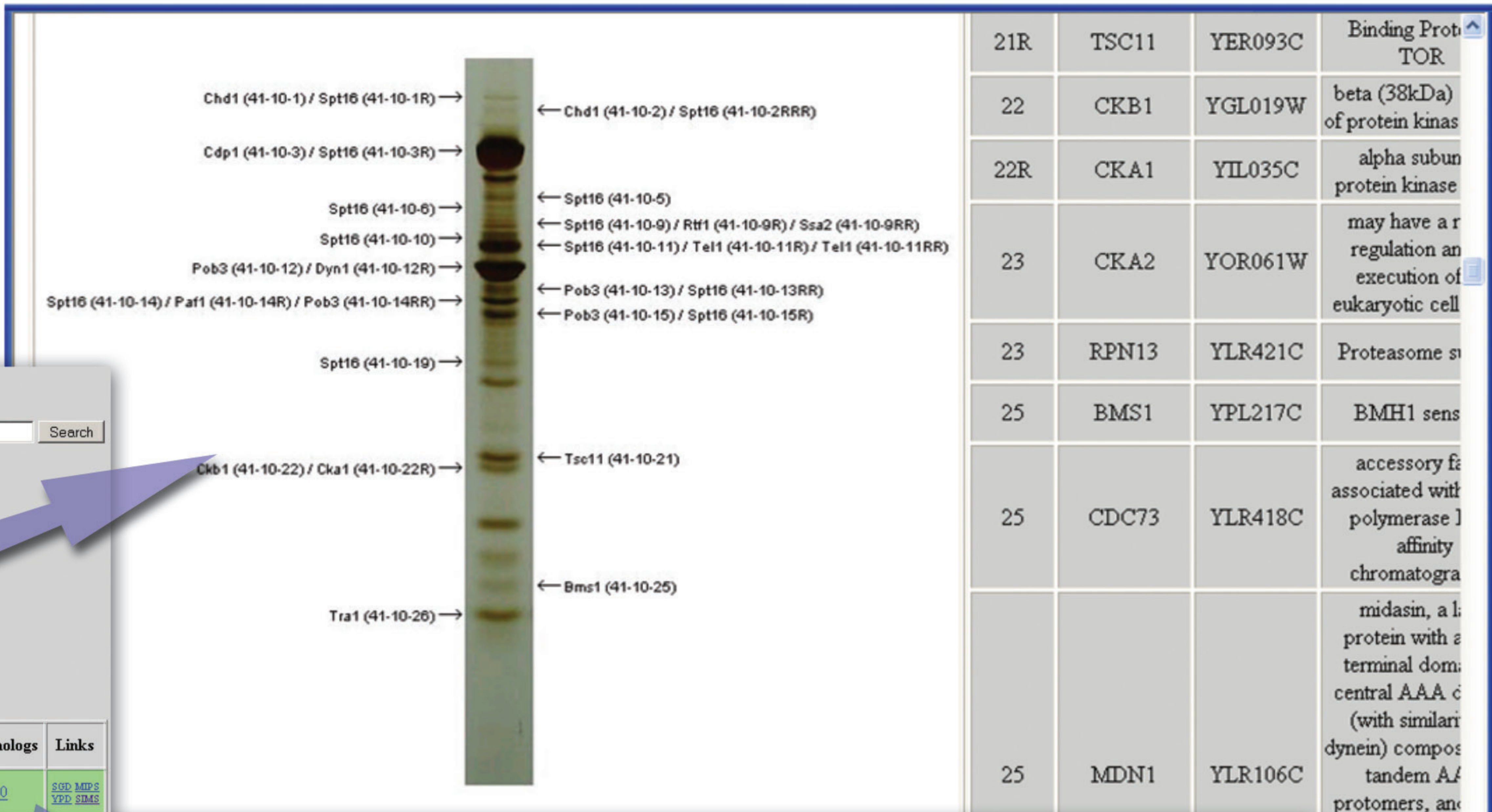
