

GeDiPNet Cluster 557 -- 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 23:18:31

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
thyroid gland development	GO:0030878	7	NKX2-5, PAX8, THRA, TUBB1, SHH, FOXE1, NKX2-1	30	30	145.34	2.564e-14	1.643e-11
thyroid hormone generation	GO:0006590	5	DUOX2, SLC26A7, SLC5A5, TPO, FOXE1	16	30	194.66	3.240e-11	1.104e-8
iodide transport	GO:0015705	3	SLC26A4, SLC26A7, SLC5A5	8	30	233.59	2.080e-7	2.335e-5
thyroid-stimulating hormone signaling pathway	GO:0038194	2	PAX8, TSHR	2	30	622.90	2.492e-6	1.813e-4
apoptotic signaling pathway	GO:0097190	4	INHBB, SHH, TNFSF12, FASLG	84	30	29.66	9.523e-6	5.233e-4
cellular response to gonadotropin stimulus	GO:0071371	2	PAX8, SLC5A5	7	30	177.97	5.206e-5	1.903e-3
copper ion transport	GO:0006825	2	FKBP4, ATP7B	11	30	113.25	1.358e-4	3.844e-3
oxalate transport	GO:0019532	2	SLC26A4, SLC26A7	11	30	113.25	1.358e-4	3.844e-3
hormone biosynthetic process	GO:0042446	2	DUOX2, TPO	12	30	103.82	1.628e-4	4.385e-3
sulfate transmembrane transport	GO:1902358	2	SLC26A4, SLC26A7	16	30	77.86	2.948e-4	6.695e-3
prostate gland development	GO:0030850	2	FKBP4, SHH	16	30	77.86	2.948e-4	6.695e-3
epithelial tube branching involved in lung morphogenesis	GO:0060441	2	SHH, NKX2-1	20	30	62.29	4.650e-4	9.063e-3
cell-cell signaling	GO:0007267	4	TSHR, TSHB, SHH, FASLG	234	30	10.65	5.085e-4	9.605e-3
hydrogen peroxide catabolic process	GO:0042744	2	DUOX2, TPO	21	30	59.32	5.134e-4	9.672e-3
animal organ development	GO:0048513	3	SHH, FOXE1, NKX2-1	102	30	18.32	5.759e-4	1.045e-2