

**Appendix D Table 6.2 List of quantified SNO-peptides ( $N = 4, 3, 2$ )**

Sequence	Acc. No.	Protein Name	Protein Ratios			$N^e$
			Protein AD/WT		Average	
			1	2		
aALEQPcEGSLTRPk	P84086	Complexin-2	0.9126	0.9107	0.9116	4
aAPQWcQGk	O08539	Myc box-dependent-interacting protein 1	0.8536	0.9593	0.9064	4
acLYAGVk	P15105	Glutamine synthetase	0.8738	1.2478	1.0608	4
acNcLLLk	D3Z6E4	Enolase	1.0005	1.1356	1.0680	4
aDcLVPSEIRk	Q9Z2Q6	Septin-5	0.8748	0.9161	0.8955	4
aHVIgTPcSk	Q63912	Oligodendrocyte-myelin glycoprotein	1.0728	1.0754	1.0741	4
akFENLck	P11499	Heat shock protein HSP 90-beta	0.9359	1.2340	1.0849	4
aVLcPPPvk	P60764	$\alpha$ S-related C3 botulinum substrate 3, isoform CRA <sup>A</sup>	0.9486	0.9090	0.9288	4
dTVQcLcVvk	P20917	Mag protein	1.1142	1.4540	1.2841	4
eAELSkGESVcLDR	P62073	mitochondrial import inner membrane translocase subunit	1.0621	0.9561	1.0091	4
ecSEVQPk	Q9CQ75	ubiquinol:ubiquinone oxidoreductase [ubiquinol] 1 alpha subcomplex s	1.0077	1.0745	1.0411	4
eFNGLGDcLtk	P48962	ADP/ATP translocase 1	0.8598	0.8412	0.8505	4
eGAPSLck	Q9Z0E0	Neurochondrin	0.9389	1.0366	0.9877	4
eGkPcIIIk	P14094	Na <sup>+</sup> /potassium-transporting ATPase subunit beta	0.9537	0.8688	0.9113	4
IVHIQAGQcGNQIGAP99024;Q9ERD7		Tubulin beta-3/5 chain	1.0172	0.9631	0.9901	4
IVHLQAGQcGNQIGAP99024;Q9ERD7		Tubulin beta-3/5 chain	1.0172	0.9631	0.9901	4
fcLDNGAk	P09411	Phosphoglycerate kinase	0.9767	0.9487	0.9627	4
fSAVALck	Q9R0P9	Ubiquitin carboxyl-terminal hydrolase isozyme L1	1.0103	1.1053	1.0578	4
fSQIcAk	P56382	ATP synthase subunit epsilon, mitochondrial	0.9774	1.0728	1.0251	4
gIFPVLck	P52480	Pyruvate kinase PKM	0.9173	1.0148	0.9660	4
gLGDCLVk	P51881	ADP/ATP translocase 2	0.9399	0.8527	0.8963	4
gLLDVTck	E9PUV4	S-phase kinase-associated protein 1	0.9958	1.0151	1.0055	4
gSSNFcVk	Q80SW1	Putative adenosylhomocysteinase 2	0.9536	1.0544	1.0040	4
gVIEcLk	Q91VA7	isocitrate dehydrogenase [NAD] subunit, mitochondri	0.9444	0.9267	0.9356	4
gYLGPEQLPDcLk	P08249	Malate dehydrogenase, mitochondrial	0.9755	0.9095	0.9425	4
icQEVLPk	O55126	Protein NipSnap homolog 2	1.1651	1.1195	1.1423	4
VSNAScTTNcLAPLA	P16858	Glyceraldehyde-3-phosphate dehydrogenase	1.6736	1.3569	1.5152	4
lcAATATILDKPEDR	O35215	D-dopachrome decarboxylase	1.0819	1.0399	1.0609	4
lcDFNPk	B1AWE0	Clathrin light chain A	0.9350	0.8912	0.9131	4
IDcAQLk	P16330	2',3'-cyclic-nucleotide 3'-phosphodiesterase	1.0262	1.0667	1.0464	4

IHQVYFDAPScVk	Q62277	Synaptophysin	0.8612	0.8809	0.8711	4
IVDVicEk	P63011	Ras-related protein Rab-3A	0.8543	0.8348	0.8446	4
ncSETQYESk	P61982	14-3-3 protein gamma	1.1615	1.1426	1.1520	4
qLIcDPSPYIPDRVQk	P50396	Rab GDP dissociation inhibitor alpha	1.0321	1.0505	1.0413	4
sADcSVEEEPWkR	P43006	Excitatory amino acid transporter 2	0.8606	0.8796	0.8701	4
scNcLLLk	Q6PHC1	Alpha-enolase	1.0372	1.2227	1.1300	4
sIPicTLk	P31254	Ubiquitin-like modifier-activating enzyme 1 Y	0.9870	1.0210	1.0040	4
tkFENLck	P07901	Heat shock protein HSP 90-alpha	0.9415	1.1602	1.0508	4
vcNPIITk	Q504P4	Heat shock cognate 71 kDa protein	0.8824	1.1729	1.0277	4
sQTTWDSGFcAVNP	O89053	Coronin	0.8453	0.9239	0.8846	4
rTVAGLAGkDPVQcSI	Q99LX0	Protein deglycase DJ-1	0.9914	1.0407	1.0160	4
yIQAAck	Q68FD5	Clathrin heavy chain 1	0.6926	1.0493	0.8709	4
yNTDcVQGLTHSk	Q6PIC6	limum/potassium-transporting ATPase subunit alph	0.9111	0.8994	0.9053	4
aLANSLAcQGk	P05064	Fructose-bisphosphate aldolase A	0.9606	0.9746	0.9676	3
aYDATcLVk	Q9R0P3	S-formylglutathione hydrolase	0.9629	1.0061	0.9845	3
dVEREDIEFick	G5E839	T-complex protein 1 subunit delta	1.0257	1.0585	1.0421	3
gVLFVPGAFTPGcSI	G3UZJ4	Peroxisome oxidoreductin-5, mitochondrial	0.9592	0.8455	0.9024	3
lcDFGSAk	Q9WV60	Glycogen synthase kinase-3 beta	1.0070	0.9821	0.9945	3
ncFASVFEk	D3YXG6	Actin-related protein 2/3 complex subunit 2	1.0434	1.0649	1.0541	3
sTLTDSLck	P58252	Elongation factor 2	0.9077	0.9388	0.9233	3
tEIQVNcPk	D6RFU9	Synaptophysin-like protein 1	1.0723	1.1691	1.1207	3
tLDcEPk	P15105	Glutamine synthetase	0.9080	0.9140	0.9110	3
TicGkGLSATVTGGQ	P60202	Myelin proteolipid protein	0.8584	0.9284	0.8934	3
vcGSNLLSIck	P60202	Myelin proteolipid protein	0.9217	1.2771	1.0994	3
vGAFTVVckDAEEAk	P05202	Aspartate aminotransferase, mitochondrial	1.0127	0.9819	0.9973	3
vLGFcHYLPEEQFpk	Q6PIC6	limum/potassium-transporting ATPase subunit alph	0.7917	0.9543	0.8730	3
yMAccLLYRGDVPk	P68373;P68368	Tubulin alpha-1C/4A chain	1.1201	1.1991	1.1596	3
aIPDLcASK	B1AQX6	SRC kinase-signaling inhibitor 1	0.88074	0.95201	0.91638	2
LDLDSckEAADGYQ	Q60864	Stress-induced-phosphoprotein 1	1.17080	0.96354	1.06717	2
aVLFcLSEDkk	P18760	Cofilin-1	1.00039	0.99737	0.99888	2
dNILIEcEAK	A0A087WNW2	Neurofascin	0.92379	0.93406	0.92892	2
eFkGLGDcLVk	P51881	ADP/ATP translocase 2	0.88527	0.94180	0.91353	2
eGVVEcSFVQSk	P08249	Malate dehydrogenase, mitochondrial	0.99128	0.86402	0.92765	2
gILLYGPPGcGk	P46460	Vesicle-fusing ATPase	0.86212	0.76464	0.81338	2

