

Contents, Supplementary File 1

Identification of the differentially expressed proteins in the mouse hippocampus following *status epilepticus*

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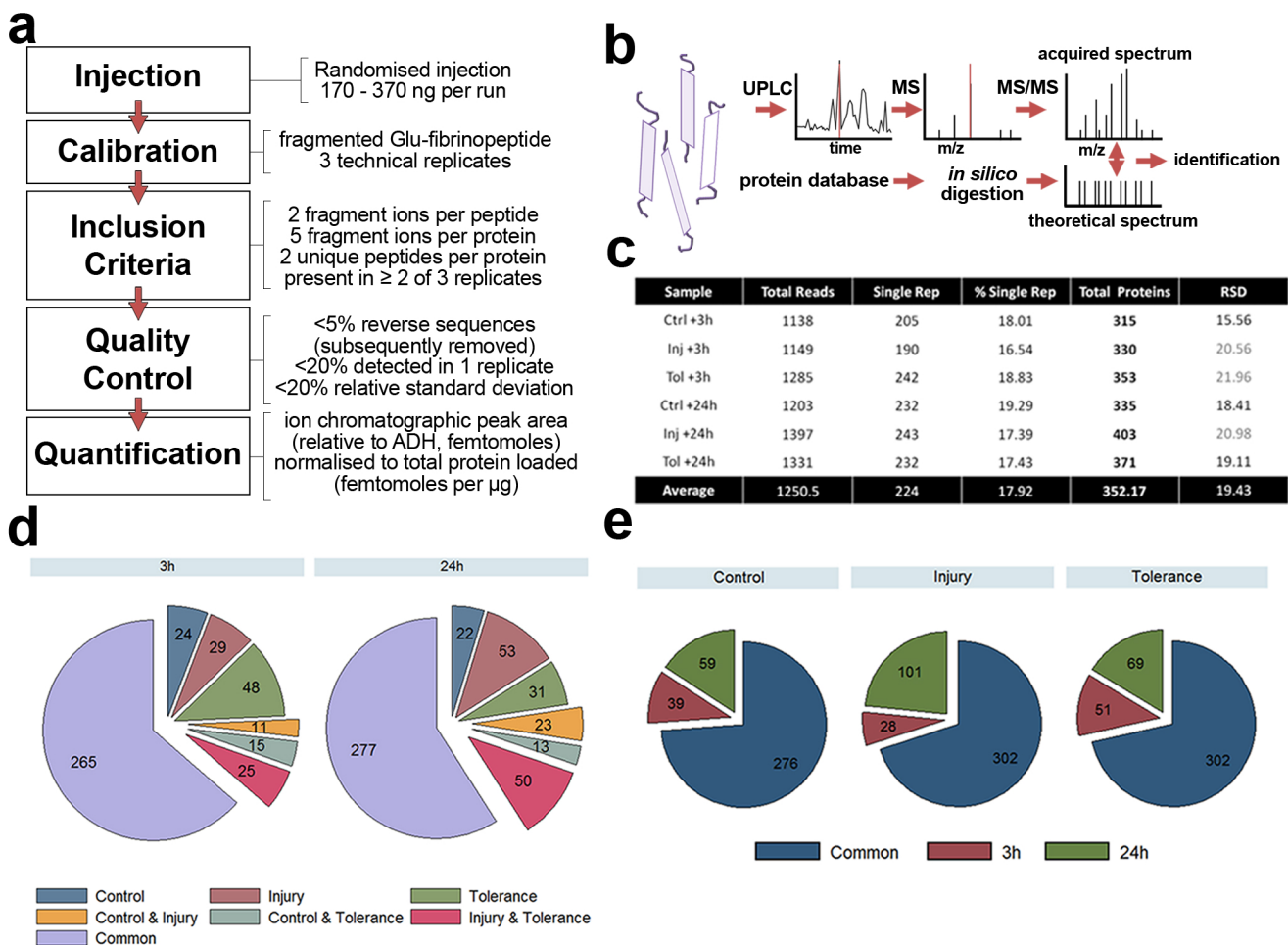


Fig. 1 Summary of proteomic profiling (a) Loading, calibration and inclusion criteria for accepted peptide fragments and proteins were defined prior to qMS analysis. Following qMS analysis, quality control criteria were applied to validate measurements and quantification of identified proteins was carried out as described in the text. (b) Depiction of the assay workflow during liquid chromatography, acquisition of protein spectra and identification of putative proteins. (c) Protein counts were merged across all replicates and read reliability was estimated. (d, e) Total counts of unique and commonly identified proteins after stratifying by treatment and timepoint were tabulated, using a ratio cutoff of $\pm 30\%$. ADH, alcohol dehydrogenase; MS, mass spectrometry; RSD, relative standard deviation; UPLC, ultra performance liquid chromatography.

Table 1

Identification of the differentially expressed proteins in the mouse hippocampus of the injury group by qMS - **Upregulated at 3h**

UniGene ID	UniProt ID	Name, Description
Mm.686	P68033	ACTC MOUSE Actin alpha cardiac muscle 1 OS Mus musculus GN Actc1 PE 1 SV 1
Mm.253090	P17427	AP2A2 MOUSE AP 2 complex subunit alpha 2 OS Mus musculus GN Ap2a2 PE 1 SV 2
Mm.26743	Q00623	APOA1 MOUSE Apolipoprotein A I OS Mus musculus GN Apoa1 PE 1 SV 1
Mm.389075	P84084	ARF5 MOUSE ADP ribosylation factor 5 OS Mus musculus GN Arf5 PE 2 SV 2
Mm.271178	Q9CQW2	ARL8B MOUSE ADP ribosylation factor like protein 8B OS Mus musculus GN Arl8b PE 2 SV 1
Mm.31395	Q00493	CBPE MOUSE Carboxypeptidase E OS Mus musculus GN Cpe PE 1 SV 2
Mm.298875	O08585	CLCA MOUSE Clathrin light chain A OS Mus musculus GN Clta PE 1 SV 1
Mm.290026	Q6IRU5	CLCB MOUSE Clathrin light chain B OS Mus musculus GN Cltb PE 2 SV 1
Mm.393405	Q9CQI6	COTL1 MOUSE Coactosin like protein OS Mus musculus GN Cotl1 PE 1 SV 3
Mm.378921	P23242	CXA1 MOUSE Gap junction alpha 1 protein OS Mus musculus GN Gja1 PE 1 SV 2
Mm.28919	Q9R0P5	DEST MOUSE Destrin OS Mus musculus GN Dstn PE 1 SV 3
Mm.27256	Q62108	DLG4 MOUSE Disks large homolog 4 OS Mus musculus GN Dlg4 PE 1 SV 1
Mm.271703	Q9DC51	GNAI3 MOUSE Guanine nucleotide binding protein G k subunit alpha OS Mus musculus GN Gnai3 PE 1 SV 3
Mm.441542	P46425	GSTP2 MOUSE Glutathione S transferase P 2 OS Mus musculus GN Gstp2 PE 2 SV 2
Mm.193539	P15864	H12 MOUSE Histone H1 2 OS Mus musculus GN Hist1h1c PE 1 SV 2
Mm.435460	Q64522	H2A2B MOUSE Histone H2A type 2 B OS Mus musculus GN Hist2h2ab PE 1 SV 3
Mm.490945	Q64525	H2B2B MOUSE Histone H2B type 2 B OS Mus musculus GN Hist2h2bb PE 1 SV 3
Mm.270681	Q61699	HS105 MOUSE Heat shock protein 105 kDa OS Mus musculus GN Hsp11 PE 1 SV 2
Mm.6388	Q61696	HS71A MOUSE Heat shock 70 kDa protein 1A OS Mus musculus GN Hspa1a PE 1 SV 2
Mm.260084	P10630	IF4A2 MOUSE Eukaryotic initiation factor 4A II OS Mus musculus GN Eif4a2 PE 2 SV 2
Mm.255822	Q6PHZ2	KCC2D MOUSE Calcium calmodulin dependent protein kinase type II subunit delta OS Mus musculus GN Cam
Mm.383180	P53657	KPYR MOUSE Pyruvate kinase isozymes R L OS Mus musculus GN Pk1r PE 2 SV 1
Mm.296082	Q9CR62	M2OM MOUSE Mitochondrial 2 oxoglutarate malate carrier protein OS Mus musculus GN Slc25a11 PE 1 SV 3
Mm.154087	Q7TSJ2	MAP6 MOUSE Microtubule associated protein 6 OS Mus musculus GN Map6 PE 1 SV 2
Mm.2326	P34884	MIF MOUSE Macrophage migration inhibitory factor OS Mus musculus GN Mif PE 1 SV 2
Mm.210857	Q61885	MOG MOUSE Myelin oligodendrocyte glycoprotein OS Mus musculus GN Mog PE 1 SV 1
Mm.393563	Q7M6Y3	PICA MOUSE Phosphatidylinositol binding clathrin assembly protein OS Mus musculus GN Picalm PE 1 SV
Mm.274432	P48453	PP2BB MOUSE Serine threonine protein phosphatase 2B catalytic subunit beta isoform OS Mus musculus G
Mm.266033	Q504M8	RAB26 MOUSE Ras related protein Rab 26 OS Mus musculus GN Rab26 PE 2 SV 1
Mm.482114	Q91ZR1	RAB4B MOUSE Ras related protein Rab 4B OS Mus musculus GN Rab4b PE 2 SV 2
Mm.334313	Q61411	RASH MOUSE GTPase HRas OS Mus musculus GN Hras1 PE 1 SV 2
Mm.297372	P62984	RL40 MOUSE Ubiquitin 60S ribosomal protein L40 OS Mus musculus GN Uba52 PE 1 SV 2
Mm.5260	P31648	SC6A1 MOUSE Sodium and chloride dependent GABA transporter 1 OS Mus musculus GN Slc6a1 PE 1 SV 2
Mm.270259	O55131	SEPT7 MOUSE Septin 7 OS Mus musculus GN Sept7 PE 1 SV 1
Mm.134191	Q99JR1	SFXN1 MOUSE Sideroflexin 1 OS Mus musculus GN Sfxn1 PE 1 SV 3
Mm.358663	Q9RON5	SYT5 MOUSE Synaptotagmin 5 OS Mus musculus GN Syt5 PE 1 SV 1
Mm.88212	P68373	TBA1C MOUSE Tubulin alpha 1C chain OS Mus musculus GN Tuba1c PE 1 SV 1
Mm.123366	Q9CQN1	TRAP1 MOUSE Heat shock protein 75 kDa mitochondrial OS Mus musculus GN Trap1 PE 1 SV 1
Mm.37214	Q92111	TRFE MOUSE Serotransferrin OS Mus musculus GN Tf PE 1 SV 1

