

GeDiPNet Cluster 593 -- 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 00:01:10

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
negative regulation of antigen processing and presentation of endogenous peptide antigen via MHC class I	GO:1904283	1	HFE	1	5	3737.40	2.676e-4	6.245e-3
regulation of iron ion transport	GO:0034756	1	HFE	2	5	1868.70	5.351e-4	9.880e-3
regulation of T cell mediated immunity	GO:0002709	1	HFE	2	5	1868.70	5.351e-4	9.880e-3
protoporphyrinogen IX metabolic process	GO:0046501	1	PPOX	3	5	1245.80	8.025e-4	1.283e-2
response to iron ion starvation	GO:1990641	1	HFE	3	5	1245.80	8.025e-4	1.283e-2
negative regulation of CD8-positive, alpha-beta T cell activation	GO:2001186	1	HFE	4	5	934.35	1.070e-3	1.514e-2
negative regulation of viral process	GO:0048525	1	MBL2	5	5	747.48	1.337e-3	1.709e-2
galactosylceramide biosynthetic process	GO:0006682	1	B4GALT3	6	5	622.90	1.605e-3	1.885e-2
cellular response to iron ion	GO:0071281	1	HFE	7	5	533.91	1.872e-3	2.050e-2
negative regulation of T cell cytokine production	GO:0002725	1	HFE	7	5	533.91	1.872e-3	2.050e-2
positive regulation of opsonization	GO:1903028	1	MBL2	9	5	415.27	2.406e-3	2.324e-2
protoporphyrinogen IX biosynthetic process	GO:0006782	1	PPOX	9	5	415.27	2.406e-3	2.324e-2
heme O biosynthetic process	GO:0048034	1	PPOX	9	5	415.27	2.406e-3	2.324e-2
positive regulation of peptide hormone secretion	GO:0090277	1	HFE	10	5	373.74	2.673e-3	2.457e-2
heme A biosynthetic process	GO:0006784	1	PPOX	10	5	373.74	2.673e-3	2.457e-2