

GeDiPNet Cluster 546 -- 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 00:01:43

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	AREG, BTC, EREG	8	9	778.63	4.321e-9	8.399e-7
heme biosynthetic process	GO:0006783	3	FECH, ALAS2, SLC25A38	27	9	230.70	2.246e-7	2.490e-5
ERBB4-ERBB4 signaling pathway	GO:0038138	2	BTC, EREG	6	9	692.11	3.090e-6	2.146e-4
epidermal growth factor receptor signaling pathway	GO:0007173	3	AREG, BTC, EREG	64	9	97.33	3.171e-6	2.191e-4
erythrocyte differentiation	GO:0030218	3	FECH, ALAS2, SLC25A38	65	9	95.83	3.324e-6	2.278e-4
heme B biosynthetic process	GO:0006785	2	FECH, ALAS2	10	9	415.27	9.260e-6	5.131e-4
positive regulation of phosphorylation	GO:0042327	2	AREG, EREG	20	9	207.63	3.900e-5	1.527e-3
positive regulation of mitotic nuclear division	GO:0045840	2	BTC, EREG	29	9	143.20	8.315e-5	2.700e-3
positive regulation of cell division	GO:0051781	2	BTC, EREG	48	9	86.51	2.299e-4	5.603e-3
response to peptide hormone	GO:0043434	2	AREG, EREG	50	9	83.05	2.496e-4	5.940e-3
positive regulation of fibroblast proliferation	GO:0048146	2	BTC, EREG	55	9	75.50	3.022e-4	6.818e-3
iron-sulfur cluster export from the mitochondrion	GO:0140466	1	ABCB7	1	9	2076.33	4.816e-4	9.241e-3
positive regulation of iron-sulfur cluster assembly	GO:1903331	1	ABCB7	1	9	2076.33	4.816e-4	9.241e-3
glycine import into mitochondrion	GO:1904983	1	SLC25A38	1	9	2076.33	4.816e-4	9.241e-3
detection of UV	GO:0009589	1	FECH	1	9	2076.33	4.816e-4	9.241e-3