SUPPLEMENTAL FIGURE LEGENDS

SUPPLEMENTAL FIGURE 1: Representative phase contrast micrographs of 3 h video-microscopy. *C. albicans* strain SC5314 was incubated in RPMI plus 10% FBS at 37°C with RAW 264.7 murine macrophages. Upper panels from left to right correspond to 20, 40 and 60 min interaction whereas lower panels correspond to 1.5, 2 and 3 h interaction.

SUPPLEMENTAL FIGURE 2: Synthetic 2D reference gel of *C. albicans* upon macrophage interaction.

SUPPLEMENTAL FIGURE 3: Expression profile of *C. albicans* genes upon macrophage interaction at two time points (bold bars correspond to 1.5 h of interaction and diagonally striped bars to 3 h of interaction, respectively). Genes were classified according to their biological function as described under "Experimental Procedures".

SUPPLEMENTAL FIGURE 4: Maps of physical and genetic interactions of up-regulated (***A***) and down-regulated (***B***) unknown genes were made using the Osprey v1.2.0 visualization program. Up-regulated genes are red-colored while down-regulated genes are green-colored. Black-colored ones represent new interacting genes. All genes represented correspond to *S. cerevisiae* orthologs (because the database employed is the BioGRID). Lines connecting genes are colored to represent the nature of known interaction(s) between a pair of genes (i.e., synthetic lethality, two-hybrid, etc). Vertices are colored to represent the GO biological processes directed by the gene product, as annotated by SGD.

SUPPLEMENTAL FIGURE 5: (***A***) Osprey interaction network containing physical and genetic interactions of actin cytoskeleton (red-colored), mitochondria (green-colored), autophagy (brown-colored), cAMP signaling (blue-colored) and apoptosis (pink-colored) related genes detected in the proteomic and genomic datasets. Black-colored genes represent new interacting genes. All genes represented correspond to *S. cerevisiae* orthologs (because the database employed is the BioGRID), as well as for Supplemental Figs 4*A* and 4*B*. Lines connecting genes are colored to represent the nature of known interaction(s) between a pair of genes (i.e., synthetic lethality, two-hybrid, etc). Vertices are colored to represent the GO biological processes directed by the gene product, as annotated by SGD. (***B***) Actin cytoskeleton sub-interaction network. (***C***) Mitochondria sub-interaction network. (***D***) Apoptosis and autophagy sub-interaction network. All interaction maps were made using the Osprey v1.2.0 visualization program.

SUPPLEMENTAL TABLE LEGENDS

SUPPLEMENTAL TABLE I: Statistical analysis of differentially expressed (increased and diminished) protein spots present in the synthetic gel from each condition (control and treated yeast cells). Central tendency (arithmetic mean) and dispersion (mean squared deviation, MSD) of the %Vol, as well as the expression ratio (treated/control yeast cells), was calculated. Identified proteins by MALDI-TOF/TOF MS, plus the probability associated with a Student's *t*-Test of over- and under-expressed proteins, with a two-tailed distribution, is also illustrated.

SUPPLEMENTAL TABLE II: *C. albicans* proteins identified by MALDI-TOF/TOF MS. The proteins are listed by their protein name, function and accession number (as described in Table

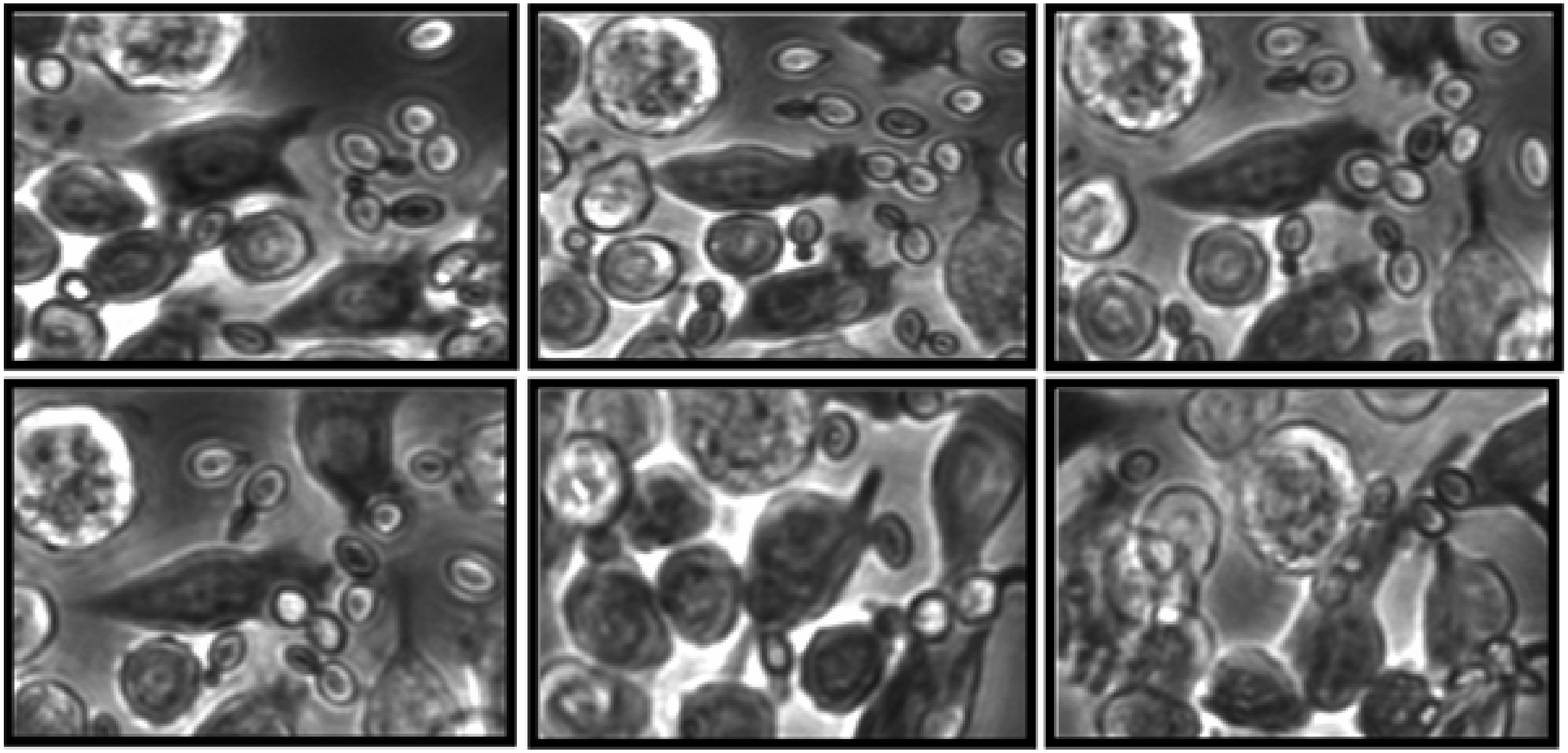
I). Underneath each entry, an overview is given of the matching peptides, which includes the observed and calculated mass, the mass deviation, the relative position of the peptide in the mature sequence, the number of miscleavages, the corresponding peptide sequence and the unmatched peptides. Also, additional information regarding the protein Mowse score, sequence coverage, number of mass values matched/searched and the search parameters used in the Mascot searches can be found. Some of the proteins identified by MS/MS ion search are supplied with their MS/MS spectra.

SUPPLEMENTAL TABLE III: Functional classification of *C. albicans* SC5314 differentially expressed genes after macrophage interaction, in at least one of the conditions tested.

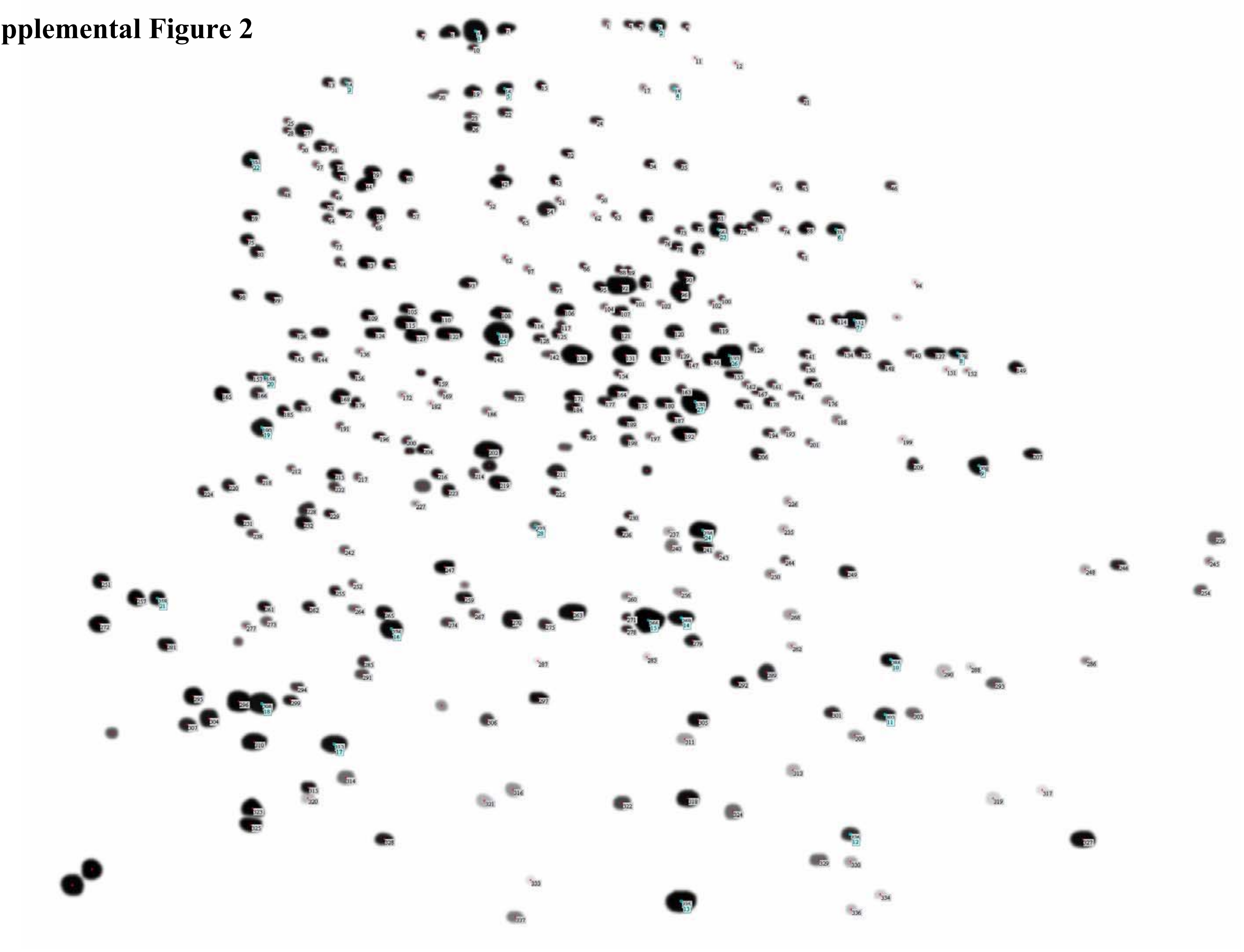
SUPPLEMENTAL TABLE IV: Evidence of functional enrichment in the genomic and proteomic datasets. Functional categories (MIPS functional classification and GO biological process) exhibiting statistically-significantly elevated membership for the set of *C. albicans* modulated genes/proteins after macrophage interaction.

SUPPLEMENTARY FIGURES

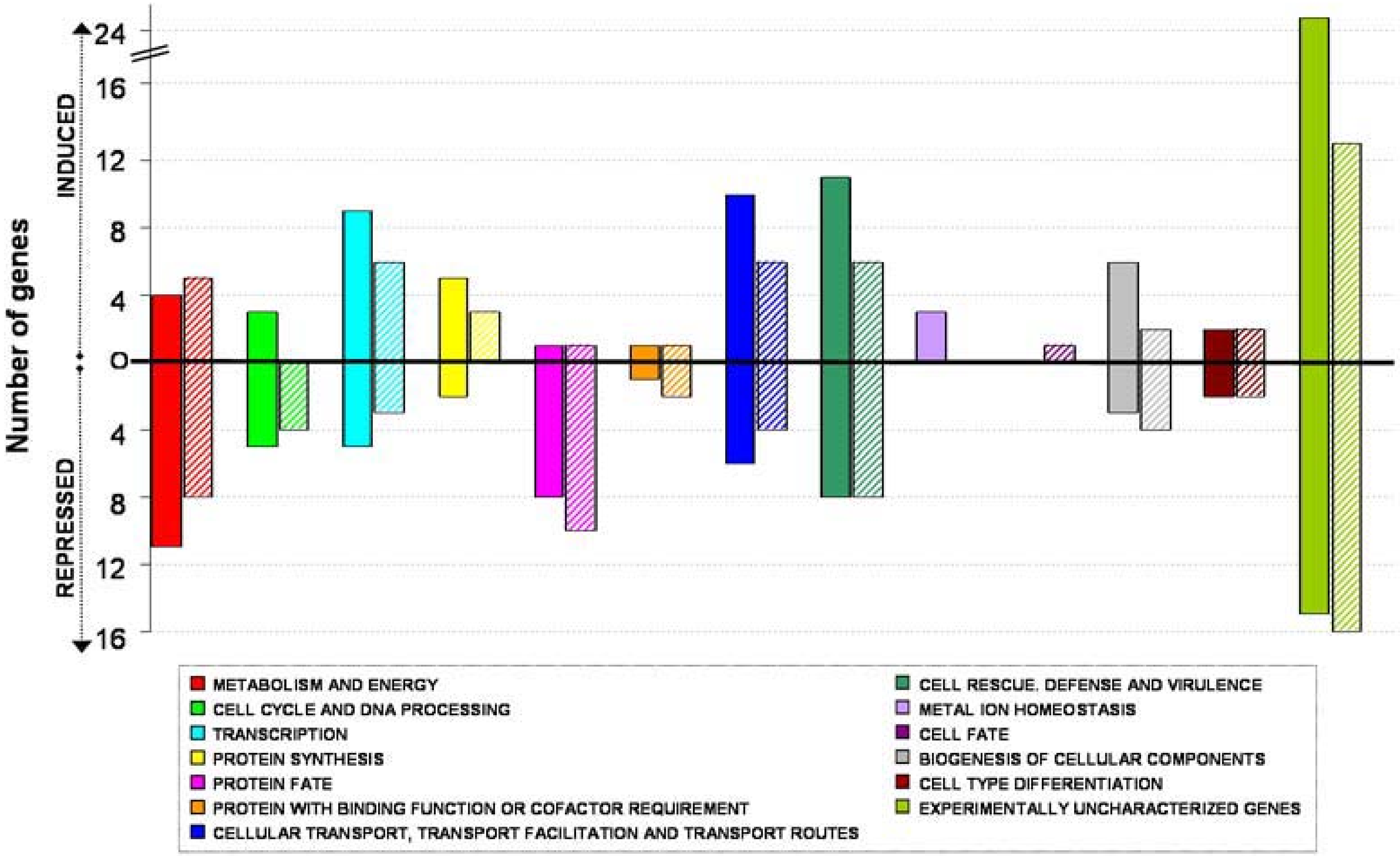
Supplemental Figure 1



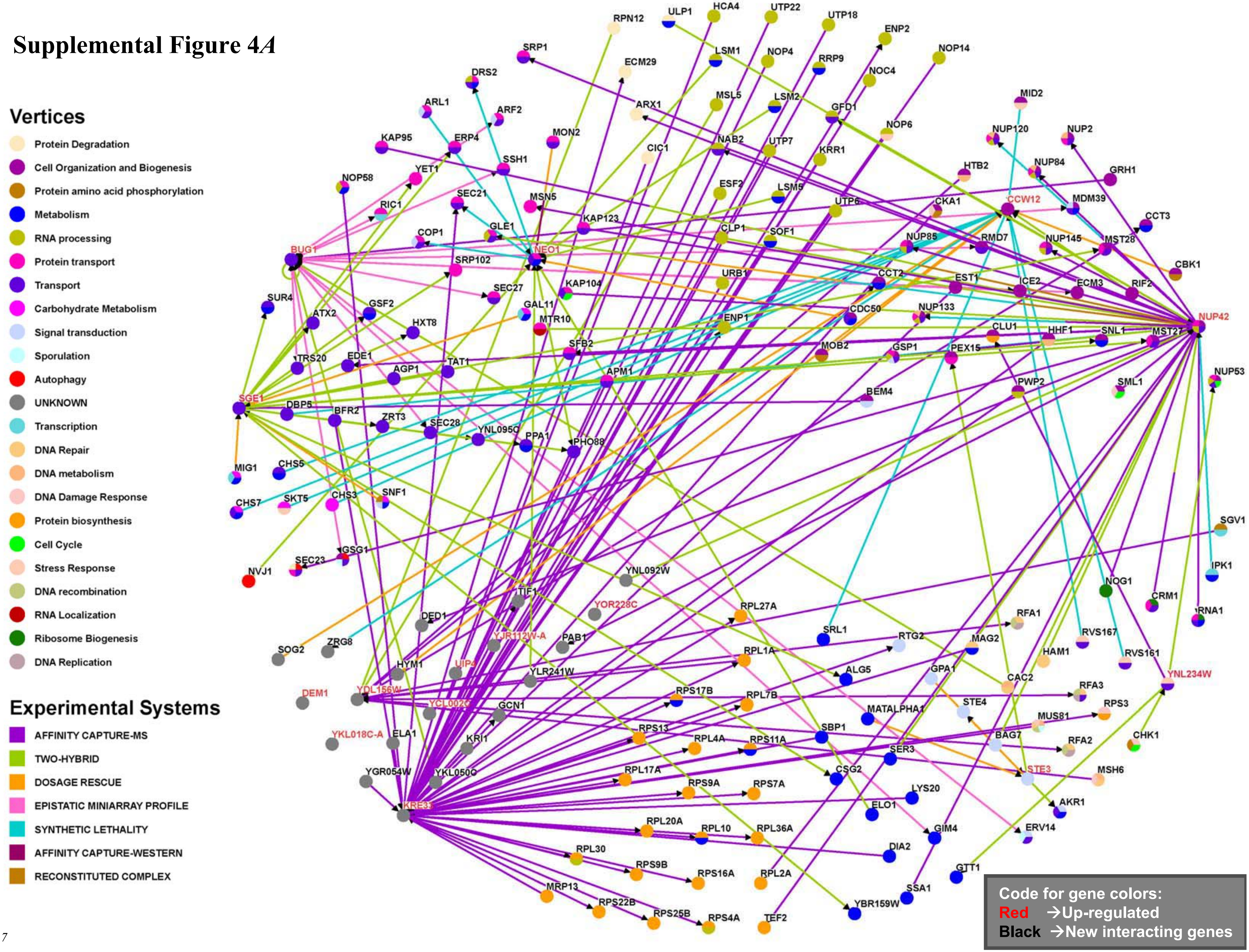
Supplemental Figure 2



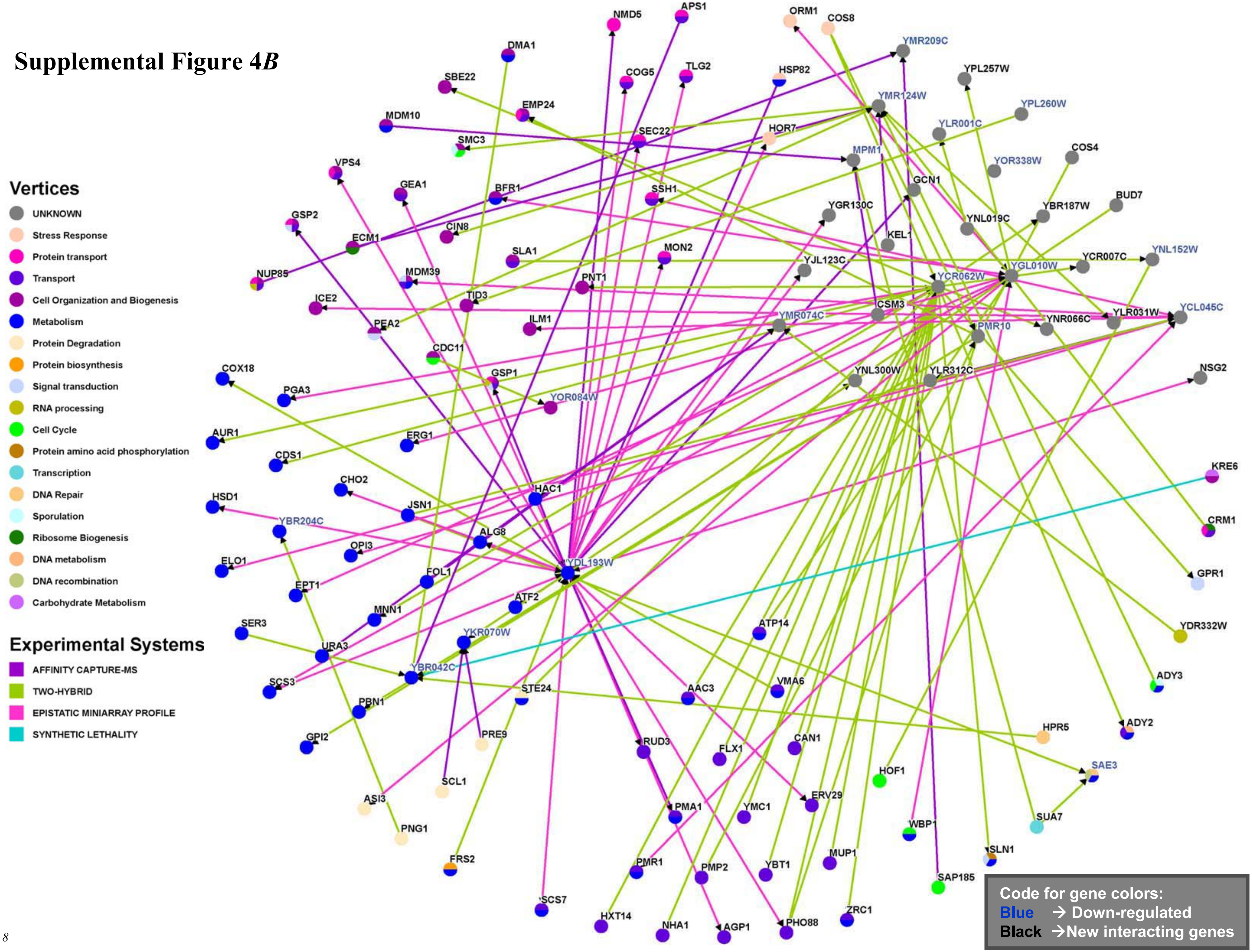
Supplemental Figure 3



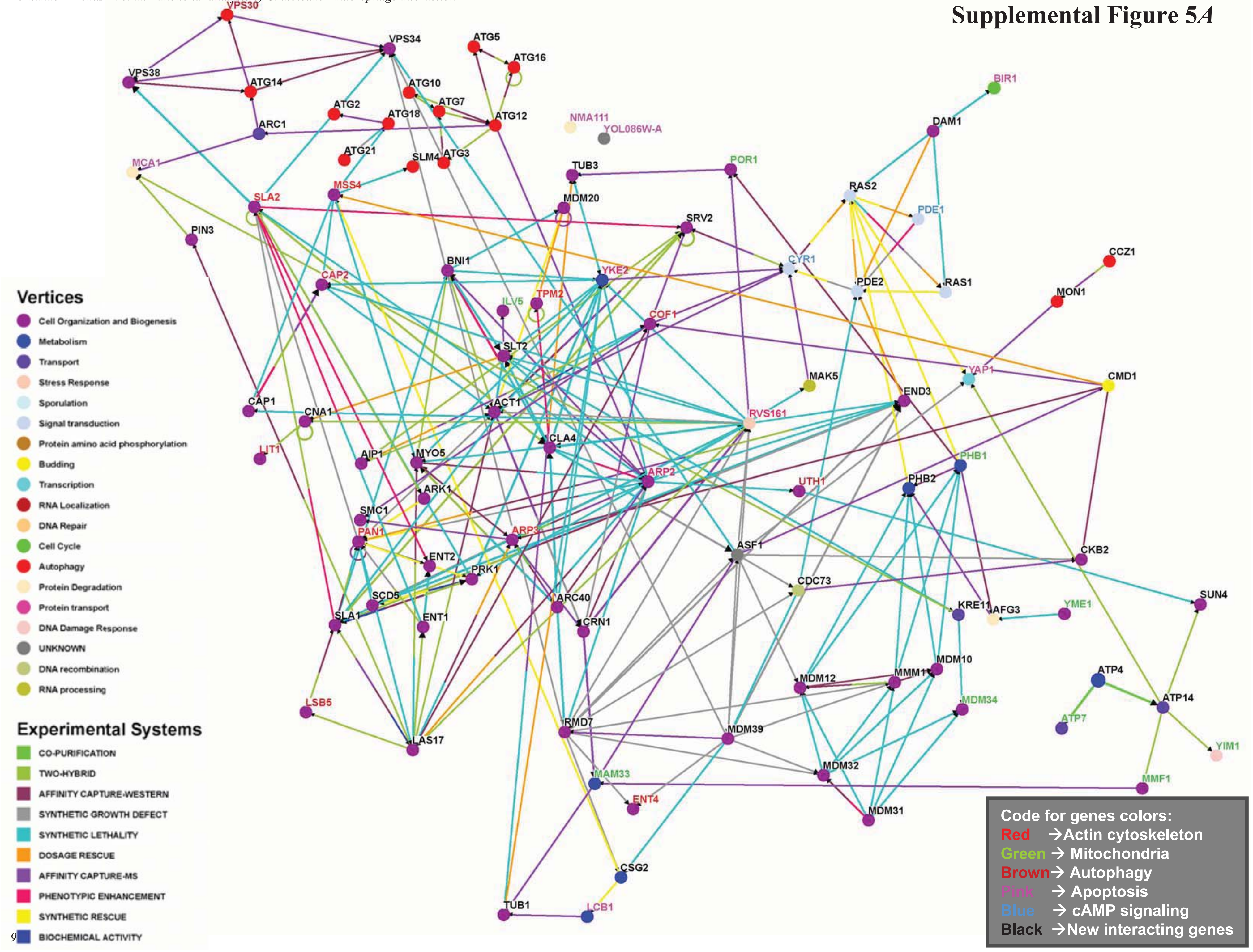
Supplemental Figure 4*A*



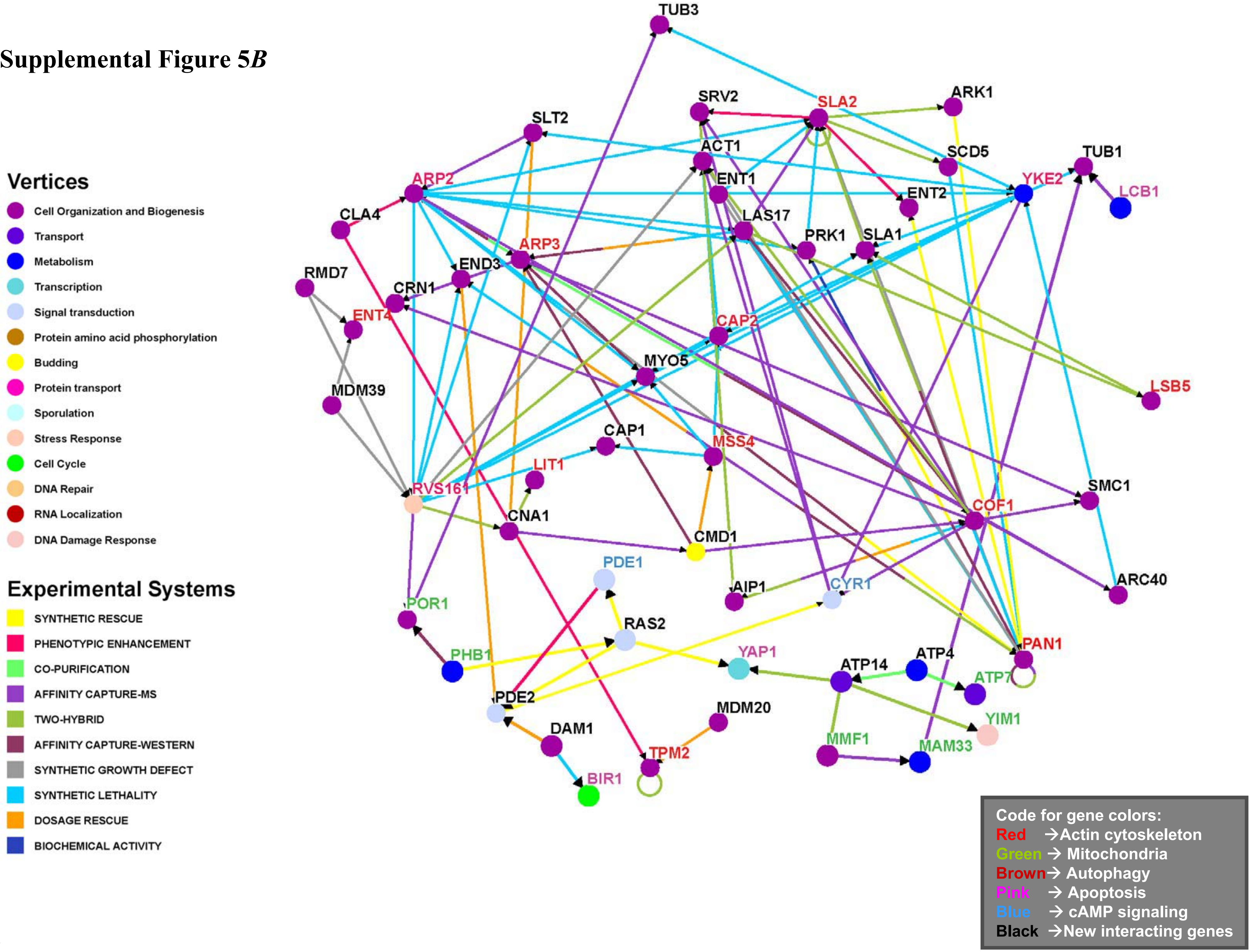
Supplemental Figure 4*B*



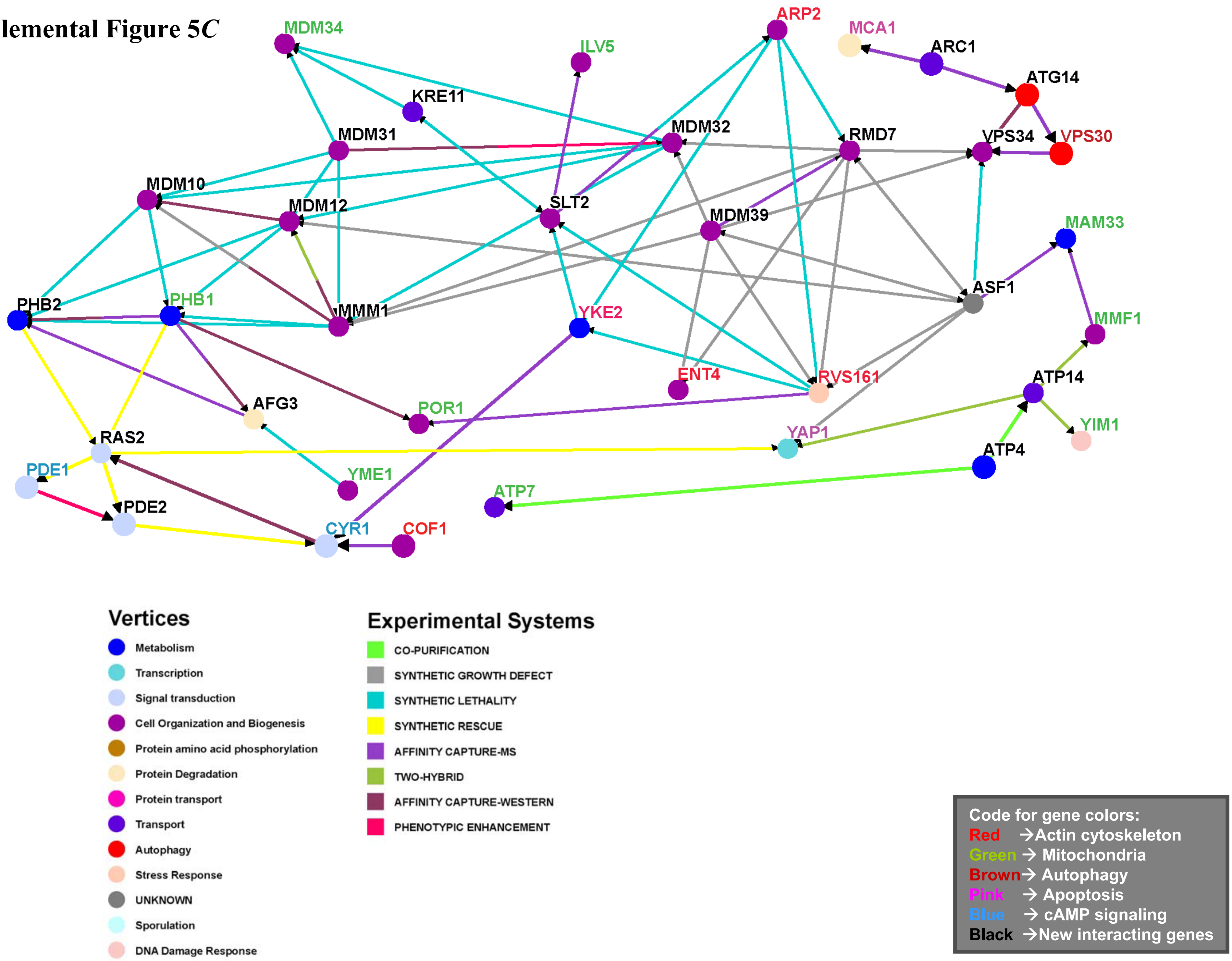
Supplemental Figure 5*A*



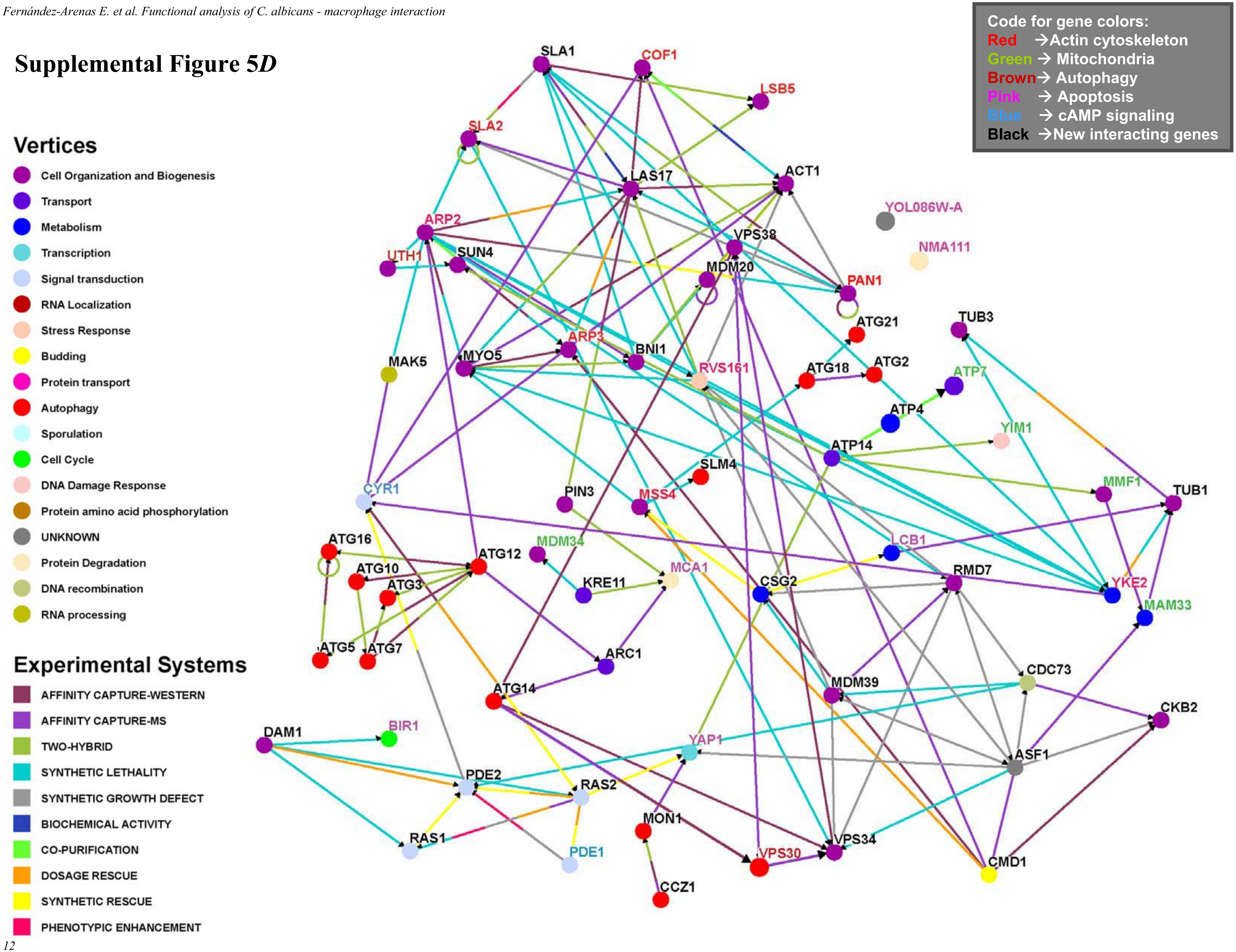
Supplemental Figure 5*B*



Supplemental Figure 5*C*



Supplemental Figure 5*D*



SUPPLEMENTAL TABLES

Supplemental Table I:

Statistical analysis of differentially expressed (amplified and diminished) protein spots present in the synthetic gel from each condition (control and treated yeast cells).

