

GeDiPNet Cluster 513 -- 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 03:23:13. · Rows: 13 · Generated: 2026-10-19 23:18:34

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
embryonic placenta development	GO:0001892	1	BPTF	26	2	359.37	2.781e-3	2.510e-2
endoderm development	GO:0007492	1	BPTF	34	2	274.81	3.636e-3	2.863e-2
cellular response to nerve growth factor stimulus	GO:1990090	1	BPTF	35	2	266.96	3.743e-3	2.900e-2
anterior/posterior pattern specification	GO:0009952	1	BPTF	112	2	83.42	1.195e-2	5.062e-2
brain development	GO:0007420	1	BPTF	244	2	38.29	2.594e-2	7.505e-2
chromatin remodeling	GO:0006338	1	BPTF	320	2	29.20	3.396e-2	8.606e-2
proteasome-mediated ubiquitin-dependent protein catabolic process	GO:0043161	1	PSMD12	343	2	27.24	3.637e-2	8.920e-2
chromatin organization	GO:0006325	1	BPTF	449	2	20.81	4.748e-2	1.042e-1
negative regulation of DNA-templated transcription	GO:0045892	1	BPTF	631	2	14.81	6.640e-2	1.273e-1
negative regulation of transcription by RNA polymerase II	GO:0000122	1	BPTF	1002	2	9.32	1.044e-1	1.700e-1
positive regulation of transcription by RNA polymerase II	GO:0045944	1	BPTF	1208	2	7.73	1.251e-1	1.918e-1
regulation of DNA-templated transcription	GO:0006355	1	BPTF	1454	2	6.43	1.496e-1	2.158e-1
regulation of transcription by RNA polymerase II	GO:0006357	1	BPTF	1602	2	5.83	1.641e-1	2.307e-1