

GeDiPNet Cluster 171 -- 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 07:31:05

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
neuromuscular process controlling posture	GO:0050884	3	GCH1, PRRT2, GLRA1	15	44	84.94	5.433e-6	3.268e-4
tetrahydrobiopterin biosynthetic process	GO:0006729	2	GCH1, SPR	8	44	106.18	1.504e-4	4.191e-3
dopamine biosynthetic process	GO:0042416	2	GCH1, TH	9	44	94.38	1.930e-4	5.037e-3
inhibitory postsynaptic potential	GO:0060080	2	CHRNA4, GLRA1	10	44	84.94	2.409e-4	5.860e-3
monoatomic ion transmembrane transport	GO:0034220	6	ANO3, CHRNA4, SCN2A, CACNA1B, KCNN2, GLRA1	404	44	6.31	3.466e-4	7.592e-3
regulation of SNARE complex assembly	GO:0035542	2	VPS16, VPS11	12	44	70.78	3.523e-4	7.676e-3
intracellular cholesterol transport	GO:0032367	2	SCP2, SERAC1	13	44	65.34	4.157e-4	8.633e-3
vacuole organization	GO:0007033	2	VPS16, VPS11	13	44	65.34	4.157e-4	8.633e-3
endosomal vesicle fusion	GO:0034058	2	VPS16, VPS11	15	44	56.63	5.579e-4	1.051e-2
response to hypoxia	GO:0001666	4	CHRNA4, TH, SLC2A1, ND1	176	44	9.65	7.694e-4	1.308e-2
monoatomic ion transport	GO:0006811	7	ATP1A3, CHRNA4, SLC30A10, SCN2A, CACNA1B, KCNN2, GLRA1	667	44	4.46	8.675e-4	1.406e-2
nitric oxide biosynthetic process	GO:0006809	2	GCH1, SPR	23	44	36.93	1.328e-3	1.830e-2
positive regulation of norepinephrine uptake	GO:0051623	1	ACTB	1	44	424.70	2.355e-3	2.546e-2
cellular response to cytochalasin B	GO:0072749	1	ACTB	1	44	424.70	2.355e-3	2.546e-2
pteridine-containing compound biosynthetic process	GO:0042559	1	GCH1	1	44	424.70	2.355e-3	2.546e-2