

GeDiPNet Cluster 364 -- 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: 2026-10-08 03:23:04. · Rows: 15 · Generated: 2026-10-07 23:26:11

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
indole metabolic process	GO:0042431	1	SLC34A1	1	6	3114.50	3.211e-4	7.182e-3
gentamycin metabolic process	GO:1901128	1	SLC34A1	1	6	3114.50	3.211e-4	7.182e-3
arsenate ion transmembrane transport	GO:1901684	1	SLC34A1	1	6	3114.50	3.211e-4	7.182e-3
positive regulation of phosphate transmembrane transport	GO:2000187	1	SLC34A1	1	6	3114.50	3.211e-4	7.182e-3
creatine biosynthetic process	GO:0006601	1	GATM	2	6	1557.25	6.421e-4	1.151e-2
muscle atrophy	GO:0014889	1	GATM	2	6	1557.25	6.421e-4	1.151e-2
response to lipid hydroperoxide	GO:0006982	1	GPX3	2	6	1557.25	6.421e-4	1.151e-2
cellular response to phosphate starvation	GO:0016036	1	SLC34A1	3	6	1038.17	9.630e-4	1.501e-2
cellular response to metal ion	GO:0071248	1	SLC34A1	3	6	1038.17	9.630e-4	1.501e-2
positive regulation of sodium-dependent phosphate transport	GO:2000120	1	SLC34A1	3	6	1038.17	9.630e-4	1.501e-2
creatine metabolic process	GO:0006600	1	GATM	4	6	778.63	1.284e-3	1.789e-2
positive regulation of membrane potential	GO:0045838	1	SLC34A1	5	6	622.90	1.605e-3	2.035e-2
galactose transmembrane transport	GO:0015757	1	SLC2A2	5	6	622.90	1.605e-3	2.035e-2
cellular response to staurosporine	GO:0072734	1	SLC34A1	5	6	622.90	1.605e-3	2.035e-2
response to parathyroid hormone	GO:0071107	1	SLC34A1	5	6	622.90	1.605e-3	2.035e-2