Table 2

Identification of the differentially expressed proteins in the mouse hippocampus of the injury group by qMS - **Downregulated at 3h**

UniGene ID	UniProt ID	Name, Description
Mm.12821	Q64436	ATP4A MOUSE Potassium transporting ATPase alpha chain 1 OS Mus musculus GN Atp4a PE 1 SV 3
Mm.136093	Q06185	ATP5I MOUSE ATP synthase subunit e mitochondrial OS Mus musculus GN Atp5i PE 1 SV 2
Mm.806	P35762	CD81 MOUSE CD81 antigen OS Mus musculus GN Cd81 PE 1 SV 1
Mm.454389	Q5SQX6	CYFP2 MOUSE Cytoplasmic FMR1 interacting protein 2 OS Mus musculus GN Cyfp2 PE 1 SV 2
Mm.246436	Q9D0M5	DYL2 MOUSE Dynein light chain 2 cytoplasmic OS Mus musculus GN Dynll2 PE 1 SV 1
Mm.433257	P39054	DYN2 MOUSE Dynamin 2 OS Mus musculus GN Dnm2 PE 1 SV 2
Mm.41502	P97807	FUMH MOUSE Fumarate hydratase mitochondrial OS Mus musculus GN Fh PE 1 SV 3
Mm.45054	Q9R111	GUAD MOUSE Guanine deaminase OS Mus musculus GN Gda PE 1 SV 1
Mm.270641	Q8BGZ1	HPCL4 MOUSE Hippocalcin like protein 4 OS Mus musculus GN Hpcal4 PE 2 SV 3
Mm.39739	Q8K0U4	HS12A MOUSE Heat shock 70 kDa protein 12A OS Mus musculus GN Hspa12a PE 1 SV 1
Mm.14825	P70404	IDHG1 MOUSE Isocitrate dehydrogenase NAD subunit gamma 1 mitochondrial OS Mus musculus GN Idh3g P
Mm.269649	P12382	K6PL MOUSE 6 phosphofructokinase liver type OS Mus musculus GN Pfkf PE 1 SV 4
Mm.235182	Q923T9	KCC2G MOUSE Calcium calmodulin dependent protein kinase type II subunit gamma OS Mus musculus GN Cam
Mm.241355	P20917	MAG MOUSE Myelin associated glycoprotein OS Mus musculus GN Mag PE 1 SV 2
Mm.1956	P08551	NFL MOUSE Neurofilament light polypeptide OS Mus musculus GN Nefl PE 1 SV 5
Mm.293716	O55125	NIPS1 MOUSE Protein NipSnap homolog 1 OS Mus musculus GN Nipsnap1 PE 1 SV 1
Mm.200859	Q61206	PA1B2 MOUSE Platelet activating factor acetylhydrolase IB subunit beta OS Mus musculus GN Pafah1b2 P
Mm.221275	Q8K0T0	RTN1 MOUSE Reticulon 1 OS Mus musculus GN Rtn1 PE 1 SV 1
Mm.378957	P54227	STMN1 MOUSE Stathmin OS Mus musculus GN Stmn1 PE 1 SV 2
Mm.3074	P68037	UB2L3 MOUSE Ubiquitin conjugating enzyme E2 L3 OS Mus musculus GN Ube2l3 PE 2 SV 1
Mm.227704	Q60931	VDAC3 MOUSE Voltage dependent anion selective channel protein 3 OS Mus musculus GN Vdac3 PE 1 SV 1
Mm.475829	Q9Z1G4	VPP1 MOUSE V type proton ATPase 116 kDa subunit a isoform 1 OS Mus musculus GN Atp6v0a1 PE 1 SV 3

Table 3

Identification of the differentially expressed proteins in the mouse hippocampus of the tolerance group by qMS - **Upregulated at 3h**

UniGene ID	UniProt ID	Name, Description
Mm.233813	P61982	1433G MOUSE 14 3 3 protein gamma OS Mus musculus GN Ywhag PE 1 SV 2
Mm.221038	Q3UJH0	AAK1 MOUSE AP2 associated protein kinase 1 OS Mus musculus GN Aak1 PE 1 SV 2
Mm.276251	P46660	AINX MOUSE Alpha internexin OS Mus musculus GN Ina PE 1 SV 2
Mm.284446	P47738	ALDH2 MOUSE Aldehyde dehydrogenase mitochondrial OS Mus musculus GN Aldh2 PE 1 SV 1
Mm.30010	Q9WV32	ARC1B MOUSE Actin related protein 2 3 complex subunit 1B OS Mus musculus GN Arpc1b PE 1 SV 4
Mm.371546	P84078	ARF1 MOUSE ADP ribosylation factor 1 OS Mus musculus GN Arf1 PE 1 SV 2
Mm.259045	P61161	ARP2 MOUSE Actin related protein 2 OS Mus musculus GN Actr2 PE 1 SV 1
Mm.273271	Q9Z1W8	AT12A MOUSE Potassium transporting ATPase alpha chain 2 OS Mus musculus GN Atp12a PE 1 SV 3
Mm.12821	Q64436	ATP4A MOUSE Potassium transporting ATPase alpha chain 1 OS Mus musculus GN Atp4a PE 1 SV 3
Mm.330524	Q99N28	CADM3 MOUSE Cell adhesion molecule 3 OS Mus musculus GN Cadm3 PE 1 SV 1
Mm.178322	Q8R464	CADM4 MOUSE Cell adhesion molecule 4 OS Mus musculus GN Cadm4 PE 1 SV 1
Mm.285993	P62204	CALM MOUSE Calmodulin OS Mus musculus GN Calm1 PE 1 SV 2
Mm.1971	P14211	CALR MOUSE Calreticulin OS Mus musculus GN Calr PE 1 SV 1
Mm.248827	P35564	CALX MOUSE Calnexin OS Mus musculus GN Canx PE 1 SV 1
Mm.26940	P48758	CBR1 MOUSE Carbonyl reductase NADPH 1 OS Mus musculus GN Cbr1 PE 1 SV 3
Mm.489675	Q91V57	CHIN MOUSE N chimaerin OS Mus musculus GN Chn1 PE 1 SV 2
Mm.44220	Q9QXT0	CNPY2 MOUSE Protein canopy homolog 2 OS Mus musculus GN Cnpy2 PE 2 SV 1
Mm.276826	P45591	COF2 MOUSE Cofilin 2 OS Mus musculus GN Cfl2 PE 1 SV 1
Mm.154358	Q55QX6	CYFP2 MOUSE Cytoplasmic FMR1 interacting protein 2 OS Mus musculus GN Cyfp2 PE 1 SV 2
Mm.158231	Q8K2B3	DHSA MOUSE Succinate dehydrogenase ubiquinone flavoprotein subunit mitochondrial OS Mus musculus
Mm.218820	Q8K1M6	DNM1L MOUSE Dynamin 1 like protein OS Mus musculus GN Dnm1l PE 1 SV 2
Mm.131135	Q9WV92	E41L3 MOUSE Band 4 1 like protein 3 OS Mus musculus GN Epb41l3 PE 1 SV 1
Mm.200497	Q8BMS1	ECHA MOUSE Trifunctional enzyme subunit alpha mitochondrial OS Mus musculus GN Hadha PE 1 SV 1
Mm.247762	Q9D8N0	EF1G MOUSE Elongation factor 1 gamma OS Mus musculus GN Eef1g PE 1 SV 3
Mm.326799	P58252	EF2 MOUSE Elongation factor 2 OS Mus musculus GN Eef2 PE 1 SV 2
Mm.395598	Q9D8Y0	EFHD2 MOUSE EF hand domain containing protein D2 OS Mus musculus GN Efhd2 PE 1 SV 1
Mm.251322	P21550	ENOB MOUSE Beta enolase OS Mus musculus GN Eno3 PE 1 SV 3
Mm.68134	Q8VDI1	ESIP1 MOUSE Epithelial stromal interaction protein 1 OS Mus musculus GN Epsti1 PE 1 SV 2
Mm.370185	P27600	GNA12 MOUSE Guanine nucleotide binding protein subunit alpha 12 OS Mus musculus GN Gna12 PE 1 SV 3
Mm.3711	Q64521	GPDM MOUSE Glycerol 3 phosphate dehydrogenase mitochondrial OS Mus musculus GN Gpd2 PE 1 SV 2
Mm.299292	P19157	GSTP1 MOUSE Glutathione S transferase P 1 OS Mus musculus GN Gstp1 PE 1 SV 2
Mm.39330	P48722	H574L MOUSE Heat shock 70 kDa protein 4L OS Mus musculus GN Hspa4l PE 1 SV 2
Mm.296181	P17156	HSP72 MOUSE Heat shock related 70 kDa protein 2 OS Mus musculus GN Hspa2 PE 1 SV 2
Mm.235123	Q8CAQ8	IMMT MOUSE Mitochondrial inner membrane protein OS Mus musculus GN Immt PE 1 SV 1
Mm.186499	Q5RKR3	ISLR2 MOUSE Immunoglobulin superfamily containing leucine rich repeat protein 2 OS Mus musculus GN I
Mm.25594	P31324	KAP3 MOUSE cAMP dependent protein kinase type II beta regulatory subunit OS Mus musculus GN Prkar2b
Mm.235182	Q923T9	KCC2G MOUSE Calcium calmodulin dependent protein kinase type II subunit gamma OS Mus musculus GN Cam
Mm.28023	Q791V5	MTCH2 MOUSE Mitochondrial carrier homolog 2 OS Mus musculus GN Mtch2 PE 1 SV 1
Mm.29513	Q9Z1P6	NDUA7 MOUSE NADH dehydrogenase ubiquinone 1 alpha subcomplex subunit 7 OS Mus musculus GN Ndufa7 P
Mm.1222	P06837	NEUM MOUSE Neuromodulin OS Mus musculus GN Gap43 PE 1 SV 1
Mm.203921	Q7TQI3	OTUB1 MOUSE Ubiquitin thioesterase OTUB1 OS Mus musculus GN Otub1 PE 1 SV 2
Mm.200859	Q61206	PA1B2 MOUSE Platelet activating factor acetylhydrolase IB subunit beta OS Mus musculus GN Pfaf1b2 P
Mm.272803	P57722	PCBP3 MOUSE Poly rC binding protein 3 OS Mus musculus GN Pcbp3 PE 2 SV 3