Group ID a)	Mean	M.S.D	% Vol of all the protein spots present in the control synthetic gel (Control yeast cells)	% Vol of all the protein spots present in the treated synthetic gel (yeast cells upon macrophage interaction)	Expression ratio	Identified protein spots
329	0.134142	0.121797	0.0123446	0.255938	20.73279005	**Cox4p**
152	0.0247655	0.0192972	0.0054683	0.0440626	8.057824187	
290	0.0586501	0.0456858	0.0129643	0.104336	8.047947055	
220	0.16948	0.130076	0.039404	0.299555	7.60214699	**Sou1p**
316	0.0589285	0.0448311	0.0140975	0.10376	7.360170243	**Ykr049p**
321	0.0621338	0.0462039	0.0159299	0.108338	6.800921537	**Gim5p**
281	0.265118	0.188743	0.0763751	0.45386	5.942512678	**Tpm2p**
286	0.04479	0.0313049	0.0134851	0.0760949	5.642887335	
81	0.0569248	0.0387309	0.0181939	0.0956557	5.257569845	
230	0.0861283	0.0567857	0.0293427	0.142914	4.870512938	
315	0.21237	0.137755	0.0746154	0.350124	4.692382538	
236	0.145896	0.0942267	0.0516691	0.240123	4.647323062	
303	0.11172	0.0712161	0.0405035	0.182936	4.516547953	**Pre3p**
289	0.227177	0.135042	0.0921343	0.362219	3.931424019	**Pre2p**
323	0.504491	0.291538	0.212953	0.796029	3.73805018	**Cof1p up**
292	0.212417	0.120942	0.0914757	0.333359	3.644235573	**Fur1p**
250	0.0533502	0.0294132	0.023937	0.0827633	3.457546894	**IPF16470**
240	0.106565	0.0575292	0.0490362	0.164095	3.346405309	
22	0.10543	0.0529608	0.0524696	0.158391	3.018719411	

270	0.411174	0.197761	0.213413	0.608936	2.853321963	
325	0.458931	0.218003	0.240928	0.676934	2.809694182	**Cof1p down**
334	0.0268572	0.0127453	0.014112	0.0396025	2.806299603	**Cox5Ap**
218	0.133056	0.0628701	0.0701861	0.195926	2.791521398	
185	0.194027	0.0904811	0.103546	0.284508	2.747648388	**Hom6p**
190	0.477249	0.216789	0.26046	0.694039	2.66466636	**Ipp1p**
318	0.496915	0.224713	0.272202	0.721628	2.651075304	**Sod1p**
159	0.109062	0.0487611	0.0603007	0.157823	2.617266466	
96	0.534122	0.237766	0.296356	0.771889	2.604600548	**Gnd1p**
285	0.159235	0.0679209	0.091314	0.227156	2.487636069	
151	0.0217829	0.0089633	0.0128196	0.0307462	2.398374364	
6	0.0700502	0.0288041	0.0412461	0.0988543	2.396694475	**Aco1p right**
324	0.159014	0.0647776	0.0942366	0.223792	2.374788564	**Rbp1p**
106	0.354385	0.137939	0.216446	0.492323	2.274576569	
10	0.0748241	0.0275697	0.0472544	0.102394	2.166867001	
155	0.236123	0.0868856	0.149238	0.323009	2.164388427	
247	0.409029	0.150426	0.258604	0.559455	2.163365609	**Ard8p**
74	0.0542737	0.0199377	0.034336	0.0742114	2.161329217	
245	0.0564346	0.0193693	0.0370653	0.075804	2.045147348	**Adk1p**
271	0.094434	0.0323466	0.0620874	0.126781	2.041976311	
275	0.180649	0.0613402	0.119309	0.24199	2.028262746	**Pre8p**
278	0.105008	0.035625	0.0693831	0.140633	2.026905687	
134	0.187956	0.0626526	0.125303	0.250608	2.000015961	
297	0.324517	0.104437	0.22008	0.428954	1.949082152	
196	0.144567	0.0463842	0.0981831	0.190951	1.944845905	
314	0.207097	0.0659345	0.141163	0.273032	1.934161218	**Cpr3p**
97	0.137835	0.0436785	0.0941569	0.181514	1.927782244	
298	0.824536	0.257666	0.56687	1.0822	1.909079683	**Tsa1p right**
100	0.0669873	0.0208636	0.0461237	0.0878509	1.90468024	
5	0.116162	0.0352488	0.080913	0.151411	1.8712815	**Aco1p left**
273	0.125031	0.0366174	0.0884136	0.161648	1.828316006	
95	0.181767	0.0517503	0.130017	0.233518	1.796057439	
204	0.221069	0.0622469	0.158822	0.283316	1.783858659	
60	0.315645	0.0852078	0.230438	0.400853	1.739526467	**Lpd1p**
23	0.0998217	0.0269111	0.0729106	0.126733	1.738197189	
115	0.485755	0.130274	0.35548	0.616029	1.732949814	

232	0.324438	0.0868907	0.237547	0.411329	1.731568911	
99	0.285219	0.0743303	0.210889	0.359549	1.704920598	**Pmi40p**
235	0.0491326	0.0124266	0.036706	0.0615591	1.67708549	
313	0.0781895	0.0194801	0.0587094	0.0976695	1.663609235	**Gpx1p**
72	0.213385	0.052784	0.160601	0.266169	1.657330901	**Zwf1p**
188	0.0653393	0.0158185	0.0495209	0.0811578	1.638859552	
76	0.0954245	0.0230466	0.0723779	0.118471	1.636839422	
293	0.152036	0.0350609	0.116975	0.187097	1.599461423	**Sod21p**
254	0.114862	0.0259612	0.0889006	0.140823	1.584050051	**Pre6p**
149	0.295022	0.064599	0.230423	0.359621	1.560699236	**Aat1p right**
18	0.292793	0.0557631	0.23703	0.348556	1.470514281	**Acs2p**
113	0.195224	0.0355296	0.159695	0.230754	1.444966968	
310	0.665539	0.119891	0.545648	0.78543	1.439444477	**Ahp1p**
111	0.651398	0.100263	0.551135	0.751661	1.36384189	**Cit1p**
335	1.16657	0.176038	0.990528	1.3426	1.355438716	**Ynk1p**
29	0.244866	0.0336347	0.211231	0.2785	1.318461779	**Ssb1p**
148	0.194888	0.0250915	0.169797	0.21998	1.295547036	**Aat1p left**
296	0.911488	0.110401	0.801087	1.02189	1.275629239	**Tsa1p left**
249	0.314036	0.0332986	0.280737	0.347334	1.237222026	**Taf14p**
202	0.866089	0.0818087	0.78428	0.947898	1.208621921	**Mdh1p**
322	0.248641	0.0234308	0.22521	0.272072	1.208081346	**Dut1p**
239	0.154908	0.0144125	0.140495	0.16932	1.205167444	**Por1p**
327	0.745265	0.0691059	0.67616	0.814371	1.204405762	**Cpr1p**
32	0.193884	0.0176804	0.176203	0.211564	1.200683303	**Ilv3p**
				TTEST (Over-expressed):	**6.49951E-17**	
138	0.452389	0.0455415	0.497931	0.406848	0.817077065	**Pot14p**
211	0.495238	0.0528237	0.548062	0.442414	0.807233488	**Snz1p**
326	0.368083	0.0397704	0.407853	0.328312	0.804976303	**Mmd1p**
268	0.103522	0.0112377	0.11476	0.0922842	0.804149529	**Tpi1p**
336	0.0632886	0.00740607	0.0706947	0.0558826	0.790477928	**Dqd1p**
71	0.490154	0.0589061	0.54906	0.431247	0.785427822	**Imh3p**
216	0.276425	0.0336645	0.310089	0.242761	0.782875239	**Mdh2p**
183	0.306759	0.0417558	0.348515	0.265003	0.760377602	
118	1.61747	0.269812	1.88728	1.34766	0.714075283	**Eno1p**
207	0.459532	0.0780127	0.537545	0.381519	0.70974337	**Tdh3p right**

177	0.30727	0.0559544	0.363225	0.251316	0.691901714	**Fba1p**
39	0.547051	0.102932	0.649983	0.444119	0.68327787	**Pdc11p**
168	0.667884	0.133931	0.801816	0.533953	0.66592959	**Ilv5p**
306	0.302281	0.0640365	0.366318	0.238245	0.650377541	**Cyp51p**
173	0.419326	0.091841	0.511167	0.327485	0.640661467	**Adh5p**
24	0.202385	0.04541	0.247795	0.156975	0.633487359	**Sdh3p**
101	0.202166	0.0472609	0.249427	0.154905	0.621043432	
226	0.0765027	0.0183073	0.09481	0.0581954	0.613810779	
154	0.148803	0.0363115	0.185114	0.112491	0.607684994	
277	0.111626	0.0274856	0.139111	0.08414	0.604840739	
52	0.0667294	0.0172623	0.0839917	0.0494671	0.588952242	
50	0.0747008	0.019437	0.0941378	0.0552637	0.58705111	
104	0.0880563	0.024075	0.112131	0.0639813	0.570594216	
65	0.105232	0.0291585	0.13439	0.076073	0.566061463	**IPF6105**
49	0.160905	0.0450772	0.205982	0.115828	0.56232098	
25	0.0990046	0.0279064	0.126911	0.0710981	0.560220154	**Ssc1p**
255	0.305169	0.0868292	0.391998	0.21834	0.556992638	**Sol3p**
87	0.0756138	0.022044	0.0976579	0.0535698	0.548545484	
36	0.381646	0.113215	0.494861	0.268431	0.542437169	
129	0.179593	0.0547268	0.234319	0.124866	0.532888925	
181	0.366087	0.113187	0.479273	0.2529	0.527674207	
198	0.419369	0.13358	0.552949	0.285788	0.516843326	**Hem13p**
233	0.195139	0.0636019	0.258741	0.131537	0.508373238	**Gpp1p**
288	0.0539416	0.0177296	0.0716712	0.036212	0.505251761	**Mxr1p**
311	0.10687	0.0352671	0.142137	0.0716028	0.503759049	**Atp7p**
62	0.0543376	0.0191179	0.0734556	0.0352197	0.47946923	
46	0.252397	0.0914043	0.343801	0.160992	0.468270889	**Cdc19p**
182	0.05213	0.0193751	0.0715051	0.0327549	0.458077815	
47	0.103737	0.0399187	0.143656	0.0638186	0.444245976	
142	0.275003	0.107462	0.382465	0.167541	0.43805577	**Adh1p**
208	1.1842	0.481388	1.66558	0.702807	0.421959317	**Tdh3p middle**
217	0.183687	0.0776411	0.261328	0.106046	0.405796547	
51	0.0692678	0.0298387	0.0991065	0.0394291	0.397845752	**Ses1p**
17	0.0853621	0.0369993	0.122361	0.0483627	0.395246034	
248	0.118625	0.0532862	0.171912	0.0653391	0.380072944	
136	0.12923	0.0614179	0.190648	0.0678119	0.355691641	

212	0.186615	0.0911616	0.277776	0.0954529	0.343632639	
209	0.56111	0.286109	0.847219	0.275001	0.324592579	**Tdh3p left**
103	0.151475	0.0787577	0.230233	0.0727173	0.315842212	**Oye32p**
227	0.120088	0.0652355	0.185324	0.0548529	0.295983791	**Sec13p**
94	0.0459817	0.02669	0.0726717	0.0192918	0.265465099	
283	0.0694929	0.042636	0.112129	0.0268569	0.239517877	**Tpi1p**
287	0.0581233	0.0425288	0.100652	0.0155945	0.154934825	
				TTEST (Under-expressed):	**3.1304E-08**	

a) Gene ID according to Image-Master 2D-Platinum nomenclature (see Supplemental Fig. 2)

Supplemental Table II:
C. albicans proteins identified by MALDI-TOF/TOF MS

Mascot Search Results

Databases employed: SWISS-PROT/TrEMBL non-redundant protein database (www.expasy.ch/sprot) and CandidaDB (genolist.Pasteur.fr/CandidaDB) as described under "Experimental Procedures"

Hom6p (PMF[a])

Match to: **CA4181|CaHOM6**; Score: **124**
homoserine dehydrogenase (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	No match to:
								771.32
1123.57	1122.56	1122.59	-0.03	188	197	1	SDVKFSDVVK	773.46
1176.58	1175.57	1175.58	-0.01	262	271	0	LPNYDADIQK	797.34
1210.63	1209.62	1209.6	0.02	115	124	1	AFSSDLKEWK	799.35
1281.65	1280.64	1280.62	0.02	303	313	0	YGFDHPFASLK	801.51
1352.78	1351.77	1351.75	0.02	28	39	0	SNIAFNVIYLAK	805.43
1994.04	1993.03	1993.03	-0.00	296	313	1	VSVEIGKYGFDHPFASLK	825.11
2099.14	2098.13	2098.12	0.01	228	247	0	ISGLEVEGPTSFPVESLIPK	833.08
2245.09	2244.08	2244.07	0.01	201	220	1	ELGYTEPDPRDDLNGLDVAR	839.1
2419.32	2418.32	2418.31	0.01	4	27	0	SVNVAIIGSGVVGSSYLSQLNNLK	841.09
2539.35	2538.35	2538.34	0.01	81	103	0	KPTVLVDNTSSPAIANYYPTFIK	843.04
2676.44	2675.43	2675.43	0	326	352	0	YPNPLIVQGAGAGAEITAHGVLADTIK	843.38
2868.43	2867.42	2867.4	0.02	49	74	0	DYSPVDLSTYETAPTQPTLSLDDLVK	845.11
2990.6	2989.59	2989.6	-0.01	323	352	1	TGRYPNPLIVQGAGAGAEITAHGVLADTIK	845.54
								848.43
								854.07
								855.07
								857.36
								861.08

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant ($p<0.05$).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **82**
Number of mass values matched: **13**
Sequence Coverage: **56%**

Matched peptides shown in **Bold Red**

1 MSK**SVNVAII GSGVVGSSYL SQLNNLKSNI AFNVIYLAK**T SEEALYSK**DY**
51 **SPVDLSTYET APTQPTLSLD DLVK**FIKGAK **KPTVLVDNTS SPAIANYYPT**
101 **FIK**EGISIAT PNKK**AFSSDL KEWK**EILQTA ELPGAGLVYH ECTVGAALPI
151 ISPLKDLIAT GDKVDKIEGI FSGTLSYIFN EFSKTEK**SDV KFSDVVK**KAK
201 **ELGYTEPDPR DDLNGLDVAR** KVTILAR**ISG LEVEGPTSFP VESLIPK**ELE
251 CVESVAEFME K**LPNYDADIQ K**VKDEAFAEN KVLRFVGKVD LNTNK**VSVEI**
301 **GKYGFDHPFA SLK**GSDNVVS IK**TGRYPNPL IVQGAGAGAE ITAHGVLADT**
351 **IK**IAERIAN

870.04
871.04
877.06
883.38
885.39
887.02
889.57
893.03
909
933.59
943.4
969.41
971.42
977.53
1020.53
1029.44
1050.12
1055.46
1057.46
1060.08
1066.1
1082.07
1098.04
1111.58
1115.48
1141.49
1143.51
1153.6
1168.6
1201.51
1229.54
1277.12
1287.55
1373.58
1433.74
1459.63

1495.83
1496.33
1518.85
1529.81
1571.82
1587.79
1909.97
2121.12
2163.07
2185.04
2225.16
2273.17
2289.15
2444.23

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications:Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 82

Lpd1p (PMF)

Match to: **CA2998|CaLPD1**; Score: **89**
dihydrolipoamide dehydrogenase (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
906.5	905.5	905.48	0.01	328	334	1	TKHDHIR
991.57	990.56	990.54	0.03	320	327	0	LIIDDQFK
1050.52	1049.51	1049.51	0	424	432	0	FIADAETQR
1235.68	1234.68	1234.68	-0.01	401	411	1	VGKFPFIANSR
1236.68	1235.67	1235.66	0.01	117	127	0	QLTGGIEMLFK
1470.79	1469.78	1469.81	-0.02	285	298	0	SDLEADVLLVAIGR
1498.69	1497.68	1497.7	-0.02	466	478	0	TCHAHPTLSEAFK
1526.81	1525.8	1525.78	0.02	131	144	1	VDYLKGAGSFVNEK
1544.79	1543.78	1543.81	-0.03	44	57	1	AAQLGLNTACIEKR
1598.87	1597.87	1597.9	-0.04	284	298	1	KSDLEADVLLVAIGR
1741.95	1740.95	1741	-0.05	185	200	1	IVTSTGILSLKEVPER
1820.91	1819.9	1819.95	-0.04	299	314	0	RPFTEGLNFEAIGLEK
2178.02	2177.02	2177.11	-0.09	299	317	1	RPFTEGLNFEAIGLEKDNK

No match to:
701.39
771.51
928.54
942.53
963.52
1007.58
1029.53
1036.58
1105.58
1229.71
1230.74
1257.63
1259.63
1297.62
1317.74
1362.71
1405.82
1410.7
1426.68
1449.83
1537.89
1581.89
1625.92
1669.94
1714
1721.77
1871
1878.95
1982.97
2127.08

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **43**
Number of mass values matched: **13**
Sequence Coverage: **27%**

Matched peptides shown in **Bold Red**

1 MLRSFKSIPA NGKLAQFVRY ASTKKYDVVV IGGGPGGYVA AIK**AAQLGLN**
51 **TACIEKR**GAL GGTCLNVGCI PSKSLLNNSH LLHQIQHEAK ERGISIQGEV
101 GVDFPKLMAA KEKAVK**QLTG GIEMLFK**KNK **VDYLKGAGSF VNEK**TVKVTP
151 IDGSEAQEVE ADHIIVATGS EPTPFPGIEI DEER**IVTSTG ILSLKEVPER**
201 LAIIGGGIIG LEMASVYARL GSKVTVIEFQ NAIGAGMDAE VAKQSQKLLA
251 KQGLDFKLGT KVVKGERDGE VVKIEVEDVK SGK**KSDLEAD VLLVAIGRRP**
301 **FTEGLNFEAI GLEKDNK**GR**L IIDDQFKTKH DHIR**VIGDVT FGPMLAHKAE
351 EEGIAAAEYI KKGHGHVNYA NIPSVMYTHP EVAWVGLNEE QLKEQGIKYK
401 **VGKFPFIANS R**AKTNMDTDG FVK**FIADAET QR**VLGVHIIG PNAGEMIAEA
451 GLALEYGAST EDISR**TCHAH PTLSEAFK**EA ALATFDKPIN F

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 43

Ilv3p (PMF)

Match to: **CA4802|CaILV3**; Score: **186**
dihydroxyacid dehydratase (by homology)

Observed	**Mr(expt)**	**Mr(calc)**	**Delta**	**Start**	**End**	**Miss**	**Peptide**	
1019.51	1018.5	1018.5	0.01	558	565	0	HWTPPEPR	
1147.6	1146.6	1146.59	0	557	565	1	KHWTPPEPR	
1176.57	1175.56	1175.56	0	148	158	0	NMPGVLMAMGR	
1210.72	1209.71	1209.71	0.01	271	280	0	NLLELDLKPR	
1321.7	1320.69	1320.69	0	461	471	1	TVCVIRYEGPK	
1470.8	1469.79	1469.78	0	205	216	1	QINNEERIDIVK	
1511.84	1510.83	1510.82	0	543	555	0	IDLLVEPDVLTER	
1565.78	1564.77	1564.76	0.02	257	270	1	EKAEECANVGFALK	
1702.91	1701.9	1701.89	0	327	342	0	ISDNTPLLADFKPSGK	
1793.9	1792.89	1792.89	0	343	359	0	YVMADLQNVGGTPAVMK	
1832.94	1831.93	1831.94	-0.01	189	204	0	IDIISAFQSYGQYLSK	
1935.08	1934.07	1934.07	0	360	377	1	YLIKEGIIDGTQLSVTGK	
1965	1963.99	1963.99	0	439	456	0	VFNDEGAFIVALENGEIK	
2226.16	2225.16	2225.05	0.1	472	493	0	GGPGMPEMLKPSSALMGYGLGK	3 Oxidation (M)
3034.68	3033.67	3033.7	-0.02	386	413	0	LADLPEGQDIVRPVSNPLKPSGHLQILK	

No match to:
1117.55
1293.08
1297.69
1518.37
1521.81
1545.64
1580.78
1631.69
2407.25

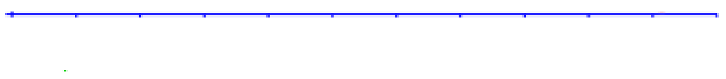
Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **24**
Number of mass values matched: **15**
Sequence Coverage: **36%**

Matched peptides shown in **Bold Red**

1 MSFVKSCRGC LRTFATSTIK HEKKLNKYSS IVTGDPSQGA SQAMLYATGF
51 SDEDFDRAQI GVGSVWWSGN PCNMHLMELN NRCSESVNKA GLKAMQFNSI
101 GVSDGITNGT EGMKYSLQSR EIIADSFETM TMAQLYDGNI AIPSCDK**NMP**
151 **GVLMAMGR**HN RPAIMVYGGT ILPGSPTCGT QNPAVADK**ID IISAFQSYGQ**
201 **YLSKQINNEE RIDIVK**HACP GPGACGGMYT ANTMASASEV LGLTLPFSSS
251 SPAVSK**EKAE ECANVGFALK NLLELDLKPR** DIVTKKSFEN AIAYIIATGG
301 STNAVLHLIA IASSFDITIT VDDFQR**ISDN TPLLADFKPS GKYVMADLQN**
351 **VGGTPAVMKY LIKEGIIDGT QLSVTGK**TIN ENLAK**LADLP EGQDIVRPVS**
401 **NPLKPSGHLQ ILK**GTLAPGS AVAKITGKEG TYFKGKAR**VF NDEGAFIVAL**
451 **ENGEIK**KGEK **TVCVIRYEGP KGGPGMPEML KPSSALMGYG LGK**DVALLTD
501 GRFSGGSHGF LIGHIVPEAA EGGPIALVED GDIIVIDADN NK**IDLLVEPD**
551 **VLTER**R**KHWT PPEPR**YKRGT LAKYAKLVSD ASKGCVTDL



Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 24

Ilv5p (PMF)

Match to: **CA1983|CaILV5**; Score: **268**
ketol-acid reducto-isomerase (by homology)

Observed	**Mr(expt)**	**Mr(calc)**	**Delta**	**Start**	**End**	**Miss**	**Peptide**
756.44	755.43	755.39	0.04	395	400	0	LRPENQ
797.41	796.4	796.37	0.03	367	372	1	SDYKER
798.47	797.46	797.43	0.03	77	82	0	LLDYFK
836.5	835.49	835.46	0.03	210	216	1	SLFKEGR
848.44	847.44	847.4	0.03	382	387	0	NMEIWR
852.46	851.45	851.41	0.04	360	366	0	SLEFNSR
864.44	863.43	863.4	0.03	382	387	0	NMEIWR Oxidation(M)
884.53	883.52	883.49	0.03	394	400	1	KLRPENQ
901.48	900.48	900.45	0.03	70	76	1	ADWPKER
977.51	976.51	976.48	0.03	328	335	0	GALDWYPR
1130.63	1129.62	1129.6	0.02	373	381	0	LEEELQTIR
1133.61	1132.6	1132.58	0.02	327	335	1	RGALDWYPR
1169.69	1168.68	1168.66	0.02	104	114	0	DNGLNVIIGVR
1181.56	1180.56	1180.54	0.02	256	265	0	EVNSDLYGER
1415.75	1414.74	1414.74	0	371	381	1	ERLEEELQTIR
1529.77	1528.76	1528.77	-0.01	171	183	0	TLYFSHGFSPVFK
1587.76	1586.76	1586.77	-0.01	56	69	0	TINFGGTEEVVHER
1610.77	1609.76	1609.77	-0.01	217	231	0	GINSSYAVWNDVTGK
1766.9	1765.89	1765.91	-0.02	338	352	0	DALKPVFEELYESVK
1804.67	1803.66	1803.69	-0.03	312	326	0	YGMDYMYDACSTTAR
1820.67	1819.67	1819.69	-0.02	312	326	0	YGMDYMYDACSTTAR Oxidation (M)
2029.08	2028.07	2028.09	-0.02	184	202	0	DLTHVEPPSNIDVILAAPK
2067.99	2066.98	2066.99	-0.01	217	235	1	GINSSYAVWNDVTGKAEEK
2244.07	2243.06	2243.1	-0.04	83	103	0	NDTFALIG LR
3077.36	3076.35	3076.44	-0.09	115	142	1	KGSSWEA FEVDEAISR

No match to:
713.49
802.43
804.45
870.42
955.52
993.5
999.5
1089.62
1152.66
1155.59
1163.56
1179.62
1609.75
1632.75
1756.66
1791.7
1814.91
1891.92
1908.94
2051.02
2090.96
2470.17

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant ($p<0.05$).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **47**
Number of mass values matched: **25**
Sequence Coverage: **57%**

Matched peptides shown in **Bold Red**

1 MSFRTTSMRM ARLATAKATL SKRTFSLLAN ATTRYTAASS AAKAMTPITS
51 IRGVK**TINFG GTEEVVHERA DWPKERLLDY FKNDTFALIG YGSQGYGQGL**
101 **NLRDNGLNVI IGVRKGSSWE AAVEDGWVPG ENLFEVDEAI SR**GTIIMDLL
151 SDAAQSETWF HIKPQLTEGK **TLYFSHGFSP VFKDLTHVEP PSNIDVILAA**
201 **PK**GSGRTVR**S LFKEGRGINS SYAVWNDVTG KAEEK**AIAMA IAIGSGYVYK
251 TTFER**EVNSD LYGER**GCLMG GIHGMFLAQY EVLRENGHTP SEAFNETVEE
301 ATQSLYPLIG K**YGMDYMYDA CSTTARRGAL DWYPR**FK**DAL KPVFEELYES**
351 **VK**NGSETKR**S LEFNSRSDYK ERLEEELQTI RNMEIWR**VGK EVR**KLRPENQ**
401

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 47

Ses1p (PMF)

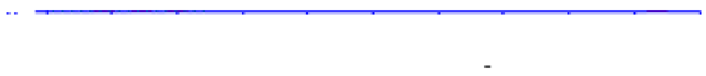
Match to: **CA1598|CaSES1** Score: **187**
seryl-tRNA synthetase (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
864.43	863.43	863.43	-0.00	288	294	0	DAWGIFR
964.43	963.42	963.43	-0.01	161	168	0	LDGYDPER
968.41	967.40	967.40	-0.00	312	318	0	SWEEFDR
1038.49	1037.48	1037.48	-0.00	130	137	0	TWTPENYK
1103.63	1102.62	1102.62	-0.00	152	160	0	LSHHEVLLR
1110.46	1109.46	1109.46	-0.00	271	279	0	YAGYSSCFR
1239.69	1238.69	1238.69	-0.00	422	432	0	EDGLVIPEVLR
1308.67	1307.67	1307.68	-0.01	1	11	0	MLDINAFLVEK + Oxidation (M)
1352.76	1351.75	1351.75	0.01	138	151	0	KPEQIAAATGAPAK
1441.76	1440.75	1440.79	-0.04	336	350	0	VVGIVSGELNNAAAK
1571.76	1570.75	1570.75	0.00	221	233	0	TAQLSQFDEELYK
1650.79	1649.78	1649.78	-0.00	397	410	0	YVHCLNSTLSATER
1718.71	1717.70	1717.70	-0.01	366	379	0	ELVSCSNCTDYQSR
2836.36	2835.35	2835.36	-0.01	105	129	0	INQVGNIVHESVVDSQDEENNELVR

No match to:
870.02
871.02
877.03
882.56
886.99
893.01
1045.53
1066.07
1082.04
1098.01
1102.6
1184.6
1276.62
1286.65
1414.74
1475.74
1480.74
1530.75
1657.87
2185.02
2200.99
2274.15

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).



Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **36**
Number of mass values matched: **14**
Sequence Coverage: **35%**

Matched peptides shown in **Bold Red**

1 **MLDINAFLVE K**GGDPEIIKA SQKKRGDSVE LVDEIIAEYK EWVKLRFDLD
51 EHNKKLNSVQ KEIGKRFKAK EDAKDLIAEK EKLSNEKKEI IEKEAEADKN
101 LRSK**INQVGN IVHESVVDSQ DEENNELVRT WTPENYKKPE QIAAATGAPA**
151 **KLSHHEVLLR LDGYDPER**GV RIVGHRGYFL RNYGVFLNQA LINYGLSFLS
201 SKGYVPLQAP VMMNKEVMAK **TAQLSQFDEE LYK**VIDGEDE KYLIATSEQP
251 ISAYHAGEWF ESPAEQLPVR **YAGYSSCFR**R EAGSHGK**DAW GIFR**VHAFEK
301 IEQFVLTEPE K**SWEEFDR**MI GCSEEFYQSL GLPYR**VVGIV SGELNNAAAK**
351 KYDLEAWFPF QQEYK**ELVSC SNCTDYQSR**N LEIRCGIKQQ NQQEKK**YVHC**
401 **LNSTLSATER** TICCILENYQ K**EDGLVIPEV LR**KYIPGEPE FIPYIKELPK
451 NTTSVKKAKG KN

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 80 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 0
Number of queries : 36

Fur1p (PMF)

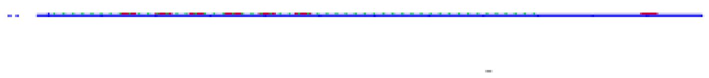
Match to: **CA2069|CaFUR1**; Score: **60**
Uracil phosphoribosyltransferase (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1013.44	1012.43	1012.41	0.02	65 -	72	0	CHGGYEYK
1080.51	1079.5	1079.47	0.03	88 -	97	0	AGESMEMGLR
1105.52	1104.51	1104.49	0.02	35 -	43	0	GDFVFYSDR
1210.63	1209.62	1209.6	0.02	179 -	188	1	AFQDKYPDVK
1261.62	1260.61	1260.59	0.02	34 -	43	1	RGDFVFYSDR
1525.89	1524.88	1524.85	0.03	108 -	120	1	ILIQRDEETALPK
1638.86	1637.85	1637.83	0.02	121 -	133	1	LFYEKLPEDISER
2007.16	2006.15	2006.13	0.02	47 -	64	0	LLVEEGLNQLPVEEAIIK

No match to:
773.46
795.52
817.48
845.54
889.57
905.53
933.58
977.62
1146.59
1447.74
1889.99

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).



Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **19**
Number of mass values matched: **8**
Sequence Coverage: **37%**

Matched peptides shown in **Bold Red**

1 MSVAKAVSKN VILLPQTNQL IGLYSIIRDQ RTK**RGDFVFY SDR**IIR**LLVE**
51 **EGLNQLPVEE AIIKCHGGYE YK**GAKFLGKI CGVSIVR**AGE SMEMGLR**DCC
101 RSVRIGK**ILI QRDEETALPK LFYEKLPEDI SER**YVFLLDP MLATGGSAMM
151 AVEVLLARGV KMDRILFLNL LAAPEGIK**AF QDKYPDVK**II TGGIDEKLDE
201 NKYIVPGLGD FGDRYYCI

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 19

Adk1p (PMF)

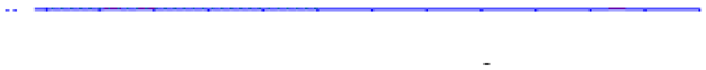
Match to: **CA1982|CaADK1**; Score: **105**
adenylate kinase, cytosolic (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	
836.48	835.47	835.47	0	162	169	0	LVHPASGR	
860.49	859.48	859.48	-0.00	238	244	0	VWSDILK	
1021.55	1020.55	1020.54	0.01	114	122	0	GFILDGFPR	
1039.6	1038.59	1038.59	0	36	46	0	MVLIGPPGAGK	
1043.57	1042.56	1042.57	-0.00	149	157	0	IDDELLVAR	
1055.6	1054.59	1054.58	0.01	36	46	0	MVLIGPPGAGK	Oxidation (M)
1339.69	1338.68	1338.68	0	212	222	0	QTEPIVAYYQK	
1551.69	1550.68	1550.68	0	57	69	0	FCACHLATGDMLR	
1567.69	1566.68	1566.67	0.01	57	69	0	FCACHLATGDMLR	Oxidation (M)
1574.82	1573.81	1573.81	0	223	237	0	TGIWSGVDASQKPTK	
1575.75	1574.75	1574.72	0.02	181	194	0	DMTDDVTGEPLVQR	
1583.91	1582.9	1582.89	0.01	144	157	1	AVELKIDDELLVAR	
1703.83	1702.82	1702.82	0	180	194	1	KDMTDDVTGEPLVQR	
1717.88	1716.87	1716.87	0	123	137	1	TIPQAEKLDSMLESR	
1733.88	1732.88	1732.87	0.01	123	137	1	TIPQAEKLDSMLESR	Oxidation (M)
1808.84	1807.83	1807.82	0.01	55	69	1	EKFCACHLATGDMLR	
1992.97	1991.96	1991.97	-0.01	85	102	0	IMDQGGLVSDEIMVNMIK	
2121.1	2120.09	2120.07	0.03	84	102	1	KIMDQGGLVSDEIMVNMIK	

No match to:
772.2
773.44
801.5
805.42
817.09
817.47
819.09
823.11
825.1
833.07
839.08
841.07
844.07
845.09
845.52
847.09
849.04
854.05
855.05
857.05
859.05
861.07
865.05
869.03
870.03
871.02
875.03
877.04
879.04
881.03

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).

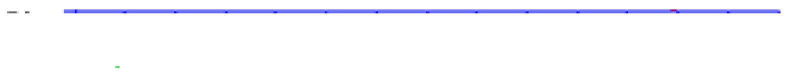


Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **94**
Number of mass values matched: **18**
Sequence Coverage: **55%**

Matched peptides shown in **Bold Red**

1 MSIEDLKNTV TKLQERIQEL EKKAGIIPDV PKSVR**MVLIG PPGAGK**GTQA
51 PNLK**EKFCAC HLATGDMLR**A QVAAKTALGV EAK**KIMDQGG LVSDEIMVNM**
101 **IK**SELENNQE CSK**GFILDGF PRTIPQAEKL DSMLESR**KTP LEK**AVELKID**
151 **DELLVAR**ITG R**LVHPASGR**S YHKLFNPPK**K DMTDDVTGEP LVQR**SDDNED
201 ALKKRLVTYH K**QTEPIVAYY QKTGIWSGVD ASQKPTKVWS DILK**CLGQN

882.57
883.03
886.01
887
889.55
893.02
895.01
897
901.01
905.51
908.99
933.58
996.6
1020.51
1028.11
1030.11
1044.09
1046.09
1050.1
1060.06
1066.08
1072.09
1076.03
1082.05
1088.07
1098.02
1111.57
1153.58
1255.13
1271.09
1277.1
1289.7
1293.08
1296.69
1309.06
1362.68



1433.72
1449.85
1465.72
1494.69
1503.7
1537.9
1565.69
1573.67
1581.93
1606.83
1918.89
2145.06
2163.06
2185.04
2201.02
2273.16
2289.17
2400.21

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 94

Ynk1p (PMF)

Match to: **CA2645|CaYNK1**; Score: **125**
Nucleoside diphosphate kinase (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
915.54	914.53	914.55	-0.02	18	26	0	GLISSILGR
950.46	949.45	949.49	-0.04	128	134	0	EIDLWFK
981.42	980.42	980.44	-0.02	105	113	0	GDFAIDMGR
997.41	996.4	996.43	-0.03	105	113	0	GDFAIDMGR Oxidation (M)
1155.65	1154.64	1154.67	-0.03	39	48	0	LVQPTESLLR
1344.73	1343.73	1343.76	-0.03	6	17	0	TFIAIKPDGVQR
1503.6	1502.59	1502.64	-0.05	114	127	0	NVCHGSDSVESANK
1679.9	1678.89	1678.94	-0.05	88	104	0	AILGATNPLQSAPGTIR
2114	2112.99	2113.08	-0.08	135	151	1	KEELVEYKPALFGWIYE
2435.02	2434.01	2434.12	-0.11	114	134	1	NVCHGSDSVESANKEIDLWFK

No match to:
861.05
877.02
893
933.42
937.49
1024.43
1039.56
1300.72
1345
1345.38
1346.73
1348.67
1366.69
1382.67
1635.89
1680.21
1680.37
1701.86
1717.84
2135.99
2151.96

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant ($p<0.05$).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **31**
Number of mass values matched: **10**
Sequence Coverage: **62%**

Matched peptides shown in **Bold Red**

1 MSDER**TFIAI KPDGVQRGLI SSILGR**FEQR GFKLVGIK**LV QPTESLLR**TH
51 YEDLQSKPFF PSLLSYMLSG PVLATVWEGK DVVKQGR**AIL GATNPLQSAP**
101 **GTIRGDFAID MGRNVCHGSD SVESANKEID LWFKKEELVE YKPALFGWIY**
151 **E**

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 31

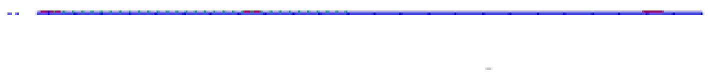
Dut1p (MS/MS b)

CA4627|CaDUT1 Mass: 16935 Total score: 45 Peptides matched: 1
dUTP pyrophosphatase

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Rank	Peptide
1	1447.7	1446.69	1446.68	0.01	0	45	1	EISLEELDNTER

Probability Based Mowse Score

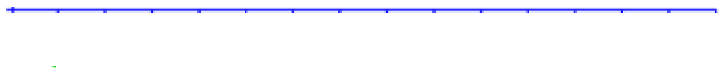
Score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 22 indicate identity or extensive homology ($p<0.05$).



Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **7%**

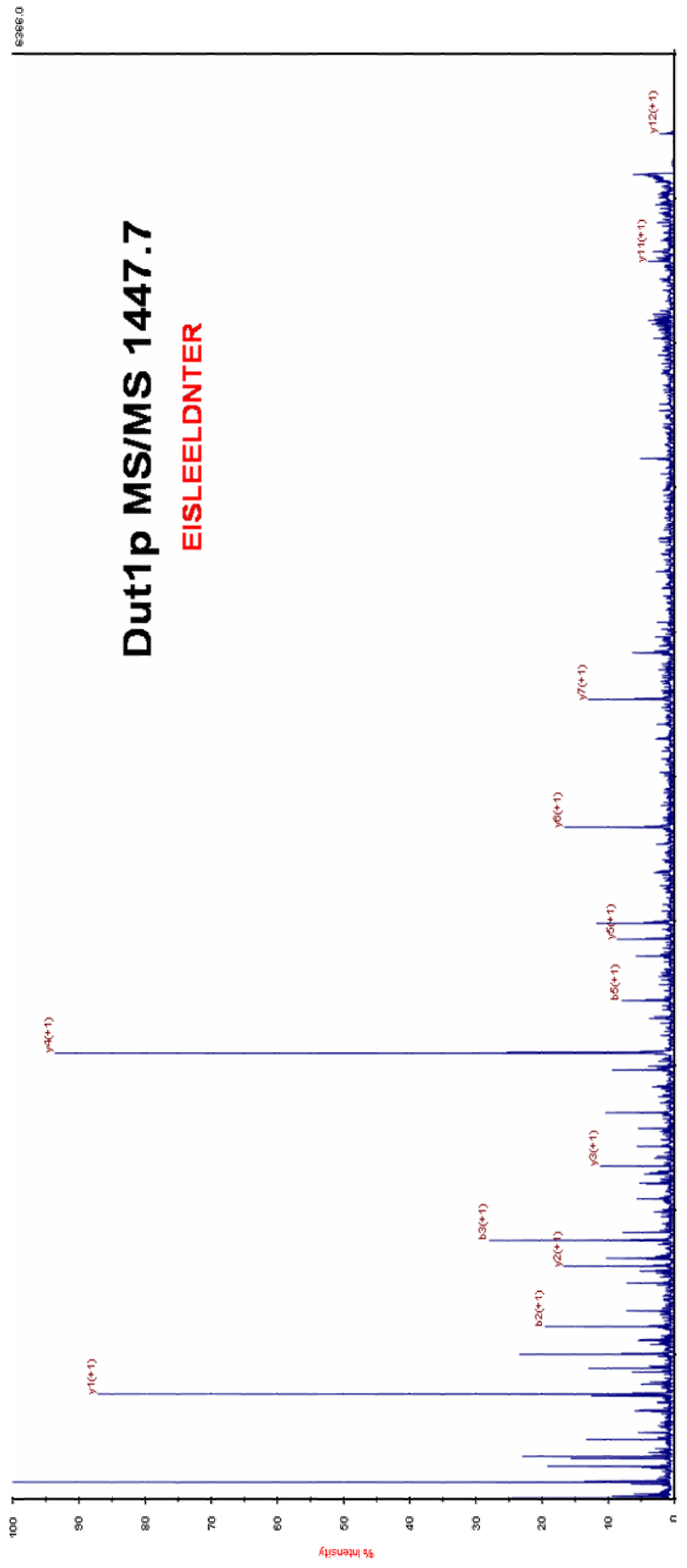
Matched peptides shown in **Bold Red**

1 MTSEDQSLKK QKLESTQSLK VYLRSPKGKV PTKGSALAAG YDLYSAEAAT
51 IPAHGQGLVS TDISIIVPIG TYGRVAPRSG LAVKHGISTG AGVIDADYRG
101 EVKVVLFNHS EKDFEIKEGD RIAQLVLEQI VNADIK**EISL EELDNTER**GE
151 GGFGSTGKN



Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 100 ppm
Fragment Mass Tolerance: ± 0.3 Da
Max Missed Cleavages : 1
Instrument type : Default
Number of queries : 1


Dut1p MS/MS 1447.7
EISLEELDNTER
6388.0
y12(+1)
y11(+1)
y7(+1)
y6(+1)
y5(+1)
b5(+1)
y4(+1)
y3(+1)
b3(+1)
y2(+1)
b2(+1)
y1(+1)
100
90
80
70
60
50
40
30
20
10
0
% Intensity

Imd3p (Imh3p, PMF)

Match to: **CA1245|CaIMH3.exon2**; Score: **184**
IMP dehydrogenase, exon 2

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
858.54	857.54	857.53	0	9	16	0	LVGIITSR
1415.79	1414.78	1414.78	0	41	53	1	KGISLTDGNELLR
1540.83	1539.82	1539.83	-0.00	160	174	0	EQAALLIEAGADALR
1558.86	1557.85	1557.85	-0.00	146	159	0	YPELQVIAGNVVTR
1622.79	1621.78	1621.75	0.03	81	94	1	NQDYPNASKSFHSK
1624.77	1623.77	1623.76	0	337	349	1	ENVDNGEIRFEFR
1695.96	1694.95	1694.96	-0.00	60	75	0	LPIVDAEGNLVSLISR
1758.87	1757.86	1757.85	0.01	331	345	1	SIDELRENVDNGEIR
1815.98	1814.98	1814.99	-0.01	144	159	1	EKYPELQVIAGNVVTR
1858.94	1857.93	1857.94	-0.00	95	111	1	QLLCGAAIGTIDADRER
1881.07	1880.06	1880.07	-0.01	58	75	1	GKLPIVDAEGNLVSLISR
1917.91	1916.9	1916.9	-0.00	350	367	0	TASAQFEGGVHGLHSYEK
1925.98	1924.98	1924.98	-0.01	209	227	0	FGVPCIADGGIGNIGHITK
2074	2072.99	2073	-0.01	350	368	1	TASAQFEGGVHGLHSYEKR
2104.01	2103	2102.99	0.01	17	34	1	DIQFHEDNKSPVSEVMTK
2154.98	2153.97	2153.94	0.03	265	285	0	GMGSIDAMQQTNTNANASTSR
2198.13	2197.12	2197.13	-0.01	286	306	1	YFSEADKVLVAQGVSGSVVDK
2205.16	2204.15	2204.16	-0.01	312	330	0	FVPYLYNGLQHSLQDIGIK
2892.39	2891.38	2891.37	0.01	228	255	0	ALALGASCVMMGGLLAGTAETPGDYFYR

No match to:
783.37
831.44
889.55
902.47
973.41
977.6
987.41
1037.5
1109.54
1169.58
1185.53
1187.51
1232.54
1243.52
1271.55
1273.55
1285.63
1293.08
1313.57
1331.56
1359.59
1399.6
1417.59
1467.71
1485.65
1503.63
1561.64
1574.79
1631.68

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **76**
Number of mass values matched: **19**
Sequence Coverage: **71%**

Matched peptides shown in **Bold Red**

1 MNGKVGGK**LV GIITSRDIQF HEDNKSPVSE VMTK**DLVVGK **KGISLTDGNE**
51 **LLR**SSKK**GKL PIVDAEGNLV SLISR**TDLQK **NQDYPNASKS FHSKQLLCGA**
101 **AIGTIDADRE R**LDKLVEAGL DVVVLDSSNG SSVFQLNMIK WIK**EKYPELQ**
151 **VIAGNVVTRE QAALLIEAGA DALR**IGMGSG SICITQEVMA CGRPQGTAVY
201 GVTEFANK**FG VPCIADGGIG NIGHITKALA LGASCVMMGG LLAGTAETPG**
251 **DYFYR**DGKRL KTYR**GMGSID AMQQTNTNAN ASTSRYFSEA DKVLVAQGVS**
301 **GSVVDK**GSIT K**FVPYLYNGL QHSLQDIGIK SIDELRENVD NGEIRFEFRT**
351 **ASAQFEGGVH GLHSYEKR**LH N

1717.72
1803.78
1812.88
1814.88
1835.89
1872.97
1939.99
1940.99
2009.16
2114.03
2181.11
2226.15
2243.22
2338.14
2405.24
2517.2
2533.32
2534.3
2551.25
2554.23
2555.21
2661.41
2684.42
2761.34
2762.34
2810.42
2891.39
2907.41

Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 76

Gua1p (IPF6105, PMF)

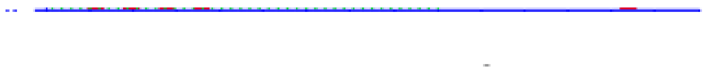
Match to: **CA3075|IPF6105** Score: **72**
similar to Saccharomyces cerevisiae Gua1p GMP synthase (glutamine-hydrolyzing) (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
948.45	947.45	947.45	-0.00	461	469	0	SVGVMGDQR
964.45	963.44	963.44	-0.01	461	469	0	SVGVMGDQR + Oxidation (M)
1071.58	1070.57	1070.57	0.00	505	514	0	IVNEVDGVAR
1092.60	1091.59	1091.60	-0.00	470	478	0	TYEQVIALR
1165.57	1164.56	1164.56	0.00	196	205	0	NFAVDICQAK
1745.81	1744.80	1744.78	0.02	38	51	0	EFNVYAEMLPCTQK + Oxidation (M)
1842.84	1841.84	1841.83	0.01	206	220	0	TNWSMENFIDTEIAR + Oxidation (M)
2052.96	2051.96	2051.95	0.00	115	132	0	EYGPATLNVEDPECALFK

No match to:
857.07
870.02
871.02
877.03
879.03
882.56
885.99
887
893.01
895.01
896.01
907.99
908.99
910.99
912.99
915
924.96
926.97
930.97
946.95
1082.06
1098.03
1114
1405.76
2164.61
2185.03
2201

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).



Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **35**
Number of mass values matched: **8**
Sequence Coverage: **16%**

Matched peptides shown in **Bold Red**

1 MSANIDDVPI EVSKVFDTIL VLDFGSQYSH LITRRLR**EFN VYAEMLPCTQ**
51 **K**IAELSWKPK GIILSGGPYS VYAEDAPHVD HDIFKLGVPI LGICYGMQEL
101 AWINGKGVAR GDKR**EYGPAT LNVEDPECAL FK**GVDHSQVW MSHGDKLHAL
151 PTGFKVVATS DNSPFCGISN ESEHIYGIQF HPEVTHTVQG KKLLK**NFAVD**
201 **ICQAKTNWSM ENFIDTEIAR** IKKLVGPTAE VIGAVSGGVD STVGAKIMKE
251 AIGDRFHAIY VDNGVMRKNE TESVKKTLDE GLGINLTVVD AGDLFLGRLK
301 GVTDPEKKRK IIGNTFIHVF EEEAAKIKPR DGSEIEYLLQ GTLYPDVIES
351 ISFKGPSQTI KTHHNVGGLL EDMKLKLIEP LRELFKDEVR HLGELLGVPE
401 DLVWRHPFPG PGLAIRVLGE VTKEQVKIAR EADAIFIEEI KKAGLYRQIS
451 QAFAALLPVK **SVGVMGDQRT YEQVIALR**AI ETLDFMTADW FIFEAAFLKK
501 VASR**IVNEVD GVAR**VTYDIT SKPPATVEWE

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 80 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 0
Number of queries : 35

Gnd1p (PMF)

Mascot Search Results

Match to: **CA5239|CaGND1**; Score: **138**
6-phosphogluconate dehydrogenase

Observed	**Mr(expt)**	**Mr(calc)**	**Delta**	**Start**	**End**	**Miss**	**Peptide**	**No match to:**
845.52	844.51	844.5	0.01	323	330	1	VEASKALK	773.44
1085.5	1084.5	1084.5	-0.00	475	483	0	DYFGAHTFK	801.49
1123.66	1122.65	1122.65	0	465	474	0	LPANLLQAQR	805.42
1187.57	1186.56	1186.57	-0.00	162	173	0	TGPSLMPGGNEK	817.09
1253.73	1252.72	1252.73	-0.00	85	94	1	ELVDQLKRPR	817.47
1258.67	1257.67	1257.67	0	380	390	0	LNNAGIALMWR	823.1
1274.68	1273.67	1273.66	0.01	380	390	0	LNNAGIALMWR Oxidation (M)	825.1
1340.72	1339.71	1339.71	-0.00	397	408	0	SVFLAEITAAYR	833.07
1362.76	1361.75	1361.76	-0.00	250	261	0	GVLDSFLIEITR	839.08
1426.69	1425.68	1425.68	0	496	506	0	DEWIHINWTGR	841.07
1495.84	1494.83	1494.83	0	462	474	1	SERLPANLLQAQR	845.09
1554.78	1553.77	1553.77	-0.00	495	506	1	KDEWIHINWTGR	849.04
1591.81	1590.8	1590.8	-0.00	145	161	0	GILFVGSGVSGGEEGAR	854.05
1640.82	1639.81	1639.81	-0.00	345	358	0	QFIDDLEQALYASK	855.05
1719.9	1718.89	1718.9	-0.00	144	161	1	KGILFVGSGVSGGEEGAR	857.34
1738.93	1737.92	1737.92	0	174	188	1	AWPHIKDIFQDVAAK	859.05
1815.92	1814.91	1814.91	0	359	374	0	IISYTQGFMLMNQAAK	861.06
1980	1978.99	1978.99	0	262	278	0	DILYYNDPTDGKPLVEK	870.02
2179.88	2178.87	2178.87	0	189	208	0	SDGEPCCDWVGDAGAGHYVK	871.02
2372.24	2371.23	2371.22	0.01	440	461	0	AIQYGIPTPAFSTALAFYDGLR	875.03
								877.04
								879.03
								881.02
								883.02
								885.02
								886.01

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **86**
Number of mass values matched: **20**
Sequence Coverage: **42%**

Matched peptides shown in **Bold Red**

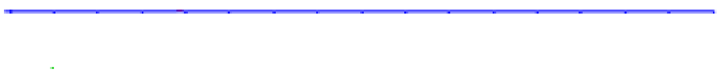
1 MKNFNALSRL SILSKQLSFN NTNSSIARGD IGLIGLAVMG QNLILNMADH
51 GYTVVAYNRT TAKVDRFLEN EAKGKSILGA HSIK**ELVDQL KRPR**RIMLLV
101 KAGAPVDEFI NQLLPYLEEG DIIIDGGNSH FPDSNRRYEE LAK**KGILFVG**
151 **SGVSGGEEGA RTGPSLMPGG NEKAWPHIKD IFQDVAAKSD GEPCCDWVGD**
201 **AGAGHYVK**MV HNGIEYGDMQ LICEAYDLMK RVGKFEDKEI GDVFATWNK**G**
251 **VLDSFLIEIT RDILYYNDPT DGKPLVEK**IL DTAGQKGTGK WTAVNALDLG
301 IPVTLIGEAV FSRCLSAMKA ER**VEASKALK** GPQVTGESPI TDKK**QFIDDL**
351 **EQALYASKII SYTQGFMLMN QAAK**DYGWK**L NNAGIALMWR** GGCIIR**SVFL**
401 **AEITAAYR**KK PDLENLLLYP FFNDAITKAQ SGWRASVGK**A IQYGIPTPAF**
451 **STALAFYDGL RSERLPANLL QAQRDYFGAH TFK**VLPGQEN ELLK**KDEWIH**
501 **INWTGR**GGDV SSTTYDA

887
889.55
893.01
895.01
901.01
908.98
933.57
943.38
954.5
977.6
1020.5
1029.42
1044.09
1050.1
1060.06
1066.08
1082.05
1098.02
1111.56
1115.45
1137.08
1137.58
1153.57
1201.49
1277.1
1287.52
1293.07
1296.69
1373.57
1433.72
1586.77
2083.04
2145.05
2163.06
2185.06
2193.94

2273.16
2289.16
2295.15
3213.53

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 86



Cdc19p (PFM)

Match to: **CA3483|CaCDC19**; Score: **172**
pyruvate kinase (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	
914.49	913.48	913.44	0.04	492	500	0	GSGHSNTVR	
1030.58	1029.57	1029.55	0.03	221	229	0	TANDVLEIR	
1128.7	1127.69	1127.67	0.03	24	34	1	RSSIIGTIGPK	
1154.71	1153.7	1153.68	0.02	80	90	0	GRPLAIALDTK	
1220.67	1219.66	1219.65	0.01	211	220	0	VHMIFASFIR	
1273.75	1272.74	1272.74	0	401	413	0	AIVVLSTSGLSAR	
1318.68	1317.67	1317.67	0	480	491	0	GDSIVTVQGWTR	
1431.8	1430.8	1430.8	0	418	429	0	YKPDVPILMVTR	
1434.77	1433.76	1433.77	-0.00	362	373	0	AIAYPQLFNELR	
1447.75	1446.74	1446.79	-0.05	418	429	0	YKPDVPILMVTR	Oxidation (M)
1462.77	1461.77	1461.79	-0.03	209	220	1	NKVHMIFASFIR	
1478.75	1477.75	1477.79	-0.04	209	220	1	NKVHMIFASFIR	Oxidation (M)
1501.78	1500.77	1500.82	-0.04	466	479	0	WAVSEAVELGIISK	
1706.94	1705.93	1705.98	-0.05	80	95	1	GRPLAIALDTKGPEIR	
1809.94	1808.93	1809	-0.08	269	285	0	GDLGIEIPAPQVFVVQK	
2251.95	2250.94	2251.01	-0.07	342	361	0	GNYPVEAVSMMHNTCLTAEK	
2254.91	2253.9	2253.99	-0.09	54	72	0	MNFSHGSYEYHQSVIDNAR	
2690.34	2689.33	2689.3	0.03	245	268	0	IENQQGVNNFDEILEVTDGVMVAR	
2698.21	2697.2	2697.27	-0.07	442	463	0	GVYPFIYDKPSIENWQEDVENR	

No match to:
728.5
778.51
822.49
822.68
823.49
832.36
1149.65
1390.78
1435.77
1472.71
1690.56
1831.93
2258.81
2270.82
2380.13
2690.1
2691.29
2692.24
2698.02
2700.15
2802.29
2802.44

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant ($p<0.05$).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **41**
Number of mass values matched: **19**
Sequence Coverage: **44%**

Matched peptides shown in **Bold Red**
1 MSHSSLSWLS NFNVETVPSK YLR**RSSIIGT IGPK**TNNVDV LVKLRKAGLN
51 VVR**MNFSHGS YEYHQSVIDN AR**KSEEVYK**G RPLAIALDTK GPEIR**TGTTI
101 GDKDYPIPPN HEMIFTTDDA YKTKCDDKVM YIDYKNITKV IAPGKIIYVD
151 DGVLSFEVIS VDDEQTLKVR SLNAGKISSH KGVNLPGTDV DLPALSEKDI
201 ADIKFGVK**NK VHMIFASFIR TANDVLEIR**K VLGEEGKDIQ IISK**IENQQG**
251 **VNNFDEILEV TDGVMVARGD LGIEIPAPQV FVVQK**QLIAK CNLAAKPVIC
301 ATQMLESMTY NPRPTRAEVS DVGNAILDGA DCVMLSGETA K**GNYPVEAVS**
351 **MMHNTCLTAE KAIAYPQLFN ELR**SLAKKPT ATTETCAVAA VSAAYEQDAK
401 **AIVVLSTSGL SAR**LVSK**YKP DVPILMVTR**N ERAAKFSHLY R**GVYPFIYDK**
451 **PSIENWQEDV ENR**LR**WAVSE AVELGIISKG DSIVTVQGWT RGSGHSNTVR**
501 IVQA

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 41

Tdh3p left (PMF)

Match to: **CA5892|CaGAP1**; Score: **114**
Glyceraldehyde-3-phosphate dehydrogenase

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1297.63	1296.62	1296.62	0	186	196	1	TVDGPSHKDWR
1500.84	1499.83	1499.82	0.01	234	247	0	VPTTDVSVVDLTVR
1656.85	1655.84	1655.84	0	75	88	1	VFQERDPANIPWGK
1766.81	1765.81	1765.79	0.01	309	322	0	LISWYDNEYGYSTR
2228.15	2227.14	2227.14	0.01	89	109	1	SGVDYVIESTGVFTKLEGAQK
2488.22	2487.21	2487.2	0.01	26	47	0	DIEVVAVNDPFIAPDYAAYMFK
2591.32	2590.31	2590.29	0.02	162	185	0	VVNDTFGIEEGLMTTVHSITATQK
2886.38	2885.37	2885.35	0.02	271	297	0	GVLGYTEDAVVSTDFLGSSYSSIFDEK
2890.49	2889.48	2889.48	0	118	144	1	VIITAPSADAPMFVVGVNEDKYTPDLK

No match to:
834.45
1628.91
1678.83
1722.82
1764.8
1768.81
1788.79
1898.03
2250.16
2510.19
2613.3
2908.38
2912.45
3018.61
3305.6

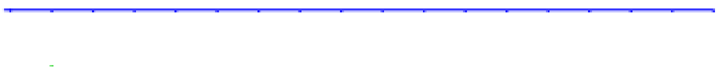
Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **24**
Number of mass values matched: **9**
Sequence Coverage: **51%**

Matched peptides shown in **Bold Red**

1 MAIKIGINGF GRIGRLVLRV ALGRK**DIEVV AVNDPFIAPD YAAYMFK**YDS
51 THGRYKGEVT ASGDDLVIDG HKIK**VFQERD PANIPWGKSG VDYVIESTGV**
101 **FTKLEGAQK**H IDAGAKK**VII TAPSADAPMF VVGVNEDKYT PDLK**IISNAS
151 CTTNCLAPLA K**VVNDTFGIE EGLMTTVHSI TATQKTVDGP SHKDWR**GGRT
201 ASGNIIPSST GAAKAVGKVI PELNGKLTGM SLR**VPTTDVS VVDLTVR**LKK
251 AASYEEIAQA IKKASEGPLK **GVLGYTEDAV VSTDFLGSSY SSIFDEK**AGI
301 LLSPTFVK**LI SWYDNEYGYS TR**VVDLLEHV AKASA



Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 24

Tdh3p middle (PMF)

Match to: **CA5892|CaGAP1**; Score: **205**
Glyceraldehyde-3-phosphate dehydrogenase

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1122.62	1121.61	1121.64	-0.04	323	332	0	VVDLLEHVAK
1145.66	1144.65	1144.67	-0.02	2	12	1	AIKIGINGFGR
1293.64	1292.63	1292.66	-0.03	251	262	0	AASYEEIAQAIK
1297.6	1296.59	1296.62	-0.03	186	196	1	TVDGPSHKDWR
1421.73	1420.72	1420.76	-0.04	251	263	1	AASYEEIAQAIKK
1500.8	1499.79	1499.82	-0.03	234	247	0	VPTTDVSVVDLTVR
1601.78	1600.77	1600.8	-0.03	89	103	0	SGVDYVIESTGVFTK
1612.84	1611.84	1611.77	0.06	57	72	0	GEVTASGDDLVIDGHK
1656.83	1655.82	1655.84	-0.02	75	88	1	VFQERDPANIPWGK
1766.78	1765.77	1765.79	-0.02	309	322	0	LISWYDNEYGYSTR
1833.89	1832.88	1832.91	-0.03	145	161	0	IISNASCTTNCLAPLAK
1903.91	1902.9	1902.93	-0.03	55	72	1	YKGEVTASGDDLVIDGHK
2228.11	2227.11	2227.14	-0.03	89	109	1	SGVDYVIESTGVFTKLEGAQK
2591.27	2590.27	2590.29	-0.03	162	185	0	VVNDTFGIEEGLMTTVHSITATQK
2886.34	2885.34	2885.35	-0.01	271	297	0	GVLGYTEDAVVSTDFLGSSYSSIFDEK
2890.46	2889.45	2889.48	-0.03	118	144	1	VIITAPSADAPMFVVGVNEDKYTPDLK

No match to:
834.42
1167.66
1253.61
1410.68
1443.72
1580.87
1625.91
1628.88
1654.81
1672.83
1678.79
1722.8
1782.77
1788.75
1857
1898.01
1925.91
1955.03
2250.09
2543.27
2613.27
2908.34

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant ($p<0.05$).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **38**
Number of mass values matched: **16**
Sequence Coverage: **65%**

Matched peptides shown in **Bold Red**

1 M**AIKIGINGF GR**IGRLVLRV ALGRKDIEVV AVNDPFIAPD YAAYMFKYDS
51 THGR**YKGEVT ASGDDLVIDG HK**IK**VFQERD PANIPWGKSG VDYVIESTGV**
101 **FTKLEGAQK**H IDAGAKK**VII TAPSADAPMF VVGVNEDKYT PDLKIISNAS**
151 **CTTNCLAPLA KVVNDTFGIE EGLMTTVHSI TATQKTVDGP SHKDWR**GGRT
201 ASGNIIPSST GAAKAVGKVI PELNGKLTGM SLR**VPTTDVS VVDLTVR**LKK
251 **AASYEEIAQA IKK**ASEGPLK **GVLGYTEDAV VSTDFLGSSY SSIFDEK**AGI
301 LLSPTFVK**LI SWYDNEYGYS TRVVDLLEHV AK**ASA

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 38

Adh1p (PMF)

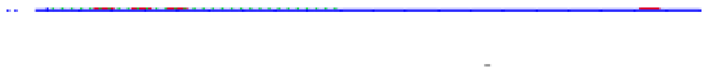
Match to: **CA4765|CaADH1** Score: **98**
alcohol dehydrogenase (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1103.70	1102.69	1102.69	0.00	353	363	0	VVLVGLPAHAK
1145.65	1144.65	1144.65	-0.00	364	374	0	VTAPVFDAVVK
1271.59	1270.58	1270.58	-0.00	388	398	0	DTAEAIDFFSR
1316.75	1315.74	1315.74	0.00	407	418	0	IVGLSDLPEVFK
1510.79	1509.78	1509.78	-0.00	96	109	0	AVVFDTNGGQLVYK
1574.85	1573.84	1573.85	-0.01	339	352	0	AIDQSVEYVRPLGK
1638.81	1637.80	1637.80	-0.00	322	338	0	ATDGGPHGAINVSVSEK
2035.07	2034.06	2034.06	0.00	148	168	0	LPLVGGHEGAGVVVGMGENVK + Oxidation (

No match to:
861.07
871.03
877.04
879.04
880.46
881.26
893.02
895.02
897.01
908.99
911
996.6
1060.07
1066.08
1082.05
1088.07
1098.03
1399.68
1456.69
1511.77
1544.78
1562.81
1619.83
2185.02
2200.98
2298.17

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).



Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **34**
Number of mass values matched: **8**
Sequence Coverage: **25%**

Matched peptides shown in **Bold Red**

1 MQASLFRIFR GASLTTTTAA ASFTATATAG ATTAKTLSGS TVLRKSYKRT
51 YSSSVLSSPE LFFFHQFNNN KRYCHTTTTT NTKTIMSEQI PKTQK**AVVFD**
101 **TNGGQLVYK**D YPVPTPKPNE LLIHVKYSGV CHTDLHAWKG DWPLATK**LPL**
151 **VGGHEGAGVV VGMGENVK**GW KIGDFAGIKW LNGSCMSCEF CQQGAEPNCG
201 EADLSGYTHD GSFEQYATAD AVQAAKIPAG TDLANVAPIL CAGVTVYKAL
251 KTADLAAGQW VAISGAGGGL GSLAVQYARA MGLRVVAIDG GDEKGEFVKS
301 LGAEAYVDFT KDKDIVEAVK K**ATDGGPHGA INVSVSEKAI DQSVEYVRPL**
351 **GKVVLVGLPA HAKVTAPVFD AVVK**SIEIKG SYVGNRK**DTA EAIDFFSR**GL
401 IKCPIK**IVGL SDLPEVFK**LM EEGKILSRYV LDTS

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 80 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 0
Number of queries : 34

Tpi1p (PMF)

Match to: **CA5950|CaTPI1** Score: **89**
Triose phosphate isomerase

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
932.47	931.46	931.46	0.00	195	203	0	SIGAEQAEK
1007.55	1006.55	1006.54	0.00	206	215	0	ILYGGSVNGK
1043.53	1042.52	1042.52	-0.00	4	12	0	QFFVGGNFK
1047.53	1046.52	1046.52	0.00	136	145	0	GGVTLDVCAR
1386.77	1385.76	1385.75	0.01	18	29	0	QQITSIIDNLNK
1431.75	1430.74	1430.74	-0.01	123	134	0	VILCIGETLEER
1487.79	1486.78	1486.78	0.01	56	69	0	QPTVAIGAQNVFDK

No match to:
855.08
861.08
871.02
877.04
881.03
887.01
893.02
908.99
1008.54
1026.5
1050.11
1060.06
1066.08
1072.1
1082.05
1098.02
1175.62
1189.62
1270.67
1277.11
1293.08
1453.74
1470.75
1522.8
1751.93
1909.02
2185
2200.99

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **35**
Number of mass values matched: **7**
Sequence Coverage: **30%**

Matched peptides shown in **Bold Red**

1 MAR**QFFVGGN FK**ANGTK**QQI TSIIDNLNK**A DLPKDVEVVI CPPALYLGLA
51 VEQNK**QPTVA IGAQNVFDK**S CGAFTGETCA SQILDVGASW TLTGHSERRT
101 IIKESDEFIA EKTKFALDTG VK**VILCIGET LEER**K**GGVTL DVCAR**QLDAV
151 SKIVSDWSNI VVAYEPVWAI GTGLAATPED AEETHKGIRA HLAK**SIGAEQ**
201 **AEK**TR**ILYGG SVNGK**NAKDF KDKANVDGFL VGGASLKPEF VDIIKSRL

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 80 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 0
Number of queries : 35

Adh5p (PMF)

Match to: **CA2391|CaADH5**; Score: **101**
probable alcohol dehydrogenase (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
709.34	708.33	708.32	0.01	325	331	0	AGGYEGR
978.53	977.52	977.5	0.02	323	331	1	LRAGGYEGR
1063.55	1062.54	1062.53	0.01	294	303	0	EAFELAAQGK
1256.59	1255.58	1255.57	0.01	283	293	0	GSFWGTSMDLR
1599.95	1598.94	1598.91	0.03	304	318	0	VKPNVAHAPLSELPK
2322.35	2321.35	2321.3	0.05	255	277	0	GTIVPVGLGATSLNINLADLDLR
2639.43	2638.42	2638.35	0.07	140	164	0	IPDNVTSEEAAAITDAVLTPYHAIK
2892.75	2891.74	2891.63	0.11	255	282	1	GTIVPVGLGATSLNINLADLDLREITVK
3093.74	3092.73	3092.64	0.09	136	164	1	NLVKIPDNVTSEEAAAITDAVLTPYHAIK

No match to:
832.31
952.55
1024.59
1035.56
1085.58
1150.53
1198.55
1322.67
1593.79
1615.76
1656.98
1836.05
1893.09
2113
2138.21
2268.17
2274.1
2278.22
2291.1
2348.13
2379.37
2624.46
2660.42
2696.43
2950.75
3073.75
3131.75
3150.77

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **37**
Number of mass values matched: **9**
Sequence Coverage: **30%**

Matched peptides shown in **Bold Red**

1 MSIPSTQYGF FYNKASGLNL KKDLPVNKPG AGQLLLKVDA VGLCHSDLHV
51 LYEGLDCGDN YVMGHEIAGT VAELGEEVSE FAVGDRVACV GPNGCGLCKH
101 CLTGNDNVCT KSFLDWFGLG YNGGYEQFLL VKRPR**NLVKI PDNVTSEEAA**
151 **AITDAVLTPY HAIK**SAGVGP ASNILIIGAG GLGGNAIQVA KAFGAKVTVL
201 DKKDKARDQA KAFGADQVYS ELPDSVLPGS FSACFDFVSV QATYDLCQKY
251 CEPK**GTIVPV GLGATSLNIN LADLDLREIT VKGSFWGTSM DLREAFELAA**
301 **QGKVKPNVAH APLSELPK**YM EK**LRAGGYEG R**VVFNP

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 37

Sol3p (PMF)

Match to: **CA1704|CaSOL3**; Score: **62**
weak multicopy suppressor of los1-1 (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1021.54	1020.53	1020.52	0	21	28	0	YVIEQQNK
1175.57	1174.56	1174.57	-0.00	97	106	0	NLPQETTNMK
1323.76	1322.75	1322.76	-0.00	107	118	0	LHVIDQSLLTGK
1813.92	1812.91	1812.93	-0.01	173	188	0	DELISYISDSPKPPPR
1858.81	1857.8	1857.83	-0.03	63	76	1	AQWDKWEVYFSDER
2454.29	2453.28	2453.28	0	168	188	1	LLEERDELISYISDSPKPPPR

No match to:
935.51
1143.63
1172.7
1199.63
1206.62
1208.63
1224.57
1243.72
1327.69
1339.7
1473.81
1536.85
1568.84
1571.75
1578.8
1701.81
1724.53
1863.74
1959.91
2046.01
2256.11
2275.11
2545.21

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).

Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **29**
Number of mass values matched: **6**
Sequence Coverage: **25%**

Matched peptides shown in **Bold Red**

1 MSTKVYSYSD SQDVANSVGK **YVIEQQNK**AI EANGSFKIAL SGGSLGKILK
51 QALIDNKEIG SK**AQWDKWEV YFSDER**LVPL YHPDSNFGLF NEMVLK**NLPQ**
101 **ETTNMKLHVI DQSLLTGK**DG KLDDLVDQAK DQEIAKEYAN GLPKQFDLIL
151 LGCGPDGHTC SLFPGHK**LLE ERDELISYIS DSPKPPPR**RI TFTFPVLENA
201 KAIAFVATGA GKAPVLREIF SGQSKLPCAL VNDIKTGVSV SWFVDSPAVE
251 GVDVLTSKY

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 29

Gpp1p (PMF)

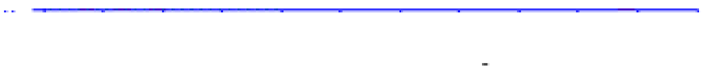
Match to: **CA5788|CARHR2**; Score: **108**
DL-glycerol phosphatase

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
717.28	716.28	716.3	-0.03	52	57	0	TSHGCR
724.34	723.33	723.36	-0.02	219	224	0	DLSSFR
1309.64	1308.63	1308.67	-0.03	153	164	0	GKPHPQGYQAAR
1319.55	1318.54	1318.59	-0.05	165	175	0	DTLGYHDAHYK
1443.77	1442.76	1442.81	-0.05	118	131	0	WAVVTSGTLPLATK
1461.74	1460.73	1460.77	-0.04	40	51	0	TRPHVDPEEIIR
1473.73	1472.72	1472.79	-0.06	176	190	0	VVVFEDAPAGITAGK
1791.88	1790.87	1790.92	-0.05	135	149	0	LLSIERPDCFITAEK
2009.93	2008.92	2008.97	-0.05	191	209	1	GAGAMVVGICSTYDPEKVR
2120.08	2119.08	2119.13	-0.06	135	152	1	LLSIERPDCFITAEKVTK
2138.06	2137.05	2136.95	0.1	237	254	0	VVVDDYFYADEQFLQESA

No match to:
713.42
731.32
744.4
756.41
757.45
793.4
815.46
832.29
841.04
845.51
855.02
861.03
877.01
892.98
905.44
1033.46
1066.02
1082.01
1153.52
1178.6
1234.64
1262.61
1273.71
1287.68
1293.23
1309.91

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).



Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **64**
Number of mass values matched: **11**
Sequence Coverage: **51%**

Matched peptides shown in **Bold Red**

1 MTKTQQPAVF YVHAALFDCD GTLVNSTGAI SEFWRDFGK**T RPHVDPEEII**
51 **RTSHGCR**TFD VIAKWSPEDA IEEQVTAWEG AIPDTFGHHA KPIPGSVELV
101 KSFDKLSKEA TENGKQR**WAV VTSGTLPLAT K**WLK**LLSIER PDCFITAEKV**
151 **TKGKPHPQGY QAARDTLGYH DAHYKVVVFE DAPAGITAGK GAGAMVVGIC**
201 **STYDPEKVR**K SGANIVVK**DL SSFR**IDSYNK ETDEFK**VVVD DYFYADEQFL**
251 **QESA**

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 64

1310.65
1331.62
1341.56
1347.6
1361.77
1405.79
1445.33
1449.82
1493.8
1495.74
1499.69
1511.72
1537.88
1553.84
1581.88
1614.85
1625.92
1638.83
1669.94
1707.73
1713.97
1773.91
1805.88
2023.93
2063.01
2134.1
2228.08

Sdh3p (Sdh12p, PMF)

Match to: **CA2470|CaSDH12** Score: **89**
Succinate dehydrogenase (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1026.51	1025.50	1025.50	0.00	245	254	0	TIMATGGYGR
1042.50	1041.49	1041.49	0.00	245	254	0	TIMATGGYGR + Oxidation (M)
1125.60	1124.59	1124.59	0.00	69	79	0	AAFGLVSEGFK
1133.56	1132.55	1132.55	-0.00	339	348	0	AITMEINEGR
1149.56	1148.55	1148.55	0.00	339	348	0	AITMEINEGR + Oxidation (M)
1350.63	1349.62	1349.62	-0.00	306	318	0	GEGGFLVNSEGER
1502.75	1501.75	1501.75	-0.01	467	480	0	DNLQPGTPIPDHAK
1543.77	1542.76	1542.78	-0.02	602	615	0	HTLSYQETVGGPVR
1836.80	1835.79	1835.81	-0.02	122	137	0	GSDWLGDQDAIHYMTK
1852.81	1851.80	1851.81	-0.01	122	137	0	GSDWLGDQDAIHYMTK + Oxidation (M)
2103.96	2102.95	2102.97	-0.02	221	239	0	DGACIGIIAYNEEDGTLHR
2797.22	2796.21	2796.26	-0.04	418	445	0	SADGNDEVVPGLLACGEAACASVHGANR

No match to:
861.08
871.03
877.04
886
893.02
895.02
897.01
899.03
908.99
910.99
915.01
917
924.97
930.98
1046.6
1094.54
1104.04
1112.55
1117.59
1150.56
1155.57
1176.55
1178.61
1191.53
1244.62
1549.67

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).

modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **12**
Sequence Coverage: **21%**

Matched peptides shown in **Bold Red**

1 MLTSLRNQVK SSAVTKRLLS SSSVRSQVIG SNVKGQDFNA AKYMSQKYHV
51 VDHEYDCVVV GAGGAGLR**AA FGLVSEGFK**T ACVSKLFPTR SHTVAAQGGI
101 NAALGNMHAD DWHWHFYDTV K**GSDWLGDQD AIHYMTK**EAP ASIYELEHYG
151 VPFSRNDEGR IYQRAFGGQS KEFGKGGQAY RTCAVADRTG HALLHSLYGQ
201 SLRHDCHFFI EFFAMDLMMK **DGACIGIIAY NEEDGTLHR**F FANR**TIMATG**
251 **GYGR**AYFSCT SAHTCTGDGY AMVSRAGLPL EDLEFVQFHP SGIYGSGCLI
301 TEGAR**GEGGF LVNSEGER**FM ERYAPSAKDL ASRDVVSR**AI TMEINEGR**GV
351 GPEKDHMYLQ LSHIPAPVLK ERLPGISETA HIFAGVDVTK EPIPILPTVH
401 YNMGGIPTNW KGEVLKK**SAD GNDEVVPGLL ACGEAACASV HGANR**LGANS
451 LLDLVVFGRA VAHTIR**DNLQ PGTPIPDHAK** DIGYESIANL DKLRNANGSK
501 PTADIRLEMQ KTMQKGCAVF RTQETLDQCV EHIGEVDKSF EDVKTTDRSM
551 IWNSDLVETL ELQNLLTCAT QTAASAAART ESRGAHSRDD FPDRDDVNWR
601 K**HTLSYQETV GGPVR**LDYRD VVKTTLDEND CKPVPPAKRV Y

1606.83
1671.86
1840.9
1873.93
1889.93
1913.86
1929.86
2057.91
2185.01
2200.97
2282.16
2706.24

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 80 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 0
Number of queries : 50

Tpi1p (MS/MS)

CA5950|CaTPI1 Mass: 26880 Total score: 23 Peptides matched: 1
Triose phosphate isomerase

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Rank	Peptide
1	**1043.5**	**1042.49**	**1042.52**	**-0.03**	**0**	**23**	**1**	**QFFVGGNFK**

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 16 indicate peptides with significant homology (p<0.05).
Individual ions scores > 20 indicate identity or extensive homology (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **4%**

Matched peptides shown in **Bold Red**
1 MAR**QFFVGGN FK**ANGTKQQI TSIIDNLNKA DLPKDVEVVI CPPALYLGLA
51 VEQNKQPTVA IGAQNVFDKS CGAFTGETCA SQILDVGASW TLTGHSERRT
101 IIKESDEFIA EKTKFALDTG VKVILCIGET LEERKGGVTL DVCARQLDAV
151 SKIVSDWSNI VVAYEPVWAI GTGLAATPED AEETHKGIRA HLAKSIGAEQ
201 AEKTRILYGG SVNGKNAKDF KDKANVDGFL VGGASLKPEF VDIIKSRL

Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.3 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of queries : 1

Tdh3p right (PMF)

Match to: **CA5892|CaGAP1**; Score: **185**
Glyceraldehyde-3-phosphate dehydrogenase

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
835.39	834.39	834.36	0.02	48	54	0	YDSTHGR
1122.6	1121.59	1121.64	-0.05	323	332	0	VVDLLEHVAK
1145.64	1144.63	1144.67	-0.04	2	12	1	AIKIGINGFGR
1293.62	1292.61	1292.66	-0.05	251	262	0	AASYEEIAQAIK
1297.58	1296.57	1296.62	-0.05	186	196	1	TVDGPSHKDWR
1421.7	1420.69	1420.76	-0.06	251	263	1	AASYEEIAQAIKK
1500.76	1499.76	1499.82	-0.06	234	247	0	VPTTDVSVVDLTVR
1601.74	1600.73	1600.8	-0.07	89	103	0	SGVDYVIESTGVFTK
1612.8	1611.8	1611.77	0.02	57	72	0	GEVTASGDDLVIDGHK
1656.78	1655.78	1655.84	-0.06	75	88	1	VFQERDPANIPWGK
1766.73	1765.72	1765.79	-0.07	309	322	0	LISWYDNEYGYSTR
1833.83	1832.83	1832.91	-0.09	145	161	0	IISNASCTTNCLAPLAK
1903.85	1902.85	1902.93	-0.08	55	72	1	YKGEVTASGDDLVIDGHK
2228.04	2227.03	2227.14	-0.11	89	109	1	SGVDYVIESTGVFTKLEGAQK
2591.18	2590.17	2590.29	-0.12	162	185	0	VVNDTFGIEEGLMTTVHSITATQK
2886.23	2885.22	2885.35	-0.13	271	297	0	GVLGYTEDAVVSTDFLGSSYSSIFDEK

No match to:

834.42
1167.64
1253.59
1313.58
1410.65
1443.69
1580.84
1628.84
1654.77
1670.78
1672.78
1678.75
1713.82
1721.78
1764.74
1782.72
1788.7
1798.73
1897.95
1919.92
1954.98
2250.02
2543.18
2613.17
2890.34
2908.23

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant ($p<0.05$).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **43**
Number of mass values matched: **16**
Sequence Coverage: **60%**

Matched peptides shown in **Bold Red**

1 M**AIKIGINGF GR**IGRLVLRV ALGRKDIEVV AVNDPFIAPD YAAYMFK**YDS**
51 **THGRYKGEVT ASGDDLVIDG HK**IK**VFQERD PANIPWGKSG VDYVIESTGV**
101 **FTKLEGAQK**H IDAGAKKVII TAPSADAPMF VVGVNEDKYT PDLK**IISNAS**
151 **CTTNCLAPLA KVVNDTFGIE EGLMTTVHSI TATQKTVDGP SHKDWR**GGRT
201 ASGNIIPSST GAAKAVGKVI PELNGKLTGM SLR**VPTTDVS VVDLTVR**LKK
251 **AASYEEIAQA IKK**ASEGPLK **GVLGYTEDAV VSTDFLGSSY SSIFDEK**AGI
301 LLSPTFVK**LI SWYDNEYGYS TRVVDLLEHV AK**ASA

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 43

Fba1p (PMF)

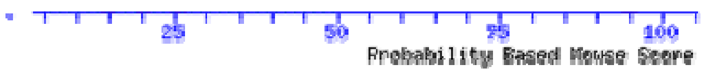
Match to: **CA5180|CaFBA1**; Score: **95**
fructose-bisphosphate aldolase (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1470.64	1469.63	1469.7	-0.07	17	28	1	DVKDLFDYAQEK
1714.82	1713.81	1713.88	-0.07	78	94	0	DQAASIAGSIAAAHYIR
2063.02	2062.02	2062.07	-0.05	95	113	0	AIAPTYGIPVVLHTDHCAK
2150.09	2149.08	2149.12	-0.04	52	72	1	DNKAPIILQTSQGGAAYFAGK
2170.03	2169.02	2169.06	-0.04	193	211	0	DALYTSPETVFAVYESLHK
2191.13	2190.12	2190.16	-0.04	95	114	1	AIAPTYGIPVVLHTDHCAKK
2228.15	2227.15	2227.13	0.01	73	94	1	GVDNKDQAASIAGSIAAAHYIR
2245.16	2244.15	2244.21	-0.06	29	51	0	GFAIPAINVTSSSTVVAALEAAR
2982.4	2981.39	2981.33	0.07	133	159	0	TGTPLFSSHMLDLSEETDDENIATCAK

No match to:
745.26
749.3
860.96
876.94
956.32
1128.41
1169.57
1219.55
1317.7
1347.65
1361.72
1405.75
1449.76
1469.64
1471.63
1493.79
1537.84
1550.71
1551.71
1581.87
1625.88
1669.93
1681.76
1794.78
2085
2100.98
2172.06
2186.08
2188.05
2285.13

Probability Based Mowse Score

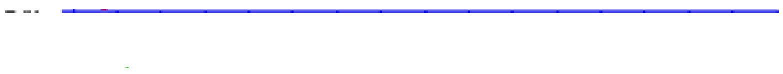
Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant ($p<0.05$).



Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **39**
Number of mass values matched: **9**
Sequence Coverage: **40%**

Matched peptides shown in **Bold Red**

1 MAPPAVLSKS GVIYGK**DVKD LFDYAQEKGF AIPAINVTSS STVVAALEAA**
51 **RDNKAPIILQ TSQGGAAYFA GKGVDNKDQA ASIAGSIAAA HYIRAIAPTY**
101 **GIPVVLHTDH CAKK**LLPWFD GMLKADEEFF AK**TGTPLFSS HMLDLSEETD**
151 **DENIATCAK**Y FERMAKMGQW LEMEIGITGG EEDGVNNEHV EK**DALYTSPE**
201 **TVFAVYESLH K**ISPNFSIAA AFGNVHGVYK PGNVQLRPEI LGDHQVYAKK
251 QIGTDAKHPL YLVFHGGSGS TQEEFNTAIK NGVVKVNLDT DCQYAYLTGI
301 RDYVTNKIEY LKAPVGNPEG ADKPNKKYFD PRVWVREGEK TMSKRIAEAL
351 DIFHTKGQL



Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm

Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 39

Pdc11p (PMF)

Match to: **CA2474|CaPDC11**; Score: **121**
Pyruvate decarboxylase (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	**No match to:**
								1543.77
745.35	744.34	744.36	-0.02	9	13	0	FFFER	1678.85
781.37	780.36	780.39	-0.03	377	382	0	VSSWFR	1966.86
1621.82	1620.81	1620.83	-0.02	307	319	1	NIVEFHSDYTKIR	2040.89
1941.03	1940.02	1940.04	-0.02	209	226	0	LISEASNPVILVDACAIR	2290.09
1983.87	1982.87	1982.89	-0.02	45	63	0	WAGNANELNAGYAADGYAR	2519.35
2094.04	2093.03	2093.06	-0.03	383	402	0	EGDIIITETGTSAFGIVQSR	2523.24
2105.08	2104.08	2104.1	-0.02	112	129	0	QLLLHHTLGNGDFTVFHR	2576.35
2441.26	2440.25	2440.25	0	157	177	0	DAYVYQRPVYIGLPSNLVDMK	2676.43
2466.25	2465.24	2465.28	-0.04	383	405	1	EGDIIITETGTSAFGIVQSRFPK	
2639.31	2638.31	2638.31	-0.00	130	153	1	MFKNISQTSAFIADINSAPAEIDR	

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **19**
Number of mass values matched: **10**
Sequence Coverage: **25%**

Matched peptides shown in **Bold Red**

1 MSEITLGR**FF FER**LHQLKVD TVFGLPGDFN LALLDKIYEV EGMR**WAGNAN**
51 **ELNAGYAADG YAR**VNPNGLS ALVSTFGVGE LSLTNAIAGS YSEHVGVINL
101 VGVPSSSAQA K**QLLLHHTLG NGDFTVFHRM FKNISQTSAF IADINSAPAE**
151 **IDR**CIR**DAYV YQRPVYIGLP SNLVDMK**VPK SLLDKKIDLS LHPNDPESQT
201 EVIETVEK**LI SEASNPVILV DACAIR**HNCK PEVAKLIEET QFPVFTTPMG
251 KSSVDESNPR FGGVYVGSLS KPEVKESVES ADLILSIGAL LSDFNTGSFS
301 YGYKTR**NIVE FHSDYTKIR**Q ATFPGVQMKE ALQKLLTTVK KSINPNYTPV
351 PVPETKLINT PAAPSTPLTQ EYLWTK**VSSW FREGDIIITE TGTSAFGIVQ**
401 **SRFPK**NSIGI SQVLWGSIGY TVGATCGAAM AAQELDPKRR VILFVGDGSL
451 QLTVQEISTM CKWECNNTYL FVLNNDGYTI ERLIHGEKAQ YNDIQPWNNL
501 QLLPLFNAKD YETKRISTVG ELNDLFADKA FAVPDKIRMV EVMLPTMDAP

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 19

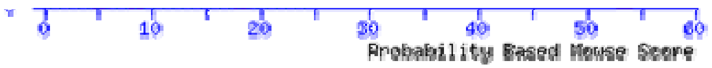
Eno1p (MS/MS)

CA3874|CaENO1 Mass: 47203 Total score: 53 Peptides matched: 1
Enolase I (2-phosphoglycerate dehydratase)

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Rank	Peptide
1	1159.61	1158.6	1158.6		0	0	53	1 IGSEVYHNLK

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 24 indicate identity or extensive homology (p<0.05).



Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **2%**

Matched peptides shown in **Bold Red**

1 MSYATKIHARYVYDSRGNPTVEVDFTTDKGLFRSIVPSGASTGVHEALEL
51 RDGDKSKWLGKGVLKAVANVNDIIAPALIKAKIDVVDQAKIDEFLLSLDG
101 TPNKSKLGANAILGVSLAAANAAAAAQGIPLYKHIANISNAKKGKFVLPV
151 PFQNVLNGGSHAGGALAFQEFMIAPTGVSTFSEALR**IGSEVYHNLK**SLTK
201 KKYGQSAGNVGDEGGVAPDIKTPKEALDLIMDAIDKAGYKGKVGIAMDVA
251 SSEFYKDGKYDLDFKNPESDPSKWLSGPQLADLYEQLISEYPIVSIEDPF
301 AEDDWDAWVHFFERVGDKIQIVGDDLTVTNPTRIKTAIEKKAANALLLKV
351 NQIGTLTESIQAANDSYAAGWGVMVSHRSGETEDTFIADLSVGLRSGQIK
401 TGAPARSERLAKLNQILRIEEELGSEAIYAGKDFQKASQL

Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 100 ppm
Fragment Mass Tolerance: ± 0.3 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of queries : 1

Ard8p (MS/MS)

CA3288|CaArd8 Mass: 30881 Total score: 35 Peptides matched: 1
D-arabinitol dehydrogenase

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Rank	Peptide
1	1644.9	1643.89	1643.92	-0.03	0	35	1	VNTLSPGYILTPLTR

Probability Based Mowse Score

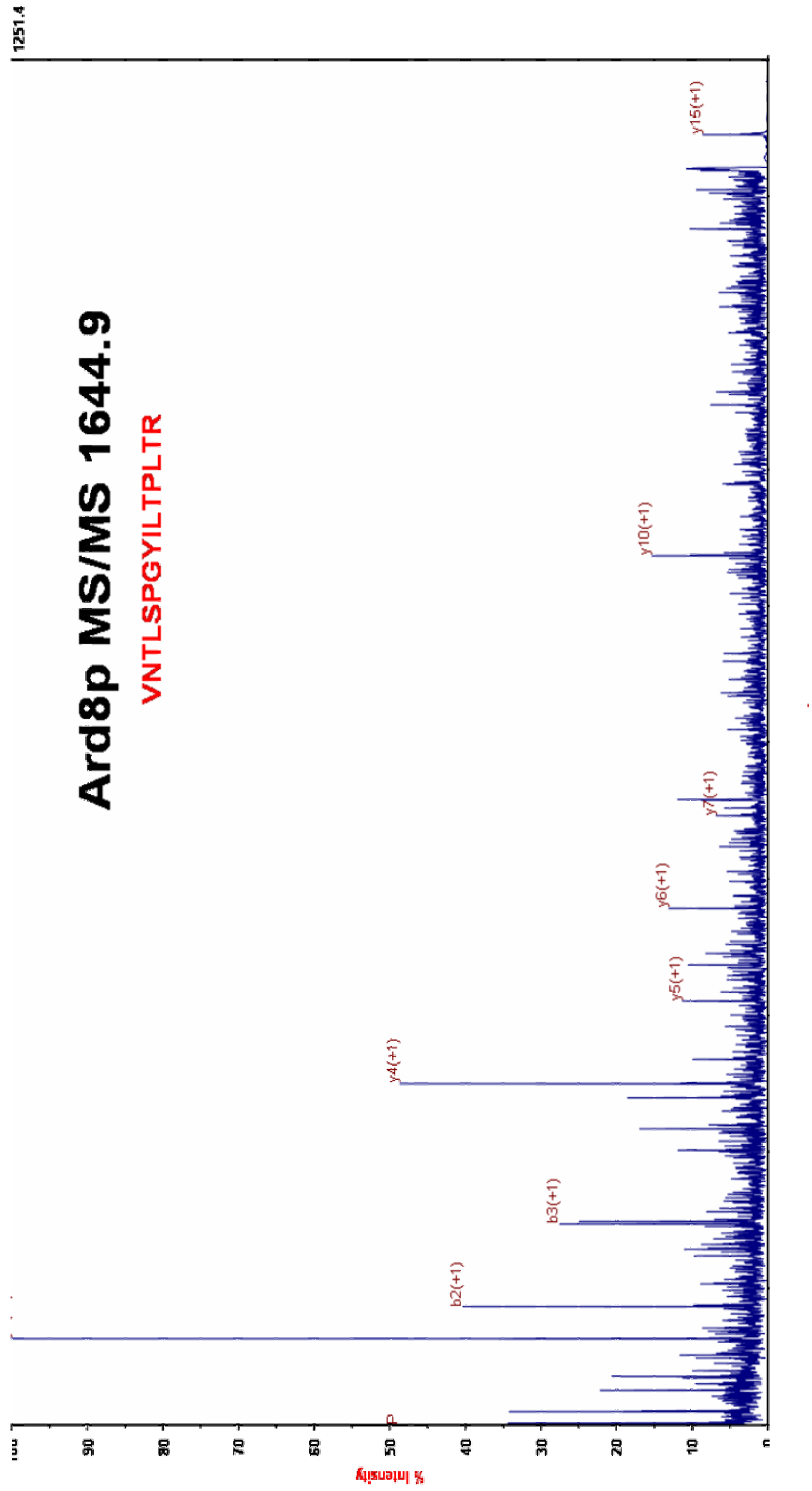
Score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 15 indicate peptides with significant homology (p<0.05).
Individual ions scores > 22 indicate identity or extensive homology (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **5%**

Matched peptides shown in **Bold Red**
1 MDSAYWSYDN IVPSFRLDGK LVILTGGSGG LAAVVSRALL AKGADVALVD
51 MNLERTQQAA RDVLQWGEEQ MKGKYESPIG QVSAWSCNIG DAEAVDLTFK
101 AINEHHGKIS SVLVNTAGYA ENFPAEEYPA KNAENLMKVN GLGSFYVSQA
151 FARPLIQNNM TGSIILIGSM SGTIVNDPQP QCMYNMSKTG VIHLARSLAC
201 EWAKYNIR**VN TLSPGYILTP LTR**NVISGHT EMKTEWESKI PMKRMAEPKE
251 FVGSILYLAS ESASSYTTGH NLVVDGGYEC W

Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 100 ppm
Fragment Mass Tolerance: ± 0.3 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of queries : 1


Ard8p MS/MS 1644.9
VNTLSPGYILTPLTR
1251.4
y15(+1)
y10(+1)
y7(+1)
y6(+1)
y5(+1)
y4(+1)
b3(+1)
b2(+1)
% Intensity
100
90
80
70
60
50
40
30
20
10
0

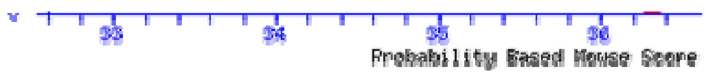
Sou1p (MS/MS)

CA3771|CaSOU1 Mass: 30304 Total score: 36 Peptides matched: 1
Sorbitol utilization protein Sou1p [Candida albicans]

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Rank	Peptide
1	**1641.89**	**1640.88**	**1640.91**	**-0.03**	**0**	**36**	**1**	**APQLPSNVLDLFSLK**

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 15 indicate peptides with significant homology (p<0.05).
Individual ions scores > 22 indicate identity or extensive homology (p<0.05).



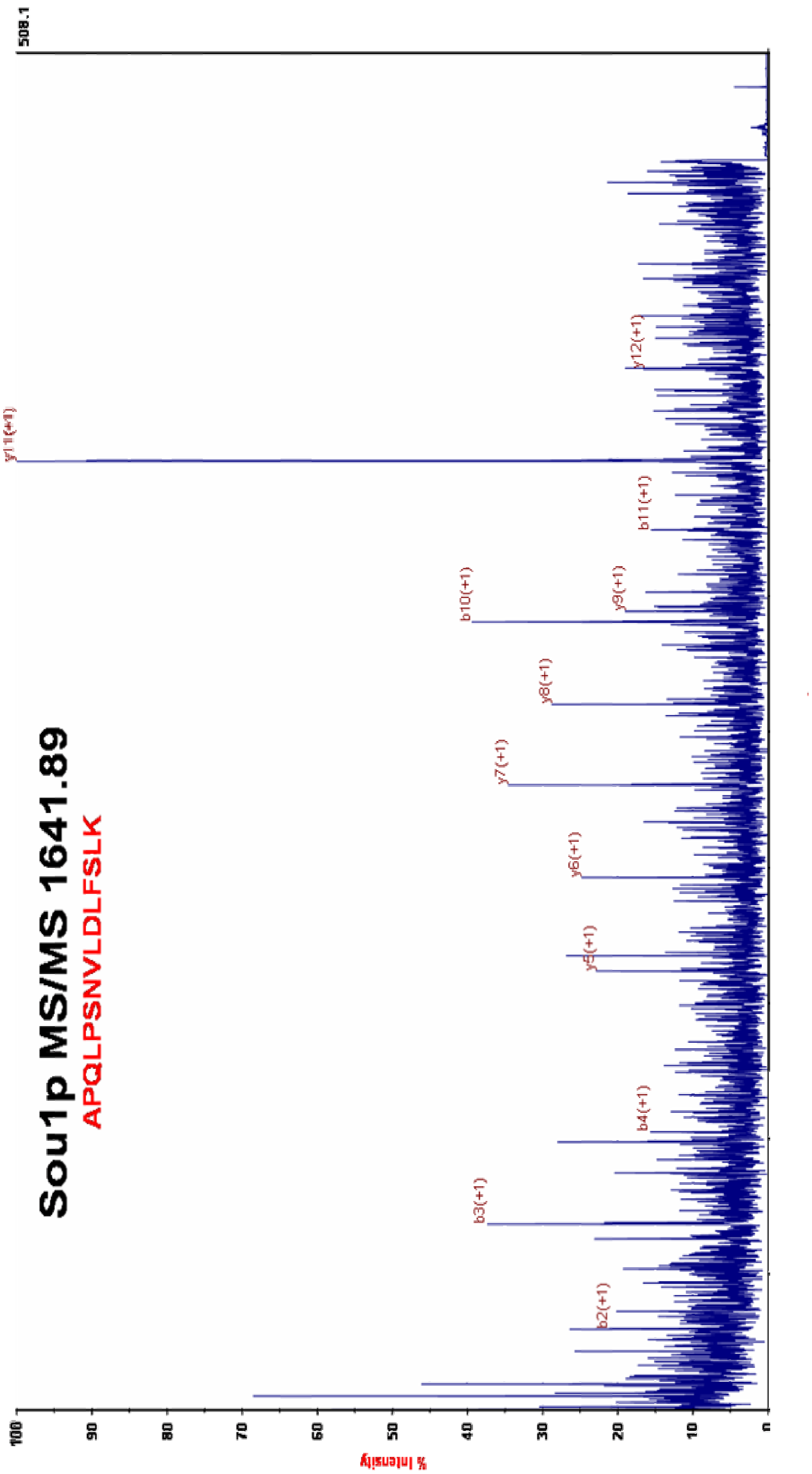
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **5%**

Matched peptides shown in **Bold Red**

1 MSEEIISFTN PALGPLPTK**A PQLPSNVLDL FSLK**GKVASV TGSSGGIGWA
51 VAEAFAQAGA DVAIWYNSKP ADAKAEYLTE KYGVKAKAYK CNVTDPNDVS
101 KVINEIEKDF GTIDIFVANA GVAWTDGPEI DVQGYDQWKK IVDCDLNGVY
151 YCAHTVGQIF KKNKSGSLII TSSMSGTIVN IPQLQAPYNA AKAACTHLAK
201 SLSVEWASFG ARVNSISPGY ILTDIADFAD PEMKKKWWQL TPLGREGLPQ
251 ELVGAYLYLA SNASTYTTGS NIAVDGGYTC P

Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 100 ppm
Fragment Mass Tolerance: ± 0.3 Da
Max Missed Cleavages : 1
Instrument type : Default
Number of queries : 1


Sou1p MS/MS 1641.89
APQLPSNVLDLFSLK
% Intensity
100
90
80
70
60
50
40
30
20
10
0
508.1
b2(+1)
b3(+1)
b4(+1)
y5(+1)
y6(+1)
y7(+1)
y8(+1)
b10(+1)
y9(+1)
b11(+1)
y11(+1)
y12(+1)

Acs2p (PMF)

Match to: **CA2858|CaACS2**; Score: **115**
acetyl-coenzyme-A synthetase (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	Miss	Peptide
856.53	855.52	855.52	0	597	0	ELVLQVR
901.52	900.51	900.51	0	605	0	TIGPFAAPK
949.51	948.51	948.51	-0.00	357	0	FWQIVEK
1157.66	1156.66	1156.66	-0.00	136	0	VAGVLQSWGIK
1162.59	1161.58	1161.58	0	198	1	ALITCDEGKR
1176.59	1175.59	1175.6	-0.01	51	0	DPQGFFGPLAK
1182.58	1181.57	1181.57	-0.00	20	1	ETPKEFFER
1196.61	1195.6	1195.59	0	533	0	VDDVVNVSGHR
1210.6	1209.59	1209.59	-0.00	33	0	GHIHDVNQYK
1224.55	1223.54	1223.54	0	522	0	DHDGYYWIR
1289.58	1288.57	1288.56	0.01	249	0	DYYWDVETAK
1346.72	1345.71	1345.71	-0.00	366	0	ATHFYVAPTALR
1380.69	1379.68	1379.68	0	237	0	TNNPEIHLTEGR
1402.72	1401.72	1401.73	-0.01	120	0	DSHILTYGDLLR
1409.73	1408.72	1408.72	0	531	1	GRVDDVVNVSGHR
1437.71	1436.7	1436.66	0.04	522	1	DHDGYYWIRGR
1490.74	1489.73	1489.71	0.02	485	1	DHWPSMARTVYK
1626.79	1625.78	1625.78	-0.00	62	0	ELLSWDHDFHTVK
1679.86	1678.85	1678.85	-0.00	382	1	AGEQEIAKYDLSSLR
1732.94	1731.93	1731.93	0	171	0	LGAAHSVIFAGFSAGSIK

No match to:
822.41
827.4
847.4
905.48
963.48
971.5
1082.59
1107.55
1164.58
1165.58
1189.65
1256.59
1272.7
1364.68
1384.7
1421.71
1435.72
1455.72
1477.71
1707.87
1807.94
1829.89
1835.97
2229.14
2239.99
2247.06
2248.12
2261.99
2266.98
2317.16

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **20**
Sequence Coverage: **29%**

Matched peptides shown in **Bold Red**

1 MPTEQTHNVV HEANGVKLR**E TPKEFFER**QP NK**GHIHDVNQ YK**QMYEQSIK
51 **DPQGFFGPLA KELLSWDHDF HTVK**SGTLKN GDAAWFLGGE LNASYNCVDR
101 HAFANPDKPA LICEADDEK**D SHILTYGDLL R**EVSK**VAGVL QSWGIK**KGDT
151 VAVYLPMNAQ AIIAMLAIAR **LGAAHSVIFA GFSAGSIK**DR VNDASCK**ALI**
201 **TCDEGKR**GGR TTNIKKLCDE ALVDCPTVEK VLVYKR**TNNP EIHLTEGRDY**
251 **YWDVETAK**FP GYLPPVSVNS EDPLFLLYTS GSTGTPKGVV HSTAGYLLGA
301 ALSTKYIFDI HPEDILFTAG DVGWITGHTY ALYGPLLLGV PTIIFEGTPA
351 YPDYGR**FWQI VEK**HK**ATHFY VAPTALR**LLR K**AGEQEIAKY DLSSLR**TLGS
401 VGEPISPDIW EWYNEFVGKN QCHISDTYWQ TESGSHLIAP LAGVVPNKPG
451 SASYPFFGID AALIDPVTGV EIEGNDAEGV LAIK**DHWPSM ARTVYK**NHTK
501 YMDTYMNPYP GYYFTGDGAA R**DHDGYYWIR GRVDDVVNVS GHR**LSTAEIE
551 AALIEDKKVS EAAVVGIHDD ITGQAVIAYV ALKEGNSDED SEGLRK**ELVL**
601 **QVR**K**TIGPFA APK**SVIIVQD LPKTRSGKIM RRILRKVSSN EADQLGDIST

651 LSNPQSVEGI ISAFGAQFGK K

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 50

Oye32p* (IPF7817, PMF)

MS-Fit search results

Rank	**1**
MOWSE Score	**1.54E+09**
# (%) Masses Matched	**20/87 (22%)**
Protein MW (Da)/pI	**47545.2 / 5.94**
Species	**IPF7817 putative NADH-dependent flavin oxidoreductase (by homology)**
PACALBI_prot.txt Accession #	**Candida**
Protein Name	**CA3564**

1. 20/87 matches (22%). 47545.2 Da, pI = 5.94. Acc. # Candida. IPF7817 putative NADH-dependent flavin oxidoreductase (by homology). CA3564.

m/z submitted	**MH+ matched**	**Delta ppm**	**start**	**end**	**Peptide Sequence**
863.4446	-863.4488	4.7865	204	211	(K)DFGAAARR(A)
1033.5767	1033.5795	-2.703	201	210	(R)VVKDFGAAAR(R)
1047.5916	1047.5951	-3.3899	333	341	(R)EPIHVPLSR(A)
1113.6238	1113.6268	-2.7108	417	425	(K)QQIVDLIER(T)
1262.7308	1262.7333	-1.975	136	147	(K)QLIAIQLGHGGR(K)
1274.5212	1274.5289	-6.037	243	253	(R)TDEYGGSFENR(T)
1343.7255	1343.7323	-5.1066	266	277	(K)SSIPNDVPVFLR(I)
1398.7578	1398.7745	-11.948	124	135	(K)LKPIVDYAHSQK(Q)
1430.6206	1430.63	-6.5986	242	253	(K)RTDEYGGSFENR(T)
1445.8116	1445.8229	-7.7649	330	341	(K)ELREPIHVPLSR(A)
1522.7383	1522.7502	-7.8014	306	320	(K)GIALVDVSSGGNDYR(Q)
1531.6749	1531.6777	-1.8263	243	255	(R)TDEYGGSFENRTR(F)
1596.8135	1596.8273	-8.6872	369	382	(K)YLEEGTFDLALIGR(G)
1700.9026	1700.9124	-5.7779	387	401	(R)NPGLVWEFADKLGVR(L)
1752.9171	1752.9285	-6.4722	149	164	(K)ASGQPLFLHLEQVADK(S)
1881.0139	1881.0234	-5.054	148	164	(R)KASGQPLFLHLEQVADK(S)
1984.0353	1984.0789	-21.9801	351	368	(K)LLVSCVGGLEKDPELLNK(Y)
2001.0029	2001.0154	-6.2206	306	324	(K)GIALVDVSSGGNDYRQPPR(S)
2059.9473	2059.946	0.6048	278	296	(R)ISAAENSPDPEAWTIEDSK(K)
2188.0549	2188.041	6.375	278	297	(R)ISAAENSPDPEAWTIEDSKK(L)

67 unmatched masses

828.2739
833.0651
839.0705
848.0341
849.036
854.0464
855.0466
859.0394
861.0609
865.0094
869.0234
870.017
871.019
875.012
877.0333
879.0208
885.993
886.9911
890.9935
893.0114
900.968
901.9627
902.9587
904.9644
918.9313
1020.5428
1044.0826
1060.0536
1066.0701
1076.0273
1082.0426
1085.5022
1092.0022
1096.5974
1098.0127
1123.655
1187.5709
1220.6243
1253.7257
1271.0739
1296.6981
1340.7162
1427.7949
1490.7577
1493.7327
1495.8247
1504.7783
1554.7656
1579.7905
1591.7964
1621.8463
1640.8201
1719.8892
1768.957
1979.9849
2083.0022
2093.0752
2145.0308
2163.0569
2179.8855
2185.043
2201.9668
2274.1692
2290.1345
2466.1589
2560.2021
3212.5266

The matched peptides cover 42% (185/432 AA's) of the protein.

1 MTVPYQVKPSDEIKGAPEVSYYTPEQPVPAGTFYPQSSDEVAPKIFQPLK
51 IGKLALPNRIGVSPMCQYSADYNFEATPYHLIHYGSLVNRGPGITIVEST
101 AVSPEGGLSPHDLGIWKDEQAE**KLKPIVDYAHSQKQLIAIQLGHGGRKAS**
151 GQPLFLHLEQVADKSVNGFADKAVAPSALAFRPNGNLPVPNELTKDEIK**R**
201 VVKDFGAAARRAVEISGFDAVEIHGAHGYLINEFYSPISNK**RTDEYGGSF**
251 ENRTRFLKEVIDSV**KSSIPNDVPVFLRISAAENSPDPEAWTIEDSKKL**AD
301 ILVE**KGIALVDVSSGGNDYRQPPRS**GIS**KELREPIHVPLSRA**IKQHVGD**K**
351 LLVSCVGGLEKDPELLNKYLEEGTFDLALIGRGFL**RNPGLVWEFADKLGV**
401 RLHQALQLGWGFWPN**KQQIVDLIERT**SKLEVN

Search Parameters

Considered modifications: | **Oxidation of M** |

Min. # Peptides to Match	Peptide Mass Tolerance (+/-)	Peptide Masses are	Digest used	Max. # Missed cleavages	Cysteines Modified by	Peptide N terminus/ C Terminus	Input # Peptide Masses
4	**50.000 ppm**	**monoisotopic**	**Trypsin**	**1**	**carbamidomethylation**	**Hydrogen (H)/Free Acid (O H)**	**87**

Erg10 (Pot14p, PMF)

Match to: **CA0290|CaPOT14**; Score: **225**
acetyl-CoA acetyltransferase (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
968.59	967.58	967.61	-0.03	270	278	0	ELGLKPLAK
973.46	972.45	972.48	-0.03	279	287	0	INGWGEAAR
1034.43	1033.42	1033.44	-0.02	166	174	0	CAADHGFTR
1107.5	1106.5	1106.52	-0.03	175	183	0	EQQDEFAIK
1179.56	1178.55	1178.58	-0.03	148	157	0	DGLLDVYEQK
1259.67	1258.66	1258.69	-0.03	197	207	0	FNQEIAPVTIK
1293.64	1292.63	1292.66	-0.03	136	147	0	FGDSTLIDGIQK
1332.7	1331.69	1331.73	-0.04	1	12	0	MVPPVYIVSTAR
1484.79	1483.79	1483.82	-0.04	253	267	0	INDGAAALILVSEAK
1566.85	1565.84	1565.88	-0.04	288	302	0	NPIDFTIAPALAVPK
1572.83	1571.82	1571.87	-0.05	194	207	1	QGKFNQEIAPVTIK
1613.74	1612.73	1612.77	-0.04	175	187	1	EQQDEFAIKSYQK
1747.84	1746.83	1746.89	-0.06	236	252	1	AVFQKENGTVTGPNASK
1905.89	1904.88	1904.91	-0.03	376	395	0	IGCAGVCNGGGGASSIVIEK
1940.92	1939.91	1939.97	-0.06	341	360	0	LNAYGGAVALGHPLGCSGAR
2122.9	2121.89	2121.95	-0.06	166	183	1	CAADHGFTREQQDEFAIK
2450.19	2449.18	2449.25	-0.07	13	36	0	TPIGSFQGTLSSLTYSDLGAHAVK
2454.18	2453.18	2453.23	-0.06	136	157	1	FGDSTLIDGIQKDGLLDVYEQK
2521.26	2520.25	2520.35	-0.1	279	302	1	INGWGEAARNPIDFTIAPALAVPK

No match to:
926.43
956.44
977.57
1030.48
1047.52
1062.46
1258.68
1272.66
1281.65
1316.68
1318.63
1334.61
1350.6
1449.81
1479.71
1552.63
1588.83
1748.84
1829.43
1829.92
1830.43
1840.92
1906.87
2104.9
2144.96
2179.9
2228.11
2303.12
2487.13
2544.3
2710.22

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **50**
Number of mass values matched: **19**
Sequence Coverage: **49%**

Matched peptides shown in **Bold Red**

1 **MVPPVYIVST ARTPIGSFQG TLSSLTYSDL GAHAVK**AALN KVPQIKPEDV
51 DEIVFGGVLQ ANVGQAPARQ VALKAGLTDK IVASTVNKVC ASGLKAIIIG
101 AQNIICGTSD IVVVGGAESM TNTPYYLPTA RNGAR**FGDST LIDGIQKDGL**
151 **LDVYEQK**LMG VAAEK**CAADH GFTREQQDEF AIKSYQK**AGN ALK**QGKFNQE**
201 **IAPVTIK**GVR GKPDVVVEKD EEIEKFNEAK LKSAR**AVFQK ENGTVTGPNA**
251 **SKINDGAAAL ILVSEAK**LK**E LGLKPLAKIN GWGEAARNPI DFTIAPALAV**
301 **PK**AVKHAGLT LDQVDFFELN EAFSVVGLAN AEICQIPLEK **LNAYGGAVAL**
351 **GHPLGCSGAR** IVVTLLSVLI QEGGK**IGCAG VCNGGGGASS IVIEK**VDSDF
401 KL

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 50

Hem13p (PMF)

Match to: **CA0517|CaHEM13**; Score: **233**
by homology S. cerev.: coproporphyrinogen III oxidase

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
732.42	731.41	731.4	0.01	18	23	0	MEALIR
755.4	754.39	754.38	0.01	197	202	1	HRGETR
771.45	770.44	770.43	0.01	318	323	0	KPIEWV
844.44	843.44	843.44	0	253	258	0	NWQQIR
909.52	908.51	908.51	0	80	87	0	LPPQAVER
1000.54	999.54	999.54	0	253	259	1	NWQQIRR
1010.5	1009.49	1009.49	0	165	171	0	WFHQQHK
1075.54	1074.53	1074.52	0	41	48	0	FHTDTWLR
1206.6	1205.59	1205.59	-0.00	243	252	1	KDTPYTPEQK
1248.64	1247.63	1247.63	0.01	272	283	0	GTQFGLQTPGSR
1267.67	1266.67	1266.66	0.01	262	271	0	YVEFNLVLDR
1307.59	1306.58	1306.57	0.01	188	196	0	WCDEYFFIK
1435.68	1434.67	1434.66	0.01	187	196	1	KWCDEYFFIK
1480.78	1479.78	1479.78	-0.01	260	271	1	GRYVEFNLVLDR
1550.77	1549.76	1549.77	-0.01	172	184	1	DALDKFDPELYPK
1600.75	1599.74	1599.73	0.01	188	198	1	WCDEYFFIKHR
1643.85	1642.85	1642.83	0.01	2	15	0	VTTEQIHDTSFPIR
1903.93	1902.92	1902.92	0	244	258	1	DTPYTPEQKNWQQIR
1928.98	1927.97	1927.98	-0.00	2	17	1	VTTEQIHDTSFPIRER
1971.11	1970.1	1970.11	-0.00	69	87	1	GGVNISIVHGKLPPQAVER
2060.02	2059.01	2059.02	-0.01	1	17	1	MVTTEQIHDTSFPIRER
2111.06	2110.06	2110.08	-0.02	223	241	0	IVESCFDAFIPAYAPIVAK
2184.08	2183.07	2183.08	-0.00	203	222	0	GIGGIFFDDFDSKPADEILK
2267.2	2266.2	2266.18	0.01	223	242	1	IVESCFDAFIPAYAPIVAKR
2497.26	2496.26	2496.28	-0.02	262	283	1	YVEFNLVLDRGTQFGLQTPGSR
2729.38	2728.38	2728.38	-0.01	26	48	1	QQQITDAIAELDTVKFHTDTWLR

No match to:
707.39
727.43
730.4
738.37
762.43
815.48
827.5
866.42
876.44
899.54
915.52
993.54
998.54
1014.52
1021.59
1032.49
1053.59
1065.56
1106.58
1111.6
1155.64
1162.62
1183.58
1229.72
1245.69
1273.76
1284.6
1289.71
1317.77
1329.61

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant ($p<0.05$).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **107**
Number of mass values matched: **26**
Sequence Coverage: **58%**

Matched peptides shown in **Bold Red**

1 **MVTTEQIHDT SFPIRERMEA LIR**LK**QQQIT DAIAELDTVK FHTDTWLR**GD
51 NGGGGQSMVL QNGTTFEK**GG VNISIVHGKL PPQAVER**MRA DHSNLKGSSK
101 DGSVNFFACG LSLVIHPINP HAPTTHANYR YFETSDPETN EIQTWWFGGG
151 ADLTPSYLYE EDAK**WFHQQH KDALDKFDPE LYPK**YK**KWCD EYFFIKHRGE**
201 **TRGIGGIFFD DFDSKPADEI LKIVESCFDA FIPAYAPIVA KRKDTPYTPE**
251 **QKNWQQIRRG RYVEFNLVLD RGTQFGLQTP GSR**VESILMS LPATASWVYD
301 HHPEPGSEED KLLQVLK**KPI EWV**

1333.74
1358.66
1361.82
1362.71
1377.78
1421.8
1449.86
1465.82
1509.85
1537.91
1549.8
1553.87
1581.95
1588.73
1597.9
1625.97
1641.93
1664.82
1669.98
1685.96
1700.86
1714.03
1726.81
1727.87
1729.98
1758.04
1774
1784.87
1802.06
1810.87
1818.03
1841.94
1846.08
1884.97
1888.55
1890.13

1911.58
1912.56
1919.95
1934.11
1994.09
2032.03
2043.97
2057.98
2149.04
2480.88
2481.81
2642.4
2659.36
2970.54
3950.99

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 107

Snz1p (PMF)

Match to: **CA4184|CaSNZ1**; Score: **154**
stationary phase protein by homology

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
763.36	762.35	762.34	0.01	52	57	0	SNQVCR
891.43	890.42	890.44	-0.02	51	57	1	KSNQVCR
919.46	918.46	918.47	-0.01	166	173	1	KDIEEASK
928.51	927.5	927.52	-0.02	128	135	1	NLGEALRR
974.49	973.49	973.5	-0.02	136	144	0	INEGAAMIR
990.49	989.48	989.5	-0.01	136	144	0	INEGAAMIR Oxidatio
1130.59	1129.58	1129.6	-0.02	135	144	1	RINEGAAMIR
1146.58	1145.58	1145.6	-0.02	135	144	1	RINEGAAMIR Oxidati
1160.6	1159.59	1159.61	-0.02	176	185	0	TETEIVELAR
1180.61	1179.6	1179.62	-0.02	118	127	1	FKVPFVCGAR
1401.77	1400.77	1400.79	-0.02	174	185	1	LKTETEIVELAR
1416.68	1415.68	1415.71	-0.03	16	29	0	GGVIMDVVNADQAK
1510.84	1509.83	1509.87	-0.03	189	201	0	VPTELLIQVIEEK
1532.73	1531.73	1531.75	-0.02	30	44	0	IAEAAGACAVMALER
1542.77	1541.76	1541.78	-0.02	248	261	0	AIVNATTHYNDPVK
1548.74	1547.73	1547.74	-0.01	30	44	0	IAEAAGACAVMALER
1858.84	1857.83	1857.86	-0.03	145	162	1	CKGEAGTGDVSSAV
1909.07	1908.06	1908.09	-0.03	186	201	1	ELRVPTELLIQVIEEK

No match to:
817.45
832.32
861.49
926.49
1084.55
1089.61
1194.62
1431.74
1445.74
1484.73
1502.71
1524.76
1546.75
1562.73
1677.81
1766.78
1841.82
1857.8
1872.86
1891.06
2174.12
3122.63
3278.7

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **41**
Number of mass values matched: **18**
Sequence Coverage: **44%**

Matched peptides shown in **Bold Red**

1 MSDFKVKAGL AQMLK**GGVIM DVVNADQAKI AEAAGACAVM ALER**IPAEMR
51 **KSNQVCR**MSD PKMIKDIMET VKIPVMAKCR IGHFTESQIL EALGVDYIDE
101 SEVLTPADTV YHIDKTK**FKV PFVCGARNLG EALRRINEGA AMIRCKGEAG**
151 **TGDVSSAVDH IR**TIK**KDIEE ASKLKTETEI VELARELRVP TELLIQVIEE**

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 41

Ipp1p (PMF)

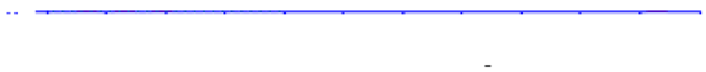
Match to: **CA0870|CaIPP1**; Score: **113**
inorganic pyrophosphatase (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
923.44	922.44	922.43	0.01	186	192	0	ATNEWFR
1284.74	1283.74	1283.73	0.01	43	53	0	TILNMIVEVPR
1392.82	1391.81	1391.8	0.01	157	169	0	VIVIDVNDPLAPK
1407.71	1406.71	1406.7	0.01	277	288	1	SIDKWFFISGAH
1560.72	1559.72	1559.68	0.04	116	129	0	GDNDPLDVCEIGEK
1759.82	1758.82	1758.81	0.01	114	129	1	AKGDNDPLDVCEIGEK
1775.88	1774.87	1774.88	-0.01	141	156	0	VLGVMALLDEGETDWK
1783.79	1782.78	1782.78	0	216	230	0	YAEEVIGECAEAWEK
1833.97	1832.97	1832.96	0	170	185	0	LNDIEDVETHLPGLLR
1885.04	1884.03	1884.03	0	43	58	1	TILNMIVEVPRWTNAK
1923.89	1922.88	1922.88	-0.00	196	212	0	IPDGKPENQFAFSGECK
2156.07	2155.06	2155.06	0.01	24	42	0	DGKPVSPFHDIPLYANEEK
2328.13	2327.13	2327.13	0	193	212	1	IYKIPDGKPENQFAFSGECK

No match to:
781.34
791.98
795.41
917.49
922.41
953.43
967.45
1071.44
1164.56
1169.62
1171.55
1211.53
1223.49
1255.57
1257.57
1271.55
1293.09
1385.63
1395.54
1429.68
1444.63
1445.64
1464.73
1466.74
1472.67
1475.59
1481.68
1485.63
1487.64
1522.71

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).



Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **88**
Number of mass values matched: **13**
Sequence Coverage: **52%**

Matched peptides shown in **Bold Red**
1 MSSYSTRQVG AANTLDYKVY IEK**DGKPVSP FHDIPLYANE EKTILNMIVE**
51 **VPRWTNAK**LE ISKEQKLNPI IQDTKKGKLR FVRNCFPHHG YIHNYGAFPQ
101 TWEDPNQSHP ETK**AKGDNDP LDVCEIGEK**V ATVGEVKQVK **VLGVMALLDE**
151 **GETDWKVIVI DVNDPLAPKL NDIEDVETHL PGLLRATNEW FRIYKIPDGK**
201 **PENQFAFSGE CK**NKK**YAEEV IGECAEAWEK** LIKGESVDSK GIDLTNTTLS
251 STPSYSDAAA QEIPSASPAP AAPIDK**SIDK WFFISGAH**

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 88

1532.67
1549.66
1559.68
1562.82
1572.69
1573.92
1574.69
1587.68
1599.74
1606.77
1617.72
1639.89
1647.66
1655.89
1657.76
1661.83
1675.71
1703.75
1733.7
1757.87
1773.84
1797.88
1803.75
1807.81
1815.85
1817.92
1819.83
1846.97
1855.91
1871.95
1889.79
1893.9
1897.87
1912.91
1975.83
1999.05
2194.02
2228.14
2251.04
2333.15
2342.15
2350.16
2543.27
2550.24
2557.28

Taf14p (Anc1p, PMF)

Match to: **CA0331|CaANC1**; Score: **69**
TFIIF subunit, transcription initiation factor (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1512.87	1511.86	1511.81	0.05	75	86	1	KIQHDLNFLQEK
1629.92	1628.92	1628.87	0.05	26	39	0	VTYTLHPTFANPIR
1696.95	1695.95	1695.89	0.05	87	101	0	YVNDHVISIPVSPTR
1946.05	1945.04	1944.98	0.06	179	195	0	LSEDDLIVVVQMVTDNR
2099.21	2098.2	2098.16	0.05	22	39	1	ILDKVTYTLHPTFANPIR
2400.2	2399.19	2399.12	0.07	203	223	0	NDVDNGEFTMDLYTLPDSLLK
2794.47	2793.46	2793.38	0.08	108	136	1	LLAETGSLPFEESGAGASSANSGSIGTKR

No match to:
771.34
771.51
777.22
795.44
797.35
799.36
815.53
845.55
857.37
859.56
885.4
889.58
903.6
933.6
943.41
969.43
971.44
1029.45
1055.46
1115.49
1137.63
1141.51
1143.53
1201.53
1227.55
1229.56
1245.55
1287.57
1315.59

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant ($p<0.05$).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Number of mass values searched: **50**
Number of mass values matched: **7**
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **47%**

Matched peptides shown in **Bold Red**

1 MRKWSVQISM LDSQGKEHPA K**ILDKVTYTL HPTFANPIR**T LKQQPFRVEE
51 QGWGEFDIPI AVHILGIPGK AGER**KIQHDL NFLQEKYVND HVISIPVSPT**
101 **R**NPALNK**LLA ETGSLPFEES GAGASSANSG SIGTKR**KLES SNGATATAAT
151 SADNKSKKSK GAMKGNIDLE KLSQGLTK**LS EDDLIVVVQM VTDNR**TNEMN
201 IK**NDVDNGEF TMDLYTLPDS LLK**SLWDYVK KHTGEA

1373.61
1389.58
1433.76
1459.65
1545.69
1631.73
1717.76
1804.81
2042.07
2252.08
2325.26
2454.33
2639.4
3214.49

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 50

Aco1p right (PMF)

Match to: **CA3546|CaACO1** Score: **141**
aconitate hydratase (by homology)

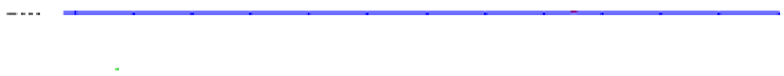
Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	No match to:
893.42	892.41	892.41	0.00	235	242	0	MSGWTSPK	877.05
922.47	921.47	921.47	0.00	670	677	0	EHAALEPR	878.04
1037.53	1036.53	1036.53	-0.00	464	472	0	NTIVSSFNR	882.57
1080.61	1079.60	1079.60	0.00	45	53	0	HLENVEIVK	893.02
1204.66	1203.66	1203.66	-0.01	56	65	0	LNRPLTYAEK	921.45
1311.63	1310.63	1310.63	0.00	638	649	0	YDGVPQTAAAYR	982.44
1359.70	1358.70	1358.70	-0.01	550	562	0	ASVEVVISPTSDR	996.61
1403.64	1402.63	1402.64	-0.01	146	157	0	EVYDFLSTACAK	1046.59
1406.72	1405.71	1405.72	-0.01	410	422	0	ALYTVSPGSEQVR	1167.71
1651.75	1650.75	1650.76	-0.02	655	669	0	WVVIGDENFGEGSSR	1175.57
1889.84	1888.83	1888.83	0.00	377	393	0	VGLIGSCTNSSYEDMTR	1191.53
1905.82	1904.82	1904.82	-0.01	377	393	0	VGLIGSCTNSSYEDMTR + Oxidation (M)	1428.74
1948.93	1947.93	1947.94	-0.02	66	81	0	LLYGHLDDPHNQEIER	2185
								2200.99
								2208
								3040.43

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **29**
Number of mass values matched: **13**
Sequence Coverage: **18%**

Matched peptides shown in **Bold Red**
1 MLSASRTALR APRSVRGLAT ASLTKDSQVN QNLLESHSFI NYKK**HLENVE**
51 **IVK**SR**LNRPL TYAEKLLYGH LDDPHNQEIE R**GVSYLKLRP DRVACQDATA
101 QMAILQFMSA GIPQVATPST VHCDHLIQAQ VGGPKDLARA IDLNK**EVYDF**
151 **LSTACAK**YNL GFWKPGSGII HQIVLENYAF PGALLIGTDS HTPNAGGLGQ
201 LAIGVGGADA VDVMSGLPWE LKAPKIIGVK LTGK**MSGWTS PK**DIILKLAG
251 ITTVKGGTGS IVEYFGSGVD TFSCTGMGTI CNMGAEIGAT TSVFPFNDSM
301 VDYLNATGRS EIAQFAQVYK KDFLSADEGA EYDQVIEIDL NTLEPHINGP
351 FTPDLATPVS KMKETAIANG WPLEVK**VGLI GSCTNSSYED MTR**AASIIKD
401 AGAHGLKSK**A LYTVSPGSEQ VR**ATIARDGQ LKTFEDFGGV VMANACGPCI
451 GQWDRQDIKK GDK**NTIVSSF NR**NFTARNDG NPATHAFVAS PEMATVYAIS
501 GDLGFNPITD TLVGADGKEF KLKEPQGVGL PPDGYDPGEN TYQAPPEDR**A**
551 **SVEVVISPTS DR**LQKLSPFK PWDGKDAERL PILIKAVGKT TTDHISMAGP
601 WLKYRGHLEN ISNNYMIGAI NAENGKANEV RNHYTGK**YDG VPQTAAAYR**D
651 AGHK**WVVIGD ENFGEGSSRE HAALEPR**FLG GFAIITKSFA RIHETNLKKQ
701 GLLPLNFKNP ADYDKINFDD EVDLIGLTTL APGKDVILRV HPKEGEAWEA
751 VLTHTFNSEQ LEWFKHGSAL NFIKSKY



Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 80 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 0
Number of queries : 29

Aco1p right (PMF)

Match to: **CA3546|CaACO1** Score: **102**
aconitate hydratase (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
922.47	921.47	921.47	-0.00	670	677	0	EHAALEPR
1037.54	1036.53	1036.53	-0.00	464	472	0	NTIVSSFNR
1080.60	1079.59	1079.60	-0.00	45	53	0	HLENVEIVK
1204.67	1203.66	1203.66	0.00	56	65	0	LNRPLTYAEK
1311.63	1310.62	1310.63	-0.00	638	649	0	YDGVPQTAAAYR
1359.70	1358.70	1358.70	-0.01	550	562	0	ASVEVVISPTSDR
1403.65	1402.64	1402.64	-0.00	146	157	0	EVYDFLSTACAK
1406.72	1405.71	1405.72	-0.01	410	422	0	ALYTVSPGSEQVR
1651.76	1650.75	1650.76	-0.02	655	669	0	WVVIGDENFGEGSSR
1889.82	1888.82	1888.83	-0.01	377	393	0	VGLIGSCTNSSYEDMTR
1905.82	1904.81	1904.82	-0.01	377	393	0	VGLIGSCTNSSYEDMTR + Oxidation (M)
1948.93	1947.93	1947.94	-0.02	66	81	0	LLYGHLDDPHNQEIER

No match to:
855.06
857.07
861.07
870.03
871.02
875.04
876.04
877.04
879.04
882.57
886
887
889.01
892.01
893.02
895.02
902.98
908.99
921.45
928.49
944.46
994.14
996.6
1046.59
1050.1
1066.08
1082.05
1098.03
1167.71
1175.55
1428.76
2185

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).