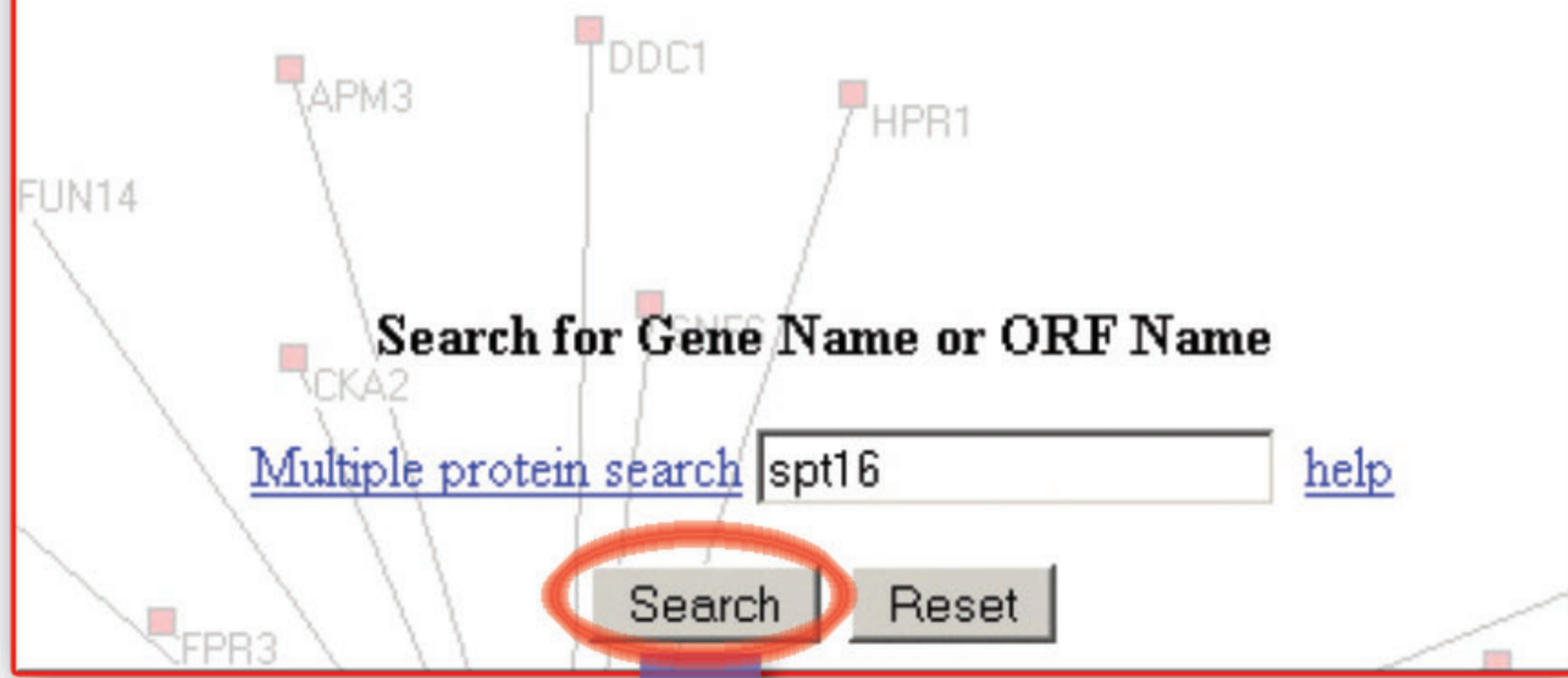


