

GeDiPNet Cluster 166 -- 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 17:42:16

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Defective MTRR causes methylmalonic aciduria and homocystinuria type cblE	Reactome	1	MTRR	2	13	461.92	2.164e-3	2.417e-2
Defective MTR causes methylmalonic aciduria and homocystinuria type cblG	Reactome	1	MTRR	2	13	461.92	2.164e-3	2.417e-2
TFAP2 (AP-2) family regulates transcription of other transcription factors	Reactome	1	CITED2	4	13	230.96	4.323e-3	3.983e-2
NGF processing	Reactome	1	PCSK5	4	13	230.96	4.323e-3	3.983e-2
Sulfur amino acid metabolism	Reactome	1	MTRR	6	13	153.97	6.478e-3	5.190e-2
FOXO-mediated transcription of cell death genes	Reactome	1	CITED2	9	13	102.65	9.703e-3	6.739e-2
Regulation of gene expression by Hypoxia-inducible Factor	Reactome	1	CITED2	11	13	83.99	1.185e-2	7.599e-2
Assembly of active LPL and LIPC lipase complexes	Reactome	1	PCSK5	11	13	83.99	1.185e-2	7.599e-2
Activation of the TFAP2 (AP-2) family of transcription factors	Reactome	1	CITED2	12	13	76.99	1.292e-2	7.945e-2
Physiological factors	Reactome	1	NKX2-5	12	13	76.99	1.292e-2	7.945e-2
YAP1- and WWTR1 (TAZ)-stimulated gene expression	Reactome	1	NKX2-5	14	13	65.99	1.506e-2	8.714e-2
Methylation	Reactome	1	MTRR	14	13	65.99	1.506e-2	8.714e-2
Cobalamin transport and metabolism	KEGG	1	MTRR	18	13	51.32	1.932e-2	1.008e-1
Cobalamin (Cbl, vitamin B12) transport and metabolism	Reactome	1	MTRR	21	13	43.99	2.251e-2	1.100e-1
Signaling by BMP	Reactome	1	BMPR2	28	13	32.99	2.990e-2	1.285e-1