

GeDiPNet Cluster 148 -- 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: 2026-10-08 06:39:28

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
beta-catenin-TCF complex assembly	GO:1904837	1	KMT2D	1	13	1437.46	6.957e-4	1.221e-2
right ventricular compact myocardium morphogenesis	GO:0003226	1	CHD7	1	13	1437.46	6.957e-4	1.221e-2
heart morphogenesis	GO:0003007	2	CHD7, EPHB4	61	13	47.13	7.988e-4	1.336e-2
heterochromatin formation	GO:0031507	2	KMT2D, SMARCA2	70	13	41.07	1.051e-3	1.591e-2
negative regulation of protein localization to nucleolus	GO:1904750	1	POLR1A	2	13	718.73	1.391e-3	1.874e-2
regulation of growth hormone secretion	GO:0060123	1	CHD7	3	13	479.15	2.086e-3	2.373e-2
olfactory nerve development	GO:0021553	1	CHD7	3	13	479.15	2.086e-3	2.373e-2
cranial nerve development	GO:0021545	1	CHD7	4	13	359.37	2.780e-3	2.776e-2
oocyte growth	GO:0001555	1	KMT2D	4	13	359.37	2.780e-3	2.776e-2
nucleolar large rRNA transcription by RNA polymerase I	GO:0042790	1	POLR1A	4	13	359.37	2.780e-3	2.776e-2
chromatin organization	GO:0006325	3	KMT2D, CHD7, KAT6A	449	13	9.60	3.293e-3	3.043e-2
regulation of axon diameter	GO:0031133	1	KEL	5	13	287.49	3.474e-3	3.132e-2
ear morphogenesis	GO:0042471	1	CHD7	5	13	287.49	3.474e-3	3.132e-2
intracellular magnesium ion homeostasis	GO:0010961	1	KEL	6	13	239.58	4.167e-3	3.398e-2
positive regulation of cytoplasmic mRNA processing body assembly	GO:0010606	1	CNOT1	6	13	239.58	4.167e-3	3.398e-2