gLYDGPVcEVSVTPk	O08553	Dihydropyrimidinase-related protein 2	1.13003	0.91432	1.02217	2
gYSIPEcQk	Q9CZU6	Citrate synthase, mitochondrial	0.97983	0.88645	0.93314	2
icSPDKMIGFSETAk	P46460	Vesicle-fusing ATPase	1.46104	0.93618	1.19861	2
iNMcGLTTk	P05201	Aspartate aminotransferase, cytoplasmic	0.99850	1.02442	1.01146	2
iVSSkDYcVTANSk	D3Z736	L-lactate dehydrogenase	0.90204	0.98859	0.94532	2
IVIVGDGAcGk	Q9QUI0	Transforming protein RhoA	0.99164	0.94253	0.96708	2
IVLcEVFk	P15105	Glutamine synthetase	0.94081	0.83750	0.88916	2
nIInkDGGSYVck	O35136	Neural cell adhesion molecule 2	0.82052	0.88730	0.85391	2
nkGVVLGGcGDk	P61922	4-aminobutyrate aminotransferase, mitochondrial	1.15574	1.05495	1.10535	2
qIFGDYkTTIcGk	P60202	Myelin proteolipid protein	1.07930	1.05734	1.06832	2
rALANSLAcQGk	P05064	Fructose-bisphosphate aldolase A	1.31710	1.01798	1.16754	2
sTcTYVGAak	Q9DCZ1	GMP reductase 1	1.00902	1.14037	1.07469	2
tcLLNETGDEPFQYkN	P15105	Glutamine synthetase	1.08496	0.85608	0.97052	2
vGAFTVVck	P05202	Aspartate aminotransferase, mitochondrial	0.91613	1.06947	0.99280	2
yEVAVPLck	Q5UE59	Kinesin light chain 1	1.02298	1.06128	1.04213	2
acSLAk	P63101	14-3-3 protein zeta/delta	0.51472	N.A.	0.51472	2
dcLPELk	E9PUD2	Dynamin-1-like protein	0.94241	N.A.	0.94241	2
eAVAick	Q2NKI4	Protein kinase C	0.85623	N.A.	0.85623	2
fGSGPck	Q9D7N9	Adipocyte plasma membrane-associated protein	1.06813	N.A.	1.06813	2
fILScADDk	P63005	Platelet-activating factor acetylhydrolase IB subunit alpha	0.75326	N.A.	0.75326	2
fRGYSIPEcQk	Q9CZU6	Citrate synthase, mitochondrial	0.98783	N.A.	0.98783	2
gkTEIQVncPk	D6RFU9	Synaptophysin-like protein 1	0.95807	N.A.	0.95807	2
gkVNSITVDNck	D3YTR7	Adenylyl cyclase-associated protein	0.84028	N.A.	0.84028	2
iEAAcFATIkDGk	Q9D6R2	Malate dehydrogenase [NAD] subunit alpha, mitochondrial	1.02913	N.A.	1.02913	2
iIAcDGGGGALGHPk	P52503	Ubiquinol:ubiquinone oxidoreductase [ubiquinol] iron-sulfur protein 6, mitochondrial	1.40584	N.A.	1.40584	2
IIVPFcGHik	Q8VED9	Galectin-related protein	1.26601	N.A.	1.26601	2
mcLVEIEkAPk	Q91VD9	Ubiquinol:ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	0.98849	N.A.	0.98849	2
ncIGDFLk	Q6ZQ38	Cullin-associated NEDD8-dissociated protein 1	1.04642	N.A.	1.04642	2
nHTGEKLFecKk	E9Q9G3	Protein Zfp938	1.05495	N.A.	1.05495	2
nSLDcEIVSak	P40124	Adenylyl cyclase-associated protein 1	0.90126	N.A.	0.90126	2
sAPSIPkENFSclTR	P14152	Malate dehydrogenase, cytoplasmic	1.05373	N.A.	1.05373	2
sSGFcPk	A2AMH3	Choline transporter-like protein 1	1.00882	N.A.	1.00882	2
tAWRLDcAQLk	P16330	2',3'-cyclic-nucleotide 3'-phosphodiesterase	1.14900	N.A.	1.14900	2
yNPNVLPVQcTGkR	P14094	Sodium/potassium-transporting ATPase subunit beta	0.82822	N.A.	0.82822	2

