

GeDiPNet Cluster 258 -- 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: 2026-10-08 03:30:07. · Rows: 15 · Generated: 2026-10-07 22:51:22

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Retrograde endocannabinoid signaling	KEGG	5	PTGS2, GRIA1, PRKCA, GABRA4, GABRB1	149	53	7.60	4.883e-4	7.989e-3
Nicotine addiction	KEGG	3	GRIA1, GABRA4, GABRB1	41	53	16.58	7.684e-4	1.137e-2
Serotonergic synapse	KEGG	4	PLA2G4A, PTGS2, PRKCA, GABRB1	115	53	7.88	1.628e-3	2.009e-2
GABA receptor activation	Reactome	2	GABRA4, GABRB1	16	53	28.33	2.204e-3	2.504e-2
Syndecan interactions	Reactome	2	TGFB1, PRKCA	16	53	28.33	2.204e-3	2.504e-2
VEGF signaling pathway	KEGG	3	PLA2G4A, PTGS2, PRKCA	60	53	11.33	2.325e-3	2.605e-2
Long-term depression	KEGG	3	PLA2G4A, GRIA1, PRKCA	60	53	11.33	2.325e-3	2.605e-2
Trafficking of GluR2-containing AMPA receptors	Reactome	2	GRIA1, PRKCA	17	53	26.66	2.491e-3	2.744e-2
Fc epsilon RI signaling pathway	KEGG	3	PLA2G4A, LAT, PRKCA	69	53	9.85	3.462e-3	3.454e-2
Biosynthesis of EPA-derived SPMs	Reactome	1	PTGS2	1	53	226.60	4.413e-3	4.094e-2
Biosynthesis of DPAn-3 SPMs	Reactome	1	PTGS2	1	53	226.60	4.413e-3	4.094e-2
Leishmaniasis	KEGG	3	NOS2, PTGS2, TGFB1	78	53	8.72	4.889e-3	4.389e-2
Efferocytosis	KEGG	4	PTGS2, TGFB1, CALR, STAB2	157	53	5.77	5.006e-3	4.449e-2
GABAergic synapse	KEGG	3	PRKCA, GABRA4, GABRB1	89	53	7.64	7.055e-3	5.613e-2
Morphine addiction	KEGG	3	PRKCA, GABRA4, GABRB1	91	53	7.47	7.500e-3	5.820e-2