

GeDiPNet Cluster 511 -- 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: 2026-10-19 23:20:29

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Transport of connexons to the plasma membrane	Reactome	1	GJB2	1	5	2402.00	4.163e-4	5.794e-3
OAS antiviral response	Reactome	1	FLNA	9	5	266.89	3.742e-3	2.976e-2
Cell-extracellular matrix interactions	Reactome	1	FLNA	12	5	200.17	4.987e-3	3.635e-2
GP1b-IX-V activation signalling	Reactome	1	FLNA	12	5	200.17	4.987e-3	3.635e-2
RHO GTPases activate PAKs	Reactome	1	FLNA	23	5	104.43	9.540e-3	5.527e-2
Non-integrin membrane-ECM interactions	Reactome	1	COL11A2	24	5	100.08	9.953e-3	5.666e-2
MET activates PTK2 signaling	Reactome	1	COL11A2	30	5	80.07	1.243e-2	6.493e-2
Collagen chain trimerization	Reactome	1	COL11A2	44	5	54.59	1.819e-2	8.116e-2
Assembly of collagen fibrils and other multimeric structures	Reactome	1	COL11A2	51	5	47.10	2.106e-2	8.822e-2
Collagen degradation	Reactome	1	COL11A2	52	5	46.19	2.147e-2	8.925e-2
Collagen biosynthesis and modifying enzymes	Reactome	1	COL11A2	67	5	35.85	2.759e-2	1.031e-1
Recruitment and ATM-mediated phosphorylation of repair and signaling proteins at DNA double strand breaks	Reactome	1	EYA1	76	5	31.61	3.125e-2	1.106e-1
Protein digestion and absorption	KEGG	1	COL11A2	103	5	23.32	4.216e-2	1.314e-1
Platelet degranulation	Reactome	1	FLNA	123	5	19.53	5.018e-2	1.451e-1
Transcriptional misregulation in cancer	KEGG	1	EYA1	198	5	12.13	7.977e-2	1.890e-1