

Table 2

Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway enrichment for the differentially expressed proteins from A β PP/PS1 transgenic mice control (Tg-ctrl) compared with wild type mice (WT-ctrl) using KOBAS. The pathways are arranged according to the number of differentially expressed proteins in each pathway. Only the top five enriched pathways ($p < 0.05$) are listed. ↓ represents significantly downregulated ($p < 0.05$) protein. ↑ represents significantly upregulated ($p < 0.05$) protein.

Pathway	Proteins number	<i>p</i> -value	Corrected <i>p</i> -value	Accession number	Protein names	Gene names	Proteins expression
Hippocampus							
Alzheimer's disease	3	0.0073	0.2502	P12023	Amyloid beta A4 protein	APP	↑
				Q63810	Calcineurin subunit B type 1	PPP3R1	↑
				Q9D0M3	Cytochrome c1	CYC1	↓
Glutamatergic synapse	3	0.003	0.2064	Q63810	Calcineurin subunit B type 1	PPP3R1	↑
				Q99MK8	Beta-adrenergic receptor kinase 1	ADRBK1	↑
				Q61011	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-3	GNB3	↓
Oxidative phosphorylation	2	0.035	0.3776	Q9D819	Inorganic pyrophosphatase	PPA1	↓
				Q9D0M3	Cytochrome c1	CYC1	↓
Cholinergic synapse	2	0.0317	0.3776	P21278	Guanine nucleotide-binding protein subunit alpha-11	GNA11	↓
				Q61011	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-3	GNB3	↓
Serotonergic synapse	2	0.0413	0.3776	P12023	Amyloid beta A4 protein	APP	↑
				Q61011	Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-3	GNB3	↓
Medial prefrontal cortex							
Metabolic pathways	11	0.0284	0.2045	P56382	ATP synthase subunit epsilon	ATP5E	↑
				P12787	Cytochrome c oxidase subunit 5A	COX5A	↑
				P48758	Carbonyl reductase [NADPH] 1	CBR1	↓
				Q922Q4	Pyrroline-5-carboxylate reductase 2	PYCR2	↓
				Q99LB2	Dehydrogenase/reductase SDR family member 4	DHRS4	↓
				Q91VR2	ATP synthase subunit gamma	ATP5C1	↓
				O70250	Phosphoglycerate mutase 2	PGAM2	↓

				Q91XF0	Pyridoxine-5-phosphate oxidase	PNPO	↓
				Q80XN0	D-beta-hydroxybutyrate dehydrogenase	BDH1	↓
				Q99LS3	Phosphoserine phosphatase	PSPH	↓
				Q9DCC4	Pyrroline-5-carboxylate reductase 3	PYCRL	↓
Parkinson's disease	5	0.0005	0.0164	Q8CGK7	Guanine nucleotide-binding protein G(olf) subunit alpha	GNAL	↑
				P56382	ATP synthase subunit epsilon	ATP5E	↑
				P12787	Cytochrome c oxidase subunit 5A	COX5A	↑
				Q60930	Voltage-dependent anion-selective channel protein 2	VDAC2	↓
				Q91VR2	ATP synthase subunit gamma	ATP5C1	↓
Ribosome	5	0.0007	0.0164	Q9D1P0	39S ribosomal protein L13	MRPL13	↑
				P62908	40S ribosomal protein S3	RPS3	↓
				P62754	40S ribosomal protein S6	RPS6	↓
				P12970	60S ribosomal protein L7a	RPL7A	↓
				P84099	60S ribosomal protein L19	RPL19	↓
Alzheimer's disease	4	0.009	0.1298	P56382	ATP synthase subunit epsilon	ATP5E	↑
				P12787	Cytochrome c oxidase subunit 5A	COX5A	↑
				Q91VR2	ATP synthase subunit gamma	ATP5C1	↓
				P49615	Cyclin-dependent-like kinase 5	CDK5	↓
Biosynthesis of amino acids	4	0.0005	0.0164	O70250	Phosphoglycerate mutase 2	PGAM2	↓
				Q922Q4	Pyrroline-5-carboxylate reductase 2	PYCR2	↓
				Q99LS3	Phosphoserine phosphatase	PSPH	↓
				Q9DCC4	Pyrroline-5-carboxylate reductase 3	PYCRL	↓
Striatum							
Metabolic pathways	5	0.0004	0.0067	P12787	Cytochrome c oxidase subunit 5A	Cox5a	↑
				P99028	Cytochrome b-c1 complex subunit 6	Uqcrh	↑
				Q91XF0	Pyridoxine-5-phosphate oxidase	Pnpo	↑
				P10518	Delta-aminolevulinic acid dehydratase	Alad	↑
				Q9D020	Cytosolic 5-nucleotidase 3A	Nt5c3a	↓

Alzheimer's disease	2	0.0044	0.0122	P12787	Cytochrome c oxidase subunit 5A	Cox5a	↑
				P99028	Cytochrome b-c1 complex subunit 6	Uqcrh	↑
Oxidative phosphorylation	2	0.0025	0.0121	P12787	Cytochrome c oxidase subunit 5A	Cox5a	↑
				P99028	Cytochrome b-c1 complex subunit 6	Uqcrh	↑
Parkinson's disease	2	0.0028	0.0121	P12787	Cytochrome c oxidase subunit 5A	Cox5a	↑
				P99028	Cytochrome b-c1 complex subunit 6	Uqcrh	↑
Huntington's disease	2	0.005	0.0122	P12787	Cytochrome c oxidase subunit 5A	Cox5a	↑
				P99028	Cytochrome b-c1 complex subunit 6	Uqcrh	↑