

GeDiPNet Cluster 332 -- 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: 2026-10-07 03:23:06. · Rows: 15 · Generated: 2026-10-07 19:41:13

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
cell motility	GO:0048870	2	DST, SCN11A	48	9	86.51	2.299e-4	5.569e-3
reflex	GO:0060004	1	SCN11A	1	9	2076.33	4.816e-4	9.305e-3
small intestine smooth muscle contraction	GO:1990770	1	SCN11A	1	9	2076.33	4.816e-4	9.305e-3
negative regulation of growth rate	GO:0045967	1	TMPRSS4	1	9	2076.33	4.816e-4	9.305e-3
guanosine metabolic process	GO:0008617	1	DGUOK	1	9	2076.33	4.816e-4	9.305e-3
dGTP metabolic process	GO:0046070	1	DGUOK	1	9	2076.33	4.816e-4	9.305e-3
purine deoxyribonucleoside metabolic process	GO:0046122	1	DGUOK	1	9	2076.33	4.816e-4	9.305e-3
response to wounding	GO:0009611	2	TMPRSS4, DST	81	9	51.27	6.550e-4	1.143e-2
chromosomal DNA methylation maintenance following DNA replication	GO:0141119	1	DNMT1	2	9	1038.17	9.630e-4	1.467e-2
negative regulation of vascular associated smooth muscle cell differentiation involved in phenotypic switching	GO:1905931	1	DNMT1	2	9	1038.17	9.630e-4	1.467e-2
thermosensory behavior	GO:0040040	1	SCN11A	2	9	1038.17	9.630e-4	1.467e-2
behavioral response to acetic acid induced pain	GO:0061367	1	SCN11A	2	9	1038.17	9.630e-4	1.467e-2
GDP-D-mannose biosynthetic process from fructose-6-phosphate	GO:0061729	1	PMM2	2	9	1038.17	9.630e-4	1.467e-2
dAMP salvage	GO:0106383	1	DGUOK	3	9	692.11	1.444e-3	1.871e-2
GDP-mannose biosynthetic process from mannose	GO:0061728	1	PMM2	3	9	692.11	1.444e-3	1.871e-2