

GeDiPNet Cluster 451 -- 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 00:03:18

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
establishment of epithelial cell apical/basal polarity involved in camera-type eye morphogenesis	GO:0003412	1	FAT1	1	9	2076.33	4.816e-4	9.241e-3
positive regulation of protein geranylgeranylation	GO:2000541	1	MUSK	1	9	2076.33	4.816e-4	9.241e-3
negative regulation of DNA methylation-dependent heterochromatin formation	GO:0090310	1	KMT2A	2	9	1038.17	9.630e-4	1.423e-2
positive regulation of gene expression	GO:0010628	3	KMT2A, MUSK, ACTG1	504	9	12.36	1.451e-3	1.797e-2
regulation of transepithelial transport	GO:0150111	1	ACTG1	4	9	519.08	1.925e-3	2.069e-2
protein processing involved in protein targeting to mitochondrion	GO:0006627	1	PMPCA	5	9	415.27	2.406e-3	2.324e-2
cardiolipin biosynthetic process	GO:0032049	1	TAMM41	5	9	415.27	2.406e-3	2.324e-2
morphogenesis of a polarized epithelium	GO:0001738	1	ACTG1	6	9	346.06	2.887e-3	2.555e-2
protein localization to bicellular tight junction	GO:1902396	1	ACTG1	6	9	346.06	2.887e-3	2.555e-2
response to potassium ion	GO:0035864	1	KMT2A	8	9	259.54	3.847e-3	2.937e-2
tight junction assembly	GO:0120192	1	ACTG1	8	9	259.54	3.847e-3	2.937e-2
mitochondrial transcription	GO:0006390	1	TWINK	8	9	259.54	3.847e-3	2.937e-2
regulation of cilium beat frequency	GO:0003356	1	CFAP43	8	9	259.54	3.847e-3	2.937e-2
T-helper 2 cell differentiation	GO:0045064	1	KMT2A	9	9	230.70	4.327e-3	3.113e-2
skeletal muscle acetylcholine-gated channel clustering	GO:0071340	1	MUSK	9	9	230.70	4.327e-3	3.113e-2