

S2 Table: List of peptides from cytoplasmic proteins as the internal control for SILAC

quantification.

Protein ID	sequence		[M+H] ⁺	Peptide sequence ^{b, c, d}
	start	end		
EF-1a	6	20	1560.85	SHINVVVIGHVDSGK
	31	37	805.40	<u>C</u> GGIDKR
	38	44	894.49	TIEKF EK
	56	62	894.47	YAWVLDK
	56	64	1135.65	YAWVLDK LK
	56	67	1491.83	YAWVLDK LKAER
	85	96	1355.71	YQVTVIDAPGHR
	85	100	1858.98	YQVTVIDAPGHRDFIK
	101	129	2923.45	NMITGTSQAD <u>C</u> AILIAGGVGEFEAGISK
	135	146	1326.75	EHALLAFTLGVR
	147	154	884.56	QLIVAVNK
	160	170	1436.72	WDESRFQEIVK
	165	170	763.44	FQEIVK
	165	177	1582.85	FQEIVKETS NFIK
	165	178	1710.94	FQEIVKETS NFIKK
	171	177	838.43	ETS NFIK
	185	210	2908.40	TVPFVPISGWNGDNMIEATTNAPWYK
	211	217	877.44	GWEKETK
	218	224	658.43	AGVVKGK
	223	245	2548.41	GKTLLEAIDAIEQPSRPTDKPLR
	225	245	2363.29	TLLEAIDAIEQPSRPTDKPLR
	246	253	975.55	LPLQDVYK
	254	264	1025.61	IGGIGTVPVGR
	265	288	2430.33	VETGVIKPGMVVTFAPAGVTTEVK
	289	311	2550.20	SVEMHHEQLEQGVPGDNVGFNVK
	320	328	976.46	RGNV <u>C</u> GDAK
	320	333	1527.73	RGNV <u>C</u> GDAKNDPPK
	321	328	820.36	GNV<u>C</u>GDAK
	370	376	893.46	FDELLEK

	370	379	1278.63	FDELLEKNDR
	370	380	1434.73	FDELLEKNDRR
	384	390	866.47	KLEDHPK
	394	401	760.42	SGDAALVK
	402	421	2311.13	FVPSKPMCVAFSEYPPLGR
	429	437	914.57	QTVAVGVK
Pdc1p	37	44	996.48	IYEVEGMR
	128	151	2522.21	MSANISETTAMITDIATAPAEIDR
	180	209	3323.80	LLQTPIDMSLKPNDASEKEVIDTILALVK
	213	224	1375.65	NPVILADACCSR
	210	224	1689.81	DAKNPVILADACCSR
	234	249	1777.96	LIDLTQFPAFVTPMGK
	233	249	1906.05	KLIDLTQFPAFVTPMGK
	259	273	1596.86	YGGVYVGTLSKPEVK
	305	315	1356.64	NIVEFHSDHMK
	333	342	1016.60	LLTTIADAAK
	343	352	1057.62	GYKPVAVPAR
	479	484	664.41	LIHGPK
	485	505	2388.20	AQYNEIQGWDHLSLLPTFGAK
	512	520	1006.48	VATTGEWDK
	512	525	1591.80	VATTGEWDKLTQDK
	535	554	2286.19	MIEIMLPVFDAPQNLVEQAK
Pma1p	100	109	1168.53	YGLNQMADEK
	100	115	1823.92	YGLNQMADEKESLVVK
	175	184	1057.64	TLANTAVVIR
	185	215	3259.67	DGQLVEIPANEVVPGDILQLEDGTVIPTDGR
	216	239	2652.31	IVTEDCFLQIDQSAITGESLAVDK
	240	252	1456.67	HYGDQTFSSSTVK
	240	253	1612.77	HYGDQTFSSSTVKR
	253	271	2013.98	RGEGFMVVTATGDNTFVGR
	254	271	1857.88	GEGFMVVTATGDNTFVGR
	272	278	686.42	AAALVNK
	429	435	863.50	SLKQYPK
	520	548	3254.47	GEGHWEILGVMPKMDPPRDDTAQTVSEAR
	538	548	1192.54	DDTAQTVSEAR

554	566	1302.75	VKMLTGDAVGIAK
910	918	1058.51	VSTQHEKET

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.