

GeDiPNet Cluster 188 -- 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 11:58:20

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
intracellular iron ion homeostasis	GO:0006879	6	CP, SLC40A1, BMP6, FTH1, HAMP, TF	71	8	197.40	6.745e-14	3.806e-11
iron ion export across plasma membrane	GO:1903988	3	SLC40A1, HAMP, TF	3	8	2335.88	5.150e-11	1.586e-8
multicellular organismal-level iron ion homeostasis	GO:0060586	4	SLC40A1, BMP6, HAMP, TF	28	8	333.70	2.810e-10	7.212e-8
iron ion transport	GO:0006826	3	SLC40A1, FTH1, TF	31	8	226.05	2.302e-7	2.439e-5
cellular response to iron ion	GO:0071281	2	BMP6, TF	7	8	667.39	3.364e-6	2.190e-4
response to iron ion	GO:0010039	2	BMP6, HAMP	18	8	259.54	2.445e-5	1.045e-3
negative regulation of iron ion transmembrane transport	GO:0034760	1	HAMP	1	8	2335.88	4.281e-4	8.586e-3
negative regulation of iron export across plasma membrane	GO:1904039	1	HAMP	1	8	2335.88	4.281e-4	8.586e-3
negative regulation of intestinal absorption	GO:1904479	1	HAMP	1	8	2335.88	4.281e-4	8.586e-3
spleen trabecula formation	GO:0060345	1	SLC40A1	1	8	2335.88	4.281e-4	8.586e-3
positive regulation of proteasomal ubiquitin-dependent protein catabolic process	GO:0032436	2	HAMP, TF	79	8	59.14	4.860e-4	9.367e-3
gamma-aminobutyric acid secretion, neurotransmission	GO:0061534	1	BEST1	2	8	1167.94	8.560e-4	1.360e-2
negative regulation of adherens junction organization	GO:1903392	1	BMP6	2	8	1167.94	8.560e-4	1.360e-2
immune response	GO:0006955	3	BMP6, FTH1, HAMP	543	8	12.91	1.225e-3	1.714e-2
positive regulation of aldosterone biosynthetic process	GO:0032349	1	BMP6	3	8	778.63	1.284e-3	1.747e-2