

GeDiPNet Cluster 640 -- 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 00:02:39

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Breakdown of the nuclear lamina	Reactome	1	LMNA	3	4	1000.83	9.989e-4	1.132e-2
Nuclear Envelope Breakdown	Reactome	1	LMNA	9	4	333.61	2.995e-3	2.538e-2
Depolymerisation of the Nuclear Lamina	Reactome	1	LMNA	15	4	200.17	4.987e-3	3.635e-2
Initiation of Nuclear Envelope (NE) Reformation	Reactome	1	LMNA	19	4	158.03	6.314e-3	4.251e-2
Terpenoid backbone biosynthesis	KEGG	1	ZMPSTE24	23	4	130.54	7.639e-3	4.803e-2
Activation of Matrix Metalloproteinases	Reactome	1	MMP9	33	4	90.98	1.095e-2	6.008e-2
Signaling by SCF-KIT	Reactome	1	MMP9	37	4	81.15	1.227e-2	6.447e-2
Bladder cancer	KEGG	1	MMP9	41	4	73.23	1.359e-2	6.854e-2
XBP1(S) activates chaperone genes	Reactome	1	LMNA	50	4	60.05	1.655e-2	7.673e-2
EPH-ephrin mediated repulsion of cells	Reactome	1	MMP9	50	4	60.05	1.655e-2	7.673e-2
Assembly of collagen fibrils and other multimeric structures	Reactome	1	MMP9	51	4	58.87	1.688e-2	7.780e-2
Collagen degradation	Reactome	1	MMP9	52	4	57.74	1.721e-2	7.870e-2
Extra-nuclear estrogen signaling	Reactome	1	MMP9	58	4	51.77	1.918e-2	8.356e-2
Signaling by BRAF and RAF fusions	Reactome	1	LMNA	67	4	44.81	2.213e-2	9.093e-2
Degradation of the extracellular matrix	Reactome	1	MMP9	70	4	42.89	2.311e-2	9.306e-2