

GeDiPNet Cluster 50 -- 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: 2026-10-07 22:43:13

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
fibroblast growth factor receptor signaling pathway involved in orbitofrontal cortex development	GO:0035607	2	FGFR2, FGFR1	2	45	415.27	5.670e-6	3.382e-4
orbitofrontal cortex development	GO:0021769	2	FGFR2, FGFR1	3	45	276.84	1.698e-5	8.008e-4
ventricular zone neuroblast division	GO:0021847	2	FGFR2, FGFR1	3	45	276.84	1.698e-5	8.008e-4
positive regulation of phospholipase activity	GO:0010518	2	FGFR2, FGFR1	4	45	207.63	3.392e-5	1.363e-3
bone trabecula morphogenesis	GO:0061430	2	SEMA4D, VEGFA	4	45	207.63	3.392e-5	1.363e-3
positive regulation of cold-induced thermogenesis	GO:0120162	4	ESRRG, GADD45G, PRDM16, VEGFA	102	45	16.28	1.050e-4	3.206e-3
positive regulation of axon extension involved in axon guidance	GO:0048842	2	DSCAM, VEGFA	7	45	118.65	1.182e-4	3.492e-3
lung-associated mesenchyme development	GO:0060484	2	FGFR2, FGFR1	9	45	92.28	2.020e-4	5.193e-3
vascular endothelial cell response to laminar fluid shear stress	GO:0097700	2	PRKACB, PRKACA	9	45	92.28	2.020e-4	5.193e-3
high-density lipoprotein particle assembly	GO:0034380	2	PRKACB, PRKACA	10	45	83.05	2.521e-4	6.047e-3
regulation of protein processing	GO:0070613	2	PRKACB, PRKACA	11	45	75.50	3.076e-4	6.984e-3
chordate embryonic development	GO:0043009	2	FGFR2, FGFR1	11	45	75.50	3.076e-4	6.984e-3
branching involved in salivary gland morphogenesis	GO:0060445	2	FGFR2, FGFR1	12	45	69.21	3.685e-4	7.934e-3
ossification involved in bone maturation	GO:0043931	2	ADAMTS7, SEMA4D	12	45	69.21	3.685e-4	7.934e-3
mesenchymal cell differentiation	GO:0048762	2	FGFR2, FGFR1	13	45	63.89	4.349e-4	8.872e-3