

GeDiPNet Cluster 426 -- 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 09:56:42

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
muscle organ development	GO:0007517	2	FHL1, EMD	114	3	109.28	1.102e-4	3.319e-3
vacuolar proton-transporting V-type ATPase complex assembly	GO:0070072	1	VMA21	6	3	1038.17	9.630e-4	1.501e-2
nuclear membrane organization	GO:0071763	1	EMD	7	3	889.86	1.123e-3	1.656e-2
regulation of atrial cardiac muscle cell membrane depolarization	GO:0060371	1	FHL1	10	3	622.90	1.605e-3	2.035e-2
negative regulation of G2/M transition of mitotic cell cycle	GO:0010972	1	FHL1	15	3	415.27	2.406e-3	2.570e-2
positive regulation of potassium ion transmembrane transport	GO:1901381	1	FHL1	16	3	389.31	2.567e-3	2.663e-2
positive regulation of protein export from nucleus	GO:0046827	1	EMD	20	3	311.45	3.208e-3	2.987e-2
lysosomal lumen acidification	GO:0007042	1	VMA21	25	3	249.16	4.008e-3	3.336e-2
amyloid fibril formation	GO:1990000	1	EMD	29	3	214.79	4.649e-3	3.625e-2
negative regulation of fibroblast proliferation	GO:0048147	1	EMD	35	3	177.97	5.609e-3	3.937e-2
regulation of canonical Wnt signaling pathway	GO:0060828	1	EMD	37	3	168.35	5.929e-3	4.057e-2
skeletal muscle cell differentiation	GO:0035914	1	EMD	49	3	127.12	7.846e-3	4.658e-2
negative regulation of G1/S transition of mitotic cell cycle	GO:2000134	1	FHL1	58	3	107.40	9.283e-3	5.038e-2
cellular response to growth factor stimulus	GO:0071363	1	EMD	76	3	81.96	1.215e-2	5.709e-2
muscle contraction	GO:0006936	1	EMD	85	3	73.28	1.358e-2	6.045e-2