2200.96

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **45**
Number of mass values matched: **12**
Sequence Coverage: **17%**

Matched peptides shown in **Bold Red**

1 MLSASRTALR APRSVRGLAT ASLTKDSQVN QNLLESHSFI NYKK**HLENVE**
51 **IVK**SR**LNRPL TYAEKLLYGH LDDPHNQEIE R**GVSYLKLRP DRVACQDATA
101 QMAILQFMSA GIPQVATPST VHCDHLIQAQ VGGPKDLARA IDLNK**EVYDF**
151 **LSTACAK**YNL GFWKPGSGII HQIVLENYAF PGALLIGTDS HTPNAGGLGQ
201 LAIGVGGADA VDVMSGLPWE LKAPKIIGVK LTGKMSGWTS PKDIILKLAG
251 ITTVKGGTGS IVEYFGSGVD TFSCTGMGTI CNMGAEIGAT TSVFPFNDSM
301 VDYLNATGRS EIAQFAQVYK KDFLSADEGA EYDQVIEIDL NTLEPHINGP
351 FTPDLATPVS KMKETAIANG WPLEVK**VGLI GSCTNSSYED MTR**AASIIKD
401 AGAHGLKSK**A LYTVSPGSEQ VR**ATIARDGQ LKTFEDFGGV VMANACGPCI
451 GQWDRQDIKK GDK**NTIVSSF NR**NFTARNDG NPATHAFVAS PEMATVYAIS
501 GDLGFNPITD TLVGADGKEF KLKEPQGVGL PPDGYDPGEN TYQAPPEDR**A**
551 **SVEVVISPTS DR**LQKLSPFK PWDGKDAERL PILIKAVGKT TTDHISMAGP
601 WLKYRGHLEN ISNNYMIGAI NAENGKANEV RNHYTGK**YDG VPQTAAAYR**D
651 AGHK**WVVIGD ENFGEGSSRE HAALEPR**FLG GFAIITKSFA RIHETNLKKQ
701 GLLPLNFKNP ADYDKINFDD EVDLIGLTTL APGKDVILRV HPKEGEAWEA
751 VLTHTFNSEQ LEWFKHGSAL NFIKSKY

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 80 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 0
Number of queries : 45

Cit1p (PMF)

Match to: **CA3909|CaCIT1**; Score: **144**
Citrate synthase, exon 2

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	
1010.54	1009.53	1009.52	0.01	119	126	0	HVEELIDR	
1097.63	1096.62	1096.61	0.01	411	420	0	GIGMPIERPK	
1167.68	1166.67	1166.66	0.02	311	321	0	VVPGYGHAVLR	
1238.64	1237.64	1237.61	0.03	301	310	0	YLWETLNSGR	
1341.81	1340.8	1340.78	0.02	399	410	0	AFGVLPQLILDR	
1735.96	1734.95	1734.9	0.05	27	42	0	TVIGEVLLEQAYGGMR	
1739.97	1738.96	1738.93	0.03	46	61	0	GLVWEGSVLDPIEGIR	
1792.97	1791.96	1791.92	0.04	411	426	1	GIGMPIERPKSFSTEK	Oxidation (M)
1808.95	1807.95	1807.91	0.04	296	310	1	EAIEKYLWETLNSGR	
2038.18	2037.17	2037.13	0.04	43	61	1	GIKGLVWEGSVLDPIEGIR	
2187.13	2186.12	2186.12	0.01	23	42	1	EHGKTVIGEVLLEQAYGGMR	

No match to:
1049.62
1050.55
1154.65
1224.7
1398.83
1753
2095.2
2551.43

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **19**
Number of mass values matched: **11**
Sequence Coverage: **23%**

Matched peptides shown in **Bold Red**

1 MLKQRLEEIL PAKAEEVKQF KK**EHGKTVIG EVLLEQAYGG MRGIKGLVWE**
51 **GSVLDPIEGI R**FRGRTIPDI QKELPKAPGG EEPLPEALFW LLLTGEVPTD
101 AQTKALSEEF AARSALPK**HV EELIDR**SPSH LHPMAQFSIA VTALESESQF
151 AQAYAKGANK SEYWKYTYED SIDLLAKLPT IAAKIYRNVF HDGKLPAAID
201 SKLDYGANLA SLLGFGDNKE FVELMRLYLT IHSDHEGGNV SAHTTHLVGS
251 ALSSPFLSLA AGLNGLAGPL HGRANQEVLE WLFKLREELN GDYSK**EAIEK**
301 **YLWETLNSGR VVPGYGHAVL R**KTDPRYTAQ REFALKHMPD YELFKLVSNI
351 YEVAPGVLTK HGKTKNPWPN VDSHSGVLLQ YYGLTEQSFY TVLFGVSR**AF**
401 **GVLPQLILDR GIGMPIERPK SFSTEK**YIEL VKNINKA

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 19

Mdh1p (PMF)

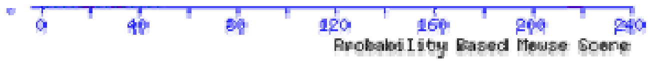
Match to: **CA5164|CaMDH1**; Score: **217**
Mitochondrial malate dehydrogenase precursor (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
705.37	704.36	704.36	-0.00	97	102	0	KPGMTR Oxidation (M)
710.4	709.39	709.39	0	215	220	0	DALVHR
1042.52	1041.51	1041.52	-0.01	206	214	1	HKDLSGETR
1178.64	1177.63	1177.63	-0.01	43	52	0	VTDLALYDIR
1233.71	1232.7	1232.71	-0.01	158	168	0	LFGVTTLDVLR
1290.64	1289.64	1289.66	-0.02	221	232	0	IQFGGDEVVQAK
1364.68	1363.67	1363.67	-0.00	103	114	0	DDLFNTNASIVR
1463.68	1462.67	1462.68	-0.02	233	248	0	DGAGSATLSMAQAGAR
1479.66	1478.65	1478.68	-0.03	233	248	0	DGAGSATLSMAQAGAR Oxidation (M)
1670.89	1669.89	1669.92	-0.03	39	52	1	LNHKVTDLALYDIR
1806.89	1805.89	1805.93	-0.04	53	71	0	GAPGVAADVSHVPTNSTVK
1914.91	1913.9	1913.94	-0.04	295	311	0	TVHPIGEISDYEEAQVK
2021.04	2020.03	2020.07	-0.04	151	168	1	GNYNPNKLFGVTTLDVLR
2610.34	2609.33	2609.33	-0.00	72	96	0	GYNPDQIEEALTGSDVIVIPAGVPR
3445.77	3444.76	3444.83	-0.06	172	205	0	FVSEVAGTNPVNENVPVVGGHSGVTIVPLLSQTK

No match to:
1054.52
1364.95
1365.67
1366.67
1952.86
2236.16
2275.09
2615.28
3467.73

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).



Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **24**
Number of mass values matched: **15**
Sequence Coverage: **56%**

Matched peptides shown in **Bold Red**

1 MFSKVATRSF SSSASNAYKV AVLGAGGGIG QPLSLLLK**LN HKVTDLALYD**
51 IRGAPGVAAD VSHVPTNSTV KGYNPDQIEE ALTGSDVIVI PAGVPRKPGM
101 TRDDLFNTNA SIVRDLAKAA ADYAPNAAVC IISNPVNSTV PIVAEVFKSK
151 GNYNPNKLFG VTTLDVLRAA R**FVSEVAGTN PVNENVPVVG GHSGVTIVPL**
201 LSQTKHKDLS GETRDALVHR IQFGGDEVVQ AKDGAGSATL SMAQAGARFA
251 GAVLDGLAGE KDVIECTFVD SPLFKDEGVD FFSTKVTLGV DGVK**TVHPIG**
301 EISDYEEAQV KEAKDTLIKN IKKGVDFVAQ NP

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 24

Mdh2p (Mdh11p, PMF)

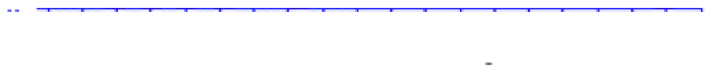
Match to: **CA5826|CaMDH11**; Score: **95**
Malate dehydrogenase (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1233.72	1232.71	1232.71	-0.00	148	158	0	LFGVTTLDIVR
1283.76	1282.75	1282.75	-0.00	316	326	0	LLEVAIEQLQK
1293.75	1292.75	1292.75	0	74	86	0	GSDLVIIPAGVPR
1415.63	1414.62	1414.66	-0.04	200	210	0	QYYDILSEEQK
1432.76	1431.75	1431.75	0	216	228	1	RVQFGGDEVVQAK
1478.79	1477.78	1477.78	-0.00	283	295	0	DLDFFSLPVQLGK
1543.77	1542.76	1542.76	0.01	200	211	1	QYYDILSEEQKK
1589.7	1588.7	1588.73	-0.03	229	244	0	NGAGSATLSMAYAGYR
2194.03	2193.02	2193.08	-0.06	296	314	1	NGITEVKYDILNQISDDEK
2510.45	2509.44	2509.42	0.02	117	140	0	AFVLVISNPVNSTVPIVAETLQAK

No match to:
889.55
905.49
933.57
977.6
1059.46
1107.54
1109.5
1145.52
1185.51
1187.51
1268.67
1273.55
1313.55
1315.56
1320.59
1332.56
1359.57
1365.65
1399.59
1417.61
1477.71
1487.65
1510.87
1532.75
1561.64
1590.73
1606.75
1631.68
1717.74
1804.76

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).

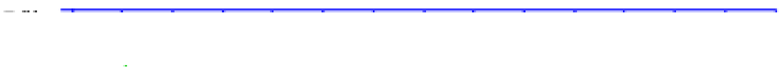


Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **51**
Number of mass values matched: **10**
Sequence Coverage: **39%**

Matched peptides shown in **Bold Red**

1 MVKVAILGAA GGIGQPLSLL TKLNPNVDEL ALFDVVNVPG VGADLSHINS
51 DSKTQSYLPK DKEDKTALAA ALK**GSDLVII PAGVPR**KPGM TRDDLFNINA
101 SIVQGLAEGI AANSPK**AFVL VISNPVNSTV PIVAETLQAK** GVYDPAR**LFG**
151 **VTTLDIVR**AN TFISQLFLDQ TKPSDFNINV VGGHSGETIV PLYSLGNSK**Q**
201 **YYDILSEEQK K**ELIK**RVQFG GDEVVQAKNG AGSATLSMAY AGYR**LAESIL
251 AAVNGKTDIV ECTFLNLDSS IKGASEARKL VK**DLDFFSLP VQLGKNGITE**
301 **VKYDILNQIS DDEK**K**LLEVA IEQLQK**NIEK GVSFAKK

1838.93
1858.87
1909.1
1918.91
2007.23
2174.17
2228.14
2399
2458.28
2516.3
3213.49



Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 51

Gim5p (PMF)

Match to: **CA2888|CaGIM5**; Score: **112**
Gim complex component (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1411.83	1410.82	1410.82	0	128	139	0	NELLNTVNLILR
1519.77	1518.77	1518.76	0.01	85	97	0	YLVDIGTGYYVEK
1567.94	1566.93	1566.92	0.01	128	140	1	NELLNTVNLILRR
1761.9	1760.89	1760.9	-0.00	83	97	1	NKYLVDIGTGYYVEK
2314.27	2313.26	2313.26	0	62	82	0	ENDLLVPLTSSLYIPGQVVTR
2404.23	2403.22	2403.19	0.03	25	46	0	SIDEEITHFTQSLQALSAAQSK
2532.29	2531.29	2531.29	0	24	46	1	KSIDEEITHFTQSLQALSAAQSK

No match to:
1071.43
1145.53
1293.07
1447.7
1639.87
1919.9
2251
2311.14
2495.28
2525.13
2623.37

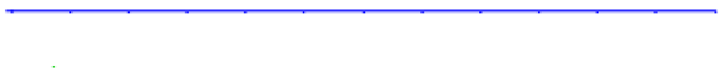
Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **18**
Number of mass values matched: **7**
Sequence Coverage: **45%**

Matched peptides shown in **Bold Red**

1 MSAAEPTNID LNSLPPQQLI EFR**KSIDEEI THFTQSLQAL SAAQSK**LKDC
51 ISSINNLEQS K**ENDLLVPLT SSLYIPGQVV TRNKYLVDIG TGYYVEK**SAD
101 KAKLGYNNKI KKLDDDAKKL KNILVQK**NEL LNTVNLILRR** KVIEMEQEQE
151 GSSAGVTN



Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 18

Rbp1p (MS/MS)

CA3676|CaRBP1 Mass: 13316 Total score: 12 Peptides matched: 1
rapamycin-binding protein

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Rank	Peptide
9	**1253.6**	**1252.59**	**1252.6**	**-0.01**	**1**	**12**	**1**	**LTNGKEFDSSR**

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 9 indicate identity or extensive homology (p<0.05).

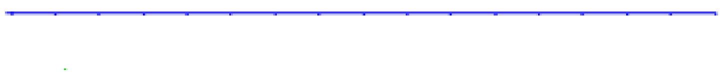
Monoisotopic mass of neutral peptide (Mr): 1252.60
Fixed modifications: Carbamidomethyl (C)
Ions Score: 12 **Matches (Bold Red):** 5/56 fragment ions using 18 most intense peaks

#	a	a*	b	b*	Seq.	y	y*	#
1	86.1		114.09		**L**			**11**
2	187.14		215.14		**T**	1140.53	1123.5	**10**
3	301.19	284.16	329.18	312.16	**N**	1039.48	1022.45	**9**
4	358.21	341.18	386.2	369.18	**G**	**925.44**	**908.41**	**8**
5	486.3	469.28	514.3	497.27	**K**	868.42	851.39	**7**
6	615.35	598.32	643.34	626.31	**E**	740.32	723.29	**6**
7	762.42	745.39	790.41	773.38	**F**	611.28	594.25	**5**
8	877.44	860.42	905.44	888.41	**D**	464.21	447.18	**4**
9	964.47	947.45	992.47	975.44	**S**	**349.18**	332.16	**3**
10	1051.51	1034.48	1079.5	1062.47	**S**	**262.15**	245.12	**2**
11					**R**	**175.12**	158.09	**1**

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **9%**

Matched peptides shown in **Bold Red**

1 MSEELPQIEI VQEGDNTTFA KPGDTVTIHY DGK**LTNGKEF DSSR**KRGKPF
51 TCTVGVGQVI KGWDISLTNN YGKGGANLPK ISKGTKAILT IPPNLAYGPR
101 GIPPIIGPNE TLVFEVELLG VNGQ



Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.3 Da
Max Missed Cleavages : 1
Instrument type : Default
Number of queries : 1

MS/MS Fragmentation of **LTNGKEFDSSR**

Cpr3p (PMF)

Match to: **CA3978|CaCPR3**; Score: **101**
cyclophilin (peptidylprolyl isomerase), mitochondrial (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1255.64	1254.63	1254.62	0	29	39	0	VFFNTSINGEK
1645.86	1644.85	1644.85	0	151	165	0	HVVFGEVVDGFDVVK
1773.95	1772.94	1772.95	-0.00	151	166	1	HVVFGEVVDGFDVVKK
1780.89	1779.88	1779.89	-0.00	79	94	0	IIPQFMLQGGDFETGK
1796.91	1795.9	1795.88	0.02	79	94	0	IIPQFMLQGGDFETGK Oxidation (M)
2417.07	2416.07	2416.07	-0.00	95	115	1	GYGGYSPTHNNDKFNDENFIK
2466.2	2465.2	2465.21	-0.02	40	60	0	QPPITFELYDDVTPITAENFR
2511.15	2510.14	2510.13	0.01	167	191	0	IESCGTSSGTPSASVVIEESGEAEK
2639.26	2638.25	2638.23	0.02	166	191	1	KIESCGTSSGTPSASVVIEESGEAEK

No match to:
841.35
869.41
887.39
973.42
1071.44
1209.56
1317.57
1346.7
1358.58
1401.6
1445.62
1475.59
1485.62
1531.66
1657.86
1667.85
1703.89
1710.88
1733.89
1785.92
1802.93
1808.88
1824.88
1846
2508.19
2508.19
2510.15
2518.19
2545.15
2653.27

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **39**
Number of mass values matched: **9**
Sequence Coverage: **57%**

Matched peptides shown in **Bold Red**

1 MFKTTLTKPL TFKSARFFST TPRAWGTK**VF FNTSINGEKQ PPITFELYDD**
51 VTPITAENFR VLCTGEKGVG YKGSIFHR**II PQFMLQGGDF ETGKGYGGYS**
101 PTHNNDKFND ENFIKKHDRP GLLSMANAGP NTNGSQFFIT TVPCPWLDGK
151 HVVFGEVVDG FDVVKKIESC GTSSGTPSAS VVIEESGEAE K

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted

Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 39

Cpr1p (Cyp1p, PMF)

Match to: **CA0972|CaCYP1**; Score: **140**
cyclophilin (peptidylprolyl isomerase), mitochondrial (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide	
716.38	715.38	715.38	0	48	53	0	GSIFHR	
737.36	736.35	736.35	0	30	35	0	TAENFR	
778.38	777.37	777.37	0	36	42	0	ALCTGEK	
948.5	947.5	947.5	0	22	29	0	LYDDVVPK	
969.47	968.46	968.46	0	81	88	0	FADENFVK	
1125.57	1124.56	1124.56	0	81	89	1	FADENFVKR	
1268.66	1267.65	1267.65	0	43	53	1	GFGYKGSIFHR	
1355.69	1354.68	1354.67	0.01	140	153	1	IESFGSGSGATSKK	
1437.8	1436.79	1436.79	0	18	29	1	ITFKLYDDVVPK	
1618.81	1617.8	1617.8	0	75	88	1	SIYGTKFADENFVK	
1627.86	1626.86	1626.86	-0.01	124	138	0	HVVFGEVTDGLDIVK	
1666.85	1665.84	1665.84	0	22	35	1	LYDDVVPKTAENFR	
1755.97	1754.96	1754.96	0	124	139	1	HVVFGEVTDGLDIVKK	
2228.09	2227.08	2227.07	0.01	54	74	0	VIPQFMLQGGDFTNFNGTGGK	
2244.07	2243.06	2243.07	0	54	74	0	VIPQFMLQGGDFTNFNGTGGK	Oxidation (M)
2925.46	2924.45	2924.44	0.01	48	74	1	GSIFHRVIPQFMLQGGDFTNFNGTGGK	
3698.81	3697.81	3697.78	0.03	90	123	0	HDRPGLLSMANAGPNTNGSQFFITTVPCPWLI	
3714.78	3713.77	3713.77	0	90	123	0	HDRPGLLSMANAGPNTNGSQFFITTVPCPWLDGK	Oxidation (M)
3854.95	3853.95	3853.88	0.07	89	123	1	RHDRPGLLSMANAGPNTNGSQFFITTVPCPWI	

No match to:
717.39
718.41
738.36
739.37
779.39
806.43
949.51
1081.59
1115.63
1116.64
1126.57
1127.57
1128.58
1137.61
1179.5
1181.63
1206.78
1269.66
1325.68
1356.69
1366.7
1381.85
1438.79
1458.67
1460.68
1549.81
1609.87
1619.82

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant ($p<0.05$).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **77**
Number of mass values matched: **19**
Sequence Coverage: **83%**

Matched peptides shown in **Bold Red**

1 MSTVYFDVSA DGQKLGK**ITF KLYDDVVPKT AENFRALCTG EKGFGYKGSI**
51 FHRVIPQFML QGGDFTNFNG TGGKSIYGTK FADENFVKRH DRPGLLSMAN
101 AGPNTNGSQF FITTVPCPWL DGKHVVFGEV TDGLDIVKKI ESFGSGSGAT
151 SKKIVIEESG QLZ

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 77

1628.87
1639.88
1649.86
1667.84
1681.79
1705.87
1756.89
1774.9
1778.91
1831.05
1920.94
2027.51
2156.17
2180.07
2266.05
2332.12
2507.2
2531.18
2926.47
2928.45
3154.46
3478.78
3651.82
3655
3699.81
3715.84
3731.79
3839.47
3855.92
3871.86

Ssb1p (PMF)

Match to: **CA3534|CaSSB1**; Score: **64**
heat shock protein 70

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1041.52	1040.51	1040.52	-0.00	352	360	0	LLSDFFDGK
1169.66	1168.65	1168.66	-0.01	162	173	0	DAGAIAGLNVLR
1242.69	1241.68	1241.69	-0.01	315	325	0	STLEPVEQVLK
1410.73	1409.72	1409.73	-0.01	303	314	1	ARFEDINSALFK
1445.76	1444.76	1444.75	0	332	345	0	SQVDEVVLVGGSTR
1469.72	1468.72	1468.72	-0.00	39	51	0	VTPSFVAFTSEER
1550.78	1549.77	1549.79	-0.02	144	157	0	AVVTVPAYFNDAQR
1729.93	1728.92	1728.94	-0.02	174	191	0	IINEPTAAAIAYGLGAGK

No match to:
824.35
828.29
842.25
844.28
868.34
879.33
883.35
885.35
901.29
911.32
913.42
927.38
1003.48
1057.43
1109.49
1288.7
1304.69
1385.75
1401.71
2216.98

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **28**
Number of mass values matched: **8**
Sequence Coverage: **16%**

Matched peptides shown in **Bold Red**

1 MADGVFQGAI GIDLGTTYSC VATYDSAVEI IANEQGNR**VT PSFVAFTSEE**
51 **R**LIGDAAKNQ AALNPKNTVF DAKRLIGRAF DDESVQKDIK SWPFKVVESN
101 GQPLIEVEYL DETKTFSPQE ISSMVLTKMK EIAEAKIGKK VEK**AVVTVPA**
151 **YFNDAQR**QAT K**DAGAIAGLN VLRIINEPTA AAIAYGLGAG K**SEKERHVLI
201 FDLGGGTFDV SLLNITGGVF TVKATAGDTH LGGQDFDTNL LEHFKKEFQK
251 KTGNDISGDA RALRRLRTAC ERAKRSLSSG TQTTVEIDSL FDGEDFSANI
301 TR**ARFEDINS ALFKSTLEPV EQVLK**DAKIS K**SQVDEVVLV GGSTR**IPKVQ
351 K**LLSDFFDGK** QLEKSINPDE AVAYGAAVQG AILTGQSTND DTKDLLLLDV
401 IPLSLGVAMQ GNVFAPVVPR NTTVPTIKRR TFTTVADHQT TVQFPVYQGE
451 RVNCTENTLL GEFDLKNIPP MQAGEPVLEA IFEVDANGIL KVTAVEKSTG
501 RSANITISNS IGRLSTEEIE KMISDAEKFK SSDDAFAKRH EQKQKLEAYV
551 ASVESTVTDP VLSAKLKKSA KDKIEAALSD ALQTLEIEES SADDYRKAEL

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 28

Cyp5p (Cyp51p, PMF)

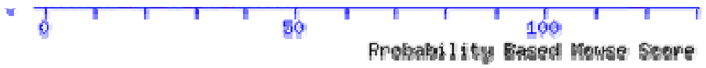
Match to: **CA5717|CaCYP51**; Score: **118**
Cyclophilin - peptidylprolyl cis-trans isomerase or PPIase (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
765.41	764.4	764.38	0.02	65	70	0	TVENFR
1193.61	1192.6	1192.6	0.01	172	181	0	DVVDYIENVK
1200.55	1199.54	1199.53	0.01	39	48	0	VYFDVEEDGK
1244.77	1243.76	1243.75	0.01	53	64	0	ITIGLFGTVVPK
1564.69	1563.68	1563.7	-0.01	118	129	1	FDDENFELKHDR
1613.79	1612.78	1612.77	0.01	39	52	1	VYFDVEEDGKSIGR
1642.85	1641.84	1641.84	0	141	155	0	NTNGSQFFITTALTK
1741.89	1740.88	1740.88	-0.00	156	171	0	WLDGAHVVFGEVLDGK
2078.99	2077.98	2077.99	-0.00	71	88	0	VLCTGELGPSYENTVFHR

No match to:
1040.98
1071.44
1266.75
1289.14
1305.12
1445.63
1537.91
1643.85
1666.82
1700.77
1951.95
2022.97
2032.02
2108.95
2118.99
2250.05
2550.23

Probability Based Mowse Score

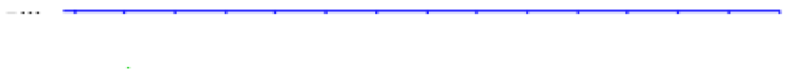
Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).



Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **26**
Number of mass values matched: **9**
Sequence Coverage: **48%**

Matched peptides shown in **Bold Red**

1 MKSLTSIALI ASIIVAFYTQ LVLGGSSNLP KNPPVTNK**VY FDVEEDGKSI**
51 GRITIGLFGT VVPKTVENFR VLCTGELGPS YENTVFHRVI KDFMIQSGDF
101 EYGQGYGGYS PTHNNGK**FDD ENFELKHDR**K YRLSMANAGK **NTNGSQFFIT**
151 TALTKWLDGA HVVFGEVLDG KDVVDYIENV KTGRGDRPVK EIKIVASGEL
201 KDSETNPSKD EL



Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 26

Ssc1p (PMF)

Match to: **CA4474|CaSSC1**; Score: **183**
Mitochondrial heat shock protein 70-related protein (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
735.38	734.37	734.37	-0.00	464	469	0	VFQGER
853.57	852.56	852.55	0.01	78	85	1	LVGIPAKR
883.58	882.57	882.57	0	189	196	0	IVGLNVLR
974.5	973.49	973.48	0.01	55	63	0	ILENSEGGR
983.55	982.55	982.55	-0.00	263	270	1	YIVDAFKK
1127.63	1126.63	1126.61	0.02	589	597	0	VQDQIQQLR
1191.59	1190.58	1190.57	0.02	105	113	1	RYEDPEVQR
1254.77	1253.77	1253.75	0.02	185	196	1	DAGKIVGLNVLR
1414.81	1413.8	1413.79	0.01	327	338	0	AQFEQLVEPLIK
1521.83	1520.83	1520.78	0.04	64	77	1	TTPSIVAFTKDGER
1542.92	1541.91	1541.88	0.03	327	339	1	AQFEQLVEPLIKK
1646.94	1645.93	1645.88	0.05	86	100	1	QAVVNPSDTLFATKR
1765.97	1764.96	1764.9	0.06	447	463	0	SQIFSTAAAGQTSVEIR
1778.97	1777.96	1777.9	0.06	136	151	0	GEQYSPQQIGGFILNK
1894.07	1893.07	1893	0.07	446	463	1	KSQIFSTAAAGQTSVEIR
1911.98	1910.98	1910.89	0.08	164	180	0	VNSAVVTCPAYFNDAQR
2040.09	2039.08	2038.99	0.09	163	180	1	KVNSAVVTCPAYFNDAQR

No match to:
745.4
1226.59
1337.71
1566.85
1591.87
1899.19
2018.04
2305.33
2321.32
2373.4
2402.43
2489.45

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant ($p<0.05$).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **29**
Number of mass values matched: **17**
Sequence Coverage: **23%**

Matched peptides shown in **Bold Red**

1 MLSARNSLKN ISRQFPKALT RAQSTAAAPT GPVIGIDLGT TNSAVAVMEG
51 KTPK**ILENSE GGRTTPSIVA FTKDGERLVG IPAKRQAVVN PSDTLFATKR**
101 LIGR**RYEDPE VQR**DINQVPY KIVKHGNGDA WLEAR**GEQYS PQQIGGFILN**
151 **K**MKETAEAAL SK**KVNSAVVT CPAYFNDAQR** QATK**DAGKIV GLNVLR**VINE
201 PTAAALAYGL EKKDGEVVAV FDLGGGTFDV SILDIGAGVF EVKSTNGDTH
251 LGGEDFDIAL VR**YIVDAFKK** ESGIDLEKDK MAIQRIREAA EKAKIELSST
301 VSTEINLPFI TADASGPKHI NQKISR**AQFE QLVEPLIKK**T IEPCKKALKD
351 AGLSTSDVSE VILVGGMSRM PKVVETVKSI FGKEPSKGIN PDEAVAMGAA
401 IQGGILAGEV KDVVLLDVTP LSLGIETMGG VFARLISRNT TIPAK**KSQIF**
451 **STAAAGQTSV EIRVFQGER**E LTRDNKLIGN FTLSGIPPAP KGVPQIEVTF
501 DIDTDGIIKV SARDKATNKD ASITVAGSSG LSDAEIEKMV NDAEKFAESD
551 KARREAIEFA NRADQLCNDT ENSLNEHKEK LSSESVQK**VQ DQIQQLR**EIV
601 LKAQAGEEVS PEELKQKTEE LQNEAINLFK DLYKDGGESS GSSEQPKN

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 29

Pre2p (MS/MS)

CA0764|CaPre2 Mass: 31545 Total score: 112 Peptides matched: 1
20S proteasome subunit (beta5)

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Rank	Peptide
1	1572.78	1571.77	1571.71	0.06	0	112	1	EGPTIYYVDSDGTR

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 21 indicate identity or extensive homology (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **5%**

Matched peptides shown in **Bold Red**

1 MNSIAQRYSHASQNDIVKEINSVHESLSSSSNIPQLELAPSIAIPPISQP
51 TDFLRAHTDDSVNPDCKIKIAHGTTTLAFRFQGGIIVAVDSRATAGNWIA
101 SQTVNKVIRINPFLLGTMAGGAADCQFWETWLGTQCRLHELREKERISVA
151 AASKILSNLVYQYKGMGLSMGTMVCGHTAK**EGPTIYYVDSDGTR**LKGDVF
201 CVGSGQTFAYGVLDSEYKWDLSVEDALYLGKRSILAATHRDAYSGGSVNL
251 YHVTEQGWTYHGNFNVGDLFWEVKEKEQSFVNVDG

Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.3 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of queries : 1

Pre3p (MS/MS)

CA5037|CaPre3 Mass: 23629 Total score: 45 Peptides matched: 1
20S proteasome subunit (beta1)

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Rank	Peptide
1	1859.9	1858.89	1858.99	-0.1	1	24	1	TALSQAIKWDGSSGGLIR

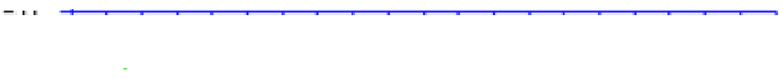
Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 14 indicate peptides with significant homology (p<0.05).
Individual ions scores > 22 indicate identity or extensive homology (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **8%**

Matched peptides shown in **Bold Red**

1 MNGISVDINH LKKGEVNLGT SIMAVTFKDG VILGADSRTT TGSYIANRVT
51 DKLTQIHDTI YCCRSGSAAD TQAVADMVKY YLQIYSSQLP PGETPTTNIA
101 ANVFQEICYN NKDNLTAGII CAGYDRKNGG SVYSIPIGGS IHKQNYAIAG
151 SGSSYIYGWC DENYKPSMEQ EQCVEFVKT**A LSQAIKWDGS SGGLIR**MVIL
201 TKNGVERRVV YLHE



Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 100 ppm
Fragment Mass Tolerance: ± 0.3 Da
Max Missed Cleavages : 1
Instrument type : Default
Number of queries : 1

Pre8p (PMF)

Match to: **CA5569|CaPRE8** Score: **78**
20S proteasome subunit Y7 (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
886.54	885.53	885.53	0.00	32	40	0	QGVTAIGIK
931.52	930.52	930.52	-0.00	111	118	0	IMVQEIAK
1122.58	1121.58	1121.58	-0.00	102	110	0	IYNEYPPVK
1175.59	1174.58	1174.58	0.00	41	51	0	CGNGVVLATER
1388.79	1387.78	1387.78	-0.00	20	31	0	LVQIEYALNAVR
2185.00	2183.99	2184.04	-0.05	2	19	0	LSIEEFCYILTFTNYSGK

No match to:
861.07
871.02
877.04
879.04
882.57
886.99
893.02
898.55
908.99
974.54
1002.55
1066.08
1082.05
1158.56
1159.55
1176.57
1278.68
1304.67
1431.75
1573.8
1805.85
2200.99

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant ($p<0.05$).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **28**
Number of mass values matched: **6**
Sequence Coverage: **26%**

Matched peptides shown in **Bold Red**

1 M**LSIEEFCYI LTFTNYSGKL VQIEYALNAV RQGVTAIGIK CGNGVVLATE**
51 **R**KANSPLIRN DTNIKVEYIT PNIGMTYSGM GPDFRVLVDR ARKLAHTNYK
101 R**IYNEYPPVK IMVQEIAK**VM QESTQSGGIR PFGVSLLVGG YDESNEGKFQ
151 LYQVDPSGSY FPWKATAIGK SSNSAKTFLE KRWNDNLQLE DGIHVALLAL
201 KECIDGELNG DNLDIAIISD PQEQLLGFKG TDIPGPRFKK LSPEEINDTL
251 DSL

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 80 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 0
Number of queries : 28

Pre6p (MS/MS)

CA4257|CaPre6 Mass: 23286 Total score: 42 Peptides matched: 1
20S proteasome subunit

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Rank	Peptide
1	1606.8	1605.79	1605.85	-0.06	0	42	1	LTLEDPVSVEYLTK

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 19 indicate peptides with significant homology (p<0.05).
Individual ions scores > 22 indicate identity or extensive homology (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **6%**

Matched peptides shown in **Bold Red**

1 MSGYDSALSIFSPDGHVFQVEYASEAVKRGTCAVGVKGKNTVVLGCEKRT
51 ALKLQDPRITPSKICKVDHHILLAFAGLNADARILVDKARVEAQSHK**LTL**
101 **EDPVSVEYLTK**YVAGVQQKYTQSGGVRPFGIATLIAGFDVRDDVPKLFQT
151 EPSGVFNAWKAHAIGRSSKTVKEFLEKHYEEDLSEEETIKLTVKSLLEVV
201 QTGAKNIEVSVLKPGAVIKKLDVDEIKKYVDAIEAEKAAEAEKKKQKSKD

Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 100 ppm
Fragment Mass Tolerance: ± 0.3 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of queries : 1

Cox4p (PMF)

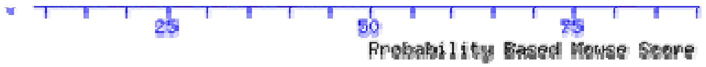
Match to: **CA4533|CaCOX4**; Score: **81**
cytochrome-c oxidase (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1111.51	1110.5	1110.49	0.01	148	157	0	YLGEPGMAHH
1151.53	1150.52	1150.53	-0.00	137	145	0	CWQCGTVLK
1569.83	1568.82	1568.84	-0.02	39	55	0	DLAEVTGAASLIGPGAK
1616.75	1615.74	1615.75	-0.01	116	128	0	GTPEQDHKPYWMK
1778.84	1777.84	1777.85	-0.01	56	71	0	EGTIPTDYEQATGLQR
1782.8	1781.79	1781.79	0	79	94	0	EGVDVFDMEMPISEGK
1873.91	1872.9	1872.91	-0.01	95	110	0	GTMQDPYLVPTYIGYR
1889.9	1888.89	1888.9	-0.01	95	110	0	GTMQDPYLVPTYIGYR Oxidation (M)
2159	2158	2158.02	-0.02	116	133	1	GTPEQDHKPYWMKVEEGK
2633.44	2632.44	2632.44	-0.01	28	55	1	AAPETAVKPAKDLAEVTGAASLIGPGAK

No match to:
771.3
773.44
797.32
799.33
817.46
845.52
857.34
883.36
885.37
889.55
933.57
943.37
969.39
971.4
977.6
1029.41
1055.43
1057.44
1101.47
1115.45
1134.5
1137.58
1141.47
1143.48
1159.47
1168.57
1185.49
1187.5
1201.49
1217.47

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).



Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **74**
Number of mass values matched: **10**
Sequence Coverage: **71%**
Matched peptides shown in **Bold Red**

1 MLSRTTFRIA RQQTRLLSTS RVLLSAK**AAP ETAVKPAKDL AEVTGAASLI**
51 GPGAKEGTIP TDYEQATGLQ RLELLGKR**EG VDVFDMEMPI SEGKGTMQDP**
101 YLVPTYIGYR YVGCK**GTPEQ DHKPYWMKVE EGK**VSR**CWQC GTVLK**AK**YLG**
151 EPGMAHH

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 74

1227.51
1229.52
1230.52
1245.52
1277.1
1287.52
1296.68
1303.5
1313.54
1373.56
1389.54
1417.59
1434.73
1459.6
1475.75
1485.61
1545.64
1589.66
1606.72
1631.68
1638.84
1647.66
1707.76
1717.7
1734.79
1777.8
1803.75
1825.89
2252.02
2551.19
2588.39
3215.37
3864.02
3887.93

Cox5Ap (PMF)

Match to: **CA2630|CaCOX5A**; Score: **112**
cytochrome-c oxidase chain V.A precursor (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1330.68	1329.67	1329.68	-0.00	129	140	0	QFASPPPITMNK
1407.73	1406.72	1406.72	0	39	51	0	ALSNAYIGNLESR
1440.63	1439.62	1439.62	0	141	151	0	EWQEQSDDYLK
1516.72	1515.71	1515.71	-0.00	85	97	0	AAYYISFGEWGPR
1571.75	1570.75	1570.77	-0.02	71	83	0	MELPWQELTPAEK
1573.8	1572.79	1572.81	-0.02	58	70	1	QDQQTLIDELKSR
1644.81	1643.8	1643.81	-0.01	84	97	1	KAAYYISFGEWGPR
1699.86	1698.85	1698.87	-0.01	71	84	1	MELPWQELTPAEKK

No match to:
1222.54
1225.14
1401.59
1475.76
1545.64
1548.69
1604.79
1638.85
1707.78
1716.85
1890.05
1951.05
2107.01
2233
2525.14
2573.26

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **24**
Number of mass values matched: **8**
Sequence Coverage: **46%**

Matched peptides shown in **Bold Red**

1 MFMRSLQRAA TKANTASITT SILRFNSTVA KSTSAAPR**AL SNAYIGNLES**
51 **R**WTSLPK**QDQ QTLIDELKSR MELPWQELTP AEKKAAYYIS FGEWGPR**TPL
101 YLPGERSQVF WITTGCIVAS VVLFFGIR**QF ASPPPITMNK EWQEQSDDYL**
151 **K**SKNANPFTG YSQVQ

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 24

Aat1p left (PMF)

Match to: **CA2661|CaAAT1**; Score: **176**
aspartate aminotransferase (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide		**No match to:**
816.43	815.42	815.41	0	122	128	0	QLIDDGR		768.54
835.47	834.46	834.46	-0.00	101	107	0	NFQSIVK		771.31
947.53	946.53	946.52	0	143	150	0	VIADFLNR		773.44
1097.54	1096.53	1096.53	0	108	116	0	NFIFNNSNK		889.55
1289.62	1288.62	1288.62	-0.00	373	382	0	SNYNWDHLLK		933.57
1401.77	1400.76	1400.77	-0.00	66	78	0	DNSGKPIIFPSVK		943.38
1403.78	1402.77	1402.78	-0.01	129	142	0	IVTAQTISGTGSLR		962.54
1450.74	1449.73	1449.73	0	295	309	0	TGSISIINSSGEASK		1029.42
1582.76	1581.75	1581.75	0	108	121	1	NFIFNNSNKDANGK		1071.59
1645.82	1644.82	1644.83	-0.01	370	382	1	LDKSNYNWDHLLK		1113.58
1664.94	1663.93	1663.94	-0.01	318	332	0	LIRPIYSSPPIHGSK		1115.45
1672.78	1671.78	1671.79	-0.01	400	413	1	LRNEYSVYATEDGR		1137.58
1696.86	1695.85	1695.87	-0.01	385	399	0	GMFVYTGLSPEQVIR		1201.5
1712.85	1711.85	1711.86	-0.01	385	399	0	GMFVYTGLSPEQVIR	Oxidation (M)	1287.53
1762.85	1761.85	1761.85	-0.01	41	56	0	ILGISEAYNNDSNPQK		1294.67
1820.04	1819.03	1819.05	-0.02	157	172	0	ILVPKPTWANHVAVFK		1296.69
1898.82	1897.81	1897.83	-0.01	173	188	0	DAGLEPEFYSYYETSK		1321.62
									1393.75
									1537.82
									1583.75
									1648.85
									1718.86
									1753.88
									2180.08
									2436.3

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant ($p<0.05$).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **42**
Number of mass values matched: **17**
Sequence Coverage: **41%**

Matched peptides shown in **Bold Red**

1 MYKTQLIKSS TQARFLAVRQ LSSTSQLLKW NDIPLAPPDK **ILGISEAYNN**
51 **DSNPQK**VNLG VGAYR**DNSGK PIIFPSVK**KA EEILLGKETE KEYTAIVGSK
101 **NFQSIVKNFI FNNSNKDANG KQLIDDGRIV TAQTISGTGS LRVIADFLNR**
151 FYSNKK**ILVP KPTWANHVAV FKDAGLEPEF YSYYETSK**ND LDYANLKKSL
201 TAAPEGSIVL LHACCHNPTG MDLTSEQWDE VLQIVQDKKF FPLVDMAYQG
251 FASGKPFEDI GLIRKLTKLA NENKIPSFAL CQSFAKNMGL YGER**TGSISI**
301 **INSSGEASK**A VESQLKK**LIR PIYSSPPIHG SK**IVEVIFDE SSGLLPQWLD
351 ELDKVVGRLN TVRSKLYEK**L DKSNYNWDHL LK**QR**GMFVYT GLSPEQVIRL**
401 **RNEYSVYATE DGR**FSISGIN DNNVDYLANA INEVIKN

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 42

Aat1p right (PMF)

Match to: **CA2661|CaAAT1**; Score: **155**
aspartate aminotransferase (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
774.44	773.43	773.43	0	310	316	0	AVESQLK
816.43	815.42	815.41	0.01	122	128	0	QLIDDGR
835.46	834.46	834.46	-0.00	101	107	0	NFQSIVK
939.45	938.45	938.43	0.02	287	294	0	NMGLYGER
947.54	946.54	946.52	0.01	143	150	0	VIADFLNR
955.45	954.44	954.42	0.02	287	294	0	NMGLYGER Oxidation (M)
1097.54	1096.53	1096.53	-0.00	108	116	0	NFIFNNSNK
1289.61	1288.6	1288.62	-0.02	373	382	0	SNYNWDHLLK
1401.79	1400.78	1400.77	0.02	66	78	0	DNSGKPIIFPSVK
1403.8	1402.79	1402.78	0.01	129	142	0	IVTAQTISGTGSLR
1664.95	1663.94	1663.94	0	318	332	0	LIRPIYSSPPIHGSK
1672.79	1671.78	1671.79	-0.00	400	413	1	LRNEYSVYATEDGR
1696.87	1695.87	1695.87	0	385	399	0	GMFVYTGLSPEQVIR
2038.03	2037.03	2037.04	-0.01	269	286	1	LANENKIPSFALCQSFAK

No match to:
773.44
798.36
845.53
941.44
962.56
1034.52
1040.97
1100.48
1110.07
1137.56
1583.76
1783.85

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant ($p<0.05$).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **26**
Number of mass values matched: **14**
Sequence Coverage: **33%**

Matched peptides shown in **Bold Red**

1 MYKTQLIKSS TQARFLAVRQ LSSTSQLLKW NDIPLAPPDK ILGISEAYNN
51 DSNPQKVNLG VGAYR**DNSGK PIIFPSVK**KA EEILLGKETE KEYTAIVGSK
101 NFQSIVKNFI FNNSNKDANG K**QLIDDGRIV TAQTISGTGS LRVIADFLNR**
151 FYSNKKILVP KPTWANHVAV FKDAGLEPEF YSYYETSKND LDYANLKKSL
201 TAAPEGSIVL LHACCHNPTG MDLTSEQWDE VLQIVQDKKF FPLVDMAYQG
251 FASGKPFEDI GLIRKLTK**LA NENKIPSFAL CQSFAKNMGL YGER**TGSISI
301 INSSGEASK**A VESQLK**K**LIR PIYSSPPIHG SK**IVEVIFDE SSGLLPQWLD
351 ELDKVVGRLN TVRSKLYEKL DK**SNYNWDHL LK**QR**GMFVYT GLSPEQVIRL**
401 RNEYSVYATE DGRFSISGIN DNNVDYLANA INEVIKN

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 26

Por1p (MS/MS)

CA0919|CaPOR1 Mass: 29748 Total score: 69 Peptides matched: 1
mitochondrial outer membrane porin (by homology)

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Rank	Peptide
1	**1557.86**	**1556.85**	**1556.77**	**0.08**	**0**	**69**	**1**	**LNFFYQQSAVNAR**

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 22 indicate identity or extensive homology (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **5%**

Matched peptides shown in **Bold Red**
1 MAPAAYSDLSKASNDLINKDFYHLSTAAVDVKTVAPNGVTFTVKGKTTKD
51 DTISASVDAKYLDKATGLTLTQGWNNANALNTKIELSELLTPGLKGELDT
101 SVVPNGARNAK**LNFFYQQSAVNAR**LFFDLLKGPIATADLVVAHDGFTAGA
151 ELGYDISSAKVNKYSVGVGYANLNYGLAATATSNLSVFSAAYFHKVSPLV
201 QVGAKATWDSIKSSNVNVEFATKYALDNTSFIKAKIADSGLTALSYTQEL
251 RPGVKLGLGASFDALKLAEPVHKLGFSLSFAA

Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 100 ppm
Fragment Mass Tolerance: ± 0.3 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of queries : 1

Sec13p* (PMF)

Rank	**1**
MOWSE Score	**4.13E+06**
# (%) Masses Matched	**12/41 (29%)**
Protein MW (Da)/pI	**33013.9 / 5.32**
Species	**CaSEC13 Protein transport protein**
PACALBI_prot.txt Accession #	**Candida**
Protein Name	**CA3392**

1. 12/41 matches (29%). 33013.9 Da, pI = 5.32. Acc. # Candida. CaSEC13 Protein transport protein. CA3392.

m/z submitted	**MH+ matched**	**Delta ppm**	**start**	**end**	**Peptide Sequence**
979.449	979.446	3.0402	254	260	(K)FPDVCWR(C)
1111.5428	1111.5384	4.0212	222	231	(R)SYIATASQDR(T)
1112.546	1112.5489	-2.5721	202	210	(K)LEGHTDWVR(D)
1131.6147	1131.6162	-1.3143	232	240	(R)TVLIWTQDR(D)
1257.6561	1257.6592	-2.4116	211	221	(R)DVAWSPSNLIR(S)
1300.6057	1300.6061	-0.3148	35	45	(K)IFDLDGTDNYK(L)
1319.6857	1319.6742	8.7218	174	185	(R)RIVSCGSDNLAK(I)
1404.6448	1404.6469	-1.5419	67	79	(K)FGSILASCSYDGK(A)
1431.7488	1431.7596	-7.5599	232	243	(R)TVLIWTQDRDGK(W)
1820.8842	1820.9005	-8.9928	247	260	(K)QLLTEEKFPDVCWR(C)
1864.8867	1864.8863	0.2048	261	278	(R)CSWSLSGNILAVSGGDNK(V)
2357.2285	2357.2406	-5.1376	46	66	(K)LITTLTGHEGPVWQVSWAHPK(F)

29 unmatched masses:

868.5473
889.5529
933.5811
1180.6208
1314.6736
1317.7596
1318.7272
1329.6948
1361.7836
1449.8333
1484.7397
1510.832
1537.8862
1562.7975
1574.8394
1581.9104
1625.9309
1795.9896
1803.8621
1847.8705
1876.8943
1909.0831
2216.9902
2228.1707
2317.1877
2371.2212
2542.2515
2661.3728
3009.4795

The matched peptides cover 43% (131/298 AA's) of the protein.

1 MVTIGNAHDDLIHDAVLDYYGKRLATCSSDKTI**KIFDLDGTDNYKLITTL**
51 **TGHEGPVWQVSWAHPKFGSILASCSYDGKA**LIWKEQPETQQWSIIAEHTV
101 HQASVNSVSWAPHELGAVLLCTSSDGKVSVVDFNDDGTTSHVIFDAHAIG
151 ANSATWAPVSTSSKDSAALKQQ**RRIVSCGSDNLAKI**WKYDAANNTYVEEA
201 **KLEGHTDWVRDVAWSPSNLIRSYIATASQDRTVLIWTQDRDGKW**Q**KQLLT**
251 **EEKFPDVCWRCSWSLSGNILAVSGGDNKV**SLWKENLQGKWESAGEVDQ

Search Parameters

Considered modifications: | **Oxidation of M** |

Min. # Peptides to Match	Peptide Mass Tolerance (+/-)	Peptide Masses are	Digest used	Max. # Missed cleavages	Cysteines Modified by	Peptide N terminus/ C Terminus	Input # Peptide Masses
4	**50.000 ppm**	**monoisotopic**	**Trypsin**	**1**	**carbamidomethylation**	**Hydrogen (H)/Free Acid (O H)**	**41**

Atp7p (PMF)

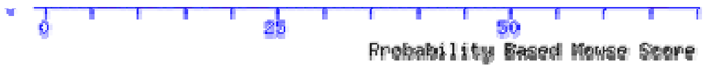
Match to: **CA1907|CaATP7**; Score: **66**
F1F0-ATPase complex, FO D subunit (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
906.48	905.47	905.44	0.03	159	165	0	WEVPGYR
979.53	978.53	978.5	0.03	93	100	0	NIEIFESK
1205.64	1204.63	1204.6	0.03	156	165	1	NGKWEVPGYR
1244.74	1243.73	1243.7	0.03	111	121	0	SVLEEISVLQK
2186.99	2185.99	2185.99	-0.01	44	61	0	EFIDLSSQSTDIDFNHYR
2315.1	2314.09	2314.09	0	43	61	1	KEFIDLSSQSTDIDFNHYR
2748.26	2747.25	2747.31	-0.06	125	149	0	EIESARPFDQLTVDDVAAASDLEEK

No match to:
773.46
797.34
801.51
805.44
817.11
817.48
825.12
833.09
839.1
841.1
845.11
845.54
847.11
849.06
854.07
855.07
857.36
858.08
859.07
861.09
864.31
870.05
871.05
877.06
881.05
887.02
889.57
893.04
909.01
933.6

Probability Based Mowse Score

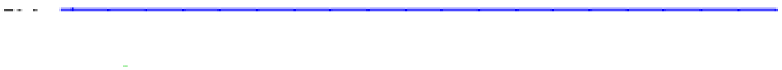
Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).



Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **62**
Number of mass values matched: **7**
Sequence Coverage: **41%**

Matched peptides shown in **Bold Red**

1 MSSVAKQAAR KVDFNKLVNG LGLTGTTASS LTAFKKRHDE AK**KEFIDLSS**
51 **QSTDIDFNHY R**SILKNSKVV DEIEKAVSGF KPVTIDVSKN LK**NIEIFESK**
101 AIENAKLTEK **SVLEEISVLQ K**TLK**EIESAR PFDQLTVDDV AAASDLEEK**V
151 TYMVK**NGKWE VPGYR**EKFGD LAAM



Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 62

943.4
1029.44
1044.12
1050.13
1060.09
1066.1
1072.12
1082.07
1088.09
1098.05
1115.48
1201.52
1206.63
1277.13
1287.56
1293.11
1296.71
1433.76
2145.04
2163.06
2185.05
2201.01
2273.15
2289.15
2527.1

Sod1p (PMF)

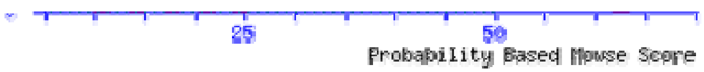
Match to: **CA4120|CaSOD1.3f**; Score: **63**
Cu,Zn-superoxide dismutase

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1071.65	1070.65	1070.64	0	112	121	1	LIGKDSILGR
1153.5	1152.49	1152.48	0.01	76	85	0	QHGAPEDDER
1375.69	1374.68	1374.68	0	122	134	0	TIVVHAGTDDYGK
1766.89	1765.89	1765.89	-0.00	142	159	0	TTGHAGARPACGVIGLTQ
2095.99	2094.98	2094.99	-0.00	122	141	1	TIVVHAGTDDYGKGGFEDSK
2844.28	2843.27	2843.26	0.01	50	75	0	GFHIHQFGDNTNGCTSAGPHFNPFGK

No match to:
773.44
801.49
817.1
817.47
825.1
833.07
839.08
841.08
845.09
845.52
847.09
849.04
850.05
854.05
855.05
858.05
859.05
861.07
866.03
869.03
870.02
871.03
877.04
886
887
889.55
893.02
895.02
905.52
908.99

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).



Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **64**
Number of mass values matched: **6**
Sequence Coverage: **52%**

Matched peptides shown in **Bold Red**

1 MIKPFLFFSV AVVRGDSKVQ GTVHFEQESE SAPTTISWEI EGNDPNALR**G**
51 **FHIHQFGDNT NGCTSAGPHF NPFGKQHGAP EDDER**HVGDL GNISTDGNGV
101 AKGTKQDLLI K**LIGKDSILG RTIVVHAGTD DYGKGGFEDS KTTGHAGARP**
151 **ACGVIGLTQ**

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 64

910.99
933.58
943.38
996.6
1029.42
1044.09
1050.1
1060.06
1066.08
1082.05
1088.06
1098.02
1104.04
1114
1115.46
1277.1
1293.07
1296.69
1309.04
1423.64
1433.73
1721.82
2163.06
2186.04
2273.15
2289.15
2789.27
3442.61

Sod21p (MS/MS)

Database : Candida 22052003 (6165 sequences; 2952183 residues)

CA5588|CaSod22.3f Mass: 18639 Total score: 72 Peptides matched: 1
superoxide dismutase, 3-prime end (by homology)

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Rank	Peptide
1	1658.85	1657.84	1657.82	0.02	0	72	1	AIWNVINWAEAESR

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 22 indicate identity or extensive homology (p<0.05).

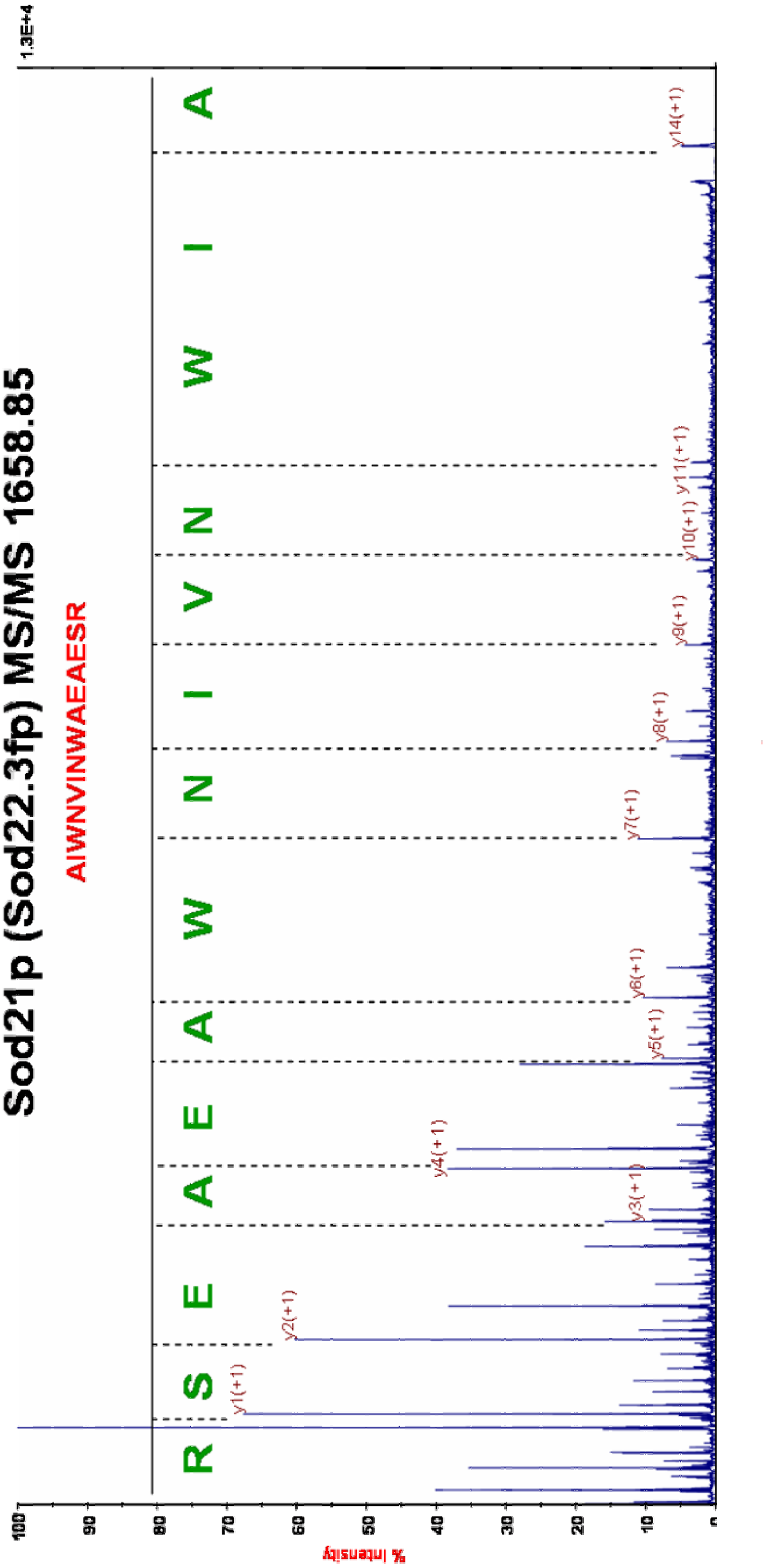
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **8%**

Matched peptides shown in **Bold Red**

1 MHVAYVNGYN AAIDALEKAV GKRDLKSVVE IQQNIKFHGG GHTNHSLFWK
51 NLAPVSKGGG KHPDTSSALG KQIVAQYGSV SNLIDITNSK LAGIQGSGWA
101 FIVKNKQNGG ALDVVTTANQ DTISAPHLVP IIAIDAWEHA YYLQYQNVKL
151 DYFK**AIWNVI NWAEAESR**YS A

Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 100 ppm
Fragment Mass Tolerance: ± 0.35 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of queries : 1


Sod21p (Sod22.3fp) MS/MS 1658.85
AIWNVINWAEAESR
1.3E+4
% Intensity
100
90
80
70
60
50
40
30
20
10
0
R
S
E
A
E
A
W
N
I
V
N
W
I
A
y1(+1)
y2(+1)
y3(+1)
y4(+1)
y5(+1)
y6(+1)
y7(+1)
y8(+1)
y9(+1)
y10(+1)
y11(+1)
y14(+1)

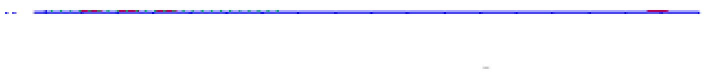
Sod21p (Sod22.3fp, MS/MS) Searched against MSDB 20020219 database (823359 sequences; 256630542 residues)

Q96UT6 Mass: 22720 Total score: 95 Peptides matched: 1
MANGANESE-CONTAINING SUPEROXIDE DISMUTASE.- Candida albicans (Yeast).

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Rank	Peptide
1	1658.85	1657.84	1657.82	0.02	0	95	1	AIWNVINWAEAESR

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 42 indicate identity or extensive homology (p<0.05).



Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 100 ppm
Fragment Mass Tolerance: ± 0.35 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of queries : 1

Gpx1p (PMF)

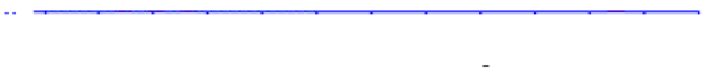
Match to: **CA0559|CaGPX1**; Score: **105**
glutathione peroxidase (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
802.48	801.47	801.47	0	115	122	0	SGVLGLTR
930.52	929.52	929.52	-0.00	44	51	1	GLEELNKK
934.5	933.49	933.49	-0.00	130	137	0	FLIDQNGK
964.52	963.52	963.52	-0.00	123	129	1	IKWNFEK
1000.46	999.45	999.45	0	36	43	0	CGFTPQYK
1082.54	1081.53	1081.54	-0.01	2	10	0	SQFYELAPK
1207.6	1206.59	1206.59	-0.00	14	23	0	GEPYPFEQLK
1353.69	1352.68	1352.68	-0.00	142	154	0	FSSLTSPESIGTK
1392.71	1391.71	1391.71	-0.00	14	25	1	GEPYPFEQLKGK
1521.75	1520.75	1520.75	-0.01	11	23	1	DAKGEPYPFEQLK

No match to:
773.44
801.49
805.42
817.09
817.47
825.1
833.07
839.08
841.07
843.07
845.09
845.52
850.05
854.05
855.05
861.07
870.02
871.02
877.04
882.57
887
889.55
893.02
908.99
933.57
996.55
1020.5
1030.11
1044.09
1050.1

Probability Based Mowse Score

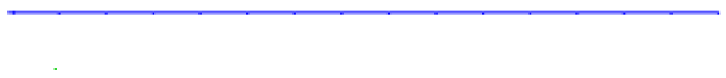
Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).



Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **64**
Number of mass values matched: **10**
Sequence Coverage: **47%**

Matched peptides shown in **Bold Red**
1 M**SQFYELAPK DAKGEPYPFE QLKGK**VVLIV NVASK**CGFTP QYKGLEELNK**
51 **K**FADQPVQIL GFPCNQFGHQ EPGSNEEIGS FCSLNYGVTF PVLDKIEVNG
101 DNTDPVYKYL KSQK**SGVLGL TRIKWNFEKF LIDQNGK**VIE R**FSSLTSPES**
151 **IGTK**IEELLK K

1060.06
1066.07
1082.04
1098.02
1111.56
1124.56
1146.55
1153.57
1277.1
1293.07
1296.68
1432.79
1433.73
1438.72
1475.76
1706.87
2146.04
2163.05
2185.05
2201.03
2221.06
2225.11
2273.15
2289.15



Search parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 64

Zwf1p (PMF)

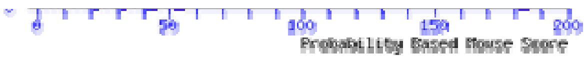
Match to: **CA2634|CaZWF1** Score: **183**

glucose-6-phosphate dehydrogenase (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
866.41	865.40	865.39	0.01	225	232	0	EAFGTEGR
881.46	880.45	880.45	0.00	325	331	0	VNIHNER
898.48	897.47	897.47	-0.00	317	324	0	AVTYAAFR
930.58	929.57	929.57	-0.00	354	361	0	IQFKPVAK
1054.60	1053.60	1053.60	0.00	332	340	0	WDGVPIVLR
1072.65	1071.64	1071.64	-0.00	153	161	0	IIIEKPFGR
1133.52	1132.51	1132.50	0.01	51	59	0	SHLEDEEFK
1174.65	1173.64	1173.64	0.00	376	385	0	VQPNEAIYLK
1211.64	1210.63	1210.63	-0.00	233	243	0	GGYFDTIGIIR
1445.81	1444.80	1444.80	-0.01	38	50	0	QLPSTVQIIGYAR
1481.66	1480.65	1480.65	0.00	426	437	0	DCYLGNHSNFVR
1511.72	1510.72	1510.72	-0.00	202	214	0	FGNELFSGVWNNK
1527.84	1526.83	1526.83	-0.00	447	460	0	LFTPLLNAVEDPAK
1611.78	1610.77	1610.78	-0.01	172	184	0	EISPLFTEDEIYR
1622.81	1621.80	1621.81	-0.01	413	425	0	DFWIPEAYEALIR
1895.98	1894.97	1894.97	0.00	280	296	0	AFDAIDINDVILGQYTK
2167.08	2166.07	2166.11	-0.03	390	409	0	IPGISTETSLTDLDLTYATR

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).



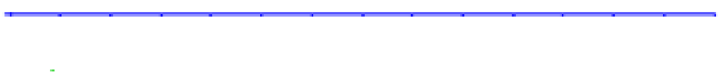
No match to:
859.56
875.51
903.57
919.54
928.54
947.59
950.51
1020.51
1046.6
1111.56
1159.63
1224.55
1246.6
1247.62
1248.62
1269.73
1298.61
1314.61
1320.58
1375.71
1386.62
1402.62
1404.67
1417.67
1428.78
1451.71
1475.75
1488.77
1514.75
1522.75

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **62**
Number of mass values matched: **17**
Sequence Coverage: **38%**

Matched peptides shown in **Bold Red**

1 MSFDSFGDYA TIVVFGASGD LAKKKTFPAL FGLFREK**QLP STVQIIGYAR**
51 **SHLEDEEFK**Q RISEHFKGGD EKTKTEFLKL VSYISGPYDT DEGYKKLESR
101 CQEYEKANKD KNDSYTPERL FYLALPPSVF TTVCEKVKKN VYPPEESKGK
151 LR**IIIEKPFG R**DLDTYREMQ K**EISPLFTED EIYR**IDHYLG KEMVKNLLVL
201 R**FGNELFSGV WNNK**HISSIQ VSFK**EAFGTE GRGGYFDTIG IIR**DVMQNHL
251 LQVLTLLTME RPVSFDPEAV RDEKVKVLK**A FDAIDINDVI LGQYTK**SEDG
301 KKPGYLDDKT VNPDSK**AVTY AAFRVNIHNE RWDGVPIVLR** AGKALDESKV
351 EIR**IQFKPVA K**GMFKEIQRN ELVIR**VQPNE AIYLK**INSKI **PGISTETSLT**
401 **DLDLTYATR**Y SK**DFWIPEAY EALIRDCYLG NHSNFVR**DDE LDVSWK**LFTP**
451 **LLNAVEDPAK** KIELQYYPYG SKGPKDLRKY LNEHGYIFSD PGTYQWPLTS
501 PNVKGKI

1537.71
1560.86
1648.84
1702.93
1917.03
1934.92
2000.99
2145.06
2168.09
2185.03
2193.05
2201.01
2309.12
2609.34
2610.32



Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 80 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 0
Number of queries : 62

Tsa1p right (IPF2431, PMF)

Match to: **CA5714|IPF2431** Score: **105**
similar to Saccharomyces cerevisiae Tsa1p thiol-specific antioxidant-like protein (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
902.53	901.52	901.53	-0.00	125	132	0	GIFLIDPK
1225.68	1224.68	1224.68	-0.01	137	147	0	QITINDLPVGR
1268.70	1267.69	1267.69	0.00	2	13	0	APVVQQPAPSFK
1562.80	1561.79	1561.80	-0.01	111	124	0	DYGVLIEEEGVALR
1670.84	1669.83	1669.84	-0.01	96	110	0	VDFPVLADTNHSLSR
1926.97	1925.96	1925.96	-0.00	15	31	0	TAVVDGVFEEVTLEQYK
2669.19	2668.19	2668.22	-0.04	165	188	0	YGEVCPANWHPGDETIKPSPEASK

No match to:
861.06
877.04
882.57
893.02
895.01
924.51
1041.53
1066.08
1082.06
1181.66
1208.66
1237.69
1247.65
1290.67
1396.8
1500.67
1545.78
1574.79
1584.79
1588.8
1600.76
1948.94
1954.93
2055.07
2112.09
2185.02
2198.09
2201.06

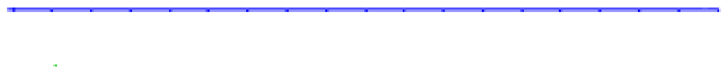
Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **35**
Number of mass values matched: **7**
Sequence Coverage: **51%**

Matched peptides shown in **Bold Red**

1 M**APVVQQPAP SFK**K**TAVVDG VFEEVTLEQY K**GKWVLLAFI PLAFTFVCPS
51 EIIAYSEAVK KFAEKDAQVL FASTDSEYTW LAWTNVARKD GGIGK**VDFPV**
101 **LADTNHSLSR DYGVLIEEEG VALRGIFLID PK**GVLR**QITI NDLPVGR**SVE
151 ESLRLLEAFQ FTEK**YGEVCP ANWHPGDETI KPSPEASK**EY FNKVNK



Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 80 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 0
Number of queries : 35

Tsa1p left (IPF2431, PMF)

Match to: **CA5714|IPF2431** Score: **59**
similar to Saccharomyces cerevisiae Tsa1p thiol-specific antioxidant-like protein (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1225.67	1224.67	1224.68	-0.02	137	147	0	QITINDLPVGR
1268.70	1267.69	1267.69	-0.00	2	13	0	APVVQQPAPSFK
1562.80	1561.79	1561.80	-0.01	111	124	0	DYGVLIEEEGVALR
1926.98	1925.97	1925.96	0.01	15	31	0	TAVVDGVFEEVTLEQYK

No match to:
861.07
871.02
877.03
879.03
881.01
887
893.01
895
908.98
1044.09
1050.11
1060.06
1066.07
1082.04
1098.02
1277.1
1293.07
2185.02
2202

Probability Based Mowse Score

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **23**
Number of mass values matched: **4**
Sequence Coverage: **27%**

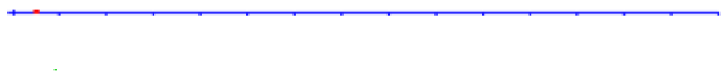
Matched peptides shown in **Bold Red**

1 M**APVVQQPAP SFK**KTAVVDG VFEEVTLEQY K**GKWVLLAFI PLAFTFVCPS

51 EIIAYSEAVK KFAEKDAQVL FASTDSEYTW LAWTNVARKD GGIGKVDFPV

101 LADTNHSLSR **DYGVLIEEEG VALR**GIFLID PKGVLR**QITI NDLPVGR**SVE

151 ESLRLLEAFQ FTEKYGEVCP ANWHPGDETI KPSPEASKEY FNKVNK



Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : MONOISOTOPIC
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 80 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 0
Number of queries : 23

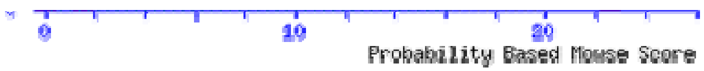
Ahp1p (IPF6629, MS/MS)

CA4127|CaIPF6629 Mass: 19360 Total score: 22 Peptides matched: 1
Putative alkyl hydroperoxide reductase (contains an AhpC or TSA family domain)

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Rank	Peptide
1	1808.8	1807.79	1807.88	-0.09	0	22	1	ELGDGFVADLTSAGMGLR

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 16 indicate peptides with significant homology (p<0.05).
Individual ions scores > 20 indicate identity or extensive homology (p<0.05).



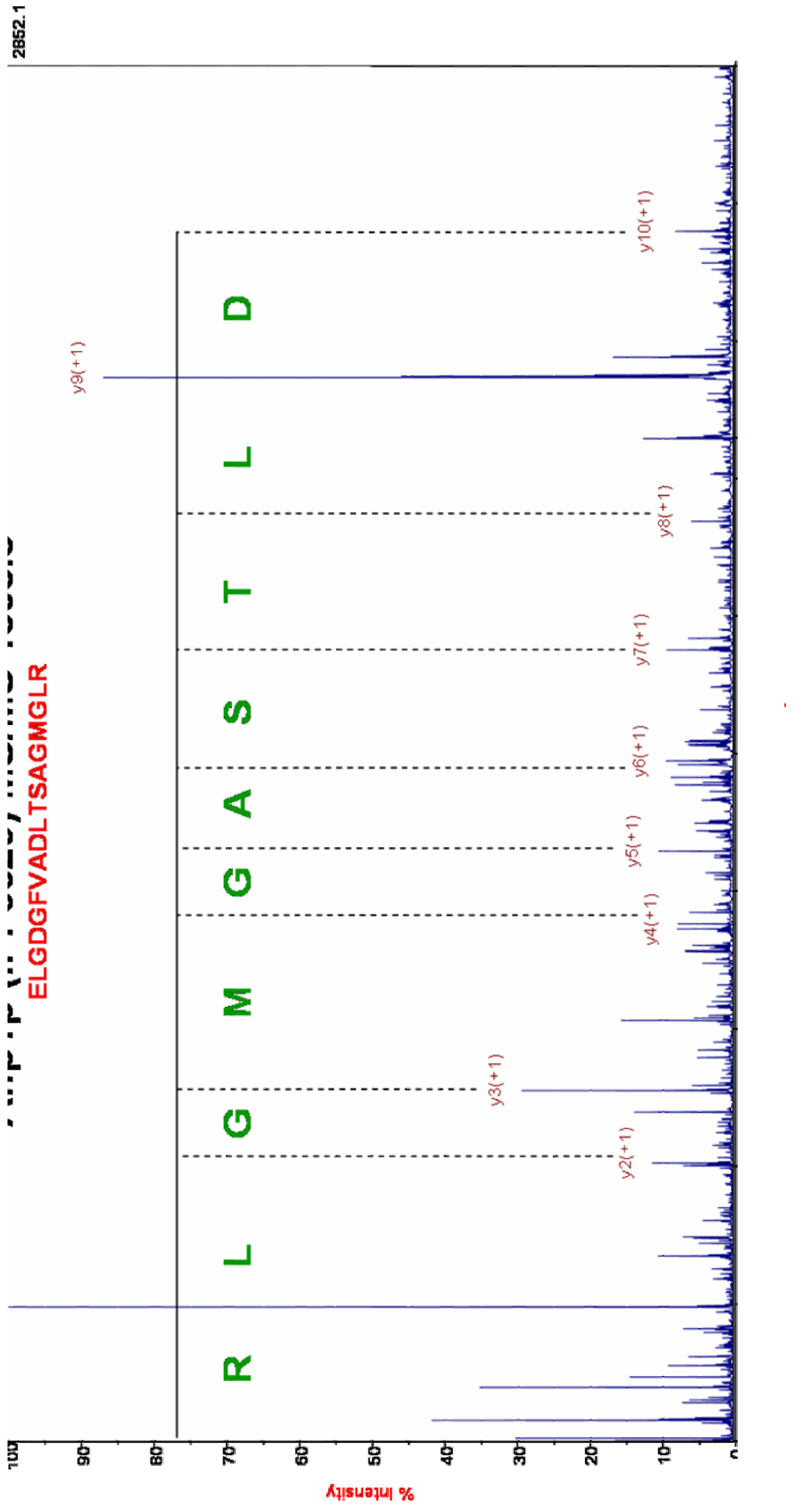
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **10%**

Matched peptides shown in **Bold Red**
1 MTDGKFPTNIEPKYIPYSKDHASLTACANPIPLDLKSLFPNNTVVVTAVP
51 GAFTPTCTEQHIPDYLKHLKDFKDKGVKKIIVLSANDPFVMAAWAKALGY
101 TDEENYVIFATDPNASISK**ELGDGFVADLTSAGMGLR**LQRYASIVVNGEI
151 TYLETEDSLGFSEISSAETILKRIHN

Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.3 Da

Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of queries : 1


2852.1
ELGDGFVADLTSAGMGLR
R
L
G
M
G
A
S
T
L
D
y2(+1)
y3(+1)
y4(+1)
y5(+1)
y6(+1)
y7(+1)
y8(+1)
y9(+1)
y10(+1)
% Intensity
0
10
20
30
40
50
60
70
80
90
100

Mxr1p (PMF)

Match to: **CA0123|CaMXR1**; Score: **70**
methionine sulfoxide reductase

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1208.7	1207.69	1207.69	0	85	94	0	LAEILDIFFK
1287.54	1286.53	1286.57	-0.04	114	124	0	SAIFTFDDEDK
1537.69	1536.68	1536.68	0	168	180	0	NSGGYECPTHFIR
1799.91	1798.9	1798.9	0.01	114	129	1	SAIFTFDDEDKSLALK
1982.01	1981	1980.99	0.01	17	33	0	LINLSAGCFWGVENVFR
2490.19	2489.18	2489.16	0.02	63	84	0	VCTGTTDYAETVQISYEPSQLK
2965.36	2964.35	2964.38	-0.03	144	167	0	IATTIETIYNWYDAEDYHQNYLTK

No match to:
767.52
771.3
773.44
783.48
801.49
811.53
817.46
827.51
855.56
857.34
883.37
889.55
899.59
915.56
933.57
943.38
943.62
959.59
977.6
987.64
996.6
1029.42
1031.67
1057.45
1075.7
1115.46
1119.73
1137.59
1141.48
1201.49

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **56**
Number of mass values matched: **7**
Sequence Coverage: **55%**

Matched peptides shown in **Bold Red**

1 MVSTISPTIL KTSTSK**LINL SAGCFWGVEN VFR**KQFTNKG LVDIKVGYAN
51 GKPSISNVTY EK**VCTGTTDY AETVQISYEP SQLKLAEILD IFFK**MHDPTT
101 VNSQGPDVGT QYR**SAIFTFD DEDKSLALK**I RDQFQKEWYP NHK**IATTIET**
151 **IYNWYDAEDY HQNYLTKNSG GYECPTHFIR** TKPKI

1217.47
1227.51
1229.53
1296.69
1303.52
1315.61
1373.57
1389.54
1401.6
1459.61
1475.76
1491.75
1545.65
1625.98
1631.68
1717.72
1827.92
3353.89
3773.96

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 56

Cof1p up (Cof1.3p, PMF)

Match to: **CA5409|CaCOF1**; Score: **71**
cofilin (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1225.65	1224.64	1224.64	-0.00	30	39	0	FVIFTLNDEK
1635.85	1634.84	1634.85	-0.01	86	99	0	IVFFTWSPDTAPVR
1782.78	1781.77	1781.78	-0.00	67	82	0	YAVYDFEYDIGGGEGK
1850.97	1849.96	1849.97	-0.01	84	99	1	SKIVFFTWSPDTAPVR
1938.88	1937.87	1937.88	-0.01	67	83	1	YAVYDFEYDIGGGEGKR
2606.22	2605.22	2605.23	-0.01	114	138	0	ALNGVAADVQGTDFSEVAYDAVHEK
2948.42	2947.41	2947.43	-0.02	114	141	1	ALNGVAADVQGTDFSEVAYDAVHEKVSR

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant ($p<0.05$).

No match to:

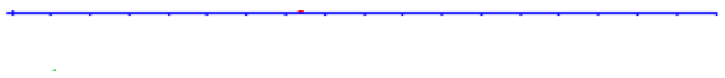
771.31
773.44
797.32
799.33
801.49
825.09
839.08
841.07
843.36
845.09
845.52
854.05
855.05
857.05
857.34
861.06
867.08
870.02
870.3
871.02
877.04
883.05
883.36
885.37
889.55
893.01
899.03
908.98
927.38
929.39
931.43
933.57
943.38
969.4
969.94
970.44
971.41
1015.43
1029.41
1050.1
1055.43
1057.44
1066.08
1072.09
1082.04
1088.06
1101.47
1115.45
1141.47
1143.48
1201.49
1217.47
1227.51
1229.51
1273.54
1287.53
1303.5
1313.54
1373.56
1389.55
1459.59
1475.22
1475.72
1545.63
1631.67
1651.84
1657.83
1667.84

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **85**
Number of mass values matched: **7**
Sequence Coverage: **49%**

Matched peptides shown in **Bold Red**

```
  1 MSFFLFFSVT VADESLTAFN DLKLGRKYKF VIFTLNDEKT QIVVEQTSTE
 51 QEYDAFLEKL PENECRYAVY DFEYDIGGGE GKRSKIVFFT WSPDTAPVRA
101 KMVYASSKDS LRRALNGVAA DVQGTDFSEV AYDAVHEKVS RGTH
```

1766.88
1960.87
1976.84
1995.91
2093.08
2163.06
2186.04
2221.16
2273.15
2763.31



Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 85

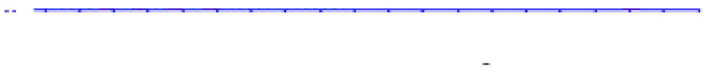
Cof1p down (Co1.3p down, PMF)

Match to: **CA5409|CaCOF1**; Score: **90**
cofilin (by homology)

Observed	**Mr(expt)**	**Mr(calc)**	**Delta**	**Start**	**End**	**Miss**	**Peptide**
1225.59	1224.58	1224.64	-0.05	30	39	0	FVIFTLNDEK
1635.81	1634.81	1634.85	-0.04	86	99	0	IVFFTWSPDTAPVR
1782.76	1781.75	1781.78	-0.03	67	82	0	YAVYDFEYDIGGGEGK
1850.95	1849.94	1849.97	-0.03	84	99	1	SKIVFFTWSPDTAPVR
1938.86	1937.85	1937.88	-0.03	67	83	1	YAVYDFEYDIGGGEGKR
2358.14	2357.13	2357.13	0	40	59	0	TQIVVEQTSTEQEYDAFLEK
2606.26	2605.26	2605.23	0.03	114	138	0	ALNGVAADVQGTDFSEVAYDAVHEK
2948.49	2947.48	2947.43	0.05	114	141	1	ALNGVAADVQGTDFSEVAYDAVHEKVSR

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).



