

GeDiPNet Cluster 318 -- 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: 2026-10-07 03:23:06. · Rows: 15 · Generated: 2026-10-07 15:52:53

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
ERBB2-EGFR signaling pathway	GO:0038134	3	BTC, AREG, EREG	8	35	200.22	3.349e-7	3.341e-5
ERBB4-ERBB4 signaling pathway	GO:0038138	2	BTC, EREG	6	35	177.97	5.088e-5	1.824e-3
heme B biosynthetic process	GO:0006785	2	FECH, ALAS2	10	35	106.78	1.519e-4	4.136e-3
epidermal growth factor receptor signaling pathway	GO:0007173	3	BTC, AREG, EREG	64	35	25.03	2.319e-4	5.603e-3
synaptic vesicle docking	GO:0016081	2	STX1A, UNC13C	13	35	82.14	2.624e-4	6.119e-3
intracellular copper ion homeostasis	GO:0006878	2	PRND, PRNP	18	35	59.32	5.117e-4	9.703e-3
positive regulation of phosphorylation	GO:0042327	2	AREG, EREG	20	35	53.39	6.339e-4	1.127e-2
vesicle docking	GO:0048278	2	STX1A, STX6	21	35	50.85	6.998e-4	1.197e-2
heme biosynthetic process	GO:0006783	2	FECH, ALAS2	27	35	39.55	1.162e-3	1.658e-2
synaptic vesicle exocytosis	GO:0016079	2	STX1A, UNC13C	28	35	38.14	1.249e-3	1.732e-2
vesicle fusion	GO:0006906	2	STX1A, STX6	28	35	38.14	1.249e-3	1.732e-2
positive regulation of mitotic nuclear division	GO:0045840	2	BTC, EREG	29	35	36.82	1.340e-3	1.797e-2
negative regulation of T cell receptor signaling pathway	GO:0050860	2	CBLB, PRNP	30	35	35.59	1.434e-3	1.871e-2
positive regulation of ATF6-mediated unfolded protein response	GO:1903893	1	ATF6	1	35	533.91	1.873e-3	2.187e-2
fructosamine catabolic process	GO:0030392	1	ALDH1A1	1	35	533.91	1.873e-3	2.187e-2