

GeDiPNet Cluster 392 -- 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: 2026-10-09 17:38:07

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
negative regulation of synaptic transmission, glutamatergic	GO:0051967	3	DRD2, DRD3, HTR2A	10	20	280.31	1.252e-7	1.450e-5
positive regulation of DNA biosynthetic process	GO:2000573	3	PDGFB, PDGFRB, HTR2A	12	20	233.59	2.292e-7	2.429e-5
regulation of dopamine secretion	GO:0014059	3	DRD2, DRD3, HTR2A	15	20	186.87	4.731e-7	4.441e-5
behavioral response to cocaine	GO:0048148	3	DRD2, DRD3, HTR2A	17	20	164.89	7.061e-7	6.221e-5
regulation of amine transport	GO:0051952	2	DRD2, DRD3	2	20	934.35	1.088e-6	8.911e-5
positive regulation of ERK1 and ERK2 cascade	GO:0070374	5	PDE8B, PDGFB, PDGFRB, DRD2, HTR2A	201	20	23.24	1.862e-6	1.375e-4
acid secretion	GO:0046717	2	DRD2, DRD3	3	20	622.90	3.263e-6	2.147e-4
positive regulation of metanephric mesenchymal cell migration by platelet-derived growth factor receptor-beta signaling pathway	GO:0035793	2	PDGFB, PDGFRB	3	20	622.90	3.263e-6	2.147e-4
positive regulation of mitotic nuclear division	GO:0045840	3	PDGFB, PDGFRB, DRD3	29	20	96.66	3.763e-6	2.405e-4
regulation of secretion by cell	GO:1903530	2	DRD2, DRD3	4	20	467.18	6.521e-6	3.745e-4
response to histamine	GO:0034776	2	DRD2, DRD3	4	20	467.18	6.521e-6	3.745e-4
smooth muscle adaptation	GO:0014805	2	PDGFB, PDGFRB	4	20	467.18	6.521e-6	3.745e-4
response to cocaine	GO:0042220	3	DRD2, DRD3, HTR2A	35	20	80.09	6.713e-6	3.834e-4
regulation of dopamine uptake involved in synaptic transmission	GO:0051584	2	DRD2, DRD3	5	20	373.74	1.086e-5	5.599e-4
adenylate cyclase-inhibiting dopamine receptor signaling pathway	GO:0007195	2	DRD2, DRD3	5	20	373.74	1.086e-5	5.599e-4