TAP Database Search



21R	TSC11	YER093C	Binding Prob TOR
22	CKB1	YGL019W	beta (38kDa) of protein kinase
22R	CKA1	YIL035C	alpha subunit protein kinase
23	CKA2	YOR061W	may have a r regulation an execution of eukaryotic cell
23	RPN13	YLR421C	Proteasome s
25	BMS1	YPL217C	BMH1 sens
25	CDC73	YLR418C	accessory fa associated with polymerase I affinity chromatogra
25	MDN1	YLR106C	midasin, a li protein with a terminal dom central AAA d (with similar dynein) compos tandem AA protomers, and terminal M-d

Interaction View
For bait SPT16(YGL207W) Search for Gene Name or ORF Name

Data filtered by Z_SCORE >= 1.0 and Confidence value >= 90 %

Gene Name	ORF Name	SGD Description	GO Annotation	Homologs	Links
SPT16	YGL207W	global regulator of transcription	P RNA elongation from Pol II promoter P chromatin modeling P regulation of global transcription from Pol II promoter	0	SGD MIPS YPD SIMS

Bait Common protein Possible cross contaminations

The following bound to SPT16(YGL207W) when it was used as bait. For details see LCMS data MalDI data for SPT16(YGL207W)

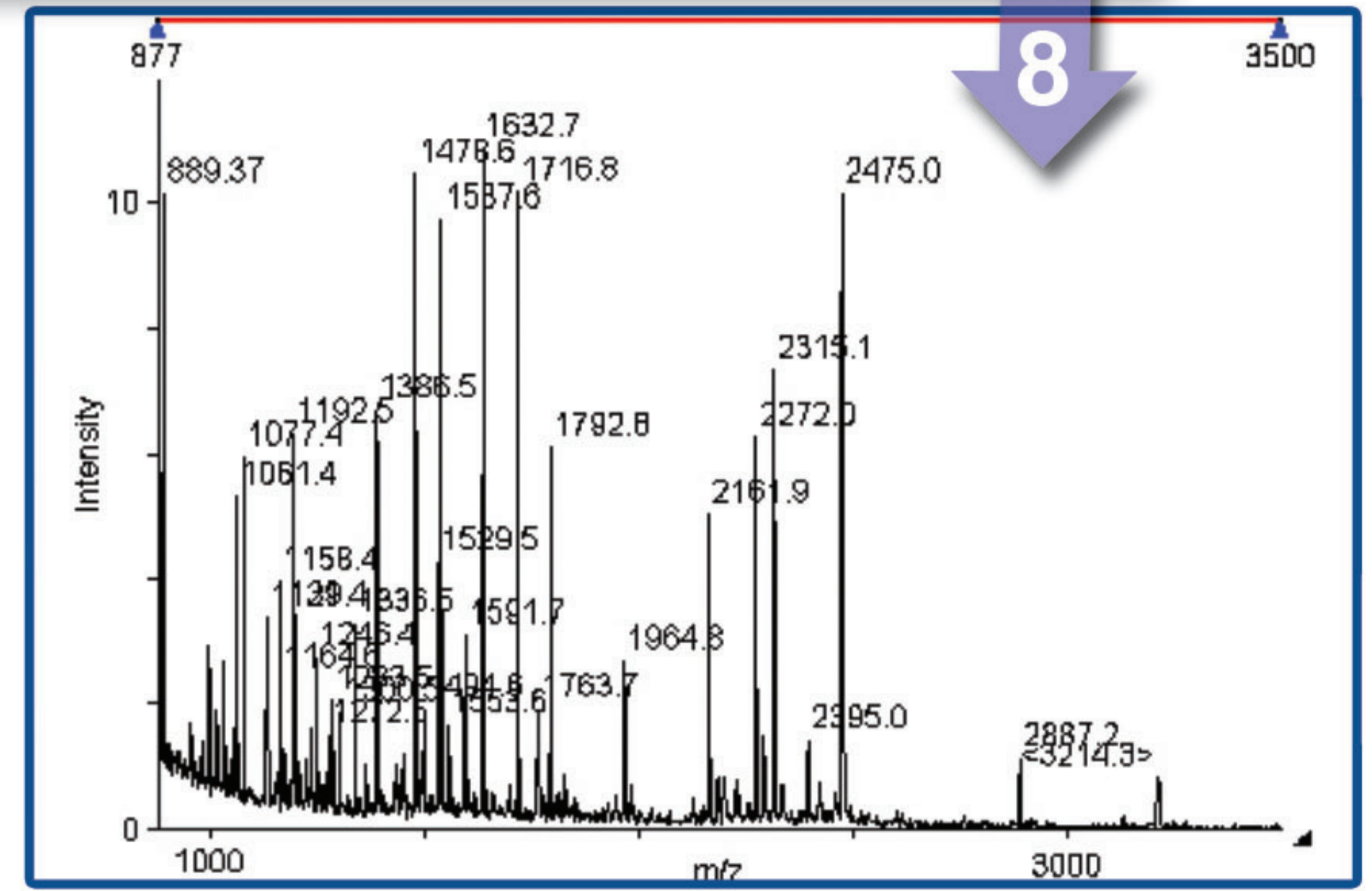
Gene Name	ORF Name	SGD Description	Localization (Molecules/Cell)	Source	L_Score	#Peptides (%)	Sum of score	Max_Maldi	Homologs	Links
SPT16	YGL207W	global regulator of transcription	nucleus (18500)	GFP	L	12/14	297(99.6)	29524.8	4.56	0
POB3	YML069W	binds to catalytic subunit of DNA polymerase alpha (PolIp)	nucleus (22400)	GFP	M	10/12	130(3.61)	469.51	6.53	1e-124
PAF1	YBR279W	RNA polymerase II-associated, nuclear protein that may serve as both a positive and negative regulator of a subset of genes, perhaps operating in parallel with Gal1Ip	nucleus (1040)	GFP	L	7/14	36(99.6)	3558.5	6.69	1e-10

