

## GeDiPNet Cluster 553 -- 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](http://gedipnet.bicnirrh.res.in). Data as of: 2026-10-20 03:30:09. · Rows: 15 · Generated: 2026-10-19 23:22:00

| Pathway                                         | Source   | Overlap Genes | Overlap Gene Names | Pathway Gene Count | Cluster Gene Count | Fold Enrichment | P-value  | FDR Q-value |
|-------------------------------------------------|----------|---------------|--------------------|--------------------|--------------------|-----------------|----------|-------------|
| Molybdenum cofactor biosynthesis                | Reactome | 2             | MOCS1, MOCS2       | 6                  | 4                  | 1000.83         | 1.247e-6 | 5.046e-5    |
| Folate biosynthesis                             | KEGG     | 2             | MOCS1, MOCS2       | 28                 | 4                  | 214.46          | 3.136e-5 | 7.518e-4    |
| Virion - Rotavirus                              | KEGG     | 1             | ITGA2              | 2                  | 4                  | 1501.25         | 6.660e-4 | 8.310e-3    |
| Biosynthesis of cofactors                       | KEGG     | 2             | MOCS1, MOCS2       | 154                | 4                  | 38.99           | 9.637e-4 | 1.102e-2    |
| Cytoskeleton in muscle cells                    | KEGG     | 2             | DAAM2, ITGA2       | 232                | 4                  | 25.88           | 2.173e-3 | 2.024e-2    |
| Sulfur relay system                             | KEGG     | 1             | MOCS2              | 8                  | 4                  | 375.31          | 2.662e-3 | 2.343e-2    |
| Syndecan interactions                           | Reactome | 1             | ITGA2              | 16                 | 4                  | 187.66          | 5.319e-3 | 3.801e-2    |
| Laminin interactions                            | Reactome | 1             | ITGA2              | 28                 | 4                  | 107.23          | 9.294e-3 | 5.428e-2    |
| MET activates PTK2 signaling                    | Reactome | 1             | ITGA2              | 30                 | 4                  | 100.08          | 9.956e-3 | 5.666e-2    |
| ECM proteoglycans                               | Reactome | 1             | ITGA2              | 51                 | 4                  | 58.87           | 1.688e-2 | 7.780e-2    |
| Integrin cell surface interactions              | Reactome | 1             | ITGA2              | 81                 | 4                  | 37.07           | 2.671e-2 | 1.011e-1    |
| Arrhythmogenic right ventricular cardiomyopathy | KEGG     | 1             | ITGA2              | 86                 | 4                  | 34.91           | 2.834e-2 | 1.046e-1    |
| ECM-receptor interaction                        | KEGG     | 1             | ITGA2              | 89                 | 4                  | 33.74           | 2.932e-2 | 1.069e-1    |
| Small cell lung cancer                          | KEGG     | 1             | ITGA2              | 93                 | 4                  | 32.28           | 3.062e-2 | 1.097e-1    |
| Hypertrophic cardiomyopathy                     | KEGG     | 1             | ITGA2              | 99                 | 4                  | 30.33           | 3.257e-2 | 1.134e-1    |