

GeDiPNet Cluster 566 -- 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: 8 · Generated: 2026-10-20 00:03:01

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
The canonical retinoid cycle in rods (twilight vision)	Reactome	2	ABCA4, CYP4V2	20	3	400.33	7.896e-6	2.399e-4
Retinoid cycle disease events	Reactome	1	ABCA4	13	3	307.95	3.244e-3	2.694e-2
Intrinsic Pathway of Fibrin Clot Formation	Reactome	1	KLKB1	23	3	174.06	5.735e-3	4.000e-2
Endogenous sterols	Reactome	1	CYP4V2	25	3	160.13	6.232e-3	4.212e-2
Activation of Matrix Metalloproteinases	Reactome	1	KLKB1	33	3	121.31	8.221e-3	5.037e-2
ABC transporters	KEGG	1	ABCA4	45	3	88.96	1.120e-2	6.095e-2
ABC-family proteins mediated transport	Reactome	1	ABCA4	81	3	49.42	2.010e-2	8.587e-2
Complement and coagulation cascades	KEGG	1	KLKB1	88	3	45.49	2.182e-2	9.013e-2