

GeDiPNet Cluster 583 -- 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 00:02:38

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Oncogene Induced Senescence	Reactome	3	ERF, MDM4, TP53	33	36	30.33	1.269e-4	2.285e-3
Stabilization of p53	Reactome	2	MDM4, TP53	11	36	60.66	4.724e-4	6.397e-3
Central carbon metabolism in cancer	KEGG	3	FGFR2, FGFR1, TP53	71	36	14.10	1.229e-3	1.327e-2
Regulation of TP53 Activity through Methylation	Reactome	2	MDM4, TP53	19	36	35.12	1.447e-3	1.498e-2
Signaling by FGFR1 amplification mutants	Reactome	1	FGFR1	1	36	333.61	2.998e-3	2.538e-2
Signaling by FGFR2 amplification mutants	Reactome	1	FGFR2	1	36	333.61	2.998e-3	2.538e-2
Signaling by FGFR2 fusions	Reactome	1	FGFR2	1	36	333.61	2.998e-3	2.538e-2
Defective SLC6A18 may confer susceptibility to iminoglycinuria and/or hyperglycinuria	Reactome	1	SLC6A18	1	36	333.61	2.998e-3	2.538e-2
Prostate cancer	KEGG	3	FGFR2, FGFR1, TP53	98	36	10.21	3.095e-3	2.604e-2
Regulation of TP53 Degradation	Reactome	2	MDM4, TP53	36	36	18.53	5.162e-3	3.730e-2
Regulation of TP53 Expression	Reactome	1	TP53	2	36	166.81	5.986e-3	4.098e-2
PI3K Cascade	Reactome	2	FGFR2, FGFR1	39	36	17.11	6.038e-3	4.123e-2
Signaling by plasma membrane FGFR1 fusions	Reactome	1	FGFR1	3	36	111.20	8.966e-3	5.313e-2
FGFR1c and Klotho ligand binding and activation	Reactome	1	FGFR1	3	36	111.20	8.966e-3	5.313e-2
Gastric cancer	KEGG	3	FGFR2, TERT, TP53	150	36	6.67	1.009e-2	5.710e-2