

SUPPORTING INFORMATION.

S1 Table: List of peptides from cell wall proteins for SILAC quantification.

Protein ID	Sequence		[M+H] ⁺	Peptide Sequence ^{b, c, d}
	Start	End		
Bgl2p	111	128	1940.05	IKESTVAGFLVGSEALYR
Crh1p	68	73	809.42	WFTDLK
	74	79	653.35	HAGEIK
	74	91	1877.94	HAGEIKYGS DGLSMTLAK
	80	91	1242.60	YGS DGLSMTLAK
	92	99	992.52	RYDNPSLK
	93	99	836.42	YDNPSLK
	100	108	1122.53	SNFYIMYGK
	109	114	714.48	LEVILK
	187	197	1326.63	TTWYLDGESVR
	252	261	1082.57	VIVTDYSTGK
252	262	1210.67	VIVTDYSTGKK	
263	285	2498.07	YTYGDQSGSWESIEADGGSIYGR	
Crh2p	60	74	1827.79	YFSHDSCMPVPICK
	80	96	874.43	FKDYSSK
	124	134	1078.55	NSGGTVLSSTR
Cwp1p	32	49	1946.93	SGSDLQYLSVYSDNGTLK
	50	66	1641.76	LGSGSGSFEATITDDGK
	50	68	1882.94	LGSGSGSFEATITDDGKLK
	106	114	959.48	SSSGFYAIK
	106	124	2030.97	SSSGFYAIKD GSSYIFSSK
	115	124	1090.51	DGSSYIFSSK
	125	139	1545.79	QSDDATGVAIRPTSK
Ccw12p	117	133	1476.91	ALPAAGALLAGAAALLL
Ccw14p	38	60	2676.10	SSSTCDSLNQVTCYCEHENSAVK

	38	61	2804.19	SSST<u>C</u>DSL<u>N</u>QV<u>T</u>C<u>Y</u>CEHENS<u>A</u>V<u>K</u>K
	61	80	2260.00	K<u>C</u>L<u>D</u>S<u>I</u>C<u>P</u>N<u>N</u>D<u>A</u>D<u>A</u>A<u>Y</u>S<u>A</u>F<u>K</u>
	62	80	2131.91	<u>C</u>L<u>D</u>S<u>I</u>C<u>P</u>N<u>N</u>D<u>A</u>D<u>A</u>A<u>Y</u>S<u>A</u>F<u>K</u>
Cwp2p	76	92	1458.78	AAVGMGAGALAAAAMLL
Ecm33p	162	172	1331.72	KVNVFNINNNR
	163	172	1203.62	VNVFNINNNR
	248	262	1575.82	VGQSL<u>S</u>I<u>V</u>S<u>N</u>D<u>E</u>L<u>S</u>K
	285	291	792.43	VIDGFNK
	337	351	1623.78	LQSN<u>G</u>A<u>I</u>Q<u>G</u>D<u>S</u>F<u>V</u><u>C</u>K
Exg2p	208	218	1205.67	ILYGD <u>L</u> GWLR
Gas1p	83	90	957.58	KLNTNVIR
	106	127	2287.19	ALNDADIYVIADLAAPATSINR
	128	141	1700.78	DDPTWTV<u>D</u>L<u>F</u>N<u>S</u>Y<u>K</u>
	184	192	1186.59	QYISDKNYR
	193	207	1695.78	KIPVGYSSN<u>D</u>D<u>E</u>D<u>T</u>R
	193	209	1922.95	KIPVGYSSN<u>D</u>D<u>E</u>D<u>T</u>R<u>V</u>K
	194	207	1567.69	IPVGYSSN <u>D</u> D <u>E</u> D <u>T</u> R
	210	222	1536.60	MTDYFAC <u>G</u> DD <u>D</u> V <u>K</u>
	223	236	1753.74	ADFYGINMYEW<u>C</u>G<u>K</u>
	241	247	769.35	TSGYADR
	415	424	1193.53	YGAYSF<u>C</u>TPK
Gas3p	32	51	2246.10	FIKPSSATNSESDNEVFFVK
	52	80	3046.29	GVDYQPGGSSGYDADSDTDILSDPEV <u>C</u> AR
	81	94	1581.80	DAYAFQQLGVNTVR
	134	147	1544.72	ADPSGTYDSL <u>Y</u> LSR
	203	217	1578.78	SIPVGYSAADNTDLR
	223	242	2311.09	YLQCNSLDGNKVND <u>D</u> L <u>D</u> ISK
	293	306	1514.74	TFDEVSEGLY<u>G</u>G<u>L</u>K
	329	349	2387.16	LDDSGSLTYKDDFVNLES<u>Q</u>L<u>K</u>
	358	368	1257.59	ESEISSDSI<u>Y</u>K
Gas5p	34	45	1314.57	GNAFFNSESGER
	192	206	1573.83	QIPVGYSAADIVANR
	207	222	1829.78	QLAAEYFN <u>C</u> GDEADAR
	248	269	2652.28	MKLYQDYSVPVFLSEFG<u>C</u>N<u>Q</u>V<u>K</u>
	250	269	2393.15	LYQDYSVPVFLSEFG<u>C</u>N<u>Q</u>V<u>K</u>

