

GeDiPNet Cluster 461 -- 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: 2026-10-20 00:01:10

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
regulation of myeloid cell apoptotic process	GO:0033032	1	THRA	1	13	1437.46	6.957e-4	1.178e-2
translation at postsynapse	GO:0140242	1	EEF2	1	13	1437.46	6.957e-4	1.178e-2
negative regulation of DNA-templated transcription initiation	GO:2000143	1	THRA	2	13	718.73	1.391e-3	1.753e-2
negative regulation of RNA polymerase II transcription preinitiation complex assembly	GO:0017055	1	THRA	2	13	718.73	1.391e-3	1.753e-2
female courtship behavior	GO:0008050	1	THRA	2	13	718.73	1.391e-3	1.753e-2
positive regulation of female receptivity	GO:0045925	1	THRA	3	13	479.15	2.086e-3	2.170e-2
positive regulation of thyroid hormone receptor signaling pathway	GO:0002157	1	THRA	3	13	479.15	2.086e-3	2.170e-2
thyroid hormone receptor signaling pathway	GO:0002154	1	THRA	3	13	479.15	2.086e-3	2.170e-2
regulation of lipid catabolic process	GO:0050994	1	THRA	3	13	479.15	2.086e-3	2.170e-2
Golgi vesicle budding	GO:0048194	1	PRKCI	4	13	359.37	2.780e-3	2.510e-2
regulation of transcription by RNA polymerase II	GO:0006357	5	GRHL3, IRF6, CTR9, THRA, BRWD3	1602	13	4.49	3.296e-3	2.744e-2
cellular response to chemical stress	GO:0062197	1	PRKCI	5	13	287.49	3.474e-3	2.810e-2
establishment of apical/basal cell polarity	GO:0035089	1	PRKCI	5	13	287.49	3.474e-3	2.810e-2
regulation of thyroid hormone receptor signaling pathway	GO:0002155	1	THRA	5	13	287.49	3.474e-3	2.810e-2
inner cell mass cell differentiation	GO:0001826	1	CTR9	6	13	239.58	4.167e-3	3.062e-2