

GeDiPNet Cluster 156 -- 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: 2026-10-08 01:37:42

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	4	ABCA4, RHO, RPE65, MYO7A	20	23	104.43	4.852e-8	3.465e-6
Melanin biosynthesis	Reactome	2	OCA2, TYR	5	23	208.87	3.496e-5	9.638e-4
Phototransduction	KEGG	2	RHO, GUCY2D	29	23	36.01	1.380e-3	1.776e-2
Inactivation, recovery and regulation of the phototransduction cascade	Reactome	2	RHO, GUCY2D	33	23	31.65	1.787e-3	2.146e-2
Regulation of commissural axon pathfinding by SLIT and ROBO	Reactome	1	ROBO1	3	23	174.06	5.735e-3	4.898e-2
ATF6 (ATF6-alpha) activates chaperones	Reactome	1	ATF6	4	23	130.54	7.639e-3	5.898e-2
Role of ABL in ROBO-SLIT signaling	Reactome	1	ROBO1	4	23	130.54	7.639e-3	5.898e-2
SLIT2:ROBO1 increases RHOA activity	Reactome	1	ROBO1	4	23	130.54	7.639e-3	5.898e-2
Aryl hydrocarbon receptor signalling	Reactome	1	AHR	7	23	74.60	1.333e-2	8.341e-2
Synthesis, secretion, and inactivation of Glucose-dependent Insulinotropic Polypeptide (GIP)	Reactome	1	PAX6	7	23	74.60	1.333e-2	8.341e-2
Regulation of expression of SLITs and ROBOs	Reactome	1	ROBO1	8	23	65.27	1.522e-2	9.042e-2
Activation of the phototransduction cascade	Reactome	1	RHO	9	23	58.02	1.711e-2	9.715e-2
ATF6 (ATF6-alpha) activates chaperone genes	Reactome	1	ATF6	9	23	58.02	1.711e-2	9.715e-2
Opsins	Reactome	1	RHO	10	23	52.22	1.899e-2	1.030e-1
Purine ribonucleoside monophosphate biosynthesis	Reactome	1	ATIC	12	23	43.51	2.275e-2	1.139e-1