

GeDiPNet Cluster 261 -- 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 00:57:34

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
positive regulation of glucose mediated signaling pathway	GO:1902661	2	SMARCA4, SMARCB1	3	15	830.53	1.803e-6	1.327e-4
positive regulation of double-strand break repair	GO:2000781	3	FMN2, SMARCA4, SMARCB1	47	15	79.52	6.642e-6	3.757e-4
regulation of G1/S transition of mitotic cell cycle	GO:2000045	3	SMARCA4, SMARCB1, CDKN1B	57	15	65.57	1.193e-5	5.977e-4
positive regulation of transcription of nucleolar large rRNA by RNA polymerase I	GO:1901838	2	SMARCA4, SMARCB1	10	15	249.16	2.696e-5	1.127e-3
RNA polymerase I preinitiation complex assembly	GO:0001188	2	SMARCA4, SMARCB1	11	15	226.51	3.294e-5	1.313e-3
positive regulation of cell differentiation	GO:0045597	3	SMARCA4, SMARCB1, SOX2	83	15	45.03	3.699e-5	1.434e-3
cellular response to lithium ion	GO:0071285	2	CDKN1B, XRCC4	15	15	166.11	6.277e-5	2.133e-3
host-mediated activation of viral transcription	GO:0043923	2	SMARCA4, SMARCB1	18	15	138.42	9.133e-5	2.827e-3
negative regulation of cell growth	GO:0030308	3	SMARCA4, PTPRJ, CDKN1B	115	15	32.50	9.788e-5	2.972e-3
chromatin remodeling	GO:0006338	4	CFDP1, SMARCA4, SMARCB1, NFKBIZ	320	15	15.57	9.923e-5	3.002e-3
epithelial cell apoptotic process	GO:1904019	2	CDKN1B, NFKBIZ	20	15	124.58	1.133e-4	3.319e-3
nucleosome disassembly	GO:0006337	2	SMARCA4, SMARCB1	21	15	118.65	1.252e-4	3.582e-3
regulation of G0 to G1 transition	GO:0070316	2	SMARCA4, SMARCB1	25	15	99.66	1.785e-4	4.667e-3
regulation of nucleotide-excision repair	GO:2000819	2	SMARCA4, SMARCB1	28	15	88.99	2.246e-4	5.471e-3
regulation of mitotic metaphase/anaphase transition	GO:0030071	2	SMARCA4, SMARCB1	34	15	73.28	3.324e-4	7.201e-3