

GeDiPNet Cluster 240 -- Enriched Pathways

Pathway enrichment: KEGG + Reactome, upper-tail hypergeometric test, Benjamini-Hochberg FDR-corrected. Fold enrichment = (overlap / cluster gene count) / (pathway gene count / universe size). Top 15 pathways per cluster by q-value. See [scripts/build_cluster_enrichment.php](#) on [gedipnet.bicnirrh.res.in](#). Data as of: 2026-10-07 03:30:09. · Rows: 15 · Generated: 2026-10-07 17:51:02

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Viral mRNA Translation	Reactome	24	RPL11, RPL15, RPL18, RPL26, RPL35, RPL35A, RPL5, RPL8, RPS10, RPS15A, RPS17, RPS19	89	52	62.28	9.302e-39	6.043e-35
SRP-dependent cotranslational protein targeting to membrane	Reactome	24	RPL11, RPL15, RPL18, RPL26, RPL35, RPL35A, RPL5, RPL8, RPS10, RPS15A, RPS17, RPS19	93	52	59.60	3.113e-38	1.910e-34
Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	Reactome	24	RPL11, RPL15, RPL18, RPL26, RPL35, RPL35A, RPL5, RPL8, RPS10, RPS15A, RPS17, RPS19	95	52	58.35	5.569e-38	3.237e-34
Formation of a pool of free 40S subunits	Reactome	24	RPL11, RPL15, RPL18, RPL26, RPL35, RPL35A, RPL5, RPL8, RPS10, RPS15A, RPS17, RPS19	101	52	54.88	2.937e-37	1.545e-33
L13a-mediated translational silencing of Ceruloplasmin expression	Reactome	24	RPL11, RPL15, RPL18, RPL26, RPL35, RPL35A, RPL5, RPL8, RPS10, RPS15A, RPS17, RPS19	111	52	49.94	3.699e-36	1.857e-32
GTP hydrolysis and joining of the 60S ribosomal subunit	Reactome	24	RPL11, RPL15, RPL18, RPL26, RPL35, RPL35A, RPL5, RPL8, RPS10, RPS15A, RPS17, RPS19	112	52	49.49	4.697e-36	2.161e-32
Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	Reactome	24	RPL11, RPL15, RPL18, RPL26, RPL35, RPL35A, RPL5, RPL8, RPS10, RPS15A, RPS17, RPS19	115	52	48.20	9.482e-36	4.189e-32
Ribosome	KEGG	25	RPL11, RPL15, RPL18, RPL26, RPL35, RPL35A, RPL5, RPL8, RPS10, RPS10-NUDT3, RPS15A, RPS17	171	52	33.77	3.862e-33	1.471e-29
Major pathway of rRNA processing in the nucleolus and cytosol	Reactome	24	RPL11, RPL15, RPL18, RPL26, RPL35, RPL35A, RPL5, RPL8, RPS10, RPS15A, RPS17, RPS19	184	52	30.13	1.771e-30	5.435e-27
Coronavirus disease - COVID-19	KEGG	25	RPL11, RPL15, RPL18, RPL26, RPL35, RPL35A, RPL5, RPL8, RPS10, RPS10-NUDT3, RPS15A, RPS17	238	52	24.26	2.219e-29	5.978e-26
Formation of the ternary complex, and subsequently, the 43S complex	Reactome	12	RPS10, RPS15A, RPS17, RPS19, RPS20, RPS24, RPS26, RPS28, RPS29, RPS7, RPS15, RPS27	51	52	54.34	1.554e-18	1.021e-15
Translation initiation complex formation	Reactome	12	RPS10, RPS15A, RPS17, RPS19, RPS20, RPS24, RPS26, RPS28, RPS29, RPS7, RPS15, RPS27	58	52	47.79	8.541e-18	4.670e-15
Ribosomal scanning and start codon recognition	Reactome	12	RPS10, RPS15A, RPS17, RPS19, RPS20, RPS24, RPS26, RPS28, RPS29, RPS7, RPS15, RPS27	58	52	47.79	8.541e-18	4.670e-15
Signaling by FGFR2 amplification mutants	Reactome	1	FGFR2	1	52	230.96	4.330e-3	3.983e-2
Signaling by FGFR2 fusions	Reactome	1	FGFR2	1	52	230.96	4.330e-3	3.983e-2