

## GeDiPNet Cluster 194 -- 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 09:35:58

| Pathway                                                                                                                     | Source   | Overlap Genes | Overlap Gene Names                               | Pathway Gene Count | Cluster Gene Count | Fold Enrichment | P-value  | FDR Q-value |
|-----------------------------------------------------------------------------------------------------------------------------|----------|---------------|--------------------------------------------------|--------------------|--------------------|-----------------|----------|-------------|
| Diabetic cardiomyopathy                                                                                                     | KEGG     | 8             | AGT, ATP2A2, INS, RYR2, SLC25A4, G6PD, AGER, ACE | 205                | 34                 | 13.78           | 7.797e-8 | 5.251e-6    |
| Hypertrophic cardiomyopathy                                                                                                 | KEGG     | 6             | AGT, ATP2A2, IGF1, RYR2, TNF, ACE                | 99                 | 34                 | 21.41           | 3.005e-7 | 1.712e-5    |
| Renin-angiotensin system                                                                                                    | KEGG     | 4             | AGT, AGTR2, KLK1, ACE                            | 23                 | 34                 | 61.43           | 4.563e-7 | 2.471e-5    |
| Hormone signaling                                                                                                           | KEGG     | 7             | AGT, AGTR2, IGF1, INS, LEPR, SLC40A1, POMC       | 219                | 34                 | 11.29           | 2.156e-6 | 9.373e-5    |
| Scavenging of heme from plasma                                                                                              | Reactome | 3             | APOA1, HP, ALB                                   | 13                 | 34                 | 81.52           | 5.815e-6 | 2.145e-4    |
| Dilated cardiomyopathy                                                                                                      | KEGG     | 5             | AGT, ATP2A2, IGF1, RYR2, TNF                     | 105                | 34                 | 16.82           | 1.056e-5 | 3.508e-4    |
| Peptide ligand-binding receptors                                                                                            | Reactome | 5             | AGT, AGTR2, POMC, BDKRB1, BDKRB2                 | 106                | 34                 | 16.66           | 1.106e-5 | 3.647e-4    |
| Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs) | Reactome | 5             | APOA1, IGF1, KLK1, SPP1, ALB                     | 125                | 34                 | 14.13           | 2.463e-5 | 7.081e-4    |
| G alpha (i) signalling events                                                                                               | Reactome | 6             | AGT, AGTR2, POMC, BDKRB1, BDKRB2, S1PR1          | 249                | 34                 | 8.51            | 6.178e-5 | 1.515e-3    |
| Neuroactive ligand-receptor interaction                                                                                     | KEGG     | 7             | AGT, AGTR2, LEPR, POMC, BDKRB1, BDKRB2, S1PR1    | 370                | 34                 | 6.68            | 6.522e-5 | 1.582e-3    |
| Calcium signaling pathway                                                                                                   | KEGG     | 6             | ATP2A2, RYR2, SLC25A4, BDKRB1, BDKRB2, RYR1      | 254                | 34                 | 8.34            | 6.899e-5 | 1.654e-3    |
| Advanced glycosylation endproduct receptor signaling                                                                        | Reactome | 2             | AGER, S100B                                      | 8                  | 34                 | 88.31           | 2.155e-4 | 4.145e-3    |
| Interleukin-4 and Interleukin-13 signaling                                                                                  | Reactome | 4             | HMOX1, TNF, POMC, S1PR1                          | 108                | 34                 | 13.08           | 2.330e-4 | 4.409e-3    |
| Pathways of neurodegeneration - multiple diseases                                                                           | KEGG     | 7             | ATP2A2, RYR2, SLC25A4, TNF, SOD1, AGER, RYR1     | 480                | 34                 | 5.15            | 3.279e-4 | 5.753e-3    |
| HDL remodeling                                                                                                              | Reactome | 2             | APOA1, ALB                                       | 10                 | 34                 | 70.65           | 3.451e-4 | 5.983e-3    |