

GeDiPNet Cluster 181 -- 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 06:25:59

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Nucleotide metabolism	KEGG	7	NT5C1B, DGUOK, DTYMK, RRM2B, TK2, TYMP, GUK1	85	50	19.78	5.405e-8	3.824e-6
Pyrimidine metabolism	KEGG	5	NT5C1B, DTYMK, RRM2B, TK2, TYMP	58	50	20.71	3.954e-6	1.564e-4
Purine metabolism	KEGG	5	NT5C1B, PDE8A, DGUOK, RRM2B, GUK1	128	50	9.38	1.835e-4	3.665e-3
Interconversion of nucleotide di- and triphosphates	Reactome	3	DTYMK, RRM2B, GUK1	29	50	24.85	2.299e-4	4.365e-3
Base excision repair	KEGG	3	POLG, POLG2, LIG3	44	50	16.38	7.974e-4	1.149e-2
Pyrimidine salvage	Reactome	2	TK2, TYMP	11	50	43.67	9.121e-4	1.266e-2
Transcriptional activation of mitochondrial biogenesis	Reactome	3	POLG2, TWNK, TFAM	51	50	14.13	1.228e-3	1.582e-2
Spinocerebellar ataxia	KEGG	4	DAB1, TWNK, SLC25A4, OPA1	144	50	6.67	2.977e-3	3.060e-2
Citric acid cycle (TCA cycle)	Reactome	2	SUCLA2, SUCLG1	22	50	21.84	3.721e-3	3.585e-2
Drug metabolism - other enzymes	KEGG	3	RRM2B, TK2, TYMP	81	50	8.90	4.612e-3	4.153e-2
Citrate cycle (TCA cycle)	KEGG	2	SUCLA2, SUCLG1	30	50	16.01	6.859e-3	5.397e-2
Propanoate metabolism	KEGG	2	SUCLA2, SUCLG1	32	50	15.01	7.780e-3	5.861e-2
Regulation of Apoptosis	Reactome	1	OPA1	2	50	120.10	8.309e-3	6.108e-2
Enzymatic degradation of Dopamine by monoamine oxidase	Reactome	1	COMT	2	50	120.10	8.309e-3	6.108e-2
Enzymatic degradation of dopamine by COMT	Reactome	1	COMT	3	50	80.07	1.244e-2	7.779e-2