

GeDiPNet Cluster 573 -- 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: 2026-10-19 23:18:22

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
late endosome to vacuole transport via multivesicular body sorting pathway	GO:0032511	2	CHMP4B, TMEM50A	12	19	163.92	6.425e-5	2.229e-3
cardiac muscle cell development	GO:0055013	2	SGCD, SLC8A1	25	19	78.68	2.898e-4	6.616e-3
calcium ion homeostasis	GO:0055074	2	SGCD, SLC8A1	42	19	46.83	8.231e-4	1.308e-2
cardiac muscle contraction	GO:0060048	2	SGCD, SLC8A1	43	19	45.75	8.627e-4	1.338e-2
regulation of systemic arterial blood pressure by baroreceptor feedback	GO:0003025	1	NAV2	1	19	983.53	1.017e-3	1.477e-2
glossopharyngeal nerve development	GO:0021563	1	NAV2	1	19	983.53	1.017e-3	1.477e-2
vagus nerve development	GO:0021564	1	NAV2	1	19	983.53	1.017e-3	1.477e-2
regulation of voltage-gated sodium channel activity	GO:1905150	1	FGF12	1	19	983.53	1.017e-3	1.477e-2
relaxation of smooth muscle	GO:0044557	1	SLC8A1	1	19	983.53	1.017e-3	1.477e-2
JNK cascade	GO:0007254	2	FGF12, MAP2K4	61	19	32.25	1.729e-3	1.971e-2
smooth muscle cell apoptotic process	GO:0034390	1	MAP2K4	2	19	491.76	2.033e-3	2.137e-2
coronary vasculature morphogenesis	GO:0060977	1	SGCD	2	19	491.76	2.033e-3	2.137e-2
intrinsic apoptotic signaling pathway in response to hydrogen peroxide	GO:0036481	1	MAP2K4	3	19	327.84	3.047e-3	2.623e-2
calcium ion export	GO:1901660	1	SLC8A1	3	19	327.84	3.047e-3	2.623e-2
regulation of neuronal action potential	GO:0098908	1	FGF12	4	19	245.88	4.061e-3	3.028e-2