

## GeDiPNet Cluster 228 -- 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: 2026-10-07 03:30:09. · Rows: 15 · Generated: 2026-10-07 16:49:15

| Pathway                                                  | Source   | Overlap Genes | Overlap Gene Names                                             | Pathway Gene Count | Cluster Gene Count | Fold Enrichment | P-value   | FDR Q-value |
|----------------------------------------------------------|----------|---------------|----------------------------------------------------------------|--------------------|--------------------|-----------------|-----------|-------------|
| Nicotine addiction                                       | KEGG     | 8             | GABRA1, GABRG2, GRIN1, GRIN2A, SLC32A1, GABRD, CACNA1A, GABRB3 | 41                 | 79                 | 29.66           | 1.956e-10 | 2.644e-8    |
| Phase 0 - rapid depolarisation                           | Reactome | 6             | SCN1A, SCN1B, SCN2A, SCN9A, SCN8A, FGF13                       | 44                 | 79                 | 20.73           | 3.865e-7  | 2.144e-5    |
| Synaptic vesicle cycle                                   | KEGG     | 7             | STXBP1, SLC6A1, STX1B, UNC13A, SLC32A1, CACNA1A, DNM1          | 79                 | 79                 | 13.47           | 8.060e-7  | 4.046e-5    |
| GABAergic synapse                                        | KEGG     | 7             | GABRA1, GABRG2, SLC6A1, SLC32A1, GABRD, CACNA1A, GABRB3        | 89                 | 79                 | 11.96           | 1.818e-6  | 8.108e-5    |
| Retrograde endocannabinoid signaling                     | KEGG     | 8             | GABRA1, GABRG2, PLCB1, SLC32A1, GABRD, CACNA1A, GABRB3, MAPK10 | 149                | 79                 | 8.16            | 5.763e-6  | 2.131e-4    |
| Morphine addiction                                       | KEGG     | 6             | GABRA1, GABRG2, SLC32A1, GABRD, CACNA1A, GABRB3                | 91                 | 79                 | 10.02           | 2.857e-5  | 8.000e-4    |
| GABA receptor activation                                 | Reactome | 3             | GABRA1, GABRG2, GABRB3                                         | 16                 | 79                 | 28.50           | 1.442e-4  | 3.017e-3    |
| Taste transduction                                       | KEGG     | 5             | GABRA1, SCN2A, SCN9A, PLCB1, CACNA1A                           | 86                 | 79                 | 8.84            | 2.489e-4  | 4.634e-3    |
| HCN channels                                             | Reactome | 2             | HCN1, HCN2                                                     | 4                  | 79                 | 76.01           | 2.542e-4  | 4.704e-3    |
| Spinocerebellar ataxia                                   | KEGG     | 6             | GRIN1, GRIN2A, PLCB1, RELN, CACNA1A, MAPK10                    | 144                | 79                 | 6.33            | 3.625e-4  | 6.211e-3    |
| Assembly and cell surface presentation of NMDA receptors | Reactome | 2             | GRIN1, GRIN2A                                                  | 6                  | 79                 | 50.68           | 6.300e-4  | 9.552e-3    |
| Cholinergic synapse                                      | KEGG     | 5             | KCNQ3, PLCB1, CHAT, CACNA1A, CHRNB4                            | 115                | 79                 | 6.61            | 9.460e-4  | 1.301e-2    |
| Dopaminergic synapse                                     | KEGG     | 5             | SCN1A, GRIN2A, PLCB1, CACNA1A, MAPK10                          | 132                | 79                 | 5.76            | 1.748e-3  | 2.068e-2    |
| GABA synthesis, release, reuptake and degradation        | Reactome | 2             | STXBP1, SLC32A1                                                | 13                 | 79                 | 23.39           | 3.179e-3  | 3.207e-2    |
| Regulation of insulin secretion                          | Reactome | 2             | SLC2A1, CACNA1A                                                | 16                 | 79                 | 19.00           | 4.829e-3  | 4.289e-2    |