Mm.19825	Q8BGT8	PHIPL MOUSE Phytanoyl CoA hydroxylase interacting protein like OS Mus musculus GN Phyhipl PE 2 SV 1
Mm.21728	Q9Z2U0	PSA7 MOUSE Proteasome subunit alpha type 7 OS Mus musculus GN Psma7 PE 1 SV 1
Mm.151600	P62823	RAB3C MOUSE Ras related protein Rab 3C OS Mus musculus GN Rab3c PE 1 SV 1
Mm.37380	Q8CG50	RAB43 MOUSE Ras related protein Rab 43 OS Mus musculus GN Rab43 PE 1 SV 1
Mm.490252	P61294	RAB6B MOUSE Ras related protein Rab 6B OS Mus musculus GN Rab6b PE 1 SV 1
Mm.383182	P32883	RASK MOUSE GTPase KRas OS Mus musculus GN Kras PE 1 SV 1
Mm.290285	Q8BHD0	RB39A MOUSE Ras related protein Rab 39A OS Mus musculus GN Rab39a PE 2 SV 1
Mm.250030	P35979	RL12 MOUSE 60S ribosomal protein L12 OS Mus musculus GN Rpl12 PE 1 SV 2
Mm.252987	Q91V14	S12A5 MOUSE Solute carrier family 12 member 5 OS Mus musculus GN Slc12a5 PE 1 SV 2
Mm.346842	Q8C650	SEP10 MOUSE Septin 10 OS Mus musculus GN Sept10 PE 2 SV 1
Mm.1682	P97797	SHPS1 MOUSE Tyrosine protein phosphatase non receptor type substrate 1 OS Mus musculus GN Sirpa PE 1
Mm.205601	Q60598	SRC8 MOUSE Src substrate cortactin OS Mus musculus GN Ctnn PE 1 SV 2
Mm.378957	P54227	STMN1 MOUSE Stathmin OS Mus musculus GN Strmn1 PE 1 SV 2
Mm.328888	F6SEU4	SYGP1 MOUSE Ras GTPase activating protein SynGAP OS Mus musculus GN Syngap1 PE 3 SV 2
Mm.200843	Q91ZZ3	SYUB MOUSE Beta synuclein OS Mus musculus GN Sncb PE 1 SV 1
Mm.1287	P10637	TAU MOUSE Microtubule associated protein tau OS Mus musculus GN Mapt PE 1 SV 3
Mm.439690	P68369	TBA1A MOUSE Tubulin alpha 1A chain OS Mus musculus GN Tuba1a PE 1 SV 1
Mm.229342	P11983	TCPA MOUSE T complex protein 1 subunit alpha OS Mus musculus GN Tcp1 PE 1 SV 3
Mm.328673	P42932	TCPQ MOUSE T complex protein 1 subunit theta OS Mus musculus GN Cct8 PE 1 SV 3
Mm.293233	Q8QZT1	THIL MOUSE Acetyl CoA acetyltransferase mitochondrial OS Mus musculus GN Acat1 PE 1 SV 1
Mm.240839	P21107	TPM3 MOUSE Tropomyosin alpha 3 chain OS Mus musculus GN Tpm3 PE 1 SV 2
Mm.371667	P61089	UBE2N MOUSE Ubiquitin conjugating enzyme E2 N OS Mus musculus GN Ube2n PE 1 SV 1
Mm.276618	Q9Z1G3	VATC1 MOUSE V type proton ATPase subunit C 1 OS Mus musculus GN Atp6v1c1 PE 1 SV 4
Mm.311549	P57746	VATD MOUSE V type proton ATPase subunit D OS Mus musculus GN Atp6v1d PE 1 SV 1
Mm.27082	Q8BVE3	VATH MOUSE V type proton ATPase subunit H OS Mus musculus GN Atp6v1h PE 1 SV 1
Mm.101389	Q8BFR1	ZCCHL MOUSE Zinc finger CCCH type antiviral protein 1 like OS Mus musculus GN Zc3hav1l PE 2 SV 1

Table 4

Identification of the differentially expressed proteins in the mouse hippocampus of the tolerance group by qMS - **Downregulated at 3h**

UniGene ID	UniProt ID	Name, Description
Mm.107293	Q8BFZ3	ACTBL MOUSE Beta actin like protein 2 OS Mus musculus GN Actbl2 PE 1 SV 1
Mm.81144	P57780	ACTN4 MOUSE Alpha actinin 4 OS Mus musculus GN Actn4 PE 1 SV 1
Mm.221298	P61205	ARF3 MOUSE ADP ribosylation factor 3 OS Mus musculus GN Arf3 PE 2 SV 2
Mm.447553	P60766	CDC42 MOUSE Cell division control protein 42 homolog OS Mus musculus GN Cdc42 PE 1 SV 2
Mm.30928	Q8BH59	CMC1 MOUSE Calcium binding mitochondrial carrier protein Aralar1 OS Mus musculus GN Slc25a12 PE 1 SV 1
Mm.27732	Q9EQF6	DPYL5 MOUSE Dihydropyrimidinase related protein 5 OS Mus musculus GN Dpysl5 PE 1 SV 1
Mm.471154	Q6PER3	MARE3 MOUSE Microtubule associated protein RP EB family member 3 OS Mus musculus GN Mapre3 PE 1 SV 1
Mm.210857	Q61885	MOG MOUSE Myelin oligodendrocyte glycoprotein OS Mus musculus GN Mog PE 1 SV 1
Mm.439702	P15532	NDKA MOUSE Nucleoside diphosphate kinase A OS Mus musculus GN Nme1 PE 1 SV 1
Mm.27842	P70441	NHRF1 MOUSE Na H exchange regulatory cofactor NHE RF1 OS Mus musculus GN Slc9a3r1 PE 1 SV 3
Mm.277349	Q99LX0	PARK7 MOUSE Protein DJ 1 OS Mus musculus GN Park7 PE 1 SV 1
Mm.378993	P61027	RAB10 MOUSE Ras related protein Rab 10 OS Mus musculus GN Rab10 PE 1 SV 1
Mm.41580	Q9CZT8	RAB3B MOUSE Ras related protein Rab 3B OS Mus musculus GN Rab3b PE 1 SV 1
Mm.379375	Q8BG05	ROA3 MOUSE Heterogeneous nuclear ribonucleoprotein A3 OS Mus musculus GN Hnrnpa3 PE 1 SV 1
Mm.270259	O55131	SEPT7 MOUSE Septin 7 OS Mus musculus GN Sept7 PE 1 SV 1
Mm.396243	O55100	SNG1 MOUSE Synaptogyrin 1 OS Mus musculus GN Syngr1 PE 1 SV 2
Mm.223674	Q62277	SYPH MOUSE Synaptophysin OS Mus musculus GN Syp PE 1 SV 2
Mm.405359	P05213	TBA1B MOUSE Tubulin alpha 1B chain OS Mus musculus GN Tuba1b PE 1 SV 2
Mm.88212	P68373	TBA1C MOUSE Tubulin alpha 1C chain OS Mus musculus GN Tuba1c PE 1 SV 1
Mm.45285	A2AQ07	TBB1 MOUSE Tubulin beta 1 chain OS Mus musculus GN Tubb1 PE 1 SV 1

Table 5

Identification of the differentially expressed proteins in the mouse hippocampus of the injury group by qMS - **Upregulated at 24h**

