

## GeDiPNet Cluster 622 -- Enriched GO Terms (Biological Process)

GO term enrichment: Biological Process terms (gene2go, human/tax\_id=9606 only), upper-tail hypergeometric test, fold enrichment = (overlap / cluster gene count) / (term gene count / universe size), Benjamini-Hochberg FDR-corrected. Top 15 terms per cluster by q-value. See scripts/build\_cluster\_go\_enrichment.php on gedipnet.bicnirrh.res.in. Data as of: 2026-10-20 03:23:14. · Rows: 15 · Generated: 2026-10-19 23:18:28

| GO Term                                                       | GO ID      | Overlap Genes | Overlap Gene Names | Term Gene Count | Cluster Gene Count | Fold Enrichment | P-value  | FDR Q-value |
|---------------------------------------------------------------|------------|---------------|--------------------|-----------------|--------------------|-----------------|----------|-------------|
| establishment of protein localization to extracellular region | GO:0035592 | 1             | LTBP2              | 3               | 2                  | 3114.50         | 3.211e-4 | 7.044e-3    |
| AMPA glutamate receptor clustering                            | GO:0097113 | 1             | CHRD1              | 5               | 2                  | 1868.70         | 5.351e-4 | 9.880e-3    |
| embryonic axis specification                                  | GO:0000578 | 1             | CHRD1              | 7               | 2                  | 1334.79         | 7.491e-4 | 1.230e-2    |
| excitatory chemical synaptic transmission                     | GO:0098976 | 1             | CHRD1              | 13              | 2                  | 718.73          | 1.391e-3 | 1.753e-2    |
| supramolecular fiber organization                             | GO:0097435 | 1             | LTBP2              | 16              | 2                  | 583.97          | 1.712e-3 | 1.958e-2    |
| synapse maturation                                            | GO:0060074 | 1             | CHRD1              | 16              | 2                  | 583.97          | 1.712e-3 | 1.958e-2    |
| eye development                                               | GO:0001654 | 1             | CHRD1              | 49              | 2                  | 190.68          | 5.238e-3 | 3.415e-2    |
| protein targeting                                             | GO:0006605 | 1             | LTBP2              | 49              | 2                  | 190.68          | 5.238e-3 | 3.415e-2    |
| protein secretion                                             | GO:0009306 | 1             | LTBP2              | 65              | 2                  | 143.75          | 6.945e-3 | 3.907e-2    |
| regulation of synaptic plasticity                             | GO:0048167 | 1             | CHRD1              | 69              | 2                  | 135.41          | 7.371e-3 | 4.026e-2    |
| system development                                            | GO:0048731 | 1             | CHRD1              | 74              | 2                  | 126.26          | 7.904e-3 | 4.160e-2    |
| negative regulation of BMP signaling pathway                  | GO:0030514 | 1             | CHRD1              | 75              | 2                  | 124.58          | 8.011e-3 | 4.175e-2    |
| BMP signaling pathway                                         | GO:0030509 | 1             | CHRD1              | 88              | 2                  | 106.18          | 9.396e-3 | 4.508e-2    |
| ossification                                                  | GO:0001503 | 1             | CHRD1              | 110             | 2                  | 84.94           | 1.174e-2 | 5.020e-2    |
| transforming growth factor beta receptor signaling pathway    | GO:0007179 | 1             | LTBP2              | 112             | 2                  | 83.42           | 1.195e-2 | 5.062e-2    |