

GeDiPNet Cluster 403 -- 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: 2026-10-08 03:30:07. · Rows: 15 · Generated: 2026-10-08 18:38:29

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Collagen chain trimerization	Reactome	4	COL12A1, COL6A1, COL6A2, COL6A3	44	6	181.97	2.338e-9	2.311e-7
Assembly of collagen fibrils and other multimeric structures	Reactome	4	COL12A1, COL6A1, COL6A2, COL6A3	51	6	156.99	4.299e-9	3.989e-7
Collagen degradation	Reactome	4	COL12A1, COL6A1, COL6A2, COL6A3	52	6	153.97	4.657e-9	4.278e-7
Collagen biosynthesis and modifying enzymes	Reactome	4	COL12A1, COL6A1, COL6A2, COL6A3	67	6	119.50	1.316e-8	1.078e-6
Protein digestion and absorption	KEGG	4	COL12A1, COL6A1, COL6A2, COL6A3	103	6	77.73	7.553e-8	5.123e-6
NCAM1 interactions	Reactome	3	COL6A1, COL6A2, COL6A3	21	6	285.95	9.184e-8	6.099e-6
Signaling by PDGF	Reactome	3	COL6A1, COL6A2, COL6A3	33	6	181.97	3.759e-7	2.092e-5
ECM proteoglycans	Reactome	3	COL6A1, COL6A2, COL6A3	51	6	117.75	1.430e-6	6.659e-5
Cytoskeleton in muscle cells	KEGG	4	COL6A1, COL6A2, COL6A3, LMNA	232	6	34.51	1.975e-6	8.782e-5
Integrin cell surface interactions	Reactome	3	COL6A1, COL6A2, COL6A3	81	6	74.14	5.826e-6	2.189e-4
ECM-receptor interaction	KEGG	3	COL6A1, COL6A2, COL6A3	89	6	67.47	7.743e-6	2.779e-4
Focal adhesion	KEGG	3	COL6A1, COL6A2, COL6A3	203	6	29.58	9.166e-5	2.116e-3
Human papillomavirus infection	KEGG	3	COL6A1, COL6A2, COL6A3	333	6	18.03	3.970e-4	6.804e-3
PI3K-Akt signaling pathway	KEGG	3	COL6A1, COL6A2, COL6A3	361	6	16.63	5.035e-4	8.170e-3
Breakdown of the nuclear lamina	Reactome	1	LMNA	3	6	667.22	1.498e-3	1.890e-2