



Mascot Search Results

User : Luz Valero
 Email : lvalero@cipf.es
 Search title : Project: MLV, Spot Set: MLV\LC 100803
 MS data file : MGF combinado.txt
 Database : Sprout 20100224 (514789 sequences; 181163771 residues)
 Taxonomy : Saccharomyces Cerevisiae (baker's yeast) (6552 sequences)
 Timestamp : 6 Aug 2010 at 11:24:49 GMT
 Enzyme : Trypsin
 Variable modifications : Deamidated (NQ), Oxidation (M)
 Mass values : Monoisotopic
 Protein Mass : Unrestricted
 Peptide Mass Tolerance : ± 100 ppm
 Fragment Mass Tolerance : ± 0.6 Da
 Max Missed Cleavages : 1
 Instrument type : MALDI-TOF-TOF
 Number of queries : 1679
 Protein hits : [YL455 YEAST](#) PWWP domain-containing protein YLR455W OS=Saccharomyces cerevisiae GN=YLR455W PE=1 SV=1
[H2B1 YEAST](#) Histone H2B.1 OS=Saccharomyces cerevisiae GN=HTB1 PE=1 SV=2
[RL13A YEAST](#) 60S ribosomal protein L13-A OS=Saccharomyces cerevisiae GN=RPL13A PE=1 SV=1
[RL4A YEAST](#) 60S ribosomal protein L4-A OS=Saccharomyces cerevisiae GN=RPL4A PE=1 SV=4
[H4 YEAST](#) Histone H4 OS=Saccharomyces cerevisiae GN=HHF1 PE=1 SV=2
[TAF14 YEAST](#) Transcription initiation factor TFIID subunit 14 OS=Saccharomyces cerevisiae GN=TAF14 PE=1 SV=1
[RL12 YEAST](#) 60S ribosomal protein L12 OS=Saccharomyces cerevisiae GN=RPL12A PE=1 SV=1
[RL19 YEAST](#) 60S ribosomal protein L19 OS=Saccharomyces cerevisiae GN=RPL19A PE=1 SV=5
[RL14A YEAST](#) 60S ribosomal protein L14-A OS=Saccharomyces cerevisiae GN=RPL14A PE=1 SV=1
[RLA0 YEAST](#) 60S acidic ribosomal protein P0 OS=Saccharomyces cerevisiae GN=RPP0 PE=1 SV=1
[RL33B YEAST](#) 60S ribosomal protein L33-B OS=Saccharomyces cerevisiae GN=RPL33B PE=1 SV=2
[RS5 YEAST](#) 40S ribosomal protein S5 OS=Saccharomyces cerevisiae GN=RPS5 PE=1 SV=3
[RS17A YEAST](#) 40S ribosomal protein S17-A OS=Saccharomyces cerevisiae GN=RPS17A PE=1 SV=1
[RIM1 YEAST](#) Single-stranded DNA-binding protein RIM1, mitochondrial OS=Saccharomyces cerevisiae GN=RIM1 PE=1 SV=1
[H2A1 YEAST](#) Histone H2A.1 OS=Saccharomyces cerevisiae GN=HTA1 PE=1 SV=2
[ACT YEAST](#) Actin OS=Saccharomyces cerevisiae GN=ACT1 PE=1 SV=1
[RL6A YEAST](#) 60S ribosomal protein L6-A OS=Saccharomyces cerevisiae GN=RPL6A PE=1 SV=2
[H3 YEAST](#) Histone H3 OS=Saccharomyces cerevisiae GN=HHT1 PE=1 SV=2
[RL1 YEAST](#) 60S ribosomal protein L1 OS=Saccharomyces cerevisiae GN=RPL1A PE=1 SV=1
[RL39 YEAST](#) 60S ribosomal protein L39 OS=Saccharomyces cerevisiae GN=RPL39 PE=1 SV=3
[RS15 YEAST](#) 40S ribosomal protein S15 OS=Saccharomyces cerevisiae GN=RPS15 PE=1 SV=1
[RL7A YEAST](#) 60S ribosomal protein L7-A OS=Saccharomyces cerevisiae GN=RPL7A PE=1 SV=3
[EAF6 YEAST](#) Chromatin modification-related protein EAF6 OS=Saccharomyces cerevisiae GN=EAF6 PE=1 SV=1
[RL25 YEAST](#) 60S ribosomal protein L25 OS=Saccharomyces cerevisiae GN=RPL25 PE=1 SV=4
[RL33A YEAST](#) 60S ribosomal protein L33-A OS=Saccharomyces cerevisiae GN=RPL33A PE=1 SV=3
[RL18 YEAST](#) 60S ribosomal protein L18 OS=Saccharomyces cerevisiae GN=RPL18A PE=1 SV=1
[RL27A YEAST](#) 60S ribosomal protein L27-A OS=Saccharomyces cerevisiae GN=RPL27A PE=1 SV=1
[PIB2 YEAST](#) Phosphatidylinositol-3-phosphate-binding protein 2 OS=Saccharomyces cerevisiae GN=PIB2 PE=1 SV=1
[RL30 YEAST](#) 60S ribosomal protein L30 OS=Saccharomyces cerevisiae GN=RPL30 PE=1 SV=3
[RS19A YEAST](#) 40S ribosomal protein S19-A OS=Saccharomyces cerevisiae GN=RPS19A PE=1 SV=2
[TOR2 YEAST](#) Serine/threonine-protein kinase TOR2 OS=Saccharomyces cerevisiae GN=TOR2 PE=1 SV=3
[TAF9 YEAST](#) Transcription initiation factor TFIID subunit 9 OS=Saccharomyces cerevisiae GN=TAF9 PE=1 SV=1
[RDH54 YEAST](#) DNA repair and recombination protein RDH54 OS=Saccharomyces cerevisiae GN=RDH54 PE=1 SV=2
[GAL7 YEAST](#) Galactose-1-phosphate uridylyltransferase OS=Saccharomyces cerevisiae GN=GAL7 PE=1 SV=4
[YNG1 YEAST](#) Protein YNG1 OS=Saccharomyces cerevisiae GN=YNG1 PE=1 SV=1
[RL20 YEAST](#) 60S ribosomal protein L20 OS=Saccharomyces cerevisiae GN=RPL20A PE=1 SV=2
[RS29A YEAST](#) 40S ribosomal protein S29-A OS=Saccharomyces cerevisiae GN=RPS29A PE=1 SV=3

