

GeDiPNet Cluster 93 -- 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: 2026-10-09 03:30:08. · Rows: 15 · Generated: 2026-10-09 00:09:04

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Melanin biosynthesis	Reactome	5	OCA2, TYR, TYRP1, SLC45A2, DCT	5	44	272.95	5.220e-13	1.087e-10
Melanogenesis	KEGG	5	TYR, MC1R, TYRP1, DCT, MITF	101	44	13.51	3.188e-5	8.579e-4
Tyrosine metabolism	KEGG	3	TYR, TYRP1, DCT	36	44	22.75	3.011e-4	5.275e-3
Sodium/Calcium exchangers	Reactome	2	SLC24A5, SLC24A4	13	44	41.99	9.973e-4	1.340e-2
GABA receptor activation	Reactome	2	GABRB3, GABRG3	16	44	34.12	1.524e-3	1.858e-2
The canonical retinoid cycle in rods (twilight vision)	Reactome	2	MYO7A, RPE65	20	44	27.30	2.390e-3	2.597e-2
Defective SLC24A4 causes hypomineralized amelogenesis imperfecta (AI)	Reactome	1	SLC24A4	1	44	272.95	3.664e-3	3.528e-2
Defective SLC24A5 causes oculocutaneous albinism 6 (OCA6)	Reactome	1	SLC24A5	1	44	272.95	3.664e-3	3.528e-2
Loss of MECP2 binding ability to 5hmC-DNA	Reactome	1	MECP2	1	44	272.95	3.664e-3	3.528e-2
Defective SLC12A1 causes Bartter syndrome 1 (BS1)	Reactome	1	SLC12A1	1	44	272.95	3.664e-3	3.528e-2
Morphine addiction	KEGG	3	GABRB3, GABRG3, PDE3A	91	44	9.00	4.453e-3	4.056e-2
Nicotine addiction	KEGG	2	GABRB3, GABRG3	41	44	13.31	9.825e-3	6.858e-2
Loss of MECP2 binding ability to 5mC-DNA	Reactome	1	MECP2	3	44	90.98	1.095e-2	7.340e-2
Regulation of commissural axon pathfinding by SLIT and ROBO	Reactome	1	ROBO1	3	44	90.98	1.095e-2	7.340e-2
ATF6 (ATF6-alpha) activates chaperones	Reactome	1	ATF6	4	44	68.24	1.458e-2	8.703e-2