

GeDiPNet Cluster 200 -- Enriched GO Terms (Biological Process)

GO term enrichment: Biological Process terms (gene2go, human/tax_id=9606 only), upper-tail hypergeometric test, fold enrichment = (overlap / cluster gene count) / (term gene count / universe size), Benjamini-Hochberg FDR-corrected. Top 15 terms per cluster by q-value. See scripts/build_cluster_go_enrichment.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-08 03:23:04. · Rows: 15 · Generated: 2026-10-08 09:56:08

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
cell fate determination	GO:0001709	3	PAX6, PTCH2, PTCH1	18	9	346.06	6.281e-8	8.215e-6
negative regulation of smoothened signaling pathway	GO:0045879	3	PTCH2, PTCH1, SUFU	35	9	177.97	5.017e-7	4.749e-5
epidermal cell fate specification	GO:0009957	2	PTCH2, PTCH1	5	9	830.53	2.060e-6	1.499e-4
positive regulation of epidermal cell differentiation	GO:0045606	2	PTCH2, PTCH1	8	9	519.08	5.765e-6	3.425e-4
adherens junction organization	GO:0034332	2	SPECC1L, CDH11	34	9	122.14	1.148e-4	3.419e-3
dorsal/ventral pattern formation	GO:0009953	2	PAX6, PTCH1	47	9	88.35	2.204e-4	5.506e-3
eye development	GO:0001654	2	PAX6, SALL2	49	9	84.75	2.397e-4	5.840e-3
skin development	GO:0043588	2	PTCH2, SUFU	55	9	75.50	3.022e-4	6.904e-3
negative regulation of epithelial cell proliferation	GO:0050680	2	PAX6, PTCH1	62	9	66.98	3.841e-4	8.167e-3
response to mechanical stimulus	GO:0009612	2	PIEZO2, PTCH1	67	9	61.98	4.486e-4	9.080e-3
pancreatic A cell development	GO:0003322	1	PAX6	1	9	2076.33	4.816e-4	9.502e-3
forebrain-midbrain boundary formation	GO:0021905	1	PAX6	1	9	2076.33	4.816e-4	9.502e-3
positive regulation of cellular response to drug	GO:2001040	1	SUFU	1	9	2076.33	4.816e-4	9.502e-3
neural crest cell delamination	GO:0036032	1	SPECC1L	1	9	2076.33	4.816e-4	9.502e-3
negative regulation of osteoblast differentiation	GO:0045668	2	PTCH1, SUFU	71	9	58.49	5.036e-4	9.804e-3