

GeDiPNet Cluster 572 -- 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: 2026-10-20 03:30:09. · Rows: 15 · Generated: 2026-10-19 23:22:14

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
POU5F1 (OCT4), SOX2, NANOG repress genes related to differentiation	Reactome	1	SOX2	3	10	400.33	2.496e-3	2.231e-2
Disinhibition of SNARE formation	Reactome	1	STXBP3	5	10	240.20	4.157e-3	3.210e-2
Netrin-1 signaling	Reactome	1	NTN1	8	10	150.13	6.644e-3	4.390e-2
DCC mediated attractive signaling	Reactome	1	NTN1	11	10	109.18	9.125e-3	5.370e-2
Axon guidance	KEGG	2	NTN1, PLXNB2	183	10	13.13	9.588e-3	5.548e-2
POU5F1 (OCT4), SOX2, NANOG activate genes related to proliferation	Reactome	1	SOX2	13	10	92.38	1.078e-2	5.962e-2
Polymerase switching	Reactome	1	RFC4	14	10	85.79	1.160e-2	6.220e-2
Translesion synthesis by REV1	Reactome	1	RFC4	16	10	75.06	1.325e-2	6.742e-2
Translesion synthesis by POLK	Reactome	1	RFC4	17	10	70.65	1.407e-2	6.986e-2
Translesion synthesis by POLI	Reactome	1	RFC4	17	10	70.65	1.407e-2	6.986e-2
Polymerase switching on the C-strand of the telomere	Reactome	1	RFC4	17	10	70.65	1.407e-2	6.986e-2
Transcriptional regulation of pluripotent stem cells	Reactome	1	SOX2	17	10	70.65	1.407e-2	6.986e-2
Microtubule-dependent trafficking of connexons from Golgi to the plasma membrane	Reactome	1	TUBB4B	18	10	66.72	1.489e-2	7.218e-2
Cilium Assembly	Reactome	1	TUBB4B	19	10	63.21	1.571e-2	7.460e-2
Translesion Synthesis by POLH	Reactome	1	RFC4	19	10	63.21	1.571e-2	7.460e-2