

GeDiPNet Cluster 514 -- 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 00:02:42

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Enzymatic degradation of Dopamine by monoamine oxidase	Reactome	1	COMT	2	21	285.95	3.494e-3	2.829e-2
Enzymatic degradation of dopamine by COMT	Reactome	1	COMT	3	21	190.63	5.237e-3	3.760e-2
Reelin signalling pathway	Reactome	1	DAB1	5	21	114.38	8.714e-3	5.219e-2
Protein repair	Reactome	1	MSRA	6	21	95.32	1.045e-2	5.837e-2
Sperm Motility And Taxes	Reactome	1	CATSPER3	9	21	63.54	1.563e-2	7.438e-2
Purine metabolism	KEGG	2	NT5C1B, PDE8A	128	21	8.94	2.073e-2	8.765e-2
Purine catabolism	Reactome	1	NT5C1B	12	21	47.66	2.079e-2	8.765e-2
TP53 regulates transcription of several additional cell death genes whose specific roles in p53-dependent apoptosis remain uncertain	Reactome	1	PERP	14	21	40.85	2.422e-2	9.574e-2
Methylation	Reactome	1	COMT	14	21	40.85	2.422e-2	9.574e-2
Spinocerebellar ataxia	KEGG	2	DAB1, TWNK	144	21	7.94	2.583e-2	9.940e-2
Virion - Lassa virus and SFTS virus	KEGG	1	PCDH7	17	21	33.64	2.933e-2	1.069e-1
Homologous DNA Pairing and Strand Exchange	Reactome	1	RMI2	25	21	22.88	4.285e-2	1.326e-1
Resolution of D-loop Structures through Synthesis-Dependent Strand Annealing (SDSA)	Reactome	1	RMI2	26	21	22.00	4.453e-2	1.356e-1
Folate biosynthesis	KEGG	1	PCBD2	28	21	20.43	4.787e-2	1.413e-1
Resolution of D-loop Structures through Holliday Junction Intermediates	Reactome	1	RMI2	33	21	17.33	5.619e-2	1.548e-1