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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

1. [YL455 YEAST](#) Mass: 35487 Score: 2192 Queries matched: 62 emPAI: 19.58

PWWP domain-containing protein YLR455W OS=Saccharomyces cerevisiae GN=YLR455W PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide
15	823.3502	822.3429	822.3508	-9.59	0	19	0.25	1	K.FEENR.L 16 17
39	836.4243	835.4170	835.4439	-32.19	0	52	0.00018	1	R.ELVNAYK.E 38
409	880.4697	879.4624	879.4814	-21.61	1	29	0.042	1	K.VKLDYSR.R 408
494	922.4641	921.4568	921.5072	-54.69	0	33	0.014	1	K.RPFFDLK.A 493
559	991.4893	990.4820	990.5498	-68.42	0	40	0.0027	1	R.VEISQLFR.R 558
587	1011.5046	1010.4973	1010.5145	-16.98	0	73	1.2e-006	1	K.ETHELLNR.I 585 586 588
759	1147.6195	1146.6122	1146.6509	-33.75	1	50	0.0003	1	R.RVEISQLFR.R 760
786	1159.6066	1158.5993	1158.6033	-3.46	0	60	2.5e-005	1	K.IVAGEDPFVGR.T 784 785 787 788 789
812	1180.5673	1179.5600	1179.5771	-14.52	0	87	6e-008	1	R.ETPTEHEIK.E 811 813
1178	1515.6888	1514.6815	1514.7042	-14.95	0	124	8.2e-012	1	K.NFDDFNVFLQEK.F 1177 1179
1182	1516.6487	1515.6414	1515.6882	-30.84	0	(107)	3.7e-010	1	K.NFDDFNVFLQEK.F 1181
1238	1586.8018	1585.7945	1585.7947	-0.12	0	32	0.014	1	K.SNEESKPNIKPSK.K 1237
1259	1616.7670	1615.7597	1615.7689	-5.68	1	103	1.3e-009	1	K.NSISIKEDPEDNQK.S 1260
1276	1643.9235	1642.9162	1642.9181	-1.16	0	106	4.6e-010	1	K.EILLSWADLITELK.K 1275
1299	1683.9072	1682.8999	1682.8933	3.92	0	84	9.4e-008	1	K.VGSFPPWPAVFPQR.L 1300 1301 1302
1325	1714.8990	1713.8917	1713.8897	1.20	1	62	1.3e-005	1	K.SNEESKPNIKPSK.K 1323 1324 1326
1361	1767.8701	1766.8628	1766.8662	-1.88	0	104	8.4e-010	1	K.AIVNDPDLGEFHP LCK.E 1359 1360 1362