Sequence	Acc. No.	Protein Name	SNO Site Occupancy in WT <sup>a</sup>				Average
			%SNO in WT in each Biological Replicate				
			1	2	3	4	
aALEQPcEGSLTRPk	P84086	Complexin-2	0.21%	0.23%	0.24%	0.18%	0.22%
aAPQWcQGk	O08539	Myc box-dependent-interacting protein 1	0.28%	0.47%	0.28%	0.35%	0.35%
acLYAGVk	P15105	Glutamine synthetase	3.18%	3.37%	9.34%	8.54%	6.11%
acNcLLLk	D3Z6E4	Enolase	10.67%	10.35%	14.93%	#####	12.46%
aDcLVPSEIRk	Q9Z2Q6	Septin-5	0.11%	0.19%	0.17%	0.23%	0.18%
aHVIgTPcSk	Q63912	Oligodendrocyte-myelin glycoprotein	4.93%	3.27%	3.04%	2.75%	3.50%
akFENLck	P11499	Heat shock protein HSP 90-beta	0.96%	0.83%	0.43%	0.88%	0.78%
aVLcPPPvK	P60764	αS-related C3 botulinum substrate 3, isoform CRA <sup>A</sup>	0.31%	0.60%	0.49%	0.52%	0.48%
dTVQcLcVvK	P20917	Mag protein	3.78%	5.09%	5.52%	3.44%	4.46%
eAELSkGESVcLDR	P62073	mitochondrial import inner membrane translocase subunit	1.90%	2.53%	2.50%	2.74%	2.42%
ecSEVQPk	Q9CQ75	isovaleryl-CoA dehydrogenase [ubiquinone] 1 alpha subcomplex s	1.08%	1.17%	0.95%	0.90%	1.03%
eFNGLGDcLtk	P48962	ADP/ATP translocase 1	0.80%	0.93%	0.73%	0.45%	0.73%
eGAPSLlck	Q9Z0E0	Neurochondrin	0.74%	0.84%	0.67%	0.62%	0.72%
eGkPcIIIk	P14094	Na <sup>+</sup> /potassium-transporting ATPase subunit beta	0.33%	0.22%	0.34%	0.43%	0.33%
IVHIQAGQcGNQIGAP99024;Q9ERD7		Tubulin beta-3/5 chain	1.74%	1.38%	1.45%	1.48%	1.51%
IVHLQAGQcGNQIGAP99024;Q9ERD7		Tubulin beta-3/5 chain	1.74%	1.38%	1.45%	1.48%	1.51%
fcLDNGAk	P09411	Phosphoglycerate kinase	0.28%	0.28%	0.22%	0.21%	0.25%
fSAVALck	Q9R0P9	Ubiquitin carboxyl-terminal hydrolase isozyme L1	0.51%	0.46%	0.36%	0.48%	0.45%
fsQIcAk	P56382	ATP synthase subunit epsilon, mitochondrial	0.12%	0.14%	0.20%	0.14%	0.15%
gIFPVLck	P52480	Pyruvate kinase PKM	0.16%	0.34%	0.16%	0.30%	0.24%
gLGDCLVk	P51881	ADP/ATP translocase 2	0.87%	0.90%	0.67%	0.46%	0.73%
gLLDVTck	E9PUV4	S-phase kinase-associated protein 1	0.56%	0.72%	0.50%	0.66%	0.61%
gSSNFcVk	Q80SW1	Putative adenosylhomocysteinase 2	0.69%	0.92%	0.61%	0.76%	0.74%
gVIEcLk	Q91VA7	isocitrate dehydrogenase [NAD] subunit, mitochondrial	0.30%	0.35%	0.21%	0.31%	0.29%
gYLGPEQLPDcLk	P08249	Malate dehydrogenase, mitochondrial	0.46%	0.97%	0.45%	0.79%	0.67%
icQEVLPk	O55126	Protein NipSnap homolog 2	1.45%	1.39%	1.44%	1.44%	1.43%
VSNAScTTNcLAPLAl	P16858	Glyceraldehyde-3-phosphate dehydrogenase	0.48%	0.83%	0.06%	0.33%	0.42%
lcAATATILDKPEDR	O35215	D-dopachrome decarboxylase	1.72%	1.27%	1.56%	1.48%	1.51%
lcDFNPk	B1AWE0	Clathrin light chain A	0.33%	0.23%	0.26%	0.19%	0.25%
IDcAQLk	P16330	2',3'-cyclic-nucleotide 3'-phosphodiesterase	1.58%	2.28%	1.76%	1.83%	1.86%
IHQVYFDAPScVk	Q62277	Synaptophysin	0.43%	0.62%	0.85%	1.08%	0.75%

IVDVIcEk	P63011	Ras-related protein Rab-3A	0.91%	0.71%	0.90%	1.01%	0.88%
ncSETQYESk	P61982	14-3-3 protein gamma	7.47%	5.87%	6.58%	8.80%	7.18%
qLIcDPSYIPDRVQk	P50396	Rab GDP dissociation inhibitor alpha	0.20%	0.16%	0.08%	0.08%	0.13%
sADcSVEEEPWkR	P43006	Excitatory amino acid transporter 2	0.75%	0.44%	0.63%	0.26%	0.52%
scNcLLLk	Q6PHC1	Alpha-enolase	3.95%	3.85%	4.57%	4.32%	4.17%
sIPicTLk	P31254	Ubiquitin-like modifier-activating enzyme 1 Y	1.89%	1.43%	1.42%	1.66%	1.60%
tkFENLck	P07901	Heat shock protein HSP 90-alpha	0.14%	0.26%	0.12%	0.34%	0.22%
vcNPIITk	Q504P4	Heat shock cognate 71 kDa protein	21.74%	25.43%	25.22%	#####	24.57%
rSQTWDSGFcAVNP	O89053	Coronin	0.31%	0.30%	0.29%	0.43%	0.34%
rTVAGLAGkDPVQcSI	Q99LX0	Protein deglycase DJ-1	0.13%	0.15%	0.20%	0.23%	0.18%
yiQAAck	Q68FD5	Clathrin heavy chain 1	0.97%	0.98%	0.86%	0.80%	0.90%
yNTDcVQGLTHSk	Q6PIC6	lium/potassium-transporting ATPase subunit alph	0.92%	0.75%	0.90%	0.79%	0.84%
aLANSLAcQGk	P05064	Fructose-bisphosphate aldolase A	0.0034	0.0019	0.0032	N.A.	0.28%
aYDATcLVk	Q9R0P3	S-formylglutathione hydrolase	0.0069	0.0029	0.0030	N.A.	0.42%
dVEREDIEFick	G5E839	T-complex protein 1 subunit delta	0.0030	0.0025	0.0028	N.A.	0.28%
gVLFVPGAFTPGcSt	G3UZJ4	Peroxisredoxin-5, mitochondrial	0.0140	0.0070	0.0074	N.A.	0.95%
lcDFGSAk	Q9WV60	Glycogen synthase kinase-3 beta	0.0174	0.0156	0.0107	N.A.	1.45%
ncFASVFEk	D3YXG6	Actin-related protein 2/3 complex subunit 2	0.0377	0.0315	0.0340	N.A.	3.44%
sTLTDSLvck	P58252	Elongation factor 2	0.0143	0.0032	0.0026	N.A.	0.67%
tEIQVNcPk	D6RFU9	Synaptophysin-like protein 1	0.0179	0.1282	0.1224	N.A.	8.95%
tLDcEPk	P15105	Glutamine synthetase	0.0039	0.0009	0.0019	N.A.	0.22%
TlcGkGLSATVTGGQ	P60202	Myelin proteolipid protein	0.0324	0.0397	0.0389	N.A.	3.70%
vcGSNLLSIck	P60202	Myelin proteolipid protein	0.0212	0.0124	0.0351	N.A.	2.29%
vGAFTVVckDAEEAk	P05202	Aspartate aminotransferase, mitochondrial	0.0042	0.0007	0.0025	N.A.	0.25%
vLGFcHYYPPEEQFPl	Q6PIC6	lium/potassium-transporting ATPase subunit alph	0.0215	0.0083	0.0085	N.A.	1.28%
yMAccLLYRGDVVPk	P68373;P68368	Tubulin alpha-1C/4A chain	0.0117	0.0075	0.0073	N.A.	0.88%
aIPDLcASK	B1AQX6	SRC kinase-signaling inhibitor 1	0.47%	0.54%	N.A.	N.A.	0.51%
LDLDSckEAADGYQ	Q60864	Stress-induced-phosphoprotein 1	1.13%	1.13%	N.A.	N.A.	1.13%
aVLFcLSEdkk	P18760	Cofilin-1	0.12%	0.17%	N.A.	N.A.	0.15%
dNILIEcEak	A0A087WNW2	Neurofascin	1.79%	1.85%	N.A.	N.A.	1.82%
eFkGLGDcLVk	P51881	ADP/ATP translocase 2	0.23%	0.47%	N.A.	N.A.	0.35%
eGVVEcSFVQSk	P08249	Malate dehydrogenase, mitochondrial	2.28%	2.26%	N.A.	N.A.	2.27%
gILLYGPPGcGk	P46460	Vesicle-fusing ATPase	0.26%	0.19%	N.A.	N.A.	0.22%
gLYDGPVcEVSVTPk	O08553	Dihydropyrimidinase-related protein 2	0.01%	0.27%	N.A.	N.A.	0.14%

