

GeDiPNet Cluster 388 -- 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: 12 · Generated: 2026-10-07 20:12:20

| Pathway                                                             | Source   | Overlap Genes | Overlap Gene Names | Pathway Gene Count | Cluster Gene Count | Fold Enrichment | P-value  | FDR Q-value |
|---------------------------------------------------------------------|----------|---------------|--------------------|--------------------|--------------------|-----------------|----------|-------------|
| Platelet homeostasis                                                | Reactome | 1             | P2RX7              | 8                  | 2                  | 750.63          | 1.332e-3 | 1.681e-2    |
| Elevation of cytosolic Ca2+ levels                                  | Reactome | 1             | P2RX7              | 13                 | 2                  | 461.92          | 2.164e-3 | 2.417e-2    |
| Thiamine metabolism                                                 | KEGG     | 1             | ALPL               | 15                 | 2                  | 400.33          | 2.496e-3 | 2.686e-2    |
| The NLRP3 inflammasome                                              | Reactome | 1             | P2RX7              | 15                 | 2                  | 400.33          | 2.496e-3 | 2.686e-2    |
| Purinergic signaling in leishmaniasis infection                     | Reactome | 1             | P2RX7              | 24                 | 2                  | 250.21          | 3.993e-3 | 3.767e-2    |
| Folate biosynthesis                                                 | KEGG     | 1             | ALPL               | 28                 | 2                  | 214.46          | 4.658e-3 | 4.181e-2    |
| Post-translational modification: synthesis of GPI-anchored proteins | Reactome | 1             | ALPL               | 66                 | 2                  | 90.98           | 1.096e-2 | 7.246e-2    |
| Biosynthesis of cofactors                                           | KEGG     | 1             | ALPL               | 154                | 2                  | 38.99           | 2.548e-2 | 1.177e-1    |
| NOD-like receptor signaling pathway                                 | KEGG     | 1             | P2RX7              | 187                | 2                  | 32.11           | 3.090e-2 | 1.310e-1    |
| Calcium signaling pathway                                           | KEGG     | 1             | P2RX7              | 254                | 2                  | 23.64           | 4.185e-2 | 1.554e-1    |
| Neuroactive ligand-receptor interaction                             | KEGG     | 1             | P2RX7              | 370                | 2                  | 16.23           | 6.067e-2 | 1.894e-1    |
| Metabolic pathways                                                  | KEGG     | 1             | ALPL               | 1563               | 2                  | 3.84            | 2.434e-1 | 4.081e-1    |