

**Table S2**

**Summary of reversible redox modified cysteinyl sites changing in microglia proteins upon treatment with A $\beta$ <sub>25-35</sub> peptide.**

Proteins <sup>a</sup>	Protein names	RRM containing peptide sequence <sup>b</sup>	PEP <sup>c</sup>	Score <sup>d</sup>	Redox sensitive site <sup>e</sup>			RRM annotation <sup>f</sup>
					Cys#	resting	activated	
Q9QZB7	Actin-related protein 1	SVATLILDSLQCPIDTR	7.85E-007	157.8	291	+		
P50247	Adenosylhomocysteinase	VIITEIDPINALQAAMEGYEVTMDEACK	6.50E-014	181.24	266	+		
P47738	Aldehyde dehydrogenase	LLCGGGAAADR	1.37E-048	145.55	388		+	
Q9D0I9	Arginine-tRNA ligase, cytoplasmic	LQEVFGCAIR	4.82E-003	97.456	86		+	SSG <sup>43</sup>
Q922B2	Aspartate-tRNA ligase, cytoplasmic	VFCIGPVFR	9.16E-006	143.85	267		+	
Q9DCX2	ATP synthase subunit d	SCAEFVSGSQLR	5.01E-032	259.47	101		+	
Q80WV3	Carbohydrate sulfotransferase 2	KEGMGGPADYHALGAMEVICNSMAK	4.09E-002	38.175	399	+		
O70370	Cathepsin S	LISLSAQNLDVDCSNEEK	9.52E-122	414.82	178		+	SSG <sup>43</sup>
Q9WUU7	Cathepsin Z	HGIPDETCNNYQAK	2.18E-015	221.86	156		+	SSG <sup>43</sup>
Q9Z1Q5	Chloride intracellular channel protein 1	LHIVQVVK	6.28E-006	149.65	191		+	SNO <sup>62, 65</sup>
P18760	Cofilin-1	HELQANCYEEVKDR	2.01E-067	328.14	139		+	SSG <sup>43</sup> SNO <sup>62, 65, 66</sup>
O08749	Dihydrolipoyl dehydrogenase	VCHAHPTLSEAFR	1.82E-003	108.72	484		+	
Q9Z0J0	Epididymal secretory protein E1	SGINCPIQK	2.75E-002	57.96	99		+	
P51906	Excitatory amino acid transporter 3	NMFPENLVQACFQQYK	3.87E-002	36.993	158	+		
P06745	Glucose-6-phosphate isomerase	MIPCDFLIPVQTQHPIR	3.98E-002	40.242	404		+	SSG <sup>43</sup>
P68040	Guanine nucleotide-binding protein subunit beta-2-like 1	AEPPQCTSLAWSADGQTLFAGYTDNLVR	3.11E-003	76.152	286	+		SSG <sup>43</sup>
		LWNTLGVK	2.56E-004	117.89	138		+	SSG <sup>43</sup>
Q8BG05	Heterogeneous nuclear ribonucleoprotein A3	WGTLTDCVVMR	7.20E-003	97.734	64		+	SNO <sup>51</sup>
Q9Z2X1	Heterogeneous nuclear ribonucleoprotein F	YGDSEFTVQSTTGHCVHMR	1.05E-005	138.05	290		+	
O35737	Heterogeneous nuclear ribonucleoprotein H	GLPWSCSADEVQR	9.79E-005	142.38	22		+	
P61979	Heterogeneous nuclear ribonucleoprotein K	IIPTLEGLQLPSPTATSQLPLESDAVECLNYQHYK	2.03E-012	141.43	132	+		SSG <sup>43</sup>
		LFQECCPHSTDR	4.53E-003	99.283	185 <sup>g</sup>		+	SNO <sup>51</sup>
Q8R081	Heterogeneous nuclear ribonucleoprotein L	VFNVFLYGNVEK	2.03E-031	267.67	401	+		SNO <sup>51</sup>
		LCFSTAQHAS	1.42E-011	205.18	578		+	SSG <sup>43</sup>

