742	1149.5338	1149.5336	0.26	1	18	0.92	1	DSKLEMDNAK
<input checked="" type="checkbox"/>	1604	680.6669	2038.9789	2038.9782	0.32	0	18	0.91	1	SAFSAPTSALFSASPMAQPR + Oxidation (M)
<input checked="" type="checkbox"/>	284	508.7654	1015.5162	1015.5186	-2.30	0	18	1.2	1	DGQIEVEVK
<input checked="" type="checkbox"/>	394	364.8806	1091.6200	1091.6199	0.02	0	18	0.67	1	AAVHNLLAQR
<input checked="" type="checkbox"/>	233	486.7521	971.4896	971.4924	-2.79	0	18	0.87	1	GLEEKPGDK
<input checked="" type="checkbox"/>	901	476.2566	1425.7480	1425.7464	1.14	0	18	0.81	1	LVDIEQVSSTHAK
<input checked="" type="checkbox"/>	1099	781.3776	1560.7406	1560.7379	1.73	0	18	0.84	1	TGEQLSQESAENIR
<input checked="" type="checkbox"/>	1088	779.3815	1556.7484	1556.7439	2.90	0	18	0.95	1	KPHSVSNGSPVCMK
<input checked="" type="checkbox"/>	1966	1041.2020	3120.5842	3120.5840	0.07	1	18	0.6	1	NDLNSLVNKYNQINSNTVLFPAQSGSGVK
<input checked="" type="checkbox"/>	402	551.7620	1101.5094	1101.5091	0.33	0	18	0.56	1	SQFTTAYER
<input checked="" type="checkbox"/>	211	473.2355	944.4564	944.4563	0.17	0	17	0.86	1	EGALEEAAR
<input checked="" type="checkbox"/>	1747	1091.0520	2180.0894	2180.0943	-2.20	1	17	1.1	1	KGPFWVGDFLIDSEWVSAK
<input checked="" type="checkbox"/>	71	408.2259	814.4372	814.4371	0.20	0	17	0.6	1	MALIDPR
<input checked="" type="checkbox"/>	533	580.3070	1158.5994	1158.6033	-3.33	0	17	1.6	1	VLNETIEWR
<input checked="" type="checkbox"/>	1603	680.6666	2038.9780	2038.9782	-0.12	0	17	1.2	1	SAFSAPTSALFSASPMAQPR + Oxidation (M)
<input checked="" type="checkbox"/>	577	594.7822	1187.5498	1187.5506	-0.61	0	17	0.69	1	DGGAHFACIR

<input checked="" type="checkbox"/>	803	678.3624	1354.7102	1354.7092	0.75	1	17	1.1	1	LPDPKSLTNDQK
<input checked="" type="checkbox"/>	1515	935.4786	1868.9426	1868.9367	3.17	0	17	1.1	1	LNSLGLTQSTSYTDLEK
<input checked="" type="checkbox"/>	1145	530.2772	1587.8098	1587.8079	1.17	1	17	1.4	1	MGGWLLPGKDGNTVK + Oxidation (M)
<input checked="" type="checkbox"/>	195	466.7742	931.5338	931.5338	0.02	1	17	1.1	1	TLKNTDIK
<input checked="" type="checkbox"/>	859	463.9346	1388.7820	1388.7816	0.28	1	17	0.89	1	NKLPPIEIIYR
<input checked="" type="checkbox"/>	335	524.2680	1046.5214	1046.5219	-0.43	0	17	2.2	1	FPNLMSGPGK
<input checked="" type="checkbox"/>	960	740.8756	1479.7366	1479.7391	-1.68	1	17	1.4	1	WMIEEKATITSR + Oxidation (M)
<input checked="" type="checkbox"/>	451	558.2629	1114.5112	1114.5117	-0.44	0	17	0.72	1	FSGQFCEVAK
<input checked="" type="checkbox"/>	85	413.7370	825.4594	825.4596	-0.21	0	17	0.78	1	IVDTPGPK
<input checked="" type="checkbox"/>	264	498.7572	995.4998	995.4964	3.46	0	17	1.3	1	FLLDDINF
<input checked="" type="checkbox"/>	1065	772.3680	1542.7214	1542.7236	-1.37	1	17	0.97	1	SDAVSKLDGTYMEK
<input checked="" type="checkbox"/>	606	607.3143	1212.6140	1212.6098	3.48	1	17	1.4	1	DNLNPIEDKR
<input checked="" type="checkbox"/>	292	509.2642	1016.5138	1016.5138	0.02	0	16	2.2	1	DNIVDSLNR
<input checked="" type="checkbox"/>	1377	867.4299	1732.8452	1732.8488	-2.02	1	16	1.5	1	MPREQIILECTEAK + Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/>	671	638.3432	1274.6718	1274.6718	0.06	1	16	1.6	1	EKISPSTDSLAK
<input checked="" type="checkbox"/>	1312	566.2716	1695.7930	1695.7927	0.18	0	16	0.93	1	VGDLSPSTEMIEHFFR + Oxidation (M)
<input checked="" type="checkbox"/>	816	681.3682	1360.7218	1360.7272	-3.92	0	16	1.6	1	QALMLTVLETDK
<input checked="" type="checkbox"/>	1882	845.7419	2534.2039	2534.1997	1.65	0	16	0.91	1	IHQAAQTLQSTPPISEENNDER
<input checked="" type="checkbox"/>	388	545.2735	1088.5324	1088.5350	-2.32	0	16	2.2	1	SSSTPTLPDGGK
<input checked="" type="checkbox"/>	1107	524.2734	1569.7984	1569.7998	-0.92	0	16	1.4	1	ASAAPEELQGGTAIK
<input checked="" type="checkbox"/>	1067	772.8567	1543.6988	1543.7042	-3.46	0	16	0.82	1	YDSIDSYLSPEGAK
<input checked="" type="checkbox"/>	1185	807.9194	1613.8242	1613.8260	-1.10	0	16	1.5	1	NTLEEIAELQADIR
<input checked="" type="checkbox"/>	1032	763.3651	1524.7156	1524.7211	-3.55	1	16	1.2	1	QQMMSMRSELIR + Oxidation (M)
<input checked="" type="checkbox"/>	326	522.2720	1042.5294	1042.5295	-0.03	0	16	1.5	1	ASPLDGEAGVK
<input checked="" type="checkbox"/>	664	637.3358	1272.6570	1272.6561	0.72	0	16	2.1	1	DTVEAEAGALVAK
<input checked="" type="checkbox"/>	771	666.8270	1331.6394	1331.6405	-0.76	1	16	1.3	1	CTSRNPGIWK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	86	413.7372	825.4598	825.4596	0.31	1	16	0.92	1	KTYSSLK
<input checked="" type="checkbox"/>	349	530.3062	1058.5978	1058.5971	0.67	1	16	2.4	1	DLLKNLSEK
<input checked="" type="checkbox"/>	125	436.7272	871.4398	871.4399	-0.09	0	16	0.84	1	APEITDAR
<input checked="" type="checkbox"/>	847	691.3755	1380.7364	1380.7361	0.25	1	16	1.4	1	RTSSQYVASAIK
<input checked="" type="checkbox"/>	1244	549.6067	1645.7983	1645.7981	0.08	1	16	1.5	1	MVQDIDGLGAPGKDSK + Oxidation (M)
<input checked="" type="checkbox"/>	1127	791.8799	1581.7452	1581.7419	2.15	0	16	1.3	1	MINDDDPIVIYMK + Oxidation (M)
<input checked="" type="checkbox"/>	768	665.8650	1329.7154	1329.7140	1.11	0	16	2	1	GEIISIIGESGAGK
<input checked="" type="checkbox"/>	1096	780.8849	1559.7552	1559.7548	0.28	0	16	2.3	1	QCLENQQLIMQR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1112	787.4112	1572.8078	1572.8069	0.61	0	16	1.4	1	IEGITPDIMEQALK + Oxidation (M)
<input checked="" type="checkbox"/>	156	452.2301	902.4456	902.4457	-0.10	0	15	2.8	1	AVEEATAGR
<input checked="" type="checkbox"/>	1022	760.3724	1518.7302	1518.7348	-2.98	0	15	2.1	1	GEGLSLLNCEEIR
<input checked="" type="checkbox"/>	73	409.2368	816.4590	816.4593	-0.28	0	15	2.6	1	IDVTIEK
<input checked="" type="checkbox"/>	279	507.7615	1013.5084	1013.5076	0.81	0	15	0.82	1	NHNLIMTR + Oxidation (M)
<input checked="" type="checkbox"/>	45	394.2314	786.4482	786.4487	-0.57	0	15	4.5	1	IDVLEAK
<input checked="" type="checkbox"/>	282	508.7653	1015.5160	1015.5120	3.95	0	15	2.8	1	NGEIIPMSR
<input checked="" type="checkbox"/>	215	476.2618	950.5090	950.5072	1.89	1	15	2.7	1	AEYEAIKK
<input checked="" type="checkbox"/>	823	684.3681	1366.7216	1366.7166	3.66	0	15	1.6	1	YQLPVTTLTLMGK + Oxidation (M)
<input checked="" type="checkbox"/>	18	376.2082	750.4018	750.4024	-0.78	0	15	3.3	1	TIQSFR
<input checked="" type="checkbox"/>	1877	845.7411	2534.2015	2534.1997	0.70	0	15	1.2	1	IHQAAQTLQSTPPISEENNDER
<input checked="" type="checkbox"/>	462	562.7882	1123.5618	1123.5617	0.13	0	15	2.2	1	MEVTSCLTLK

<input checked="" type="checkbox"/>	645	629.3378	1256.6610	1256.6612	-0.13	0	15	2	1	TVILDAENSPAK
<input checked="" type="checkbox"/>	841	689.8433	1377.6720	1377.6711	0.71	0	15	1.8	1	QASMELVNSFPR
<input checked="" type="checkbox"/>	1710	713.0126	2136.0160	2136.0157	0.12	0	15	1.5	1	MSNPQQQFISDELSQLQK + Oxidation (M)
<input checked="" type="checkbox"/>	291	509.2627	1016.5108	1016.5138	-2.93	0	15	3.7	1	VDGAASAAIDK
<input checked="" type="checkbox"/>	1313	848.9044	1695.7942	1695.7927	0.93	0	15	1.7	1	VGDLSTEMIEHFRR + Oxidation (M)
<input checked="" type="checkbox"/>	853	694.3668	1386.7190	1386.7242	-3.71	0	15	2.1	1	EALEEVGATVELK
<input checked="" type="checkbox"/>	1036	764.3710	1526.7274	1526.7287	-0.79	0	15	2.3	1	YLDGTGITCLNEK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	650	630.8061	1259.5976	1259.5994	-1.36	0	15	1.8	1	DGPDSDIVLSSR
<input checked="" type="checkbox"/>	303	511.7525	1021.4904	1021.4936	-3.11	1	15	2	1	GKDLSMPMK + Oxidation (M)
<input checked="" type="checkbox"/>	371	538.3040	1074.5934	1074.5921	1.27	0	15	2.8	1	TTQLADIVSK
<input checked="" type="checkbox"/>	1037	764.3727	1526.7308	1526.7287	1.44	1	15	2.2	1	EMGGSVYLDADKVK + Oxidation (M)
<input checked="" type="checkbox"/>	1282	836.4302	1670.8458	1670.8475	-1.00	1	14	2.2	1	TKDPDLTAADLDAVR
<input checked="" type="checkbox"/>	399	366.1965	1095.5677	1095.5673	0.36	0	14	2.3	1	AVVDHINGSGK
<input checked="" type="checkbox"/>	756	662.3536	1322.6926	1322.6976	-3.77	1	14	1.5	1	LSTSSLCVTRR
<input checked="" type="checkbox"/>	599	604.7769	1207.5392	1207.5429	-3.01	1	14	0.96	1	DESSRSNAQK
<input checked="" type="checkbox"/>	30	385.1960	768.3774	768.3766	1.08	0	14	1.2	1	QGAGAPTAP
<input checked="" type="checkbox"/>	1003	752.3763	1502.7380	1502.7325	3.71	0	14	2.7	1	SGVSLSAEQNENLR
<input checked="" type="checkbox"/>	15	368.7200	735.4254	735.4279	-3.38	1	14	2.9	1	KGVTGFK
<input checked="" type="checkbox"/>	248	494.7498	987.4850	987.4848	0.30	0	14	2.3	1	YHIAMEPK
<input checked="" type="checkbox"/>	1035	764.3706	1526.7266	1526.7287	-1.31	1	14	2.4	1	EMGGSVYLDADKVK + Oxidation (M)
<input checked="" type="checkbox"/>	475	565.7666	1129.5186	1129.5186	0.06	0	14	1.2	1	SNIHMQESGK
<input checked="" type="checkbox"/>	1320	851.4335	1700.8524	1700.8556	-1.83	0	14	2.6	1	QWLSELNLPNSCLK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	498	571.7665	1141.5184	1141.5193	-0.71	0	14	1	1	FGDAFWNSAK
<input checked="" type="checkbox"/>	709	650.8593	1299.7040	1299.7034	0.50	0	14	2.7	1	IAVITNEAEVVK
<input checked="" type="checkbox"/>	1677	1049.4990	2096.9834	2096.9852	-0.83	0	14	2	1	ASIMCKPYWEWEQWLK
<input checked="" type="checkbox"/>	953	737.3938	1472.7730	1472.7769	-2.64	1	14	2.8	1	DLRPVRCLSDATK
<input checked="" type="checkbox"/>	487	569.2935	1136.5724	1136.5713	0.99	0	14	3.6	1	ADSLIYQAEK
<input checked="" type="checkbox"/>	1252	824.3999	1646.7852	1646.7821	1.89	0	14	2.1	1	MDINIDDILADLDR + Oxidation (M)
<input checked="" type="checkbox"/>	497	571.3330	1140.6514	1140.6503	1.05	0	14	2.1	1	QLLSNQPLTK
<input checked="" type="checkbox"/>	1041	765.3820	1528.7494	1528.7490	0.31	1	14	2.4	1	LRISCMISSNAYR + Oxidation (M)
<input checked="" type="checkbox"/>	190	465.2380	928.4614	928.4614	0.04	0	14	1.4	1	VPDAVSDAR
<input checked="" type="checkbox"/>	470	565.3142	1128.6138	1128.6139	-0.01	0	14	4	1	ANIIVAGESQK
<input checked="" type="checkbox"/>	1383	578.9544	1733.8414	1733.8366	2.74	1	14	2.4	1	VTERCESALQSLEGR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	363	535.7488	1069.4830	1069.4829	0.17	0	14	1.3	1	YQNVFDER
<input checked="" type="checkbox"/>	1190	808.9100	1615.8054	1615.8107	-3.23	1	14	2.7	1	FKAHDSQLAHYAK
<input checked="" type="checkbox"/>	1139	530.2761	1587.8065	1587.8079	-0.91	1	14	2.9	1	MGGWLLPGKDGNTVK + Oxidation (M)
<input checked="" type="checkbox"/>	1439	887.5150	1773.0154	1773.0149	0.33	1	14	0.48	1	QTYLVGGAVRDALLGLK
<input checked="" type="checkbox"/>	1213	813.9288	1625.8430	1625.8413	1.08	0	14	2.2	1	NYRPIEAGTTIYTK
<input checked="" type="checkbox"/>	325	522.2429	1042.4712	1042.4753	-3.91	0	14	1.3	1	QYAGASMTAK + Oxidation (M)
<input checked="" type="checkbox"/>	1329	852.4169	1702.8192	1702.8250	-3.36	1	14	2.6	1	GHKCWIFDLDISGR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1720	1073.5250	2145.0354	2145.0275	3.69	0	14	2.3	1	CIDGFGAMGFGFIEVGTVTPK
<input checked="" type="checkbox"/>	1076	773.8717	1545.7288	1545.7246	2.76	0	14	2.9	1	HMAESDWTISIVR + Oxidation (M)
<input checked="" type="checkbox"/>	1194	809.8994	1617.7842	1617.7846	-0.19	1	14	2.7	1	NTISEAGDKLEQADK
<input checked="" type="checkbox"/>	1208	812.9117	1623.8088	1623.8144	-3.42	0	14	2.7	1	NLSLSELGWDIYSK
<input checked="" type="checkbox"/>	1875	845.7408	2534.2006	2534.1997	0.35	0	14	1.6	1	IHQAAQTLQSTPPISEENNDER
<input checked="" type="checkbox"/>	764	663.8961	1325.7776	1325.7779	-0.18	1	13	0.89	1	KNLISGLGNLAAR