gYSIPEcQk	Q9CZU6	Citrate synthase, mitochondrial	0.18%	0.25%	N.A.	N.A.	0.21%
icSPDkMIGFSETAk	P46460	Vesicle-fusing ATPase	0.91%	0.99%	N.A.	N.A.	0.95%
iNMcGLTTk	P05201	Aspartate aminotransferase, cytoplasmic	0.86%	0.91%	N.A.	N.A.	0.89%
iVSSkDYcVTANSk	D3Z736	L-lactate dehydrogenase	0.63%	0.61%	N.A.	N.A.	0.62%
IVIVGDGAcGk	Q9QUI0	Transforming protein RhoA	1.65%	3.98%	N.A.	N.A.	2.82%
IVLcEVFk	P15105	Glutamine synthetase	1.53%	1.70%	N.A.	N.A.	1.62%
nIINkDGGSYVck	O35136	Neural cell adhesion molecule 2	0.34%	0.38%	N.A.	N.A.	0.36%
nkGVVLGGcGDk	P61922	4-aminobutyrate aminotransferase, mitochondrial	0.96%	1.03%	N.A.	N.A.	1.00%
qIFGDYkTTIcGk	P60202	Myelin proteolipid protein	0.53%	0.46%	N.A.	N.A.	0.50%
rALANSLAcQGk	P05064	Fructose-bisphosphate aldolase A	0.33%	0.33%	N.A.	N.A.	0.33%
sTcTYVGAAk	Q9DCZ1	GMP reductase 1	1.36%	0.73%	N.A.	N.A.	1.04%
tcLLNETGDEPFQYkN	P15105	Glutamine synthetase	0.34%	0.34%	N.A.	N.A.	0.34%
vGAFTVVck	P05202	Aspartate aminotransferase, mitochondrial	0.12%	0.21%	N.A.	N.A.	0.17%
yEVAVPLck	Q5UE59	Kinesin light chain 1	0.37%	0.41%	N.A.	N.A.	0.39%
acSLAk	P63101	14-3-3 protein zeta/delta	30.10%	25.62%	N.A.	N.A.	27.86%
dcLPELk	E9PUD2	Dynamin-1-like protein	0.99%	0.84%	N.A.	N.A.	0.92%
eAVAIck	Q2NKI4	Protein kinase C	0.01%	0.23%	N.A.	N.A.	0.12%
fGSGPck	Q9D7N9	Adipocyte plasma membrane-associated protein	1.84%	1.35%	N.A.	N.A.	1.60%
fiLScADDk	P63005	Phorbol-12-myristate-13-acetate-activating factor acetylhydrolase IB subunit alpha	3.32%	4.32%	N.A.	N.A.	3.82%
fRGYSIPEcQk	Q9CZU6	Citrate synthase, mitochondrial	0.07%	0.07%	N.A.	N.A.	0.07%
gkTEIQVncPk	D6RFU9	Synaptophysin-like protein 1	30.53%	27.68%	N.A.	N.A.	29.10%
gkVNSITVDNck	D3YTR7	Adenylyl cyclase-associated protein	2.45%	2.25%	N.A.	N.A.	2.35%
iEAAcFATIkDGk	Q9D6R2	Malate dehydrogenase [NAD] subunit alpha, mitochondrial	1.02%	1.14%	N.A.	N.A.	1.08%
iIAcDGGGGALGHPk	P52503	Malate dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	4.92%	2.10%	N.A.	N.A.	3.51%
IIVPFcGHik	Q8VED9	Galectin-related protein	1.00%	0.87%	N.A.	N.A.	0.93%
mcLVEIEkAPk	Q91VD9	Ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	0.06%	0.42%	N.A.	N.A.	0.24%
ncIGDFLk	Q6ZQ38	Cullin-associated NEDD8-dissociated protein 1	1.21%	1.11%	N.A.	N.A.	1.16%
nHTGEKLFecKk	E9Q9G3	Protein Zfp938	1.66%	1.74%	N.A.	N.A.	1.70%
nSLDcEIVSAk	P40124	Adenylyl cyclase-associated protein 1	2.45%	2.59%	N.A.	N.A.	2.52%
sAPSIPkENFScLTR	P14152	Malate dehydrogenase, cytoplasmic	0.05%	0.20%	N.A.	N.A.	0.13%
sSGFcPk	A2AMH3	Choline transporter-like protein 1	2.09%	1.32%	N.A.	N.A.	1.71%
tAWRLDcAQLk	P16330	2',3'-cyclic-nucleotide 3'-phosphodiesterase	0.29%	0.61%	N.A.	N.A.	0.45%
yNPNVLPVQcTGkR	P14094	Sodium/potassium-transporting ATPase subunit beta	0.86%	0.71%	N.A.	N.A.	0.79%

