

GeDiPNet Cluster 594 -- 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: 2026-10-20 03:23:14. · Rows: 15 · Generated: 2026-10-19 23:19:00

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
prostate epithelial cord elongation	GO:0060523	2	FGFR2, SHH	3	14	889.86	1.563e-6	1.241e-4
epithelial cell proliferation involved in salivary gland morphogenesis	GO:0060664	2	FGFR2, SHH	5	14	533.91	5.205e-6	3.268e-4
mesenchymal cell proliferation involved in lung development	GO:0060916	2	FGFR2, SHH	5	14	533.91	5.205e-6	3.268e-4
branching involved in prostate gland morphogenesis	GO:0060442	2	FGFR2, SHH	6	14	444.93	7.805e-6	4.506e-4
regulation of cell differentiation	GO:0045595	3	FGFR2, PTK2, TFAP2A	54	14	74.15	8.118e-6	4.636e-4
lung lobe morphogenesis	GO:0060463	2	FGFR2, SHH	8	14	333.70	1.456e-5	7.276e-4
limb bud formation	GO:0060174	2	FGFR2, SHH	9	14	296.62	1.871e-5	8.777e-4
lung-associated mesenchyme development	GO:0060484	2	FGFR2, SHH	9	14	296.62	1.871e-5	8.777e-4
branching involved in salivary gland morphogenesis	GO:0060445	2	FGFR2, SHH	12	14	222.46	3.425e-5	1.388e-3
lung development	GO:0030324	3	FBN1, FGFR2, SHH	108	14	37.08	6.524e-5	2.250e-3
regulation of osteoblast differentiation	GO:0045667	2	FGFR2, PTK2	17	14	157.03	7.043e-5	2.381e-3
protein autophosphorylation	GO:0046777	3	FGFR2, IRAK1, PTK2	113	14	35.44	7.465e-5	2.489e-3
embryonic digestive tract morphogenesis	GO:0048557	2	FGFR2, SHH	18	14	148.31	7.920e-5	2.600e-3
lung morphogenesis	GO:0060425	2	MAP2K2, SHH	25	14	106.78	1.548e-4	4.240e-3
kidney development	GO:0001822	3	FBN1, SHH, TFAP2A	146	14	27.43	1.597e-4	4.334e-3