

GeDiPNet Cluster 469 -- 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: 2026-10-19 23:18:54

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
muscle atrophy	GO:0014889	1	TBCE	2	3	3114.50	3.211e-4	7.044e-3
peripheral nervous system neuron axonogenesis	GO:0048936	1	TBCE	4	3	1557.25	6.421e-4	1.113e-2
post-chaperonin tubulin folding pathway	GO:0007023	1	TBCE	7	3	889.86	1.123e-3	1.550e-2
protein-DNA covalent cross-linking repair	GO:0106300	1	FAM111A	9	3	692.11	1.444e-3	1.794e-2
tubulin complex assembly	GO:0007021	1	TBCE	10	3	622.90	1.605e-3	1.885e-2
protein autoprocessing	GO:0016540	1	FAM111A	25	3	249.16	4.008e-3	3.008e-2
developmental growth	GO:0048589	1	TBCE	30	3	207.63	4.809e-3	3.273e-2
replication fork processing	GO:0031297	1	FAM111A	41	3	151.93	6.568e-3	3.799e-2
negative regulation of viral genome replication	GO:0045071	1	FAM111A	44	3	141.57	7.047e-3	3.929e-2
adult locomotory behavior	GO:0008344	1	TBCE	56	3	111.23	8.964e-3	4.407e-2
mitotic spindle organization	GO:0007052	1	TBCE	58	3	107.40	9.283e-3	4.491e-2
protein O-linked glycosylation	GO:0006493	1	B3GALNT2	71	3	87.73	1.136e-2	4.934e-2
post-embryonic development	GO:0009791	1	TBCE	82	3	75.96	1.311e-2	5.298e-2
axonogenesis	GO:0007409	1	TBCE	125	3	49.83	1.993e-2	6.510e-2
DNA replication	GO:0006260	1	FAM111A	131	3	47.55	2.088e-2	6.675e-2