<input checked="" type="checkbox"/>	860	695.8755	1389.7364	1389.7405	-2.89	1	13	2.9	1	WVFNKNVEIK
<input checked="" type="checkbox"/>	983	751.3641	1500.7136	1500.7096	2.69	1	13	1.9	1	YSDSEADIKQAFK
<input checked="" type="checkbox"/>	1064	771.8771	1541.7396	1541.7371	1.68	0	13	2	1	ECVAQGGICFAFIK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	668	637.8511	1273.6876	1273.6877	-0.08	1	13	2.8	1	EKLSTALNSPSK
<input checked="" type="checkbox"/>	1831	822.0616	2463.1630	2463.1700	-2.85	0	13	1.7	1	GVPMEDSHNIQHTNSLDDK
<input checked="" type="checkbox"/>	61	403.7224	805.4302	805.4334	-3.91	0	13	3.9	1	INFDGIK
<input checked="" type="checkbox"/>	1701	1063.0360	2124.0574	2124.0561	0.62	1	13	2.5	1	FPESVNVGFMQKVSADK
<input checked="" type="checkbox"/>	1142	530.2769	1587.8089	1587.8079	0.60	1	13	3	1	MGGWLLPGKDGNTVK + Oxidation (M)
<input checked="" type="checkbox"/>	1455	604.9829	1811.9269	1811.9274	-0.28	0	13	2.9	1	MVVTLIHPIAMDGLR + 2 Oxidation (M)
<input checked="" type="checkbox"/>	713	651.3566	1300.6986	1300.7027	-3.13	0	13	3.4	1	NAIVTVDPFPK
<input checked="" type="checkbox"/>	1256	824.9190	1647.8234	1647.8216	1.11	1	13	3.4	1	QLLEDKYGVDGANAR
<input checked="" type="checkbox"/>	158	452.7585	903.5024	903.5025	-0.09	0	13	2.8	1	AANITTSVK
<input checked="" type="checkbox"/>	453	558.3007	1114.5868	1114.5870	-0.13	0	13	2.6	1	GLSPSALIDDK
<input checked="" type="checkbox"/>	213	473.7839	945.5532	945.5535	-0.28	0	13	3.1	1	IPFIETVK
<input checked="" type="checkbox"/>	985	751.8539	1501.6932	1501.6984	-3.41	1	13	1.8	1	FHNGKTIGPDADCK
<input checked="" type="checkbox"/>	124	435.7740	869.5334	869.5334	0.00	0	13	3.8	1	LVSVSLPR
<input checked="" type="checkbox"/>	407	553.2715	1104.5284	1104.5299	-1.28	0	13	1.9	1	EGSSESLPATK
<input checked="" type="checkbox"/>	1021	760.3718	1518.7290	1518.7348	-3.78	0	13	3.2	1	VASMVNGESLEDIR
<input checked="" type="checkbox"/>	1050	512.2711	1533.7915	1533.7933	-1.20	1	13	3.8	1	IVLSTKQNCQTSR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	644	628.8463	1255.6780	1255.6786	-0.41	0	13	3	1	HSTAHLVGHAVK
<input checked="" type="checkbox"/>	368	537.8119	1073.6092	1073.6121	-2.63	0	13	3.1	1	FLDALASLPK
<input checked="" type="checkbox"/>	143	449.2247	896.4348	896.4352	-0.35	1	13	2	1	DSAYSKAR
<input checked="" type="checkbox"/>	1072	773.3810	1544.7474	1544.7430	2.86	1	13	2.7	1	NEEISQQKADDIR
<input checked="" type="checkbox"/>	336	524.2683	1046.5220	1046.5244	-2.23	1	13	4.4	1	DGKELEGTAK
<input checked="" type="checkbox"/>	391	545.8088	1089.6030	1089.6005	2.37	1	13	2.6	1	DMIRWILK + Oxidation (M)
<input checked="" type="checkbox"/>	413	554.2855	1106.5564	1106.5608	-3.90	0	13	3.9	1	DEALIDIYR
<input checked="" type="checkbox"/>	1158	799.9224	1597.8302	1597.8311	-0.55	0	13	3.6	1	LDDNIIDISITPNR
<input checked="" type="checkbox"/>	1202	810.9072	1619.7998	1619.8017	-1.17	1	13	3.9	1	KGMFIIDGGEIYR + Oxidation (M)
<input checked="" type="checkbox"/>	114	425.2393	848.4640	848.4644	-0.38	1	13	3.1	1	KLDDVLF
<input checked="" type="checkbox"/>	1090	779.8725	1557.7304	1557.7324	-1.27	1	13	2.6	1	YGGGWEVQRSYAR
<input checked="" type="checkbox"/>	306	511.7531	1021.4916	1021.4903	1.34	0	13	3	1	FPCSVVEGK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	406	553.2711	1104.5276	1104.5312	-3.23	1	13	4.6	1	DWIRTSGDR
<input checked="" type="checkbox"/>	854	694.3865	1386.7584	1386.7541	3.16	1	13	3.2	1	ELVSAMKEIVPR + Oxidation (M)
<input checked="" type="checkbox"/>	899	713.3713	1424.7280	1424.7259	1.48	1	12	3.8	1	EIDAAVKQAHTDK
<input checked="" type="checkbox"/>	337	524.2854	1046.5562	1046.5583	-1.95	0	12	4	1	AMLVDFPVR
<input checked="" type="checkbox"/>	881	707.3378	1412.6610	1412.6606	0.33	0	12	2.2	1	MSHLDDIPSTPGK + Oxidation (M)
<input checked="" type="checkbox"/>	1274	831.9061	1661.7976	1661.8009	-1.93	1	12	3.7	1	SPSAYLNNPAEERSK
<input checked="" type="checkbox"/>	226	480.7321	959.4496	959.4461	3.72	0	12	2.7	1	LDENGWAR
<input checked="" type="checkbox"/>	790	673.8612	1345.7078	1345.7062	1.21	1	12	3.2	1	STVVLRSNGNGSR
<input checked="" type="checkbox"/>	1235	821.9260	1641.8374	1641.8436	-3.76	0	12	3.1	1	GVCVFSYEQLLSLK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	755	661.3463	1320.6780	1320.6786	-0.41	1	12	4.1	1	ANKGFSSLQNK
<input checked="" type="checkbox"/>	973	746.8861	1491.7576	1491.7609	-2.20	1	12	4.7	1	SADKIFVSYATK
<input checked="" type="checkbox"/>	1014	758.8677	1515.7208	1515.7205	0.21	0	12	2.4	1	SAAFDGNYSYISTVK
<input checked="" type="checkbox"/>	246	492.7705	983.5264	983.5287	-2.34	0	12	1.9	1	VSNIEPPK
<input checked="" type="checkbox"/>	1727	719.3557	2155.0453	2155.0442	0.50	0	12	3.1	1	FDIITCMELLEHPDPQR
<input checked="" type="checkbox"/>	492	570.7778	1139.5410	1139.5393	1.50	1	12	2.6	1	YPGNRTCTTK

<input checked="" type="checkbox"/>	884	709.8787	1417.7428	1417.7412	1.14	1	12	3.8	1	SADNIIKSIENSK
<input checked="" type="checkbox"/>	866	699.8658	1397.7170	1397.7191	-1.45	1	12	3.3	1	FVDELSNAFKTK
<input checked="" type="checkbox"/>	455	559.7684	1117.5222	1117.5186	3.26	0	12	3.4	1	STCHGISAASGK
<input checked="" type="checkbox"/>	1732	722.6996	2165.0770	2165.0721	2.24	1	12	2.8	1	DLRSDNYLVVCAALNAICR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1081	776.8387	1551.6628	1551.6624	0.32	1	12	1.3	1	TWREADNCDESVK
<input checked="" type="checkbox"/>	152	451.7508	901.4870	901.4869	0.17	0	12	10	1	DLNVSIGGK
<input checked="" type="checkbox"/>	630	624.8380	1247.6614	1247.6617	-0.21	1	12	4.2	1	ICLAMEKALEK
<input checked="" type="checkbox"/>	550	389.5170	1165.5292	1165.5251	3.49	0	12	2.2	1	DSAYPEELSR
<input checked="" type="checkbox"/>	123	435.2581	868.5016	868.5018	-0.18	0	12	1.6	1	LDLLGNPK
<input checked="" type="checkbox"/>	460	562.2570	1122.4994	1122.4950	3.94	0	12	1.7	1	TAAGIWCCNGK
<input checked="" type="checkbox"/>	906	716.8350	1431.6554	1431.6525	2.07	1	12	2	1	MATARGGSGPDPGSR + Oxidation (M)
<input checked="" type="checkbox"/>	647	629.3499	1256.6852	1256.6864	-0.88	0	12	4.1	1	TLIAVLEDIAAE
<input checked="" type="checkbox"/>	259	496.7471	991.4796	991.4757	4.01	0	12	4.1	1	NDAITCVTR
<input checked="" type="checkbox"/>	404	552.7974	1103.5802	1103.5823	-1.82	0	12	4.2	1	TTLQTDGVLK
<input checked="" type="checkbox"/>	879	706.3807	1410.7468	1410.7507	-2.72	0	12	4.2	1	DYNIPIHEVLAK
<input checked="" type="checkbox"/>	317	516.7623	1031.5100	1031.5070	2.98	0	12	4.7	1	QGIDCEVLR
<input checked="" type="checkbox"/>	1826	1232.5880	2463.1614	2463.1576	1.56	1	12	2.8	1	FDINIPNHHTLFCTRDFAMR + Oxidation (M)
<input checked="" type="checkbox"/>	883	708.8575	1415.7004	1415.6979	1.77	1	12	3.7	1	MNHPDYKLNLR + Oxidation (M)
<input checked="" type="checkbox"/>	1325	851.4365	1700.8584	1700.8556	1.70	0	12	4.2	1	QWLSELNLPNSCLK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1091	779.8732	1557.7318	1557.7311	0.48	1	11	2.6	1	GNYSAVSKFIDDDK
<input checked="" type="checkbox"/>	1214	543.2985	1626.8737	1626.8763	-1.62	1	11	3.4	1	RVEVCLPIENTGLK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	256	495.7577	989.5008	989.5029	-2.09	0	11	4.6	1	DANLTTLESK
<input checked="" type="checkbox"/>	590	399.8792	1196.6158	1196.6190	-2.68	0	11	5.4	1	ATLQQFQSFK
<input checked="" type="checkbox"/>	1154	799.8845	1597.7544	1597.7592	-3.00	1	11	3.8	1	GKGQFENVMGALTCK + Oxidation (M)
<input checked="" type="checkbox"/>	737	657.8716	1313.7286	1313.7303	-1.26	1	11	4.4	1	GEQVGSLDIIRK
<input checked="" type="checkbox"/>	1028	762.4131	1522.8116	1522.8144	-1.78	1	11	3.8	1	VELFDNLKATFAR
<input checked="" type="checkbox"/>	1421	879.9471	1757.8796	1757.8730	3.78	0	11	5.4	1	QSVLADCLNNIVNAER
<input checked="" type="checkbox"/>	1543	954.4921	1906.9696	1906.9645	2.70	1	11	4.3	1	VLSGEVIPVCCGSAFKNK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	681	642.2827	1282.5508	1282.5500	0.69	0	11	1.8	1	EFGVSEEQACK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1699	708.6972	2123.0698	2123.0676	1.02	0	11	5	1	LMGKPASEVSMTELLMGLGK + 2 Oxidation (M)
<input checked="" type="checkbox"/>	693	431.2469	1290.7189	1290.7143	3.53	1	11	3.5	1	LSSVTESLKTAR
<input checked="" type="checkbox"/>	1193	809.8987	1617.7828	1617.7855	-1.62	1	11	4.4	1	MMPQSLPDTTTPKR + Oxidation (M)
<input checked="" type="checkbox"/>	283	508.7654	1015.5162	1015.5186	-2.30	0	11	6	1	DGQIEVEVK
<input checked="" type="checkbox"/>	298	510.7444	1019.4742	1019.4706	3.58	0	11	4.9	1	MGPIDTSQR + Oxidation (M)
<input checked="" type="checkbox"/>	202	470.7278	939.4410	939.4410	0.07	0	11	2.2	1	HVEEEAAR
<input checked="" type="checkbox"/>	370	538.3035	1074.5924	1074.5921	0.35	1	11	4.7	1	LEEGGLTTKK
<input checked="" type="checkbox"/>	797	677.3773	1352.7400	1352.7412	-0.85	0	11	4.1	1	NSNPGIVLSPSLR
<input checked="" type="checkbox"/>	832	687.3405	1372.6664	1372.6665	-0.06	0	11	4.2	1	ACMHPVTAMLVGK + Oxidation (M)
<input checked="" type="checkbox"/>	977	749.8636	1497.7126	1497.7172	-3.01	1	11	4.1	1	GTISNRLNEDHDK
<input checked="" type="checkbox"/>	357	532.7775	1063.5404	1063.5372	3.05	1	11	5.4	1	MPLFEKDGK
<input checked="" type="checkbox"/>	760	663.3572	1324.6998	1324.7000	-0.11	1	11	4	1	RFGHNQPSALAK
<input checked="" type="checkbox"/>	189	465.2379	928.4612	928.4614	-0.14	0	11	2.8	1	DPAAISEAR
<input checked="" type="checkbox"/>	636	627.8260	1253.6374	1253.6404	-2.36	1	11	5.5	1	NEPYRFITSK
<input checked="" type="checkbox"/>	1331	568.9413	1703.8021	1703.7962	3.43	1	11	3.5	1	TDSEDPVSDVDLTRR
<input checked="" type="checkbox"/>	918	721.8773	1441.7400	1441.7421	-1.44	1	11	4.8	1	VMSAIRNFMITK + 2 Oxidation (M)
<input checked="" type="checkbox"/>	216	477.7484	953.4822	953.4818	0.47	0	11	3.4	1	TEISSVYR

<input checked="" type="checkbox"/>	1262	829.4151	1656.8156	1656.8107	2.96	0	11	4.8	1	GGDHSELGAVDALAFAK
<input checked="" type="checkbox"/>	392	546.7754	1091.5362	1091.5393	-2.80	1	11	5.8	1	NMSIEAQRK + Oxidation (M)
<input checked="" type="checkbox"/>	542	583.2747	1164.5348	1164.5332	1.39	0	11	3.1	1	QADELVSEMK + Oxidation (M)
<input checked="" type="checkbox"/>	1152	797.8795	1593.7444	1593.7383	3.85	1	11	5.3	1	TGSGKVNQSYGHSSEK
<input checked="" type="checkbox"/>	1169	802.9096	1603.8046	1603.8068	-1.36	1	11	5.6	1	KGMFIIYDGEIYR
<input checked="" type="checkbox"/>	1382	867.9234	1733.8322	1733.8295	1.61	0	11	5.3	1	SSFAQSTLNTFVIMGK + Oxidation (M)
<input checked="" type="checkbox"/>	79	412.7289	823.4432	823.4413	2.40	1	11	7.7	1	DHAGIRR
<input checked="" type="checkbox"/>	344	528.2434	1054.4722	1054.4720	0.28	0	11	3.3	1	QYWGSASEK
<input checked="" type="checkbox"/>	348	529.2969	1056.5792	1056.5815	-2.13	0	11	5.9	1	ILLQEGEAEK
<input checked="" type="checkbox"/>	128	437.2907	872.5668	872.5695	-3.03	1	11	0.63	1	IVKIATTK
<input checked="" type="checkbox"/>	232	486.2796	970.5446	970.5447	-0.09	0	11	7.4	1	NAVPLGTTAK
<input checked="" type="checkbox"/>	1177	537.6229	1609.8469	1609.8464	0.30	0	11	3.5	1	KPFRPTSGLTSYEK
<input checked="" type="checkbox"/>	600	604.7771	1207.5396	1207.5429	-2.67	1	11	3	1	EDSSRSNAQK
<input checked="" type="checkbox"/>	180	459.2051	916.3956	916.3960	-0.40	0	11	0.53	1	CESPEPAK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	649	629.8307	1257.6468	1257.6452	1.31	0	11	5.9	1	DIDAEAALEIAK
<input checked="" type="checkbox"/>	637	627.8376	1253.6606	1253.6590	1.28	1	11	3.9	1	YPPFRACISIAK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1380	867.4309	1732.8472	1732.8420	3.00	1	11	5.8	1	DDFPNFEHGKSLLSK
<input checked="" type="checkbox"/>	456	560.3410	1118.6674	1118.6699	-2.21	0	11	1.7	1	LILTPPAAPLN
<input checked="" type="checkbox"/>	1741	725.7004	2174.0794	2174.0752	1.94	1	11	5.6	1	VMNHMDDIIIEFIKDLVVK
<input checked="" type="checkbox"/>	196	466.7742	931.5338	931.5338	0.00	0	11	4.8	1	LTQVGLSSK
<input checked="" type="checkbox"/>	324	521.7803	1041.5460	1041.5455	0.57	0	11	5.4	1	LAALPEGTDR
<input checked="" type="checkbox"/>	323	521.7803	1041.5460	1041.5455	0.57	0	11	5.4	1	LAALPEGTDR
<input checked="" type="checkbox"/>	638	627.8383	1253.6620	1253.6663	-3.37	1	11	4.4	1	VVICGDLRHSR
<input checked="" type="checkbox"/>	959	740.3995	1478.7844	1478.7868	-1.58	1	11	4.3	1	KETELELELFTK
<input checked="" type="checkbox"/>	640	628.3552	1254.6958	1254.6932	2.14	0	11	4.5	1	NNIEVVNAALAK
<input checked="" type="checkbox"/>	369	538.3030	1074.5914	1074.5921	-0.58	1	11	4.8	1	KTATLSETPK
<input checked="" type="checkbox"/>	1672	699.6735	2095.9987	2095.9956	1.45	1	11	3.7	1	SEGLSMAQHPGLSSGPEKER
<input checked="" type="checkbox"/>	1634	1029.4860	2056.9574	2056.9596	-1.05	0	11	3.1	1	SCSSSSSHLIHSLTQSSPR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	786	672.3623	1342.7100	1342.7067	2.50	1	10	8.3	1	YLYEMALIRR + Oxidation (M)
<input checked="" type="checkbox"/>	525	385.8841	1154.6305	1154.6295	0.81	1	10	5.1	1	ADLNVPVKD GK
<input checked="" type="checkbox"/>	1201	810.9070	1619.7994	1619.8017	-1.42	1	10	6.5	1	KGMFIIYDGEIYR + Oxidation (M)
<input checked="" type="checkbox"/>	781	671.3543	1340.6940	1340.6976	-2.65	0	10	4.7	1	TLQLSFDLYNK
<input checked="" type="checkbox"/>	818	681.8597	1361.7048	1361.7047	0.11	1	10	5.5	1	CILGDVSKCPVTK
<input checked="" type="checkbox"/>	1104	785.3818	1568.7490	1568.7471	1.27	1	10	4.8	1	NFEDIAEREYGVK
<input checked="" type="checkbox"/>	204	471.7470	941.4794	941.4818	-2.49	0	10	2.8	1	EDLIGNGPK
<input checked="" type="checkbox"/>	1126	791.8734	1581.7322	1581.7319	0.20	1	10	4.4	1	NTYCLYERMVK
<input checked="" type="checkbox"/>	314	516.2713	1030.5280	1030.5295	-1.40	0	10	7.7	1	AVGIVSGGEDK
<input checked="" type="checkbox"/>	753	659.8635	1317.7124	1317.7140	-1.16	0	10	5.8	1	SLLNLSLVQETK
<input checked="" type="checkbox"/>	1027	761.8620	1521.7094	1521.7059	2.30	0	10	4.7	1	TNGANTAGTFSEGP AK
<input checked="" type="checkbox"/>	857	695.3386	1388.6626	1388.6671	-3.19	0	10	4.7	1	VAEELVEETAGDK
<input checked="" type="checkbox"/>	911	720.8375	1439.6604	1439.6571	2.34	0	10	4.1	1	MTVCNLSIEMGAR + Oxidation (M)
<input checked="" type="checkbox"/>	1015	758.8679	1515.7212	1515.7205	0.47	0	10	3.9	1	SAAFDGNISYGISTVK
<input checked="" type="checkbox"/>	775	668.3494	1334.6842	1334.6864	-1.59	1	10	8.2	1	ISLGGNSKMETAK
<input checked="" type="checkbox"/>	563	586.7705	1171.5264	1171.5298	-2.87	0	10	2.6	1	IGFSYDWER
<input checked="" type="checkbox"/>	299	510.7716	1019.5286	1019.5321	-3.39	0	10	11	1	LAEVISACSK
<input checked="" type="checkbox"/>	579	596.8248	1191.6350	1191.6360	-0.80	1	10	6.2	1	AHPRGDLLEGK

