Table S3. SNO-Cys sites with significant *S*-nitrosylation level changes responding to SAC in LPS-simulated BV-2 cells

Peptide sequence	Modification	Protein group accession	Protein description	Average _LPS	Average _SAC	Fold change	*p*-value
mdcqecpegyr	c3(carbamidomethyl); c6(iodoTMT6)	B7FAV1	Filamin, alpha (Fragment) OS=Mus musculus GN=Flna PE=4 SV=1	1.4850	0.7120	2.0857	0.0278
yvdiaipcnnk	c8(iodoTMT6)	D3YTT7	40S ribosomal protein SA OS=Mus musculus GN=Rpsa-ps10 PE=3 SV=1	1.1720	0.5977	1.9610	0.0013
aqcpiver	c3(iodoTMT6)	D3YYM6	40S ribosomal protein S5 (Fragment) OS=Mus musculus GN=Rps5 PE=3 SV=1	0.8653	0.4377	1.9772	0.0097
ncltnfhgmdltr	c2(iodoTMT6)	D3Z6C3	40S ribosomal protein S3a OS=Mus musculus GN=Rps3a2 PE=3 SV=1	0.9510	0.3690	2.5772	0.0002
fgevvdctik	c7(iodoTMT6)	E9Q5B6;Q99020	Heterogeneous nuclear ribonucleoprotein D0 (Fragment) OS=Mus musculus GN=Hnrnpd PE=2 SV=1; Heterogeneous nuclear ribonucleoprotein A/B OS=Mus musculus GN=Hnrnpab PE=1 SV=1	1.0050	0.5193	1.9352	0.0004
fgevvdctlk	c7(iodoTMT6)	E9Q5B6;Q99020	Heterogeneous nuclear ribonucleoprotein D0 (Fragment) OS=Mus musculus GN=Hnrnpd PE=2 SV=1; Heterogeneous nuclear ribonucleoprotein A/B OS=Mus musculus GN=Hnrnpab PE=1 SV=1	1.0050	0.5193	1.9352	0.0004
elvldnck	c7(iodoTMT6)	F6UFG6;Q9EST5	Acidic leucine-rich nuclear phosphoprotein 32 family member A OS=Mus musculus GN=Anp32a PE=4 SV=1; Acidic leucine-rich nuclear phosphoprotein 32 family member B OS=Mus musculus GN=Anp32b PE=1 SV=1	0.8873	0.5700	1.5567	0.0093
cpnptcenmnfswr	c1(carbamidomethyl); c6(iodoTMT6)	G3UXT7	RNA-binding protein FUS (Fragment) OS=Mus musculus GN=Fus PE=4 SV=1	1.0317	0.4660	2.2139	0.0084
cagnediitlr	c1(iodoTMT6)	J3QQ26	Proliferating cell nuclear antigen OS=Mus musculus GN=Pcna-ps2 PE=3 SV=1	1.0700	0.6575	1.6274	0.0017
lvvecvmk	c5(iodoTMT6)	P04117	Fatty acid-binding protein, adipocyte OS=Mus musculus GN=Fabp4 PE=1 SV=3	1.0353	0.3270	3.1662	0.0017
alanslacqgk	c8(iodoTMT6)	P05064	Fructose-bisphosphate aldolase A OS=Mus musculus GN=Aldoa PE=1 SV=2	1.0290	0.5147	1.9994	0.0202
vigsgcnldsar	c6(iodoTMT6)	P06151	L-lactate dehydrogenase A chain OS=Mus musculus GN=Ldha PE=1 SV=3	0.9050	0.5067	1.7862	0.0049
etectyfstplllgk	c4(iodoTMT6)	P08249	Malate dehydrogenase, mitochondrial OS=Mus musculus GN=Mdh2 PE=1 SV=3	1.0310	0.5430	1.8987	0.0091
egvvecsfvqsk	c6(iodoTMT6)	P08249	Malate dehydrogenase, mitochondrial OS=Mus musculus GN=Mdh2 PE=1 SV=3	1.0377	0.6517	1.5923	0.0096
