

GeDiPNet Cluster 302 -- 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 10:37:46

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	30	400.33	6.850e-14	1.810e-11
Melanogenesis	KEGG	5	TYR, MC1R, TYRP1, DCT, MITF	101	30	19.82	4.591e-6	1.775e-4
Tyrosine metabolism	KEGG	3	TYR, TYRP1, DCT	36	30	33.36	9.499e-5	2.154e-3
Sodium/Calcium exchangers	Reactome	2	SLC24A5, SLC24A4	13	30	61.59	4.625e-4	7.502e-3
Defective SLC24A4 causes hypomineralized amelogenesis imperfecta (AI)	Reactome	1	SLC24A4	1	30	400.33	2.498e-3	2.686e-2
Defective SLC24A5 causes oculocutaneous albinism 6 (OCA6)	Reactome	1	SLC24A5	1	30	400.33	2.498e-3	2.686e-2
Defective SLC12A1 causes Bartter syndrome 1 (BS1)	Reactome	1	SLC12A1	1	30	400.33	2.498e-3	2.686e-2
Neurophilin interactions with VEGF and VEGFR	Reactome	1	KDR	4	30	100.08	9.956e-3	6.820e-2
Signaling by membrane-tethered fusions of PDGFRA or PDGFRB	Reactome	1	KDR	5	30	80.07	1.243e-2	7.776e-2
Cation-coupled Chloride cotransporters	Reactome	1	SLC12A1	7	30	57.19	1.736e-2	9.505e-2
VEGF binds to VEGFR leading to receptor dimerization	Reactome	1	KDR	8	30	50.04	1.982e-2	1.022e-1
Activation of the phototransduction cascade	Reactome	1	PDE6B	9	30	44.48	2.227e-2	1.093e-1
Interleukin-4 and Interleukin-13 signaling	Reactome	2	IRF4, NDN	108	30	7.41	2.959e-2	1.279e-1
VEGFR2 mediated cell proliferation	Reactome	1	KDR	14	30	28.60	3.443e-2	1.393e-1
Purine metabolism	KEGG	2	PDE3A, PDE6B	128	30	6.26	4.037e-2	1.526e-1