

GeDiPNet Cluster 628 -- 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: 2026-10-20 03:30:09. · Rows: 15 · Generated: 2026-10-19 23:21:08

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
snRNP Assembly	Reactome	2	SMN1, SMN2	53	7	64.74	3.956e-4	5.577e-3
Synthesis of PIPs at the ER membrane	Reactome	1	MTMR2	5	7	343.14	2.911e-3	2.492e-2
Synthesis of PIPs at the late endosome membrane	Reactome	1	MTMR2	10	7	171.57	5.815e-3	4.033e-2
Synthesis of PIPs at the early endosome membrane	Reactome	1	MTMR2	15	7	114.38	8.712e-3	5.219e-2
Processing of SMDT1	Reactome	1	SPG7	16	7	107.23	9.291e-3	5.428e-2
Elastic fibre formation	Reactome	1	FBLN5	18	7	95.32	1.045e-2	5.837e-2
Molecules associated with elastic fibres	Reactome	1	FBLN5	38	7	45.15	2.194e-2	9.030e-2
Legionellosis	KEGG	1	NAIP	56	7	30.64	3.219e-2	1.127e-1
Inositol phosphate metabolism	KEGG	1	MTMR2	73	7	23.50	4.179e-2	1.307e-1
Phosphatidylinositol signaling system	KEGG	1	MTMR2	98	7	17.51	5.575e-2	1.542e-1
NOD-like receptor signaling pathway	KEGG	1	NAIP	187	7	9.17	1.041e-1	2.213e-1
Pathogenic Escherichia coli infection	KEGG	1	NAIP	200	7	8.58	1.109e-1	2.299e-1
Salmonella infection	KEGG	1	NAIP	248	7	6.92	1.359e-1	2.596e-1
Shigellosis	KEGG	1	NAIP	250	7	6.86	1.370e-1	2.607e-1
Amyotrophic lateral sclerosis	KEGG	1	SETX	368	7	4.66	1.958e-1	3.265e-1