

GeDiPNet Cluster 454 -- 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: 2026-10-20 03:30:09. · Rows: 15 · Generated: 2026-10-20 00:03:19

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	39	10.33	1.126e-4	2.088e-3
Nicotine addiction	KEGG	3	GRIA1, GABRA4, GABRB1	41	39	22.53	3.099e-4	4.619e-3
Serotonergic synapse	KEGG	4	PLA2G4A, PTGS2, PRKCA, GABRB1	115	39	10.71	5.067e-4	6.738e-3
VEGF signaling pathway	KEGG	3	PLA2G4A, PTGS2, PRKCA	60	39	15.40	9.533e-4	1.093e-2
Long-term depression	KEGG	3	PLA2G4A, GRIA1, PRKCA	60	39	15.40	9.533e-4	1.093e-2
GABA receptor activation	Reactome	2	GABRA4, GABRB1	16	39	38.49	1.198e-3	1.300e-2
Syndecan interactions	Reactome	2	TGFB1, PRKCA	16	39	38.49	1.198e-3	1.300e-2
Trafficking of GluR2-containing AMPA receptors	Reactome	2	GRIA1, PRKCA	17	39	36.23	1.355e-3	1.425e-2
Pathways in cancer	KEGG	7	NOS2, PTGS2, TGFB1, PDGFRB, PRKCA, TCF7L2, PTCH1	533	39	4.04	1.454e-3	1.505e-2
Efferocytosis	KEGG	4	PTGS2, TGFB1, CALR, STAB2	157	39	7.85	1.619e-3	1.631e-2
Leishmaniasis	KEGG	3	NOS2, PTGS2, TGFB1	78	39	11.84	2.036e-3	1.927e-2
GABAergic synapse	KEGG	3	PRKCA, GABRA4, GABRB1	89	39	10.38	2.965e-3	2.528e-2
Morphine addiction	KEGG	3	PRKCA, GABRA4, GABRB1	91	39	10.15	3.157e-3	2.643e-2
Biosynthesis of EPA-derived SPMs	Reactome	1	PTGS2	1	39	307.95	3.247e-3	2.695e-2
Biosynthesis of DPA _n -3 SPMs	Reactome	1	PTGS2	1	39	307.95	3.247e-3	2.695e-2