<input checked="" type="checkbox"/>	1367	863.9274	1725.8402	1725.8396	0.38	1	10	5.9	1	MFSYSYTIINSTRLK + Oxidation (M)
<input checked="" type="checkbox"/>	1384	867.9290	1733.8434	1733.8407	1.60	1	10	6.4	1	GKLDWSDSAMGVPSLR + Oxidation (M)
<input checked="" type="checkbox"/>	1161	801.8903	1601.7660	1601.7620	2.52	0	10	5	1	EQWSNCP ² TIAQIR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	769	665.8705	1329.7264	1329.7292	-2.09	0	10	6.7	1	SLIITDQHIYK
<input checked="" type="checkbox"/>	793	674.3541	1346.6936	1346.6976	-2.95	1	10	7	1	SRNALIET ² CVGK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	728	437.2045	1308.5917	1308.5883	2.60	0	10	3.4	1	GCLMYLFD ² FGK + Oxidation (M)
<input checked="" type="checkbox"/>	1292	838.9202	1675.8258	1675.8273	-0.87	1	10	8.3	1	EGLKAVAAGMNPMDLK + 2 Oxidation (M)
<input checked="" type="checkbox"/>	518	575.8032	1149.5918	1149.5917	0.10	0	10	7.9	1	IDELIDSAFK
<input checked="" type="checkbox"/>	748	659.3214	1316.6282	1316.6322	-3.01	1	10	4.7	1	EVMDKYFELK + Oxidation (M)
<input checked="" type="checkbox"/>	632	625.8221	1249.6296	1249.6302	-0.48	1	10	9.5	1	ESTKIAPSFDR
<input checked="" type="checkbox"/>	509	573.7834	1145.5522	1145.5564	-3.63	1	10	5.8	1	VDEEGNKLDK
<input checked="" type="checkbox"/>	174	457.7689	913.5232	913.5233	-0.02	0	10	9.3	1	DVKPQSIK
<input checked="" type="checkbox"/>	310	514.7722	1027.5298	1027.5338	-3.87	0	10	6.2	1	YLTYQVVK
<input checked="" type="checkbox"/>	604	606.8640	1211.7134	1211.7125	0.77	1	10	2.5	1	LSAPDLLKEVK
<input checked="" type="checkbox"/>	499	571.8233	1141.6320	1141.6342	-1.93	1	10	7.2	1	LIK ² TENPAEK
<input checked="" type="checkbox"/>	840	689.3265	1376.6384	1376.6428	-3.17	0	10	5.4	1	LMQCLPNSNDVK + Oxidation (M)
<input checked="" type="checkbox"/>	865	699.8652	1397.7158	1397.7191	-2.31	1	10	5.3	1	FVDELSNAFKTK
<input checked="" type="checkbox"/>	663	636.8438	1271.6730	1271.6721	0.74	0	10	9.3	1	GVAELIQEQSAK
<input checked="" type="checkbox"/>	940	487.6069	1459.7989	1459.7969	1.33	1	10	4.8	1	SIGFLSRIPMPAR + Oxidation (M)
<input checked="" type="checkbox"/>	629	624.8070	1247.5994	1247.5993	0.10	0	10	5.3	1	NLESSISNQEK
<input checked="" type="checkbox"/>	1053	769.3703	1536.7260	1536.7242	1.18	0	10	7.5	1	MEIALDNGQFEVR + Oxidation (M)
<input checked="" type="checkbox"/>	429	557.7694	1113.5242	1113.5243	-0.08	0	10	4.3	1	YQAWQSGFK
<input checked="" type="checkbox"/>	1188	539.2805	1614.8197	1614.8148	3.02	1	10	7.1	1	VADTRMQPGGLEGLR + Oxidation (M)
<input checked="" type="checkbox"/>	1483	915.4733	1828.9320	1828.9249	3.90	1	10	7.2	1	SILRMQ ² TMSDMLFK + Oxidation (M)
<input checked="" type="checkbox"/>	1222	815.9167	1629.8188	1629.8209	-1.28	1	9	6.7	1	DEEQTI ² IERALDAK
<input checked="" type="checkbox"/>	749	659.3218	1316.6290	1316.6282	0.64	0	9	5.1	1	ETMLADLDQPGK
<input checked="" type="checkbox"/>	423	557.7688	1113.5230	1113.5243	-1.16	0	9	3.5	1	YQAWQSGFK
<input checked="" type="checkbox"/>	1542	953.4973	1904.9800	1904.9852	-2.70	1	9	6.7	1	AGTMQPA ² AFLAEAQIMKK
<input checked="" type="checkbox"/>	738	658.8273	1315.6400	1315.6376	1.82	1	9	5.5	1	HEMMLRDALGK + Oxidation (M)
<input checked="" type="checkbox"/>	1648	690.0009	2066.9809	2066.9769	1.90	0	9	5.8	1	SNDS ² SHPLWLESLNNAQR
<input checked="" type="checkbox"/>	1548	961.5095	1921.0044	1921.0091	-2.43	1	9	6.4	1	RELTSIMPV ² GSSINVFR + Oxidation (M)
<input checked="" type="checkbox"/>	122	434.7661	867.5176	867.5178	-0.18	0	9	3.7	1	VPAVL ² DVR
<input checked="" type="checkbox"/>	367	537.7753	1073.5360	1073.5353	0.70	0	9	10	1	DDL ² NIDLTR
<input checked="" type="checkbox"/>	725	436.8790	1307.6152	1307.6106	3.51	0	9	5.6	1	GGQSAALDSFER
<input checked="" type="checkbox"/>	81	412.7531	823.4916	823.4916	0.07	0	9	4.1	1	AVTVIGHK
<input checked="" type="checkbox"/>	1925	873.4214	2617.2424	2617.2516	-3.54	0	9	5.2	1	TEILV ² PDAAHG ² TNPATATMCGYTVK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1066	772.3685	1542.7224	1542.7170	3.51	1	9	5.8	1	CNGMLS ² NKSFIEK + Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/>	1702	709.3521	2125.0345	2125.0361	-0.77	1	9	6.7	1	KYTEILESAGGEVLDSQMR
<input checked="" type="checkbox"/>	1407	875.4274	1748.8402	1748.8369	1.89	1	9	7.8	1	YFNEYK ² SPGSLSTR
<input checked="" type="checkbox"/>	836	687.8777	1373.7408	1373.7415	-0.51	1	9	7.7	1	NIGGDLGGAIRGFK
<input checked="" type="checkbox"/>	365	536.2761	1070.5376	1070.5356	1.87	0	9	5.4	1	TGSV ² DTLHNK
<input checked="" type="checkbox"/>	1221	815.9161	1629.8176	1629.8144	1.98	0	9	7	1	NMQLNNISNVEVQK
<input checked="" type="checkbox"/>	976	749.8631	1497.7116	1497.7174	-3.83	0	9	6.1	1	LEGMFGFIDQVDK
<input checked="" type="checkbox"/>	1093	779.8735	1557.7324	1557.7344	-1.28	0	9	5.2	1	SSAYINATLDAMASK + Oxidation (M)
<input checked="" type="checkbox"/>	626	621.3362	1240.6578	1240.6564	1.15	0	9	6.4	1	QQVWLPVESR
<input checked="" type="checkbox"/>	651	630.8130	1259.6114	1259.6107	0.56	0	9	5.6	1	LSYYMDELVK

<input checked="" type="checkbox"/>	1435	591.9912	1772.9518	1772.9455	3.56	0	9	5.8	1	LCEAVGLSGGVLSQTLAR
<input checked="" type="checkbox"/>	653	633.2877	1264.5608	1264.5605	0.26	0	9	3.6	1	GGMILSDEDNAK + Oxidation (M)
<input checked="" type="checkbox"/>	757	662.8644	1323.7142	1323.7160	-1.31	1	9	7.2	1	QKLQHPPPHSR
<input checked="" type="checkbox"/>	25	381.2369	760.4592	760.4595	-0.40	1	9	4.2	1	FLKTPR
<input checked="" type="checkbox"/>	134	439.7132	877.4118	877.4150	-3.57	0	9	5.7	1	VMENMVR
<input checked="" type="checkbox"/>	1304	843.9544	1685.8942	1685.8882	3.56	1	9	6.4	1	INNLRAMLSQDGNLK
<input checked="" type="checkbox"/>	648	629.8299	1257.6452	1257.6427	2.01	0	9	7.8	1	AGMSSLAYFLAK
<input checked="" type="checkbox"/>	373	538.7949	1075.5752	1075.5736	1.57	1	9	6.8	1	IMLEKWEK
<input checked="" type="checkbox"/>	678	641.8545	1281.6944	1281.6969	-1.89	0	9	5.5	1	YISYPTQVLAK
<input checked="" type="checkbox"/>	241	489.3145	976.6144	976.6182	-3.82	0	9	0.31	1	VHLGVALLR
<input checked="" type="checkbox"/>	1881	845.7416	2534.2030	2534.1997	1.29	0	9	5.1	1	IHQAAQQLQSTPPISEENNDER
<input checked="" type="checkbox"/>	57	401.2618	800.5090	800.5120	-3.68	1	9	6.1	1	TKGVGVLK
<input checked="" type="checkbox"/>	898	475.9160	1424.7262	1424.7259	0.16	0	9	7.4	1	DLDPPTNNASIIR
<input checked="" type="checkbox"/>	1525	940.9679	1879.9212	1879.9284	-3.81	1	9	8.6	1	NMENIVEVAVMNFRAK + Oxidation (M)
<input checked="" type="checkbox"/>	197	467.2104	932.4062	932.4087	-2.60	0	9	1.7	1	IANEEDDK
<input checked="" type="checkbox"/>	267	500.2592	998.5038	998.5032	0.60	0	9	7	1	ILDEADAPR
<input checked="" type="checkbox"/>	201	469.7564	937.4982	937.4981	0.15	1	9	3.6	1	SYQSKLGR
<input checked="" type="checkbox"/>	770	666.3625	1330.7104	1330.7092	0.93	1	9	8.3	1	AGDAITLSEKAQK
<input checked="" type="checkbox"/>	789	672.8577	1343.7008	1343.7045	-2.68	1	9	9.9	1	EQEIVRLNSK
<input checked="" type="checkbox"/>	1406	582.9667	1745.8783	1745.8844	-3.54	1	9	8.3	1	SRETMLITVMSFGFK
<input checked="" type="checkbox"/>	851	462.2571	1383.7495	1383.7470	1.78	0	9	7.9	1	ENLITTPSRPR
<input checked="" type="checkbox"/>	779	670.8041	1339.5936	1339.5901	2.67	0	9	3.8	1	MATGIGDPQCFK + Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/>	1305	563.6080	1687.8022	1687.8022	0.01	0	9	5.3	1	AVPELCLMLNDLQNR + Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/>	1335	852.9464	1703.8782	1703.8844	-3.63	0	9	8.8	1	VFLLDYEGTLFLMK + Oxidation (M)
<input checked="" type="checkbox"/>	1342	854.9163	1707.8180	1707.8138	2.51	0	9	6.3	1	VDDNVLQCLEEYLR
<input checked="" type="checkbox"/>	643	628.8445	1255.6744	1255.6780	-2.86	1	9	10	1	HMIKCEIALAK
<input checked="" type="checkbox"/>	804	678.3629	1354.7112	1354.7139	-1.98	1	9	8.3	1	CLNAPPLRQTSR
<input checked="" type="checkbox"/>	159	452.7587	903.5028	903.5025	0.35	1	9	8.1	1	EVKNSTVK
<input checked="" type="checkbox"/>	1232	547.9398	1640.7976	1640.7915	3.67	1	9	6.6	1	DIVNMVMHHRDFK
<input checked="" type="checkbox"/>	21	377.7252	753.4358	753.4385	-3.51	0	9	0.9	1	GPPGSIVK
<input checked="" type="checkbox"/>	1271	831.9028	1661.7910	1661.7937	-1.59	1	9	6.8	1	YKDVIDSFYQEQK
<input checked="" type="checkbox"/>	1733	723.0277	2166.0613	2166.0602	0.50	0	9	8.3	1	TMITHNDGAQWMLLPPPTK + Oxidation (M)
<input checked="" type="checkbox"/>	923	482.9074	1445.7004	1445.6998	0.41	1	9	8.1	1	DISDIEGEKDGIR
<input checked="" type="checkbox"/>	930	725.8847	1449.7548	1449.7504	3.08	0	9	7.9	1	YHLFEVVDTISK
<input checked="" type="checkbox"/>	1135	529.6053	1585.7941	1585.7956	-0.97	1	9	11	1	LHAQKAIMATLMGGE + Oxidation (M)
<input checked="" type="checkbox"/>	1150	797.4182	1592.8218	1592.8272	-3.39	0	9	9.9	1	LTIPSPNMLFFGEK
<input checked="" type="checkbox"/>	1706	712.6833	2135.0281	2135.0276	0.20	1	9	7.5	1	RTAMSAATDNASELVENLSR
<input checked="" type="checkbox"/>	309	513.2660	1024.5174	1024.5164	1.01	0	9	4.8	1	TCFLSIWR
<input checked="" type="checkbox"/>	1835	822.0621	2463.1645	2463.1576	2.79	1	8	6	1	FDINIPNHHTLFCTRDFAMR + Oxidation (M)
<input checked="" type="checkbox"/>	559	585.3114	1168.6082	1168.6088	-0.46	0	8	7.2	1	INVETLHSEK
<input checked="" type="checkbox"/>	311	515.2045	1028.3944	1028.3977	-3.14	0	8	0.39	1	MVEMSCSEK + Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/>	952	737.3937	1472.7728	1472.7736	-0.49	1	8	11	1	VLSQHGIDSSRFK
<input checked="" type="checkbox"/>	805	678.8787	1355.7428	1355.7409	1.47	1	8	9.1	1	GPVAKTNSLENVK
<input checked="" type="checkbox"/>	982	751.3633	1500.7120	1500.7096	1.62	1	8	6.6	1	YSDSEADIKQAFK
<input checked="" type="checkbox"/>	1189	808.9036	1615.7926	1615.7889	2.33	1	8	8.4	1	MSIRDWPASERPR + Oxidation (M)
<input checked="" type="checkbox"/>	564	586.7708	1171.5270	1171.5298	-2.34	0	8	3.4	1	WYAEKNAYAK

<input checked="" type="checkbox"/>	459	561.2690	1120.5234	1120.5248	-1.22	0	8	7.1	1	TGGLSDTVEDK
<input checked="" type="checkbox"/>	275	503.7551	1005.4956	1005.4978	-2.19	0	8	8.9	1	SLTLADSDGK
<input checked="" type="checkbox"/>	355	532.2664	1062.5182	1062.5193	-0.98	1	8	9	1	TAEAKETADK
<input checked="" type="checkbox"/>	396	547.3088	1092.6030	1092.6035	-0.41	1	8	7.7	1	KIMIMLQ GK + 2 Oxidation (M)
<input checked="" type="checkbox"/>	882	707.8755	1413.7364	1413.7364	0.01	1	8	8.6	1	LRQVIN EWDNK
<input checked="" type="checkbox"/>	704	650.3387	1298.6628	1298.6653	-1.86	0	8	8.2	1	SDLLPPATVACR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	176	458.2480	914.4814	914.4821	-0.75	0	8	14	1	ANPATVSQK
<input checked="" type="checkbox"/>	692	646.3274	1290.6402	1290.6390	0.95	0	8	8.7	1	EAAQAI FAPMAR + Oxidation (M)
<input checked="" type="checkbox"/>	380	542.8038	1083.5930	1083.5924	0.61	0	8	8.8	1	LAL EGEPSLR
<input checked="" type="checkbox"/>	784	672.3281	1342.6416	1342.6452	-2.66	1	8	12	1	GFDVTGFRASMR
<input checked="" type="checkbox"/>	505	573.7642	1145.5138	1145.5097	3.66	0	8	3.3	1	MLSTMEGAYK + Oxidation (M)
<input checked="" type="checkbox"/>	1378	578.6228	1732.8466	1732.8414	2.99	0	8	10	1	AQQLDGAMGQLETSIR + Oxidation (M)
<input checked="" type="checkbox"/>	754	661.3295	1320.6444	1320.6496	-3.90	0	8	10	1	DLSIISSHMYR
<input checked="" type="checkbox"/>	1159	800.3870	1598.7594	1598.7585	0.57	0	8	7.7	1	ECVAQG GICFAFIK + 2 Carbamidomethyl (C)
<input checked="" type="checkbox"/>	833	687.3408	1372.6670	1372.6722	-3.74	0	8	8.9	1	VSQETDIPEEVK
<input checked="" type="checkbox"/>	943	731.3927	1460.7708	1460.7697	0.76	0	8	12	1	CNLVTVSSIFPPK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1718	714.0275	2139.0607	2139.0625	-0.87	0	8	9.1	1	LMGKPASEVSMTELLMGLGK + 3 Oxidation (M)
<input checked="" type="checkbox"/>	1049	767.8754	1533.7362	1533.7345	1.17	0	8	9	1	ELGAGVTMNEGIEAK + Oxidation (M)
<input checked="" type="checkbox"/>	589	599.3147	1196.6148	1196.6149	-0.08	0	8	11	1	QVADLVNADPR
<input checked="" type="checkbox"/>	362	535.2269	1068.4392	1068.4402	-0.89	0	8	1.3	1	EMMTA APR + 2 Oxidation (M)
<input checked="" type="checkbox"/>	951	737.3693	1472.7240	1472.7219	1.44	1	8	9.1	1	QSTSSTSHSAKAGPK
<input checked="" type="checkbox"/>	278	505.7522	1009.4898	1009.4903	-0.41	0	8	11	1	MGQLFSSPK + Oxidation (M)
<input checked="" type="checkbox"/>	1115	787.8726	1573.7306	1573.7334	-1.75	1	8	5.4	1	DVDAFFKEIESMK + Oxidation (M)
<input checked="" type="checkbox"/>	1936	883.7557	2648.2453	2648.2509	-2.14	0	8	6.1	1	AMTDVTGFLLGHLSEMCQAGVQAR
<input checked="" type="checkbox"/>	1131	792.3904	1582.7662	1582.7661	0.09	1	8	7.3	1	AYEDRVAMITGDVK + Oxidation (M)
<input checked="" type="checkbox"/>	244	491.7626	981.5106	981.5131	-2.52	0	8	6.6	1	DPVPATTPGK
<input checked="" type="checkbox"/>	670	637.8516	1273.6886	1273.6877	0.71	0	8	11	1	VSNESLISNIAK
<input checked="" type="checkbox"/>	1409	875.4278	1748.8410	1748.8437	-1.54	1	8	9.4	1	VVDAGCKVVITCDEGK + 2 Carbamidomethyl (C)
<input checked="" type="checkbox"/>	296	510.2328	1018.4510	1018.4542	-3.09	1	8	2	1	YQKYDMR + Oxidation (M)
<input checked="" type="checkbox"/>	926	724.3411	1446.6676	1446.6714	-2.62	0	8	5.5	1	ACSPAPGPWTTFR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1212	813.9268	1625.8390	1625.8413	-1.37	1	8	11	1	YHNDLIEKEIQPK
<input checked="" type="checkbox"/>	1184	538.9484	1613.8234	1613.8260	-1.64	0	8	9.6	1	NTLEEIAELQADIR
<input checked="" type="checkbox"/>	1493	921.9788	1841.9430	1841.9371	3.25	1	8	9	1	TKAGEVLLTDEHTAETK
<input checked="" type="checkbox"/>	1125	791.8729	1581.7312	1581.7345	-2.02	0	8	7.3	1	YSGTSPMSSPDAAA K
<input checked="" type="checkbox"/>	1337	569.2916	1704.8530	1704.8539	-0.52	0	8	13	1	GEMSPQIASALLMGLR + 2 Oxidation (M)
<input checked="" type="checkbox"/>	984	751.3666	1500.7186	1500.7177	0.62	0	8	9.2	1	CTCGANHALGNIVTK
<input checked="" type="checkbox"/>	529	578.7748	1155.5350	1155.5383	-2.80	1	8	6.3	1	ETCTGGFKWK
<input checked="" type="checkbox"/>	751	659.8444	1317.6742	1317.6711	2.41	1	8	15	1	MARVTVQEADK
<input checked="" type="checkbox"/>	1437	887.4845	1772.9544	1772.9560	-0.86	1	8	7.3	1	EVEAQLPEKVEYVIK
<input checked="" type="checkbox"/>	1250	823.9300	1645.8454	1645.8457	-0.15	1	8	11	1	NGSISLEEMRQALAK
<input checked="" type="checkbox"/>	696	647.8275	1293.6404	1293.6387	1.35	0	8	13	1	FLQSGINEQMK
<input checked="" type="checkbox"/>	970	745.4427	1488.8708	1488.8704	0.28	0	8	3.4	1	QVGVPYIIVFINK
<input checked="" type="checkbox"/>	745	658.8564	1315.6982	1315.7024	-3.13	0	7	12	1	YFTSTVLSLAK
<input checked="" type="checkbox"/>	878	706.3756	1410.7366	1410.7354	0.86	0	7	8.4	1	QVLEEAELLDPR
<input checked="" type="checkbox"/>	302	511.7521	1021.4896	1021.4869	2.71	0	7	13	1	HYIDFEAK
<input checked="" type="checkbox"/>	585	598.2801	1194.5456	1194.5418	3.24	1	7	5.9	1	YRYGGGHLSDA