SNO Site Occupancy in AD<sup>a</sup>

Sequence	Acc. No.	Protein Name	%SNO in AD in each Biological Replicate				Average
			1	2	3	4	
aALEQPcEGSLTRPk	P84086	Complexin-2	0.29%	0.32%	0.21%	0.22%	0.26%
aAPQWcQGk	O08539	Myc box-dependent-interacting protein 1	0.56%	0.49%	0.37%	0.44%	0.47%
acLYAGVk	P15105	Glutamine synthetase	4.58%	3.52%	6.51%	6.96%	5.39%
acNcLLLk	D3Z6E4	Enolase	12.41%	9.87%	9.83%	#####	11.17%
aDcLVPSEIRk	Q9Z2Q6	Septin-5	0.41%	0.28%	0.26%	0.27%	0.30%
aHVIgTPcSk	Q63912	Oligodendrocyte-myelin glycoprotein	3.46%	5.63%	2.12%	2.32%	3.38%
akFENLck	P11499	Heat shock protein HSP 90-beta	0.78%	0.84%	0.53%	0.73%	0.72%
aVLcPPPvk	P60764	αS-related C3 botulinum substrate 3, isoform CRA <sup>A</sup>	0.64%	0.60%	0.50%	0.66%	0.60%
dTVQcLcVvk	P20917	Mag protein	3.90%	3.83%	2.37%	4.50%	3.65%
eAELSkGESVcLDR	P62073	mitochondrial import inner membrane translocase subunit	2.10%	1.47%	1.43%	3.32%	2.08%
ecSEVQPk	Q9CQ75	isocitrate dehydrogenase [ubiquinone] 1 alpha subcomplex s	1.24%	1.21%	0.74%	1.04%	1.06%
eFNGLGDcLtk	P48962	ADP/ATP translocase 1	1.07%	1.17%	0.83%	1.14%	1.05%
eGAPSLck	Q9Z0E0	Neurochondrin	0.75%	0.76%	0.65%	0.59%	0.69%
eGkPcIIIk	P14094	Na <sup>+</sup> /potassium-transporting ATPase subunit beta	0.41%	0.19%	0.51%	0.61%	0.43%
IVHIQAGQcGNQIGAP99024;Q9ERD7		Tubulin beta-3/5 chain	1.37%	1.47%	1.04%	1.41%	1.33%
IVHLQAGQcGNQIGAP99024;Q9ERD7		Tubulin beta-3/5 chain	1.37%	1.47%	1.04%	1.41%	1.33%
fcLDNGAk	P09411	Phosphoglycerate kinase	0.33%	0.27%	0.19%	0.26%	0.26%
fSAVALck	Q9R0P9	Ubiquitin carboxyl-terminal hydrolase isozyme L1	0.43%	0.48%	0.37%	0.37%	0.41%
fSQIcAk	P56382	ATP synthase subunit epsilon, mitochondrial	0.15%	0.18%	0.13%	0.14%	0.15%
gIFPVLck	P52480	Pyruvate kinase PKM	0.36%	0.35%	0.17%	0.20%	0.27%
gLGDcLVk	P51881	ADP/ATP translocase 2	0.77%	0.80%	0.63%	0.70%	0.73%
gLLDVTck	E9PUV4	S-phase kinase-associated protein 1	0.81%	0.60%	0.56%	0.73%	0.68%
gSSNFcVk	Q80SW1	Putative adenosylhomocysteinase 2	1.10%	0.85%	0.62%	0.74%	0.83%
gVIEcLk	Q91VA7	isocitrate dehydrogenase [NAD] subunit, mitochondri	0.47%	0.38%	0.33%	0.33%	0.38%
gYLGPEQLPDcLk	P08249	Malate dehydrogenase, mitochondrial	0.78%	0.88%	0.76%	0.74%	0.79%
icQEVLPk	O55126	Protein NipSnap homolog 2	1.25%	1.33%	1.24%	1.19%	1.25%
VSNAscTTNcLAPLA	P16858	Glyceraldehyde-3-phosphate dehydrogenase	0.59%	0.52%	0.17%	0.35%	0.40%
lcAATATILdkPEDR	O35215	D-dopachrome decarboxylase	1.68%	1.41%	0.56%	1.38%	1.26%
lcDFNPk	B1AWE0	Clathrin light chain A	0.36%	0.29%	0.23%	0.26%	0.28%
IDcAQLk	P16330	2',3'-cyclic-nucleotide 3'-phosphodiesterase	1.99%	1.69%	0.50%	2.29%	1.62%
IHQVYFDAPScVk	Q62277	Synaptophysin	1.19%	0.97%	0.65%	0.73%	0.89%
IVDVIcEk	P63011	Ras-related protein Rab-3A	0.88%	0.99%	0.93%	1.00%	0.95%

ncSETQYESk	P61982	14-3-3 protein gamma	4.84%	5.78%	3.37%	6.02%	5.00%
qLIcDPSYIPDRVQk	P50396	Rab GDP dissociation inhibitor alpha	0.16%	0.15%	0.13%	0.11%	0.14%
sADcSVEEEPWkR	P43006	Excitatory amino acid transporter 2	0.40%	0.51%	0.78%	0.90%	0.65%
scNcLLLk	Q6PHC1	Alpha-enolase	4.23%	3.84%	3.00%	3.80%	3.72%
sIPicTLk	P31254	Ubiquitin-like modifier-activating enzyme 1 Y	1.98%	1.78%	1.39%	1.56%	1.68%
tkFENLck	P07901	Heat shock protein HSP 90-alpha	0.37%	0.44%	0.14%	0.20%	0.29%
vcNPIITk	Q504P4	Heat shock cognate 71 kDa protein	26.71%	26.11%	15.25%	#####	22.98%
QTTWDSGFcAVNP	O89053	Coronin	0.44%	0.54%	0.32%	0.31%	0.40%
TVAGLAGkDPVQcSI	Q99LX0	Protein deglycase DJ-1	0.23%	0.14%	0.23%	0.18%	0.20%
yIQAAck	Q68FD5	Clathrin heavy chain 1	1.42%	1.35%	0.72%	0.71%	1.05%
yNTDcVQGLTHSk	Q6PIC6	limum/potassium-transporting ATPase subunit alpha	1.08%	0.90%	0.54%	0.96%	0.87%
aLANSLAcQGk	P05064	Fructose-bisphosphate aldolase A	0.0040	0.0020	0.0018	N.A.	0.26%
aYDATcLVk	Q9R0P3	S-formylglutathione hydrolase	0.0070	0.0031	0.0029	N.A.	0.43%
dVEREDIEFick	G5E839	T-complex protein 1 subunit delta	0.0033	0.0025	0.0027	N.A.	0.28%
gVLFGVPGAFTPGcSI	G3UZJ4	Peroxisome oxidoreductin-5, mitochondrial	0.0141	0.0083	0.0083	N.A.	1.02%
lcDFGSAk	Q9WV60	Glycogen synthase kinase-3 beta	0.0145	0.0157	0.0144	N.A.	1.49%
ncFASVFEk	D3YXG6	Actin-related protein 2/3 complex subunit 2	0.0311	0.0323	0.0293	N.A.	3.09%
sTLTDSLvck	P58252	Elongation factor 2	0.0148	0.0033	0.0039	N.A.	0.73%
tEIQVNcPk	D6RFU9	Synaptophysin-like protein 1	0.0177	0.0606	0.1356	N.A.	7.13%
tLDcEPk	P15105	Glutamine synthetase	0.0044	0.0015	0.0027	N.A.	0.29%
TicGkGLSATVTGGQ	P60202	Myelin proteolipid protein	0.0969	0.0236	0.0368	N.A.	5.24%
vcGSNLLSIck	P60202	Myelin proteolipid protein	0.0041	0.0029	0.0198	N.A.	0.89%
vGAFTVVcKDAEEAk	P05202	Aspartate aminotransferase, mitochondrial	0.0038	0.0028	0.0025	N.A.	0.30%
vLGFcHYLPEEQFk	Q6PIC6	limum/potassium-transporting ATPase subunit alpha	0.0270	0.0081	0.0082	N.A.	1.44%
yMAcLLYRGDVVPk	P68373;P68368	Tubulin alpha-1C/4A chain	0.0117	0.0054	0.0061	N.A.	0.77%
aIPDLdAsk	B1AQX6	SRC kinase-signaling inhibitor 1	0.59%	0.64%	N.A.	N.A.	0.62%
LDLSSckEAADGYQ	Q60864	Stress-induced-phosphoprotein 1	1.20%	1.33%	N.A.	N.A.	1.26%
aVLFcLSEDkk	P18760	Cofilin-1	0.15%	0.16%	N.A.	N.A.	0.15%
dNILIEcEak	A0A087WNW2	Neurofascin	1.83%	2.00%	N.A.	N.A.	1.91%
eFkGLGDcLVk	P51881	ADP/ATP translocase 2	0.45%	0.38%	N.A.	N.A.	0.41%
eGVVcSFVQSk	P08249	Malate dehydrogenase, mitochondrial	2.25%	2.34%	N.A.	N.A.	2.29%
gILLYGPPGcGk	P46460	Vesicle-fusing ATPase	0.24%	0.24%	N.A.	N.A.	0.24%
gLYDGPVcEVSVTPk	O08553	Dihydropyrimidinase-related protein 2	0.16%	0.13%	N.A.	N.A.	0.15%
gYSIPEcQk	Q9CZU6	Citrate synthase, mitochondrial	0.30%	0.31%	N.A.	N.A.	0.30%



