

GeDiPNet Cluster 189 -- 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: 2026-10-09 03:30:08. · Rows: 15 · Generated: 2026-10-09 08:01:24

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Peroxisome	KEGG	3	IDH2, SOD2, IDH1	83	10	43.41	3.688e-5	9.667e-4
Homologous DNA Pairing and Strand Exchange	Reactome	2	BRCA2, PALB2	25	10	96.08	1.853e-4	3.583e-3
Resolution of D-loop Structures through Synthesis-Dependent Strand Annealing (SDSA)	Reactome	2	BRCA2, PALB2	26	10	92.38	2.007e-4	3.810e-3
Citrate cycle (TCA cycle)	KEGG	2	IDH2, IDH1	30	10	80.07	2.681e-4	4.802e-3
2-Oxocarboxylic acid metabolism	KEGG	2	IDH2, IDH1	33	10	72.79	3.250e-4	5.606e-3
Resolution of D-loop Structures through Holliday Junction Intermediates	Reactome	2	BRCA2, PALB2	33	10	72.79	3.250e-4	5.606e-3
Homologous recombination	KEGG	2	BRCA2, PALB2	41	10	58.59	5.029e-4	7.907e-3
HDR through Homologous Recombination (HRR)	Reactome	2	BRCA2, PALB2	48	10	50.04	6.896e-4	1.011e-2
Transcriptional activation of mitochondrial biogenesis	Reactome	2	IDH2, SOD2	51	10	47.10	7.785e-4	1.109e-2
Abnormal conversion of 2-oxoglutarate to 2-hydroxyglutarate	Reactome	1	IDH1	1	10	1201.00	8.326e-4	1.162e-2
NADPH regeneration	Reactome	1	IDH1	1	10	1201.00	8.326e-4	1.162e-2
Fanconi anemia pathway	KEGG	2	BRCA2, PALB2	54	10	44.48	8.726e-4	1.202e-2
Glutathione metabolism	KEGG	2	IDH2, IDH1	59	10	40.71	1.041e-3	1.384e-2
Central carbon metabolism in cancer	KEGG	2	IDH2, IDH1	71	10	33.83	1.504e-3	1.838e-2
Biosynthesis of amino acids	KEGG	2	IDH2, IDH1	75	10	32.03	1.676e-3	1.999e-2