

GeDiPNet Cluster 356 -- 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 07:21:25

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
complement activation, lectin pathway	GO:0001867	3	COLEC10, COLEC11, MASP1	13	8	539.05	1.470e-8	2.357e-6
positive regulation of opsonization	GO:1903028	2	COLEC10, COLEC11	9	8	519.08	5.765e-6	3.425e-4
cell surface pattern recognition receptor signaling pathway	GO:0002752	2	COLEC10, COLEC11	11	8	424.70	8.804e-6	4.824e-4
complement activation	GO:0006956	2	COLEC11, MASP1	35	8	133.48	9.475e-5	2.970e-3
right ventricular compact myocardium morphogenesis	GO:0003226	1	CHD7	1	8	2335.88	4.281e-4	8.766e-3
positive regulation of CD8-positive, alpha-beta cytotoxic T cell extravasation	GO:2000454	1	FADD	1	8	2335.88	4.281e-4	8.766e-3
negative regulation of cardiac muscle tissue development	GO:0055026	1	FGF3	2	8	1167.94	8.560e-4	1.393e-2
death-inducing signaling complex assembly	GO:0071550	1	FADD	2	8	1167.94	8.560e-4	1.393e-2
regulation of growth hormone secretion	GO:0060123	1	CHD7	3	8	778.63	1.284e-3	1.789e-2
olfactory nerve development	GO:0021553	1	CHD7	3	8	778.63	1.284e-3	1.789e-2
negative regulation of activation-induced cell death of T cells	GO:0070236	1	FADD	3	8	778.63	1.284e-3	1.789e-2
innate immune response	GO:0045087	3	COLEC11, MASP1, FADD	605	8	11.58	1.674e-3	2.100e-2
cranial nerve development	GO:0021545	1	CHD7	4	8	583.97	1.711e-3	2.128e-2
proteolysis	GO:0006508	3	COLEC10, COLEC11, MASP1	613	8	11.43	1.739e-3	2.151e-2
negative regulation of complement activation	GO:0045916	1	MASP1	5	8	467.18	2.139e-3	2.400e-2