

GeDiPNet Cluster 25 -- 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 17:45:31

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Hedgehog signaling pathway	KEGG	5	GLI2, PTCH2, CDON, PTCH1, SUFU	56	43	24.94	1.545e-6	7.084e-5
Pathways in cancer	KEGG	11	EDN1, GNAI3, PLCB4, FZD5, LAMB1, GLI2, MITF, PTCH2, RARB, PTCH1, SUFU	533	43	5.76	1.872e-6	8.315e-5
Basal cell carcinoma	KEGG	5	FZD5, GLI2, PTCH2, PTCH1, SUFU	63	43	22.17	2.790e-6	1.169e-4
Melanogenesis	KEGG	5	EDN1, GNAI3, PLCB4, FZD5, MITF	101	43	13.83	2.844e-5	7.973e-4
Gastric acid secretion	KEGG	4	GNAI3, PLCB4, ACTB, ACTG1	76	43	14.70	1.516e-4	3.137e-3
Hippo signaling pathway	KEGG	5	FZD5, ACTB, ACTG1, GLI2, YAP1	157	43	8.89	2.309e-4	4.381e-3
Ligand-receptor interactions	Reactome	2	CDON, PTCH1	7	43	79.80	2.600e-4	4.794e-3
Recycling pathway of L1	Reactome	3	DPYSL2, ACTB, ACTG1	40	43	20.95	3.851e-4	6.521e-3
Formation of annular gap junctions	Reactome	2	ACTB, ACTG1	11	43	50.78	6.747e-4	1.006e-2
Cell-extracellular matrix interactions	Reactome	2	ACTB, ACTG1	12	43	46.55	8.078e-4	1.159e-2
Gap junction degradation	Reactome	2	ACTB, ACTG1	12	43	46.55	8.078e-4	1.159e-2
PLC beta mediated events	Reactome	2	GNAI3, PLCB4	12	43	46.55	8.078e-4	1.159e-2
Interaction between L1 and Ankyrins	Reactome	2	ACTB, ACTG1	13	43	42.97	9.526e-4	1.308e-2
Hedgehog 'off' state	Reactome	3	GLI2, PTCH1, SUFU	56	43	14.96	1.038e-3	1.396e-2
Platelet activation	KEGG	4	GNAI3, PLCB4, ACTB, ACTG1	126	43	8.87	1.039e-3	1.396e-2