

GeDiPNet Cluster 242 -- 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 18:40:35

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
EGR2 and SOX10-mediated initiation of Schwann cell myelination	Reactome	4	EGR2, MPZ, PMP22, PRX	20	10	240.20	1.167e-9	1.225e-7
RUNX1 regulates transcription of genes involved in BCR signaling	Reactome	1	ELF2	6	10	200.17	4.986e-3	4.437e-2
Cell adhesion molecules	KEGG	2	MPZ, CNTNAP1	160	10	15.01	7.399e-3	5.789e-2
Beta-oxidation of pristanoyl-CoA	Reactome	1	AMACR	9	10	133.44	7.471e-3	5.806e-2
Activation of the phototransduction cascade	Reactome	1	RHO	9	10	133.44	7.471e-3	5.806e-2
Opsins	Reactome	1	RHO	10	10	120.10	8.298e-3	6.227e-2
Polymerase switching	Reactome	1	RFC1	14	10	85.79	1.160e-2	7.656e-2
Synthesis of bile acids and bile salts via 24-hydroxycholesterol	Reactome	1	AMACR	14	10	85.79	1.160e-2	7.656e-2
Translesion synthesis by REV1	Reactome	1	RFC1	16	10	75.06	1.325e-2	8.310e-2
Primary bile acid biosynthesis	KEGG	1	AMACR	17	10	70.65	1.407e-2	8.603e-2
Translesion synthesis by POLK	Reactome	1	RFC1	17	10	70.65	1.407e-2	8.603e-2
Translesion synthesis by POLI	Reactome	1	RFC1	17	10	70.65	1.407e-2	8.603e-2
Polymerase switching on the C-strand of the telomere	Reactome	1	RFC1	17	10	70.65	1.407e-2	8.603e-2
Translesion Synthesis by POLH	Reactome	1	RFC1	19	10	63.21	1.571e-2	9.243e-2
The canonical retinoid cycle in rods (twilight vision)	Reactome	1	RHO	20	10	60.05	1.653e-2	9.503e-2