

GeDiPNet Cluster 135 -- 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 06:59:50

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
response to lipopolysaccharide	GO:0032496	18	BLVRA, CNR2, LY96, MAPK14, NOS2, NQO1, RELA, TNF, VCAM1, FOS, IL1B, MAPK1	161	151	13.84	8.827e-16	6.938e-13
cellular response to lipopolysaccharide	GO:0071222	18	CXCL8, IL6, LY96, MAPK14, NOS2, NR1H3, NR1H4, RELA, SERPINE1, TNF, CD68, HMGB1	187	151	11.91	1.261e-14	8.051e-12
bile acid and bile salt transport	GO:0015721	9	ATP8B1, ABCB11, ABCC2, ABCC3, NR1H4, SLC10A1, SLC51A, SLC51B, SLCO1A2	26	151	42.84	3.209e-13	1.627e-10
positive regulation of gene expression	GO:0010628	23	CXCL8, EGR1, ID4, IGF1, IL6, MAPK14, NFE2L2, NR1H2, RDX, RELA, TLR2, TNF	504	151	5.65	1.745e-11	6.056e-9
positive regulation of miRNA transcription	GO:1902895	10	AGT, EGR1, IL6, NR1H2, RELA, TNF, WT1, FOS, JUN, TGFB1	56	151	22.10	2.276e-11	7.604e-9
inflammatory response	GO:0006954	22	BLVRA, CCL7, CNR2, CXCL2, CXCL8, IL6, LY96, NFE2L2, NOS2, NR1H4, RELA, TLR2	467	151	5.83	2.716e-11	8.913e-9
positive regulation of interleukin-8 production	GO:0032757	10	IL6, NOS2, RELA, SERPINE1, TLR2, TNF, HMGB1, IL1B, MYD88, TLR4	65	151	19.04	1.076e-10	3.069e-8
stress-activated MAPK cascade	GO:0051403	7	MAPK13, MAPK14, MAP3K7, MAPK1, MAPK3, MAPK8, TLR4	23	151	37.66	4.302e-10	1.051e-7
lipopolysaccharide-mediated signaling pathway	GO:0031663	8	LY96, MAPK14, TLR2, MAPK1, MAPK3, MYD88, NOS3, TLR4	38	151	26.05	6.007e-10	1.432e-7
positive regulation of interleukin-6 production	GO:0032755	11	IL6, MAPK13, NOS2, RELA, TLR2, TNF, HMGB1, IL1B, MYD88, TGFB1, TLR4	103	151	13.22	7.006e-10	1.633e-7
positive regulation of ERK1 and ERK2 cascade	GO:0070374	14	FGA, ICAM1, IGF1, SLC30A10, TNF, ACTA2, CCN2, HMGB1, IL1B, JUN, MAPK3, TGFB1	201	151	8.62	9.562e-10	2.155e-7
cellular response to tumor necrosis factor	GO:0071356	11	CXCL8, MAPK14, NFE2L2, RELA, VCAM1, COL1A1, FOS, MAP3K7, MAPK1, MAPK3, ABCB1	107	151	12.72	1.059e-9	2.354e-7
positive regulation of chemokine production	GO:0032722	8	EGR1, IL6, TLR2, TNF, HMGB1, IL1B, MYD88, TLR4	49	151	20.20	5.139e-9	9.547e-7
response to ethanol	GO:0045471	10	CAT, CYP7A1, RELA, SLC10A1, TNF, VCAM1, CD68, FOS, MYD88, TGFB1	110	151	11.25	2.067e-8	3.211e-6
JNK cascade	GO:0007254	8	TNF, IL1B, JUN, MAP3K7, MAPK8, MAPK9, MYD88, TLR4	61	151	16.23	3.092e-8	4.505e-6