

GeDiPNet Cluster 604 -- 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: 9 · Generated: 2026-10-20 00:02:22

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
mRNA decay by 5' to 3' exoribonuclease	Reactome	1	LSM3	14	6	142.98	6.975e-3	4.528e-2
Non-integrin membrane-ECM interactions	Reactome	1	DDR2	24	6	83.40	1.193e-2	6.320e-2
Vasopressin regulates renal water homeostasis via Aquaporins	Reactome	1	RAB11FIP2	43	6	46.55	2.130e-2	8.893e-2
Base excision repair	KEGG	1	TDP1	44	6	45.49	2.179e-2	9.002e-2
Nonhomologous End-Joining (NHEJ)	Reactome	1	TDP1	69	6	29.01	3.399e-2	1.161e-1
RNA degradation	KEGG	1	LSM3	78	6	25.66	3.835e-2	1.244e-1
Spliceosome	KEGG	1	LSM3	162	6	12.36	7.827e-2	1.873e-1
mRNA Splicing - Major Pathway	Reactome	1	LSM3	183	6	10.94	8.803e-2	2.005e-1
Endocytosis	KEGG	1	RAB11FIP2	250	6	8.01	1.186e-1	2.396e-1