

GeDiPNet Cluster 168 -- 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 15:05:03

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	52	59.89	4.924e-4	9.455e-3
optic nerve development	GO:0021554	2	NAV2, SLC25A46	15	52	47.92	7.792e-4	1.284e-2
cardiac muscle cell development	GO:0055013	2	SGCD, SLC8A1	25	52	28.75	2.187e-3	2.379e-2
negative regulation of Ras protein signal transduction	GO:0046580	2	MFN2, RABGEF1	25	52	28.75	2.187e-3	2.379e-2
regulation of systemic arterial blood pressure by baroreceptor feedback	GO:0003025	1	NAV2	1	52	359.37	2.783e-3	2.708e-2
glossopharyngeal nerve development	GO:0021563	1	NAV2	1	52	359.37	2.783e-3	2.708e-2
vagus nerve development	GO:0021564	1	NAV2	1	52	359.37	2.783e-3	2.708e-2
dendritic transport	GO:0098935	1	RABGEF1	1	52	359.37	2.783e-3	2.708e-2
pyrimidine nucleoside transport	GO:0015864	1	SLC28A3	1	52	359.37	2.783e-3	2.708e-2
regulation of voltage-gated sodium channel activity	GO:1905150	1	FGF12	1	52	359.37	2.783e-3	2.708e-2
relaxation of smooth muscle	GO:0044557	1	SLC8A1	1	52	359.37	2.783e-3	2.708e-2
Spemann organizer formation at the anterior end of the primitive streak	GO:0060064	1	WNT3	1	52	359.37	2.783e-3	2.708e-2
hypoxanthine catabolic process	GO:0009114	1	XDH	1	52	359.37	2.783e-3	2.708e-2
xanthine catabolic process	GO:0009115	1	XDH	1	52	359.37	2.783e-3	2.708e-2
pyridoxal 5'-phosphate salvage	GO:0009443	1	PDXK	1	52	359.37	2.783e-3	2.708e-2