UniGene ID	UniProt ID	Name, Description
Mm.221038	Q3UHJ0	AAK1 MOUSE AP2 associated protein kinase 1 OS Mus musculus GN Aak1 PE 1 SV 2
Mm.686	P68033	ACTC MOUSE Actin alpha cardiac muscle 1 OS Mus musculus GN Actc1 PE 1 SV 1
Mm.284446	P47738	ALDH2 MOUSE Aldehyde dehydrogenase mitochondrial OS Mus musculus GN Aldh2 PE 1 SV 1
Mm.271178	Q9CQW2	ARL8B MOUSE ADP ribosylation factor like protein 8B OS Mus musculus GN Arl8b PE 2 SV 1
Mm.150319	Q641P0	ARP3B MOUSE Actin related protein 3B OS Mus musculus GN Actr3b PE 2 SV 1
Mm.394300	Q8BLQ9	CADM2 MOUSE Cell adhesion molecule 2 OS Mus musculus GN Cadm2 PE 1 SV 2
Mm.203965	Q6ZQ38	CAND1 MOUSE Cullin associated NEDD8 dissociated protein 1 OS Mus musculus GN Cand1 PE 2 SV 2
Mm.19142	P47753	CAZA1 MOUSE F actin capping protein subunit alpha 1 OS Mus musculus GN Capza1 PE 1 SV 4
Mm.31395	Q00493	CBPE MOUSE Carboxypeptidase E OS Mus musculus GN Cpe PE 1 SV 2
Mm.806	P35762	CD81 MOUSE CD81 antigen OS Mus musculus GN Cd81 PE 1 SV 1
Mm.44220	Q9QXT0	CNPY2 MOUSE Protein canopy homolog 2 OS Mus musculus GN Cnpy2 PE 2 SV 1
Mm.23692	Q60737	CSK21 MOUSE Casein kinase II subunit alpha OS Mus musculus GN Csnk2a1 PE 1 SV 2
Mm.378921	P23242	CXA1 MOUSE Gap junction alpha 1 protein OS Mus musculus GN Gja1 PE 1 SV 2
Mm.472264	Q9JLM8	DCLK1 MOUSE Serine threonine protein kinase DCLK1 OS Mus musculus GN Dclk1 PE 1 SV 1
Mm.210863	Q9WV69	DEMA MOUSE Dematin OS Mus musculus GN Epb49 PE 1 SV 1
Mm.246436	Q9D0M5	DYL2 MOUSE Dynein light chain 2 cytoplasmic OS Mus musculus GN Dynll2 PE 1 SV 1
Mm.5305	P68040	GBLP MOUSE Guanine nucleotide binding protein subunit beta 2 like 1 OS Mus musculus GN Gnb2l1 PE 1 S
Mm.102080	Q8VE33	GD1L1 MOUSE Ganglioside induced differentiation associated protein 1 like 1 OS Mus musculus GN Gdap1
Mm.393508	O70443	GNAZ MOUSE Guanine nucleotide binding protein G z subunit alpha OS Mus musculus GN Gnaz PE 2 SV 4
Mm.282351	P48774	GSTM5 MOUSE Glutathione S transferase Mu 5 OS Mus musculus GN Gstm5 PE 1 SV 1
Mm.193539	P15864	H12 MOUSE Histone H1 2 OS Mus musculus GN Hist1h1c PE 1 SV 2
Mm.245931	P27661	H2AX MOUSE Histone H2A x OS Mus musculus GN H2afx PE 1 SV 2
Mm.378937	Q9R257	HEBP1 MOUSE Heme binding protein 1 OS Mus musculus GN Hebp1 PE 1 SV 1
Mm.279821	P60843	IF4A1 MOUSE Eukaryotic initiation factor 4A I OS Mus musculus GN Eif4a1 PE 2 SV 1
Mm.246466	Q6WVG3	KCD12 MOUSE BTB POZ domain containing protein KCTD12 OS Mus musculus GN Kctd12 PE 1 SV 1
Mm.16563	P00342	LDHC MOUSE L lactate dehydrogenase C chain OS Mus musculus GN Ldhc PE 1 SV 2
Mm.298251	Q9JIA1	LGI1 MOUSE Leucine rich glioma inactivated protein 1 OS Mus musculus GN Lgi1 PE 1 SV 1
Mm.334011	Q8BMF3	MAON MOUSE NADP dependent malic enzyme mitochondrial OS Mus musculus GN Me3 PE 1 SV 2
Mm.248907	P31938	MP2K1 MOUSE Dual specificity mitogen activated protein kinase kinase 1 OS Mus musculus GN Map2k1 PE
Mm.27570	Q9CQZ5	NDUA6 MOUSE NADH dehydrogenase ubiquinone 1 alpha subcomplex subunit 6 OS Mus musculus GN Ndufa6 P
Mm.279823	Q9D8B4	NDUAB MOUSE NADH dehydrogenase ubiquinone 1 alpha subcomplex subunit 11 OS Mus musculus GN Ndufa11
Mm.375824	Q99LY9	NDU55 MOUSE NADH dehydrogenase ubiquinone iron sulfur protein 5 OS Mus musculus GN Ndufs5 PE 1 SV
Mm.317293	Q80Z24	NEGR1 MOUSE Neuronal growth regulator 1 OS Mus musculus GN Negr1 PE 1 SV 1
Mm.326702	Q810U3	NFASC MOUSE Neurofascin OS Mus musculus GN Nfasc PE 1 SV 1
Mm.208439	Q810U4	NRCAM MOUSE Neuronal cell adhesion molecule OS Mus musculus GN Nrcam PE 1 SV 2
Mm.490272	Q60597	ODO1 MOUSE 2 oxoglutarate dehydrogenase mitochondrial OS Mus musculus GN Ogdh PE 1 SV 3
Mm.296221	Q9D2G2	ODO2 MOUSE Dihydrodipicolylsine residue succinyltransferase component of 2 oxoglutarate dehydrogenase
Mm.544	Q62048	PEA15 MOUSE Astrocytic phosphoprotein PEA 15 OS Mus musculus GN Pea15 PE 1 SV 1
Mm.36241	O35129	PHB2 MOUSE Prohibitin 2 OS Mus musculus GN Phb2 PE 1 SV 1
Mm.274432	P48453	PP2BB MOUSE Serine threonine protein phosphatase 2B catalytic subunit beta isoform OS Mus musculus G
Mm.29824	Q11011	PSA MOUSE Puromycin sensitive aminopeptidase OS Mus musculus GN Npepps PE 1 SV 2
Mm.30210	Q9QUM9	PSA6 MOUSE Proteasome subunit alpha type 6 OS Mus musculus GN Psma6 PE 1 SV 1
Mm.151600	P62823	RAB3C MOUSE Ras related protein Rab 3C OS Mus musculus GN Rab3c PE 1 SV 1

Mm.305750	P14115	RL27A MOUSE 60S ribosomal protein L27a OS Mus musculus GN Rpl27a PE 2 SV 5
Mm.380435	P99027	RLA2 MOUSE 60S acidic ribosomal protein P2 OS Mus musculus GN Rplp2 PE 1 SV 3
Mm.246990	Q9E997	RTN3 MOUSE Reticulon 3 OS Mus musculus GN Rtn3 PE 1 SV 2
Mm.5260	P31648	SC6A1 MOUSE Sodium and chloride dependent GABA transporter 1 OS Mus musculus GN Slc6a1 PE 1 SV 2
Mm.33343	Q8R3V5	SHLB2 MOUSE Endophilin B2 OS Mus musculus GN Sh3glb2 PE 2 SV 2
Mm.10	Q64674	SPEE MOUSE Spermidine synthase OS Mus musculus GN Srm PE 2 SV 1
Mm.393311	Q8BWF0	SSDH MOUSE Succinate semialdehyde dehydrogenase mitochondrial OS Mus musculus GN Aldh5a1 PE 1 SV 1
Mm.328888	F6SEU4	SYGP1 MOUSE Ras GTPase activating protein SynGAP OS Mus musculus GN Syngap1 PE 3 SV 2
Mm.5102	P46097	SYT2 MOUSE Synaptotagmin 2 OS Mus musculus GN Syt2 PE 1 SV 1
Mm.24183	Q9R1Q8	TAGL3 MOUSE Transgelin 3 OS Mus musculus GN Tagln3 PE 1 SV 1
Mm.405359	P05213	TBA1B MOUSE Tubulin alpha 1B chain OS Mus musculus GN Tuba1b PE 1 SV 2
Mm.379227	Q9CWF2	TBB2B MOUSE Tubulin beta 2B chain OS Mus musculus GN Tubb2b PE 1 SV 1
Mm.213292	Q9CZW5	TOM70 MOUSE Mitochondrial import receptor subunit TOM70 OS Mus musculus GN Tomm70a PE 1 SV 2
Mm.136648	Q9CYZ2	TPD54 MOUSE Tumor protein D54 OS Mus musculus GN Tpd52l2 PE 1 SV 1
Mm.274346	Q9Z0P5	TWF2 MOUSE Twinfilin 2 OS Mus musculus GN Twf2 PE 1 SV 1
Mm.27082	Q8BVE3	VATH MOUSE V type proton ATPase subunit H OS Mus musculus GN Atp6v1h PE 1 SV 1

Table 6

Identification of the differentially expressed proteins in the mouse hippocampus of the injury group by qMS - **Downregulated at 24h**