Submit to FunSpec Submit to GO Term Finder

SPT16(YGL207W) bound to the following proteins as a prey.

Gene Name	ORF Name	SGD Description	Localization (Molecules/Cell)	Source	L_Score	#Peptides (%)	Sum of score	Max_Maldi	Homologs	Links
SPT16	YGL207W	global regulator of transcription	nucleus (18500)	GFP	L	11/61	291(99.6)	28927.2	4.56	0
HTA2	YBL003C	Histone H2A (HTA1 and HTA2 code for nearly identical proteins)	nucleus (32100)	GFP	L	7/61	45(99.6)	4466.2	4.44	3e-40
PAF1	YBR279W	RNA polymerase II-associated, nuclear protein that may serve as both a positive and negative regulator of a subset of genes, perhaps operating in parallel with Gal1Ip	nucleus (1040)	GFP	L	3/61	20(99.6)	1992.0	3.91	1e-10

Band number	Gene Name	Orf Name	SGD Description	SGD Gene Product	Final_score
1	CHD1	YER164W	Sole S. cerevisiae member of CHD gene family containing Chromodomain, Helicase domain, and DNA-binding domain	transcriptional regulator	1.95
2	SPT16	YGL207W	global regulator of transcription		4.08
3	SPT16	YGL207W	global regulator of transcription		4.48
4	CTR9	YOL145C	CTR9 is required for normal CLN1 and CLN2 G1 cyclin expression		1.83
5	YMR247C	YMR247C			0.44
6	SPT16	YGL207W	global regulator of transcription		4.46
7	CTR9	YOL145C	CTR9 is required for normal CLN1 and CLN2 G1 cyclin expression		2.63
8	SPT16	YGL207W	global regulator of transcription		4.19
9	SPT16	YGL207W	global regulator of transcription		2.88
10	CTF19	YPL018W	Chromosome Transmission Fidelity	kinetochore protein	1.8



LC-MS/MS Data
LC-MS/MS data for bait SPT16(YGL207W)

Gene Name	ORF Name	SGD Description	GO Annotation	Links
SPT16	YGL207W	global regulator of transcription	P RNA elongation from Pol II promoter P chromatin modeling P regulation of global transcription from Pol II promoter	SGD MIPS YPD SIMS

Bait Common protein

DB 13 AS180303 284 23,24 DTASelect COMBINED.html

Gene Name	ORF Name	SGD Description	SGD Gene Product	Number of peptides	Probability	Ambiguous	Cross Contamination	Links
SPT16	YGL207W	global regulator of transcription		36	99.6	No	No	SGD MIPS YPD SIMS
POB3	YML069W	binds to catalytic subunit of DNA polymerase alpha (PolIp)	DNA polymerase delta binding protein	31	99.6	No	No	SGD MIPS YPD SIMS
STO1	YMR125W	Large subunit of the nuclear cap-binding protein complex	Large subunit of the nuclear cap-binding protein complex	3	99.6	No	No	SGD MIPS YPD SIMS

