

GeDiPNet Cluster 516 -- 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 00:01:21

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
positive regulation of nitric-oxide synthase activity	GO:0051000	2	GCH1, INS	3	6	2076.33	2.577e-7	2.794e-5
tetrahydrobiopterin biosynthetic process	GO:0006729	2	GCH1, SPR	8	6	778.63	2.404e-6	1.760e-4
dopamine biosynthetic process	GO:0042416	2	GCH1, NR4A2	9	6	692.11	3.090e-6	2.146e-4
nitric oxide biosynthetic process	GO:0006809	2	GCH1, SPR	23	6	270.83	2.167e-5	9.822e-4
pteridine-containing compound biosynthetic process	GO:0042559	1	GCH1	1	6	3114.50	3.211e-4	7.044e-3
general adaptation syndrome	GO:0051866	1	NR4A2	1	6	3114.50	3.211e-4	7.044e-3
regulation of lung blood pressure	GO:0014916	1	GCH1	2	6	1557.25	6.421e-4	1.113e-2
negative regulation of glycogen catabolic process	GO:0045818	1	INS	2	6	1557.25	6.421e-4	1.113e-2
pteridine-containing compound metabolic process	GO:0042558	1	GCH1	3	6	1038.17	9.630e-4	1.423e-2
habenula development	GO:0021986	1	NR4A2	3	6	1038.17	9.630e-4	1.423e-2
tetrahydrobiopterin metabolic process	GO:0046146	1	GCH1	4	6	778.63	1.284e-3	1.669e-2
positive regulation of nitric oxide mediated signal transduction	GO:0010750	1	INS	4	6	778.63	1.284e-3	1.669e-2
positive regulation of dendritic spine maintenance	GO:1902952	1	INS	5	6	622.90	1.605e-3	1.885e-2
negative regulation of respiratory burst involved in inflammatory response	GO:0060266	1	INS	5	6	622.90	1.605e-3	1.885e-2
cellular response to corticotropin-releasing hormone stimulus	GO:0071376	1	NR4A2	5	6	622.90	1.605e-3	1.885e-2