

GeDiPNet Cluster 81 -- 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 02:10:18

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
response to glucocorticoid	GO:0051384	4	ADIPOQ, BCHE, TNF, UCP3	53	34	41.48	2.510e-6	1.766e-4
negative regulation of blood coagulation	GO:0030195	3	APOE, F2, SERPINE1	16	34	103.05	3.032e-6	2.051e-4
regulation of renal output by angiotensin	GO:0002019	2	ACE, AGT	2	34	549.62	3.213e-6	2.150e-4
positive regulation of angiogenesis	GO:0045766	5	PTGIS, SERPINE1, HMOX1, ITGB2, IL1A	159	34	17.28	9.545e-6	5.132e-4
decidualization	GO:0046697	3	PTGIS, SPP1, VDR	25	34	65.95	1.231e-5	6.211e-4
negative regulation of proteolysis	GO:0045861	3	F2, SERPINE1, TP53	27	34	61.07	1.562e-5	7.514e-4
response to macrophage colony-stimulating factor	GO:0036005	2	SPP1, TNF	4	34	274.81	1.924e-5	8.837e-4
positive regulation of protein-containing complex disassembly	GO:0043243	2	TNF, IGF1R	4	34	274.81	1.924e-5	8.837e-4
cellular response to lipopolysaccharide	GO:0071222	5	CXCL9, MMP3, SERPINE1, TNF, IL1A	187	34	14.70	2.091e-5	9.445e-4
positive regulation of reactive oxygen species metabolic process	GO:2000379	3	F2, TP53, AGT	34	34	48.50	3.168e-5	1.290e-3
maintenance of blood vessel diameter homeostasis by renin-angiotensin	GO:0002034	2	ACE, AGT	5	34	219.85	3.202e-5	1.301e-3
cellular extravasation	GO:0045123	2	ITGB2, TNF	5	34	219.85	3.202e-5	1.301e-3
regulation of systemic arterial blood pressure by renin-angiotensin	GO:0003081	2	ACE, AGT	6	34	183.21	4.798e-5	1.772e-3
positive regulation of nitric oxide biosynthetic process	GO:0045429	3	APOE, ITGB2, TNF	42	34	39.26	6.018e-5	2.103e-3
positive regulation of cholesterol metabolic process	GO:0090205	2	APOE, AGT	7	34	157.03	6.709e-5	2.290e-3