	317	329	1600.79	LTDFENLKNEYSK
Mkc7p	305	321	1988.06	YAGDLYTIPIINTLQHR
Pry3	121	130	1085.49	STAEIGCGYK
Plb2p	101	111	1110.54	IGIACSGGGYR
Pst1p	126	140	1604.93	LITLPAISSFTSNIK
	246	262	1913.00	LNTIGQTFSIVSNDYLK
	319	326	762.36	GGADVESK
Pir1p	246	255	1079.54	SSGTLEMNLK
	246	263	1820.94	SSGTLEMNLKGGILTDGK
	246	265	2034.07	SSGTLEMNLKGGILTDGKGR
Pir2p	318	327	1093.56	TSGTLEMNLK
	318	335	1834.96	TSGTLEMNLKGGILTDGK
	318	337	2048.08	TSGTLEMNLKGGILTDGKGR
Pir3p	307	325	2271.05	HIGSQCHEVYLQAIDLIDC
Cis3p	127	149	2452.22	DSSCKNSGTLELTLKDGVLTDAK
	127	151	2665.35	DSSCKNSGTLELTLKDGVLTDAKGR
	132	141	1075.60	NSGTLELTLK
	132	149	1875.01	NSGTLELTLKDGVLTDAK
	132	151	2088.13	NSGTLELTLKDGVLTDAKGR
	142	149	818.43	DGVLTDAK
	142	151	1031.55	DGVLTDAKGR
Ssa1p	35	47	1471.71	TTPSFVAFTDTER
	125	136	1327.66	MKETAESYLGAK
	137	153	1897.93	VNDAVVTVPAYFNDSQR
	158	169	1199.67	DAGTIAGLNVLRL
	170	186	1787.99	IINEPTAAAIAAYGLDKK
	218	233	1675.73	ATAGDTHLGGEDFDNR
	234	243	1274.69	LVNHFIQEFK
	249	255	833.41	DLSTNQR
	297	308	1526.74	ARFEELCADLFR
	326	339	1459.78	SQVDEIVLVGGSTR
	507	514	961.52	LSKEDIEK
Scw4p	135	148	1533.69	GITYTPYESSGACK
	149	167	2019.04	SASEVASDLAQLTDFPVIR
	168	181	1686.78	LYGTDCNQVENVFK

	189	207	2185.15	VFLGIYYVDQIQDGVNTIK
	292	308	1986.04	NTVAQDSGKWLLEQIQR
	301	308	1085.61	WLLEQIQR
	309	317	1064.52	VWTAC <u>CD</u> GKK
	370	378	909.43	ADGAYGVEK
	370	386	1871.88	ADGAYGVEKYWGILSNE
	379	386	981.47	YWGILSNE
Scw10p	138	151	1576.66	GITYSPYND<u>D</u>G<u>S</u>C<u>K</u>
	152	170	2065.02	STAQVASDLEQLTGFDNIR
	171	186	1822.90	LYGVDC<u>S</u>QVENVLQAK
	321	343	2436.19	DVVITETGWPSKGDTYGEAVPSK
	344	354	1131.60	ANQEAAISSIK
	355	372	2053.93	SS<u>C</u>GSSAYLFTAFNDLW<u>K</u>
Tdh3p	47	53	835.37	YDSTHGR
	54	70	1882.93	YAGEVSHDDKHIIVDGK
	117	137	2207.11	VVITAPSSTAPMFVMGVNEEK
	117	143	2914.46	VVITAPSSTAPMFVMGVNEEKYTSDLK
	144	160	1705.86	IVSNASCTTNCLAPLAK
	161	184	2575.31	VINDAFGIEEGLMTTVHSLTATQK
	185	195	1297.63	TVDGPSHKDWR
	199	213	1374.72	TASGNIIPSSTGAAK
	232	246	1470.84	VPTVDVSVVDLTVK
	247	258	1481.78	LNKETTYDEIKK
	308	321	1752.79	LVSWDNEYGYSTR
	322	332	1179.67	VVDLVEHVAKA
Tos1p	355	367	1575.66	TLQYGDAS<u>C</u><u>S</u>C<u>W</u>K
	368	385	1943.87	TG<u>C</u>GEMDLFEILTAGSDK
	412	421	1051.54	AAVIFNSSDK

Note:

- Mass for singly charged peptide with Lys-D0 labeling.
- Peptides were from trypsin digestion with up to three Lys or Arg miss-cleavage.
- The underlined cysteines were carbamidomethyl modified with a 57.02 Da increase in mass.
- Peptide sequences in bold were used for SILAC quantification.