eqwsncptigqir	c6(iodoTMT6)	P10605	Cathepsin B OS=Mus musculus GN=Ctsb PE=1 SV=2	1.0340	0.5663	1.8258	0.0116
heqnidcgggyvk	c7(iodoTMT6)	P14211	Calreticulin OS=Mus musculus GN=Calr PE=1 SV=1	0.8660	0.4200	2.0619	0.0205
vnqigsvtesiqack	c14(iodoTMT6)	P17182;P21550	Alpha-enolase OS=Mus musculus GN=Eno1 PE=1 SV=3; Beta-enolase OS=Mus musculus GN=Eno3 PE=1 SV=3	1.0673	0.4930	2.1650	0.0001
vnqigsvteslqack	c14(iodoTMT6)	P17182;P21550	Alpha-enolase OS=Mus musculus GN=Eno1 PE=1 SV=3; Beta-enolase OS=Mus musculus GN=Eno3 PE=1 SV=3	1.0673	0.4930	2.1650	0.0001
iipgfmcqggdftr	c7(iodoTMT6)	P17742	Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia PE=1 SV=2	0.9500	0.5750	1.6522	0.0015
itisdcgql	c6(iodoTMT6)	P17742	Peptidyl-prolyl cis-trans isomerase A OS=Mus musculus GN=Ppia PE=1 SV=2	0.9230	0.5003	1.8448	0.0020
iavaaqncyk	c8(iodoTMT6)	P17751	Triosephosphate isomerase OS=Mus musculus GN=Tpi1 PE=1 SV=4	0.9083	0.3797	2.3924	0.0038
mlpdkdcr	c7(iodoTMT6)	P18760	Cofilin-1 OS=Mus musculus GN=Cfl1 PE=1 SV=3	1.1967	0.5667	2.1118	0.0444
llcgllsdr	c3(iodoTMT6)	P34884	Macrophage migration inhibitory factor OS=Mus musculus GN=Mif PE=1 SV=2	0.9630	0.3873	2.4862	0.0048
slveasssgvsvlslcek	c16(iodoTMT6)	P50580	Proliferation-associated protein 2G4 OS=Mus musculus GN=Pa2g4 PE=1 SV=3	0.9733	0.3840	2.5347	0.0323
gtdimytgtldcwr	c12(iodoTMT6)	P51881	ADP/ATP translocase 2 OS=Mus musculus GN=Slc25a5 PE=1 SV=3	0.9535	0.6983	1.3654	0.0100
ntgiictigpasr	c6(iodoTMT6)	P52480	Pyruvate kinase isozymes M1/M2 OS=Mus musculus GN=Pkm PE=1 SV=4	1.0103	0.6387	1.5819	0.0002
egalceenmr	c5(iodoTMT6)	P58252	Elongation factor 2 OS=Mus musculus GN=Eef2 PE=1 SV=2	1.0083	0.5863	1.7197	0.0016
ytcsfcgk	c3(carbamidomethyl); c6(iodoTMT6)	P61514	60S ribosomal protein L37a OS=Mus musculus GN=Rpl37a PE=2 SV=2	1.0230	0.4830	2.1180	0.0028
fdtgnlcmvtgganlgr	c7(iodoTMT6)	P62702	40S ribosomal protein S4, X isoform OS=Mus musculus GN=Rps4x PE=2 SV=2	0.8677	0.3053	2.8417	0.0014
dlttagavtqcyr	c11(iodoTMT6)	P62717	60S ribosomal protein L18a OS=Mus musculus GN=Rpl18a PE=1 SV=1	1.1605	0.4895	2.3708	0.0007
ssgeivycgqvfek	c8(iodoTMT6)	P62717	60S ribosomal protein L18a OS=Mus musculus GN=Rpl18a PE=1 SV=1	0.9170	0.3435	2.6696	0.0052
yddmaacmk	c7(iodoTMT6)	P63101	14-3-3 protein zeta/delta OS=Mus musculus GN=Ywhaz PE=1 SV=1	1.1013	0.5633	1.9550	0.0128
qahlcvlasncdepmyvk	c5(carbamidomethyl); c11(iodoTMT6)	P63323	40S ribosomal protein S12 OS=Mus musculus GN=Rps12 PE=1 SV=2	0.9450	0.5965	1.5842	0.0218