No match to:
773.37
801.42
805.35
817.4
825.03
832.99
839.01
841.01
845.02
845.45
848.97
853.98
854.98
861
869.96
870.96
876.97
882.5
885.93
886.93
889.48
892.95
902.91
908.92
917.35
933.51
969.88
970.38
1020.44
1044.03
1046.99
1047.49
1050.04

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **73**
Number of mass values matched: **8**
Sequence Coverage: **63%**

Matched peptides shown in **Bold Red**

1 MSFFLFFSVT VADESLTAFN DLKLGRKYK**F VIFTLNDEKT QIVVEQTSTE**
51 **QEYDAFLEK**L PENECR**YAVY DFEYDIGGGE GKRSKIVFFT WSPDTAPVR**A
101 KMVYASSKDS LRR**ALNGVAA DVQGTDFSEV AYDAVHEKVS R**GTH

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 73

1060
1066.01
1081.98
1097.96
1111.5
1129.51
1153.51
1277.05
1293.03
1433.67
1474.68
1475.18
1591.8
1651.81
1657.8
1667.8
1766.85
1882.94
1894.88
1920.87
1960.86
1995.89
2093.08
2163.06
2185.05
2221.18
2225.16
2273.16
2289.18
2763.38
2952.82
3257.62

Tmp2p (PMF)

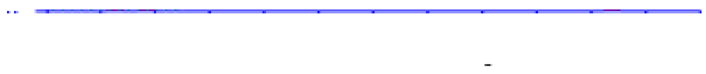
Match to: **CA5116|CaTPM2.3**; Score: **208**
Tropomyosin

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
860.49	859.48	859.48	0.01	103	109	1	LRETDVK
873.48	872.48	872.47	0	110	116	1	AEQLERK
876.48	875.47	875.47	-0.00	98	104	1	ETTEKLR
956.44	955.43	955.42	0.01	73	80	0	TSNENYTK
1046.59	1045.58	1045.57	0.01	54	62	0	LETSLNEIK
1058.56	1057.55	1057.55	-0.00	34	42	0	DNQIQALTR
1062.54	1061.53	1061.54	-0.00	16	24	1	SDELSDRIK
1084.53	1083.52	1083.52	0	73	81	1	TSNENYTKK
1086.52	1085.51	1085.5	0.02	63	72	0	EAADESHSLK
1146.58	1145.58	1145.57	0.01	7	15	1	LDAEKWQEK
1157.64	1156.63	1156.65	-0.01	2	11	1	INNLKLDAEK
1317.66	1316.65	1316.66	-0.01	105	115	1	ETDVKAEQLER
1543.76	1542.75	1542.76	-0.01	130	142	1	KFEELTETYNAAK
1545.77	1544.76	1544.72	0.04	82	94	0	NQVLEEELEEADK
1563.76	1562.75	1562.75	0	117	129	1	VASLESEKEEWEK
1673.84	1672.83	1672.82	0.02	81	94	1	KNQVLEEELEEADK
1900.94	1899.93	1899.94	-0.01	82	97	1	NQVLEEELEEADKNLK
2171.07	2170.06	2170.09	-0.02	25	42	1	ELEQENLEKDNQIQALTR
2244.13	2243.12	2243.15	-0.03	44	62	1	NQVLEEEVEKLETSLNEIK

No match to:
885.5
886.51
892.25
906.51
922.45
928.49
933.51
949.5
955.49
971.48
979.43
996.61
1059.57
1100.57
1106.52
1107.58
1123.58
1128.6
1175.57
1299.65
1329.66
1339.65
1374.68
1393.65
1445.75
1449.77
1480.73
1496.7
1586.83
1691.83

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant ($p<0.05$).

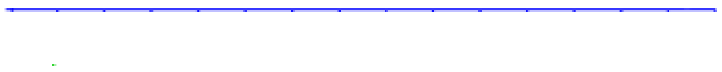


1714.93
1728.92
1771.89
1797.81
1819.94
1948.9
2029
2153.03
2175.09
2299.18
2372.23
2412.24
2489.22
2531.28
2540.35
2617.33
2758.4
2772.39
2788.43
2886.44
2986.42
3214.66
3219.56
3311.65
3331.63
3439.7

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **75**
Number of mass values matched: **19**
Sequence Coverage: **90%**

Matched peptides shown in **Bold Red**

1 M**INNLKLDAE KWQEKSDELS DRIKELEQEN LEKDNQIQAL TR**K**NQVLEEE**
51 **VEKLETSLNE IKEAADESHS LKTSNENYTK KNQVLEEELE EADKNLKETT**
101 **EKLRETDVKA EQLERKVASL ESEKEEWEKK FEELTETYNA AK**AELDEISQ
151 QLEAI



Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 75

Pmi40p (PMF)

Match to: **CA0988|CaPMI40**; Score: **70**

mannose-6-phosphate isomerase (PHOSPHOMANNOSE ISOMERASE) (PMI)(PHOSPHOHEXOMUTASE)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
868.53	867.52	867.52	0	242	248	0	LPELIQR
1017.53	1016.52	1016.51	0.01	333	340	0	MPLQEFPR
1033.52	1032.51	1032.51	0.01	333	340	0	MPLQEFPR Oxidation (M)
1119.58	1118.57	1118.57	0	228	236	1	TDREPQVFK
1120.6	1119.59	1119.6	-0.01	118	128	0	LGAQLHAADPK
1157.62	1156.62	1156.62	-0.00	61	70	0	AIDLNNQTLR
1273.67	1272.66	1272.66	-0.00	331	340	1	QKMPLQEFPR
1289.68	1288.68	1288.66	0.02	331	340	1	QKMPLQEFPR Oxidation (M)
1531.67	1530.66	1530.66	0.01	9	20	0	IQCGYQNYDWGK
1719.86	1718.85	1718.85	-0.00	209	223	1	LMNTDDDVIKQQTAK

No match to:
882.57
908.49
945.5
986.6
1040.47
1096.54
1308.66
1383.59
1396.73
1475.78
1482.76
1667.75
1705.84
1756.86
1758.88
1823.77
1866.96
1873.82
1918.01
1947.15
2222.92

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **31**
Number of mass values matched: **10**
Sequence Coverage: **16%**

Matched peptides shown in **Bold Red**

1 MSSEKLFR**IQ CGYQNYDWGK** IGSSSAVAQF VHNSDPSITI DETKPYAELW
51 MGTHPSVPSK **AIDLNNQTLR** DLVTAKPQEY LGESIITKFG SSKELPFLFK
101 VLSIEKVLSI QAHPDKK**LGA QLHAADPK**NY PDDNHKPEMA IAVTDFEGFC
151 GFKPLDQLAK TLATVPELNE IIGQELVDEF ISGIKLPAEV GSQDDVNNRK
201 LLQKVFGK**LM NTDDDVIKQQ TAK**LLER**TDR EPQVFK**DIDS R**LPELIQR**LN
251 KQFPNDIGLF CGCLLLNHVG LNKGEAMFLQ AKDPHAYISG DIIECMAASD
301 NVVRAGFTPK FKDVKNLVEM LTYSYESVEK **QKMPLQEFPR** SKGDAVKSVL
351 YDPPIAEFSV LQTIFDKSKG GKQVIEELNG PSIVIATNGK GTIQITGDDS
401 TKQKIDTGYV FFVAPGSSIE LTADSDNQDQ DFTTYRAFVE A

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 31

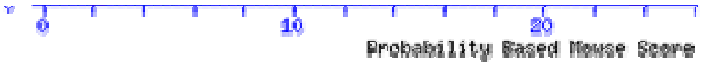
Mmd1p (MS/MS)

CA2578|CaMMD1 Mass: 13139 Total score: 24 Peptides matched: 1
Maintenance of mitochondrial DNA (by homology)

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Rank	Peptide
1	**1134.56**	**1133.55**	**1133.56**	**-0.01**	**0**	**24**	**1**	**YFSEHKPAR**

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 16 indicate peptides with significant homology (p<0.05).
Individual ions scores > 22 indicate identity or extensive homology (p<0.05).



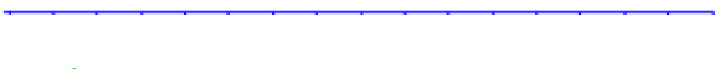
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **8%**

Matched peptides shown in **Bold Red**

1 MRLLTISSCL GFIYVSGQIP YTPDNKPLPA SATIADYAEQ AIQNVSNILE
51 ASNSSLNHIV KANIFLTDMG AQFGEFNKVY AK**YFSEHKPA R**SCVAVKELP
101 LGVPLEIEVV AIEKDDTKL

Monoisotopic mass of neutral peptide (Mr): 1133.56
Fixed modifications: Carbamidomethyl (C)
Ions Score: 24 **Matches (Bold Red):** 16/38 fragment ions using 41 most intense peaks

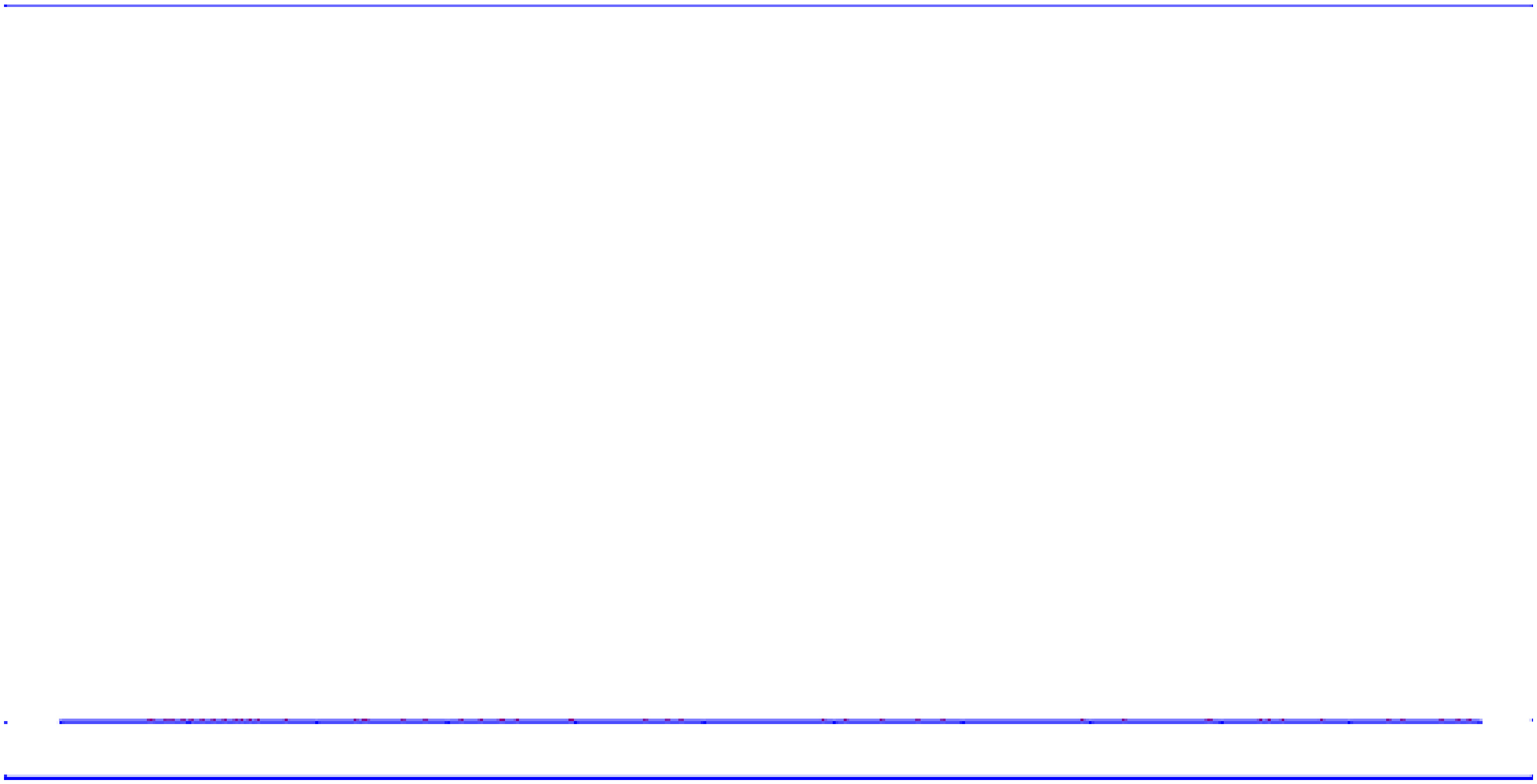
#	a	a*	b	b*	Seq.	y	y*	#
1	**136.08**		164.07		**Y**			**9**
2	**283.14**		**311.14**		**F**	971.51	954.48	**8**
3	370.18		**398.17**		**S**	**824.44**	807.41	**7**
4	499.22		527.21		**E**	737.41	720.38	**6**
5	**636.28**		**664.27**		**H**	**608.36**	**591.34**	**5**
6	764.37	747.35	**792.37**	775.34	**K**	**471.3**	**454.28**	**4**
7	861.43	844.4	**889.42**	872.39	**P**	**343.21**	**326.18**	**3**
8	932.46	915.44	960.46	943.43	**A**	246.16	229.13	**2**
9					**R**	**175.12**	158.09	**1**



Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.3 Da
Max Missed Cleavages : 1
Instrument type : Default
Number of queries : 1

MS/MS Fragmentation of **YFSEHKPAR**



YKR049p (IPF13867, MS/MS)

CA4437|CaIPF13867 Mass: 19774 Total score: 28 Peptides matched: 1
Member of the DUF1687 domain of unknown function family. Low similarity to *S. cerevisiae* FMP46p involved in oxidative stress response

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Rank	Peptide
1	**1954.89**	**1953.88**	**1953.88**	**0**	**0**	**28**	**1**	**TFSPAEYQMIYDTFNK**

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 17 indicate peptides with significant homology (p<0.05).
Individual ions scores > 22 indicate identity or extensive homology (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **9%**

Matched peptides shown in **Bold Red**

1 MSLFRSLQNS PSTISIFHNS SIPLSNKLYD ILEKAYDTQP EKPKHEFQID
51 LMKNKMPTYD QYKLIVDKYL KGSTSKTILH NCFPFLHDSK TELYNSKGNV
101 VTVKGVEWAN K**TFSPAEYQM IYDTFNK**LQE SSDQSINTIA SNVFQAPLVV
151 DWDNDVIAGD EETLKAILSK YN

Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 200 ppm
Fragment Mass Tolerance: ± 0.35 Da
Max Missed Cleavages : 1
Instrument type : MALDI-TOF-TOF
Number of queries : 1

IPF16470 (MS/MS)

Match to: **CA2002|IPF16470**; Score: **100**
Protein containing an alanine racemase N-terminal domain high similarity to uncharacterized S. cerevisiae Ybl036p

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Rank	Peptide
1	**1547.78**	**1546.77**	**1546.78**	**-0.01**	**0**	**100**	**1**	**HFGENYVQELIAK**

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 22 indicate identity or extensive homology ($p<0.05$).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Sequence Coverage: **4%**

Matched peptides shown in **Bold Red**

1 MRTILTRSIF KFRYPNIIQR TMSSTSTSTS TPSFPEPTEA RKQELITNYN
51 NTLQQVQSLN PKVNLVAVSK LKPSSDIMAL YSIGVR**HFGE NYVQELIAK**S
101 QELPNDIKWH FIGGLQSGKA KDLSKHVANL YAVETIDSLK KCKQLDNTRV
151 KVEGDDINVF LQINTSGEEQ KSGFQNLQDI ESTVEFLLSS DCKKLKFLGL
201 MTIGSFNESI SNENDKENQD FKKLVEMKQI LDSKYNLNLE LSMGMSNDFQ
251 QAIKQGSTSV RVGTTIFGSR PPSQQQK

Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Fragment Mass Tolerance: ± 0.3 Da
Max Missed Cleavages : 1
Instrument type : Default
Number of queries : 1

Dqd1p (IPF10071, PMF)

Match to: **CA0996|IPF10071**; Score: **83**
catabolic 3-dehydroquinase (by homology)

Observed	Mr(expt)	Mr(calc)	Delta	Start	End	Miss	Peptide
1506.74	1505.73	1505.73	0	112	123	1	EPFRHQSYLSDK
1606.97	1605.96	1605.96	0	5	19	0	VLLINGPNLNLLGTR
1924.95	1923.94	1923.94	-0.00	24	41	0	YGTTSLSDIEQAAIEQAK
2090.19	2089.18	2089.19	-0.01	5	23	1	VLLINGPNLNLLGTREPEK
2344.28	2343.27	2343.27	-0.00	91	111	0	DALLGTAIPFIEVHITNVHQR
2408.19	2407.18	2407.18	0	20	41	1	EPEKYGTTSLSDIEQAAIEQAK

No match to:
949.54
1065.65
1401.6
1459.61
1471.67
1475.59
1475.76
1485.63
1487.63
1503.63
1573.68
1638.87
1659.7
1675.71
1761.74
1803.75
1847.79
1890.78
1994.95
2129.12
2250.99
2269.05

Probability Based Mowse Score

Score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 50 are significant (p<0.05).

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **28**
Number of mass values matched: **6**
Sequence Coverage: **47%**

Matched peptides shown in **Bold Red**

1 MVKK**VLLING PNLNLLGTRE PEKYGTTSLS DIEQAAIEQA K**LKNNDSEVL
51 VFQSNTEGFI IDRIHEAKRQ GVGFVVINAG AYTHTSVGIR **DALLGTAIPF**
101 **IEVHITNVHQ REPFRHQSYL SDK**AVAVICG LGVYGYTAAI EYALNY

Search Parameters

Type of search : Peptide Mass Fingerprint
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Oxidation (M)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 50 ppm
Peptide Charge State : 1+
Max Missed Cleavages : 1
Number of queries : 28

a) Peptide Mass Fingerprint (PMF) type of search
b) MS/MS Ion search
*** MS-Fit search results, www.prospector.ucsf.edu**

Supplemental Table III:

Functional classification of *Candida albicans* SC5314 differentially expressed genes after macrophage interaction, in at least one of the conditions tested.

GENE ID [a)]	GENE NAME [b)]	BIOLOGICAL FUNCTION [c)]	1.5 h [d)]	3 h [d)]
METABOLISM AND ENERGY				
1- METABOLISM				
CA1084	IPF1036	Member of the CoA-transferase III family, has a region of low similarity to a region of alpha-methylacyl-CoA racemase (human AMACR), which is upregulated in prostate cancer and associated with sensory motor neuropathy and pigmentary retinopathy	2.01	1.52
CA1319	IPF3144	Protein containing a pyridoxamine 5'-phosphate oxidase domain, has low similarity to uncharacterized *Schizosaccharomyces pombe* Spac1952.08cp	0.55	
1.1 Amino-acid metabolism				
CA2570	PRO3	Member of the delta 1-pyrroline-5-carboxylate reductase (P5CR) family	0.55	1.21
CA5419	PRS1	Phosphoribosylpyrophosphate (PRPP) synthetase	0.55	0.99
CA6139	ADE2	Phosphoribosylaminoimidazole carboxylase	0.56	0.94
1.2 Nitrogen and sulfur metabolism				
CA5925	MET8	Siroheme synthase, involved in sulfate assimilation	2.42	3.92
CA5480	MET5	Similar to *Saccharomyces cerevisiae* MET4, a transcriptional activator of sulfur metabolism	1.93	1.74
CA4610	MET30	Protein with high similarity to *S. cerevisiae* Met30p, which targets proteins for ubiquitination by interacting with the SCF complex and regulates sulfur assimilation genes, contains an F-box domain and seven WD domains (WD-40 repeat)	0.65	0.55
1.3 Nucleotide metabolism				
CA2345	HNT1	Adenosine monophosphoramidase	0.52	0.49
1.5 C-compound and carbohydrate metabolism				
CA4724	PDC2	Member of the DDE superfamily endonuclease family, has low similarity to pyruvate decarboxylase regulatory protein (*S. cerevisiae* Pdc2p), which acts in metabolism	1.90	1.65
CA2697	IPF9167	Protein containing an FGGY family of carbohydrate kinases N-terminal domain, has high similarity to *S. cerevisiae* Ydr109p	0.88	0.58

CA3559	PGI1	Glucose-6-phosphate isomerase	0.78	0.57
CA4041	GAL10	UDP-glucose 4-epimerase	0.76	0.53
CA4123	AMS1	Protein with high similarity to *S. cerevisiae* Ams1p, which is an alpha-Mannosidase that hydrolyzes terminal non-reducing alpha-D-mannose residues from alpha-D-mannosides. Contains glycosyl hydrolases family 38 N- and C-terminal domains	0.69	0.46
CA6057	SOR1	Protein with high similarity to *S. cerevisiae* Sor1p, which is a sorbitol dehydrogenase (L-iditol 2-dehydrogenase). Member of the zinc-binding dehydrogenase family, which catalyze reversible oxidation of ethanol to acetaldehyde	0.67	0.48
CA4044	GAL7	UDP-glucose-hexose-1-phosphate uridylyltransferase, contains galactose-1-phosphate uridyl transferase N-terminal and C-terminal domains, which are involved in binding Zn and Fe	0.57	0.60
CA3309	PFK26	Protein containing a 6-phosphofructo-2-kinase domain, which catalyze formation and degradation of fructose-2, 6-bisphosphate, has a region of low similarity to a region of *S. cerevisiae* Pfk26p, which is 6-Phosphofructose-2-kinase	0.56	
CA4040	GAL1	Galactokinase, catalyzes the first step in galactose metabolism	0.55	
CA1593	MIG1	Transcriptional regulator of some genes whose products are involved in aspects of metabolism such as gluconeogenesis and energy generation	0.30	

1.6 Lipid, fatty-acid, isoprenoid, TCA and glyoxylate metabolism

CA4030	EBP4	Oxidoreductase with estrogen-binding properties. Has strong similarity to *Candida albicans* Ebp1p, which is an oxidoreductase with estrogen-binding properties, contains an NADH:flavin oxidoreductase or NADH oxidase family domain	3.61	3.92
CA1505	POT1	Acetyl-CoA C-acyltransferase, peroxisomal	3.03	2.45
CA5471	OAR1	Protein containing a short chain dehydrogenase domain, has low similarity to *S. cerevisiae* Oar1p, which is a 3-oxoacyl-(acyl-carrier-protein) reductase	2.51	2.23
CA1353	ERG1	Squalene epoxidase	1.35	1.90

1.7 Metabolism of vitamins. cofactors. and prosthetic groups

CA4818	PHH1	Putative protein binding (pterin 4 alpha carbinolamine dehydratase domain)	0.84	0.52
CA5655	IPF18080	Protein possibly involved in pantothenate biosynthesis	0.83	0.57
CA4773	IPF3340	Similar to *S. cerevisiae* YDR196c, a protein of unknown function localised to ER involved in biosynthesis of vitamins, cofactors, and prosthetic groups	0.53	
CA0054	RIB4	6,7-dimethyl-8-ribityllumazine synthase	0.46	

INFORMATION PATHWAYS

2- CELL CYCLE AND DNA PROCESSING

CA1799	HOP2	Protein similar to *S. cerevisiae* Hop2p, required with Mnd1p in meiosis for pairing of homologous chromosomes and double stranded break repair	3.03	
CA5743	SLD3	Similar to *S. cerevisiae* Sld3p, an essential protein that may be involved in DNA replication through its association with Cdc45p	1.97	5.15
CA3393	IPF6748	Similar to *S. cerevisiae* Far3p, protein involved in G1 cell cycle arrest in response to pheromone, in a pathway different from the Far1p-dependent pathway	1.92	1.48
CA5226	RIM15	Protein kinase involved in the RIM pathway	0.82	0.54
CA3411	CLG1	Putative cyclin dependent protein kinase regulator	0.72	0.51
CA0440	IPF12473	Similar to *S. cerevisiae* Src1p, protein that may play a role in anaphase sister chromatid separation, expression is cell cycle-regulated	0.53	
CA0748	TFS1	Similar to *S. cerevisiae* Tfs1p, a cdc25-dependent nutrient- and ammonia-response cell-cycle regulator	0.53	0.56
CA4698	CDC25	Guanine nucleotide-releasing factor, cdc25-dependent nutrient- and ammonia-response cell-cycle regulator (involved in filamentous growth)	0.53	
CA5353	IML2	Protein with moderate similarity to *S. cerevisiae* Iml2p, which has a role in stability of artificial minichromosomes	0.49	
CA0526	BUB3	Cell cycle arrest protein	0.41	0.40

3- TRANSCRIPTION

3.1 RNA synthesis

CA1993	IPF6614	Putative Glycine tRNA ligase	2.53	3.43
CA5222	PTA1	Similar to *S. cerevisiae* Pta1p pre-tRNA processing protein	2.18	1.13
CA1717	HAP6	Protein containing a histone-like transcription factor (CBF or NF-Y) and archaeal histone domain. Has a region of high similarity to a region of component of *S. cerevisiae* Hap3p, which is a component of heterotrimeric CCAAT-binding factor	2.10	1.98
CA5491	MIG2	Protein containing two zinc finger C2H2 type repeats, which bind nucleic acids. Has moderate similarity to a region of *Aspergillus niger* CreA, which is a carbon catabolite transcriptional repressor	1.78	
CA5237	ZMS1	Protein containing a Zinc finger C2H2 type repeat, has low similarity to *S. cerevisiae* Zms1p, which positively regulates the expression of *S. cerevisiae* Gut1p, S. cerevisiae Gut2p and *S. cerevisiae* Atp9p and is required for normal growth on glycerol	0.48	0.33
CA3639	IPF9251	Putative transcription factor: fungal Zn2 Cys2 cluster domain	0.43	0.34

3.2 RNA processing

CA5883	SLU7	Protein with low similarity to *S. cerevisiae* Slu7p, which is a pre-mRNA splicing factor affecting 3' splice site choice and required for the second catalytic step of splicing	3.16	2.66
CA0758	PAP11	Poly(A) polymerase by homology to *S. cerevisiae*	3.02	1.00
CA1438	NOP58	Nucleolar protein required for pre-18S rRNA processing	2.82	1.41
CA4567	SEN34	Putative tRNA splicing factor. Similar to *S. cerevisiae* SEN34, a tRNA splicing endonuclease gamma subunit	2.10	2.30
CA2546	RPC31	DNA-directed RNA polymerase III, 5-prime end (by homology)	2.08	1.55
CA2071	IPF6971	Internal fragment ,nuclear mRNA splicing via spliceosome by homology with LSM7 Sm-like (Lsm) protein	1.91	4.59
CA0923	ERB1	Similar to *S. cerevisiae* Erb1p, a protein required for maturation of the 25S and 5.8S ribosomal RNAs	1.85	3.15
CA1998	IPF6605	Similar to *S. cerevisiae* Trm82p, a protein required for 7-methylguanosine modification of yeast tRNA	1.83	
CA0098	IPF16479	Putative RNA binding	1.58	1.76
CA2167	IPF4553	Putative transcription factor	0.60	0.47
CA6154	SNU13	Similar to *S. cerevisiae* Snu13p U4/U6.U5 snRNP associated protein	0.57	
CA2094	YTH2	Member of the zinc finger C-x8-C-x5-C-x3-H type family, which bind DNA or RNA	0.56	0.90
CA2323	SMD2	U1 snRNP protein of the Sm class protein (by homology), involved in nuclear mRNA splicing, via spliceosome	0.53	

4- PROTEIN SYNTHESIS

4.1- Ribosome biogenesis

CA0908	MRPL31	Mitochondrial ribosomal protein	3.71	1.59
CA1941	RLP24	Member of the ribosomal L24e family, which are part of the large ribosomal subunit. Has moderate similarity to *Caenorhabditis elegans* RPL-24.2, which is involved in larval development	1.85	1.41
CA4307	IPF20013	Protein containing a calcineurin-like phosphoesterase domain, has low similarity to uncharacterized *S. cerevisiae* Ynl217p, which may be involved in protein biosynthesis	1.76	1.49
CA3009	MRPL19	Ribosomal protein	1.75	1.52
CA1770	NSA1	Putative binding protein	1.55	1.76
CA4588	BEL1	Protein of the 40S ribosomal subunit	1.14	1.75
CA1629	NPI46	Proline cis-trans isomerase	0.85	1.75
CA4785	RSM7	Protein containing a ribosomal S7p or S5e domain, which are present in the small ribosomal subunit. Has moderate similarity to uncharacterized *S. cerevisiae* Rsm7p, which is a putative mitochondrial ribosomal protein S7	0.52	

4.2 Translation

4.2.1 Translation initiation

CA3016	CDC332	Protein containing an eukaryotic initiation factor 4E domain, has a region of low similarity to a region of *C. elegans* IFE-4, which binds to the mRNA cap structure	1.80	1.17
CA0667	TIF5	Translation initiation factor eIF5	0.56	1.23

5- PROTEIN FATE

5.1 Protein folding and stabilization

CA4684	HSP78.5f	Heat shock protein of clpb family of ATP-dependent proteases, mitochondrial, 5-prime end	0.77	0.47
CA0265	STI1	Stress-induced protein	0.70	0.50
CA1230	SSA4	Heat shock protein 70	0.58	0.49
CA4683	HSP78.3f	Heat shock protein of clpb family of ATP-dependent proteases, mitochondrial, 3-prime end	0.58	0.34
CA2076	ERO1	Required for protein disulfide bond formation in the ER	0.54	

5.2 Protein targeting. sorting and translocation

CA2009	IPF1732	Putative Phenylalanyl-tRNA synthetase (intramitochondrial protein sorting)	0.53	0.51

5.3 Protein modification and degradation

CA1287	IPF5545	Member of the UBX (ubiquitin-regulatory) domain containing family, similar to *S. cerevisiae* Ubx5p, which may be involved in proteasome function	1.94	1.35
CA1950	JIP5	Putative nucleolar protein, possibly involved in modification by ubiquitination/deubiquitination	0.87	1.95
CA2854	RPN4	26S proteasome subunit	0.70	0.51
CA1288	KSP1	Serine/threonine protein kinase	0.69	0.45
CA4806	IPF1155	Putative dipeptidase	0.66	0.52
CA1988	IPF19749	Low similarity to C. glabrata *CAGL0F03311g* with high similarity to S. cerevisiae Ksp1p, which is a serine/threonine kinase that suppresses prp20 mutant when overproduced, involved in protein modification	0.64	0.52
CA5565	QRI8	E2 ubiquitin-conjugation enzyme	0.58	0.87
CA3786	UFD1	Ubiquitin fusion degradation protein	0.57	
CA0724	IPF13398	Putative protein kinase	0.54	0.39
CA3818	IPF6695	Member of the peptidase family M49, has moderate similarity to dipeptidylpeptidase III (human DPP3)	0.51	
CA0663	PUP2	20S proteasome subunit (alpha5)	0.46	0.90

5.4 Assembly of protein complexes

CA4218	ACP1	Protein with high similarity to *S. cerevisiae* Acp1p, which is an acyl carrier protein and component of mitochondrial type II fatty acid synthase. Contains a phosphopantetheine attachment site domain	0.92	0.55
CA6049	IPF4935	Putative cytochrome oxidase assembly factor (by homology)	1.12	0.48

6- PROTEIN WITH BINDING FUNCTION OR COFACTOR REQUIREMENT

6.2Nucleic acid binding

CA1714	NAB2	Nuclear poly(A)-RNA-binding protein	2.04	
CA2359	IPF8952	Similar to *S. cerevisiae* Rpa34p nonessential component of RNA-polI	1.07	1.85
CA0684	IPF4450	Member of the type 1 reverse transcriptase (RNA-dependent DNA polymerase) family	0.77	0.45
CA2146	IPF12799	Protein containing a ZZ zinc finger	0.72	0.52
CA0277	RNH1	Protein containing two RNase H domains, has a region of low similarity to ribonuclease H1 (human RNASEH1), which binds to double stranded RNA and DNA-RNA hybrids and degrades the RNA strand of DNA-RNA hybrids	0.54	0.74

7- CELLULAR TRANSPORT, TRANSPORT FACILITATION AND TRANSPORT ROUTES

7.1 Transported compounds

7.1.1 Ion transport

CA3615	GIT1	Glycerophosphoinositol transporter. Has high similarity to *S. cerevisiae* Git1p, which is a protein involved in inositol metabolism and possibly inorganic phosphate transporter	3.22	2.69
CA4886	PHO83	Member of the major facilitator superfamily and the sugar (and other) transporter family, has weak similarity to a region of mouse Slc22a6, which mediates the exchange of organic anions, dicarboxylate, and para-aminohippurate	2.18	3.09
CA5160	PHO89	Na+-coupled phosphate transport	1.28	2.83
CA1365	IPF11849	Protein containing a globin domain, has a region of moderate similarity to a region of *S. cerevisiae* Ynl234p, which is a hemoprotein involved in the nitrogen starvation response, heat shock response and osmotic response. Putative oxygen transporter activity	1.80	
CA1645	PMC1	Ca2+-transporting P-type ATPase, involved in sensitivity to fluconazole	1.28	1.75

7.1.2 C-compound and carbohydrate transport

CA3414	HXT1	Putative low-affinity glucose permease, involved in calcium ion transport, by homology with *S. cerevisiae* HXT11	2.32	2.04
CA3161	MCH	Member of the major facilitator super-family, similar to monocarboxylate transporter homolog 5 (*S. cerevisiae* MCH5)	1.84	1.26
CA1070	HXT61	High-affinity hexose transporter, by homology with *S. cerevisiae* HXT6	1.13	0.53
CA0783	ACR1	Protein with high similarity to *S. cerevisiae* Sfc1p, which is a mitochondrial membrane succinate-fumarate transporter, member of the mitochondrial carrier protein family of membrane transporters	0.57	1.00

7.1.3 Amino acid transport

CA3387	MUP3	Very low affinity methionine permease	2.53	1.11
CA5039	GAP2	General amino acid permease	1.99	

7.1.4 Drug/Lipid transport

CA5225	ACB1	Protein with high similarity to acyl-coenzyme-A binding protein. Transports newly synthesized acyl-CoA esters from fatty acid synthetase (Fas1p-Fas2p) to acyl-CoA-consuming processes	1.73	3.43
CA3895	CDR4	Multidrug resistance protein	0.76	0.56
CA0785	IPF14603	Member of the scramblase family which are involved in the redistribution of phospholipids after cell activation or injury, has high similarity to uncharacterized *S. cerevisiae* Yjr100p	0.53	0.71

7.1.5 Electron transport

CA2631	NUO1	Protein with high similarity to Fe-S subunit of the NADH-ubiquinone oxidoreductase complex I (human NDUFS8), which an iron-sulfur electron transfer carrier that is associated with Leigh's syndrome, contains two iron-sulfur cluster (4Fe-4S) binding domains	0.49	

7.1.6 Vitamin/Cofactor transport

CA5295	IPF1954	Protein with similarity to *S. cerevisiae* Tna1p, which is a nicotinic acid permease	3.64	3.89

7.2 Transport facilitation

7.2.1 ABC Transporters

CA4190	IPF7530	ATP-binding-cassette protein (by homology to *A.gambiae*)	0.46	0.25

7.3 Transport routes

7.3.1 Non-vesicular ER transport

CA1072	SBH1	Protein involved in translocation into the ER	3.33	2.43
CA5881	SSS1	ER protein-translocase complex subunit	2.70	2.64

7.3.2 Vesicular transport (Golgi network. etc.)

CA5433	SFT1	SNARE-like protein	2.35	2.97
CA1697	IPF16758	ER to Golgi vesicle-mediated transport by homology with *S. cerevisiae* RUD3, a Golgi matrix protein involved in the structural organization of the cis-Golgi	1.94	0.99
CA0830	APL5	AP-3 complex subunit, gamma-adaptin	1.16	0.57
CA0483	SEC9	Transport protein	0.54	0.71
CA5142	IPF1022	Similar to *S. cerevisiae* Erv29p ER-Golgi transport vesicle protein	0.46	0.40

7.3.3 Vacuolar transport

CA0982	VPS62	Protein with high similarity to *S. cerevisiae* Vps62p, which is a class F vacuolar protein sorting protein involved in the Saccharomyces cerevisiae Prc1p vacuolar trafficking pathway	0.66	0.56

7.3.5 Cellular import: Endocytosis

CA5534	SCD5	Similar to *S. cerevisiae* SCD5, a suppressor of clathrin deficiency 5.	1.82	2.26

PERCEPTION AND RESPONSE TO STIMULI

8- CELLULAR COMMUNICATION/SIGNAL TRANSDUCTION MECHANISM

8.1 cAMP mediated signal transduction

CA4205	FGR38	Filamentous Growth Regulator, involved in G-protein signaling, coupled to cAMP nucleotide second messenger with adenylate cyclase activity. Similar to*S. cerevisiae* Cyr1p (adenylate cyclase)	1.49	2.07
CA4137	PDE1	Low-affinity cyclic nucleotide phosphodiesterase	0.47	

9- CELL RESCUE DEFENSE AND VIRULENCE

9.1 Stress response

CA5764	PSR2	Similar to *S. cerevisiae* Psr2p plasma membrane phosphatase required for sodium stress response	2.61	1.89
CA0358	IPF17488.5f	Similar to *S. cerevisiae* SPT23, a dosage-dependent suppressor of Ty-induced promotor mutations, involved in cold shock response	2.10	2.04
CA0386	IPF4065	Possible stress protein	1.90	1.19
CA1673	PST2	1,4-benzoquinone reductase	1.02	0.52
CA4018	MOG1	Similar to *S. cerevisiae* MOG1, a multicopy suppressor of gsp1, involved in nuclear protein import, interacts with Gsp1p, Sln1p, Ypd1p and Skn7p, plays a role in osmoregulation by activating SLN1-SKN7 signal transduction, nuclear localization of Skn7p and osmotic response gene expression	0.79	0.53

9.1.1 Oxidative stress response and Detoxification

CA4884	ALK6	N-alkane inducible cytochrome P-450, involucrated in detoxification involving cytochrome P450	5.61	2.35
CA2687	IFU6.3f	Putative ortholog of *S. cerevisiae* Gre2p, (by homology with *C. albicans* IFU6.5f) which is a Methylglyoxal reductase (NADPH-dependent). Putative Dihydrokgempferol-4-reductase possibly involved in detoxification by modification	3.21	2.72
CA0772	UGA11.exon2	4-aminobutyrate aminotransferase, exon 2 (by homology)	2.17	2.29
CA1039	BOP1	Strong similarity to *S. cerevisiae* hypothetical protein YPL221w. Protein involved in outer chain mannosylation and detoxification	1.87	1.12
CA2190	AOX1	Alternative oxidase	1.79	1.14
CA0559	GPX1	Glutathione peroxidase	0.64	0.38
CA2659	NDH2	NADH dehydrogenase	0.58	
CA1564	GAD1	Glutamate decarboxylase	0.58	0.39
CA0971	AHP2	Similar to *S. cerevisiae* Ahp1p which is an alkyl hydroperoxide reductase	0.57	
CA4437	YKR049	Member of the DUF1687 domain of unknown function family. Similar to *S. cerevisiae* FMP46, which is a putative redox protein containing a thioredoxin fold	0.53	0.68
CA6010	TRX1	Thioredoxin	0.54	0.76

9.1.2 DNA damage repair

CA2827	RAD2	Structure-specific nuclease of the nucleotide excision repairosome	2.11	1.10
CA2114	PSY2	Similar to *S. cerevisiae* Platinum sensitivity 2 (Psy2p), a member of the Protein Phosphatase 4 cisplatin sensitive complex (PP4cs) involved in DNA repair and the histone H2A phosphatase complex (HTP-C) required to exit the DNA damage checkpoint	1.98	1.13
CA4273	CAC2	Similar to *S. cerevisiae* Cac2p, chromatin assembly complex subunit 2, likely to associate with PCNA (Pol30p), functions in nucleosome assembly linked with DNA replication and in double-strand DNA break repair	1.78	1.31
CA5485	RAD1.53f	Member of the ERCC4 domain family, has moderate similarity to *S. cerevisiae* Rad1p, which is a component of the nucleotide excision repairosome	1.33	2.25

9.2 Disease, virulence and defense

9.2.1 Pathogenesis

CA0744	IPF14919	Similar to *C. albicans* mucin protein (by homology with *C. albicans* IPF14282)	2.71	
CA0541	IPF14574	Protein containing a DUF814 domain of unknown function, which are found in putative fibronectin or fibrinogen binding protein	1.88	2.63
CA5713	ALS6	Agglutinin-like protein	1.84	2.10
CA0448	ALS10	Agglutinin-like protein	1.80	1.11
CA1619	MIT1	Protein required for mannosylation of inositol phosphoceramide (IPC) and production of phospholipomannan, involved in evasion of host defense response	0.54	
CA5613	IPF525	Low similarity to human estrogen responsive finger protein	0.79	0.53

9.2.2 Response to toxins

CA3606	RTA3	Member of the RTA1-like protein family, which may be involved with response to toxin. Has strong similarity to uncharacterized *C. albicans* Rta4p which has a region of moderate similarity to *S. cerevisiae* Rsb1p, which is a likely long-chain base (LCB) flippase that releases sphingoid LCBs from the cytoplasm to the medium	0.75	0.56

10- INTERACTION WITH THE CELLULAR ENVIRONMENT

10.1 Metal ion homeostasis

CA5884	SLF1	Copper homeostasis protein	2.69	1.14
CA3415	FRE30.53	Member of the ferric reductase like transmembrane component family, which may bind FAD and move electrons across the plasma membrane, internal fragment. Has strong similarity to *S. cerevisiae* ferric reductase Fre2p and *C. albicans* Fre10p	1.76	1.07
CA3416	FRE30.3	Member of the ferric reductase like transmembrane component family, which may bind FAD and move electrons across the plasma membrane, 5-prime end fragment. Has strong similarity to *S. cerevisiae* ferric reductase Fre2p and *C. albicans* Fre10p	1.75	1.55

DEVELOPMENTAL PROCESSES

11- CELL FATE: CELL DEATH

11.1 Apoptosis

CA2984	IPF12606.3eoc	Putative serine protease. Possibly involved in promoting apoptosis following heat shock or exposure to hydrogen peroxide, by homolgy with *S. cerevisiae* NMA111	3.54 /3.16[e)]	2.77/6.25

11.2 Aging

CA5232	SUN42	Putative cell wall beta-glucosidase with high homology to *S. cerevisiae* Uth1p involved in aging process and determination of life span and viability upon starvation as well as autophagy	0.52/0.07	0.64/1.82
CA0183	CAP1	Transcriptional activator involved in oxidative stress response and aging	0.52	

12- BIOGENESIS OF CELLULAR COMPONENTS

12.1 Cell wall

CA5400	KRE62.3f	Glucan synthase subunit, 3-prime end (by homology with *S. cerevisiae* Kre6p)	2.61	2.01
CA1905	PIR32	Putative structural constituent of cell wall	2.15	
CA4245	PGA21	Putative cell wall protein. Similar to *S. cerevisiae* Tip1p, a major cell wall mannoprotein with possible lipase activity	2.11	1.39
CA0788	IPF14107	Similar to *S. cerevisiae* DAN4, a member of the seripauperin and TIP1 family. Has low similarity to cell surface flocculin (S. cerevisiae Muc1p), which is required for invasive and pseudohyphal growth	2.12	1.65
CA3642	PGA19	Putative GPI-anchored protein	1.97	2.04
CA4679	PGA17	Putative GPI-anchored protein	1.96	1.17
CA5936	SLK19	Lysine/glutamic acid-rich protein involved in cell wall biogenesis and organization and required for normal virulence	0.76	0.49
CA4894	IPF1617	Low similarity to *S. cerevisiae* Ecm13p, a protein possibly involved in cell wall structure or biosynthesis	0.68	0.56
CA3706	PSA2	Member of the nucleotidyl transferase family, similar to *C. albicans* Psa1p, a Mannose-1-phosphate guanyltransferase	0.57	0.44
CA4577	MKK2	Protein kinase of MEK, similat to *S. cerevisiae* MKK1, a serine/threonine protein kinase involved in cell wall integrity pathway	0.53	