1365	1771.9667	1770.9594	1771.0131	-30.30	1	118	3.9e-011	1	K.EILLSWADLITELKK.E	1366	
1435	1872.8380	1871.8307	1871.9417	-59.31	1	40	0.0023	1	R.IYENS DTKRPF DLK.A	1436	
1465	1924.8684	1923.8611	1923.9326	-37.17	0	137	4.8e-013	1	K.ELDQDSIHNFILEH SK.N	1464	
1559	2166.0366	2165.0293	2165.1116	-38.02	1	74	1e-006	1	R.LKELDQDSIHNFILEH SK.N	1558	
1566	2173.0940	2172.0867	2172.0811	2.60	1	72	1.7e-006	1	R.ETPTEHEIKETHELLNR.I	1564	1565
1609	2320.0815	2319.0742	2319.0444	12.9	1	69	2.9e-006	1	K.NFDDFNVFLQEKFEENR.L	1610	

2. [H2B1 YEAST](#) Mass: 14244 Score: 597 Queries matched: 20 emPAI: 9.64
Histone H2B.1 OS=Saccharomyces cerevisiae GN=HTB1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide			
3	816.4480	815.4407	815.4501	-11.50	0	43	0.0018	1	R.EIQTAVR.L	4	5	
534	953.5785	952.5712	952.5957	-25.69	0	77	2.2e-007	1	R.LILPGELAK.H	535		
768	1153.5146	1152.5073	1152.5339	-23.04	0	66	5.1e-006	1	K.ETYSSYIYK.V	767	769	770
855	1211.5848	1210.5775	1210.5942	-13.79	0	22	0.14	1	K.QTHPDTGISQK.S	856		
941	1281.6166	1280.6093	1280.6288	-15.23	1	83	1.2e-007	1	R.KETYSSYIYK.V	942	944	
1364	1771.8693	1770.8620	1770.8611	0.55	0	113	1.3e-010	1	K.SMSILNSFVNDIFER.I	1363		
1367	1772.8547	1771.8474	1771.8451	1.33	0	(76)	6.6e-007	1	K.SMSILNSFVNDIFER.I	1368		
1376	1787.8594	1786.8521	1786.8560	-2.15	0	(34)	0.01	1	K.SMSILNSFVNDIFER.I	1375		

Proteins matching the same set of peptides:

[H2B2 YEAST](#) Mass: 14229 Score: 597 Queries matched: 20
Histone H2B.2 OS=Saccharomyces cerevisiae GN=HTB2 PE=1 SV=2

3. [RL13A YEAST](#) Mass: 22540 Score: 232 Queries matched: 18 emPAI: 1.93
60S ribosomal protein L13-A OS=Saccharomyces cerevisiae GN=RPL13A PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide			
423	883.4380	882.4308	882.4460	-17.27	1	11	1.3	1	R.KHWQER.V	422		
459	901.4444	900.4371	900.4454	-9.16	0	8	3.8	1	K.VHFDQAGK.K			
536	964.5001	963.4928	963.5137	-21.70	0	18	0.43	1	K.AAGLTAAYAR.T			
552	981.5323	980.5251	980.5403	-15.56	0	9	3	1	R.TIGIAVDHR.R	553		
825	1193.5463	1192.5390	1192.5473	-6.90	0	53	0.00012	1	R.AVQDNGESAFR.T	824		
828	1194.5422	1193.5349	1193.5313	3.07	0	(40)	0.0027	1	R.AVQDNGESAFR.T			
829	1194.5422	1193.5349	1193.5313	3.07	0	(31)	0.021	1	R.AVQDNGESAFR.T			
1008	1333.6390	1332.6317	1332.6422	-7.87	0	73	1.4e-006	1	R.NQEIFDANVQR.L	1007	1009	1010
1649	2653.2180	2652.2107	2652.3395	-48.54	0	84	8.8e-008	1	K.APEAEQVLSAAATFPIAQPATDVEAR.A	1650		
1666	2953.3923	2952.3850	2952.4828	-33.13	1	31	0.016	1	R.NGKAPEAEQVLSAAATFPIAQPATDVEAR.A	1667		

4. [RL4A YEAST](#) Mass: 39068 Score: 200 Queries matched: 9 emPAI: 0.46
60S ribosomal protein L4-A OS=Saccharomyces cerevisiae GN=RPL4A PE=1 SV=4

