

GeDiPNet Cluster 511 -- 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 03:23:14. · Rows: 15 · Generated: 2026-10-20 00:00:31

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
sensory perception of sound	GO:0007605	3	COL11A2, EYA1, GJB2	162	5	69.21	6.315e-6	3.815e-4
otic vesicle morphogenesis	GO:0071600	1	EYA1	1	5	3737.40	2.676e-4	6.245e-3
regulation of membrane repolarization during atrial cardiac muscle cell action potential	GO:1905000	1	FLNA	1	5	3737.40	2.676e-4	6.245e-3
regulation of membrane repolarization during cardiac muscle cell action potential	GO:1905031	1	FLNA	1	5	3737.40	2.676e-4	6.245e-3
positive regulation of secondary heart field cardioblast proliferation	GO:0072513	1	EYA1	3	5	1245.80	8.025e-4	1.283e-2
tubulin deacetylation	GO:0090042	1	FLNA	3	5	1245.80	8.025e-4	1.283e-2
formation of radial glial scaffolds	GO:0021943	1	FLNA	4	5	934.35	1.070e-3	1.514e-2
establishment of Sertoli cell barrier	GO:0097368	1	FLNA	4	5	934.35	1.070e-3	1.514e-2
soft palate development	GO:0060023	1	COL11A2	5	5	747.48	1.337e-3	1.709e-2
adenylate cyclase-inhibiting dopamine receptor signaling pathway	GO:0007195	1	FLNA	5	5	747.48	1.337e-3	1.709e-2
protein localization to bicellular tight junction	GO:1902396	1	FLNA	6	5	622.90	1.605e-3	1.885e-2
gap junction-mediated intercellular transport	GO:1990349	1	GJB2	6	5	622.90	1.605e-3	1.885e-2
negative regulation of transcription by RNA polymerase I	GO:0016479	1	FLNA	7	5	533.91	1.872e-3	2.050e-2
mesodermal cell fate specification	GO:0007501	1	EYA1	7	5	533.91	1.872e-3	2.050e-2
striated muscle tissue development	GO:0014706	1	EYA1	7	5	533.91	1.872e-3	2.050e-2