

GeDiPNet Cluster 465 -- 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 23:18:38

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
bone maturation	GO:0070977	1	MBTPS2	3	2	3114.50	3.211e-4	7.044e-3
regulation of response to endoplasmic reticulum stress	GO:1905897	1	MBTPS2	4	2	2335.88	4.281e-4	8.531e-3
ATF6-mediated unfolded protein response	GO:0036500	1	MBTPS2	8	2	1167.94	8.560e-4	1.331e-2
regulation of cholesterol biosynthetic process	GO:0045540	1	MBTPS2	12	2	778.63	1.284e-3	1.669e-2
membrane protein intracellular domain proteolysis	GO:0031293	1	MBTPS2	14	2	667.39	1.498e-3	1.821e-2
positive regulation of cholesterol biosynthetic process	GO:0045542	1	MBTPS2	24	2	389.31	2.567e-3	2.402e-2
NLS-bearing protein import into nucleus	GO:0006607	1	MBTPS2	27	2	346.06	2.888e-3	2.555e-2
mitotic G2 DNA damage checkpoint signaling	GO:0007095	1	MBTPS2	36	2	259.54	3.849e-3	2.937e-2
positive regulation of transcription by RNA polymerase II	GO:0045944	2	MBTPS2, YY2	1208	2	15.47	4.176e-3	3.063e-2
endoplasmic reticulum unfolded protein response	GO:0030968	1	MBTPS2	58	2	161.09	6.198e-3	3.697e-2
cholesterol metabolic process	GO:0008203	1	MBTPS2	107	2	87.32	1.142e-2	4.959e-2
response to endoplasmic reticulum stress	GO:0034976	1	MBTPS2	113	2	82.69	1.206e-2	5.083e-2
protein maturation	GO:0051604	1	MBTPS2	134	2	69.73	1.429e-2	5.531e-2
steroid metabolic process	GO:0008202	1	MBTPS2	135	2	69.21	1.440e-2	5.537e-2
proteolysis	GO:0006508	1	MBTPS2	613	2	15.24	6.453e-2	1.256e-1