

GeDiPNet Cluster 442 -- 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 00:02:55

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Vitamin E	Reactome	1	TTPA	1	10	1201.00	8.326e-4	9.853e-3
Defective DHDDS causes retinitis pigmentosa 59	Reactome	1	NUS1	2	10	600.50	1.665e-3	1.665e-2
Response to elevated platelet cytosolic Ca2+	Reactome	1	PRKCG	3	10	400.33	2.496e-3	2.231e-2
Telomere C-strand (Lagging Strand) Synthesis	Reactome	1	PCNA	5	10	240.20	4.157e-3	3.210e-2
Arachidonate production from DAG	Reactome	1	ABHD12	5	10	240.20	4.157e-3	3.210e-2
Disinhibition of SNARE formation	Reactome	1	PRKCG	5	10	240.20	4.157e-3	3.210e-2
Synthesis of Dolichyl-phosphate	Reactome	1	NUS1	6	10	200.17	4.986e-3	3.635e-2
Calmodulin induced events	Reactome	1	PRKCG	7	10	171.57	5.815e-3	4.033e-2
Phase 1 - inactivation of fast Na+ channels	Reactome	1	KCND3	7	10	171.57	5.815e-3	4.033e-2
Spinocerebellar ataxia	KEGG	2	KCND3, PRKCG	144	10	16.68	6.032e-3	4.120e-2
Processive synthesis on the C-strand of the telomere	Reactome	1	PCNA	8	10	150.13	6.644e-3	4.390e-2
Hepatitis B	KEGG	2	PCNA, PRKCG	163	10	14.74	7.670e-3	4.816e-2
Processive synthesis on the lagging strand	Reactome	1	PCNA	10	10	120.10	8.298e-3	5.062e-2
Removal of the Flap Intermediate from the C-strand	Reactome	1	PCNA	11	10	109.18	9.125e-3	5.370e-2
Mismatch repair (MMR) directed by MSH2:MSH6 (MutSalpha)	Reactome	1	PCNA	14	10	85.79	1.160e-2	6.220e-2