

GeDiPNet Cluster 602 -- 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: 8 · Generated: 2026-10-19 23:18:23

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
regulation of cAMP/PKA signal transduction	GO:01411161	1	PDE10A	5	2	1868.70	5.351e-4	9.880e-3
cGMP catabolic process	GO:0046069	1	PDE10A	5	2	1868.70	5.351e-4	9.880e-3
regulation of adenylate cyclase-activating G protein-coupled receptor signaling pathway	GO:0106070	1	PDE10A	5	2	1868.70	5.351e-4	9.880e-3
negative regulation of cGMP-mediated signaling	GO:0010754	1	PDE10A	6	2	1557.25	6.421e-4	1.113e-2
cAMP catabolic process	GO:0006198	1	PDE10A	9	2	1038.17	9.630e-4	1.423e-2
negative regulation of cAMP/PKA signal transduction	GO:0141162	1	PDE10A	28	2	333.70	2.995e-3	2.594e-2
DNA-templated transcription	GO:0006351	1	LINC00473	113	2	82.69	1.206e-2	5.083e-2
signal transduction	GO:0007165	1	PDE10A	2125	2	4.40	2.145e-1	2.801e-1