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide	
1118	1444.6537	1443.6464	1443.6491	-1.86	0	70	2e-006	1	K.AGHQTSAESWGTR.A	1117
1270	1630.8755	1629.8682	1629.8726	-2.69	1	9	2.9	1	R.RGPLVVYAEADNGIVK.A	1269
1442	1881.0544	1880.0471	1880.0506	-1.86	0	100	2.1e-009	1	K.IPEIPLVVSTDLESIQK.T	1443
1538	2112.0085	2111.0012	2111.1334	-62.63	0	28	0.042	1	R.IINSSEIQSAIRPAGQATQK.R	1537
1647	2611.4763	2610.4690	2610.4242	17.2	0	10	1.3	1	R.NVPGVETANVASLNLQLAPGAHLGR.F	

Proteins matching the same set of peptides:

[RL4B YEAST](#) Mass: 39038 Score: 200 Queries matched: 9
60S ribosomal protein L4-B OS=Saccharomyces cerevisiae GN=RPL4B PE=1 SV=2

5. [H4 YEAST](#) Mass: 11361 Score: 157 Queries matched: 6 emPAI: 1.32
Histone H4 OS=Saccharomyces cerevisiae GN=HHF1 PE=1 SV=2

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide			
806	1178.6044	1177.5971	1177.6343	-31.54	0	51	0.00027	1	R.ISGLIYEEVR.A	805		
994	1325.7372	1324.7299	1324.7463	-12.34	0	71	1.7e-006	1	R.DNIQGITKPAIR.R	995	996	997

6. [TAF14 YEAST](#) Mass: 27423 Score: 156 Queries matched: 2 emPAI: 0.19
Transcription initiation factor TFIID subunit 14 OS=Saccharomyces cerevisiae GN=TAF14 PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide	
1446	1888.9402	1887.9329	1887.9248	4.30	0	101	2.1e-009	1	K.LNEDDLVGVVQMTDNK.T	1447

7. [RL12 YEAST](#) Mass: 17812 Score: 155 Queries matched: 3 emPAI: 0.31
60S ribosomal protein L12 OS=Saccharomyces cerevisiae GN=RPL12A PE=1 SV=1

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide	
1316	1707.8073	1706.8000	1706.8951	-55.71	0	103	1.2e-009	1	K.HSGNIQLDEIIEIAR.Q	1317
1643	2563.2266	2562.2193	2562.2602	-15.94	1	4	9.1	2	R.VDFKNPHDIEGINAGEIIEIPEN.-	

8. [RL19 YEAST](#) Mass: 21691 Score: 122 Queries matched: 9 emPAI: 0.56
60S ribosomal protein L19 OS=Saccharomyces cerevisiae GN=RPL19A PE=1 SV=5

Query	Observed	Mr(expt)	Mr(calc)	ppm	Miss	Score	Expect	Rank	Peptide				
787	1159.6066	1158.5993	1158.5629	31.5	1	21	0.2	4	K.ALNFEAEARR.L	784	786	788	789
1129	1454.7131	1453.7058	1453.8041	-67.62	1	1	17	7	R.EARLPSQVVWIR.R				
1470	1929.8440	1928.8367	1928.9228	-44.62	0	81	1.6e-007	1	K.VWLDPNETSEIAQANSR.N				

[1513](#) [2058.0264](#) [2057.0191](#) [2057.0177](#) 0.67 1 57 4.8e-005 1 [R.KVWLPNETSEIAQANSR.N](#) [1514](#)

9. [RL14A_YEAST](#) Mass: 15158 Score: 104 Queries matched: 3 emPAI: 0.88
60S ribosomal protein L14-A OS=Saccharomyces cerevisiae GN=RPL14A PE=1 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[862](#) [1212.7017](#) [1211.6944](#) [1211.7125](#) -14.93 0 63 9.2e-006 1 [K.LAAIVEIIDQK.K](#) [863](#)
[1509](#) [2051.2119](#) [2050.2046](#) [2050.1939](#) 5.23 0 37 0.0027 1 [R.QAINLGQVLTPLTFALPR.G](#)

Proteins matching the same set of peptides:

[RL14B_YEAST](#) Mass: 15144 Score: 104 Queries matched: 3
60S ribosomal protein L14-B OS=Saccharomyces cerevisiae GN=RPL14B PE=1 SV=1