icSPDkMIGFSETAk	P46460	Vesicle-fusing ATPase	1.07%	0.93%	N.A.	N.A.	1.00%
iNMcGLTTk	P05201	Aspartate aminotransferase, cytoplasmic	0.80%	0.80%	N.A.	N.A.	0.80%
iVSSkDYcVTANSk	D3Z736	L-lactate dehydrogenase	0.45%	0.61%	N.A.	N.A.	0.53%
IVIVGDGAcGk	Q9QUI0	Transforming protein RhoA	1.75%	3.53%	N.A.	N.A.	2.64%
IVLcEVFk	P15105	Glutamine synthetase	1.97%	1.83%	N.A.	N.A.	1.90%
nIINkDGGSYVck	O35136	Neural cell adhesion molecule 2	0.38%	0.71%	N.A.	N.A.	0.54%
nkGVVLGGcGDk	P61922	4-aminobutyrate aminotransferase, mitochondrial	0.82%	0.82%	N.A.	N.A.	0.82%
qIFGDYkTTIcGk	P60202	Myelin proteolipid protein	0.19%	0.61%	N.A.	N.A.	0.40%
rALANSLAcQGk	P05064	Fructose-bisphosphate aldolase A	0.38%	0.41%	N.A.	N.A.	0.40%
sTcTYVGAak	Q9DCZ1	GMP reductase 1	1.39%	0.81%	N.A.	N.A.	1.10%
tcLLNETGDEPFQYkN	P15105	Glutamine synthetase	0.36%	0.45%	N.A.	N.A.	0.40%
vGAFTVVck	P05202	Aspartate aminotransferase, mitochondrial	0.15%	0.15%	N.A.	N.A.	0.15%
yEVAVPLck	Q5UE59	Kinesin light chain 1	0.42%	0.35%	N.A.	N.A.	0.38%
acSLAk	P63101	14-3-3 protein zeta/delta	54.95%	53.87%	N.A.	N.A.	54.41%
dcLPELk	E9PUD2	Dynamin-1-like protein	0.71%	0.89%	N.A.	N.A.	0.80%
eAVAIck	Q2NKI4	Protein kinase C	0.22%	0.31%	N.A.	N.A.	0.27%
fGSGPck	Q9D7N9	Adipocyte plasma membrane-associated protein	1.27%	2.40%	N.A.	N.A.	1.83%
fILScADDk	P63005	Platelet-activating factor acetylhydrolase IB subunit alpha	2.25%	4.28%	N.A.	N.A.	3.27%
fRGYSIPEcQk	Q9CZU6	Citrate synthase, mitochondrial	0.45%	0.39%	N.A.	N.A.	0.42%
gkTEIQVncPk	D6RFU9	Synaptophysin-like protein 1	21.72%	34.70%	N.A.	N.A.	28.21%
gkVNSITVDNck	D3YTR7	Adenylyl cyclase-associated protein	2.32%	3.31%	N.A.	N.A.	2.81%
iEAAcFATIkDGk	Q9D6R2	Malate dehydrogenase [NAD] subunit alpha, mitochondrial	0.84%	1.00%	N.A.	N.A.	0.92%
iIAcDGGGGALGHPk	P52503	Malate dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	1.49%	4.74%	N.A.	N.A.	3.12%
IIVPFcGHik	Q8VED9	Galectin-related protein	0.24%	1.30%	N.A.	N.A.	0.77%
mcLVEIEkAPk	Q91VD9	Ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	0.26%	0.29%	N.A.	N.A.	0.28%
ncIGDFLk	Q6ZQ38	Cullin-associated NEDD8-dissociated protein 1	0.98%	0.93%	N.A.	N.A.	0.96%
nHTGEKLFecKk	E9Q9G3	Protein Zfp938	1.39%	1.45%	N.A.	N.A.	1.42%
nSLDcEIVSAk	P40124	Adenylyl cyclase-associated protein 1	2.93%	2.73%	N.A.	N.A.	2.83%
sAPSIPKENFScLTR	P14152	Malate dehydrogenase, cytoplasmic	0.17%	0.24%	N.A.	N.A.	0.20%
sSGFcPk	A2AMH3	Choline transporter-like protein 1	0.89%	2.32%	N.A.	N.A.	1.61%
tAWRLDcAQLk	P16330	2',3'-cyclic-nucleotide 3'-phosphodiesterase	0.41%	0.91%	N.A.	N.A.	0.66%
yNPNVLPVQcTGkR	P14094	Sodium/potassium-transporting ATPase subunit beta	0.72%	0.74%	N.A.	N.A.	0.73%

AD/WT in Each Biological Replicate<sup>b</sup>

Sequence

Acc. No.

Protein Name

Log<sub>2</sub>SNO(AD/WT)

