

GeDiPNet Cluster 313 -- 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 13:51:46

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Synthesis of Prostaglandins (PG) and Thromboxanes (TX)	Reactome	2	PTGES, PTGS2	12	33	60.66	4.750e-4	7.659e-3
Scavenging of heme from plasma	Reactome	2	APOL1, HBB	13	33	55.99	5.604e-4	8.695e-3
RHO GTPases activate PAKs	Reactome	2	FLNA, MYH9	23	33	31.65	1.787e-3	2.103e-2
Biosynthesis of EPA-derived SPMs	Reactome	1	PTGS2	1	33	363.94	2.748e-3	2.889e-2
Biosynthesis of DPAn-3 SPMs	Reactome	1	PTGS2	1	33	363.94	2.748e-3	2.889e-2
African trypanosomiasis	KEGG	2	APOL1, HBB	37	33	19.67	4.592e-3	4.139e-2
Biosynthesis of electrophilic i%-3 PUFA oxo-derivatives	Reactome	1	PTGS2	2	33	181.97	5.488e-3	4.649e-2
Reversal of alkylation damage by DNA dioxygenases	Reactome	1	FTO	2	33	181.97	5.488e-3	4.649e-2
TCF7L2 mutants don't bind CTBP	Reactome	1	TCF7L2	3	33	121.31	8.221e-3	6.073e-2
Biosynthesis of DHA-derived SPMs	Reactome	1	PTGS2	3	33	121.31	8.221e-3	6.073e-2
Abacavir transmembrane transport	Reactome	1	SLC22A2	3	33	121.31	8.221e-3	6.073e-2
Cushing syndrome	KEGG	3	AGT, SCARB1, TCF7L2	155	33	7.04	8.663e-3	6.297e-2
Ovarian steroidogenesis	KEGG	2	PTGS2, SCARB1	52	33	14.00	8.910e-3	6.406e-2
Neurotransmitter clearance	Reactome	1	SLC22A2	4	33	90.98	1.095e-2	7.246e-2
Arachidonic acid metabolism	KEGG	2	PTGES, PTGS2	63	33	11.55	1.288e-2	7.942e-2