10. [RLA0_YEAST](#) Mass: 33745 Score: 100 Queries matched: 7 emPAI: 0.54
60S acidic ribosomal protein P0 OS=Saccharomyces cerevisiae GN=RPP0 PE=1 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[907](#) [1242.6322](#) [1241.6249](#) [1241.6292](#) -3.40 1 33 0.011 1 [K.LREYLEEYK.S](#) [908](#)
[933](#) [1267.6234](#) [1266.6161](#) [1266.6132](#) 2.29 0 59 3.4e-005 1 [R.GFLSDLPDFEK.L](#) [932](#)
[945](#) [1283.5876](#) [1282.5803](#) [1282.6670](#) -67.56 0 7 4.3 1 [R.AGAVAPEDIWVR.A](#)
[1540](#) [2131.0801](#) [2130.0728](#) [2130.0528](#) 9.40 0 42 0.0014 1 [K.SLFVVGVDNVSSQMQHEVR.K](#) [1541](#)

11. [RL33B_YEAST](#) Mass: 12161 Score: 92 Queries matched: 2 emPAI: 0.48
60S ribosomal protein L33-B OS=Saccharomyces cerevisiae GN=RPL33B PE=1 SV=2
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[1345](#) [1750.8683](#) [1749.8610](#) [1749.8937](#) -18.69 0 84 1.2e-007 1 [K.IEGVATPQEAQFYLGR.K](#) [1346](#)

12. [RSS_YEAST](#) Mass: 25023 Score: 89 Queries matched: 7 emPAI: 0.48
40S ribosomal protein S5 OS=Saccharomyces cerevisiae GN=RPS5 PE=1 SV=3
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[835](#) [1196.6398](#) [1195.6325](#) [1195.6462](#) -11.43 0 14 0.85 1 [R.QPIFVAHTAGR.Y](#) [834](#)
[928](#) [1264.6189](#) [1263.6116](#) [1263.6459](#) -27.14 0 34 0.01 1 [K.DASLVVDYVQVR.Q](#) [927](#)
[1015](#) [1339.7987](#) [1338.7914](#) [1338.7983](#) -5.14 0 58 2.2e-005 1 [R.VNQAIALLTIGAR.E](#) [1016](#)
[1234](#) [1584.6962](#) [1583.6889](#) [1583.6919](#) -1.89 1 3 11 1 [R.LTNSLMMNGRNNGK.K](#)

13. [RS17A_YEAST](#) Mass: 15779 Score: 84 Queries matched: 4 emPAI: 0.84
40S ribosomal protein S17-A OS=Saccharomyces cerevisiae GN=RPS17A PE=1 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[956](#) [1296.7513](#) [1295.7440](#) [1295.7561](#) -9.33 0 50 0.00021 1 [K.LPLSVINVAQR.D](#) [957](#)
[1241](#) [1591.7026](#) [1590.6953](#) [1590.7889](#) -58.85 0 45 0.00078 1 [K.DQYVPEVSALDSR.S](#) [1242](#)

Proteins matching the same set of peptides:

[RS17B_YEAST](#) Mass: 15794 Score: 84 Queries matched: 4
40S ribosomal protein S17-B OS=Saccharomyces cerevisiae GN=RPS17B PE=1 SV=1

14. [RIM1_YEAST](#) Mass: 15377 Score: 73 Queries matched: 7 emPAI: 0.87
Single-stranded DNA-binding protein RIM1, mitochondrial OS=Saccharomyces cerevisiae GN=RIM1 PE=1 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[1276](#) [1643.9235](#) [1642.9162](#) [1642.9505](#) -20.87 1 32 0.014 2 [K.GTTLSLVQKDIINLLK.N](#) [1275](#)
[1296](#) [1676.7678](#) [1675.7605](#) [1675.7550](#) 3.29 0 52 0.00017 1 [R.IGSEFTEHTSANNNR.Y](#) [1295](#)
[1501](#) [2014.9335](#) [2013.9262](#) [2014.0160](#) -44.56 1 15 0.74 2 [R.KGALVYVEADAANYVFER.D](#)
[1521](#) [2082.9358](#) [2081.9285](#) [2081.9654](#) -17.69 1 18 0.31 1 [R.IGSEFTEHTSANNNRYLK.Y](#)
[1522](#) [2082.9358](#) [2081.9285](#) [2081.9654](#) -17.69 1 (14) 0.79 3 [R.IGSEFTEHTSANNNRYLK.Y](#)

