

GeDiPNet Cluster 494 -- 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: 2026-10-19 23:21:21

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Netrin-1 signaling	Reactome	2	DCC, NTN1	8	5	600.50	3.879e-6	1.329e-4
DCC mediated attractive signaling	Reactome	2	DCC, NTN1	11	5	436.73	7.615e-6	2.329e-4
Axon guidance	KEGG	3	DCC, NTN1, ROBO3	183	5	39.38	3.403e-5	8.054e-4
ROBO receptors bind AKAP5	Reactome	1	ROBO3	3	5	800.67	1.249e-3	1.343e-2
Regulation of commissural axon pathfinding by SLIT and ROBO	Reactome	1	ROBO3	3	5	800.67	1.249e-3	1.343e-2
Caspase activation via Dependence Receptors in the absence of ligand	Reactome	1	DCC	4	5	600.50	1.664e-3	1.665e-2
Retrograde neurotrophin signalling	Reactome	1	DNAL4	11	5	218.36	4.572e-3	3.438e-2
Homologous DNA Pairing and Strand Exchange	Reactome	1	RAD51	25	5	96.08	1.037e-2	5.824e-2
Resolution of D-loop Structures through Synthesis-Dependent Strand Annealing (SDSA)	Reactome	1	RAD51	26	5	92.38	1.078e-2	5.963e-2
Resolution of D-loop Structures through Holliday Junction Intermediates	Reactome	1	RAD51	33	5	72.79	1.367e-2	6.870e-2
Transcriptional Regulation by E2F6	Reactome	1	RAD51	35	5	68.63	1.449e-2	7.115e-2
HDR through Single Strand Annealing (SSA)	Reactome	1	RAD51	37	5	64.92	1.531e-2	7.347e-2
Presynaptic phase of homologous DNA pairing and strand exchange	Reactome	1	RAD51	39	5	61.59	1.613e-2	7.583e-2
Homologous recombination	KEGG	1	RAD51	41	5	58.59	1.696e-2	7.797e-2
Pathways in cancer	KEGG	2	DCC, RAD51	533	5	9.01	1.798e-2	8.066e-2