

GeDiPNet Cluster 494 -- 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: 2026-10-20 00:01:21

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
anterior/posterior axon guidance	GO:0033564	2	DCC, NTN1	5	5	1494.96	5.726e-7	5.463e-5
neuron migration	GO:0001764	3	DCC, NTN1, ROBO3	132	5	84.94	3.410e-6	2.325e-4
axon guidance	GO:0007411	3	DCC, NTN1, ROBO3	192	5	58.40	1.052e-5	5.649e-4
response to glucoside	GO:1904631	1	RAD51	1	5	3737.40	2.676e-4	6.245e-3
regulation of glial cell migration	GO:1903975	1	NTN1	1	5	3737.40	2.676e-4	6.245e-3
axonogenesis	GO:0007409	2	DCC, NTN1	125	5	59.80	4.381e-4	8.683e-3
mitotic recombination-dependent replication fork processing	GO:1990426	1	RAD51	2	5	1868.70	5.351e-4	9.880e-3
positive regulation of axon guidance	GO:1902669	1	ROBO3	2	5	1868.70	5.351e-4	9.880e-3
spinal cord ventral commissure morphogenesis	GO:0021965	1	DCC	3	5	1245.80	8.025e-4	1.283e-2
dorsal/ventral axon guidance	GO:0033563	1	DCC	3	5	1245.80	8.025e-4	1.283e-2
negative regulation of negative chemotaxis	GO:0050925	1	ROBO3	3	5	1245.80	8.025e-4	1.283e-2
DNA recombinase assembly	GO:0000730	1	RAD51	3	5	1245.80	8.025e-4	1.283e-2
chemorepulsion of axon	GO:0061643	1	NTN1	3	5	1245.80	8.025e-4	1.283e-2
Cdc42 protein signal transduction	GO:0032488	1	NTN1	3	5	1245.80	8.025e-4	1.283e-2
cellular response to cisplatin	GO:0072719	1	RAD51	4	5	934.35	1.070e-3	1.514e-2