

GeDiPNet Cluster 523 -- 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: 2026-10-20 00:03:20

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Defective PMM2 causes PMM2-CDG (CDG-1a)	Reactome	1	PMM2	1	16	750.63	1.332e-3	1.409e-2
RNA Polymerase II Transcription Elongation	Reactome	2	MLLT1, SUPT16H	59	16	25.44	2.724e-3	2.384e-2
Formation of RNA Pol II elongation complex	Reactome	2	MLLT1, SUPT16H	61	16	24.61	2.909e-3	2.492e-2
Synthesis of GDP-mannose	Reactome	1	PMM2	3	16	250.21	3.992e-3	3.122e-2
SUMOylation of DNA methylation proteins	Reactome	1	DNMT1	4	16	187.66	5.319e-3	3.801e-2
RNA Polymerase II Pre-transcription Events	Reactome	2	MLLT1, SUPT16H	84	16	17.87	5.443e-3	3.862e-2
Phosphonate and phosphinate metabolism	KEGG	1	PCYT2	6	16	125.10	7.968e-3	4.940e-2
Transport and synthesis of PAPS	Reactome	1	SLC35B2	6	16	125.10	7.968e-3	4.940e-2
Transport of nucleotide sugars	Reactome	1	SLC35B2	9	16	83.40	1.193e-2	6.320e-2
Presynaptic depolarization and calcium channel opening	Reactome	1	CACNA2D1	12	16	62.55	1.588e-2	7.505e-2
Synthesis of PE	Reactome	1	PCYT2	12	16	62.55	1.588e-2	7.505e-2
Caspase-mediated cleavage of cytoskeletal proteins	Reactome	1	ADD1	12	16	62.55	1.588e-2	7.505e-2
TP53 Regulates Transcription of Caspase Activators and Caspases	Reactome	1	PIDD1	12	16	62.55	1.588e-2	7.505e-2
Purine salvage	Reactome	1	DGUOK	13	16	57.74	1.719e-2	7.864e-2
KSRP (KHSRP) binds and destabilizes mRNA	Reactome	1	EXOSC9	15	16	50.04	1.981e-2	8.517e-2