GeDiPNet Cluster 658 -- 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: 2026-10-22 03:23:16. · Rows: 10 · Generated: 2026-10-21 23:30:24

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
mRNA 3'-end processing by stem-loop binding and cleavage	GO:0006398	1	CPSF3	6	3	1038.17	9.630e-4	1.373e-2
co-transcriptional mRNA 3'-end processing, cleavage and polyadenylation pathway	GO:0180010	1	CPSF3	9	3	692.11	1.444e-3	1.721e-2
mRNA 3'-end processing	GO:0031124	1	CPSF3	27	3	230.70	4.329e-3	3.043e-2
positive regulation of G1/S transition of mitotic cell cycle	GO:1900087	1	CPSF3	51	3	122.14	8.166e-3	4.170e-2
synapse organization	GO:0050808	1	PCDHGC4	72	3	86.51	1.151e-2	4.883e-2
negative regulation of neuron apoptotic process	GO:0043524	1	PCDHGC4	160	3	38.93	2.547e-2	7.323e-2
homophilic cell adhesion via plasma membrane adhesion molecules	GO:0007156	1	PCDHGC4	167	3	37.30	2.657e-2	7.471e-2
mRNA processing	GO:0006397	1	CPSF3	410	3	15.19	6.439e-2	1.245e-1
nervous system development	GO:0007399	1	PCDHGC4	631	3	9.87	9.792e-2	1.615e-1
cell adhesion	GO:0007155	1	PCDHGC4	665	3	9.37	1.030e-1	1.673e-1