

GeDiPNet Cluster 447 -- 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: 2026-10-20 03:23:14. · Rows: 15 · Generated: 2026-10-19 23:18:21

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
proteolysis involved in protein catabolic process	GO:0051603	5	PSMB4, PSMB8, PSMA3, PSMB9, PSMB10	53	7	251.85	3.162e-12	1.352e-9
proteasome-mediated ubiquitin-dependent protein catabolic process	GO:0043161	5	PSMB4, PSMB8, PSMA3, PSMB9, PSMB10	343	7	38.92	4.124e-8	6.023e-6
proteasome assembly	GO:0043248	2	POMP, PSMG2	11	7	485.38	6.605e-6	3.941e-4
proteolysis	GO:0006508	3	PSMB8, PSMB9, PSMB10	613	7	13.06	1.114e-3	1.550e-2
chaperone-mediated protein complex assembly	GO:0051131	1	PSMG2	24	7	111.23	8.957e-3	4.406e-2
negative regulation of inflammatory response to antigenic stimulus	GO:0002862	1	PSMB4	26	7	102.68	9.700e-3	4.577e-2
mitotic spindle assembly checkpoint signaling	GO:0007094	1	PSMG2	30	7	88.99	1.119e-2	4.890e-2
antigen processing and presentation	GO:0019882	1	PSMB8	48	7	55.62	1.785e-2	6.127e-2
T cell proliferation	GO:0042098	1	PSMB10	51	7	52.34	1.895e-2	6.335e-2
humoral immune response	GO:0006959	1	PSMB10	58	7	46.03	2.153e-2	6.772e-2
fat cell differentiation	GO:0045444	1	PSMB8	93	7	28.71	3.433e-2	8.631e-2
cell morphogenesis	GO:0000902	1	PSMB10	119	7	22.43	4.374e-2	9.916e-2
immune system process	GO:0002376	2	PSMB8, PSMB9	943	7	5.66	4.510e-2	1.009e-1
ubiquitin-dependent protein catabolic process	GO:0006511	1	PSMA3	257	7	10.39	9.240e-2	1.571e-1
regulation of cell cycle	GO:0051726	1	PSMG2	262	7	10.19	9.412e-2	1.588e-1