

GeDiPNet Cluster 274 -- 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 14:13:01

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
glucose homeostasis	GO:0042593	2	INSR, HNF1A	134	2	139.46	5.104e-5	1.829e-3
regulation of pronephros size	GO:0035565	1	HNF1A	2	2	4671.75	2.140e-4	5.282e-3
positive regulation of meiotic cell cycle	GO:0051446	1	INSR	2	2	4671.75	2.140e-4	5.282e-3
regulation of female gonad development	GO:2000194	1	INSR	2	2	4671.75	2.140e-4	5.282e-3
renal D-glucose absorption	GO:0035623	1	HNF1A	3	2	3114.50	3.211e-4	7.027e-3
positive regulation of protein-containing complex disassembly	GO:0043243	1	INSR	4	2	2335.88	4.281e-4	8.586e-3
positive regulation of developmental growth	GO:0048639	1	INSR	4	2	2335.88	4.281e-4	8.586e-3
positive regulation of respiratory burst	GO:0060267	1	INSR	7	2	1334.79	7.491e-4	1.251e-2
exocrine pancreas development	GO:0031017	1	INSR	10	2	934.35	1.070e-3	1.569e-2
dendritic spine maintenance	GO:0097062	1	INSR	11	2	849.41	1.177e-3	1.664e-2
regulation of glycogen biosynthetic process	GO:0005979	1	INSR	11	2	849.41	1.177e-3	1.664e-2
male sex determination	GO:0030238	1	INSR	12	2	778.63	1.284e-3	1.747e-2
neuron projection maintenance	GO:1990535	1	INSR	13	2	718.73	1.391e-3	1.837e-2
positive regulation of cellular component organization	GO:0051130	1	INSR	16	2	583.97	1.712e-3	2.068e-2
positive regulation of DNA-templated transcription	GO:0045893	2	INSR, HNF1A	778	2	24.02	1.731e-3	2.086e-2