

GeDiPNet Cluster 395 -- Enriched Pathways

Pathway enrichment: KEGG + Reactome, upper-tail hypergeometric test, Benjamini-Hochberg FDR-corrected. Fold enrichment = (overlap / cluster gene count) / (pathway gene count / universe size). Top 15 pathways per cluster by q-value. See scripts/build_cluster_enrichment.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-07 03:30:09. · Rows: 15 · Generated: 2026-10-07 04:04:17

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Parkinson disease	KEGG	4	SNCA, PRKN, SLC18A2, PSMD3	268	19	9.43	7.214e-4	1.061e-2
Hh mutants that don't undergo autocatalytic processing are degraded by ERAD	Reactome	2	SHH, PSMD3	56	19	22.58	3.470e-3	3.412e-2
Hedgehog ligand biogenesis	Reactome	2	SHH, PSMD3	60	19	21.07	3.974e-3	3.763e-2
Inhibition of nitric oxide production	Reactome	1	NOS2	3	19	210.70	4.739e-3	4.229e-2
Nitric oxide stimulates guanylate cyclase	Reactome	1	NOS2	3	19	210.70	4.739e-3	4.229e-2
Mitochondrial transcription initiation	Reactome	1	TFAM	3	19	210.70	4.739e-3	4.229e-2
Pathways of neurodegeneration - multiple diseases	KEGG	4	SNCA, NOS2, PRKN, PSMD3	480	19	5.27	6.053e-3	4.964e-2
HHAT G278V abrogates palmitoylation of Hh-Np	Reactome	1	SHH	4	19	158.03	6.314e-3	5.105e-2
Neurotransmitter clearance	Reactome	1	BCHE	4	19	158.03	6.314e-3	5.105e-2
ABC-family proteins mediated transport	Reactome	2	ABCB1, PSMD3	81	19	15.61	7.132e-3	5.537e-2
Synthesis of 5-eicosatetraenoic acids	Reactome	1	PON1	6	19	105.35	9.457e-3	6.631e-2
Release of Hh-Np from the secreting cell	Reactome	1	SHH	7	19	90.30	1.102e-2	7.274e-2
Ligand-receptor interactions	Reactome	1	SHH	7	19	90.30	1.102e-2	7.274e-2
Antigen processing: Ubiquitination & Proteasome degradation	Reactome	3	PRKN, FBXO7, PSMD3	309	19	6.14	1.204e-2	7.651e-2
Amyloid fiber formation	Reactome	2	SNCA, PRKN	109	19	11.60	1.262e-2	7.860e-2