SIMS SUMMARY

View SEQUEST-STATQUEST-SIMS Summary

SIMS

No	File name	Confidence	Xcorr	DSeq	Sequence	Locus	Links	PS	PSRank	Int	DV
	23,24.0330.0330.1	0.999	3.6135	0.4735	KALADWQQDKL	YGL207W	TAP SGD MIPS YPD QD	470	1	5/10	
	23,24.0335.0335.1	0.981	1.7589	0.1880	KALADWQQD	YGL207W	TAP SGD MIPS YPD QD	363	1	5/8	
	23,24.0380.0380.1	0.999	2.6705	0.1920	RFLIDPSEEMAN.N	YGL207W	TAP SGD MIPS YPD QD	110	1	2/12	
	23,24.1324.1324.1	0.997	2.4184	0.3648	LNIDFDVFK.K	YGL207W	TAP SGD MIPS YPD QD	107	2154	1/8	
	23,24.1384.1384.1	0.997	2.4432	0.2613	KEVESVIEVEKT	YGL207W	TAP SGD MIPS YPD QD	76	1816	1/12	

Spectrum Key:

Unique	Filename	XCorr	DeltaCN	Precursor	M+H+ Mass	Rank by Sp	Ion Proportion	Copies	Sequence
13	AS180303_284_23,24.0519.0519.1	0.9272	0.0695	843.39	196	4170.04	1		L.DETEPPR.F
13	AS180303_284_23,24.1669.1669.1	1.0074	8.0E-4	626.55	26	5000.04	1		Q.LYNGNC.I
13	AS180303_284_23,24.0951.0951.1	2.7166	0.1751	1418.37	1	6500.04	1		F.YFNNEEDNNK.K
13	AS180303_284_23,24.0845.0845.1	1.5954	0.1499	798.5	4	6670.04	1		K.VPSKPR.N
13	AS180303_284_23,24.1125.1125.1	2.3545	0.3054	1086.51	1	6670.04	1		K.ALADVVQDK.L
13	AS180303_284_23,24.1397.1397.1	1.6087	0.0562	797.58	6	8000.04	2		R.IHVDWK.S
13	AS180303_284_23,24.1021.1021.1	1.3739	0.0972	743.55	5	7500.04	1		K.TVGIPEK.D
13	AS180303_284_23,24.0987.0987.1	1.5357	0.0666	957.4	56	5000.04	1		K.DFNKPVTH.I
13	AS180303_284_23,24.1134.1134.2	3.9346	0.2516	1925.68	1	7140.04	1		R.RYGDEDELEQEER.R
13	AS180303_284_23,24.1327.1327.1	0.9751	0.0956	649.28	91	5000.04	1		R.VPSTVF.I
13	AS180303_284_23,24.1418.1418.1	0.8619	0.0795	587.48	31	5000.04	1		K.NPILM.G
13	AS180303_284_23,24.0517.0517.1	1.868	0.1809	991.23	4	6500.04	1		F.NSPGSSGGISK.K
13	AS180303_284_23,24.1422.1422.1	1.7291	0.1891	1288.49	1	5000.04	1		D.AIAEASNGLLTVE.N
13	AS180303_284_23,24.0545.0545.1	0.9877	0.1182	1200.37	159	2270.04	1		S.AADANGDPSEPR.Q
13	AS180303_284_23,24.1697.1697.1	1.8204	0.1783	997.67	1	7140.04	1		L.NIDFDVFK.K
13	AS180303_284_23,24.1923.1923.1	2.6245	0.1394	1475.51	1	5770.04	1		K.LFDDVIALDINSAGK.T
13	AS180303_284_23,24.0447.0447.1	1.875	0.15	1060.36	46	3890.04	3		A.DANGDPSEPR.Q
13	AS180303_284_23,24.1585.1585.1	1.3715	0.1667	927.3	8	6430.04	1		L.SYEFPATL.I