P21956	Lactadherin	ITLRLELLGC	3.73E-010	130.98	463	+		SS with 308 <sup>67</sup>
Q3V3R1	Monofunctional C1-tetrahydrofolate synthase	EAGLDITHICLPPDSGEDEIIDEILK	4.04E-002	38.237	129	+		SSG <sup>43</sup>
Q922Q1	MOSC domain-containing protein 2	CVLTTVDPDTGHDR	3.98E-002	43.813	274	+		
Q7TPV4	Myb-binding protein 1A	SVFGHICPHLTPR	9.99E-004	124.21	676		+	SNO <sup>51</sup>
O08709	Peroxiredoxin-6	DFTPVCTTELGR	1.79E-031	169.65	47		+	SSG <sup>43, 44</sup> SNO <sup>65, 66, 68</sup>
Q9WUA3	6-phosphofructokinase	LGITNLCVIGGDGSLTGANLFR	2.83E-027	240.71	122	+		
Q9DCD0	6-phosphogluconate dehydrogenase, decarboxylating	SAVDNCQDSWR	5.00E-024	250.7	402		+	
Q9DBJ1	Phosphoglycerate mutase 1	YADLTEDQLPSCESLK	1.05E-043	300.03	153		+	SSG <sup>43</sup> SNO <sup>65, 66</sup>
Q61233	Plastin-2	KLENCNYAVDLGK	1.71E-022	237.32	460		+	SSG <sup>43</sup>
P62962	Profilin-1	CYEMASHLR	2.90E-008	166.09	128		+	
P17918	Proliferating cell nuclear antigen	DLSHIGDAVVISCAK	1.54E-022	244.44	162		+	SSG <sup>43</sup> SNO <sup>51, 65</sup>
P50580	Proliferation-associated protein 2G4	AAHLCAEAALR	9.21E-006	137.95	149		+	
Q9R0Q7	Prostaglandin E synthase 3	LTFSCLGGSDFNK	2.68E-022	232.6	402		+	SSG <sup>43</sup> SNO <sup>65</sup>
Q9R1P4	Proteasome subunit alpha type-1	LLCNFMR	5.43E-003	103.29	85		+	SSG <sup>43</sup>
Q9CQ89	Protein CutA	LAACVNLIPIQTSIYEWK	6.06E-003	86.367	94	+		
P27773	Protein disulfide-isomerase A3	FIQDSIFGLCPHMTEDNKDLIQGK	5.48E-012	177.73	244		+	SNO <sup>69</sup> SSG <sup>43</sup>
E9PZD9	Protein E330020D12Rik	AQGQRPCGFR	3.42E-002	45.161	49	+		
E9Q817	Protein Nfx11	KCCPGNCPPCDQNCGR	4.25E-002	26.292	492/493/ 497/500 <sup>h</sup>		+	
P52480	Pyruvate kinase isozymes M1/M2	AEGSDVANAVLDGADCIMLSGETAKGDYPLEAVR	2.65E-027	219.26	358	+		SSG <sup>43</sup>
P63001	Ras-related C3 botulinum toxin substrate 1	HHCPNTPHILVGTK	1.15E-002	74.475	105		+	SNO <sup>51</sup>
Q91VI7	Ribonuclease inhibitor	SLLELQMSSNPLGDEGVQELCK	2.17E-036	276.68	357	+		
Q5XJF6	Ribosomal protein	FSVCVLGDQQHCDEAK	1.34E-011	203.7	74 <sup>g</sup>		+	
P47962	60S ribosomal protein L5	IEGDMIVCAAYAHLPK	2.05E-004	119.65	76		+	SSG <sup>43</sup>
P62918	60S ribosomal protein L8	AQLNIGNVLPVGTMPGIVCCLEEKPGDR	6.11E-005	107.17	114/115 <sup>h</sup>	+		
P35979	60S ribosomal protein L12	EILGTAQSVGCNVDGR	5.11E-031	261.64	141		+	SSG <sup>43</sup>

P62830	60S ribosomal protein L23	ECADLWPR	7.07E-003	72.485	125		+	SSG <sup>43</sup>
P14115	60S ribosomal protein L27a	NQSFCTVNLDK	1.65E-022	232.5	70		+	
P83882	60S ribosomal protein L36a	LECVEPNCR	8.84E-005	134.26	72 <sup>g</sup>		+	
Q9R0P3	S-formylglutathione hydrolase	CPALYWLSGLTCTEQNFISK	2.26E-003	99.891	56 <sup>h</sup>		+	
O55143	Sarcoplasmic/endoplasmic reticulum calcium ATPase 2	CHQYDGLVELATICALCNDLSALDYNEAK	3.75E-002	36.142	417 <sup>g</sup>		+	
Q9CZ7	Serine hydroxymethyltransferase	YYGGAEVVDEIELLCQR	3.05E-004	115.68	119		+	
Q6PDM2	Serine/arginine-rich splicing factor 1	EAGDVCYADVYR	1.07E-006	172.13	148		+	
P80316	T-complex protein 1 subunit epsilon	ETGANLAICQWGFDEANHLLQLQGLPAVR	7.28E-008	135.54	302		+	
P80318	T-complex protein 1 subunit gamma	IPGGIIEDSCVLR	2.17E-010	200.93	213		+	SSG <sup>43</sup> SNO <sup>51, 69</sup>
		TLIQNCGASTIR	7.10E-144	265.22	455		+	SSG <sup>43</sup> SNO <sup>51</sup>
Q9R233	Tapasin	VSLTPAPVVWAAPGEAPPELLCLASHFFPAEGLEVK	5.96E-010	138.41	318		+	
Q921F2	TAR DNA-binding protein 43	VTEDENDEPIEIPSEDDGTVLLSTVTAQFPACGLR	1.47E-002	63.203	39		+	
Q91WM3	U3 small nucleolar RNA-interacting protein 2	QLDPLCDIPLVGFINSLK	3.83E-009	173.98	416		+	
P62814	V-type proton ATPase subunit B, brain isoform	SDFEENGSMDNVCLFLNLANPTIER	5.28E-003	71.428	258		+	
P20152	Vimentin	QVQSLTCEVDALK	1.95E-005	158.58	328		+	SSG <sup>43</sup> SNO <sup>51, 66, 70</sup>

<sup>a</sup> UniProtKB protein identifier.

<sup>b</sup> Sequence of peptides identified by shotgun proteomics as containing cysteinyl residues specifically sensible to the A $\beta$ <sub>25-35</sub> treatment in BV2 cells.

<sup>c</sup> Peptide Posterior Error Probability (PEP) score, calculated by MaxQuant algorithms; the smaller the PEP, the more certain is the identification of a peptide.

<sup>d</sup> Andromeda score for the best associated MS/MS spectrum allowing identification in the shotgun proteomics analysis.

<sup>e</sup> Specific cysteinyl residue proved to lose (+, in the resting cell column) or to gain (+, in the activated cell column) the RRM upon beta amyloid treatment.

<sup>f</sup> Literature references on post-translational modifications annotated up to now for each of specific cysteinyl residues proved in our work carrying RRM. SS, disulphide bridge; SSG, Mixed disulphide bridge with glutathione; SNO, nitrosothiols. Numbers refer to those in the Reference section of the manuscript.

<sup>g</sup> Indicates certain identification of the RRM site due to the presence in MS/MS spectra of discriminating ions.

<sup>h</sup> Indicates ambiguous RRM sites due to lack of discriminating ions.