

GeDiPNet Cluster 616 -- 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 00:01:12

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
tRNA aminoacylation for protein translation	GO:0006418	3	WARS2, NARS2, TARS2	36	5	311.45	6.549e-8	8.908e-6
translation	GO:0006412	4	WARS2, MTFMT, NARS2, TARS2	310	5	48.22	3.666e-7	3.747e-5
RNA import into mitochondrion	GO:0035927	1	PNPT1	1	5	3737.40	2.676e-4	6.245e-3
nuclear polyadenylation-dependent mRNA catabolic process	GO:0071042	1	PNPT1	1	5	3737.40	2.676e-4	6.245e-3
mitochondrial tryptophanyl-tRNA aminoacylation	GO:0070183	1	WARS2	1	5	3737.40	2.676e-4	6.245e-3
conversion of methionyl-tRNA to N-formyl-methionyl-tRNA	GO:0071951	1	MTFMT	1	5	3737.40	2.676e-4	6.245e-3
mitochondrial threonyl-tRNA aminoacylation	GO:0070159	1	TARS2	1	5	3737.40	2.676e-4	6.245e-3
asparaginyl-tRNA aminoacylation	GO:0006421	1	NARS2	2	5	1868.70	5.351e-4	9.880e-3
mitochondrial RNA 5'-end processing	GO:0000964	1	PNPT1	2	5	1868.70	5.351e-4	9.880e-3
tryptophanyl-tRNA aminoacylation	GO:0006436	1	WARS2	2	5	1868.70	5.351e-4	9.880e-3
rRNA import into mitochondrion	GO:0035928	1	PNPT1	3	5	1245.80	8.025e-4	1.283e-2
mitochondrial mRNA catabolic process	GO:0000958	1	PNPT1	3	5	1245.80	8.025e-4	1.283e-2
positive regulation of mitochondrial RNA catabolic process	GO:0000962	1	PNPT1	3	5	1245.80	8.025e-4	1.283e-2
mitochondrial RNA 3'-end processing	GO:0000965	1	PNPT1	3	5	1245.80	8.025e-4	1.283e-2
threonyl-tRNA aminoacylation	GO:0006435	1	TARS2	3	5	1245.80	8.025e-4	1.283e-2