

GeDiPNet Cluster 398 -- 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 07:25:07

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
hemostasis	GO:0007599	4	F2, F5, PROZ, F9	55	4	339.76	6.715e-11	1.983e-8
blood coagulation	GO:0007596	4	F2, F5, PROZ, F9	106	4	176.29	9.780e-10	2.127e-7
proteolysis	GO:0006508	3	F2, PROZ, F9	613	4	22.86	1.371e-4	3.903e-3
response to vitamin K	GO:0032571	1	F5	3	4	1557.25	6.421e-4	1.151e-2
neutrophil-mediated killing of gram-negative bacterium	GO:0070945	1	F2	5	4	934.35	1.070e-3	1.602e-2
regulation of body fluid levels	GO:0050878	1	F2	7	4	667.39	1.498e-3	1.953e-2
positive regulation of phospholipase C-activating G protein-coupled receptor signaling pathway	GO:1900738	1	F2	7	4	667.39	1.498e-3	1.953e-2
negative regulation of platelet activation	GO:0010544	1	F2	9	4	519.08	1.925e-3	2.259e-2
cytolysis by host of symbiont cells	GO:0051838	1	F2	11	4	424.70	2.353e-3	2.546e-2
ligand-gated ion channel signaling pathway	GO:1990806	1	F2	11	4	424.70	2.353e-3	2.546e-2
negative regulation of astrocyte differentiation	GO:0048712	1	F2	11	4	424.70	2.353e-3	2.546e-2
thrombin-activated receptor signaling pathway	GO:0070493	1	F2	11	4	424.70	2.353e-3	2.546e-2
regulation of blood coagulation	GO:0030193	1	F2	11	4	424.70	2.353e-3	2.546e-2
negative regulation of fibrinolysis	GO:0051918	1	F2	12	4	389.31	2.566e-3	2.663e-2
positive regulation of blood coagulation	GO:0030194	1	F2	15	4	311.45	3.207e-3	2.987e-2