15. [H2A1_YEAST](#) Mass: 13981 Score: 70 Queries matched: 6 emPAI: 1.80
Histone H2A.1 OS=Saccharomyces cerevisiae GN=HTA1 PE=1 SV=2
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[143](#) [850.4579](#) [849.4506](#) [849.5184](#) -79.85 0 37 0.006 1 [R.HLQLAIR.N](#) [142](#)
[482](#) [917.4772](#) [916.4699](#) [916.5131](#) -47.10 0 41 0.0026 1 [K.AGLTFPVGR.V](#) [481](#)
[1631](#) [2409.3350](#) [2408.3277](#) [2408.3904](#) -26.00 0 35 0.0048 1 [K.LLGNVTIAQGGVLPNIHQNLPLK.K](#) [1630](#)

Proteins matching the same set of peptides:

[H2A2_YEAST](#) Mass: 13981 Score: 70 Queries matched: 6
Histone H2A.2 OS=Saccharomyces cerevisiae GN=HTA2 PE=1 SV=2

16. [ACT_YEAST](#) Mass: 41663 Score: 64 Queries matched: 2 emPAI: 0.12
Actin OS=Saccharomyces cerevisiae GN=ACT1 PE=1 SV=1
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[1381](#) [1790.8209](#) [1789.8136](#) [1789.8846](#) -39.67 0 51 0.00018 1 [K.SYELPDGQVITIGNER.F](#) [1382](#)

17. [RL6A_YEAST](#) Mass: 19949 Score: 61 Queries matched: 5 emPAI: 0.62
60S ribosomal protein L6-A OS=Saccharomyces cerevisiae GN=RPL6A PE=1 SV=2
Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[592](#) [1017.4751](#) [1016.4678](#) [1016.4967](#) -28.43 0 46 0.00064 1 [K.FNVEYFAK.E](#) [591](#)

[849](#) [1202.5614](#) [1201.5541](#) [1201.5914](#) -31.00 1 5 8 1 [K.NGDKPHMLKF.-](#)
[1156](#) [1479.9226](#) [1478.9153](#) [1478.9184](#) -2.11 0 22 0.058 1 [R.ASLVPGTVLILLAGR.F](#) [1155](#)

18. [H3_YEAST](#) Mass: 15347 Score: 57 Queries matched: 4 emPAI: 0.37
 Histone H3 OS=Saccharomyces cerevisiae GN=HHT1 PE=1 SV=2
 Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[574](#) [1004.5665](#) [1003.5592](#) [1003.5815](#) -22.15 0 52 0.00018 1 [R.YKPGTVALR.E](#) [575](#) [576](#) [577](#)

19. [RL1_YEAST](#) Mass: 24470 Score: 51 Queries matched: 2 emPAI: 0.22
 60S ribosomal protein L1 OS=Saccharomyces cerevisiae GN=RPL1A PE=1 SV=1
 Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[1422](#) [1845.9209](#) [1844.9136](#) [1844.9057](#) 4.29 1 51 0.00018 1 [K.AGKFPTPVSHNDLYGK.V](#) [1423](#)

20. [RL39_YEAST](#) Mass: 6338 Score: 43 Queries matched: 3 emPAI: 1.08
 60S ribosomal protein L39 OS=Saccharomyces cerevisiae GN=RPL39 PE=1 SV=3
 Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[978](#) [1307.6797](#) [1306.6724](#) [1306.7258](#) -40.86 0 5 8.7 1 [K.QNRPLPQWIR.L](#)
[1110](#) [1435.8182](#) [1434.8109](#) [1434.8208](#) -6.86 1 38 0.0035 1 [K.QNRPLPQWIR.L](#) [1109](#)

21. [RS15_YEAST](#) Mass: 15992 Score: 42 Queries matched: 2 emPAI: 0.35
 40S ribosomal protein S15 OS=Saccharomyces cerevisiae GN=RPS15 PE=1 SV=1
 Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[1076](#) [1391.7618](#) [1390.7545](#) [1390.7568](#) -1.65 0 40 0.0026 1 [K.LAAPENKPAVPR.T](#) [1077](#)

22. [RL7A_YEAST](#) Mass: 27621 Score: 37 Queries matched: 7 emPAI: 0.19
 60S ribosomal protein L7-A OS=Saccharomyces cerevisiae GN=RPL7A PE=1 SV=3
 Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[878](#) [1219.5929](#) [1218.5856](#) [1218.5894](#) -3.11 0 1 21 4 [K.HFIQGSFGNR.E](#)
[883](#) [1226.5504](#) [1225.5431](#) [1225.6204](#) -63.03 0 13 0.91 1 [K.LSNPSGGWGVPR.K](#) [884](#)
[1490](#) [1979.9709](#) [1978.9636](#) [1978.9650](#) -0.67 1 37 0.0047 1 [K.HFIQGSFGNREEFINK.L](#) [1488](#) [1489](#) [1491](#)

