

GeDiPNet Cluster 242 -- 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 20:39:43

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
vesicle-mediated transport	GO:0016192	13	KIF5A, AP5Z1, TFG, KIF1A, KIF1C, AP4B1, AP4E1, AP4M1, AP4S1, VAMP1, ZFYVE27, TRAPPC2	326	154	4.84	3.146e-6	2.073e-4
retrograde neuronal dense core vesicle transport	GO:1990049	3	KIF5A, KIF1A, KIF1C	5	154	72.81	5.423e-6	3.203e-4
autophagosome organization	GO:1905037	3	SPG11, ATP13A2, ZFYVE26	5	154	72.81	5.423e-6	3.203e-4
lipid metabolic process	GO:0006629	21	BSCL2, CPT1C, FAR1, SPART, B4GALNT1, DDHD1, FA2H, PNPLA6, GBA2, DDHD2, CYP2U1, CYP7B1	840	154	3.03	5.628e-6	3.296e-4
endoplasmic reticulum tubular network formation	GO:0071787	3	RTN2, ARL6IP1, ZFYVE27	6	154	60.67	1.078e-5	5.522e-4
positive regulation of mitochondrial fission	GO:0090141	4	DDHD1, DDHD2, PRKN, DNM1L	22	154	22.06	2.890e-5	1.187e-3
regulation of mitochondrion organization	GO:0010821	4	ATP13A2, PRKN, DNM1L, SQSTM1	22	154	22.06	2.890e-5	1.187e-3
endoplasmic reticulum tubular network membrane organization	GO:1990809	3	RTN2, ATL1, ARL6IP1	8	154	45.50	2.982e-5	1.215e-3
endosome organization	GO:0007032	5	WASHC5, USP8, ALS2, SQSTM1, USP50	45	154	13.48	3.335e-5	1.326e-3
macroautophagy	GO:0016236	6	VPS37A, RAB3GAP2, PRKN, VCP, TBK1, SQSTM1	77	154	9.46	4.159e-5	1.569e-3
SREBP signaling pathway	GO:0032933	3	ERLIN1, ERLIN2, SREBF2	9	154	40.45	4.446e-5	1.650e-3
protein targeting	GO:0006605	5	SORL1, AP4B1, AP4E1, AP4M1, AP4S1	49	154	12.38	5.070e-5	1.819e-3
mitochondrial DNA replication	GO:0006264	3	POLG, POLG2, TWNK	11	154	33.09	8.628e-5	2.711e-3
autophagy	GO:0006914	9	AP5Z1, ATP13A2, PRKN, VCP, SQSTM1, DNAJC16, DNM2, RETREG1, TECPR2	221	154	4.94	9.242e-5	2.848e-3
protein transport	GO:0015031	16	RTN2, UBAP1, KPNA3, WASHC5, AP5Z1, VPS37A, PGAP1, AP4B1, AP4E1, AP4M1, AP4S1, BICD2	667	154	2.91	1.281e-4	3.644e-3