<input checked="" type="checkbox"/>	1445	897.9099	1793.8052	1793.8027	1.40	1	7	6.7	1	EETSNS E EQATKQTGR
<input checked="" type="checkbox"/>	1789	581.5689	2322.2465	2322.2406	2.54	0	7	5	1	VQPSAM L PPDQPQITGLVLF R + Oxidation (M)
<input checked="" type="checkbox"/>	843	689.8704	1377.7262	1377.7252	0.75	1	7	11	1	SVLKGGPLSDSYR
<input checked="" type="checkbox"/>	1138	794.8915	1587.7684	1587.7681	0.19	0	7	8.6	1	LVYSDLSHPESWR
<input checked="" type="checkbox"/>	623	619.8533	1237.6920	1237.6918	0.20	0	7	4.8	1	DLPTVDLAIGPK
<input checked="" type="checkbox"/>	401	549.7771	1097.5396	1097.5361	3.19	1	7	13	1	M YRAPSVMK + Oxidation (M)
<input checked="" type="checkbox"/>	485	568.7579	1135.5012	1135.4993	1.74	1	7	5.4	1	KEEGSENSEK
<input checked="" type="checkbox"/>	928	724.8964	1447.7782	1447.7745	2.61	1	7	8.5	1	MIVEG P VLYGDK
<input checked="" type="checkbox"/>	560	586.2806	1170.5466	1170.5492	-2.15	0	7	4.9	1	AFLCGQNYAGK
<input checked="" type="checkbox"/>	1309	846.9174	1691.8202	1691.8222	-1.17	1	7	12	1	EGLK S VAA G MNPMDLK + 2 Oxidation (M)
<input checked="" type="checkbox"/>	1676	1049.4990	2096.9834	2096.9852	-0.83	0	7	9.5	1	ASIMCKPYWEWEQWLK
<input checked="" type="checkbox"/>	1284	837.4136	1672.8126	1672.8169	-2.54	0	7	11	1	NSQFAGG P LGNPNTAK
<input checked="" type="checkbox"/>	345	528.2701	1054.5256	1054.5229	2.56	1	7	7.8	1	M KFNSSIGR + Oxidation (M)
<input checked="" type="checkbox"/>	1206	811.8962	1621.7778	1621.7770	0.52	0	7	11	1	NDSLLCVGLDPDPHK
<input checked="" type="checkbox"/>	1180	805.9322	1609.8498	1609.8464	2.15	0	7	7.6	1	KPFRPTSGLT S YEK
<input checked="" type="checkbox"/>	474	565.7665	1129.5184	1129.5226	-3.69	1	7	5.8	1	YQEC G KAFK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1094	779.8749	1557.7352	1557.7392	-2.53	0	7	7.1	1	CTCGANHALGNIVTK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1482	915.4283	1828.8420	1828.8486	-3.59	0	7	8	1	QSLQ C SSVPSQSPNGGQR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1818	816.7303	2447.1691	2447.1654	1.50	1	7	8.8	1	VLFHVYCF S SKNMDDFLGDAVK
<input checked="" type="checkbox"/>	343	528.2433	1054.4720	1054.4688	3.07	0	7	7.9	1	C MSNFALGR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1293	419.9941	1675.9473	1675.9509	-2.13	1	7	4.2	1	ALSYVQLKAGVSDVVK
<input checked="" type="checkbox"/>	1302	843.4152	1684.8158	1684.8164	-0.34	0	7	9.7	1	GSGTLCEALLMTQAFK + Oxidation (M)
<input checked="" type="checkbox"/>	1413	876.9324	1751.8502	1751.8512	-0.57	1	7	12	1	C TVEAGYPGVLSTRDK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	731	655.8540	1309.6934	1309.6886	3.67	1	7	7.5	1	FAM C IKVLGGSK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	876	704.8878	1407.7610	1407.7623	-0.88	1	7	9	1	NSFVHKLHPTTK
<input checked="" type="checkbox"/>	243	491.7455	981.4764	981.4767	-0.27	1	7	8.6	1	DKFTTENK
<input checked="" type="checkbox"/>	1240	549.2839	1644.8299	1644.8235	3.88	1	7	11	1	IFF M RNFNNWIK + Oxidation (M)
<input checked="" type="checkbox"/>	1098	781.3776	1560.7406	1560.7380	1.71	0	7	10	1	DPTSTSTINAQSPSR
<input checked="" type="checkbox"/>	1641	689.0236	2064.0490	2064.0570	-3.88	0	7	19	1	QQQLMQLINDLAMIFMK
<input checked="" type="checkbox"/>	1054	769.3987	1536.7828	1536.7784	2.91	1	7	10	1	FIENEGGK V SGSVSK
<input checked="" type="checkbox"/>	493	571.3138	1140.6130	1140.6139	-0.74	0	7	7.7	1	SGLPGQIVDQK
<input checked="" type="checkbox"/>	862	699.3411	1396.6676	1396.6699	-1.62	0	7	12	1	M VQMICLLCVR + Carbamidomethyl (C); 2 Oxidation (M)
<input checked="" type="checkbox"/>	1026	761.4038	1520.7930	1520.7942	-0.77	1	7	13	1	STLTMK C LTEPIK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1101	781.8747	1561.7348	1561.7406	-3.65	1	7	11	1	ENLREMI E ESANK
<input checked="" type="checkbox"/>	1187	539.2767	1614.8083	1614.8035	2.93	1	7	11	1	ALEEGVTPRQL C DK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1756	735.7035	2204.0887	2204.0808	3.57	0	7	12	1	SGESEDSTIADLAVALNSGQIK
<input checked="" type="checkbox"/>	759	663.3228	1324.6310	1324.6342	-2.36	0	7	14	1	M IMTTTHFLGK + Oxidation (M)
<input checked="" type="checkbox"/>	1007	756.8705	1511.7264	1511.7216	3.21	0	7	11	1	QENHGLSLVSLGDEK
<input checked="" type="checkbox"/>	1490	920.4493	1838.8840	1838.8828	0.70	0	7	13	1	TSL L MMIMGELEPSAGK + 2 Oxidation (M)
<input checked="" type="checkbox"/>	1020	506.5928	1516.7566	1516.7562	0.26	1	7	12	1	FE G KSEINGFVYK
<input checked="" type="checkbox"/>	364	536.2407	1070.4668	1070.4702	-3.17	1	7	5.6	1	YGG S AMKDDK
<input checked="" type="checkbox"/>	1444	892.9547	1783.8948	1783.8927	1.22	1	7	12	1	RVLVELNDQYYNMK
<input checked="" type="checkbox"/>	975	747.3872	1492.7598	1492.7629	-2.05	0	7	12	1	LMGIESQGM L LAAK + 2 Oxidation (M)
<input checked="" type="checkbox"/>	707	650.8312	1299.6478	1299.6493	-1.10	0	7	10	1	LSDILNVH E MDK + Oxidation (M)
<input checked="" type="checkbox"/>	752	659.8456	1317.6766	1317.6776	-0.72	0	7	12	1	STDLLVAGEAAGSK
<input checked="" type="checkbox"/>	1120	526.9608	1577.8606	1577.8599	0.41	1	7	7.6	1	VI S ESMDILFRIR

<input checked="" type="checkbox"/>	1195	540.2687	1617.7843	1617.7861	-1.14	0	7	13	1	FGSYCVSNLSIFPK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	60	403.2343	804.4540	804.4527	1.62	1	7	16	1	MAKGAVTK
<input checked="" type="checkbox"/>	164	455.7606	909.5066	909.5032	3.79	0	7	12	1	ASAAHVVAGK
<input checked="" type="checkbox"/>	1457	605.6429	1813.9069	1813.9104	-1.97	1	7	11	1	AQECGQAADNLVLKAAR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	609	608.8260	1215.6374	1215.6420	-3.78	0	7	15	1	IPLEIMDLEK + Oxidation (M)
<input checked="" type="checkbox"/>	262	498.7500	995.4854	995.4859	-0.41	0	7	12	1	GSVGFLLMNR + Oxidation (M)
<input checked="" type="checkbox"/>	669	637.8511	1273.6876	1273.6877	-0.08	0	7	13	1	VSNESLISNIAK
<input checked="" type="checkbox"/>	1721	716.0195	2145.0367	2145.0347	0.94	1	7	12	1	MRHYEIMIILDPAQDER + Oxidation (M)
<input checked="" type="checkbox"/>	724	435.9007	1304.6803	1304.6758	3.42	0	7	18	1	ISTTLINQMER
<input checked="" type="checkbox"/>	1506	931.9840	1861.9534	1861.9567	-1.77	1	7	16	1	DQALLSKAVQCLNTSSK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	735	657.3565	1312.6984	1312.6986	-0.15	0	7	11	1	EAPAQLASALSAGK
<input checked="" type="checkbox"/>	825	685.2847	1368.5548	1368.5504	3.28	0	7	1.9	1	ESMESGWDLDK + Oxidation (M)
<input checked="" type="checkbox"/>	1436	591.9915	1772.9527	1772.9520	0.39	1	7	8.9	1	TVDIETKEAVLATVER
<input checked="" type="checkbox"/>	1762	741.7075	2222.1007	2222.1075	-3.07	1	7	11	1	QLCGLVESLFLERQALMEK
<input checked="" type="checkbox"/>	1260	826.9364	1651.8582	1651.8642	-3.58	1	6	14	1	EIQAVSNLSGQKHK
<input checked="" type="checkbox"/>	782	448.2224	1341.6454	1341.6421	2.44	0	6	14	1	QTFGGTCLLQMK + Oxidation (M)
<input checked="" type="checkbox"/>	1290	838.4043	1674.7940	1674.7988	-2.85	0	6	12	1	TQDDILSYIETSYK
<input checked="" type="checkbox"/>	1040	764.8688	1527.7230	1527.7205	1.65	1	6	12	1	DEFADGASYLQGKK
<input checked="" type="checkbox"/>	1366	863.3862	1724.7578	1724.7635	-3.29	1	6	4.6	1	NSQNSVSNVDCCKSK
<input checked="" type="checkbox"/>	1266	830.9156	1659.8166	1659.8113	3.24	0	6	16	1	LMIPNITQYSPCK + Oxidation (M)
<input checked="" type="checkbox"/>	1370	864.4446	1726.8746	1726.8712	2.00	0	6	11	1	KPDEFLAEQLHAAMK
<input checked="" type="checkbox"/>	1272	554.9382	1661.7928	1661.7930	-0.16	1	6	13	1	DGQTDKGNILDDIMK
<input checked="" type="checkbox"/>	203	471.2415	940.4684	940.4654	3.22	0	6	15	1	VEIFYDR
<input checked="" type="checkbox"/>	1463	912.9733	1823.9320	1823.9352	-1.74	1	6	13	1	HHPLTDRTLAMIFEK + Oxidation (M)
<input checked="" type="checkbox"/>	1638	1031.4890	2060.9634	2060.9626	0.43	1	6	9.5	1	RDITLDDMYHEVSFAIH
<input checked="" type="checkbox"/>	1229	819.9295	1637.8444	1637.8422	1.39	1	6	14	1	MTIPSPNMLFFRGK
<input checked="" type="checkbox"/>	633	625.8237	1249.6328	1249.6343	-1.13	0	6	22	1	AEWLKPYTDK
<input checked="" type="checkbox"/>	750	659.3489	1316.6832	1316.6870	-2.88	1	6	19	1	RGQVAEGMALAK + Oxidation (M)
<input checked="" type="checkbox"/>	958	740.3993	1478.7840	1478.7803	2.56	1	6	12	1	MNLGEPYILKSAK + Oxidation (M)
<input checked="" type="checkbox"/>	1464	912.9736	1823.9326	1823.9339	-0.68	0	6	13	1	GGSDAIYSNMVLEIHK + Oxidation (M)
<input checked="" type="checkbox"/>	531	386.5437	1156.6093	1156.6088	0.44	1	6	16	1	LDSAPEKAQAK
<input checked="" type="checkbox"/>	141	442.6922	883.3698	883.3705	-0.77	0	6	2	1	MSETSSSR
<input checked="" type="checkbox"/>	701	649.8514	1297.6882	1297.6851	2.45	1	6	14	1	QQVQDALNARR
<input checked="" type="checkbox"/>	1170	802.9102	1603.8058	1603.8093	-2.18	1	6	13	1	SVDTSSLDKWPELK
<input checked="" type="checkbox"/>	1192	540.2680	1617.7822	1617.7855	-2.03	1	6	13	1	MMPQSLPDTTTPKR + Oxidation (M)
<input checked="" type="checkbox"/>	885	710.3245	1418.6344	1418.6289	3.92	0	6	5.7	1	VCFYSNSFNPGK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	419	556.7615	1111.5084	1111.5042	3.83	0	6	7.4	1	VEMGMYPGK
<input checked="" type="checkbox"/>	944	731.3940	1460.7734	1460.7697	2.56	0	6	13	1	IILNIFNGEMGPK + Oxidation (M)
<input checked="" type="checkbox"/>	130	437.7484	873.4822	873.4807	1.76	0	6	38	1	ILTAEKAK
<input checked="" type="checkbox"/>	530	579.2719	1156.5292	1156.5257	3.10	0	6	8.4	1	FMTSQMTPAK + Oxidation (M)
<input checked="" type="checkbox"/>	1633	686.6592	2056.9558	2056.9484	3.60	1	6	9.2	1	SGQSALCDALFSSQSSKER + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1381	867.4314	1732.8482	1732.8519	-2.12	0	6	17	1	LTNDTSSTYIAASYVK
<input checked="" type="checkbox"/>	842	460.2488	1377.7246	1377.7299	-3.90	1	6	15	1	VLADPGCHRVR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	87	414.6876	827.3606	827.3596	1.30	0	6	2.6	1	GSAGYMSR
<input checked="" type="checkbox"/>	1679	1053.5490	2105.0834	2105.0860	-1.23	0	6	13	1	ATLTQAMSVTAAMDLLSPLR + Oxidation (M)
<input checked="" type="checkbox"/>	1079	774.8635	1547.7124	1547.7151	-1.70	0	6	11	1	NWTASTCVRPDNK + Carbamidomethyl (C)

<input checked="" type="checkbox"/>	1362	860.9251	1719.8356	1719.8402	-2.66	1	6	14	1	ENAIKHMSYHAYLK + Oxidation (M)
<input checked="" type="checkbox"/>	874	702.8836	1403.7526	1403.7521	0.40	1	6	13	1	IVQYRIENDVR
<input checked="" type="checkbox"/>	1134	793.8964	1585.7782	1585.7809	-1.64	1	6	12	1	LRS DGTATPVQNGDR
<input checked="" type="checkbox"/>	467	564.3066	1126.5986	1126.5982	0.37	0	6	13	1	SDLHSVLTQK
<input checked="" type="checkbox"/>	1205	811.4150	1620.8154	1620.8116	2.37	1	6	17	1	LNTGMAFMIKHSQK + Oxidation (M)
<input checked="" type="checkbox"/>	1500	926.9893	1851.9640	1851.9631	0.49	1	6	13	1	NWLATLRA YFQNEVK
<input checked="" type="checkbox"/>	165	455.7612	909.5078	909.5072	0.68	0	6	8.6	1	VPHPIY GK
<input checked="" type="checkbox"/>	948	732.8938	1463.7730	1463.7694	2.49	0	6	13	1	ILTAMVTPFTADGK
<input checked="" type="checkbox"/>	1736	1085.5270	2169.0394	2169.0450	-2.57	1	6	13	1	LAYGPEGREPRPDEIADR
<input checked="" type="checkbox"/>	1915	864.1125	2589.3157	2589.3109	1.86	0	6	13	1	VINDNFGIIEGLMTTVHATTATQK + Oxidation (M)
<input checked="" type="checkbox"/>	1009	757.8600	1513.7054	1513.7083	-1.85	0	6	11	1	MAVSTIFSQDSNSK
<input checked="" type="checkbox"/>	1564	976.9811	1951.9476	1951.9455	1.09	1	6	12	1	ASMSMNLRTAVSDDAVIR + Oxidation (M)
<input checked="" type="checkbox"/>	785	672.3356	1342.6566	1342.6517	3.65	0	6	14	1	ATTHWVVTEDGK
<input checked="" type="checkbox"/>	875	470.2474	1407.7204	1407.7180	1.66	0	6	20	1	MQGSVTEFLKPR + Oxidation (M)
<input checked="" type="checkbox"/>	75	409.2372	816.4598	816.4593	0.72	0	6	21	1	LEEVS IK
<input checked="" type="checkbox"/>	788	672.8276	1343.6406	1343.6429	-1.71	1	6	13	1	EQGGQQGAADAGKK
<input checked="" type="checkbox"/>	1182	807.8925	1613.7704	1613.7719	-0.92	1	6	14	1	GSKMEDVIFSGSSVR + Oxidation (M)
<input checked="" type="checkbox"/>	93	418.2427	834.4708	834.4712	-0.38	1	6	23	1	DL LYRR
<input checked="" type="checkbox"/>	971	745.8575	1489.7004	1489.7017	-0.85	1	6	13	1	CLENKQMTDVPR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	931	725.8859	1449.7572	1449.7576	-0.22	1	6	15	1	VRQAQSEYVAATK
<input checked="" type="checkbox"/>	1724	718.3530	2152.0372	2152.0299	3.38	0	6	15	1	PINSFENYPMSWKPSIDK
<input checked="" type="checkbox"/>	746	658.8568	1315.6990	1315.6983	0.55	1	6	20	1	ESKSPLTG GELAK
<input checked="" type="checkbox"/>	1356	573.2911	1716.8515	1716.8505	0.58	1	6	17	1	YLESNKQHVMPIDK + Oxidation (M)
<input checked="" type="checkbox"/>	618	616.8094	1231.6042	1231.6091	-3.98	1	6	18	1	MAGAATGSRTPGR
<input checked="" type="checkbox"/>	1886	845.7428	2534.2066	2534.1997	2.71	0	6	12	1	IHQAAQTLQSTPPISEENNDER
<input checked="" type="checkbox"/>	1338	853.9124	1705.8102	1705.8103	-0.01	1	6	15	1	CIHVPM TQCKTFGK + 2 Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1502	927.4833	1852.9520	1852.9577	-3.07	1	6	16	1	NCLPVNT PQSRIQNAAK
<input checked="" type="checkbox"/>	382	362.8383	1085.4931	1085.4964	-3.06	1	6	6.7	1	MYTRWADK + Oxidation (M)
<input checked="" type="checkbox"/>	1514	934.9870	1867.9594	1867.9581	0.75	1	6	14	1	TAAA AVAWASRFYEVAGK
<input checked="" type="checkbox"/>	739	658.8285	1315.6424	1315.6376	3.65	0	5	11	1	MHQMTLAEIAR + Oxidation (M)
<input checked="" type="checkbox"/>	1871	845.7389	2534.1949	2534.1997	-1.90	0	5	12	1	IHQAAQTLQSTPPISEENNDER
<input checked="" type="checkbox"/>	532	579.7455	1157.4764	1157.4771	-0.59	0	5	1.9	1	SSSSGMFN GER
<input checked="" type="checkbox"/>	56	401.2394	800.4642	800.4643	-0.11	0	5	31	1	IIEVAEK
<input checked="" type="checkbox"/>	1354	859.4323	1716.8500	1716.8539	-2.22	1	5	17	1	KAAGDMEILCPGIGAQK + Oxidation (M)
<input checked="" type="checkbox"/>	817	681.8594	1361.7042	1361.7013	2.16	0	5	17	1	VFEMNPELVIR + Oxidation (M)
<input checked="" type="checkbox"/>	1353	858.9176	1715.8206	1715.8222	-0.92	0	5	15	1	DDLPLMANTSHMLVK + 2 Oxidation (M)
<input checked="" type="checkbox"/>	1895	849.7410	2546.2012	2546.2031	-0.75	1	5	13	1	GVAATRSMASGGGVPTDEEQATGLER
<input checked="" type="checkbox"/>	334	524.2614	1046.5082	1046.5067	1.52	0	5	17	1	VVDDMP SLR + Oxidation (M)
<input checked="" type="checkbox"/>	1211	813.9001	1625.7856	1625.7905	-3.00	1	5	18	1	FANMGAQMVKEVASK + Oxidation (M)
<input checked="" type="checkbox"/>	584	598.2796	1194.5446	1194.5485	-3.24	0	5	11	1	MGCQATQLTSR
<input checked="" type="checkbox"/>	1458	605.6672	1813.9798	1813.9799	-0.06	1	5	11	1	GVISNSGGPVRVYSLPGR
<input checked="" type="checkbox"/>	1359	859.9259	1717.8372	1717.8345	1.58	0	5	17	1	SSFAQSTLNTFVTMGK
<input checked="" type="checkbox"/>	135	439.7529	877.4912	877.4909	0.36	0	5	24	1	DVAVVF TK
<input checked="" type="checkbox"/>	1043	765.8740	1529.7334	1529.7395	-3.98	0	5	13	1	SAEIPMPASLDDIR + Oxidation (M)
<input checked="" type="checkbox"/>	1830	616.7980	2463.1629	2463.1626	0.11	0	5	11	1	SPPNQDAQEGRPDSPTAEVVDVR
<input checked="" type="checkbox"/>	412	554.2667	1106.5188	1106.5212	-2.16	0	5	13	1	MSNQVMLPR + 2 Oxidation (M)

