

GeDiPNet Cluster 441 -- 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 23:18:15

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
membrane docking	GO:0022406	1	CHP1	1	7	2669.57	3.746e-4	7.813e-3
positive regulation of protein transport	GO:0051222	1	CHP1	2	7	1334.79	7.491e-4	1.230e-2
cellular response to glutathione	GO:0072753	1	AFG3L2	2	7	1334.79	7.491e-4	1.230e-2
glutathione import into mitochondrion	GO:0160007	1	AFG3L2	2	7	1334.79	7.491e-4	1.230e-2
methionyl-tRNA aminoacylation	GO:0006431	1	MARS2	2	7	1334.79	7.491e-4	1.230e-2
positive regulation of sodium:proton antiporter activity	GO:0032417	1	CHP1	3	7	889.86	1.123e-3	1.550e-2
mitochondrial RNA 3'-end processing	GO:0000965	1	MTPAP	3	7	889.86	1.123e-3	1.550e-2
regulation of calcium import into the mitochondrion	GO:0110097	1	AFG3L2	3	7	889.86	1.123e-3	1.550e-2
negative regulation of phosphatase activity	GO:0010923	1	CHP1	3	7	889.86	1.123e-3	1.550e-2
negative regulation of cell fate commitment	GO:0010454	1	NKX6-2	3	7	889.86	1.123e-3	1.550e-2
positive regulation of protein glycosylation	GO:0060050	1	CHP1	4	7	667.39	1.498e-3	1.821e-2
anterograde neuronal dense core vesicle transport	GO:1990048	1	KIF1C	4	7	667.39	1.498e-3	1.821e-2
negative regulation of protein autophosphorylation	GO:0031953	1	CHP1	4	7	667.39	1.498e-3	1.821e-2
mitochondrial mRNA polyadenylation	GO:0097222	1	MTPAP	4	7	667.39	1.498e-3	1.821e-2
mitochondrial protein quality control	GO:0141164	1	AFG3L2	4	7	667.39	1.498e-3	1.821e-2