

GeDiPNet Cluster 90 -- 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: 2026-10-07 03:23:06. · Rows: 15 · Generated: 2026-10-07 16:26:34

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
branching involved in salivary gland morphogenesis	GO:0060445	3	FGFR2, FGF8, FGFR1	12	53	88.15	4.655e-6	2.836e-4
fibroblast growth factor receptor signaling pathway involved in orbitofrontal cortex development	GO:0035607	2	FGFR2, FGFR1	2	53	352.58	7.893e-6	4.329e-4
lipid droplet organization	GO:0034389	3	RAB18, RAB3GAP1, TBC1D20	18	53	58.76	1.706e-5	7.925e-4
orbitofrontal cortex development	GO:0021769	2	FGFR2, FGFR1	3	53	235.06	2.363e-5	1.019e-3
ventricular zone neuroblast division	GO:0021847	2	FGFR2, FGFR1	3	53	235.06	2.363e-5	1.019e-3
establishment of protein localization to endoplasmic reticulum membrane	GO:0097051	2	RAB3GAP1, RAB3GAP2	3	53	235.06	2.363e-5	1.019e-3
positive regulation of endoplasmic reticulum tubular network organization	GO:1903373	2	RAB3GAP1, RAB3GAP2	3	53	235.06	2.363e-5	1.019e-3
fibroblast growth factor receptor signaling pathway	GO:0008543	4	FGFR2, FGF8, FGFR1, KLB	60	53	23.51	2.500e-5	1.062e-3
pharyngeal system development	GO:0060037	3	FGF8, PTCH1, FOXI3	21	53	50.37	2.763e-5	1.148e-3
motor neuron axon guidance	GO:0008045	3	FGF8, SEMA3A, CHN1	24	53	44.07	4.180e-5	1.575e-3
positive regulation of phospholipase activity	GO:0010518	2	FGFR2, FGFR1	4	53	176.29	4.718e-5	1.720e-3
positive regulation of protein lipidation	GO:1903061	2	RAB3GAP1, RAB3GAP2	4	53	176.29	4.718e-5	1.720e-3
positive regulation of mesenchymal cell proliferation	GO:0002053	3	FGFR2, ARHGAP5, FGFR1	26	53	40.68	5.348e-5	1.892e-3
camera-type eye development	GO:0043010	4	RAB3GAP1, TBC1D20, WT1, ARHGAP35	74	53	19.06	5.728e-5	1.990e-3
cell fate commitment	GO:0045165	4	FGFR2, FGF8, GAS1, KDM6B	75	53	18.80	6.038e-5	2.065e-3