Proteins matching the same set of peptides:

[RL7B_YEAST](#) Mass: 27679 Score: 37 Queries matched: 7
 60S ribosomal protein L7-B OS=Saccharomyces cerevisiae GN=RPL7B PE=1 SV=3

23. [EAF6_YEAST](#) Mass: 12887 Score: 34 Queries matched: 2 emPAI: 0.45
 Chromatin modification-related protein EAF6 OS=Saccharomyces cerevisiae GN=EAF6 PE=1 SV=1
 Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[1320](#) [1708.7250](#) [1707.7177](#) [1707.7098](#) 4.64 0 34 0.007 1 [K.SHSHADSAFNNDR.I](#) [1319](#)

24. [RL25_YEAST](#) Mass: 15748 Score: 33 Queries matched: 2 emPAI: 0.36
 60S ribosomal protein L25 OS=Saccharomyces cerevisiae GN=RPL25 PE=1 SV=4
 Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[1120](#) [1446.7407](#) [1445.7334](#) [1445.7436](#) -7.01 0 31 0.021 1 [K.VIEQPITSETAMK.K](#) [1119](#)

25. [RL33A_YEAST](#) Mass: 12147 Score: 33 Queries matched: 1 emPAI: 0.48
 60S ribosomal protein L33-A OS=Saccharomyces cerevisiae GN=RPL33A PE=1 SV=3
 Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[1334](#) [1736.8760](#) [1735.8687](#) [1735.8781](#) -5.40 0 33 0.012 1 [K.IEGVATPQDAQFYLGK.R](#)

26. [RL18_YEAST](#) Mass: 20551 Score: 33 Queries matched: 8 emPAI: 0.27
 60S ribosomal protein L18 OS=Saccharomyces cerevisiae GN=RPL18A PE=1 SV=1
 Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[475](#) [910.4159](#) [909.4087](#) [909.4279](#) -21.19 0 30 0.017 1 [R.HFGMGPHK.G](#) [476](#)
[477](#) [914.5159](#) [913.5086](#) [913.5345](#) -28.36 0 14 0.86 3 [K.GQNTLILR.G](#) [478](#)
[734](#) [1124.6393](#) [1123.6320](#) [1123.6462](#) -12.60 0 6 4.1 2 [K.INRPPVSVSR.I](#) [736](#)
[1004](#) [1331.7097](#) [1330.7024](#) [1330.7093](#) -5.16 0 24 0.12 1 [K.TVVVGTVDDAR.I](#) [1005](#)

27. [RL27A_YEAST](#) Mass: 15522 Score: 32 Queries matched: 4 emPAI: 0.36
 60S ribosomal protein L27-A OS=Saccharomyces cerevisiae GN=RPL27A PE=1 SV=1
 Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[1159](#) [1490.7744](#) [1489.7671](#) [1489.7790](#) -7.97 0 12 1.8 1 [K.SHPFGHALVAGIER.Y](#) [1160](#)
[1244](#) [1594.7565](#) [1593.7492](#) [1593.7635](#) -8.94 0 32 0.014 1 [K.SVSTETFEQPSQR.E](#) [1243](#)

Proteins matching the same set of peptides:

[RL27B_YEAST](#) Mass: 15496 Score: 32 Queries matched: 4
 60S ribosomal protein L27-B OS=Saccharomyces cerevisiae GN=RPL27B PE=1 SV=1

28. [PIB2_YEAST](#) Mass: 70574 Score: 32 Queries matched: 2 emPAI: 0.07
 Phosphatidylinositol-3-phosphate-binding protein 2 OS=Saccharomyces cerevisiae GN=PIB2 PE=1 SV=1

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[1139](#) 1471.7726 1470.7653 1470.7864 -14.35 0 32 0.017 1 K.QQIQSPAMVSILR.K [1140](#)

29. [RL30_YEAST](#) Mass: 11408 Score: 31 Queries matched: 1 emPAI: 0.52
60S ribosomal protein L30 OS=Saccharomyces cerevisiae GN=RPL30 PE=1 SV=3

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[1398](#) 1816.8730 1815.8657 1815.8792 -7.40 0 31 0.021 1 K.VVYFQGGNNELGTAVGK.L

30. [RS19A_YEAST](#) Mass: 15907 Score: 30 Queries matched: 3 emPAI: 0.35
40S ribosomal protein S19-A OS=Saccharomyces cerevisiae GN=RPS19A PE=1 SV=2

