

GeDiPNet Cluster 328 -- 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 15:02:58

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
visceral muscle development	GO:0007522	1	MYH6	1	8	2335.88	4.281e-4	8.586e-3
regulation of heart growth	GO:0060420	1	MYH6	2	8	1167.94	8.560e-4	1.360e-2
negative regulation of G2/M1 transition of meiotic cell cycle	GO:0110031	1	PKMYT1	3	8	778.63	1.284e-3	1.747e-2
regulation of carbon utilization	GO:0043609	1	PRKAG2	3	8	778.63	1.284e-3	1.747e-2
oocyte differentiation	GO:0009994	1	NPM2	4	8	583.97	1.711e-3	2.068e-2
muscle system process	GO:0003012	1	MYH6	5	8	467.18	2.139e-3	2.343e-2
regulation of fatty acid oxidation	GO:0046320	1	PRKAG2	5	8	467.18	2.139e-3	2.343e-2
positive regulation of DNA metabolic process	GO:0051054	1	NPM2	6	8	389.31	2.566e-3	2.584e-2
positive regulation of meiotic nuclear division	GO:0045836	1	NPM2	6	8	389.31	2.566e-3	2.584e-2
positive regulation of transcription of Notch receptor target	GO:0007221	1	MAML3	7	8	333.70	2.993e-3	2.816e-2
atrial cardiac muscle tissue morphogenesis	GO:0055009	1	MYH6	7	8	333.70	2.993e-3	2.816e-2
regulation of D-glucose import	GO:0046324	1	PRKAG2	8	8	291.98	3.420e-3	3.030e-2
regulation of fatty acid metabolic process	GO:0019217	1	PRKAG2	11	8	212.35	4.700e-3	3.564e-2
cAMP biosynthetic process	GO:0006171	1	ADCY9	11	8	212.35	4.700e-3	3.564e-2
in utero embryonic development	GO:0001701	2	MYH6, ADCY9	252	8	18.54	4.807e-3	3.579e-2