

GeDiPNet Cluster 229 -- 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: 2026-10-07 03:30:09. · Rows: 15 · Generated: 2026-10-07 06:28:35

Pathway	Source	Overlap Genes	Overlap Gene Names	Pathway Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
Type I hemidesmosome assembly	Reactome	11	ITGB4, PLEC, KRT14, KRT5, ITGA6, LAMB3, CD151, DST, LAMA3, LAMC2, COL17A1	11	34	353.24	1.530e-29	4.224e-26
Assembly of collagen fibrils and other multimeric structures	Reactome	10	ITGB4, PLEC, COL7A1, ITGA6, LAMB3, CD151, DST, LAMA3, LAMC2, COL17A1	51	34	69.26	9.071e-17	4.140e-14
Laminin interactions	Reactome	7	ITGB4, COL7A1, ITGA6, LAMB3, LAMA3, LAMC2, ITGA3	28	34	88.31	8.561e-13	1.895e-10
ECM-receptor interaction	KEGG	7	ITGB4, ITGA6, LAMB3, FREM2, LAMA3, LAMC2, ITGA3	89	34	27.78	4.417e-9	4.238e-7
Formation of the cornified envelope	Reactome	7	KRT14, KRT5, PKP1, DSP, JUP, CSTA, KRT2	130	34	19.02	6.244e-8	4.353e-6
Anchoring fibril formation	Reactome	4	COL7A1, LAMB3, LAMA3, LAMC2	15	34	94.20	7.147e-8	4.879e-6
MET activates PTK2 signaling	Reactome	4	LAMB3, LAMA3, LAMC2, ITGA3	30	34	47.10	1.392e-6	6.508e-5
Keratinization	Reactome	6	KRT14, KRT5, PKP1, DSP, JUP, KRT2	152	34	13.94	3.737e-6	1.496e-4
Arrhythmogenic right ventricular cardiomyopathy	KEGG	5	ITGB4, ITGA6, ITGA3, DSP, JUP	86	34	20.54	3.956e-6	1.564e-4
Small cell lung cancer	KEGG	5	ITGA6, LAMB3, LAMA3, LAMC2, ITGA3	93	34	18.99	5.821e-6	2.146e-4
Focal adhesion	KEGG	6	ITGB4, ITGA6, LAMB3, LAMA3, LAMC2, ITGA3	203	34	10.44	1.963e-5	5.893e-4
Cytoskeleton in muscle cells	KEGG	6	ITGB4, PLEC, ITGA6, ITGA3, DSP, JUP	232	34	9.14	4.164e-5	1.102e-3
Toxoplasmosis	KEGG	4	ITGA6, LAMB3, LAMA3, LAMC2	112	34	12.62	2.679e-4	4.916e-3
Human papillomavirus infection	KEGG	6	ITGB4, ITGA6, LAMB3, LAMA3, LAMC2, ITGA3	333	34	6.36	3.030e-4	5.406e-3
Apoptotic cleavage of cell adhesion proteins	Reactome	2	PKP1, DSP	11	34	64.22	4.211e-4	6.964e-3