<input checked="" type="checkbox"/>	1563	651.6563	1951.9471	1951.9496	-1.28	0	5	14	1	GLVACTGNQFCGQAIETK
<input checked="" type="checkbox"/>	1667	1046.0010	2089.9874	2089.9838	1.76	0	5	12	1	MSQESSLSTVSTTSLVFDR + Oxidation (M)
<input checked="" type="checkbox"/>	1373	866.4232	1730.8318	1730.8323	-0.25	1	5	17	1	KQQDSSSEDTPPVVK
<input checked="" type="checkbox"/>	1621	1025.5070	2048.9994	2049.0057	-3.05	1	5	18	1	CVRMC E EVVGAVALGTVEK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	366	537.2762	1072.5378	1072.5401	-2.06	0	5	20	1	QGDEVIGEVK
<input checked="" type="checkbox"/>	1749	728.0316	2181.0730	2181.0698	1.47	0	5	15	1	GEVTVGMDVMIDINVIFEGK + Oxidation (M)
<input checked="" type="checkbox"/>	1310	847.4090	1692.8034	1692.7995	2.33	0	5	13	1	QEAWELVTFEGEGAK
<input checked="" type="checkbox"/>	1527	941.4627	1880.9108	1880.9057	2.73	0	5	16	1	GTIQAAPYGGWEGQATFK
<input checked="" type="checkbox"/>	1581	989.4882	1976.9618	1976.9547	3.62	1	5	18	1	ICDEVAVMENGKVIEQ GK + Oxidation (M)
<input checked="" type="checkbox"/>	1042	765.3848	1528.7550	1528.7522	1.87	0	5	19	1	GPVFNHSTGQTEEEK
<input checked="" type="checkbox"/>	1167	802.9089	1603.8032	1603.7988	2.77	1	5	17	1	VEVSGAAVD S LDLDRM
<input checked="" type="checkbox"/>	1632	1028.4960	2054.9774	2054.9830	-2.70	1	5	18	1	EEQIKSSSTMNLDELFGK
<input checked="" type="checkbox"/>	963	742.3572	1482.6998	1482.6959	2.66	1	5	16	1	YQTNPMRVLDCCK + Oxidation (M)
<input checked="" type="checkbox"/>	821	684.3354	1366.6562	1366.6512	3.66	0	5	20	1	FMIEEVMPEVK + Oxidation (M)
<input checked="" type="checkbox"/>	1858	839.0653	2514.1741	2514.1771	-1.19	0	5	11	1	DNLSCIMVTYPSTHG V YEQTIK + Oxidation (M)
<input checked="" type="checkbox"/>	1307	564.6494	1690.9264	1690.9301	-2.18	1	5	10	1	QPAMIHRALLGSIER
<input checked="" type="checkbox"/>	1529	942.4921	1882.9696	1882.9683	0.71	1	5	15	1	MLHSSDVNLQKQALQR + Oxidation (M)
<input checked="" type="checkbox"/>	1251	549.9348	1646.7826	1646.7875	-3.01	0	5	15	1	MDQFAVFGNPVAH S K
<input checked="" type="checkbox"/>	479	566.2569	1130.4992	1130.4988	0.43	0	5	7.2	1	YTVMCEELK + Oxidation (M)
<input checked="" type="checkbox"/>	288	508.7847	1015.5548	1015.5563	-1.42	0	5	25	1	SPLGARPYR
<input checked="" type="checkbox"/>	1424	883.4159	1764.8172	1764.8110	3.56	1	5	14	1	VPQQACREPFLS C CK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	495	571.3307	1140.6468	1140.6502	-2.97	0	5	18	1	ELES L IRPGK
<input checked="" type="checkbox"/>	1311	847.9329	1693.8512	1693.8531	-1.10	1	5	25	1	KMSSNLLCEIVSWK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1662	694.6710	2080.9912	2080.9986	-3.59	1	5	18	1	VMQEEALSAENFDEKLTK
<input checked="" type="checkbox"/>	1029	508.9439	1523.8099	1523.8065	2.24	1	5	15	1	IRVGMNPNHVLK + Oxidation (M)
<input checked="" type="checkbox"/>	732	656.3311	1310.6476	1310.6506	-2.28	0	5	16	1	NAQDYIAFLEK
<input checked="" type="checkbox"/>	1504	929.9762	1857.9378	1857.9432	-2.87	0	5	18	1	EENLNAGSNVSATALLQK
<input checked="" type="checkbox"/>	688	643.8521	1285.6896	1285.6877	1.49	1	5	24	1	RIAELDEEIAK
<input checked="" type="checkbox"/>	1061	771.4221	1540.8296	1540.8249	3.08	1	5	13	1	KWIERPLIDDEK
<input checked="" type="checkbox"/>	234	487.2413	972.4680	972.4665	1.60	0	5	11	1	ADAYGHGIGL
<input checked="" type="checkbox"/>	1350	858.4254	1714.8362	1714.8308	3.17	1	5	17	1	GASRGPNEVMENDVLK
<input checked="" type="checkbox"/>	700	649.8239	1297.6332	1297.6376	-3.39	0	5	16	1	VMQYFELSPGK
<input checked="" type="checkbox"/>	905	716.3434	1430.6722	1430.6751	-2.02	0	5	13	1	MDLLNYQYLDK + Oxidation (M)
<input checked="" type="checkbox"/>	1023	760.4225	1518.8304	1518.8341	-2.39	1	5	13	1	FCVGTGRLGLALQK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1650	691.3307	2070.9703	2070.9640	3.03	1	5	15	1	GDKTNHGEP E LNASSIGMAK + Oxidation (M)
<input checked="" type="checkbox"/>	1394	871.4210	1740.8274	1740.8253	1.22	0	5	17	1	HAEVAHAML E NGTAYK
<input checked="" type="checkbox"/>	1365	862.9128	1723.8110	1723.8055	3.22	1	5	15	1	AQAALGMN M KTMNAEK + Oxidation (M)
<input checked="" type="checkbox"/>	465	563.7514	1125.4882	1125.4907	-2.14	1	5	6.4	1	MSKNTEGMGR + Oxidation (M)
<input checked="" type="checkbox"/>	962	742.3561	1482.6976	1482.7024	-3.21	1	5	18	1	KCDEYIEALNTGK
<input checked="" type="checkbox"/>	1227	818.9387	1635.8628	1635.8688	-3.62	1	5	18	1	ILNVTTEMLKMATR + Oxidation (M)
<input checked="" type="checkbox"/>	1013	758.8671	1515.7196	1515.7205	-0.59	0	5	16	1	SAAFDGMNSY G ISTVK
<input checked="" type="checkbox"/>	464	563.7505	1125.4864	1125.4859	0.45	0	5	6.2	1	TSELDMSESK
<input checked="" type="checkbox"/>	242	489.7540	977.4934	977.4930	0.43	0	5	32	1	NAYEVAVGR
<input checked="" type="checkbox"/>	1802	792.0480	2373.1222	2373.1311	-3.75	1	5	17	1	VGAGFYAKTAGADPAAVAYEAMDK
<input checked="" type="checkbox"/>	528	578.7747	1155.5348	1155.5342	0.53	0	5	13	1	MGAGSSSYR P K + Oxidation (M)
<input checked="" type="checkbox"/>	687	643.8517	1285.6888	1285.6878	0.82	0	5	25	1	VISVTSVNPGE G K

<input checked="" type="checkbox"/>	813	679.8354	1357.6562	1357.6547	1.11	0	5	17	1	GLIPMEGDEELR
<input checked="" type="checkbox"/>	1248	823.9099	1645.8052	1645.8060	-0.45	1	5	21	1	KSQAGASELGPFS DPR
<input checked="" type="checkbox"/>	1340	854.9150	1707.8154	1707.8138	0.98	1	5	17	1	DPTKAGGFILESECGK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	163	455.7605	909.5064	909.5032	3.57	1	5	19	1	ATKHVQNL
<input checked="" type="checkbox"/>	239	487.7906	973.5666	973.5630	3.73	1	5	11	1	GEGVKIMLK
<input checked="" type="checkbox"/>	1341	854.9152	1707.8158	1707.8138	1.21	1	5	18	1	DPTKAGGFILESECGK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	848	692.3788	1382.7430	1382.7445	-1.07	1	5	17	1	LYEELQKYVAK
<input checked="" type="checkbox"/>	1347	856.9388	1711.8630	1711.8604	1.57	1	5	23	1	CTPFKSSNFEGVVLK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1092	779.8734	1557.7322	1557.7320	0.18	0	5	14	1	CGFAVFAEQMISK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1485	915.9280	1829.8414	1829.8396	1.03	0	5	12	1	VIGLMMTACDLCSVTK + 2 Carbamidomethyl (C); 2 Oxidation (M)
<input checked="" type="checkbox"/>	1148	795.4048	1588.7950	1588.7953	-0.16	1	5	20	1	EKTCVIGNGMVDPK
<input checked="" type="checkbox"/>	1719	1070.5380	2139.0614	2139.0591	1.08	0	5	19	1	LMNSICEIFGVSQBEILSK
<input checked="" type="checkbox"/>	1241	823.4239	1644.8332	1644.8367	-2.13	0	5	19	1	LSYLLYQMLCGIR + Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/>	562	586.7700	1171.5254	1171.5220	2.98	0	5	8.5	1	TSEPYCPTFK
<input checked="" type="checkbox"/>	573	589.8362	1177.6578	1177.6608	-2.48	1	5	7.6	1	ITSRIFQWK
<input checked="" type="checkbox"/>	1228	818.9393	1635.8640	1635.8654	-0.85	1	5	20	1	VIQLCTGDLGFSAKK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1168	535.6085	1603.8037	1603.8028	0.54	1	5	21	1	MGKSASGALWLDPOK + Oxidation (M)
<input checked="" type="checkbox"/>	766	664.8618	1327.7090	1327.7096	-0.39	1	5	23	1	ASAAQPDVSVGPKAK
<input checked="" type="checkbox"/>	1273	554.9385	1661.7937	1661.7939	-0.16	1	5	19	1	NPMVSVACVGVCPKDK + Oxidation (M)
<input checked="" type="checkbox"/>	1924	873.0768	2616.2086	2616.2047	1.48	0	4	11	1	LMISSEYVMTSTSHESSEQLR + 2 Oxidation (M)
<input checked="" type="checkbox"/>	1704	712.3505	2134.0297	2134.0299	-0.12	1	4	23	1	AVEQIDMFDCVLPTRNAR
<input checked="" type="checkbox"/>	1441	888.4360	1774.8574	1774.8526	2.72	0	4	20	1	ASSDLGVEWIEFHTGK
<input checked="" type="checkbox"/>	1914	648.0319	2588.0985	2588.0980	0.21	1	4	2.3	1	SNCTGGSSPANSNTGYEERACTLGR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1303	843.4485	1684.8824	1684.8858	-1.99	0	4	21	1	VALCNWAELTPEVLK
<input checked="" type="checkbox"/>	932	725.8875	1449.7604	1449.7656	-3.57	0	4	23	1	VIWEDYFPLLR
<input checked="" type="checkbox"/>	964	743.3937	1484.7728	1484.7704	1.65	1	4	23	1	ACRRPSLTIMHGK + Oxidation (M)
<input checked="" type="checkbox"/>	1546	640.9944	1919.9614	1919.9687	-3.83	1	4	19	1	AQADKSSSLLDVTELEK
<input checked="" type="checkbox"/>	1813	608.0478	2428.1621	2428.1634	-0.53	0	4	19	1	AIISTGVGQHQMWAQFYNYK + Oxidation (M)
<input checked="" type="checkbox"/>	1281	835.4229	1668.8312	1668.8262	3.03	1	4	24	1	CNPILHEICRCAGIK
<input checked="" type="checkbox"/>	1643	1033.5070	2064.9994	2064.9914	3.91	1	4	25	1	SKANPWGSEFMGTWQMPK
<input checked="" type="checkbox"/>	711	651.3224	1300.6302	1300.6333	-2.34	1	4	19	1	DCAAVEKGPILDA
<input checked="" type="checkbox"/>	263	498.7524	995.4902	995.4892	1.06	1	4	18	1	GISRMSMAK + Oxidation (M)
<input checked="" type="checkbox"/>	1646	1034.4950	2066.9754	2066.9810	-2.67	1	4	18	1	YAGSKEALGTFQPNWENR
<input checked="" type="checkbox"/>	1839	822.0631	2463.1675	2463.1603	2.91	1	4	15	1	VLFHVYCFSKNMDDFLGDAVK + Oxidation (M)
<input checked="" type="checkbox"/>	710	650.8594	1299.7042	1299.7034	0.63	1	4	26	1	KDGQVLGEDVLK
<input checked="" type="checkbox"/>	1198	540.9390	1619.7952	1619.8016	-3.96	0	4	25	1	INGAHHSTVQGPSSTK
<input checked="" type="checkbox"/>	1678	701.6705	2101.9897	2101.9925	-1.33	1	4	16	1	FLYCMEGINRASAASGEVK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1146	530.2775	1587.8107	1587.8104	0.18	1	4	21	1	TKDESILSGSLSHSK
<input checked="" type="checkbox"/>	175	458.2480	914.4814	914.4821	-0.75	0	4	35	1	ANPATVSQK
<input checked="" type="checkbox"/>	20	376.2386	750.4626	750.4640	-1.75	1	4	14	1	TYKLVK
<input checked="" type="checkbox"/>	1306	563.6096	1687.8070	1687.8062	0.48	0	4	18	1	LLENMPMPWEQIR + 2 Oxidation (M)
<input checked="" type="checkbox"/>	214	476.2390	950.4634	950.4610	2.58	0	4	22	1	QAWAFSNK
<input checked="" type="checkbox"/>	504	573.7638	1145.5130	1145.5097	2.96	0	4	8	1	MLSTMEGAYK + Oxidation (M)
<input checked="" type="checkbox"/>	1258	551.6031	1651.7875	1651.7842	1.98	0	4	23	1	FATYAGPQDDAEVLR
<input checked="" type="checkbox"/>	1868	845.3975	2533.1707	2533.1723	-0.64	1	4	12	1	MGVEDIESMLNHRSGMLGLAGER + 2 Oxidation (M)
<input checked="" type="checkbox"/>	1668	697.6708	2089.9906	2089.9838	3.25	0	4	15	1	MSQESSLSTVSTTSLVFDR + Oxidation (M)