UniGene ID	UniProt ID	Name, Description
Mm.34319	Q9CQV8	1433B MOUSE 14 3 3 protein beta alpha OS Mus musculus GN Ywhab PE 1 SV 3
Mm.234700	P62259	1433E MOUSE 14 3 3 protein epsilon OS Mus musculus GN Ywhae PE 1 SV 1
Mm.409488	P68510	1433F MOUSE 14 3 3 protein eta OS Mus musculus GN Ywhah PE 1 SV 2
Mm.289630	P68254	1433T MOUSE 14 3 3 protein theta OS Mus musculus GN Ywhaq PE 1 SV 1
Mm.107293	Q8BFZ3	ACTBL MOUSE Beta actin like protein 2 OS Mus musculus GN Actbl2 PE 1 SV 1
Mm.28521	Q8R5C5	ACTY MOUSE Beta contractin OS Mus musculus GN Actr1b PE 1 SV 1
Mm.227583	O55143	AT2A2 MOUSE Sarcoplasmic endoplasmic reticulum calcium ATPase 2 OS Mus musculus GN At2a2 PE 1 SV 2
Mm.274540	Q3UHL1	CAMKV MOUSE CaM kinase like vesicle associated protein OS Mus musculus GN Camkv PE 1 SV 2
Mm.58836	Q9CZU6	CISY MOUSE Citrate synthase mitochondrial OS Mus musculus GN Cs PE 1 SV 1
Mm.298875	O08585	CLCA MOUSE Clathrin light chain A OS Mus musculus GN Clta PE 1 SV 1
Mm.290026	Q6IRU5	CLCB MOUSE Clathrin light chain B OS Mus musculus GN Cltb PE 2 SV 1
Mm.298947	O35215	DOPD MOUSE D dopachrome decarboxylase OS Mus musculus GN Ddt PE 1 SV 3
Mm.441620	Q8BZ98	DYN3 MOUSE Dynamin 3 OS Mus musculus GN Dnm3 PE 1 SV 1
Mm.254629	B2RSH2	GNAI1 MOUSE Guanine nucleotide binding protein G i subunit alpha 1 OS Mus musculus GN Gnai1 PE 2 SV 5
Mm.170587	P43274	H14 MOUSE Histone H1 4 OS Mus musculus GN Hist1h1e PE 1 SV 2
Mm.262527	Q8CGP6	H2A1H MOUSE Histone H2A type 1 H OS Mus musculus GN Hist1h2ah PE 1 SV 3
Mm.14287	P16627	HS71L MOUSE Heat shock 70 kDa protein 1 like OS Mus musculus GN Hspa1l PE 2 SV 4
Mm.397111	P63005	LIS1 MOUSE Platelet activating factor acetylhydrolase IB subunit alpha OS Mus musculus GN Pafah1b1 P
Mm.5246	P17742	PPIA MOUSE Peptidyl prolyl cis trans isomerase A OS Mus musculus GN Ppia PE 1 SV 2
Mm.378993	P61027	RAB10 MOUSE Ras related protein Rab 10 OS Mus musculus GN Rab10 PE 1 SV 1
Mm.41580	Q9CZT8	RAB3B MOUSE Ras related protein Rab 3B OS Mus musculus GN Rab3b PE 1 SV 1
Mm.155896	O88569	ROA2 MOUSE Heterogeneous nuclear ribonucleoproteins A2 B1 OS Mus musculus GN Hnrnpa2b1 PE 1 SV 2
Mm.258633	Q60864	STIP1 MOUSE Stress induced phosphoprotein 1 OS Mus musculus GN Stip1 PE 1 SV 1
Mm.439759	P61264	STX1B MOUSE Syntaxin 1B OS Mus musculus GN Stx1b PE 1 SV 1
Mm.29845	Q9WUM5	SUCA MOUSE Succinyl CoA ligase ADP GDP forming subunit alpha mitochondrial OS Mus musculus GN Suc
Mm.187079	Q8CHC4	SYNJ1 MOUSE Synaptotagmin 1 OS Mus musculus GN Synj1 PE 1 SV 3
Mm.223674	Q62277	SYPH MOUSE Synaptophysin OS Mus musculus GN Syp PE 1 SV 2
Mm.7420	Q9D6F9	TBB4A MOUSE Tubulin beta 4A chain OS Mus musculus GN Tubb4a PE 1 SV 3
Mm.328673	P42932	TCPQ MOUSE T complex protein 1 subunit theta OS Mus musculus GN Cct8 PE 1 SV 3
Mm.1104	Q02053	UBA1 MOUSE Ubiquitin like modifier activating enzyme 1 OS Mus musculus GN Uba1 PE 1 SV 1
Mm.29807	Q9R0P9	UCHL1 MOUSE Ubiquitin carboxyl terminal hydrolase isozyme L1 OS Mus musculus GN Uchl1 PE 1 SV 1
Mm.101389	Q8BFR1	ZCCHL MOUSE Zinc finger CCCH type antiviral protein 1 like OS Mus musculus GN Zc3hav1l PE 2 SV 1

Table 7

Identification of the differentially expressed proteins in the mouse hippocampus of the tolerance group by qMS - **Upregulated at 24h**

UniGene ID	UniProt ID	Name, Description
Mm.3118	P61164	ACTZ MOUSE Alpha centractin OS Mus musculus GN Actr1a PE 2 SV 1
Mm.389075	P84084	ARF5 MOUSE ADP ribosylation factor 5 OS Mus musculus GN Arf5 PE 2 SV 2
Mm.174998	Q8VEH3	ARL8A MOUSE ADP ribosylation factor like protein 8A OS Mus musculus GN Arl8a PE 2 SV 1
Mm.197534	Q8BKX1	BAIP2 MOUSE Brain specific angiogenesis inhibitor 1 associated protein 2 OS Mus musculus GN Baiap2 P
Mm.2755	Q08331	CALB2 MOUSE Calretinin OS Mus musculus GN Calb2 PE 1 SV 3
Mm.1971	P14211	CALR MOUSE Calreticulin OS Mus musculus GN Calr PE 1 SV 1
Mm.128627	Q8R1Q8	DC1L1 MOUSE Cytoplasmic dynein 1 light intermediate chain 1 OS Mus musculus GN Dync1l1 PE 1 SV 1
Mm.250414	O35098	DPYL4 MOUSE Dihydropyrimidinase related protein 4 OS Mus musculus GN Dpysl4 PE 1 SV 1
Mm.278458	P26883	FKB1A MOUSE Peptidyl prolyl cis trans isomerase FKBP1A OS Mus musculus GN Fkbp1a PE 1 SV 2
Mm.436562	Q64467	G3PT MOUSE Glyceraldehyde 3 phosphate dehydrogenase testis specific OS Mus musculus GN Gapdhs PE 1
Mm.41737	P63213	GBG2 MOUSE Guanine nucleotide binding protein G I G S G O subunit gamma 2 OS Mus musculus GN Gng2
Mm.1239	P03995	GFAP MOUSE Glial fibrillary acidic protein OS Mus musculus GN Gfap PE 1 SV 4
Mm.394930	Q9WV60	GSK3B MOUSE Glycogen synthase kinase 3 beta OS Mus musculus GN Gsk3b PE 1 SV 2
Mm.8048	Q07133	H1T MOUSE Histone H1t OS Mus musculus GN Hist1h1t PE 2 SV 4
Mm.14287	P16627	HS71L MOUSE Heat shock 70 kDa protein 1 like OS Mus musculus GN Hspa1l PE 2 SV 4
Mm.240965	Q80TL4	K1045 MOUSE Protein KIAA1045 OS Mus musculus GN Kiaa1045 PE 1 SV 2
Mm.397111	P63005	LIS1 MOUSE Platelet activating factor acetylhydrolase IB subunit alpha OS Mus musculus GN Pfah1b1 P
Mm.210857	Q61885	MOG MOUSE Myelin oligodendrocyte glycoprotein OS Mus musculus GN Mog PE 1 SV 1
Mm.200859	Q61206	PA1B2 MOUSE Platelet activating factor acetylhydrolase IB subunit beta OS Mus musculus GN Pfah1b2 P
Mm.456635	P62141	PP1B MOUSE Serine threonine protein phosphatase PP1 beta catalytic subunit OS Mus musculus GN Ppp1cb
Mm.295252	Q9CR16	PPID MOUSE Peptidyl prolyl cis trans isomerase D OS Mus musculus GN Ppid PE 1 SV 3
Mm.208883	Q9Z2U1	PSA5 MOUSE Proteasome subunit alpha type 5 OS Mus musculus GN Psma5 PE 1 SV 1
Mm.482241	P42669	PURA MOUSE Transcriptional activator protein Pur alpha OS Mus musculus GN Pura PE 1 SV 1
Mm.27806	Q9WUB3	PYGM MOUSE Glycogen phosphorylase muscle form OS Mus musculus GN Pygm PE 1 SV 3
Mm.32870	P59279	RAB2B MOUSE Ras related protein Rab 2B OS Mus musculus GN Rab2b PE 2 SV 1
Mm.260157	P35276	RAB3D MOUSE Ras related protein Rab 3D OS Mus musculus GN Rab3d PE 1 SV 1
Mm.482114	Q91ZR1	RAB4B MOUSE Ras related protein Rab 4B OS Mus musculus GN Rab4b PE 2 SV 2
Mm.27348	P63321	RALA MOUSE Ras related protein Ral A OS Mus musculus GN Rala PE 1 SV 1
Mm.261448	Q80ZJ1	RAP2A MOUSE Ras related protein Rap 2a OS Mus musculus GN Rap2a PE 1 SV 2
Mm.45148	Q8BHC1	RB39B MOUSE Ras related protein Rab 39B OS Mus musculus GN Rab39b PE 2 SV 1
Mm.397450	P14148	RL7 MOUSE 60S ribosomal protein L7 OS Mus musculus GN Rpl7 PE 2 SV 2
Mm.298745	P62270	RS18 MOUSE 40S ribosomal protein S18 OS Mus musculus GN Rps18 PE 1 SV 3
Mm.399829	P97351	RS3A MOUSE 40S ribosomal protein S3a OS Mus musculus GN Rps3a PE 1 SV 3
Mm.159143	Q9DA97	SEP14 MOUSE Septin 14 OS Mus musculus GN Sept14 PE 2 SV 2
Mm.134191	Q99JR1	SFXN1 MOUSE Sideroflexin 1 OS Mus musculus GN Sfxn1 PE 1 SV 3
Mm.104540	Q9DB05	SNAA MOUSE Alpha soluble NSF attachment protein OS Mus musculus GN Napa PE 1 SV 1
Mm.273053	P47758	SRPRB MOUSE Signal recognition particle receptor subunit beta OS Mus musculus GN Srprb PE 1 SV 1
Mm.187079	Q8CHC4	SYNJ1 MOUSE Synaptojanin 1 OS Mus musculus GN Synj1 PE 1 SV 3
Mm.430772	Q9QZM0	UBQL2 MOUSE Ubiquilin 2 OS Mus musculus GN Ubqln2 PE 1 SV 2
Mm.28643	P63044	VAMP2 MOUSE Vesicle associated membrane protein 2 OS Mus musculus GN Vamp2 PE 1 SV 2
Mm.260456	Q9QY76	VAPB MOUSE Vesicle associated membrane protein associated protein B OS Mus musculus GN Vapb PE 2 SV
Mm.276618	Q9Z1G3	VATC1 MOUSE V type proton ATPase subunit C 1 OS Mus musculus GN Atp6v1c1 PE 1 SV 4
Mm.406120	O88342	WDR1 MOUSE WD repeat containing protein 1 OS Mus musculus GN Wdr1 PE 1 SV 3
Mm.298132	Q8BGF3	WDR92 MOUSE WD repeat containing protein 92 OS Mus musculus GN Wdr92 PE 2 SV 1

