

GeDiPNet Cluster 339 -- 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 12:09:52

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
DNA-templated transcription termination	GO:0006353	3	SETX, SMN1, SMN2	13	14	308.03	9.531e-8	1.171e-5
positive regulation of macrophage fusion	GO:0034241	2	TYROBP, TREM2	5	14	533.91	5.205e-6	3.159e-4
microglial cell activation involved in immune response	GO:0002282	2	TYROBP, TREM2	5	14	533.91	5.205e-6	3.159e-4
T cell activation via T cell receptor contact with antigen bound to MHC molecule on antigen presenting cell	GO:0002291	2	TYROBP, TREM2	8	14	333.70	1.456e-5	7.111e-4
nervous system development	GO:0007399	5	SPG7, SETX, NAIP, SMN1, SMN2	631	14	10.58	6.713e-5	2.290e-3
amyloid-beta clearance	GO:0097242	2	TYROBP, TREM2	17	14	157.03	7.043e-5	2.381e-3
apoptotic cell clearance	GO:0043277	2	TYROBP, TREM2	22	14	121.34	1.194e-4	3.517e-3
spliceosomal complex assembly	GO:0000245	2	SMN1, SMN2	28	14	95.34	1.948e-4	5.068e-3
spliceosomal snRNP assembly	GO:0000387	2	SMN1, SMN2	29	14	92.05	2.092e-4	5.321e-3
RNA splicing, via transesterification reactions	GO:0000375	2	SMN1, SMN2	30	14	88.99	2.240e-4	5.570e-3
response to axon injury	GO:0048678	2	TYROBP, TREM2	37	14	72.15	3.420e-4	7.512e-3
pyroptotic inflammatory response	GO:0070269	2	TREM2, NAIP	40	14	66.74	4.000e-4	8.380e-3
semaphorin-plexin signaling pathway	GO:0071526	2	TYROBP, TREM2	43	14	62.08	4.625e-4	9.272e-3
regulation of biological quality	GO:0065008	2	TYROBP, TREM2	45	14	59.32	5.066e-4	9.833e-3
osteoclast differentiation	GO:0030316	2	TYROBP, TREM2	49	14	54.48	6.007e-4	1.105e-2