lip_psite_pair	delta_psite_lip	psite_Log2FC	Qvalue(LiP)	Log2FC(LiP_norm)
HOG1_IQDPQMTGYVSTR_T174	0	5.538	0.01	1.758
HOG1_IQDPQMTGYVSTR_S178	4	5.538	0.01	1.758
YLR257W_SYQSAEQEIDHTAPEK_S200	4.5	2.725	0.032	1.257
PAR32_TSSPNNNAPIVVGR_S141	11.5	−2.481	0.027	1.077
PAR32_TSSPNNNAPIVVGR_S138	14.5	−2.481	0.027	1.077
PAL1_SFDMPQLNTR_S64	10.5	−1.576	0.034	1.055
PAL1_SFDMPQLNTR_S61	7.5	2.585	0.034	1.055
PAL1_SFDMPQLNTR_S60	6.5	2.585	0.034	1.055
STE20_APAQETVTTPTSKPAQAR_T573	0.5	1.169	0.041	0.989
SEC31_VATPLSGGVPPAPLPK_T1050	5.5	2.795	0.028	0.986
SEC31_VATPLSGGVPPAPLPK_S1053	2.5	2.795	0.028	0.986
NET1_TTSNPSSILHDLPR_S1059	11.5	−1.269	0.035	0.942
FAR8_EAGSELHDLEK_T132	10	3.632	0.039	0.856
HAL5_FQEIECK_S275	12	−2.26	0.037	0.792
NUP2_NETSKPVFSF_T392	8.5	1.53	0.046	0.767
PRS5_ENYTFESHPGTPVSSSL_T127	2	1.976	0.033	0.74
BNI5_TIVVGGDNEYNHESSR_S263	18.5	2.259	0.039	0.729
SIS1_GGMGGMPGGFR_S173	10	1.54	0.033	0.682
MAK11_IMFGEK_S380	10.5	−1.122	0.041	0.678
KEL1_LDDLLER_S1003	10	1.424	0.042	0.615
SWA2_VDFSAPPLVPTNSTTK_S79	4.5	2.16	0.039	0.581
PAR32_PSPVLLPLK_S49	7	2.638	0.034	0.564
PAR32_PSPVLLPLK_S47	5	4.489	0.034	0.564
PAR32_PSPVLLPLK_S39	3	3.804	0.034	0.564
ABP1_NSIPAPK_S481	2	2.494	0.045	0.561
ABP1_NSIPAPK_S478	5	2.128	0.045	0.561
YPK1_GTINPSNSSVVPVR_T57	5.5	−6.359	0.038	0.518
PRS5_ENYTFESHPGTPVSS_Y119	5	1.291	0.046	0.509
PRS5_ENYTFESHPGTPVSS_T120	4	1.976	0.046	0.509
AKL1_TIGSDEALANEK_S541	2.5	1.127	0.044	0.46
BOI1_YGNLNDSASNIGK_S104	0	2.774	0.04	0.45
TSA1_NGTVLPCNWTPGAATIKPT_T174	0	1.951	0.034	0.373
EDE1_VATPSIPQQPIPLK_T1307	4.5	1.891	0.041	0.36
NET1_SSIVEEDIVSR_S278	4	1.541	0.035	0.312
PRM5_LLNSPESDGSVNR_S288	9	7.701	0.048	0.309
CLA4_NDQSTPQTMR_S477	15.5	2.113	0.04	0.176
BRO1_ASVVGGPPLLPQK_S740	7	5.345	0.032	0.149
BRO1_ASVVGGPPLLPQK_S728	5	7.838	0.032	0.149
EIS1_NVEDLPTQLEK_T720	1	1.96	0.047	−0.203
ABP1_SSAAPPPPPR_S515	3.5	2.179	0.049	−0.222
TIF4631_DSFITTR_S908	2	2.887	0.031	−0.224
SSB1_LSSEEIEK_S515	2.5	2.246	0.043	−0.231
WHI4_SFNDPFGLETISQR_S274	9.5	−2.846	0.041	−0.249
WHI4_SFNDPFGLETISQR_S258	6.5	10.84	0.041	−0.249
WHI4_SFNDPFGLETISQR_S254	10.5	10.371	0.041	−0.249
HXT2_LETDESPIQTK_S20	12	−1.119	0.027	−0.251
HXT2_LETDESPIQTK_S17	15	−1.119	0.027	−0.251
RPL7A_TAEQVAAER_T22	4	3.155	0.027	−0.333
POL3_IDDEDTPQLEK_S30	11	−1.624	0.027	−0.36
RAM1_ELETDTTEAR_S38	14.5	2.613	0.036	−0.362
PTK2_SSVALQDLIK_S105	3.5	1.414	0.049	−0.373
CKI1_VQESRPGSVR_S14	7.5	2.03	0.036	−0.379
YHR097C_LPSYEEAAGTPK_T76	3.5	1.631	0.047	−0.395
RAS2_NVNSSTTVVNAR_S225	1.5	3.117	0.044	−0.424
RAS2_NVNSSTTVVNAR_S224	2.5	3.117	0.044	−0.424
GPD2_SDSAVSIVHLK_S75	0	−2.608	0.049	−0.478
RTN1_LGPISNLVK_S206	6	4.879	0.042	−0.5
PBS2_LNEQTGSDNGSAVK_S38	10.5	−1.487	0.032	−0.516
TOP2_ENTPEQDDVATK_T1306	11.5	−1.343	0.026	−0.55
YRA1_SLDEIIGSNK_S8	4.5	−1.766	0.032	−0.559
YRA1_SLEDLDK_S211	3	3.604	0.035	−0.601
RCN2_TDPGVTGVDSSSLNK_S156	17	−1.21	0.04	−0.668
RCN2_TDPGVTGVDSSSLNK_S152	13	−1.21	0.04	−0.668
BUG1_DELIAAVEK_T274	16	2.168	0.025	−0.679
HRK1_SFLNFIGR_S37	3.5	2.188	0.042	−0.68
YDL121C_DTEESLGHDSASAS_S82	6.5	2.653	0.041	−0.763
YDL121C_DTEESLGHDSASAS_S80	4.5	2.653	0.041	−0.763
TPS3_VDCNNQELSNNK_S56	14.5	−1.105	0.033	−0.788
TPS3_VDCNNQELSNNK_S53	11.5	−1.105	0.033	−0.788
SUI3_SVSADAEAEK_S57	4.5	−1.599	0.042	−0.818
ENT1_SDENDDDLQR_S177	9.5	−1.217	0.034	−0.958
ENT1_SDENDDDLQR_S175	7.5	−1.217	0.034	−0.958
KRE6_AIASSPSLNSNLSK_S136	0.5	2.596	0.045	−1.014
YPR036W-A_VIPSLSPVSQPSSR_S32	9.5	−2.585	0.03	−1.892
PXL1_NVSAAPSVPVTMK_S63	4	−1.347	0.033	−2.279
PXL1_NVSAAPSVPVTMK_S53	14	−4.458	0.033	−2.279
HXT1_SNSSNSYELESGR_S9	10	5.423	0.027	−2.528
HXT1_SNSSNSYELESGR_S3	16	5.423	0.027	−2.528
HXT1_SNSSNSYELESGR_S15	4	2.908	0.027	−2.528