

## GeDiPNet Cluster 390 -- 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](https://gedipnet.bicnirrh.res.in/scripts/build_cluster_enrichment.php) on [gedipnet.bicnirrh.res.in](https://gedipnet.bicnirrh.res.in). Data as of: 2026-10-07 03:30:09. · Rows: 15 · Generated: 2026-10-07 10:47:42

| Pathway                                                                                                                     | Source   | Overlap Genes | Overlap Gene Names                                   | Pathway Gene Count | Cluster Gene Count | Fold Enrichment | P-value   | FDR Q-value |
|-----------------------------------------------------------------------------------------------------------------------------|----------|---------------|------------------------------------------------------|--------------------|--------------------|-----------------|-----------|-------------|
| Assembly of collagen fibrils and other multimeric structures                                                                | Reactome | 7             | COL17A1, LAMB3, MMP20, COL7A1, LAMC2, COL1A1, COL1A2 | 51                 | 31                 | 53.18           | 3.948e-11 | 6.229e-9    |
| Anchoring fibril formation                                                                                                  | Reactome | 5             | LAMB3, COL7A1, LAMC2, COL1A1, COL1A2                 | 15                 | 31                 | 129.14          | 2.409e-10 | 3.174e-8    |
| ECM-receptor interaction                                                                                                    | KEGG     | 6             | ITGB6, LAMB3, LAMC2, DSPP, COL1A1, COL1A2            | 89                 | 31                 | 26.12           | 8.860e-8  | 5.898e-6    |
| Post-translational protein phosphorylation                                                                                  | Reactome | 6             | AMBN, AMELX, ENAM, FAM20A, FAM20C, AMTN              | 108                | 31                 | 21.52           | 2.820e-7  | 1.618e-5    |
| Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs) | Reactome | 6             | AMBN, AMELX, ENAM, FAM20A, FAM20C, AMTN              | 125                | 31                 | 18.60           | 6.704e-7  | 3.439e-5    |
| MET activates PTK2 signaling                                                                                                | Reactome | 4             | LAMB3, LAMC2, COL1A1, COL1A2                         | 30                 | 31                 | 51.66           | 9.497e-7  | 4.651e-5    |
| Type I hemidesmosome assembly                                                                                               | Reactome | 3             | COL17A1, LAMB3, LAMC2                                | 11                 | 31                 | 105.66          | 2.534e-6  | 1.083e-4    |
| Collagen chain trimerization                                                                                                | Reactome | 4             | COL17A1, COL7A1, COL1A1, COL1A2                      | 44                 | 31                 | 35.22           | 4.587e-6  | 1.774e-4    |
| Extracellular matrix organization                                                                                           | Reactome | 3             | COL7A1, COL1A1, COL1A2                               | 15                 | 31                 | 77.48           | 6.938e-6  | 2.471e-4    |
| ECM proteoglycans                                                                                                           | Reactome | 4             | ITGB6, DSPP, COL1A1, COL1A2                          | 51                 | 31                 | 30.39           | 8.339e-6  | 2.880e-4    |
| Collagen degradation                                                                                                        | Reactome | 4             | MMP20, COL7A1, COL1A1, COL1A2                        | 52                 | 31                 | 29.80           | 9.017e-6  | 3.084e-4    |
| Collagen biosynthesis and modifying enzymes                                                                                 | Reactome | 4             | COL17A1, COL7A1, COL1A1, COL1A2                      | 67                 | 31                 | 23.13           | 2.485e-5  | 7.134e-4    |
| Laminin interactions                                                                                                        | Reactome | 3             | LAMB3, COL7A1, LAMC2                                 | 28                 | 31                 | 41.51           | 4.883e-5  | 1.253e-3    |
| Integrin cell surface interactions                                                                                          | Reactome | 4             | ITGB6, COL7A1, COL1A1, COL1A2                        | 81                 | 31                 | 19.13           | 5.260e-5  | 1.333e-3    |
| Protein digestion and absorption                                                                                            | KEGG     | 4             | COL17A1, COL7A1, COL1A1, COL1A2                      | 103                | 31                 | 15.05           | 1.343e-4  | 2.845e-3    |