Average

Statistics

			1	2	3	4	Average	Status
aALEQPcEGSLTRPk	P84086	Complexin-2	0.4505	0.4419	-0.1440	0.3197	0.2670	0.1144
aAPQWcQGk	O08539	Myc box-dependent-interacting protein 1	0.9791	0.0452	0.4153	0.3412	0.4452	0.0050
acLYAGVk	P15105	Glutamine synthetase	0.5249	0.0651	-0.5202	#####	-0.0561	0.9941
acNcLLLk	D3Z6E4	Enolase	0.2180	-0.0686	-0.6034	#####	-0.1493	0.5670
aDcLVPSEIRk	Q9Z2Q6	Septin-5	1.8684	0.5275	0.5759	0.2461	0.8045	0.0001
aHVIGTPcSk	Q63912	Oligodendrocyte-myelin glycoprotein	-0.5117	0.7846	-0.5223	#####	-0.1242	0.8758
akFENLck	P11499	Heat shock protein HSP 90-beta	-0.3059	0.0092	0.2798	#####	-0.0701	0.6820
aVLcPPPVK	P60764	s-related C3 botulinum substrate 3, isoform CRA	1.0732	0.0063	0.0197	0.3620	0.3653	0.0099
dTVQcLcVVK	P20917	Mag protein	0.0445	-0.4088	-1.2226	0.3883	-0.2996	0.5204
eAELSkGESVcLDR	P62073	ndrial import inner membrane translocase subunit	0.1490	-0.7862	-0.8035	0.2754	-0.2913	0.4000
ecSEVQPk	Q9CQ75	ehydrogenase [ubiquinone] 1 alpha subcomplex s	0.1985	0.0472	-0.3525	0.1992	0.0231	0.8565
eFNGLGDcLTK	P48962	ADP/ATP translocase 1	0.4103	0.3300	0.1760	1.3245	0.5602	0.0001
eGAPSLck	Q9Z0E0	Neurochondrin	0.0199	-0.1386	-0.0270	#####	-0.0496	0.1140
eGkPcIIIk	P14094	dium/potassium-transporting ATPase subunit beta	0.3158	-0.1716	0.5931	0.4897	0.3068	0.1409
IVHIQAGQcGNQIGAP99024;Q9ERD7		Tubulin beta-3/5 chain	-0.3376	0.0929	-0.4754	#####	-0.1975	0.2996
IVHLQAGQcGNQIGAP99024;Q9ERD7		Tubulin beta-3/5 chain	-0.3376	0.0929	-0.4754	#####	-0.1975	0.3112
fcLDNGAk	P09411	Phosphoglycerate kinase	0.2713	-0.0802	-0.1814	0.3228	0.0831	0.4135
fSAVALck	Q9R0P9	Ubiquitin carboxyl-terminal hydrolase isozyme L1	-0.2347	0.0588	0.0327	#####	-0.1341	0.4113
fSQIcAk	P56382	ATP synthase subunit epsilon, mitochondrial	0.3692	0.3852	-0.5728	#####	0.0335	0.9702
gIFPVLck	P52480	Pyruvate kinase PKM	1.1829	0.0106	0.0715	#####	0.1836	0.5898
gLGDCLVk	P51881	ADP/ATP translocase 2	-0.1650	-0.1676	-0.0960	0.5994	0.0427	0.9776
gLLDVTck	E9PUV4	S-phase kinase-associated protein 1	0.5406	-0.2577	0.1623	0.1363	0.1454	0.4586
gSSNFcVk	Q80SW1	Putative adenosylhomocysteinase 2	0.6643	-0.1133	0.0448	#####	0.1371	0.8567
gVIEcLk	Q91VA7	citrate dehydrogenase [NAD] subunit, mitochondri	0.6567	0.1230	0.6436	0.0924	0.3790	0.0112
gYLGPEQLPDcLk	P08249	Malate dehydrogenase, mitochondrial	0.7648	-0.1372	0.7641	#####	0.3227	0.4009
icQEVLpk	O55126	Protein NipSnap homolog 2	-0.2176	-0.0702	-0.2146	#####	-0.1946	0.0001
VSNAScTTNcLAPLA	P16858	Glyceraldehyde-3-phosphate dehydrogenase	0.3024	-0.6845	1.3756	0.0934	0.2717	0.5715
lcAATATILDKPEDR	O35215	D-dopachrome decarboxylase	-0.0315	0.1560	-1.4866	#####	-0.3674	0.5910
lcDFNPk	B1AWE0	Clathrin light chain A	0.1276	0.3709	-0.1872	0.4441	0.1889	<i>p</i> -value <sup>c</sup> 0.2803
IDcAQLk	P16330	2',3'-cyclic-nucleotide 3'-phosphodiesterase	0.3350	-0.4310	-1.8011	0.3248	-0.3931	0.5140
IHQVYFDAPScVk	Q62277	Synaptophysin	1.4570	0.6545	-0.3867	#####	0.2886	0.5371
IVDVicEk	P63011	Ras-related protein Rab-3A	-0.0517	0.4822	0.0410	#####	0.1144	0.7002
ncSETQYESk	P61982	14-3-3 protein gamma	-0.6262	-0.0231	-0.9669	#####	-0.5412	0.0001

qLIcDPSYIPDRVQk	P50396	Rab GDP dissociation inhibitor alpha	-0.3036	-0.1113	0.8005	0.4130	0.1997	0.5233
sADcSVEEEPWkR	P43006	Excitatory amino acid transporter 2	-0.9181	0.2007	0.3097	1.7850	0.3443	0.5737
scNcLLLk	Q6PHC1	Alpha-enolase	0.0987	-0.0044	-0.6092	#####	-0.1746	0.2841
sIPicTLk	P31254	Ubiquitin-like modifier-activating enzyme 1 Y	0.0660	0.3143	-0.0243	#####	0.0667	0.6889
tkFENLck	P07901	Heat shock protein HSP 90-alpha	1.3780	0.7556	0.2315	#####	0.4014	0.4517
vcNPIITk	Q504P4	Heat shock cognate 71 kDa protein	0.2973	0.0384	-0.7254	#####	-0.1274	0.6792
rSQTTWDSGFcAVNP	O89053	Coronin	0.4778	0.8408	0.1276	#####	0.2502	0.2792
rTVAGLAGkDPVQcSI	Q99LX0	Protein deglycase DJ-1	0.8801	-0.0709	0.1638	#####	0.1638	0.6983
yiQAAck	Q68FD5	Clathrin heavy chain 1	0.5480	0.4657	-0.2436	#####	0.1504	0.4008
yNTDcVQGLTHSk	Q6PIC6	lium/potassium-transporting ATPase subunit alph	0.2369	0.2677	-0.7383	0.2721	0.0096	0.9914
aLANSLAcQGk	P05064	Fructose-bisphosphate aldolase A	0.2341	0.0785	-0.8474	N.A.	-0.1783	0.8996
aYDATcLVk	Q9R0P3	S-formylglutathione hydrolase	0.0350	0.1230	-0.0664	N.A.	0.0305	0.6013
dVEREDIEFck	G5E839	T-complex protein 1 subunit delta	0.1278	0.0360	-0.0713	N.A.	0.0309	0.5980
gVLFGVPGAFTPGcSl	G3UZJ4	Peroxiredoxin-5, mitochondrial	0.0028	0.2365	0.1582	N.A.	0.1325	0.0001
lcDFGSAk	Q9WV60	Glycogen synthase kinase-3 beta	-0.2625	0.0102	0.4307	N.A.	0.0595	0.6405
ncFASVFEk	D3YXG6	Actin-related protein 2/3 complex subunit 2	-0.2776	0.0359	-0.2126	N.A.	-0.1514	0.3060
sTLTDSLvck	P58252	Elongation factor 2	0.0481	0.0602	0.5832	N.A.	0.2305	0.0001
tEIQVNcPk	D6RFU9	Synaptophysin-like protein 1	-0.0175	-1.0799	0.1473	N.A.	-0.3167	0.6339
tLDcEPk	P15105	Glutamine synthetase	0.1995	0.7419	0.5202	N.A.	0.4872	0.0001
TlcGkGLSATVTGGQl	P60202	Myelin proteolipid protein	1.5800	-0.7499	-0.0821	N.A.	0.2493	0.9019
vcGSNLLSIck	P60202	Myelin proteolipid protein	-2.3845	-2.0908	-0.8259	N.A.	-1.7671	0.0001
vGAFTVVcKDAEEAk	P05202	Aspartate aminotransferase, mitochondrial	-0.1372	2.0528	-0.0195	N.A.	0.6321	0.9063
vLGFcHYYLPEEQFPk	Q6PIC6	lium/potassium-transporting ATPase subunit alph	0.3267	-0.0293	-0.0553	N.A.	0.0807	0.8991
yMAccLLYRGDVVPk	P68373;P68368	Tubulin alpha-1C/4A chain	0.0029	-0.4891	-0.2625	N.A.	-0.2496	0.2935
aIPDLcASk	B1AQX6	SRC kinase-signaling inhibitor 1	0.23736	0.32390	N.A.	N.A.	0.28063	0.04240
LDLDSScKEAADGYQ	Q60864	Stress-induced-phosphoprotein 1	0.23007	0.08065	N.A.	N.A.	0.15536	0.07317
aVLFcLSEDkk	P18760	Cofilin-1	-0.10437	0.28248	N.A.	N.A.	0.08906	0.18848
dNILIEcEak	A0A087WNW2	Neurofascin	0.10857	0.03083	N.A.	N.A.	0.06970	0.03809
eFkGLGDcLVk	P51881	ADP/ATP translocase 2	-0.31653	0.93377	N.A.	N.A.	0.30862	0.57713
eGVVEcSFVQSk	P08249	Malate dehydrogenase, mitochondrial	0.04496	-0.01661	N.A.	N.A.	0.01418	0.03017
gILLYGPPGcGk	P46460	Vesicle-fusing ATPase	0.36109	-0.10476	N.A.	N.A.	0.12817	0.22636
gLYDGPVcEVSVTPk	O08553	Dihydropyrimidinase-related protein 2	-1.05619	4.67067	N.A.	N.A.	1.80724	1.36180
gYSIPEcQk	Q9CZU6	Citrate synthase, mitochondrial	0.31043	0.73054	N.A.	N.A.	0.52048	0.20446
icSPDkMIGFSETAk	P46460	Vesicle-fusing ATPase	-0.07862	0.22710	N.A.	N.A.	0.07424	0.14928

