

GeDiPNet Cluster 131 -- 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 23:58:45

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Voltage gated Potassium channels	Reactome	2	KCND3, KCNH2	43	15	37.24	1.276e-3	1.674e-2
Opioid Signalling	Reactome	1	PDYN	3	15	266.89	3.743e-3	3.650e-2
CREB3 factors activate genes	Reactome	1	CREBRF	5	15	160.13	6.230e-3	5.168e-2
NOSTRIN mediated eNOS trafficking	Reactome	1	CAV1	5	15	160.13	6.230e-3	5.168e-2
Biosynthesis of maresin-like SPMs	Reactome	1	CYP3A4	6	15	133.44	7.472e-3	5.806e-2
Phase 1 - inactivation of fast Na+ channels	Reactome	1	KCND3	7	15	114.38	8.712e-3	6.435e-2
Phase 3 - rapid repolarisation	Reactome	1	KCNH2	8	15	100.08	9.951e-3	6.966e-2
Spinocerebellar ataxia	KEGG	2	KCND3, PDYN	144	15	11.12	1.353e-2	8.407e-2
FOXO-mediated transcription of cell cycle genes	Reactome	1	CAV1	11	15	72.79	1.366e-2	8.453e-2
Physiological factors	Reactome	1	NPPA	12	15	66.72	1.489e-2	8.912e-2
Phagosome	KEGG	2	MRC2, CTSS	155	15	10.33	1.556e-2	9.184e-2
eNOS activation	Reactome	1	CAV1	13	15	61.59	1.612e-2	9.396e-2
Trafficking and processing of endosomal TLR	Reactome	1	CTSS	13	15	61.59	1.612e-2	9.396e-2
YAP1- and WWTR1 (TAZ)-stimulated gene expression	Reactome	1	NPPA	14	15	57.19	1.735e-2	9.779e-2
Tuberculosis	KEGG	2	MRC2, CTSS	181	15	8.85	2.085e-2	1.085e-1