

GeDiPNet Cluster 394 -- 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: 2026-10-09 03:23:08. · Rows: 15 · Generated: 2026-10-08 23:31:03

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
monoamine transport	GO:0015844	2	SLC6A3, SLC18A2	9	6	692.11	3.090e-6	2.051e-4
dopamine transport	GO:0015872	2	SLC6A3, SLC18A2	10	6	622.90	3.862e-6	2.454e-4
neurotransmitter transport	GO:0006836	2	SLC6A3, SLC18A2	57	6	109.28	1.360e-4	3.818e-3
regulation of CD4-positive, alpha-beta T cell activation	GO:2000514	1	AGER	1	6	3114.50	3.211e-4	7.094e-3
mitochondrial tryptophanyl-tRNA aminoacylation	GO:0070183	1	WARS2	1	6	3114.50	3.211e-4	7.094e-3
L-alanine catabolic process, by transamination	GO:0019481	1	AGXT2	1	6	3114.50	3.211e-4	7.094e-3
N(omega),N(omega)-dimethyl-L-arginine catabolic process	GO:2001299	1	AGXT2	1	6	3114.50	3.211e-4	7.094e-3
serotonin secretion by mast cell	GO:0002552	1	SLC18A2	1	6	3114.50	3.211e-4	7.094e-3
somato-dendritic dopamine secretion	GO:0099123	1	SLC18A2	1	6	3114.50	3.211e-4	7.094e-3
locomotory behavior	GO:0007626	2	SLC6A3, SLC18A2	99	6	62.92	4.110e-4	8.412e-3
glycine biosynthetic process, by transamination of glyoxylate	GO:0019265	1	AGXT2	2	6	1557.25	6.421e-4	1.140e-2
negative regulation of blood circulation	GO:1903523	1	AGER	2	6	1557.25	6.421e-4	1.140e-2
regulation of T cell mediated cytotoxicity	GO:0001914	1	AGER	2	6	1557.25	6.421e-4	1.140e-2
negative regulation of connective tissue replacement involved in inflammatory response wound healing	GO:1904597	1	AGER	2	6	1557.25	6.421e-4	1.140e-2
positive regulation of DNA-templated DNA replication	GO:2000105	1	AGER	2	6	1557.25	6.421e-4	1.140e-2