

GeDiPNet Cluster 527 -- 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 03:23:13. · Rows: 15 · Generated: 2026-10-19 23:18:37

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
cellular response to glucagon stimulus	GO:0071377	2	GNAS, PRKAR1A	11	14	242.69	2.856e-5	1.203e-3
adenylate cyclase-activating adrenergic receptor signaling pathway	GO:0071880	2	GPR101, GNAS	14	14	190.68	4.719e-5	1.771e-3
cardiac muscle cell proliferation	GO:0060038	2	PRKAR1A, ARID2	28	14	95.34	1.948e-4	4.990e-3
positive regulation of receptor signaling pathway via JAK-STAT	GO:0046427	2	GH1, PRL	40	14	66.74	4.000e-4	8.181e-3
endocytosis	GO:0006897	3	TSC2, HRAS, SH3GL1	223	14	17.96	5.538e-4	1.014e-2
positive regulation of MAPK cascade	GO:0043410	3	GPR101, GH1, HRAS	224	14	17.88	5.611e-4	1.024e-2
positive regulation of lactation	GO:1903489	1	PRL	2	14	667.39	1.498e-3	1.821e-2
response to nutrient levels	GO:0031667	2	GH1, PRL	79	14	33.79	1.554e-3	1.869e-2
female pregnancy	GO:0007565	2	GNAS, PRL	80	14	33.37	1.593e-3	1.885e-2
neural tube closure	GO:0001843	2	TSC2, STIL	85	14	31.41	1.796e-3	2.015e-2
bone maturation	GO:0070977	1	GH1	3	14	444.93	2.246e-3	2.244e-2
regulation of protein localization to chromatin	GO:1905634	1	SETD2	3	14	444.93	2.246e-3	2.244e-2
positive regulation of miRNA metabolic process	GO:2000630	1	HRAS	3	14	444.93	2.246e-3	2.244e-2
microtubule cytoskeleton organization involved in mitosis	GO:1902850	1	SETD2	4	14	333.70	2.994e-3	2.594e-2
prolactin signaling pathway	GO:0038161	1	PRL	4	14	333.70	2.994e-3	2.594e-2