<input checked="" type="checkbox"/>	631	625.2905	1248.5664	1248.5656	0.68	0	4	15	1	GGMILSDEDNAK
<input checked="" type="checkbox"/>	1136	794.3728	1586.7310	1586.7287	1.51	0	4	14	1	SAYSVFQDMPEVEK + Oxidation (M)
<input checked="" type="checkbox"/>	1165	535.6082	1603.8028	1603.8028	-0.02	1	4	21	1	MGKSASGALWLDPOK + Oxidation (M)
<input checked="" type="checkbox"/>	1291	838.4293	1674.8440	1674.8432	0.48	1	4	22	1	ALAEAEAIRAMMAAPK + 2 Oxidation (M)
<input checked="" type="checkbox"/>	915	481.2836	1440.8290	1440.8300	-0.71	1	4	13	1	EGIAATVVALLARAS
<input checked="" type="checkbox"/>	1681	1054.0220	2106.0294	2106.0301	-0.31	1	4	20	1	SKPSSPTATDINSSASASRSR
<input checked="" type="checkbox"/>	941	730.9075	1459.8004	1459.7956	3.33	0	4	17	1	TVEDAAILMSVLAK
<input checked="" type="checkbox"/>	1629	1028.4940	2054.9734	2054.9700	1.68	1	4	25	1	TNFTCKPKSCLGSMNPR + Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/>	376	540.2550	1078.4954	1078.4965	-0.94	0	4	15	1	DMEIAQTQK + Oxidation (M)
<input checked="" type="checkbox"/>	1045	766.9081	1531.8016	1531.8028	-0.75	1	4	28	1	VISDNAELTCARLK
<input checked="" type="checkbox"/>	1820	818.0759	2451.2059	2451.2063	-0.19	1	4	22	1	KELCEGNSVSENHIPPILLER + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1448	899.9998	1797.9850	1797.9836	0.80	1	4	11	1	EEAVEVTRLVLEAVGGK
<input checked="" type="checkbox"/>	1199	540.9393	1619.7961	1619.8017	-3.50	1	4	28	1	KGMFIIYDGEIYR + Oxidation (M)
<input checked="" type="checkbox"/>	682	642.3173	1282.6200	1282.6241	-3.12	1	4	28	1	CRLEAWLQHA + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1216	814.9012	1627.7878	1627.7876	0.18	1	4	21	1	NKNGASVVMSTYTEK
<input checked="" type="checkbox"/>	210	473.2193	944.4240	944.4273	-3.47	1	4	5.5	1	YTGDKMSK + Oxidation (M)
<input checked="" type="checkbox"/>	1070	772.9367	1543.8588	1543.8643	-3.56	1	4	14	1	TKGEMVLIVEGKPK + Oxidation (M)
<input checked="" type="checkbox"/>	1155	799.8951	1597.7756	1597.7776	-1.23	1	4	21	1	FINEYHKEVYEK
<input checked="" type="checkbox"/>	192	465.7397	929.4648	929.4679	-3.25	1	4	30	1	ANDRDIAR
<input checked="" type="checkbox"/>	1215	543.6030	1627.7872	1627.7916	-2.74	0	4	22	1	GDFVVTCTGNVDIIK
<input checked="" type="checkbox"/>	347	529.2857	1056.5568	1056.5564	0.46	0	4	26	1	VAVLDQDAAR
<input checked="" type="checkbox"/>	496	381.2241	1140.6505	1140.6503	0.18	0	4	22	1	LIDAVIVGADR
<input checked="" type="checkbox"/>	574	590.3039	1178.5932	1178.5900	2.78	1	4	35	1	NMNALRVSMK + Oxidation (M)
<input checked="" type="checkbox"/>	1587	1004.9760	2007.9374	2007.9353	1.05	1	4	18	1	GGTDLAACLANTLNKMEDR + Oxidation (M)
<input checked="" type="checkbox"/>	1861	840.0654	2517.1744	2517.1749	-0.21	1	4	14	1	IECMRGGQWNPSPMISIQIPVR + Oxidation (M)
<input checked="" type="checkbox"/>	904	716.3433	1430.6720	1430.6751	-2.16	0	4	17	1	MDLLNYQYLDK + Oxidation (M)
<input checked="" type="checkbox"/>	1492	921.9768	1841.9390	1841.9458	-3.64	1	4	22	1	LSYHPMLGELAEAGAKR
<input checked="" type="checkbox"/>	869	700.8544	1399.6942	1399.6983	-2.91	1	4	19	1	AKENTTDALYFK
<input checked="" type="checkbox"/>	1533	948.4730	1894.9314	1894.9321	-0.37	0	4	28	1	LSGSIPFVFPSPACVCGSK
<input checked="" type="checkbox"/>	1498	618.3280	1851.9622	1851.9625	-0.20	0	4	23	1	VLQVINPGNPTGQVQTR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1660	1041.4960	2080.9774	2080.9834	-2.87	0	4	21	1	MSAEAEAIVTTATADVSSPSK + Oxidation (M)
<input checked="" type="checkbox"/>	929	725.3932	1448.7718	1448.7735	-1.17	0	4	30	1	NIHDAALAEVLQR
<input checked="" type="checkbox"/>	516	575.7695	1149.5244	1149.5203	3.57	0	4	14	1	WDHFSTTR
<input checked="" type="checkbox"/>	133	439.7001	877.3856	877.3851	0.62	0	4	9.6	1	ICEQEEK
<input checked="" type="checkbox"/>	1330	568.6143	1702.8211	1702.8196	0.89	1	4	24	1	CDINIKEDVAEEVAR
<input checked="" type="checkbox"/>	592	599.7797	1197.5448	1197.5448	0.03	0	4	15	1	YQCTVSNAAAGK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1279	834.4413	1666.8680	1666.8712	-1.90	1	4	20	1	QVCPELEKAQPGALK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	909	719.8854	1437.7562	1437.7576	-0.93	0	4	26	1	TSELVAIHAGIGDR
<input checked="" type="checkbox"/>	1269	554.9371	1661.7895	1661.7856	2.31	1	4	24	1	STPQDNKTISEAESR
<input checked="" type="checkbox"/>	1645	1034.4940	2066.9734	2066.9765	-1.47	0	4	23	1	QVTSWSEASMLLTAAAMDR
<input checked="" type="checkbox"/>	1069	772.8915	1543.7684	1543.7639	2.94	0	3	40	1	LAMWIMHLDNIR + 2 Oxidation (M)
<input checked="" type="checkbox"/>	1396	872.4415	1742.8684	1742.8687	-0.12	0	3	28	1	DQLLQSLNEGDVIDGK
<input checked="" type="checkbox"/>	1717	1070.5370	2139.0594	2139.0670	-3.53	1	3	28	1	DYNRIIAMLSPDEQALFK + Oxidation (M)
<input checked="" type="checkbox"/>	690	644.2800	1286.5454	1286.5489	-2.67	0	3	5.1	1	MDDNLFEEFK
<input checked="" type="checkbox"/>	795	675.8397	1349.6648	1349.6616	2.44	0	3	33	1	TAVETGPAGAYWK
<input checked="" type="checkbox"/>	1795	776.7468	2327.2186	2327.2234	-2.06	1	3	17	1	KLDSPQTAHSSSLIAGHTGPVPK

<input checked="" type="checkbox"/>	1860	839.7380	2516.1922	2516.1927	-0.22	1	3	20	1	DIGFKGVIFSDDLTMEGACGAGGIK + Oxidation (M)
<input checked="" type="checkbox"/>	1691	708.3464	2122.0174	2122.0153	0.98	1	3	22	1	EQMSAFHLAFNSIKENEK
<input checked="" type="checkbox"/>	921	723.8483	1445.6820	1445.6820	0.02	0	3	23	1	MTKPETPEETQR
<input checked="" type="checkbox"/>	1496	925.4562	1848.8978	1848.9040	-3.31	1	3	29	1	FADECKDIATVEQRPK
<input checked="" type="checkbox"/>	1513	934.9865	1867.9584	1867.9540	2.36	1	3	22	1	HELNYDDVALGRLPTR
<input checked="" type="checkbox"/>	1550	641.6515	1921.9327	1921.9269	3.01	1	3	26	1	TIDQDYINIEDKNDVK
<input checked="" type="checkbox"/>	1708	1068.5400	2135.0654	2135.0656	-0.08	0	3	24	1	NCQQQLWLGLLPMTVSGR + Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/>	63	404.2225	806.4304	806.4286	2.25	0	3	79	1	GYAEVLR
<input checked="" type="checkbox"/>	1486	611.3185	1830.9337	1830.9264	3.97	1	3	26	1	AGIPADALEQYGHYKAK
<input checked="" type="checkbox"/>	1838	822.0624	2463.1654	2463.1740	-3.51	0	3	20	1	TSLNVSFNPEFLDCQIHEVK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1788	775.0882	2322.2428	2322.2406	0.94	1	3	14	1	LLLKLSPPFHGGTSVSYTSMIR + Oxidation (M)
<input checked="" type="checkbox"/>	1754	1103.0500	2204.0854	2204.0896	-1.86	1	3	27	1	CPSVTPPEGGALSFLADRLSR
<input checked="" type="checkbox"/>	254	495.7575	989.5004	989.5043	-3.86	0	3	29	1	HADLPGPQR
<input checked="" type="checkbox"/>	617	615.7912	1229.5678	1229.5710	-2.59	0	3	14	1	AMEHDGQSLVK + Oxidation (M)
<input checked="" type="checkbox"/>	1296	841.9333	1681.8520	1681.8457	3.77	1	3	26	1	EYQNMNRNASISILK + Oxidation (M)
<input checked="" type="checkbox"/>	1713	1070.0140	2138.0134	2138.0096	1.81	1	3	21	1	AADLTGADV EAMMRSIAGTAR + 2 Oxidation (M)
<input checked="" type="checkbox"/>	780	671.3439	1340.6732	1340.6765	-2.41	1	3	25	1	AFKVPGYYPQA
<input checked="" type="checkbox"/>	856	695.3381	1388.6616	1388.6572	3.21	0	3	23	1	DEAGIVEWVESR
<input checked="" type="checkbox"/>	1420	878.9324	1755.8502	1755.8501	0.07	0	3	21	1	SNLELYQYQTAMAPK
<input checked="" type="checkbox"/>	1815	612.2952	2445.1517	2445.1524	-0.30	1	3	20	1	MAVMEMACPGAPGSAVGQQKELPK + Oxidation (M)
<input checked="" type="checkbox"/>	1903	855.0831	2562.2275	2562.2377	-3.99	0	3	20	1	ADPSYGILYAYISTLNIDDETTK
<input checked="" type="checkbox"/>	153	451.7799	901.5452	901.5419	3.75	1	3	15	1	MSKIKPAK
<input checked="" type="checkbox"/>	625	619.8701	1237.7256	1237.7282	-2.03	1	3	7	1	EVKLSPPIVEK
<input checked="" type="checkbox"/>	956	738.3420	1474.6694	1474.6722	-1.86	0	3	16	1	MPEQAQQGEQSVK + Oxidation (M)
<input checked="" type="checkbox"/>	491	570.7648	1139.5150	1139.5168	-1.58	0	3	9.8	1	MGLYSPSEK
<input checked="" type="checkbox"/>	810	679.3434	1356.6722	1356.6673	3.62	0	3	26	1	SALTEQYYNLR
<input checked="" type="checkbox"/>	1415	877.8895	1753.7644	1753.7584	3.46	0	3	8.6	1	GSWDSENFWLDPSSK
<input checked="" type="checkbox"/>	1899	1281.1150	2560.2154	2560.2149	0.23	1	3	23	1	MEPRVAEAVETGEEDVIMEALR + Oxidation (M)
<input checked="" type="checkbox"/>	974	498.5851	1492.7335	1492.7350	-1.05	0	3	31	1	FNYAVNYALSGFK
<input checked="" type="checkbox"/>	936	728.3704	1454.7262	1454.7228	2.39	1	3	28	1	IVATWYKMGQDK + Oxidation (M)
<input checked="" type="checkbox"/>	1086	777.8787	1553.7428	1553.7443	-0.91	1	3	24	1	AMHEPVPMDRTVR + Oxidation (M)
<input checked="" type="checkbox"/>	1716	1070.5370	2139.0594	2139.0596	-0.07	1	3	30	1	RASEYADIQIENQISQFK
<input checked="" type="checkbox"/>	1909	860.0731	2577.1975	2577.1905	2.72	0	3	20	1	TEWGNLME TLSQGEDETPLQVK + Oxidation (M)
<input checked="" type="checkbox"/>	1559	968.9884	1935.9622	1935.9546	3.93	1	3	30	1	DLAMRICEHYVTITQK + Oxidation (M)
<input checked="" type="checkbox"/>	1740	1088.0440	2174.0734	2174.0684	2.33	1	3	32	1	TIASKIWYALFEDDPYSR
<input checked="" type="checkbox"/>	1285	558.6132	1672.8178	1672.8243	-3.91	0	3	30	1	GDCTSQVVLLGHPYK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1171	803.4000	1604.7854	1604.7902	-2.96	1	3	36	1	ECGKIQEALDCLVK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1568	654.6304	1960.8694	1960.8666	1.43	1	3	11	1	GMSCNHCVARIEEAVGR + 2 Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/>	1722	1075.5480	2149.0814	2149.0799	0.73	1	3	27	1	YLMPDPIETLAAAKTLCDK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	420	556.7618	1111.5090	1111.5075	1.36	0	3	13	1	MNMLLAEMK + 2 Oxidation (M)
<input checked="" type="checkbox"/>	1352	858.9170	1715.8194	1715.8189	0.34	1	3	25	1	LDQATFDEMLKSFR + Oxidation (M)
<input checked="" type="checkbox"/>	1680	703.0148	2106.0226	2106.0229	-0.16	1	3	28	1	LKLGSPPTNGNSAAPSPESEP
<input checked="" type="checkbox"/>	476	565.7672	1129.5198	1129.5226	-2.46	1	3	12	1	CQFFSGEKK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	706	650.3680	1298.7214	1298.7194	1.61	1	3	31	1	IEDLREAAAIK
<input checked="" type="checkbox"/>	1411	875.4282	1748.8418	1748.8437	-1.05	0	3	32	1	AGMDGLVCSALEAQALK + Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/>	1889	846.0700	2535.1882	2535.1959	-3.04	1	3	20	1	MGGQVTV DHEHRMGEPVGTLDVR + Oxidation (M)

<input checked="" type="checkbox"/>	534	580.7539	1159.4932	1159.4962	-2.51	1	3	7.9	1	MGCSSSSTKTR + Oxidation (M)
<input checked="" type="checkbox"/>	1176	805.9037	1609.7928	1609.7970	-2.56	1	3	29	1	MPWRLPTGHQLCR + Oxidation (M)
<input checked="" type="checkbox"/>	1928	877.0797	2628.2173	2628.2121	1.97	1	3	17	1	EVPSMEEIFQACAQEDLKVTMAK + 2 Oxidation (M)
<input checked="" type="checkbox"/>	1389	580.2759	1737.8059	1737.8097	-2.22	0	3	24	1	DGQFIAFPTEEDIEK
<input checked="" type="checkbox"/>	1489	919.9811	1837.9476	1837.9421	3.01	1	3	28	1	QIHEASLEESSETPLKK
<input checked="" type="checkbox"/>	1220	544.2796	1629.8170	1629.8210	-2.44	0	3	37	1	ATVDEALALEGAESVR
<input checked="" type="checkbox"/>	1073	515.9244	1544.7514	1544.7551	-2.44	0	3	27	1	TEPEPVFWFYVK
<input checked="" type="checkbox"/>	1108	785.9073	1569.8000	1569.8045	-2.86	1	3	27	1	DIAARMTLVHANSR + Oxidation (M)
<input checked="" type="checkbox"/>	1200	540.9395	1619.7967	1619.7977	-0.64	0	3	35	1	MEYTPSPKQLSSR
<input checked="" type="checkbox"/>	705	650.3419	1298.6692	1298.6693	-0.03	0	3	32	1	FANVIGYMIGAK + Oxidation (M)
<input checked="" type="checkbox"/>	1207	542.2718	1623.7936	1623.7967	-1.90	0	3	28	1	VADLPTPLYAMYDR
<input checked="" type="checkbox"/>	1360	859.9578	1717.9010	1717.9073	-3.65	0	3	29	1	VDAVICDGFVGNVLLK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1836	616.7985	2463.1649	2463.1563	3.50	1	3	23	1	DAGYKIVTHMMPDLPNVDFER + Oxidation (M)
<input checked="" type="checkbox"/>	1900	854.4136	2560.2190	2560.2261	-2.78	1	3	25	1	LGMEEGEAIESPMVSRVIENAQR + Oxidation (M)
<input checked="" type="checkbox"/>	954	492.2557	1473.7453	1473.7423	2.00	1	3	48	1	QTVDEALKDAQTR
<input checked="" type="checkbox"/>	1123	791.3825	1580.7504	1580.7538	-2.11	1	3	26	1	AEVNMKSSDALAAMK + Oxidation (M)
<input checked="" type="checkbox"/>	1520	940.4343	1878.8540	1878.8608	-3.61	0	3	20	1	NNNNYNNNNIFPNSVK
<input checked="" type="checkbox"/>	621	619.2941	1236.5736	1236.5710	2.18	0	3	24	1	FMALNDYHAR
<input checked="" type="checkbox"/>	537	581.7616	1161.5086	1161.5124	-3.25	1	3	9.5	1	KYMDNSNYK
<input checked="" type="checkbox"/>	947	488.9316	1463.7730	1463.7766	-2.47	1	3	27	1	SNSGKTIISSALMR
<input checked="" type="checkbox"/>	1783	1148.0740	2294.1334	2294.1365	-1.33	1	3	26	1	QFLSQYLPAPQGMERTLDGK + Oxidation (M)
<input checked="" type="checkbox"/>	138	442.1967	882.3788	882.3793	-0.52	0	3	6.3	1	EAELMQF + Oxidation (M)
<input checked="" type="checkbox"/>	1024	760.9106	1519.8066	1519.8068	-0.13	0	3	27	1	ADAVLLEVCLAFTR
<input checked="" type="checkbox"/>	1705	712.3669	2134.0789	2134.0841	-2.45	1	3	30	1	RVTDLVVGHPLNMDDTAGPK
<input checked="" type="checkbox"/>	558	584.3564	1166.6982	1166.7023	-3.45	1	3	11	1	KNLNPLEVLK
<input checked="" type="checkbox"/>	1499	618.3286	1851.9640	1851.9631	0.45	1	3	27	1	NWLATLRAFYQNEVK
<input checked="" type="checkbox"/>	1669	523.9803	2091.8921	2091.8886	1.66	0	3	7.8	1	GKPIESSCMYGTCCLLWGK + 2 Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/>	1484	610.6710	1828.9912	1828.9869	2.31	0	3	21	1	MAHFALVSLSVTVNVNK
<input checked="" type="checkbox"/>	1259	826.9103	1651.8060	1651.8100	-2.39	1	3	28	1	INAACRLNDISYSR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1626	1028.4940	2054.9734	2054.9765	-1.48	0	3	35	1	LGLMPDGENMILDLESHR + Oxidation (M)
<input checked="" type="checkbox"/>	1673	1049.0070	2095.9994	2095.9963	1.49	1	3	25	1	FDHVGVFAPFSREBTEAAK
<input checked="" type="checkbox"/>	762	663.8126	1325.6106	1325.6108	-0.09	0	2	20	1	MMNPFANASIAK + 2 Oxidation (M)
<input checked="" type="checkbox"/>	1553	644.9655	1931.8747	1931.8795	-2.52	1	2	16	1	LQEHCDNEYNRVLDK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1487	611.6465	1831.9177	1831.9172	0.27	1	2	36	1	EACPIISNAMLVGDKAK + Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/>	1556	646.0239	1935.0499	1935.0466	1.71	1	2	18	1	AVAIPDFFERSTALLGK
<input checked="" type="checkbox"/>	1619	683.3271	2046.9595	2046.9646	-2.53	1	2	23	1	GYSYDLQVEEAYDLARR
<input checked="" type="checkbox"/>	1666	697.3301	2088.9685	2088.9662	1.08	0	2	26	1	YWGIPVPWQCSSCSAHR
<input checked="" type="checkbox"/>	1764	742.3799	2224.1179	2224.1205	-1.18	1	2	31	1	VHRLMSGPLGGDQMGSLVAR + Oxidation (M)
<input checked="" type="checkbox"/>	266	500.2558	998.4970	998.4974	-0.36	0	2	22	1	WLSGFFSR
<input checked="" type="checkbox"/>	1547	961.4805	1920.9464	1920.9429	1.86	0	2	33	1	SVGTYGDAEVEAIQNLQK
<input checked="" type="checkbox"/>	11	362.7380	723.4614	723.4643	-3.96	1	2	3.1	1	VPGVPPK
<input checked="" type="checkbox"/>	1121	790.8900	1579.7654	1579.7698	-2.74	1	2	36	1	GKSLANMLAEGMAAGK + 2 Oxidation (M)
<input checked="" type="checkbox"/>	1011	596.2330	1515.6772	1515.6801	-1.94	1	2	14	1	SIEDNHDDTSQKK
<input checked="" type="checkbox"/>	580	597.8332	1193.6518	1193.6478	3.41	1	2	29	1	MELLEYLKR
<input checked="" type="checkbox"/>	1743	726.3317	2175.9733	2175.9796	-2.91	1	2	15	1	MFSSNYRSLNFGDNPWVK
<input checked="" type="checkbox"/>	1280	834.9178	1667.8210	1667.8236	-1.51	1	2	32	1	AMAGSLGNVSARIFCR + Oxidation (M)