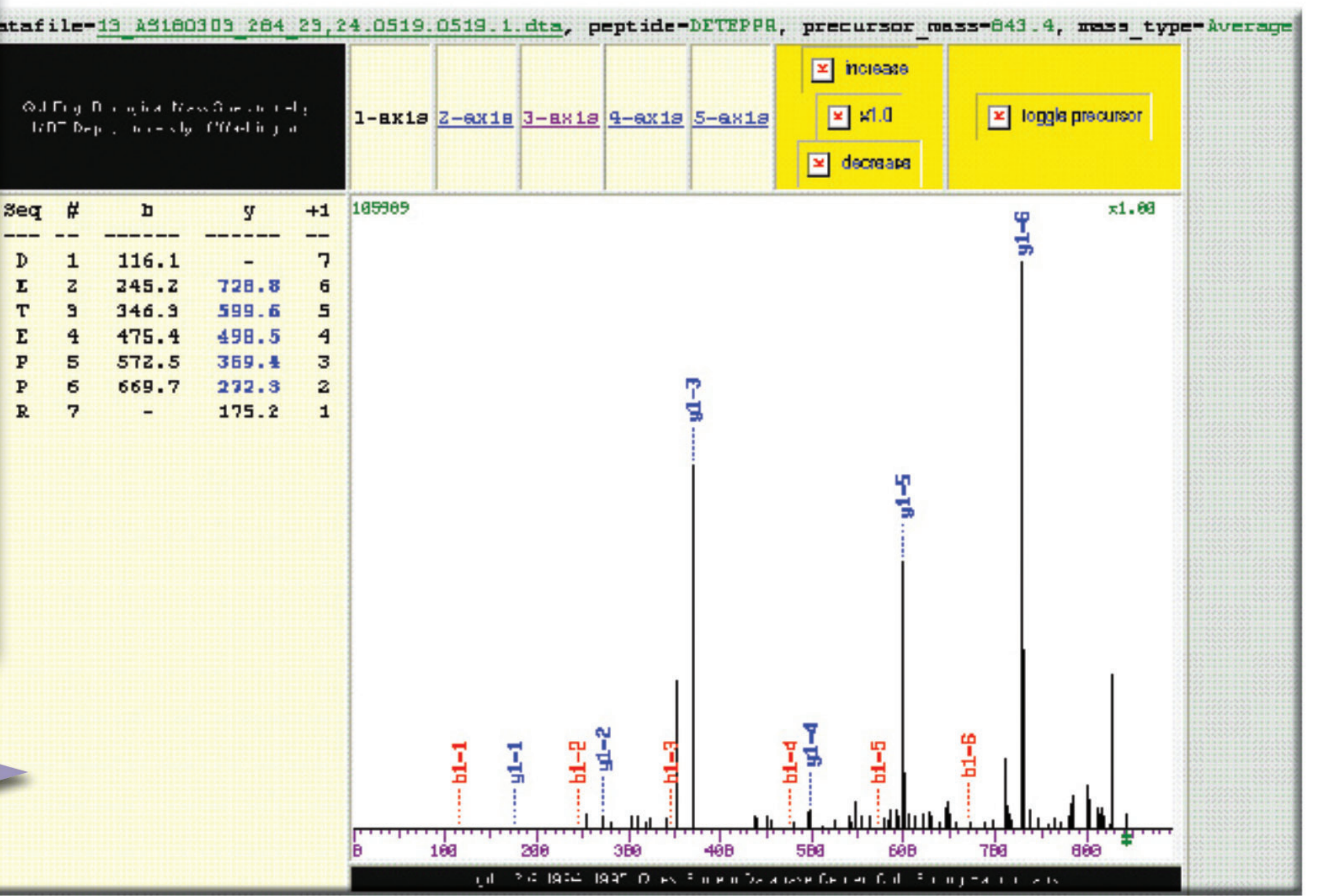


Figure S6. A comprehensive database of the yeast interactome (<http://tap.med.utoronto.ca/>). Querying of a protein name (1) leads to an interaction view summarizing the results of all purifications involving the queried protein, as well as links to YPD, SGD, MIPS and BioGRID databases. Links from this table lead to details of the LC/MS/MS (2) or MALDI-TOF (6 and 7) experiments. From the LC/MS/MS page, mass spectrum search algorithm scores (2 and 3) and spectral images (5) can be retrieved, in addition to results from SIMS site-specific modification searches (4). Similarly, the link to the MALDI-TOF data allows for retrieval of search algorithm scores (7), silver-stained gels (6) and spectral images (8).