

GeDiPNet Cluster 379 -- 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 13:35:49

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
vasodilation	GO:0042311	5	ACE, AGTR2, BDKRB2, TNF, S100A1	50	20	93.44	1.679e-9	3.469e-7
response to ethanol	GO:0045471	4	G6PD, SOD1, TNF, S100B	110	20	33.98	5.121e-6	3.117e-4
response to macrophage colony-stimulating factor	GO:0036005	2	SPP1, TNF	4	20	467.18	6.521e-6	3.780e-4
inflammatory response	GO:0006954	6	HP, AGTR2, BDKRB1, BDKRB2, NFE2L2, TNF	467	20	12.00	6.788e-6	3.907e-4
response to hydrogen peroxide	GO:0042542	3	HMOX1, HP, SOD1	39	20	71.87	9.348e-6	5.051e-4
blood vessel remodeling	GO:0001974	3	ATP7A, ACE, AGTR2	42	20	66.74	1.172e-5	5.975e-4
positive regulation of smooth muscle cell proliferation	GO:0048661	3	HMOX1, S1PR1, TNF	52	20	53.90	2.241e-5	9.930e-4
response to salt stress	GO:0009651	2	BDKRB2, TNF	9	20	207.63	3.900e-5	1.521e-3
intracellular iron ion homeostasis	GO:0006879	3	HMOX1, SLC40A1, SOD1	71	20	39.48	5.720e-5	2.023e-3
negative regulation of heart rate	GO:0010459	2	AGTR2, TNF	12	20	155.73	7.136e-5	2.402e-3
regulation of blood pressure	GO:0008217	3	SOD1, ACE, AGTR2	83	20	33.77	9.120e-5	2.892e-3
positive regulation of canonical NF-kappaB signal transduction	GO:0043123	4	HMOX1, TNF, S100A4, S100B	232	20	16.11	9.593e-5	2.998e-3
negative regulation of ferroptosis	GO:0110076	2	HMOX1, NFE2L2	14	20	133.48	9.827e-5	3.049e-3
removal of superoxide radicals	GO:0019430	2	ATP7A, SOD1	15	20	124.58	1.133e-4	3.385e-3
angiotensin-activated signaling pathway	GO:0038166	2	ACE, AGTR2	16	20	116.79	1.294e-4	3.745e-3