Table 8

Identification of the differentially expressed proteins in the mouse hippocampus of the tolerance group by qMS - **Downregulated at 24h**

UniGene ID	UniProt ID	Name, Description
Mm.686	P68033	ACTC MOUSE Actin alpha cardiac muscle 1 OS Mus musculus GN Actc1 PE 1 SV 1
Mm.290482	O89053	COR1A MOUSE Coronin 1A OS Mus musculus GN Coro1a PE 1 SV 5
Mm.7286	O88712	CTBP1 MOUSE C terminal binding protein 1 OS Mus musculus GN Ctbp1 PE 1 SV 2
Mm.433257	P39054	DYN2 MOUSE Dynamin 2 OS Mus musculus GN Dnm2 PE 1 SV 2
Mm.21740	O35737	HNRH1 MOUSE Heterogeneous nuclear ribonucleoprotein H OS Mus musculus GN Hnrnh1 PE 1 SV 3
Mm.6388	Q61696	HS71A MOUSE Heat shock 70 kDa protein 1A OS Mus musculus GN Hspa1a PE 1 SV 2
Mm.251013	P70168	IMB1 MOUSE Importin subunit beta 1 OS Mus musculus GN Kpnb1 PE 1 SV 2
Mm.235123	Q8CAQ8	IMMT MOUSE Mitochondrial inner membrane protein OS Mus musculus GN Immt PE 1 SV 1
Mm.269649	P12382	K6PL MOUSE 6 phosphofructokinase liver type OS Mus musculus GN Pfk1 PE 1 SV 4
Mm.28023	Q791V5	MTCH2 MOUSE Mitochondrial carrier homolog 2 OS Mus musculus GN Mtch2 PE 1 SV 1
Mm.490272	Q60597	ODO1 MOUSE 2 oxoglutarate dehydrogenase mitochondrial OS Mus musculus GN Ogdh PE 1 SV 3
Mm.206159	Q8K183	PDXK MOUSE Pyridoxal kinase OS Mus musculus GN Pdxk PE 1 SV 1
Mm.4598	Q61361	PGCB MOUSE Brevican core protein OS Mus musculus GN Bcan PE 1 SV 2
Mm.217764	Q9D0F9	PGM1 MOUSE Phosphoglucomutase 1 OS Mus musculus GN Pgm1 PE 1 SV 4
Mm.5260	P31648	SC6A1 MOUSE Sodium and chloride dependent GABA transporter 1 OS Mus musculus GN Slc6a1 PE 1 SV 2
Mm.42944	Q9WTX5	SKP1 MOUSE S phase kinase associated protein 1 OS Mus musculus GN Skp1 PE 1 SV 3
Mm.5102	P46097	SYT2 MOUSE Synaptotagmin 2 OS Mus musculus GN Syt2 PE 1 SV 1
Mm.200843	Q91Z23	SYUB MOUSE Beta synuclein OS Mus musculus GN Sncb PE 1 SV 1
Mm.29182	Q93092	TALDO MOUSE Transaldolase OS Mus musculus GN Taldo1 PE 1 SV 2
Mm.439690	P68369	TBA1A MOUSE Tubulin alpha 1A chain OS Mus musculus GN Tuba1a PE 1 SV 1
Mm.405359	P05213	TBA1B MOUSE Tubulin alpha 1B chain OS Mus musculus GN Tuba1b PE 1 SV 2
Mm.27082	Q8BVE3	VATH MOUSE V type proton ATPase subunit H OS Mus musculus GN Atp6v1h PE 1 SV 1

Proteomic analysis after status epilepticus identifies UCHL1 as protective against hippocampal injury (Neurochemical Research)

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Contents, Supplementary File 2

Source data for Figure 2

Figure 2-1, page 2	GOstat analysis, up- and down-regulated proteins following injury, sampled at 3h
Figure 2-2, page 4	GOstat analysis, up- and down-regulated proteins following injury, sampled at 24h
Figure 2-3, page 6	GOstat analysis, up- and down-regulated proteins following tolerance, sampled at 3h
Figure 2-4, page 8	GOstat analysis, up- and down-regulated proteins following tolerance, sampled at 24h

Figure 2-3 - Source data file for Figure 2

GStat analysis, for up-and-down-regulated proteins (±30%) following treatment (T0), sampled at 3h
 performed online at <http://gostat.wehi.edu.au/cg-bin/gostat.pl>

Search parameters

Against default GO database
 used database MGI (see <http://geneontology.org/gene-associations/readme/mgi.README>)
 minimal length of GO path 3
 Subset Biological Process (BP), Cellular Component (CC), Molecular Function (MF)
 maximum p-value 50
 maximum number of GOs over/under
 representation no
 clustered no
 multiple test FDR (Benjamini)

Datasets run
 T0 +30 (3h) 5769
 T0 -30 (3h) 1820
Successful annotations by Gostat
 5769
 1820
Success following manual re-annotation*
 6359
 2020
 (*using DAVID and Uniprot)

