

GeDiPNet Cluster 205 -- 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: 2026-10-08 03:23:04. · Rows: 15 · Generated: 2026-10-08 08:47:36

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
SRP-dependent cotranslational protein targeting to membrane	GO:0006614	5	SRP19, SRP54, SEC61A1, SRP68, SRPRA	10	74	126.26	2.106e-10	5.491e-8
granulocyte differentiation	GO:0030851	4	CLPB, SRP54, AP3B1, CSF3	15	74	67.34	2.992e-7	3.075e-5
granulocyte colony-stimulating factor signaling pathway	GO:0038158	3	JAGN1, CSF3, HAX1	5	74	151.52	5.927e-7	5.451e-5
neutrophil chemotaxis	GO:0030593	5	SRP54, CSF3R, CXCR2, IL1B, TGFB2	55	74	22.96	2.531e-6	1.778e-4
defense response	GO:0006952	7	CSF3R, ACKR1, FCGR2B, IFNA2, STAT2, TNF, WAS	163	74	10.84	3.720e-6	2.414e-4
cotranslational protein targeting to membrane	GO:0006613	3	SRP19, SEC61A1, SRPRA	10	74	75.76	7.012e-6	4.015e-4
SRP-dependent cotranslational protein targeting to membrane, signal sequence recognition	GO:0006617	3	SRP19, SRP54, SRPRA	14	74	54.11	2.103e-5	9.480e-4
protein targeting to ER	GO:0045047	3	SRP54, SEC61A1, SRPRA	15	74	50.51	2.621e-5	1.120e-3
response to hypoxia	GO:0001666	6	ABCB1, CHRN2, MTHFR, TGFB2, TGFB3, TNF	176	74	8.61	6.986e-5	2.368e-3
positive regulation of macrophage derived foam cell differentiation	GO:0010744	3	CSF2, IL1B, TNF	21	74	36.08	7.532e-5	2.507e-3
inflammatory response	GO:0006954	9	TCIRG1, CXCR2, ACKR1, AP3B1, C5, FCGR2B, IFNA2, IL1B, TNF	467	74	4.87	9.219e-5	2.913e-3
positive regulation of fever generation	GO:0031622	2	IL1B, TNF	4	74	126.26	9.235e-5	2.917e-3
cellular response to lipopolysaccharide	GO:0071222	6	GFI1, ABCB1, CSF2, CSF3, IL1B, TNF	187	74	8.10	9.763e-5	3.037e-3
cell morphogenesis	GO:0000902	5	AP3B1, CDH13, PTPRO, SS18, TGFB2	119	74	10.61	1.092e-4	3.296e-3
cardiac muscle cell proliferation	GO:0060038	3	TGFB2, TGFB3, GATA6	28	74	27.06	1.819e-4	4.829e-3