ymaccllyr	c4(carbamidomethyl); c5(iodoTMT6)	P68373;P05213;Q3UX10	Tubulin alpha-1C chain OS=Mus musculus GN=Tuba1c PE=1 SV=1; Tubulin alpha-1B chain OS=Mus musculus GN=Tuba1b PE=1 SV=2; Tubulin alpha chain-like 3 OS=Mus musculus GN=Tubal3 PE=2 SV=2	1.0262	0.5958	1.7222	0.0005
mivecvmnnatctr	c5(iodoTMT6); c12(carbamidomethyl)	Q05816	Fatty acid-binding protein, epidermal OS=Mus musculus GN=Fabp5 PE=1 SV=3	0.9944	0.4451	2.2342	0.0006
mivecvmnnatctr	c5(carbamidomethyl); c12(iodoTMT6)	Q05816	Fatty acid-binding protein, epidermal OS=Mus musculus GN=Fabp5 PE=1 SV=3	1.0442	0.5742	1.8185	0.0029
alendpdcr	c8(iodoTMT6)	Q61233;Q99K51	Plastin-2 OS=Mus musculus GN=Lcp1 PE=1 SV=4; Plastin-3 OS=Mus musculus GN=Pls3 PE=1 SV=3	1.0927	0.4777	2.2875	0.0007
tseslcqnnmvilk	c6(iodoTMT6)	Q6P5F9	Exportin-1 OS=Mus musculus GN=Xpo1 PE=1 SV=1	0.9123	0.5150	1.7715	0.0187

Peptide sequence	Modification	Protein group accession	Protein description	Average _LPS	Average _SAC	Fold change	*p*-value
gsqfgqscclr	c8(carbamidomethyl); c9(iodoTMT6)	Q8CGC7	Bifunctional glutamate/proline--tRNA ligase OS=Mus musculus GN=Eprs PE=1 SV=4	0.9557	0.4427	2.1589	0.0317
gsqfgqscclr	c8(iodoTMT6); c9(carbamidomethyl)	Q8CGC7	Bifunctional glutamate/proline--tRNA ligase OS=Mus musculus GN=Eprs PE=1 SV=4	0.9557	0.4427	2.1589	0.0317
eirpvcr	c6(iodoTMT6)	Q8VDW0;Q9Z1N5	ATP-dependent RNA helicase DDX39A OS=Mus musculus GN=Ddx39a PE=2 SV=1; Spliceosome RNA helicase Ddx39b OS=Mus musculus GN=Ddx39b PE=1 SV=1	1.0080	0.5017	2.0093	0.0001
qactpmfr	c3(iodoTMT6)	Q9CZN7	Serine hydroxymethyltransferase OS=Mus musculus GN=Shmt2 PE=2 SV=1	1.0793	0.4983	2.1659	0.0003
sgqgafgnmcr	c10(iodoTMT6)	Q9D8E6	60S ribosomal protein L4 OS=Mus musculus GN=Rpl4 PE=1 SV=3	1.1427	0.6060	1.8856	0.0018
nalanplycpdyr	c9(iodoTMT6)	Q9DB77	Cytochrome b-c1 complex subunit 2, mitochondrial OS=Mus musculus GN=Uqcrc2 PE=1 SV=1	0.9547	0.6230	1.5324	0.0016
savdncqdswr	c6(iodoTMT6)	Q9DCD0	6-phosphogluconate dehydrogenase, decarboxylating OS=Mus musculus GN=Pgd PE=2 SV=3	0.9530	0.4890	1.9489	0.0001
ligpncpgvinpgeck	c6(carbamidomethyl); c15(iodoTMT6)	Q9WUM5	Succinyl-CoA ligase [ADP/GDP-forming] subunit alpha, mitochondrial OS=Mus musculus GN=Suclg1 PE=1 SV=4	1.0530	0.6720	1.5670	0.0178

Note: Multi-Cys peptides with a single SNO-Cys are highlighted in green, and multi-Cys peptides with 2 SNO-Cys sites are highlighted in red.