T0 Up 3h BP

Best GOs (Max 50)	GO term	Genes	Count	Total	P-Value	Gene	Search Term	GOs
GO:0001914	protein transport	atp6v1d atp6a atp6b1c1 atp2aa6v1h	63	18253	3.42E-04	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	hydrogen transport	atp6v1d atp6a atp6b1c1 atp2aa6v1h	5	58	0.00042	aat1	Mm22108	GO:000468 GO:0008150
GO:0001914	oxidative phosphorylation	atp6v1d atp6a atp6b1c1 atp2aa6v1h	4	51	0.0002	aat1	Mm22108	GO:000468 GO:0008150
GO:007010	cytoskeleton organization and biogenesis	epq4-10 naa cat tuba1a krasraspa mapt smn1	8	447	0.00077	aat1	Mm22446	GO:0008152 GO:0008153
GO:0006918	energy coupled proton transport, down electrochemical gradient	atp6v1d atp6a atp6b1c1 atp2aa6v1h	3	31	0.00077	aat1	Mm22108	GO:000468 GO:0008150
GO:041946	ATP synthesis coupled proton transport	atp6v1d atp6a atp6b1c1 atp2aa6v1h	3	31	0.00077	aat1	Mm22108	GO:000468 GO:0008150
GO:041919	localization	atp6a atp2 aa6v1h atp6b1c1 atp2aa6v1h	20	2619	0.00077	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	coenzyme metabolic process	3 ac12a6 ywhag adm1	5	159	0.0106	aat1	Mm22108	GO:000468 GO:0008150
GO:0007474	ATP biosynthetic process	atp6v1d atp6a atp6b1c1 atp2aa6v1h	3	36	0.0108	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	nucleoside phosphate metabolic process	atp6v1d atp6a atp6b1c1 atp2aa6v1h	3	36	0.0108	aat1	Mm22108	GO:000468 GO:0008150
GO:0030306	cortical actin cytoskeleton organization and biogenesis	epq4-10 cat	2	8	0.0111	aat1	Mm22446	GO:0008152 GO:0008153
GO:0006918	ATP metabolic process	atp6v1d atp6a atp6b1c1 atp2aa6v1h	3	36	0.0111	aat1	Mm22108	GO:000468 GO:0008150
GO:0019142	monovent inorganic cation transport	atp6v1d atp6a atp6b1c1 atp2aa6v1h	6	286	0.0111	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	cofactor metabolic process	atp6v1d atp6a atp6b1c1 atp2aa6v1h	6	187	0.0111	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	ribonucleoside triphosphate biosynthetic process	atp6v1d atp6a atp6b1c1 atp2aa6v1h	3	45	0.0111	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	purine nucleoside triphosphate biosynthetic process	atp6v1d atp6a atp6b1c1 atp2aa6v1h	3	45	0.0111	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	purine nucleoside triphosphate biosynthetic process	atp6v1d atp6a atp6b1c1 atp2aa6v1h	3	45	0.0111	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	cofactor biosynthesis and biogenesis	epq4-10 naa cat	2	10	0.0111	aat1	Mm22446	GO:0008152 GO:0008153
GO:0006918	nucleoside triphosphate biosynthetic process	atp6v1d atp6a atp6b1c1 atp2aa6v1h	3	48	0.0111	aat1	Mm22108	GO:000468 GO:0008150
GO:041814	regulation of long-term neuronal synaptic plasticity	syngap1 kras	2	11	0.0111	aat1	Mm22108	GO:000468 GO:0008150
GO:0031111	negative regulation of microtubule polymerisation or depolymerisation	mapt smn1	2	11	0.0111	aat1	Mm22108	GO:000468 GO:0008150
GO:0007015	microtubule depolymerisation	mapt smn1	2	11	0.0111	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	purine nucleoside triphosphate metabolic process	syngap1 pkrab2 kras	3	49	0.0111	aat1	Mm22108	GO:000468 GO:0008150
GO:0007474	learning	syngap1 pkrab2 kras	3	49	0.0111	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	ribonucleoside triphosphate metabolic process	atp6v1d atp6a atp6b1c1 atp2aa6v1h	3	50	0.0111	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	purine nucleoside triphosphate metabolic process	atp6v1d atp6a atp6b1c1 atp2aa6v1h	3	51	0.0115	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	group transfer coenzyme metabolic process	atp6v1d atp6a atp6b1c1 atp2aa6v1h	3	54	0.0128	aat1	Mm22108	GO:000468 GO:0008150
GO:0031110	regulation of microtubule polymerisation or depolymerisation	mapt smn1	2	13	0.0129	aat1	Mm22108	GO:000468 GO:0008150
GO:0007474	nucleoside triphosphate metabolic process	atp6v1d atp6a atp6b1c1 atp2aa6v1h	3	56	0.0129	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	cation transport	atp6v1d atp6a atp6b1c1 atp2aa6v1h	7	459	0.0129	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	purine nucleoside triphosphate biosynthetic process	atp6v1d atp6a atp6b1c1 atp2aa6v1h	3	57	0.0129	aat1	Mm22108	GO:000468 GO:0008150
GO:0031110	microtubule polymerisation or depolymerisation	mapt smn1	2	14	0.0129	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	regulation of neuronal synaptic plasticity	syngap1 kras	2	14	0.0129	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	cellular TCR mediated signal transduction	rab34a syngap1 grn12 krasrasb3	3	81	0.0144	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	ribonucleoside biosynthetic process	atp6v1d atp6a atp6b1c1 atp2aa6v1h	3	81	0.0144	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	purine nucleoside biosynthetic process	atp6v1d atp6a atp6b1c1 atp2aa6v1h	3	81	0.0144	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	purine nucleoside biosynthetic process	atp6v1d atp6a atp6b1c1 atp2aa6v1h	3	85	0.0154	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	learning and memory	syngap1 pkrab2 kras	3	49	0.0154	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	ribonucleoside metabolic process	atp6v1d atp6a atp6b1c1 atp2aa6v1h	3	70	0.0162	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	actin cytoskeleton organization and biogenesis	epq4-10 naa cat	2	74	0.0162	aat1	Mm22446	GO:0008152 GO:0008153
GO:0006918	purine nucleoside metabolic process	atp6v1d atp6a atp6b1c1 atp2aa6v1h	3	74	0.0162	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	regulation of synaptic plasticity	syngap1 kras	2	21	0.0255	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	actin filament based process	epq4-10 cat kras sirpa	4	165	0.0237	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	visual behaviour	syngap1 kras	2	22	0.0237	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	visual perception	syngap1 kras	2	22	0.0237	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	regulation of synapse structure and activity	syngap1 kras	2	23	0.0254	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	coenzyme biosynthetic process	atp6v1d atp6a atp6b1c1 atp2aa6v1h	3	83	0.0259	aat1	Mm22108	GO:000468 GO:0008150
GO:0031111	negative regulation of microtubule polymerisation	smn1	1	1	0.0266	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	cellular component organisation and biogenesis	syngap1 tuba1a rab39 mapt smn1 epq4-10 arf1 rpl12 ep1a	16	213	0.0358	aat1	Mm22108	GO:000468 GO:0008150

T0 Up 3h CC

Best GOs (Max 50)	GO term	Genes	Count	Total	P-Value	Gene	Search Term	GOs
GO:0005832	cytoplasm	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	63	18253	5.40E-05	aat1	Mm22108	GO:0005739 GO:0016020
GO:0042334	prokin complex	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	15	1558	2.25E-03	aat1	Mm22942	GO:0005739 GO:0016020
GO:0030291	macromolecular complex	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	17	1963	0.00235	aat1	Mm22942	GO:0005739 GO:0005885 GO:0019528 GO:0042995
GO:0007474	learning and memory	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	6	229	0.0037	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	mitochondrial inner membrane	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	6	238	0.0037	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	mitochondrial membrane	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	6	248	0.0037	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	Asp23 protein complex	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	6	248	0.0037	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	cell projection	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	7	344	0.0037	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	learning and memory	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	6	229	0.0037	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	mitochondrial envelope	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	6	268	0.0038	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	cytoskeleton	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	10	859	0.0096	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	neuron projection	syngap1 ga43 tpm3 mapt	4	116	0.0096	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	mitochondrial part	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	6	316	0.0096	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	cytoplasmic part	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	21	3058	0.0096	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	membrane fraction	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	7	446	0.0099	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	mitochondrion	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	10	920	0.0099	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	cell fraction	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	7	498	0.0103	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	envelope	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	6	375	0.0115	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	organelle envelope	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	6	375	0.0115	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	cytoskeletal part	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	7	520	0.0118	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	organelle membrane	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	7	522	0.0118	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	intric to membrane	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	8	567	0.0138	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	integral to membrane	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	8	562	0.0154	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	vacuolar protein-transferring V-type ATPase, V1 domain	atp6v1h	1	1	0.0154	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	proton-transferring V-type ATPase, V1 domain	atp6v1h	1	1	0.0154	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	cleavage furrow	atp6v1h	1	2	0.0315	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	intracellular part	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	40	8417	0.0351	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	intracellular	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	41	8708	0.0351	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	glycogen 3-phosphate dehydrogenase complex	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	1	3	0.0403	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	podosome	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	1	3	0.0403	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	non-membrane-bound organelle	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	1	1463	0.0412	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	non-membrane-bound organelle	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	1	1463	0.0412	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	cell cortex	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	2	47	0.0412	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	intracellular organelle part	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3a	15	2287	0.0412	aat1	Mm22108	GO:000468 GO:0008150
GO:0006918	organelle part	act1 eef1g smn1 ssha mapt pcrab2 pafah1b2 tmem4 enc3						

Figure 2.4 - Source data file for Figure 2

Gostat analysis, for up-and down-regulated proteins (≥30% following tolerance (ToI), sampled at 24h
performed online at <http://gostat.welhi.edu.au/cg-bin/gostat.pl>

Search parameters

Against default GO database
used database MGI (see http://geneontology.org/gene-associations/readme/mgi_README)
minimal length of GO path 3
Subset Biological Process (BP), Cellular Component (CC), Molecular Function (MF)
maximal p-value 0.1
maximal number of GOs representation 50
clustered over/under no
multiple test FDR (Benjamini)

Datasets run 44/44
ToI >30 (24h) 20/22
ToI <30 (24h) 20/22

ToI Up 24h BP

Best GOs (Max. 50)	GO term	Genes	Count	Total	P-Value	Gene	Search Term	GOs
GO:000684	small GTPase mediated signal transduction	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	44	18253	3.27E-05	actr1a	Mm 3118	GO:016192
GO:0019043	cellular component organization and biogenesis	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	9	337	0.00111	actr1a	Mm 3118	GO:000888 GO:0007284 GO:0015031 GO:0016192
GO:0011719	localization	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	17	2619	0.00127	actr1a	Mm 3118	GO:0007284 GO:000888 GO:0015031 GO:0016192
GO:0007242	intracellular signaling cascade	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	11	865	0.00131	atp1b1c1	Mm 27618	GO:0007185 GO:0007286 GO:0007399 GO:0048647
GO:0016192	vesicle-mediated transport	actr1a rac1b3o balap2 arf1a dync111 rab3d rala rab2b	7	401	0.00234	calb2	Mm 2755	GO:0006457 GO:0030886 GO:0040020
GO:0008104	transport	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	14	2259	0.0119	dyx4c4	Mm 250414	GO:0006457
GO:0016192	establishment of cellular localization	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	8	710	0.0119	dyx4c4	Mm 250414	GO:0006457
GO:0016192	cellular localization	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	8	722	0.0119	dyx4c4	Mm 250414	GO:0006457
GO:0016192	establishment of localization	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	14	2320	0.0124	dyx4c4	Mm 250414	GO:0006457
GO:0016192	regulation of exocytosis	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	2	16	0.028	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0016192	regulation of transport	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	3	84	0.028	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0016192	stem cell self-renewal	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	2	21	0.028	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0016192	regulation of glycolysis	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	6	697	0.0307	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0046130	male gamete generation	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	4	195	0.0310	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0046130	synaptic vesicle transport	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	2	23	0.0308	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0046130	intracellular transport	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	1	1	0.0307	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0046130	positive regulation of protein export from nucleus	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	1	1	0.0307	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0046130	regulation of glycolysis	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	1	1	0.0307	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	glucan metabolic process	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	2	31	0.0307	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	glycogen metabolic process	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	2	31	0.0307	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	glycogen storage	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	4	250	0.0455	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	energy reserve metabolic process	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	2	35	0.0455	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	protein transport	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	6	624	0.0476	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	protein folding	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	6	130	0.0478	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	organelle organization and biogenesis	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	6	656	0.0482	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	establishment of protein localization	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	2	47	0.0545	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	regulation of protein export from nucleus	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	4	292	0.0578	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	sexual reproduction	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	2	47	0.0581	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	cellular polysaccharide metabolic process	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	2	47	0.0581	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	polysaccharide metabolic process	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	2	47	0.0581	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	cell cycle	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	6	708	0.0584	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	protein localization	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	3	3	0.064	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	acetylation	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	1	3	0.064	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	retrograde axon cargo transport	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	4	324	0.064	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	cellular homeostasis	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	4	324	0.064	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	cell motility	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	6	731	0.0643	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	macromolecule localization	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	3	178	0.0661	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	regulation of progression through cell cycle	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	3	178	0.0661	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	regulation of cell cycle	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	1	4	0.0661	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	glycogen catabolic process	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	1	4	0.0661	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	carbohydrate process	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	1	4	0.0661	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	positive regulation of carbohydrate metabolic process	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	1	4	0.0661	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	regulation of cell cycle	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	1	4	0.0661	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	regulation of meiosis	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	3	183	0.0714	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	ribonucleoprotein complex biogenesis and assembly	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	2	86	0.0719	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821
GO:0006792	energy derivation by oxidation of organic compounds	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	2	86	0.0719	gpcr2a	Mm 43662	GO:0006096 GO:0030317 GO:0049821