<input checked="" type="checkbox"/>	1823	821.7194	2462.1364	2462.1379	-0.61	0	2	20	1	LMQPLMMSDNPPDES DLGLLTK
<input checked="" type="checkbox"/>	824	684.3686	1366.7226	1366.7205	1.60	0	2	33	1	QQIDLGA VNNAPK
<input checked="" type="checkbox"/>	1074	515.9246	1544.7520	1544.7471	3.17	0	2	31	1	ENLFTGS NNPLDPK
<input checked="" type="checkbox"/>	1238	823.3900	1644.7654	1644.7640	0.90	1	2	25	1	DAYWIAM NSSSLKCK + Oxidation (M)
<input checked="" type="checkbox"/>	1923	872.7475	2615.2207	2615.2256	-1.89	1	2	24	1	MVQLPFV CGVWSSAAGMDKEIMK + 2 Oxidation (M)
<input checked="" type="checkbox"/>	1157	799.9056	1597.7966	1597.7923	2.75	1	2	35	1	AMFGVY NEKLGDVR
<input checked="" type="checkbox"/>	656	634.8284	1267.6422	1267.6448	-2.04	0	2	33	1	IEPSQAV YSFK
<input checked="" type="checkbox"/>	957	492.5650	1474.6732	1474.6762	-2.07	0	2	18	1	VLESGFY EQMTR + Oxidation (M)
<input checked="" type="checkbox"/>	1297	842.4234	1682.8322	1682.8257	3.86	1	2	37	1	SSTAT TSCINGRSTAVK
<input checked="" type="checkbox"/>	1524	627.6471	1879.9195	1879.9163	1.68	1	2	36	1	ELNTDE KEQLQTSFAK
<input checked="" type="checkbox"/>	1952	744.8655	2975.4329	2975.4231	3.30	1	2	25	1	EPMQVY LELLQKMATCAWTYSQAQK + Oxidation (M)
<input checked="" type="checkbox"/>	1851	624.7969	2495.1585	2495.1499	3.44	0	2	22	1	SSSAGQ WANSLLILSMEFSSNHR
<input checked="" type="checkbox"/>	1509	622.3047	1863.8923	1863.8884	2.10	1	2	37	1	IIEVEE LSETERMDQR + Oxidation (M)
<input checked="" type="checkbox"/>	1782	573.5525	2290.1809	2290.1892	-3.63	1	2	28	1	GILGLR ASMFIDYVQHIADR + Oxidation (M)
<input checked="" type="checkbox"/>	1916	864.7473	2591.2201	2591.2149	2.01	0	2	26	1	IEIYD NSHISGTHPYGVMVCGK + Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/>	1137	794.3960	1586.7774	1586.7763	0.74	1	2	35	1	DMSFN PPVAGPPSKK + Oxidation (M)
<input checked="" type="checkbox"/>	1808	806.0607	2415.1603	2415.1563	1.66	0	2	27	1	TEIIVP DAAHGTNPATAVMCGYK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	502	572.7573	1143.5000	1143.4978	1.92	0	2	7.7	1	SSMGS NAAAYTR
<input checked="" type="checkbox"/>	774	667.8167	1333.6188	1333.6197	-0.64	1	2	26	1	HYQKQ SDGLCR
<input checked="" type="checkbox"/>	1653	520.2387	2076.9257	2076.9179	3.74	1	2	14	1	HPEYNL CMKNDLMQPR + Carbamidomethyl (C); 2 Oxidation (M)
<input checked="" type="checkbox"/>	712	651.3553	1300.6960	1300.6987	-2.03	0	2	52	1	TVVGGG DSIAAANK
<input checked="" type="checkbox"/>	1887	845.7448	2534.2126	2534.2080	1.81	1	2	32	1	ELRSH PNECFCSGCTAVTIK + 2 Carbamidomethyl (C)
<input checked="" type="checkbox"/>	223	479.2776	956.5406	956.5403	0.35	1	2	70	1	SKPTSP GKR
<input checked="" type="checkbox"/>	1423	881.4479	1760.8812	1760.8767	2.60	1	2	39	1	KL SHLQAELDEMYGK
<input checked="" type="checkbox"/>	500	572.7562	1143.4978	1143.4940	3.34	0	2	12	1	TMIAF DMDGK + Oxidation (M)
<input checked="" type="checkbox"/>	1283	558.6085	1672.8037	1672.8025	0.70	0	2	35	1	MQAAS GQLQQTHMVK + Oxidation (M)
<input checked="" type="checkbox"/>	1657	694.3434	2080.0084	2080.0119	-1.72	1	2	37	1	QNVGSY RASGANINLNQMK + Oxidation (M)
<input checked="" type="checkbox"/>	483	567.3304	1132.6462	1132.6492	-2.59	1	2	28	1	INFK SALEVI
<input checked="" type="checkbox"/>	1391	580.6081	1738.8025	1738.7978	2.67	1	2	25	1	MRPT SGCSKDDTIQK + Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/>	949	735.3516	1468.6886	1468.6868	1.27	1	2	30	1	KL SDDIQMNFDK + Oxidation (M)
<input checked="" type="checkbox"/>	1690	1061.0090	2120.0034	2119.9997	1.78	1	2	31	1	WDFN QDPMAVDKLAEGIR + Oxidation (M)
<input checked="" type="checkbox"/>	1798	788.0870	2361.2392	2361.2369	0.97	0	2	28	1	IAIYP GTFDPITYGHLDVITR
<input checked="" type="checkbox"/>	468	564.7593	1127.5040	1127.5070	-2.59	0	2	14	1	HFPC SPESK
<input checked="" type="checkbox"/>	802	452.2039	1353.5899	1353.5904	-0.40	0	2	15	1	AQSNAM LEMAEK + 2 Oxidation (M)
<input checked="" type="checkbox"/>	1268	554.6155	1660.8247	1660.8268	-1.26	1	2	40	1	SSQT SLPSQLENKDK
<input checked="" type="checkbox"/>	1449	600.3358	1797.9856	1797.9850	0.34	0	2	20	1	RPVL VLQNDGLYQQR
<input checked="" type="checkbox"/>	747	439.5770	1315.7092	1315.7070	1.62	0	2	36	1	MSWA AVLAVAAAR
<input checked="" type="checkbox"/>	1038	764.3755	1526.7364	1526.7334	2.02	1	2	32	1	GRFT SEMVMVQAR + Oxidation (M)
<input checked="" type="checkbox"/>	837	688.3555	1374.6964	1374.6966	-0.08	0	2	51	1	CGTP PAYVAPEVLR
<input checked="" type="checkbox"/>	919	722.3135	1442.6124	1442.6143	-1.31	0	2	8.9	1	SCTV SVHCSNHR + 2 Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1534	632.9786	1895.9140	1895.9121	0.99	0	2	35	1	AGTVM FEIANVSEELMR
<input checked="" type="checkbox"/>	839	688.8420	1375.6694	1375.6700	-0.41	1	2	38	1	QMRGM GIDEALR
<input checked="" type="checkbox"/>	539	388.5714	1162.6924	1162.6961	-3.24	1	2	9.1	1	LEKY GVTLIK
<input checked="" type="checkbox"/>	1287	837.9120	1673.8094	1673.8116	-1.31	1	2	39	1	MQLPE EMRAEVTPK + Oxidation (M)
<input checked="" type="checkbox"/>	1535	633.3071	1896.8995	1896.8961	1.77	1	2	30	1	IDKVY CADVKPEMEGK + Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/>	74	409.2371	816.4596	816.4606	-1.19	1	2	60	1	RNFP VGK

<input checked="" type="checkbox"/>	1333	852.9224	1703.8302	1703.8268	2.05	1	2	48	1	RFVVQDTGGWEPDAK
<input checked="" type="checkbox"/>	1901	854.7433	2561.2081	2561.2036	1.73	1	2	29	1	ASGVLTTSCGNTITCYLKASAACR + 3 Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1918	865.0768	2592.2086	2592.2173	-3.36	1	2	25	1	TAFSFEFFPPKTEDGVDNLFER
<input checked="" type="checkbox"/>	927	483.5998	1447.7776	1447.7743	2.27	1	2	35	1	SQRSLQTSLVSSR
<input checked="" type="checkbox"/>	1314	848.9250	1695.8354	1695.8290	3.78	0	2	39	1	ACIIFFEIDAVGGAR
<input checked="" type="checkbox"/>	1462	912.9317	1823.8488	1823.8447	2.27	1	2	32	1	MDKFSLSHMSVWQGR + Oxidation (M)
<input checked="" type="checkbox"/>	1824	616.7971	2463.1593	2463.1563	1.23	1	2	26	1	DAGYKIVTHMMPDLPNVDFER + Oxidation (M)
<input checked="" type="checkbox"/>	1969	1041.5360	3121.5862	3121.5828	1.09	1	2	27	1	AGKGLEIDIFQELLDGDMGLEIFPAVQMLR + 2 Oxidation (M)
<input checked="" type="checkbox"/>	1728	1078.5310	2155.0474	2155.0554	-3.69	1	2	35	1	GMLDGNLLYQWLSMSKQR + Oxidation (M)
<input checked="" type="checkbox"/>	1369	576.6136	1726.8190	1726.8158	1.87	0	2	37	1	MTMLFSATLPEDVEK + Oxidation (M)
<input checked="" type="checkbox"/>	642	628.8123	1255.6100	1255.6092	0.71	1	2	39	1	RVAVHDDMTGR
<input checked="" type="checkbox"/>	461	562.3434	1122.6722	1122.6761	-3.41	1	2	9	1	IKLHSGEVIK
<input checked="" type="checkbox"/>	727	655.3020	1308.5894	1308.5914	-1.52	1	2	20	1	MEPRMSSGSNLR + 2 Oxidation (M)
<input checked="" type="checkbox"/>	1234	821.9106	1641.8066	1641.8124	-3.53	1	2	37	1	RVLDDVGGNGYHGWR
<input checked="" type="checkbox"/>	1576	988.0262	1974.0378	1974.0431	-2.64	1	2	37	1	LQMIVCSATLHAFEVKK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	610	610.8013	1219.5880	1219.5866	1.16	1	2	45	1	KENQELSMNK
<input checked="" type="checkbox"/>	1129	528.2741	1581.8005	1581.7960	2.84	1	2	37	1	IIEKMATFEIDEK + Oxidation (M)
<input checked="" type="checkbox"/>	538	581.7620	1161.5094	1161.5059	3.04	1	2	12	1	YKFCASCAR + 2 Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1218	815.9095	1629.8044	1629.8097	-3.25	0	2	36	1	VSVSDDNLIIEPSK
<input checked="" type="checkbox"/>	910	720.3627	1438.7108	1438.7061	3.31	1	2	51	1	LTQRACGFLMDK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1364	862.4238	1722.8330	1722.8359	-1.63	1	2	40	1	AAAMASRENFQAELEK + Oxidation (M)
<input checked="" type="checkbox"/>	822	684.3621	1366.7096	1366.7092	0.32	1	1	34	1	QHDKLLDELEK
<input checked="" type="checkbox"/>	506	573.7645	1145.5144	1145.5175	-2.68	0	1	14	1	YQMQYELR + Oxidation (M)
<input checked="" type="checkbox"/>	945	732.3279	1462.6412	1462.6374	2.66	1	1	18	1	CDPKATGVWGPWM + Oxidation (M)
<input checked="" type="checkbox"/>	1494	923.9878	1845.9610	1845.9618	-0.43	1	1	38	1	SVTEGIDAMGEVTIRLR
<input checked="" type="checkbox"/>	1518	625.9894	1874.9464	1874.9407	3.01	0	1	43	1	NSLLSEIIGLMEAAEGGR + Oxidation (M)
<input checked="" type="checkbox"/>	1752	732.7014	2195.0824	2195.0818	0.25	1	1	42	1	SNVDVSSGVEDEDPKRPLPR
<input checked="" type="checkbox"/>	1585	1003.0050	2003.9954	2003.9952	0.10	1	1	43	1	QSYHLTVKAFNVPDEEK
<input checked="" type="checkbox"/>	1893	637.0535	2544.1849	2544.1777	2.83	1	1	23	1	VSVYHPSTMKLETICYANDPYAR
<input checked="" type="checkbox"/>	740	658.8287	1315.6428	1315.6480	-3.95	0	1	34	1	TPGGSSGSAAVAAR
<input checked="" type="checkbox"/>	1130	528.2745	1581.8017	1581.8039	-1.40	0	1	45	1	ITHDFVSYSLSVSK
<input checked="" type="checkbox"/>	142	442.7631	883.5116	883.5127	-1.17	1	1	33	1	SKPKEAPK
<input checked="" type="checkbox"/>	1984	745.7733	3723.8301	3723.8447	-3.91	1	1	22	1	TYLWRCQFLLPFVSLGMLCFGALIGLCACICR + 2 Carbamidomethyl (C)
<input checked="" type="checkbox"/>	695	647.8193	1293.6240	1293.6243	-0.22	0	1	46	1	QCMVMAIQVQK + Oxidation (M)
<input checked="" type="checkbox"/>	763	442.8792	1325.6158	1325.6108	3.77	0	1	27	1	QAEVQMFLCNK + Oxidation (M)
<input checked="" type="checkbox"/>	820	682.8679	1363.7212	1363.7208	0.34	1	1	41	1	ALQTYSRALADR
<input checked="" type="checkbox"/>	1316	425.6848	1698.7101	1698.7155	-3.20	0	1	7	1	ADLFNMLGDDESGSGR + Oxidation (M)
<input checked="" type="checkbox"/>	1456	605.3138	1812.9196	1812.9152	2.43	1	1	36	1	QAKELAAANMTPEAAAAR
<input checked="" type="checkbox"/>	1738	724.3607	2170.0603	2170.0557	2.10	1	1	40	1	SFTCTLFAPAWHYEKLEK
<input checked="" type="checkbox"/>	1116	788.8932	1575.7718	1575.7715	0.21	1	1	45	1	ASISMLRSEHPVSF + Oxidation (M)
<input checked="" type="checkbox"/>	1786	767.7186	2300.1340	2300.1365	-1.11	1	1	42	1	MPEGAQGLSLSKPSPLGCGRR + Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/>	1385	868.4299	1734.8452	1734.8471	-1.09	1	1	43	1	SNPEIFCGITRTNAR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	416	555.7540	1109.4934	1109.4957	-2.05	1	1	36	1	EMMSSQNRK
<input checked="" type="checkbox"/>	1450	600.3359	1797.9859	1797.9850	0.51	0	1	23	1	RPVVLVQNDGLYQQR
<input checked="" type="checkbox"/>	472	565.7659	1129.5172	1129.5148	2.21	0	1	15	1	DMMLNTVYK + Oxidation (M)
<input checked="" type="checkbox"/>	1263	829.9059	1657.7972	1657.7988	-0.91	0	1	44	1	LYYNDYNIIEGIGPK

<input checked="" type="checkbox"/>	607	607.3248	1212.6350	1212.6364	-1.08	1	1	42	1	IWERGGGVSPR
<input checked="" type="checkbox"/>	481	566.8142	1131.6138	1131.6135	0.27	1	1	50	1	DLQEVTAATK
<input checked="" type="checkbox"/>	1834	822.0620	2463.1642	2463.1603	1.57	0	1	31	1	TGDFCIIPPNSFALGCTIEYFR
<input checked="" type="checkbox"/>	473	565.7663	1129.5180	1129.5192	-1.06	0	1	16	1	QYPEYGFAR
<input checked="" type="checkbox"/>	1334	852.9462	1703.8778	1703.8737	2.43	1	1	49	1	VLGTGTQQIRTNCSAR
<input checked="" type="checkbox"/>	1426	883.4262	1764.8378	1764.8426	-2.71	0	1	39	1	NMLPDYAVVAEPTCVK + Oxidation (M)
<input checked="" type="checkbox"/>	1908	1289.1150	2576.2154	2576.2176	-0.85	1	1	33	1	DAVEWAAEAEARGAGEILLTSM ^{DR} + Oxidation (M)
<input checked="" type="checkbox"/>	1532	632.6510	1894.9312	1894.9315	-0.16	1	1	50	1	SKGVLVGSSTMNVMMPK + Oxidation (M)
<input checked="" type="checkbox"/>	1288	837.9121	1673.8096	1673.8157	-3.60	1	1	45	1	YDKMWLLSMIQSK + 2 Oxidation (M)
<input checked="" type="checkbox"/>	1731	1083.5450	2165.0754	2165.0675	3.69	0	1	39	1	FDGVVLDLGVSSMQLDIADR + Oxidation (M)
<input checked="" type="checkbox"/>	1068	515.5961	1543.7665	1543.7664	0.02	1	1	58	1	QNQVSMPPSKGVEK + Oxidation (M)
<input checked="" type="checkbox"/>	1857	629.5507	2514.1737	2514.1764	-1.07	1	1	28	1	MASVGTLPASSMATKQSNASICA ^{EK} + 2 Oxidation (M)
<input checked="" type="checkbox"/>	1166	535.6083	1603.8031	1603.8062	-1.94	1	1	44	1	RCTDLCLIQPSIDK
<input checked="" type="checkbox"/>	867	699.8727	1397.7308	1397.7303	0.38	1	1	43	1	YGKLV ^{PATAGHDLG}
<input checked="" type="checkbox"/>	1419	585.9241	1754.7505	1754.7491	0.78	1	1	10	1	NWMEVTMEEEEK ^{GK} + Oxidation (M)
<input checked="" type="checkbox"/>	1639	688.3277	2061.9613	2061.9677	-3.11	1	1	29	1	ELSAYMRL ^{LLDLDSSYR} + Oxidation (M)
<input checked="" type="checkbox"/>	1567	981.0089	1960.0032	1960.0014	0.96	1	1	41	1	YIKESNHQLQSVSVNSK
<input checked="" type="checkbox"/>	1848	830.7346	2489.1820	2489.1903	-3.36	0	1	34	1	IGDDNLLMINAHIAHDCQ ^{IGNR} + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1012	758.8647	1515.7148	1515.7140	0.55	1	1	29	1	YSFTPGDVRTAM ^R + Oxidation (M)
<input checked="" type="checkbox"/>	1501	927.4342	1852.8538	1852.8472	3.56	1	1	30	1	EKGISSDNESVASCNSVK
<input checked="" type="checkbox"/>	454	559.3087	1116.6028	1116.6042	-1.19	0	1	39	1	LFCFSIIFK
<input checked="" type="checkbox"/>	1186	808.3636	1614.7126	1614.7171	-2.74	0	1	16	1	CQAVGDPYCTFVAK + 2 Carbamidomethyl (C)
<input checked="" type="checkbox"/>	70	407.7371	813.4596	813.4596	0.05	0	1	53	1	TPGGIIEK
<input checked="" type="checkbox"/>	908	479.9731	1436.8975	1436.8966	0.60	1	1	1.6	1	TLALLQ ^{AELPLKK}
<input checked="" type="checkbox"/>	1431	886.4255	1770.8364	1770.8294	3.97	0	1	45	1	FCCASPGSVVLGHGAPR + 2 Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1897	640.5483	2558.1641	2558.1669	-1.09	1	1	19	1	DFGKMTANSVSVATCEQLTYYSK + Oxidation (M)
<input checked="" type="checkbox"/>	1898	854.0733	2559.1981	2559.2073	-3.60	1	1	29	1	SWMCRQCGSFLSTQPTVSPFFIGK
<input checked="" type="checkbox"/>	1224	544.6025	1630.7857	1630.7886	-1.77	1	1	43	1	GFQAEPAQMRAGAPGK + Oxidation (M)
<input checked="" type="checkbox"/>	1759	736.3757	2206.1053	2206.1117	-2.92	1	1	47	1	DVTIFSANELSQAQEDKIAK
<input checked="" type="checkbox"/>	1640	516.7418	2062.9381	2062.9306	3.65	1	1	28	1	MKAIYWTSEDGSVYEER
<input checked="" type="checkbox"/>	1810	806.3952	2416.1638	2416.1654	-0.67	1	1	40	1	QALAQYLP ^{SLEQIMDKYMDK} + 2 Oxidation (M)
<input checked="" type="checkbox"/>	961	741.3675	1480.7204	1480.7158	3.17	1	1	50	1	YSDQELKQQTNK
<input checked="" type="checkbox"/>	1642	689.3388	2064.9946	2064.9938	0.36	1	1	48	1	QEPKNYMPNFAE ^{EIALR} + Oxidation (M)
<input checked="" type="checkbox"/>	1777	1139.0680	2276.1214	2276.1181	1.48	1	1	42	1	LEPIPQLKCVGGTAGCDSYTPK
<input checked="" type="checkbox"/>	1951	992.4886	2974.4440	2974.4515	-2.54	0	1	35	1	TTDVTGEVILPEGTEMVMPGDNVTINVK + Oxidation (M)
<input checked="" type="checkbox"/>	1379	867.4306	1732.8466	1732.8420	2.66	1	1	52	1	DDFPNFEGHKSLLSK
<input checked="" type="checkbox"/>	1175	804.9052	1607.7958	1607.8003	-2.75	0	1	60	1	QDAATTNTVSTVSVSK
<input checked="" type="checkbox"/>	1019	759.3701	1516.7256	1516.7232	1.62	0	1	37	1	FETTAVNTLFC ^{SK} + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1453	900.9526	1799.8906	1799.8845	3.43	1	1	45	1	GCHVMSGTPGRVLDMIK
<input checked="" type="checkbox"/>	1845	828.0544	2481.1414	2481.1451	-1.49	1	1	25	1	MGRTGVDIVSLDWTVDMAEGCAR
<input checked="" type="checkbox"/>	297	510.2523	1018.4900	1018.4866	3.43	1	1	71	1	EPNGMARTK + Oxidation (M)
<input checked="" type="checkbox"/>	978	500.5952	1498.7638	1498.7667	-1.97	0	1	44	1	EPPTYLGLPANA ^{EK}
<input checked="" type="checkbox"/>	966	495.9587	1484.8543	1484.8562	-1.31	1	1	19	1	DVIILSLVRSNEK
<input checked="" type="checkbox"/>	1299	562.2538	1683.7396	1683.7345	3.02	1	1	19	1	MASFHKGAAGDSMGSSK + Oxidation (M)
<input checked="" type="checkbox"/>	1317	850.4290	1698.8434	1698.8498	-3.74	1	1	42	1	KMEITYLSQDLSQK + Oxidation (M)
<input checked="" type="checkbox"/>	639	628.3203	1254.6260	1254.6278	-1.41	0	1	46	1	MSQFTNVAITK + Oxidation (M)