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[1468](#) 1928.9600 1927.9527 1927.9428 5.14 0 30 0.022 1 R.DVAAQDFINAYASFLQR.Q [1469](#)
[1576](#) 2199.9216 2198.9143 2198.9691 -24.91 1 13 0.92 1 K.TSSGNEMPPQDAEGWFYKR.A

Proteins matching the same set of peptides:

[RS19B_YEAST](#) Mass: 15881 Score: 30 Queries matched: 3
40S ribosomal protein S19-B OS=Saccharomyces cerevisiae GN=RPS19B PE=1 SV=2

31. [TOR2_YEAST](#) Mass: 281390 Score: 30 Queries matched: 6 emPAI: 0.02
Serine/threonine-protein kinase TOR2 OS=Saccharomyces cerevisiae GN=TOR2 PE=1 SV=3

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[3](#) 816.4480 815.4407 815.4501 -11.48 0 30 0.033 3 R.LAANTLGR.L [4](#)
[759](#) 1147.6195 1146.6122 1146.6430 -26.87 1 12 1.7 7 K.AALSIEKMR.I
[1039](#) 1358.6974 1357.6901 1357.7275 -27.55 0 1 23 2 R.VLIPSSDIEVMR.L [1037](#)
[1550](#) 2154.9753 2153.9680 2154.1797 -98.26 0 4 8 1 R.IHSPVLVDQAEVSHELIR.M

32. [TAF9_YEAST](#) Mass: 17304 Score: 28 Queries matched: 2 emPAI: 0.32
Transcription initiation factor TFIID subunit 9 OS=Saccharomyces cerevisiae GN=TAF9 PE=1 SV=1

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[818](#) 1190.6544 1189.6471 1189.6012 38.6 0 28 0.044 1 K.ELMLQLAAER.N [819](#)

33. [RDH54_YEAST](#) Mass: 104087 Score: 27 Queries matched: 6 emPAI: 0.05
DNA repair and recombination protein RDH54 OS=Saccharomyces cerevisiae GN=RDH54 PE=1 SV=2

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[16](#) 823.3502 822.3429 822.3065 44.2 0 1 14 10 R.NSPDMDK.M
[831](#) 1194.5613 1193.5540 1193.5961 -35.29 1 27 0.052 1 R.QLMKNLSLQK.F [828](#) [830](#)
[928](#) 1264.6189 1263.6116 1263.5587 41.9 1 12 1.8 8 R.NSPDMDKMAVR.N [927](#)

34. [GAL7_YEAST](#) Mass: 42358 Score: 26 Queries matched: 2 emPAI: 0.12
Galactose-1-phosphate uridylyltransferase OS=Saccharomyces cerevisiae GN=GAL7 PE=1 SV=4

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[40](#) 842.4913 841.4840 841.4406 51.6 0 26 0.04 1 R.ATGNLNPR.Y [41](#)

35. [YNG1_YEAST](#) Mass: 25334 Score: 26 Queries matched: 2 emPAI: 0.21
Protein YNG1 OS=Saccharomyces cerevisiae GN=YNG1 PE=1 SV=1

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[1605](#) 2294.9866 2293.9793 2294.0558 -33.36 1 26 0.046 1 R.LMQTIDLFKNEDEPGMER.A [1606](#)

36. [RL20_YEAST](#) Mass: 20424 Score: 26 Queries matched: 1 emPAI: 0.27
60S ribosomal protein L20 OS=Saccharomyces cerevisiae GN=RPL20A PE=1 SV=2

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[1457](#) 1907.9803 1906.9730 1906.9748 -0.94 0 26 0.06 1 K.ASGEIVSINQINEAHPK.V

37. [RS29A_YEAST](#) Mass: 6656 Score: 25 Queries matched: 2 emPAI: 1.01
40S ribosomal protein S29-A OS=Saccharomyces cerevisiae GN=RPS29A PE=1 SV=3

Query Observed Mr(expt) Mr(calc) ppm Miss Score Expect Rank Peptide
[1067](#) 1379.6636 1378.6563 1378.6531 2.37 0 25 0.081 1 M.AHENVWFSHPR.R [1066](#)

Proteins matching the same set of peptides:

[RS29B_YEAST](#) Mass: 6723 Score: 25 Queries matched: 2
40S ribosomal protein S29-B OS=Saccharomyces cerevisiae GN=RPS29B PE=1 SV=3