ToI Up 24h CC

Best GOs (Max. 50)	GO term	Genes	Count	Total	P-Value	Gene	Search Term	GOs
GO:0005829	cytoplasm	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	44	8214	3.40E-05	actr1a	Mm 3118	GO:0005737 GO:0005854 GO:0005889 GO:0005896 GO:0005918 GO:0005984 GO:0015629
GO:0005829	intracellular	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	35	8708	2.24E-03	actr1a	Mm 3118	GO:0005737 GO:0005854 GO:0005889 GO:0005896 GO:0005918 GO:0005984 GO:0015629
GO:0044248	Zygomycota	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	2	5	0.00234	actr1a	Mm 3118	GO:0005737 GO:0005854 GO:0005889 GO:0005896 GO:0005918 GO:0005984 GO:0015629
GO:0005829	cytoskeletal part	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	3	468	0.00235	actr1a	Mm 3118	GO:0005737 GO:0005854 GO:0005889 GO:0005896 GO:0005918 GO:0005984 GO:0015629
GO:0044244	intracellular part	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	32	8417	0.0138	actr1a	Mm 3118	GO:0005737 GO:0005854 GO:0005889 GO:0005896 GO:0005918 GO:0005984 GO:0015629
GO:0006829	cytosol	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	5	337	0.0208	actr1a	Mm 3118	GO:0005737 GO:0005854 GO:0005889 GO:0005896 GO:0005918 GO:0005984 GO:0015629
GO:0006829	cytoskeletal part	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	3	94	0.0208	actr1a	Mm 3118	GO:0005737 GO:0005854 GO:0005889 GO:0005896 GO:0005918 GO:0005984 GO:0015629
GO:0006829	macromolecular complex	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	12	1863	0.0209	actr1a	Mm 3118	GO:0005737 GO:0005854 GO:0005889 GO:0005896 GO:0005918 GO:0005984 GO:0015629
GO:0006829	microtubule associated complex	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	3	102	0.0209	actr1a	Mm 3118	GO:0005737 GO:0005854 GO:0005889 GO:0005896 GO:0005918 GO:0005984 GO:0015629
GO:0044244	intracellular non-membrane-bound organelle	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	10	1463	0.0209	actr1a	Mm 3118	GO:0005737 GO:0005854 GO:0005889 GO:0005896 GO:0005918 GO:0005984 GO:0015629
GO:0044248	non-membrane-bound organelle	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	10	1463	0.0209	actr1a	Mm 3118	GO:0005737 GO:0005854 GO:0005889 GO:0005896 GO:0005918 GO:0005984 GO:0015629
GO:0006829	secretory granule	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	2	38	0.0246	actr1a	Mm 3118	GO:0005737 GO:0005854 GO:0005889 GO:0005896 GO:0005918 GO:0005984 GO:0015629
GO:0006829	ribosome	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	17	526	0.0256	actr1a	Mm 3118	GO:0005737 GO:0005854 GO:0005889 GO:0005896 GO:0005918 GO:0005984 GO:0015629
GO:0006829	intracellular membrane	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	5	567	0.0277	actr1a	Mm 3118	GO:0005737 GO:0005854 GO:0005889 GO:0005896 GO:0005918 GO:0005984 GO:0015629
GO:0006829	integral to membrane	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	4	567	0.0277	actr1a	Mm 3118	GO:0005737 GO:0005854 GO:0005889 GO:0005896 GO:0005918 GO:0005984 GO:0015629
GO:0006829	cell	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	41	13677	0.0277	actr1a	Mm 3118	GO:0005737 GO:0005854 GO:0005889 GO:0005896 GO:0005918 GO:0005984 GO:0015629
GO:0044244	cell part	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	41	13677	0.0277	actr1a	Mm 3118	GO:0005737 GO:0005854 GO:0005889 GO:0005896 GO:0005918 GO:0005984 GO:0015629
GO:0044248	Zygomycota membrane	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	1	4	0.0602	actr1a	Mm 3118	GO:0005737 GO:0005854 GO:0005889 GO:0005896 GO:0005918 GO:0005984 GO:0015629
GO:0006829	DNA replication factor complex	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	1	5	0.0714	actr1a	Mm 3118	GO:0005737 GO:0005854 GO:0005889 GO:0005896 GO:0005918 GO:0005984 GO:0015629
GO:0006829	dynactin complex	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	1	7	0.0846	actr1a	Mm 3118	GO:0005737 GO:0005854 GO:0005889 GO:0005896 GO:0005918 GO:0005984 GO:0015629

ToI Up 24h MF

Best GOs (Max. 50)	GO term	Genes	Count	Total	P-Value	Gene	Search Term	GOs
GO:0005245	GTP binding	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	44	8214	9.12E-05	actr1a	Mm 3118	GO:0005737 GO:0005854 GO:0005889 GO:0005896 GO:0005918 GO:0005984 GO:0015629
GO:0032541	ribonucleotide binding	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	11	325	0.00235	actr1a	Mm 3118	GO:0005737 GO:0005854 GO:0005889 GO:0005896 GO:0005918 GO:0005984 GO:0015629
GO:0032541	guanylate nucleotide binding	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	11	325	0.00235	actr1a	Mm 3118	GO:0005737 GO:0005854 GO:0005889 GO:0005896 GO:0005918 GO:0005984 GO:0015629
GO:0032543	ribonucleotide binding	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	16	1554	0.00235	actr1a	Mm 3118	GO:0005737 GO:0005854 GO:0005889 GO:0005896 GO:0005918 GO:0005984 GO:0015629
GO:0032545	purine ribonucleotide binding	rac1b3o balap2 arf1a dync111 rab3d rala rab2b	16	1554	0.00235	actr1a	Mm 3118	GO:0005737 GO:0005854 GO:0005889 GO:0005896 GO:0005918 GO:0005984 GO:0015629
GO:0004616	nucleotide binding	rac1b3o balap2 arf1a						

GO:0043748	protein polymerization	tuba to tuba1a	2	39	0.0159	pki	Mm29949	GO:0006096	
GO:0006222	water-soluble vitamin metabolic process	pkc	2	39	0.0159	pkc2	Mm21754	GO:0006096	
GO:0044961	skeletal myofibril assembly	act1	1	1	0.0168	pkp1a	Mm4264	GO:0006112	
GO:003340	muscle thin filament assembly	act1	1	1	0.0168	pkc	Mm5265	GO:0006110	GO:0006336
GO:0006096	glycolysis	pki	2	46	0.0175	snb	Mm20043	GO:0042417	
GO:0044961	cellular macromolecule catabolic process	pki	1	1	0.0168	pkc2	Mm5102	GO:0006110	
GO:0042410	vitamin B9 biosynthetic process	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0042410	vitamin B1 metabolic process	pkc	1	2	0.0243	tuba1a	Mm43660	GO:0007117	GO:0005258
GO:0006096	pyridoxine biosynthetic process	pkc	1	2	0.0243	tuba1b	Mm39213	GO:0007018	GO:0005258
GO:0006096	vitamin metabolic process	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0006096	transport	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0006096	establishment of localization	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0006096	microtubule-based movement	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0006096	cardiac myofibril assembly	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0006096	macromolecule catabolic process	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0006096	ribosomal protein import into nucleus	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0006096	cytoskeleton-dependent intracellular transport	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0044961	cellular metabolic process	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0006096	cardiac muscle morphogenesis	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0006096	cardiac muscle cell development	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0044961	localization	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0006096	muscle morphogenesis	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0006096	pentose-phosphate shunt	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0006096	NADPH regeneration	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0044961	cellular catabolic process	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0006096	coenzyme metabolic process	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0006096	cytoskeleton organization and biogenesis	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0006096	myofibril assembly	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0006096	NADP metabolic process	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0006096	stabilized muscle cell development	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0006096	protein import into nucleus, docking	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0006096	muscle cell development	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0006096	microtubule-based process	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0006096	nucleotide metabolic process	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0006096	telomere organization and biogenesis	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0044961	water-soluble vitamin biosynthetic process	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098
GO:0006096	telomere maintenance	pkc	1	2	0.0243	tblot1	Mm29182	GO:0009775	GO:0006098

Tot Down 24h CC

Best GOs (Max. 50)

GO:0044446

GO:0044422

GO:0007017

GO:0000241

GO:003340

GO:0006096

GO:0044961

GO:0042410

GO:0006096

GO:0044961

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