

## GeDiPNet Cluster 66 -- 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: 2026-10-08 03:30:07. · Rows: 15 · Generated: 2026-10-08 03:10:47

| Pathway                                     | Source   | Overlap Genes | Overlap Gene Names                                                       | Pathway Gene Count | Cluster Gene Count | Fold Enrichment | P-value   | FDR Q-value |
|---------------------------------------------|----------|---------------|--------------------------------------------------------------------------|--------------------|--------------------|-----------------|-----------|-------------|
| Urea cycle                                  | Reactome | 7             | ASS1, ARG1, ASL, NAGS, SLC25A15, CPS1, OTC                               | 10                 | 36                 | 233.53          | 1.394e-16 | 5.526e-14   |
| Biosynthesis of amino acids                 | KEGG     | 10            | ASS1, ARG1, ASL, CTH, MAT1A, NAGS, PHGDH, PSPH, CPS1, OTC                | 75                 | 36                 | 44.48           | 1.081e-14 | 3.108e-12   |
| Arginine biosynthesis                       | KEGG     | 7             | ASS1, ARG1, ASL, NAGS, CPS1, OTC, GLUD1                                  | 23                 | 36                 | 101.53          | 2.771e-13 | 6.235e-11   |
| Metabolic pathways                          | KEGG     | 22            | ASS1, AHCY, ALDH6A1, ARG1, ASL, CTH, GAMT, GCLC, HMGCL, IVD, MAT1A, NAGS | 1563               | 36                 | 4.70            | 1.753e-11 | 2.835e-9    |
| Carbon metabolism                           | KEGG     | 7             | ALDH6A1, PCCA, PCCB, PHGDH, PSPH, CPS1, GLUD1                            | 115                | 36                 | 20.31           | 4.075e-8  | 2.947e-6    |
| Alanine, aspartate and glutamate metabolism | KEGG     | 5             | ASS1, ASL, CPS1, GLUD1, ALDH4A1                                          | 37                 | 36                 | 45.08           | 7.372e-8  | 5.019e-6    |
| Valine, leucine and isoleucine degradation  | KEGG     | 5             | ALDH6A1, HMGCL, IVD, PCCA, PCCB                                          | 48                 | 36                 | 34.75           | 2.828e-7  | 1.625e-5    |
| Cysteine and methionine metabolism          | KEGG     | 5             | AHCY, CTH, GCLC, MAT1A, PHGDH                                            | 52                 | 36                 | 32.08           | 4.256e-7  | 2.322e-5    |
| One carbon pool by folate                   | KEGG     | 4             | AHCY, CTH, MAT1A, TYMS                                                   | 38                 | 36                 | 35.12           | 4.667e-6  | 1.831e-4    |
| Glycine, serine and threonine metabolism    | KEGG     | 4             | CTH, GAMT, PHGDH, PSPH                                                   | 40                 | 36                 | 33.36           | 5.754e-6  | 2.169e-4    |
| Arginine and proline metabolism             | KEGG     | 4             | ARG1, GAMT, PRODH, ALDH4A1                                               | 50                 | 36                 | 26.69           | 1.419e-5  | 4.558e-4    |
| Proline catabolism                          | Reactome | 2             | PRODH, ALDH4A1                                                           | 3                  | 36                 | 222.41          | 2.616e-5  | 7.614e-4    |
| Propionyl-CoA catabolism                    | Reactome | 2             | PCCA, PCCB                                                               | 5                  | 36                 | 133.44          | 8.687e-5  | 2.021e-3    |
| Propanoate metabolism                       | KEGG     | 3             | ALDH6A1, PCCA, PCCB                                                      | 32                 | 36                 | 31.28           | 1.156e-4  | 2.545e-3    |
| Sulfur amino acid metabolism                | Reactome | 2             | AHCY, MAT1A                                                              | 6                  | 36                 | 111.20          | 1.301e-4  | 2.803e-3    |