

GeDiPNet Cluster 400 -- 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 12:22:26

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Melanin biosynthesis	Reactome	2	OCA2, TYR	5	10	480.40	6.232e-6	2.256e-4
The canonical retinoid cycle in rods (twilight vision)	Reactome	2	RPE65, MYO7A	20	10	120.10	1.176e-4	2.554e-3
Regulation of commissural axon pathfinding by SLIT and ROBO	Reactome	1	ROBO1	3	10	400.33	2.496e-3	2.686e-2
ATF6 (ATF6-alpha) activates chaperones	Reactome	1	ATF6	4	10	300.25	3.327e-3	3.313e-2
Role of ABL in ROBO-SLIT signaling	Reactome	1	ROBO1	4	10	300.25	3.327e-3	3.313e-2
SLIT2:ROBO1 increases RHOA activity	Reactome	1	ROBO1	4	10	300.25	3.327e-3	3.313e-2
Aryl hydrocarbon receptor signalling	Reactome	1	AHR	7	10	171.57	5.815e-3	4.841e-2
Synthesis, secretion, and inactivation of Glucose-dependent Insulinotropic Polypeptide (GIP)	Reactome	1	PAX6	7	10	171.57	5.815e-3	4.841e-2
Regulation of expression of SLITs and ROBOs	Reactome	1	ROBO1	8	10	150.13	6.644e-3	5.278e-2
ATF6 (ATF6-alpha) activates chaperone genes	Reactome	1	ATF6	9	10	133.44	7.471e-3	5.688e-2
Signaling by ROBO receptors	Reactome	1	ROBO1	12	10	100.08	9.951e-3	6.820e-2
Synthesis, secretion, and inactivation of Glucagon-like Peptide-1 (GLP-1)	Reactome	1	PAX6	14	10	85.79	1.160e-2	7.504e-2
Phase I - Functionalization of compounds	Reactome	1	AHR	21	10	57.19	1.735e-2	9.505e-2
Xenobiotics	Reactome	1	AHR	24	10	50.04	1.981e-2	1.022e-1
Endogenous sterols	Reactome	1	AHR	25	10	48.04	2.063e-2	1.046e-1