12.2 Actin cytoskeleton

CA0623	MSS4	Phosphatidylinositol-4-phosphate 5-kinase. Has high homology to *S.cerevisiae* Mss4p that is a multicopy suppressor of Stt4 mutation 4, a phosphatidylinositol-4-phosphate 5-kinase that is required for proper organization of the actin cytoskeleton	0.53	

12.3 Mitochondrion

CA2016	YIM1	Similar to *S. cerevisiae* Yim1p mitochondrial inner membrane protease	0.55	
CA1779	MDM34	Possible essential for maintaining wild-type mitochondrial morphology (by homology)	0.73	0.42

13- CELL TYPE DIFFERENTIATION

13.1 fungal cell type differentiation

CA1610	LAS1	Protein involved in cell morphogenesis, cytoskeletal regulation and bud formation	3.76	2.48
CA4027	IPF7174	Protein with moderate similarity to uncharacterized *S. cerevisiae* Rdi1p a small GTPase mediated signal transduction. Possibly involved in budding, cell polarity and filament formation	2.28	
CA1402	ECE1	Cell Elongation Protein	2.21	0.95
CA1621	HYR10	Protein with low similarity to *C. albicans* Hyr1p, which is a hyphal-specific cell wall protein	2.20	1.21
CA5780	IPF1123	Protein with high similarity to *S. cerevisiae* TGL4, a Triacylglycerol lipase 4 involved in spore wall assembly	1.22	0.55
CA4193	IPF7535	Member of the UBX (ubiquitin-regulatory) domain containing family, has low similarity to *S. cerevisiae* Ubx7p, which is involved in tetrad formation	0.67	0.50
CA5425	BDF1	Sporulation protein	0.54	0.71

EXPERIMENTALLY UNCHARACTERIZED GENES[f]

CA4032	IPF11081	Unknown function	4.21	2.59
CA4229	IPF12480.5*	Protein containing a DUF699 putative ATPase domain, has high similarity to *S. cerevisiae* Kre33p	3.74	3.30
CA3276	IPF6263	Unknown function	3.52	5.21
CA3216	IPF13038*	Unknown function, similar to *S. cerevisiae* YKL018C-A	3.50	2.06
CA4334	IPF2082*	Unknown function, similar to *S. cerevisiae* Sge1p , a crystal violet resistance protein	3.14	1.15
CA3142	IPF9211.5f	Unknown function, 3-prime end	2.95	1.75
CA2152	IPF7899	Member of the PCI (proteasome. COP9-complex and eIF3) or PINT (Proteasome. Int-6. Nip-1 and TRIP-15) domain containing family	2.94	1.42
CA3125	IPF8921.5eoc	Unknown function, 5-prime end	2.93	4.29
CA5458	IPF274	Unknown function	2.90	3.80
CA0167	IPF19160	Unknown function	2.84	2.59
CA0644	IPF17131	Unknown function	2.82	0.89
CA5192	HOK	Unknown function	2.77	4.43
CA1898	IPF11998*	Unknown function, similar to *S. cerevisiae* Ccw12p, a cell wall mannoprotein	2.72	1.87
CA4851	IPF5818	Unknown function	2.68	3.53
CA2983	IPF18396	Unknown function	2.51	3.77

CA5408	IPF1551*	Unknown function, similar to *S. cerevisiae* UIP4	2.48	2.65
CA4590	IPF2218*	Unknown function, similar to *S. cerevisiae* YDL156w, a protein of unknown function localised to cytoplasm and nucleus	2.48	2.01
CA3810	IPF9230*	Unknown function, similar to *S. cerevisiae* Ste3p pheromone a-factor receptor	2.42	2.08
CA3232	IPF17727.3	Unknown function, 3-prime end	2.41	1.98
CA3644	IPF4126*	Unknown function, similar to *S. cerevisiae* NEO1, a P-type ATPase, a proposed aminophospholipid translocase	2.34	1.77
CA0193	IPF6493*	Unknown function, contains a globin domain and has homology to *S. cerevisiae* YNL234W, an hemoprotein with similarity to mammalian globins	2.21	0.92
CA0611	IPF17542	Unknown function	2.18	1.17
CA6120	IPF132*	Unknown function, similar to *S. cerevisiae* Nup42p, which is a nuclear pore protein involved in the nuclear export of heat shock mRNAs	2.17	
CA0589	IPF13080*	Unknown function, similar to *S. cerevisiae* YJR112w-a, a conserved hypothetical protein	2.17	
CA3910	IPF3293*	Unknown function, similar to *S. cerevisiae* Dem1p, a protein of unknown function localised to mitochondria	2.16	
CA4121	IPF7081	Unknown function	2.08	2.04
CA0683	IPF14519.5f	Unknown function	2.08	1.30
CA3712	IPF7891	Unknown function	2.03	
CA3972	IPF6504*	Unknown function, similar to *S. cerevisiae* Bug1p,a protein of unknown function localised to golgi-ER transport vesicles	1.84	
CA0085	IPF16201	Unknown function	1.83	1.35
CA5133	IPF5129	Unknown function	1.82	3.74
CA3585	IFT1	Unknown function	1.80	2.49
CA5624	IPF501*	Protein of unknown function, similar to uncharacterized *S. cerevisiae* Ycl002p	1.80	0.99
CA4825	IPF1205	Unknown function	1.79	
CA3108	IPF11826*	Unknown function, similar to *S. cerevisiae* YOR228c, a protein of unknown function localised to mitochondria	1.75	1.41
CA3533	IPF13450	Unknown function	1.50	1.98
CA5912	IPF5966	Unknown function	1.46	1.77
CA4673	MPU1	Protein of unknown function, has low similarity to uncharacterized *Cryptococcus neoformans* Cnj02700_D	1.18	1.75
CA3999	IPF10447*	Unknown function, similar to *S. cerevisiae* YBR204c, a protein with similarity to serine-active lipases, localized to lipid droplets	1.13	0.54
CA0273	IPF19066*	Protein containing an alpha or beta hydrolase fold domain, has similarity to *S. cerevisiae* Yor084w, a peroxisomal matrix protein of unknown molecular function	0.64	0.55
CA5603	IPF553*	Member of the fasciclin domain family, has similarity to uncharacterized *S. cerevisiae* Ylr001p	1.04	0.57

CA1882	IPF19934	Unknown function	0.95	0.55
CA0815	IPF16231	Unknown function	0.92	0.51
CA0670	YKR70*	Unknown function, similar to *S. cerevisiae* YKR070w, a protein of unknown function localised to mitochondria	0.92	0.58
CA3986	XJP6	Unknown function	0.90	0.52
CA1098	IPF12316*	Unknown function, similar to *S. cerevisiae* Sae3p, a protein involved in sporulation in the absence of Spo11p, functions with Mei5p and Dmc1p during meiotic recombination	0.82	0.43
CA4081	IPF2523	Member of the bacterial domain of unknown function (DUF377) containing family	0.73	0.52
CA4951	IPF13607*	Member of the DUF1212 domain of unknown function family, which may be membrane proteins, has high similarity to *S. cerevisiae* Pmr10p, a protein regulated by alpha factor	0.72	0.58
CA1235	IPF20079*	Unknown function, similar to *S. cerevisiae* YMR074c, a protein of unknown function localised to cytoplasm and nucleus	0.71	0.47
CA0005	MPM1*	Unknown function, similar to *S. cerevisiae* Mpm1p, a mitochondrial membrane protein	0.70	0.27
CA4735	IPF7726*	Unknown function, similar to *S. cerevisiae* YPL260w, a protein of unknown function localised to cytoplasm and nucleus	0.68	0.55
CA4220	IPF8762	Unknown function	0.62	0.39
CA3268	RPS620b	Unknown function, similar to *C. albicans* RPS620a/Mrs107p	0.61	0.58
CA2547	IPF14911*	Protein containing a C2 domain, similar to *S. cerevisiae* YNL152w, a protein which may be involved in calcium-dependent phospholipid binding	0.58	0.70
CA5535	IPF2839	Member of the SPFH domain or Band 7 family, which may regulate cation conductance, has low similarity to a region of *C. elegans* MEC-2, which is a protein required for chemotaxis and function of touch receptors	0.57	0.46
CA3132	IPF8904*	Protein with unknown function that contains a SWIRM domain, has moderate similarity to *S. cerevisiae* Yor338p	0.57	0.36
CA0086	IPF16598*	Member of the phospholipid and glycerol acyltransferase family, has moderate similarity to *S. cerevisiae* Ybr042p	0.56	1.03
CA1223	IPF14870*	Unknown function, similar to *S. cerevisiae* YCL045c, a protein of unknown function localised to ER	0.56	0.75
CA6160	IPF1835	Unknown function	0.55	0.98
CA4787	IPF3364	Unknown function	0.54	
CA4637	IPF1514	Unknown function	0.50	
CA2021	IPF17283*	Unknown function, similar to *S. cerevisiae* YCR062w, a protein that may be involved in response to heat and high salinity	0.50	0.46
CA0782	IPF16253	Protein containing an RNA recognition motif (RRM. RBD. or RNP)	0.50	0.65
CA6094	IPF53*	Protein of unknown function, has moderate similarity to uncharacterized *S. cerevisiae* Ydl193p, which is a protein of unknown function that associates with lipid particles and with the endoplasmic reticulum	0.44	

CA4560	IPF8038*	Unknown function, similar to *S. cerevisiae* YMR124w, a protein of unknown function localised to bud	0.48
CA3078	IPF19970*	Member of the N2227-like protein family, which may be involved in stress response, similar to *S. cerevisiae* YMR209c, a protein of unknown function localised to cytoplasm	0.45
CA5924	IPF2822	Unknown function	0.42
CA4529	IPF4395*	Member of the DUF962 domain of unknown function family, homology with *S. cerevisiae* YGL010w, a protein of unknown function localised to ER	0.28

a) Gene ID according to CandidaDB (http://www.genolist.pasteur.fr/CandidaDB) database

b) Gene name according to MycopathPD (Proteome Bioknowledge Library, https://www.proteome.com/control/tools/proteome) database

c) Gene functions were assigned as described under "Experimental Procedures"

d)The average expression ratio from four different microarray experiments, using two biological samples and dye-swapping is shown. Values >1.75 signify that the genes were up-regulated in treated yeast cells (exposed to macrophages) compared to control yeast cells; values < 0.57 signify that the genes were down-regulated in treated yeast cells compared to control yeast cells.

e) Red values represents RT-PCR results (data not shown)

f) Asterisks denote differentially expressed unknown genes employed in the networks analyses (see Supplemental Fig. 4*A* and 4*B*)

Supplementary Table IV
Evidence of functional enrichment in the genomic and proteomic datasets.

(Created using FunSpec)

The p-values represent the probability that the intersection of a given list with any given functional category occurs by chance.

MIPS Functional Classification of up-regulated genes (259 categories)

Category	p-value	Proteins in category	K (number identified)	F (total assigned)
TRANSPORT FACILITATION	0.0002541	PHO89 GIT1 SSS1 SBH1 PMC1 MUP3 HXT1 YIL166C GAP1 PHO84 MCH5 SGE1	12	312
SUBCELLULAR LOCALISATION	0.0004763	PTA1 SEN34 HAP3 TIP1 GRS1 GIT1 RDI1 PDC2 SSS1 SLU7 SBH1 PMC1 HOP2 NAB2 ERG1 RAD2 MUP3 HXT1 POT1 CYR1 RPA34 SAG1 DAN4 SFT1 MRPL31 PIR3 PAP1 GAP1 LAS1 CAC2 PHO84 ASC1 MRPL24 MET4 LSM7 RPC31 MRPL19 CDC33 RUD3 NOP58 RAD1	41	2256
plasma membrane	0.001513	GIT1 MUP3 HXT1 CYR1 SAG1 GAP1 PHO84	7	145
homeostasis of phosphate	0.00278	PHO89 PHO84	2	7
regulation of nitrogen and sulfur utilization	0.004633	MET8 UGA1 MET4	3	29
phosphate transport	0.005822	PHO89 PHO84	2	10
cellular import	0.006316	MUP3 HXT1 GAP1 PHO84 SCD5	5	100
REGULATION OF /	0.008494	PHO89 SLF1 PMC1 CYR1	7	198

INTERACTION WITH CELLULAR ENVIRONMENT		PHO84 FAR3 FRE3		
other lipid, fatty-acid and isoprenoid metabolism activities	0.009863	TIP1 OAR1	2	13
homeostasis of anions	0.009863	PHO89 PHO84	2	13
cell wall	0.009915	TIP1 DAN4 PIR3	3	38
homeostasis of cations	0.01164	PHO89 SLF1 PMC1 PHO84 FRE3	5	116
ionic homeostasis	0.01619	PHO89 SLF1 PMC1 PHO84 FRE3	5	126
nucleus	0.01673	PTA1 SEN34 HAP3 SLU7 HOP2 NAB2 RAD2 RPA34 PAP1 LAS1 CAC2 MET4 LSM7 RPC31 NOP58 RAD1	16	774
second messenger mediated signal transduction	0.02348	CYR1	1	2
lipid and fatty-acid transport	0.02499	GIT1 ACB1	2	21
anion transporters (Cl, SO4, PO4, etc.)	0.02499	PHO89 PHO84	2	21
mRNA processing (splicing, 5'-, 3'-end processing)	0.02571	PTA1 SLU7 NAB2 PAP1 LSM7	5	142
homeostasis of other cations	0.02965	PHO89 PMC1	2	23
amino acid transport	0.02965	MUP3 GAP1	2	23
other transport facilitators	0.03069	SSS1 SBH1 MCH5	3	58
lipid, fatty-acid and isoprenoid metabolism	0.03917	TIP1 GIT1 ACB1 ERG1 POT1 OAR1	6	213
nitrogen and sulfur	0.04421	MET8 UGA1 MET4	3	67

metabolism				
detoxification involving cytochrome P450	0.04641	DIT2	1	4

GO Biological Process of Up-regulated genes (1380 categories)

Category	**p-value**	**Proteins in category**	**K (number identified)**	**F (total assigned)**
cell growth and/or maintenance [GO:0008151]	0.002994	PTA1 SEN34 HAP3 TIP1 GRS1 MET8 PHO89 GIT1 PDC2 SSS1 SLU7 TRM82 DIT2 SLF1 SBH1 PMC1 HOP2 NSA1 SLD3 NAB2 MIG2 UGA1 ACB1 ERG1 RAD2 MUP3 HXT1 POT1 CYR1 RPA34 SAG1 SFT1 OAR1 MRPL31 PIR3 PAP1 GAP1 LAS1 PSR2 CAC2 PHO84 FAR3 MRPL24 MET4 LSM7 RPC31 MRPL19 CDC33 RUD3 MCH5 NOP58 SCD5 FRE3 RAD1 SGE1	55	3657
phosphate transport [GO:0006817]	0.004693	PHO89 PHO84	2	9
fatty acid metabolism [GO:0006631]	0.007274	ACB1 POT1 OAR1	3	34
di-, tri-valent inorganic cation homeostasis [GO:0030005]	0.01065	SLF1 PMC1 FRE3	3	39
nucleotide-excision repair, DNA incision, 3' to lesion [GO:0006295]	0.01181	RAD2	1	1
siroheme biosynthesis [GO:0019354]	0.01181	MET8	1	1

inorganic anion transport [GO:0015698]	0.01308	PHO89 PHO84	2	15
metal ion homeostasis [GO:0006875]	0.0148	SLF1 PMC1 FRE3	3	44
co-translational membrane targeting [GO:0006613]	0.01483	SSS1 SBH1	2	16
mRNA polyadenylation [GO:0006378]	0.01483	PTA1 PAP1	2	16
transport [GO:0006810]	0.01488	PHO89 GIT1 SSS1 SBH1 PMC1 NAB2 MUP3 HXT1 SFT1 GAP1 PHO84 RUD3 MCH5 FRE3 SGE1	15	698
nucleotide-excision repair, DNA incision, 5' to lesion [GO:0006296]	0.02348	RAD1	1	2
double-strand break repair via single-strand annealing, removal of non-homologous ends [GO:0000736]	0.02348	RAD1	1	2
glycyl-tRNA aminoacylation [GO:0006426]	0.02348	GRS1	1	2
protein-membrane targeting [GO:0006612]	0.02728	SSS1 SBH1	2	22
amino acid transport [GO:0006865]	0.02965	MUP3 GAP1	2	23
mRNA metabolism [GO:0016071]	0.03069	PTA1 PAP1 LSM7	3	58
nucleobase, nucleoside, nucleotide and nucleic acid	0.03178	PTA1 SEN34 HAP3 GRS1 PDC2 SLU7 TRM82 SLD3 NAB2 MIG2 RAD2 RPA34 PAP1	19	1046

metabolism [GO:0006139]		CAC2 MET4 LSM7 RPC31 NOP58 RAD1		
anion transport [GO:0006820]	0.03211	PHO89 PHO84	2	24
heterophilic cell adhesion [GO:0007157]	0.03501	SAG1	1	3
transcription termination [GO:0006353]	0.03501	GRS1	1	3
agglutination (sensu *Saccharomyces*) [GO:0007334]	0.03501	SAG1	1	3
RNA processing [GO:0006396]	0.04409	PTA1 SEN34 SLU7 TRM82 PAP1 LSM7 NOP58	7	277
G-protein signaling, coupled to cyclic nucleotide second messenger [GO:0007187]	0.04641	CYR1	1	4
calcium ion transport [GO:0006816]	0.04641	PMC1	1	4
removal of non-homologous ends [GO:0000735]	0.04641	RAD1	1	4
nucleosome assembly [GO:0006334]	0.04641	CAC2	1	4
cell-cell adhesion [GO:0016337]	0.04641	SAG1	1	4
tRNA processing [GO:0008033]	0.04837	PTA1 SEN34	2	30
nucleotide-excision repair [GO:0006289]	0.04837	RAD2 RAD1	2	30

MIPS Functional Classification of down-regulated genes (259 categories)

Category	p-value	Proteins in category	K (number identified)	F (total assigned)
METABOLISM	5.536e-05	GAL7 GAL10 PGI1 STP4 PSA1 HNT1 GAL3 MSS4 HXT6 PPN1 PRO3 AMS1 MIG2 YHL018W MET30 PFK26 SFC1 SOR1 PRS1 ACP1 CDC25 RNH1 GAD1 RAS2 RIB4 ADE2 PDR5 PIP2 SUR1	29	1066
stress response	0.0004671	HSP78 SSA4 HYR1 AHP1 YAP1 QRI8 RAS2 STI1 MKK2	9	175
C-compound and carbohydrate metabolism	0.002916	GAL7 GAL10 PGI1 PSA1 GAL3 HXT6 AMS1 MIG2 PFK26 SFC1 SOR1 CDC25 RAS2	13	415
perception of nutrients and nutritional adaptation	0.004175	TFS1 CDC25 RAS2	3	25
regulation of C-compound and carbohydrate utilization	0.004943	GAL3 MIG2 PFK26 SFC1 CDC25 RAS2	6	120
cytoplasmic and nuclear degradation	0.009766	RPN4 UFD1 PUP2 MET30 QRI8	5	99
plasma membrane	0.01212	MSS4 HXT6 SEC9 CDC25 RAS2 PDR5	6	145
regulation of nucleotide metabolism	0.0123	CDC25 RAS2	2	13
nucleotide metabolism	0.01331	HNT1 PRS1 CDC25 RNH1 RAS2 ADE2	6	148
mitotic cell cycle and cell cycle control	0.01719	CLG1 MET30 SIM1 TRX1 TFS1 CDC25 RAS2 BUB3 SLK19 MKK2	10	352

CELL FATE	0.02435	MSS4 SEC9 PUP2 SIM1 PRS1 BDF1 QRI8 RAS2 STI1 SUR1 MKK2	11	427
cell cycle	0.03456	CLG1 PUP2 MET30 SIM1 TRX1 TFS1 CDC25 RAS2 BUB3 SLK19 MKK2	11	451

GO Biological Process of Down-regulated genes (1380 categories)

Category	**p-value**	**Proteins in category**	**K (number identified)**	**F (total assigned)**
hexose metabolism [GO:0019318]	1.443e-06	GAL7 GAL10 PGI1 PSA1 GAL3 MIG2 PFK26 SOR1	8	63
alcohol metabolism [GO:0006066]	1.972e-06	GAL7 GAL10 PGI1 PSA1 GAL3 MIG2 PFK26 SOR1 NDE1	9	88
monosaccharide metabolism [GO:0005996]	2.921e-06	GAL7 GAL10 PGI1 PSA1 GAL3 MIG2 PFK26 SOR1	8	69
cell growth and/or maintenance [GO:0008151]	9.534e-05	ECM13 GAL7 GAL10 PGI1 RPN4 STP4 PSA1 GAL3 MSS4 HSP78 HXT6 PPN1 SNU13 PRO3 SSA4 RIM15 AMS1 MIG2 CLG1 MDM34 SEC9 UFD1 VPS62 PUP2 ERV29 KSP1 MET30 PFK26 SIM1 HYR1 MOG1 SFC1 RSM7 SOR1 PRS1 ACP1 TRX1 AHP1 SMD2 CDC25 BDF1 YAP1 SRC1 ERO1 QRI8 NDE1 YIM1 SKY1 RNH1 GAD1 RAS2 YOL075C RIB4 BUB3 STI1 RSB1 ADE2 PDR5 SLK19 PIP2 SUR1 MKK2 APL5 TIF5 YTH1	65	3657
galactose metabolism [GO:0006012]	0.0001777	GAL7 GAL10 GAL3	3	9

carbohydrate metabolism [GO:0005975]	0.0003023	GAL7 GAL10 PGI1 PSA1 GAL3 AMS1 MIG2 PFK26 SOR1	9	165
mannose metabolism [GO:0006013]	0.0005155	PSA1 SOR1	2	3
response to oxidative stress [GO:0006979]	0.0007756	HYR1 TRX1 AHP1 YAP1	4	32
fructose metabolism [GO:0006000]	0.001689	PFK26 SOR1	2	5
protein folding [GO:0006457]	0.002184	HSP78 SSA4 ERO1 STI1	4	42
metabolism [GO:0008152]	0.002197	GAL7 GAL10 PGI1 RPN4 STP4 PSA1 GAL3 HSP78 PPN1 SNU13 PRO3 SSA4 RIM15 AMS1 MIG2 SEC9 UFD1 VPS62 PUP2 ERV29 KSP1 MET30 PFK26 HYR1 MOG1 RSM7 SOR1 PRS1 ACP1 TRX1 AHP1 SMD2 YAP1 ERO1 QRI8 NDE1 YIM1 SKY1 RNH1 GAD1 RIB4 STI1 ADE2 PIP2 SUR1 MKK2 APL5 TIF5 YTH1	49	2693
response to drug [GO:0042493]	0.003277	YAP1 SKY1 PDR5	3	23
response to stress [GO:0006950]	0.004604	HSP78 SSA4 RIM15 PUP2 HYR1 TRX1 AHP1 YAP1	8	199
redox homeostasis [GO:0045454]	0.007279	TRX1 AHP1	2	10
response to chemical substance [GO:0042221]	0.01168	YAP1 SKY1 PDR5	3	36
regulation of protein-nucleus import [GO:0042306]	0.01324	SKY1	1	1
mannose inositol phosphoceramide	0.01324	SUR1	1	1

metabolism [GO:0006675]				
succinate transport [GO:0015744]	0.01324	SFC1	1	1
adenylate cyclase activation [GO:0007190]	0.01324	RAS2	1	1
fumarate transport [GO:0015741]	0.01324	SFC1	1	1
positive regulation of protein-nucleus import [GO:0042307]	0.01324	SKY1	1	1
actin cable assembly [GO:0045011]	0.01324	MSS4	1	1
mature ribosome assembly [GO:0042256]	0.01324	TIF5	1	1
protein thiol-disulfide exchange [GO:0006467]	0.01324	ERO1	1	1
RAS protein signal transduction [GO:0007265]	0.01627	CDC25 RAS2	2	15
mRNA processing [GO:0006397]	0.02238	SNU13 UFD1 SMD2 SKY1 YTH1	5	122
start control point of mitotic cell cycle [GO:0007089]	0.02631	CDC25	1	2
inositolphosphoceramide metabolism [GO:0006673]	0.02631	SUR1	1	2
nucleotide-sugar biosynthesis [GO:0009226]	0.02631	PSA1	1	2
fructose 2,6-bisphosphate metabolism [GO:0006003]	0.02631	PFK26	1	2
GDP-mannose biosynthesis [GO:0009298]	0.02631	PSA1	1	2
G-protein signaling, adenylate cyclase activating pathway	0.02631	RAS2	1	2

[GO:0007189]				
response to biotic stimulus [GO:0009607]	0.03205	HYR1 TRX1 AHP1 YAP1	4	91
monosaccharide biosynthesis [GO:0046364]	0.03663	PGI1 PSA1	2	23
hexose biosynthesis [GO:0019319]	0.03663	PGI1 PSA1	2	23
glutamine metabolism [GO:0006541]	0.03921	PRO3	1	3
polyphosphate metabolism [GO:0006797]	0.03921	PPN1	1	3
cell communication [GO:0007154]	0.03964	HYR1 TRX1 AHP1 CDC25 YAP1 SKY1 RAS2 PDR5 MKK2	9	348
alcohol biosynthesis [GO:0046165]	0.0427	PGI1 PSA1	2	25
protein targeting [GO:0006605]	0.0486	HSP78 SSA4 VPS62 MOG1 YIM1 SKY1	6	200

MIPS Functional Classification of over-expressed proteins (259 categories)

Category	**p-value**	**In Category from Cluster**	**k**	**f**
SUBCELLULAR LOCALISATION	2.096e-10	IPP1 SSB1 CPR1 ADK1 PMI40 LPD1 COX4 SOD2 ARD1 FUR1 GND1 TPM2 PRE3 ILV3 SOD1 YNK1 MDH1 COF1 AAT2 AHP1 ACO1 TSA1 CPR3 PRE8 GIM5 COX5A POR1 FPR1 SPS19 ZWF1 CIT1 PRE6 TAF14 PRE2	34	2256
cytoplasm	9.469e-08	IPP1 SSB1 CPR1 ADK1 PMI40 ARD1 FUR1 GND1 SOD1 YNK1 AAT2 ACO1 TSA1 GIM5 FPR1 ZWF1	16	554
ENERGY	2.698e-06	LPD1 COX4 GND1 MDH1 ACS2 ACO1 COX5A SPS19 ZWF1 CIT1	10	252
tricarboxylic-acid	1.634e-05	LPD1 MDH1 ACO1 CIT1	4	25

pathway (citrate cycle, Krebs cycle, TCA cycle)				
CELL RESCUE, DEFENSE AND VIRULENCE	0.0003017	CPR1 SOD2 PRE3 SOD1 GPX1 AHP1 TSA1 ZWF1	8	278
detoxification	0.0004333	SOD2 SOD1 GPX1 TSA1 ZWF1	5	102
protein folding and stabilization	0.0005029	CPR1 CPR3 GIM5 FPR1	4	59
pentose-phosphate pathway	0.00139	GND1 ZWF1	2	9
peroxisome	0.001878	AAT2 AHP1 SPS19	3	39
PROTEIN FATE (folding, modification, destination)	0.003336	CPR1 ARD1 PRE3 COF1 CPR3 PRE8 GIM5 FPR1 PRE6 PRE2	10	594
cytoplasmic and nuclear degradation	0.003463	PRE3 PRE8 PRE6 PRE2	4	99
amino acid biosynthesis	0.006472	LPD1 ILV3 HOM6 AAT2	4	118
nucleotide metabolism	0.01411	DUT1 ADK1 FUR1 YNK1	4	148
endoplasmic reticulum	0.0172	PRE3 PRE8 PRE6 PRE2	4	157
proteolytic degradation	0.01831	PRE3 PRE8 PRE6 PRE2	4	160
phosphate metabolism	0.01851	IPP1 TAF14	2	33
glyoxylate cycle	0.0377	ACO1	1	6
oxidation of fatty acids	0.04385	SPS19	1	7
regulation of phosphate utilization	0.04996	TAF14	1	8

GO Biological Process of Over-expressed proteins (1380 categories)

Category	p-value	In Category from Cluster	k	f
oxygen and reactive oxygen species	2.309e-06	SOD2 SOD1 GPX1 AHP1 TSA1	5	35

metabolism [GO:0006800]				
organic acid metabolism [GO:0006082]	9.037e-06	LPD1 MDH1 ACS2 ACO1 SPS19 CIT1	6	79
carboxylic acid metabolism [GO:0019752]	9.037e-06	LPD1 MDH1 ACS2 ACO1 SPS19 CIT1	6	79
energy pathways [GO:0006091]	5.464e-05	COX4 MDH1 ACO1 COX5A POR1 ZWF1 CIT1	7	159
energy derivation by oxidation of organic compounds [GO:0015980]	5.464e-05	COX4 MDH1 ACO1 COX5A POR1 ZWF1 CIT1	7	159
catabolism [GO:0009056]	6.435e-05	DUT1 LPD1 PRE3 AAT2 PRE8 SPS19 ZWF1 PRE6 PRE2	9	289
tricarboxylic acid cycle [GO:0006099]	0.000104	MDH1 ACO1 CIT1	3	15
glutamate metabolism [GO:0006536]	0.000104	AAT2 ACO1 CIT1	3	15
citrate metabolism [GO:0006101]	0.0002364	ACO1 CIT1	2	4
acetate biosynthesis [GO:0019413]	0.0002364	LPD1 ACS2	2	4
cell growth and/or maintenance [GO:0008151]	0.000278	DUT1 SSB1 CPR1 PMI40 LPD1 COX4 SOD2 ARD1 FUR1 GND1 TPM2 PRE3 ILV3 SOD1 HOM6 GPX1 MDH1 COF1 AAT2 AHP1 ACS2 ACO1 TSA1 CPR3 PRE8 GIM5 COX5A POR1 SPS19 ZWF1 CIT1 PRE6 TAF14 PRE2	34	3657
TCA intermediate metabolism [GO:0006100]	0.0002959	MDH1 ACO1 CIT1	3	21
acetyl-CoA metabolism [GO:0006084]	0.0003925	LPD1 ACS2	2	5
acetate metabolism [GO:0006083]	0.0005863	LPD1 ACS2	2	6

actin polymerization and/or depolymerization [GO:0008154]	0.0008175	TPM2 COF1	2	7
response to oxidative stress [GO:0006979]	0.001051	GPX1 AHP1 TSA1	3	32
glutamine family amino acid metabolism [GO:0009064]	0.001257	AAT2 ACO1 CIT1	3	34
regulation of redox homeostasis [GO:0030503]	0.001731	AHP1 TSA1	2	10
glutamate biosynthesis [GO:0006537]	0.002964	ACO1 CIT1	2	13
amine biosynthesis [GO:0009309]	0.002983	LPD1 ILV3 ACO1 CIT1	4	95
organic acid biosynthesis [GO:0016053]	0.003444	LPD1 ACS2	2	14
carboxylic acid biosynthesis [GO:0046394]	0.003444	LPD1 ACS2	2	14
aerobic respiration [GO:0009060]	0.005023	COX4 COX5A POR1	3	55
cellular respiration [GO:0045333]	0.005554	COX4 COX5A POR1	3	57
ubiquitin-dependent protein catabolism [GO:0006511]	0.005556	PRE3 PRE8 PRE6 PRE2	4	113
fatty acid catabolism [GO:0009062]	0.006383	SPS19	1	1
superoxide metabolism [GO:0006801]	0.006383	SOD1	1	1
nucleotide catabolism [GO:0009166]	0.006383	DUT1	1	1
organic acid catabolism [GO:0016054]	0.006383	SPS19	1	1

carboxylic acid catabolism [GO:0046395]	0.006383	SPS19	1	1
protein-ligand dependent protein catabolism [GO:0019941]	0.007273	PRE3 PRE8 PRE6 PRE2	4	122
coenzyme metabolism [GO:0006732]	0.009064	LPD1 ACS2 ZWF1	3	68
actin filament depolymerization [GO:0030042]	0.01273	COF1	1	2
lipid catabolism [GO:0016042]	0.01273	SPS19	1	2
acetyl-CoA biosynthesis from pyruvate [GO:0006086]	0.01273	LPD1	1	2
mannose biosynthesis [GO:0019307]	0.01273	PMI40	1	2
proteolysis and peptidolysis [GO:0006508]	0.01317	PRE3 PRE8 PRE6 PRE2	4	145
protein catabolism [GO:0030163]	0.01793	PRE3 PRE8 PRE6 PRE2	4	159
malate metabolism [GO:0006108]	0.01903	MDH1	1	3
mannose metabolism [GO:0006013]	0.01903	PMI40	1	3
response to biotic stimulus [GO:0009607]	0.01987	GPX1 AHP1 TSA1	3	91
homeostasis [GO:0019725]	0.02164	SOD1 AHP1 TSA1	3	94
actin filament organization [GO:0007015]	0.02912	TPM2 COF1	2	42
propionate metabolism	0.03152	ACO1	1	5

[GO:0019541]				
response to stress [GO:0006950]	0.03698	PRE3 GPX1 AHP1 TSA1	4	199
copper homeostasis [GO:0006878]	0.0377	SOD1	1	6
negative regulation of meiosis [GO:0045835]	0.0377	CPR1	1	6
actin cytoskeleton organization and biogenesis [GO:0030036]	0.0431	TPM2 COF1	2	52
pentose-phosphate shunt [GO:0006098]	0.04385	ZWF1	1	7
threonine metabolism [GO:0006566]	0.04385	HOM6	1	7
cell wall mannoprotein biosynthesis [GO:0000032]	0.04996	PMI40	1	8
histone deacetylation [GO:0016575]	0.04996	CPR1	1	8

MIPS Functional Classification of under-expressed proteins (259 categories)

Category	**p-value**	**In Category from Cluster**	**k**	**f**
ENERGY	1.401e-10	CDC19 ADH5 TPI1 TDH3 ENO1 ATP7 FBA1 SDH3 PDC1 ADH1 MDH2 OYE3	12	252
C-compound and carbohydrate utilization	5.962e-08	CDC19 ADH5 TPI1 TDH3 ENO1 RHR2 FBA1 PDC1 ADH1 MDH2	10	261
METABOLISM	1.132e-07	CDC19 ADH5 HEM13 TPI1 MXR1 TDH3 ENO1 YHR112C RHR2 FBA1 PDC1 ILV5 IMD4 GUA1 ADH1 MDH2 ERG10	17	1066
glycolysis and gluconeogenesis	2.984e-07	CDC19 TPI1 TDH3 ENO1 FBA1	5	35
C-compound and	4.42e-06	CDC19 ADH5 TPI1 TDH3 ENO1 RHR2	10	415

carbohydrate metabolism		FBA1 PDC1 ADH1 MDH2		
cytoplasm	8.179e-06	CDC19 SES1 HEM13 TPI1 TDH3 ENO1 FBA1 PDC1 ADH1 MDH2 ERG10	11	554
fermentation	0.000357	ADH5 PDC1 ADH1	3	33
SUBCELLULAR LOCALISATION	0.003881	CDC19 SES1 HEM13 TPI1 CPR5 TDH3 ENO1 SSC1 ATP7 FBA1 SDH3 PDC1 SEC13 ILV5 ADH1 MDH2 ERG10	17	2256
respiration	0.006134	ATP7 SDH3 PDC1	3	88
purine ribonucleotide metabolism	0.01579	IMD4 GUA1	2	45
other amino acid metabolism activities	0.02136	MXR1	1	5
other cell division and DNA synthesis activities	0.02558	SNZ1	1	6
protein folding and stabilization	0.0263	CPR5 SSC1	2	59
stress response	0.0383	MXR1 SSC1 SNZ1	3	175
mitochondrial transport	0.04597	SSC1 ATP7	2	80

GO Biological Process of Under-expressed proteins (1380 categories)

Category	p-value	In Category from Cluster	k	f
alcohol metabolism [GO:0006066]	5.335e-11	CDC19 ADH5 TPI1 TDH3 ENO1 RHR2 FBA1 PDC1 MDH2	9	88
energy pathways [GO:0006091]	4.849e-10	CDC19 TPI1 TDH3 ENO1 RHR2 FBA1 SDH3 PDC1 ADH1 MDH2	10	159
energy derivation by oxidation of organic compounds [GO:0015980]	4.849e-10	CDC19 TPI1 TDH3 ENO1 RHR2 FBA1 SDH3 PDC1 ADH1 MDH2	10	159
alcohol biosynthesis [GO:0046165]	5.912e-10	TPI1 TDH3 ENO1 RHR2 FBA1 MDH2	6	25
main pathways of	1.602e-09	CDC19 TPI1 TDH3 ENO1 FBA1 SDH3	7	53

carbohydrate metabolism [GO:0006092]		MDH2		
glycolysis [GO:0006096]	4.245e-09	CDC19 TPI1 TDH3 ENO1 FBA1	5	16
gluconeogenesis [GO:0006094]	1.949e-08	TPI1 TDH3 ENO1 FBA1 MDH2	5	21
glucose metabolism [GO:0006006]	2.231e-08	CDC19 TPI1 TDH3 ENO1 FBA1 MDH2	6	44
glucose catabolism [GO:0006007]	2.515e-08	CDC19 TPI1 TDH3 ENO1 FBA1	5	22
hexose catabolism [GO:0019320]	2.515e-08	CDC19 TPI1 TDH3 ENO1 FBA1	5	22
monosaccharide biosynthesis [GO:0046364]	3.204e-08	TPI1 TDH3 ENO1 FBA1 MDH2	5	23
hexose biosynthesis [GO:0019319]	3.204e-08	TPI1 TDH3 ENO1 FBA1 MDH2	5	23
monosaccharide catabolism [GO:0046365]	3.204e-08	CDC19 TPI1 TDH3 ENO1 FBA1	5	23
alcohol catabolism [GO:0046164]	6.208e-08	CDC19 TPI1 TDH3 ENO1 FBA1	5	26
hexose metabolism [GO:0019318]	2.033e-07	CDC19 TPI1 TDH3 ENO1 FBA1 MDH2	6	63
carbohydrate catabolism [GO:0016052]	2.984e-07	CDC19 TPI1 TDH3 ENO1 FBA1	5	35
monosaccharide metabolism [GO:0005996]	3.524e-07	CDC19 TPI1 TDH3 ENO1 FBA1 MDH2	6	69
carbohydrate biosynthesis [GO:0016051]	2.502e-06	TPI1 TDH3 ENO1 FBA1 MDH2	5	53
carbohydrate metabolism [GO:0005975]	4.398e-06	CDC19 TPI1 TDH3 ENO1 FBA1 SDH3 MDH2	7	165
fermentation [GO:0006113]	3.136e-05	RHR2 PDC1 ADH1	3	15
metabolism [GO:0008152]	4.752e-05	CDC19 ADH5 SES1 HEM13 TPI1 MXR1 TDH3 ENO1 SOL3 MMF1 RHR2	22	2693

		SSC1 FBA1 SDH3 PDC1 SEC13 ILV5 SNZ1 GUA1 ADH1 MDH2 ERG10		
biosynthesis [GO:0009058]	0.0001126	SES1 HEM13 TPI1 TDH3 ENO1 MMF1 RHR2 FBA1 ILV5 MDH2 ERG10	11	731
organic acid metabolism [GO:0006082]	0.0003293	CDC19 SDH3 PDC1 MDH2	4	79
cell growth and/or maintenance [GO:0008151]	0.0005964	CDC19 ADH5 SES1 HEM13 TPI1 CPR5 MXR1 TDH3 ENO1 SOL3 MMF1 RHR2 SSC1 ATP7 FBA1 SDH3 PDC1 SEC13 ILV5 SNZ1 GUA1 ADH1 MDH2 ERG10	24	3657
pyruvate metabolism [GO:0006090]	0.0007875	CDC19 PDC1	2	10
branched chain family amino acid biosynthesis [GO:0009082]	0.0009599	MMF1 ILV5	2	11
isoleucine biosynthesis [GO:0009097]	0.004308	MMF1	1	1
non-selective vesicle assembly [GO:0006902]	0.004308	SEC13	1	1
catabolism [GO:0009056]	0.007045	CDC19 TPI1 TDH3 ENO1 FBA1	5	289
polyol biosynthesis [GO:0046173]	0.008599	RHR2	1	2
glycerol biosynthesis [GO:0006114]	0.008599	RHR2	1	2
GMP metabolism [GO:0046037]	0.008599	GUA1	1	2
non-selective vesicle endocytosis [GO:0016193]	0.008599	SEC13	1	2
malate metabolism [GO:0006108]	0.01287	MDH2	1	3
isoleucine metabolism [GO:0006549]	0.01287	MMF1	1	3
oxidative phosphorylation, succinate to ubiquinone	0.01713	SDH3	1	4

[GO:0006121]				
succinate metabolism [GO:0006105]	0.01713	SDH3	1	4
ethanol fermentation [GO:0019655]	0.02136	PDC1	1	5
glycolytic fermentation [GO:0019660]	0.02558	PDC1	1	6
pyridoxine metabolism [GO:0008614]	0.02558	SNZ1	1	6
glycerol metabolism [GO:0006071]	0.02979	RHR2	1	7
polyol metabolism [GO:0019751]	0.02979	RHR2	1	7
ethanol metabolism [GO:0006067]	0.03397	PDC1	1	8
purine nucleoside monophosphate metabolism [GO:0009126]	0.04229	GUA1	1	10