

GeDiPNet Cluster 437 -- 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](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 00:02:52

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Degradation of the extracellular matrix	Reactome	3	FBN1, MMP2, MMP9	70	7	73.53	6.527e-6	2.044e-4
Activation of Matrix Metalloproteinases	Reactome	2	MMP2, MMP9	33	7	103.98	1.524e-4	2.648e-3
Bladder cancer	KEGG	2	MMP2, MMP9	41	7	83.69	2.362e-4	3.742e-3
EPH-ephrin mediated repulsion of cells	Reactome	2	MMP2, MMP9	50	7	68.63	3.520e-4	5.090e-3
Collagen degradation	Reactome	2	MMP2, MMP9	52	7	65.99	3.808e-4	5.410e-3
Extra-nuclear estrogen signaling	Reactome	2	MMP2, MMP9	58	7	59.16	4.739e-4	6.412e-3
Endocrine resistance	KEGG	2	MMP2, MMP9	99	7	34.66	1.375e-3	1.443e-2
Interleukin-4 and Interleukin-13 signaling	Reactome	2	MMP2, MMP9	108	7	31.77	1.634e-3	1.642e-2
Metabolism of vitamin K	Reactome	1	VKORC1	3	7	571.90	1.748e-3	1.725e-2
Leukocyte transendothelial migration	KEGG	2	MMP2, MMP9	116	7	29.58	1.882e-3	1.821e-2
Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)	Reactome	2	FBN1, MMP2	125	7	27.45	2.181e-3	2.030e-2
Ion influx/efflux at host-pathogen interface	Reactome	1	ATP7A	4	7	428.93	2.330e-3	2.129e-2
Relaxin signaling pathway	KEGG	2	MMP2, MMP9	130	7	26.40	2.356e-3	2.147e-2
Pathways in cancer	KEGG	3	MMP2, MMP9, VHL	533	7	9.66	2.661e-3	2.343e-2
Estrogen signaling pathway	KEGG	2	MMP2, MMP9	139	7	24.69	2.689e-3	2.359e-2