

GeDiPNet Cluster 299 -- 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: 2026-10-07 03:23:06. · Rows: 15 · Generated: 2026-10-07 09:09:15

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
regulation of G0 to G1 transition	GO:0070316	10	SMARCB1, ARID1A, ARID1B, ARID2, DPF2, SMARCA2, SMARCA4, SMARCC2, SMARCD1, SMARCE1	25	20	373.74	4.200e-25	1.348e-21
regulation of nucleotide-excision repair	GO:2000819	10	SMARCB1, ARID1A, ARID1B, ARID2, DPF2, SMARCA2, SMARCA4, SMARCC2, SMARCD1, SMARCE1	28	20	333.70	1.684e-24	4.991e-21
regulation of mitotic metaphase/anaphase transition	GO:0030071	10	SMARCB1, ARID1A, ARID1B, ARID2, DPF2, SMARCA2, SMARCA4, SMARCC2, SMARCD1, SMARCE1	34	20	274.81	1.677e-23	4.548e-20
positive regulation of myoblast differentiation	GO:0045663	10	SMARCB1, ARID1A, ARID1B, ARID2, SMARCA2, SMARCA4, SMARCC2, SMARCD1, SMARCE1, SOX4	47	20	198.80	6.582e-22	1.354e-18
positive regulation of double-strand break repair	GO:2000781	10	SMARCB1, ARID1A, ARID1B, ARID2, DPF2, SMARCA2, SMARCA4, SMARCC2, SMARCD1, SMARCE1	47	20	198.80	6.582e-22	1.354e-18
positive regulation of cell differentiation	GO:0045597	11	SMARCB1, RPS6KA3, ARID1A, ARID1B, ARID2, SMARCA2, SMARCA4, SMARCC2, SMARCD1, SMARCE1, NF2	83	20	123.83	1.083e-21	2.153e-18
regulation of G1/S transition of mitotic cell cycle	GO:2000045	10	SMARCB1, ARID1A, ARID1B, ARID2, DPF2, SMARCA2, SMARCA4, SMARCC2, SMARCD1, SMARCE1	57	20	163.92	5.462e-21	1.022e-17
positive regulation of T cell differentiation	GO:0045582	9	SMARCB1, ARID1A, ARID1B, ARID2, SMARCA2, SMARCA4, SMARCC2, SMARCD1, SMARCE1	40	20	210.23	5.911e-20	9.572e-17
nucleosome disassembly	GO:0006337	7	SMARCB1, ARID1A, ARID2, SMARCA4, SMARCC2, SMARCD1, SMARCE1	21	20	311.45	5.667e-17	5.762e-14
chromatin remodeling	GO:0006338	12	SMARCB1, ARID1A, ARID1B, ARID2, BICRA, DPF2, KDM8, SMARCA2, SMARCA4, SMARCC2, SMARCD1, SMARCE1	320	20	35.04	5.770e-17	5.833e-14
positive regulation of stem cell population maintenance	GO:1902459	8	SMARCB1, ARID1A, BICRA, DPF2, SMARCA2, SMARCA4, SMARCD1, SMARCE1	47	20	159.04	1.052e-16	9.999e-14
nervous system development	GO:0007399	11	SMARCB1, ARID1A, ARID1B, DPF2, SMARCA2, SMARCA4, SMARCC2, SMARCD1, SMARCE1, SOX11, SOX4	631	20	16.29	7.605e-12	2.863e-9
chromatin organization	GO:0006325	10	SMARCB1, ARID1A, ARID1B, ARID2, DPF2, KDM8, SMARCA4, SMARCC2, SMARCD1, SMARCE1	449	20	20.81	8.652e-12	3.220e-9
positive regulation of DNA-templated transcription	GO:0045893	11	ARID1A, ARID1B, BICRA, KDM8, SMARCA2, SMARCA4, SMARCC2, SMARCD1, SMARCE1, SOX11, SOX4	778	20	13.21	7.238e-11	2.142e-8
transcription initiation-coupled chromatin remodeling	GO:0045815	5	SMARCB1, ARID1A, ARID1B, SMARCA4, SMARCD1	41	20	113.95	5.976e-10	1.426e-7