

GeDiPNet Cluster 200 -- 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 11:31:29

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Homologous DNA Pairing and Strand Exchange	Reactome	2	BRCA2, PALB2	25	8	120.10	1.156e-4	2.516e-3
Resolution of D-loop Structures through Synthesis-Dependent Strand Annealing (SDSA)	Reactome	2	BRCA2, PALB2	26	8	115.48	1.252e-4	2.685e-3
Citrate cycle (TCA cycle)	KEGG	2	IDH2, IDH1	30	8	100.08	1.673e-4	3.395e-3
2-Oxocarboxylic acid metabolism	KEGG	2	IDH2, IDH1	33	8	90.98	2.029e-4	3.948e-3
Resolution of D-loop Structures through Holliday Junction Intermediates	Reactome	2	BRCA2, PALB2	33	8	90.98	2.029e-4	3.948e-3
Homologous recombination	KEGG	2	BRCA2, PALB2	41	8	73.23	3.143e-4	5.562e-3
HDR through Homologous Recombination (HRR)	Reactome	2	BRCA2, PALB2	48	8	62.55	4.313e-4	7.101e-3
Fanconi anemia pathway	KEGG	2	BRCA2, PALB2	54	8	55.60	5.461e-4	8.522e-3
Glutathione metabolism	KEGG	2	IDH2, IDH1	59	8	50.89	6.518e-4	9.795e-3
Abnormal conversion of 2-oxoglutarate to 2-hydroxyglutarate	Reactome	1	IDH1	1	8	1501.25	6.661e-4	9.955e-3
NADPH regeneration	Reactome	1	IDH1	1	8	1501.25	6.661e-4	9.955e-3
Central carbon metabolism in cancer	KEGG	2	IDH2, IDH1	71	8	42.29	9.429e-4	1.299e-2
Biosynthesis of amino acids	KEGG	2	IDH2, IDH1	75	8	40.03	1.052e-3	1.409e-2
Pancreatic cancer	KEGG	2	BRAF, BRCA2	77	8	38.99	1.108e-3	1.465e-2
Peroxisome	KEGG	2	IDH2, IDH1	83	8	36.17	1.286e-3	1.638e-2