

GeDiPNet Cluster 414 -- 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 07:41:50

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	8	GP6, ITGB3, PLAT, F3, GP1BA, P2RY12, VWF, ITGA2	106	19	74.23	5.880e-14	3.383e-11
hemostasis	GO:0007599	5	GP6, F3, GP1BA, P2RY12, VWF	55	19	89.41	2.066e-9	4.253e-7
platelet activation	GO:0030168	5	GP6, ITGB3, GP1BA, P2RY12, VWF	69	19	71.27	6.615e-9	1.196e-6
positive regulation of leukocyte migration	GO:0002687	3	ITGB3, ITGA2, ITGA2B	19	19	155.29	8.546e-7	7.291e-5
cell-substrate adhesion	GO:0031589	3	ITGB3, VWF, ITGA2	25	19	118.02	2.021e-6	1.451e-4
cell adhesion	GO:0007155	7	DSCAM, ITGB3, GP1BA, VWF, CDH15, ITGA2, ITGA2B	665	19	10.35	2.428e-6	1.682e-4
collagen-activated signaling pathway	GO:0038065	2	GP6, ITGA2	6	19	327.84	1.466e-5	7.039e-4
platelet aggregation	GO:0070527	3	GP6, ITGB3, P2RY12	49	19	60.22	1.594e-5	7.542e-4
smooth muscle cell migration	GO:0014909	2	ITGB3, PLAT	9	19	218.56	3.511e-5	1.379e-3
positive regulation of positive chemotaxis	GO:0050927	2	F3, ITGA2	11	19	178.82	5.357e-5	1.894e-3
mesodermal cell differentiation	GO:0048333	2	ITGB3, ITGA2	13	19	151.31	7.589e-5	2.467e-3
positive regulation of cell adhesion mediated by integrin	GO:0033630	2	ITGB3, P2RY12	16	19	122.94	1.165e-4	3.396e-3
dendrite self-avoidance	GO:0070593	2	DSCAM, PALLD	16	19	122.94	1.165e-4	3.396e-3
positive regulation of smooth muscle cell migration	GO:0014911	2	ITGB3, ITGA2	17	19	115.71	1.320e-4	3.726e-3
integrin-mediated signaling pathway	GO:0007229	3	ITGB3, ITGA2, ITGA2B	100	19	29.51	1.354e-4	3.792e-3