

GeDiPNet Cluster 36 -- 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 16:26:49

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
blood coagulation	GO:0007596	51	F2, F5, FGG, PROC, F10, GGCX, GNAQ, SERPINC1, VKORC1, F7, ITGB3, PLAT	106	281	32.00	2.744e-65	1.790e-60
hemostasis	GO:0007599	38	F2, F5, FGG, PROC, F10, SERPINC1, F7, PLAU, PROS1, SERPING1, THBD, F3	55	281	45.95	2.239e-57	6.527e-53
fibrinolysis	GO:0042730	14	F2, FGG, PLAT, PLAU, PROS1, SERPING1, FGA, FGB, GP1BA, KLKB1, PLG, F12	19	281	49.00	2.376e-22	5.327e-19
platelet activation	GO:0030168	18	F2, FGG, ITGB3, VWF, P2RY12, ACTN1, ADAMTS13, FGA, FGB, GP1BA, GP1BB, GP6	69	281	17.35	7.756e-18	9.104e-15
platelet aggregation	GO:0070527	16	ACTB, FGG, ITGB3, FERMT3, P2RY12, TUBB1, GNAS, ACTN1, FGA, FGB, FLNA, GATA1	49	281	21.71	9.562e-18	1.119e-14
positive regulation of phosphatidylinositol 3-kinase/protein kinase B signal transduction	GO:0051897	27	F2, FLT1, KDR, VEGFA, APP, NTRK2, PARK7, PROS1, TNF, TGFB1, P2RY12, JAK2	217	281	8.27	2.831e-17	3.038e-14
platelet formation	GO:0030220	12	CASP3, TPM4, TUBB1, ACTN1, GATA1, MPIG6B, MPL, MYH9, NBEAL2, PTPN11, PTPRJ, WDR1	24	281	33.25	2.434e-16	2.140e-13
megakaryocyte development	GO:0035855	10	THPO, FLI1, FLNA, GP1BA, GP1BB, GP9, MPIG6B, PTPN11, VPS33B, MEIS1	23	281	28.91	4.852e-13	2.367e-10
positive regulation of ERK1 and ERK2 cascade	GO:0070374	20	FGG, ITGB3, KDR, VEGFA, APP, APOE, HLA-DRB1, NPY, TNF, TGFB1, THPO, EPO	201	281	6.62	2.785e-11	9.114e-9
plasminogen activation	GO:0031639	7	FGG, PLAT, PLAU, F11, FGA, FGB, KLKB1	12	281	38.79	1.198e-10	3.375e-8
negative regulation of fibrinolysis	GO:0051918	7	F2, PLAT, PLAU, THBD, PLG, HRG, SERPINE1	12	281	38.79	1.198e-10	3.375e-8
positive regulation of platelet activation	GO:0010572	7	JAK2, FLNA, GP1BA, GP1BB, GP9, PTPRJ, SELP	13	281	35.81	2.563e-10	6.652e-8
blood coagulation, intrinsic pathway	GO:0007597	6	F8, FLNA, GP1BA, GP1BB, GP9, F12	8	281	49.88	2.993e-10	7.654e-8
angiogenesis	GO:0001525	22	HMOX1, APOLD1, CASP8, COL4A1, COL4A2, FLT1, ITGA2B, ITGAV, ITGB3, KDR, MMP2, VEGFA	284	281	5.15	3.726e-10	9.238e-8
blood coagulation, fibrin clot formation	GO:0072378	6	FGG, ITGB3, F13A1, FGA, FGB, F13B	9	281	44.33	8.866e-10	2.011e-7