

GeDiPNet Cluster 158 -- 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: 2026-10-10 03:23:26. · Rows: 15 · Generated: 2026-10-10 06:05:05

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
iron-sulfur cluster assembly	GO:0016226	4	ABCB7, GLRX5, HSPA9, HSCB	27	46	60.18	5.410e-7	5.119e-5
ERBB2-EGFR signaling pathway	GO:0038134	3	BTC, AREG, EREG	8	46	152.34	7.750e-7	6.882e-5
erythrocyte differentiation	GO:0030218	4	ALAS2, HSPA9, SLC25A38, FECH	65	46	25.00	1.949e-5	9.094e-4
heme biosynthetic process	GO:0006783	3	ALAS2, SLC25A38, FECH	27	46	45.14	3.917e-5	1.548e-3
ERBB4-ERBB4 signaling pathway	GO:0038138	2	BTC, EREG	6	46	135.41	8.836e-5	2.863e-3
heme B biosynthetic process	GO:0006785	2	ALAS2, FECH	10	46	81.25	2.634e-4	6.337e-3
intracellular oxygen homeostasis	GO:0032364	2	ALAS2, SOD2	10	46	81.25	2.634e-4	6.337e-3
[2Fe-2S] cluster assembly	GO:0044571	2	GLRX5, HSCB	11	46	73.86	3.215e-4	7.283e-3
synaptic vesicle docking	GO:0016081	2	STX1A, UNC13C	13	46	62.50	4.545e-4	9.285e-3
epidermal growth factor receptor signaling pathway	GO:0007173	3	BTC, AREG, EREG	64	46	19.04	5.236e-4	1.022e-2
intracellular iron ion homeostasis	GO:0006879	3	ABCB7, ALAS2, GLRX5	71	46	17.17	7.096e-4	1.252e-2
intracellular copper ion homeostasis	GO:0006878	2	PRND, PRNP	18	46	45.14	8.845e-4	1.445e-2
positive regulation of phosphorylation	GO:0042327	2	AREG, EREG	20	46	40.62	1.095e-3	1.652e-2
response to cadmium ion	GO:0046686	2	SOD2, PRNP	21	46	38.69	1.208e-3	1.751e-2
vesicle docking	GO:0048278	2	STX1A, STX6	21	46	38.69	1.208e-3	1.751e-2