

GeDiPNet Cluster 580 -- 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: 13 · Generated: 2026-10-20 00:03:18

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
rRNA modification in the nucleus and cytosol	Reactome	2	DKC1, NOP10	12	4	500.42	5.485e-6	1.772e-4
Telomere Extension By Telomerase	Reactome	2	DKC1, NOP10	16	4	375.31	9.969e-6	2.906e-4
Ribosome biogenesis in eukaryotes	KEGG	2	DKC1, NOP10	125	4	48.04	6.360e-4	8.050e-3
Fructose catabolism	Reactome	1	TKFC	5	4	600.50	1.664e-3	1.665e-2
DDX58/IFIH1-mediated induction of interferon-alpha/beta	Reactome	1	TKFC	17	4	176.62	5.651e-3	3.957e-2
Fructose and mannose metabolism	KEGG	1	TKFC	34	4	88.31	1.128e-2	6.123e-2
Glycerolipid metabolism	KEGG	1	TKFC	64	4	46.91	2.115e-2	8.845e-2
Inflammatory bowel disease	KEGG	1	MAF	66	4	45.49	2.180e-2	9.007e-2
RIG-I-like receptor signaling pathway	KEGG	1	TKFC	72	4	41.70	2.377e-2	9.466e-2
Th1 and Th2 cell differentiation	KEGG	1	MAF	93	4	32.28	3.062e-2	1.097e-1
Carbon metabolism	KEGG	1	TKFC	115	4	26.11	3.776e-2	1.234e-1
Transcriptional misregulation in cancer	KEGG	1	MAF	198	4	15.16	6.434e-2	1.673e-1
Metabolic pathways	KEGG	1	TKFC	1563	4	1.92	4.275e-1	5.524e-1