iNMcGLTTk	P05201	Aspartate aminotransferase, cytoplasmic	-0.19216	-0.10612	N.A.	N.A.	-0.14914	0.04216
iVSSkDYcVTANSk	D3Z736	L-lactate dehydrogenase	-0.00205	-0.48095	N.A.	N.A.	-0.24150	0.23259
IVIVGDGAcGk	Q9QUI0	Transforming protein RhoA	-0.17377	0.08540	N.A.	N.A.	-0.04419	0.12669
IVLcEVFk	P15105	Glutamine synthetase	0.10508	0.36118	N.A.	N.A.	0.23313	0.12519
nIInkDGGSYVck	O35136	Neural cell adhesion molecule 2	0.89751	0.16996	N.A.	N.A.	0.53373	0.34922
nkGVVLGGcGDk	P61922	4-aminobutyrate aminotransferase, mitochondrial	-0.33616	-0.23906	N.A.	N.A.	-0.28761	0.04757
qIFGDYkTTIcGk	P60202	Myelin proteolipid protein	0.39437	-1.44943	N.A.	N.A.	-0.52753	0.79794
rALANSLAcQGk	P05064	Fructose-bisphosphate aldolase A	0.31437	0.23079	N.A.	N.A.	0.27258	0.04096
sTcTYVGAak	Q9DCZ1	GMP reductase 1	0.03826	0.16066	N.A.	N.A.	0.09946	0.05996
tcLLNETGDEPFQYkN	P15105	Glutamine synthetase	0.39460	0.05859	N.A.	N.A.	0.22659	0.16395
vGAFTVVck	P05202	Aspartate aminotransferase, mitochondrial	0.33423	-0.46982	N.A.	N.A.	-0.06780	RSD <sup>d</sup> 0.38419
yEVAVPLck	Q5UE59	Kinesin light chain 1	-0.23231	0.17303	N.A.	N.A.	-0.02964	0.19737
acSLAk	P63101	14-3-3 protein zeta/delta	0.86839	1.07243	N.A.	N.A.	0.97041	0.09984
dcLPELk	E9PUD2	Dynamin-1-like protein	-0.48637	0.08837	N.A.	N.A.	-0.19900	0.27803
eAVAIck	Q2NKI4	Protein kinase C	4.07588	0.41524	N.A.	N.A.	2.24556	1.20695
fGSGPck	Q9D7N9	Adipocyte plasma membrane-associated protein	-0.54058	0.82692	N.A.	N.A.	0.14317	0.62420
fiLScADDk	P63005	Platelet-activating factor acetylhydrolase IB subunit alpha	-0.55823	-0.01480	N.A.	N.A.	-0.28651	0.26324
fRGYSIPEcQk	Q9CZU6	Citrate synthase, mitochondrial	2.65783	2.43360	N.A.	N.A.	2.54572	0.10968
gkTEIQVncPk	D6RFU9	Synaptophysin-like protein 1	-0.49151	0.32643	N.A.	N.A.	-0.08254	0.39049
gkVNSITVDNck	D3YTR7	Adenylyl cyclase-associated protein	-0.08192	0.55964	N.A.	N.A.	0.23886	0.30936
iEAAcFATIkDGk	Q9D6R2	Malate dehydrogenase [NAD] subunit alpha, mitochondrial	-0.27494	-0.19484	N.A.	N.A.	-0.23489	0.03925
iIAcDGGGGALGHPk	P52503	Malate dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial	-1.72081	1.17468	N.A.	N.A.	-0.27306	1.07913
IIVPFcGHik	Q8VED9	Galectin-related protein	-2.04590	0.58144	N.A.	N.A.	-0.73223	1.02022
mcLVEIEkAPk	Q91VD9	Ubiquinone oxidoreductase 75 kDa subunit, mitochondrial	2.11820	-0.51381	N.A.	N.A.	0.80219	1.02132
ncIGDFLk	Q6ZQ38	Cullin-associated NEDD8-dissociated protein 1	-0.30031	-0.25118	N.A.	N.A.	-0.27574	0.02408
nHTGEKLFecKk	E9Q9G3	Protein Zfp938	-0.26051	-0.26019	N.A.	N.A.	-0.26035	0.00015
nSLDcEIVSAk	P40124	Adenylyl cyclase-associated protein 1	0.25472	0.07335	N.A.	N.A.	0.16403	0.08878
sAPSIPkENFSclTR	P14152	Malate dehydrogenase, cytoplasmic	1.69024	0.24261	N.A.	N.A.	0.96642	0.65543
sSGFcPk	A2AMH3	Choline transporter-like protein 1	-1.22800	0.81194	N.A.	N.A.	-0.20803	0.86095
tAWRLDcAQLk	P16330	2',3'-cyclic-nucleotide 3'-phosphodiesterase	0.51452	0.58109	N.A.	N.A.	0.54780	0.03262
yNPNVLPVQcTGkR	P14094	Sodium/potassium-transporting ATPase subunit beta	-0.26728	0.05510	N.A.	N.A.	-0.10609	0.15735