

GeDiPNet Cluster 27 -- 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: 2026-10-07 22:56:51

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
regulation of blood pressure	GO:0008217	12	ACTA2, AGT, EDN1, SCNN1G, EDNRB, REN, SOD1, SOD2, LEP, POMC, PTGS2, SCNN1A	83	240	11.26	6.624e-10	1.501e-7
glomerular basement membrane development	GO:0032836	6	NPHS1, MYO1E, WT1, COL4A4, MPV17, COL4A3	10	240	46.72	8.482e-10	1.873e-7
kidney development	GO:0001822	13	CD2AP, MYO1E, WT1, AGT, LAMA5, GATA3, REN, SGPL1, TNS2, BMP7, AGTR1, RHOA	146	240	6.93	5.237e-8	7.043e-6
tRNA threonylcarbamoyladenosine modification	GO:0002949	4	GON7, OSGEP, TPRKB, YRDC	5	240	62.29	1.314e-7	1.542e-5
nephron development	GO:0072006	5	NUP107, NUP133, NUP160, NUP85, ITGA3	11	240	35.39	1.454e-7	1.684e-5
positive regulation of T cell proliferation	GO:0042102	9	BTNL2, CD28, IL1B, IL2, NCK1, NCK2, PTPRC, TNFSF4, LEP	67	240	10.46	1.831e-7	2.042e-5
podocyte differentiation	GO:0072112	5	CD2AP, PTPRO, WT1, EDN1, EDNRB	12	240	32.44	2.467e-7	2.621e-5
collagen-activated tyrosine kinase receptor signaling pathway	GO:0038063	5	COL4A1, COL4A5, COL4A3, COL1A1, COL4A2	12	240	32.44	2.467e-7	2.621e-5
glomerulus development	GO:0032835	5	CD2AP, MYO1E, PLCE1, PTPRO, WT1	13	240	29.95	3.966e-7	3.882e-5
cell-cell adhesion	GO:0098609	14	NPHS1, ITGB4, KIRREL2, MYH9, CDH12, FAT1, ICAM1, ITGB2, CD2, ITGA3, TNXB, BMP7	218	240	5.00	9.176e-7	7.787e-5
positive regulation of nitric oxide biosynthetic process	GO:0045429	7	EDN1, ITGB2, IL1B, SOD2, APOE, IFNG, PTGS2	42	240	12.98	9.715e-7	8.159e-5
peptide antigen assembly with MHC class II protein complex	GO:0002503	5	HLA-DQA1, HLA-DQB1, HLA-DRB1, HLA-DRB5, B2M	16	240	24.33	1.304e-6	1.038e-4
positive regulation of cell population proliferation	GO:0008284	22	EMP2, EDN1, FN1, REG1A, TGFB1, FGFR4, PAK1, EDNRB, F2, BTC, EPO, FGF2	532	240	3.22	1.543e-6	1.190e-4
cell adhesion	GO:0007155	25	NPHS1, EMP2, CCN2, FN1, ITGB4, KIRREL2, LAMA5, LAMB2, MYH10, MYH9, SPP1, CDH12	665	240	2.93	1.642e-6	1.248e-4
symbiont entry into host cell	GO:0046718	10	ACE2, HAVCR1, MYH10, MYH9, SCARB2, ICAM1, AGTR1, CTSB, CTSL, DPP4	112	240	6.95	1.822e-6	1.363e-4