<input checked="" type="checkbox"/>	1226	546.2708	1635.7906	1635.7848	3.55	1	1	51	1	ALVEICTEMEKEGK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	386	544.3276	1086.6406	1086.6437	-2.84	0	1	29	1	NVTIVPGLFK
<input checked="" type="checkbox"/>	458	561.2682	1120.5218	1120.5257	-3.39	1	1	66	1	MPPMTKAEGK + 2 Oxidation (M)
<input checked="" type="checkbox"/>	1113	525.2888	1572.8446	1572.8471	-1.61	1	1	38	1	TISLRVDEAELATR
<input checked="" type="checkbox"/>	697	432.5977	1294.7713	1294.7721	-0.66	1	1	8.1	1	ETLVGRVVGPIR
<input checked="" type="checkbox"/>	1968	781.1545	3120.5889	3120.5840	1.58	1	1	28	1	NDLNSLVNKYNQINSNTVLFPAQSGSGVK
<input checked="" type="checkbox"/>	508	573.7658	1145.5170	1145.5209	-3.37	0	1	24	1	TSCCSLYTIR
<input checked="" type="checkbox"/>	1508	932.9408	1863.8670	1863.8632	2.05	0	1	33	1	MSAASNIEEGSLIDAQGR + Oxidation (M)
<input checked="" type="checkbox"/>	1902	855.0714	2562.1924	2562.1964	-1.55	1	1	31	1	MCIQSKAMNEASHSHLGLVFR + Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/>	1357	573.2916	1716.8530	1716.8465	3.79	1	1	58	1	TDPEMGSLLRQLSDR
<input checked="" type="checkbox"/>	1637	1031.4820	2060.9494	2060.9441	2.58	1	1	37	1	RAMADPEVQQIMSDPAMR + Oxidation (M)
<input checked="" type="checkbox"/>	272	501.2925	1000.5704	1000.5706	-0.11	1	1	1.2e+002	1	HLLFDKTK
<input checked="" type="checkbox"/>	616	614.2993	1226.5840	1226.5853	-0.99	0	1	30	1	ITYEAIQDMK + Oxidation (M)
<input checked="" type="checkbox"/>	1097	781.3725	1560.7304	1560.7251	3.43	1	1	42	1	YCKGMGIVQPYMR + Oxidation (M)
<input checked="" type="checkbox"/>	1686	1057.0040	2111.9934	2111.9906	1.35	0	1	39	1	SGSPQVYSSSSGGGATLIGGGR
<input checked="" type="checkbox"/>	1864	631.0533	2520.1841	2520.1890	-1.93	0	1	32	1	MWPNSSSLGPCFRPTNITLEER + Oxidation (M)
<input checked="" type="checkbox"/>	675	640.3909	1278.7672	1278.7660	0.99	0	1	9.3	1	IIGGGQPLGIVAGK
<input checked="" type="checkbox"/>	1237	822.3994	1642.7842	1642.7780	3.81	1	1	33	1	WEFQKGEAFYGP
<input checked="" type="checkbox"/>	1295	559.6567	1675.9483	1675.9509	-1.56	1	1	18	1	DGVTLTLKQLSAVFGK
<input checked="" type="checkbox"/>	1799	788.4139	2362.2199	2362.2128	2.97	1	1	37	1	RSEIPADIVTSSGSLDHPHISPK
<input checked="" type="checkbox"/>	1569	654.9567	1961.8483	1961.8537	-2.79	1	1	12	1	AYGEKSSQTSPCSQGYGR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	221	479.2772	956.5398	956.5403	-0.49	0	1	94	1	VERPSTLR
<input checked="" type="checkbox"/>	1917	864.7485	2591.2237	2591.2247	-0.39	1	1	34	1	EALLDPEMSKYSVIMLDEAHER + Oxidation (M)
<input checked="" type="checkbox"/>	1963	1028.5110	3082.5112	3082.5110	0.05	1	1	40	1	WQGLTGKTIDLHVGDICDFEFLAETFK
<input checked="" type="checkbox"/>	1526	941.4627	1880.9108	1880.9125	-0.86	1	1	47	1	KAAECFGSQCVVVAIDGK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1555	968.5305	1935.0464	1935.0539	-3.87	0	1	29	1	KPLLSAVCPGFLIYTEK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1583	996.4988	1990.9830	1990.9861	-1.52	1	1	54	1	TGDVARWLDNGAVEYLGR
<input checked="" type="checkbox"/>	1953	992.8245	2975.4517	2975.4568	-1.71	1	1	42	1	ECLELYNLGFLFAPFYSEGFYRIK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1758	1104.0590	2206.1034	2206.0953	3.70	1	1	49	1	MLREFNVEANVGNPQVAYR
<input checked="" type="checkbox"/>	1814	609.0483	2432.1641	2432.1642	-0.02	1	1	42	1	MPQLNSGEGDELGANDELIRFK
<input checked="" type="checkbox"/>	1301	842.9230	1683.8314	1683.8324	-0.55	1	1	60	1	NINGESCLMFAIKTK + Oxidation (M)
<input checked="" type="checkbox"/>	1890	846.0738	2535.1996	2535.1965	1.22	1	1	41	1	KFDEWVAPTPEVADMQNHLHR + Oxidation (M)
<input checked="" type="checkbox"/>	127	436.7749	871.5352	871.5378	-2.98	0	1	35	1	ILVESALK
<input checked="" type="checkbox"/>	1842	620.7969	2479.1585	2479.1624	-1.57	1	1	31	1	REYGIDPGIEHYGCMLDLIGR + Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/>	1870	845.7217	2534.1433	2534.1417	0.62	1	1	21	1	TELFDLDDMRELLSSCNNTYR
<input checked="" type="checkbox"/>	1964	1544.6770	3087.3394	3087.3347	1.53	0	1	8	1	LPCPEDCVISEWGPWTALPCNPSGSR + 3 Carbamidomethyl (C)
<input checked="" type="checkbox"/>	68	407.2048	812.3950	812.3963	-1.52	0	1	32	1	MPPANQR
<input checked="" type="checkbox"/>	1255	824.9149	1647.8152	1647.8185	-1.95	1	1	57	1	ISNCIIDMNRIGR + Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/>	1410	875.4279	1748.8412	1748.8477	-3.68	0	1	57	1	MNYNDPLEPAMIITK
<input checked="" type="checkbox"/>	1755	735.7032	2204.0878	2204.0837	1.86	1	1	49	1	MAYKANFHPLEGLIDGAWR + Oxidation (M)
<input checked="" type="checkbox"/>	1521	470.7218	1878.8581	1878.8636	-2.91	0	0	40	1	ESSFNSFLGDSSGISFAK
<input checked="" type="checkbox"/>	1734	1084.0380	2166.0614	2166.0568	2.13	0	0	56	1	VLDSMLPFFTGIYGNPHSR + Oxidation (M)
<input checked="" type="checkbox"/>	1978	1060.2100	3177.6082	3177.5971	3.50	1	0	29	1	MISLLETQQSENDIKMQVLMSEIEQLK
<input checked="" type="checkbox"/>	1416	439.4493	1753.7681	1753.7652	1.68	0	0	17	1	EDGFVVVDEEDVCIGCR
<input checked="" type="checkbox"/>	1865	841.0692	2520.1858	2520.1811	1.87	0	0	36	1	FGVSASAPVMAMPAGAAAGGAAAEK
<input checked="" type="checkbox"/>	1390	869.9594	1737.9042	1737.9050	-0.41	0	0	42	1	IDLNNYSFLVQSVAR

<input checked="" type="checkbox"/>	1418	585.6169	1753.8289	1753.8305	-0.93	0	0	46	1	MTTVVAGSSNQDEFIR
<input checked="" type="checkbox"/>	1930	881.4102	2641.2088	2641.2177	-3.37	1	0	26	1	DVELNELEPEKQPMNAADGAAAGEK + Oxidation (M)
<input checked="" type="checkbox"/>	1164	535.6080	1603.8022	1603.7963	3.66	1	0	51	1	VHCNDFLIKSICR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1349	858.4241	1714.8336	1714.8288	2.84	1	0	49	1	NWPPHRSEATDLHR
<input checked="" type="checkbox"/>	217	478.2879	954.5612	954.5611	0.21	1	0	31	1	IRDSLVR
<input checked="" type="checkbox"/>	801	677.8014	1353.5882	1353.5904	-1.62	1	0	25	1	DSMRDDLMDIK + Oxidation (M)
<input checked="" type="checkbox"/>	1345	855.9316	1709.8486	1709.8461	1.52	1	0	51	1	CHPWHPGGVDPVPEK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1779	1139.0750	2276.1354	2276.1333	0.92	0	0	57	1	LLSQPMALPPCTEPTFQGLPH
<input checked="" type="checkbox"/>	1832	616.7981	2463.1633	2463.1695	-2.52	1	0	35	1	CTELPEKLPVTTEMVECSLER + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1847	830.7345	2489.1817	2489.1903	-3.48	0	0	44	1	IGDDNLLMINAHIAHDCCQIGNR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1935	883.7548	2648.2426	2648.2496	-2.64	0	0	36	1	VTAMPTAPTLLNMAPNDEIISMDR + 3 Oxidation (M)
<input checked="" type="checkbox"/>	808	453.2111	1356.6115	1356.6132	-1.28	0	0	28	1	LCAQNAFYENK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1197	540.9387	1619.7943	1619.7890	3.25	0	0	54	1	DSGETESLIVSQLDK
<input checked="" type="checkbox"/>	418	556.7614	1111.5082	1111.5047	3.23	0	0	28	1	HHYESTNPK
<input checked="" type="checkbox"/>	1082	777.3671	1552.7196	1552.7232	-2.27	0	0	39	1	YSSCEPIVPGGYK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1929	878.7519	2633.2339	2633.2301	1.43	1	0	31	1	LMYEHNLQRTACSMTHGPFPGVK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1106	785.8427	1569.6708	1569.6763	-3.48	0	0	13	1	MSNMSIQDDVTTGLR + Oxidation (M)
<input checked="" type="checkbox"/>	1332	568.9429	1703.8069	1703.8036	1.93	1	0	45	1	DKMLSIQINDPSTEN
<input checked="" type="checkbox"/>	1797	787.3868	2359.1386	2359.1379	0.27	1	0	48	1	MPHKIGFVVVSSSGHEDGFSAR + Oxidation (M)
<input checked="" type="checkbox"/>	1932	882.4584	2644.3534	2644.3564	-1.15	1	0	43	1	ICHSKTPSLTSSLSQC DIVISAIGK + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1674	1049.0080	2096.0014	2096.0037	-1.07	1	0	43	1	NWKVTDASLFEMLNWK
<input checked="" type="checkbox"/>	1776	755.6832	2264.0278	2264.0267	0.48	0	0	27	1	MANDQHTELETEFTLDQVK + Oxidation (M)
<input checked="" type="checkbox"/>	205	471.7553	941.4960	941.4971	-1.07	0	0	53	1	DWGLLNPK
<input checked="" type="checkbox"/>	1454	904.9750	1807.9354	1807.9390	-1.94	1	0	59	1	TVEMIEEGDLKYLR
<input checked="" type="checkbox"/>	1854	836.0656	2505.1750	2505.1660	3.58	0	0	44	1	TDDPGSGFTTVWNAVSELNGDPK
<input checked="" type="checkbox"/>	1907	859.7447	2576.2123	2576.2145	-0.85	1	0	42	1	YDPEYVLLLSGDHIYKMDYDK
<input checked="" type="checkbox"/>	1944	920.7999	2759.3779	2759.3800	-0.76	1	0	41	1	QGRESGAQVLVYDMPLLIENGEVVK
<input checked="" type="checkbox"/>	674	640.2551	1278.4956	1278.4978	-1.66	0	0	2	1	CMGPMTHCTGK + 2 Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1560	970.9720	1939.9294	1939.9230	3.31	1	0	47	1	LMEMEQLSSLRETEK + Oxidation (M)
<input checked="" type="checkbox"/>	1122	527.6028	1579.7866	1579.7915	-3.15	0	0	68	1	LIYEMAGIDEALAR + Oxidation (M)
<input checked="" type="checkbox"/>	1442	889.4586	1776.9026	1776.9054	-1.52	1	0	78	1	ALRLSGGDHCHAGTVVGK
<input checked="" type="checkbox"/>	1008	757.3453	1512.6760	1512.6766	-0.37	1	0	38	1	NIKDICYTADDDK
<input checked="" type="checkbox"/>	694	647.3254	1292.6362	1292.6408	-3.50	0	0	70	1	ALGTNAHMGHLR + Oxidation (M)
<input checked="" type="checkbox"/>	1052	768.8707	1535.7268	1535.7323	-3.58	0	0	64	1	NQEMVLSCLDALK + Carbamidomethyl (C); Oxidation (M)
<input checked="" type="checkbox"/>	1910	860.3917	2578.1533	2578.1470	2.42	1	0	21	1	MLDGMRRALFLNSGQVCLCSER + Carbamidomethyl (C); 3 Oxidation (M)
<input checked="" type="checkbox"/>	421	556.7620	1111.5094	1111.5080	1.27	1	0	24	1	MSGPRGGSYGK + Oxidation (M)
<input checked="" type="checkbox"/>	1959	1002.8290	3005.4652	3005.4661	-0.30	1	0	41	1	SGMIKMQTLADIGVFSQFIGMLTDSR + 2 Oxidation (M)
<input checked="" type="checkbox"/>	586	598.7632	1195.5118	1195.5074	3.75	1	0	18	1	KMSENGTCNR + Carbamidomethyl (C)
<input checked="" type="checkbox"/>	1729	1079.0290	2156.0434	2156.0428	0.31	1	0	53	1	METAINIGFACSLLRQDMK + Oxidation (M)
<input checked="" type="checkbox"/>	512	574.7373	1147.4600	1147.4644	-3.82	0	0	6.6	1	MGYWDADYK
<input checked="" type="checkbox"/>	1124	791.8373	1581.6600	1581.6657	-3.59	0	0	10	1	EFTDGNLYFSDMK + Oxidation (M)
<input checked="" type="checkbox"/>	1592	674.9915	2021.9527	2021.9451	3.74	1	0	52	1	MNFQEAWEKQPMSPKPR + Oxidation (M)
<input checked="" type="checkbox"/>	1117	788.8936	1575.7726	1575.7715	0.72	1	0	64	1	ASISMLRSEHPVSF + Oxidation (M)
<input checked="" type="checkbox"/>	1294	838.9813	1675.9480	1675.9509	-1.68	0	0	19	1	VVSHLIGLLDPSIDAK
<input checked="" type="checkbox"/>	1	448.2766	447.2693							
<input checked="" type="checkbox"/>	2	478.3141	477.3068							

<input checked="" type="checkbox"/>	3	492.2802	491.2729
<input checked="" type="checkbox"/>	4	495.3405	494.3332
<input checked="" type="checkbox"/>	5	503.1075	502.1002
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<input checked="" type="checkbox"/>	9	362.2227	722.4308
<input checked="" type="checkbox"/>	12	362.7383	723.4620
<input checked="" type="checkbox"/>	14	367.7216	733.4286
<input checked="" type="checkbox"/>	16	737.4592	736.4519
<input checked="" type="checkbox"/>	19	376.2309	750.4472
<input checked="" type="checkbox"/>	23	379.2485	756.4824
<input checked="" type="checkbox"/>	24	381.2210	760.4274
<input checked="" type="checkbox"/>	26	382.2198	762.4250
<input checked="" type="checkbox"/>	27	383.2043	764.3940
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<input checked="" type="checkbox"/>	29	384.7514	767.4882
<input checked="" type="checkbox"/>	32	385.7411	769.4676
<input checked="" type="checkbox"/>	36	388.3422	774.6698
<input checked="" type="checkbox"/>	37	388.3422	774.6698
<input checked="" type="checkbox"/>	38	388.3423	774.6700
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<input checked="" type="checkbox"/>	40	388.3424	774.6702
<input checked="" type="checkbox"/>	41	392.2874	782.5602
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<input checked="" type="checkbox"/>	44	392.7485	783.4824
<input checked="" type="checkbox"/>	50	398.2509	794.4872
<input checked="" type="checkbox"/>	51	398.2510	794.4874
<input checked="" type="checkbox"/>	52	398.7744	795.5342
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<input checked="" type="checkbox"/>	54	399.7383	797.4620
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<input checked="" type="checkbox"/>	65	406.2485	810.4824
<input checked="" type="checkbox"/>	66	406.7643	811.5140
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<input checked="" type="checkbox"/>	69	407.2879	812.5612
<input checked="" type="checkbox"/>	78	411.7475	821.4804
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<input checked="" type="checkbox"/>	94	420.2641	838.5136
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Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin
Variable modifications : [Carbamidomethyl \(C\)](#), [Oxidation \(M\)](#)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 4 ppm
Fragment Mass Tolerance : ± 0.4 Da
Max Missed Cleavages : 1
Instrument type : ESI-TRAP
Number of queries : 1987

Mascot: <http://www.matrixscience.com/>