

GeDiPNet Cluster 442 -- 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 00:01:24

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
adult walking behavior	GO:0007628	2	AGTPBP1, ABHD12	34	10	109.92	1.433e-4	4.000e-3
positive regulation of deoxyribonuclease activity	GO:0032077	1	PCNA	1	10	1868.70	5.351e-4	9.880e-3
negative regulation of establishment of blood-brain barrier	GO:0090212	1	TTPA	1	10	1868.70	5.351e-4	9.880e-3
developmental induction	GO:0031128	1	NKX2-1	1	10	1868.70	5.351e-4	9.880e-3
lipid metabolic process	GO:0006629	4	ABHD12, TTPA, NUS1, TPP1	840	10	8.90	6.848e-4	1.170e-2
response to toxic substance	GO:0009636	2	PRKCG, TTPA	83	10	45.03	8.570e-4	1.331e-2
anterograde axonal transport of mitochondrion	GO:0098957	1	AGTPBP1	2	10	934.35	1.070e-3	1.514e-2
forebrain neuron fate commitment	GO:0021877	1	NKX2-1	2	10	934.35	1.070e-3	1.514e-2
epithelial cell differentiation	GO:0030855	2	PCNA, TPP1	110	10	33.98	1.498e-3	1.821e-2
ventricular cardiac muscle cell membrane repolarization	GO:0099625	1	KCND3	3	10	622.90	1.605e-3	1.885e-2
mitotic telomere maintenance via semi-conservative replication	GO:1902990	1	PCNA	3	10	622.90	1.605e-3	1.885e-2
protein deglutamylation	GO:0035608	1	AGTPBP1	3	10	622.90	1.605e-3	1.885e-2
retrograde axonal transport of mitochondrion	GO:0098958	1	AGTPBP1	3	10	622.90	1.605e-3	1.885e-2
positive regulation of mismatch repair	GO:0032425	1	PRKCG	3	10	622.90	1.605e-3	1.885e-2
regulation of response to food	GO:0032095	1	PRKCG	3	10	622.90	1.605e-3	1.885e-2