

GeDiPNet Cluster 88 -- 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 15:01:48

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
replicative senescence	GO:0090399	4	TP53, ATM, ATR, CDKN2A	16	32	145.99	1.270e-8	2.105e-6
cellular response to gamma radiation	GO:0071480	4	TP53, ATM, ATR, MDM2	28	32	83.42	1.408e-7	1.616e-5
intrinsic apoptotic signaling pathway by p53 class mediator	GO:0072332	4	TP53, PYCARD, FHIT, WWOX	29	32	80.55	1.632e-7	1.827e-5
regulation of cell cycle	GO:0051726	7	TP53, ATM, CCND1, RB1, BAP1, MDM2, CDKN2A	262	32	15.60	2.452e-7	2.575e-5
apoptotic process	GO:0006915	10	TP53, BIRC5, PYCARD, RB1, MDM2, CDKN2A, WNT7A, FHIT, VEGFA, WWOX	747	32	7.82	2.846e-7	2.917e-5
apoptotic signaling pathway	GO:0097190	5	TP53, P2RX7, PYCARD, TNF, CDKN2A	84	32	34.76	2.978e-7	3.029e-5
positive regulation of signal transduction by p53 class mediator	GO:1901798	3	RPS15, SMARCA4, CDKN2A	13	32	134.76	1.289e-6	1.015e-4
negative regulation of cell growth	GO:0030308	5	TP53, NPPA, RB1, SMARCA4, CDKN2A	115	32	25.39	1.426e-6	1.098e-4
positive regulation of gene expression	GO:0010628	8	TP53, ATM, P2RX7, MDM2, TNF, CDKN2A, WNT7A, VEGFA	504	32	9.27	1.575e-6	1.191e-4
regulation of cellular response to heat	GO:1900034	3	ATM, MTOR, ATR	15	32	116.79	2.047e-6	1.467e-4
regulation of G1/S transition of mitotic cell cycle	GO:2000045	4	CCND1, RB1, SMARCA4, CDKN2A	57	32	40.98	2.624e-6	1.787e-4
establishment of RNA localization to telomere	GO:0097694	2	ATM, ATR	2	32	583.97	2.841e-6	1.904e-4
establishment of protein-containing complex localization to telomere	GO:0097695	2	ATM, ATR	2	32	583.97	2.841e-6	1.904e-4
positive regulation of telomerase catalytic core complex assembly	GO:1904884	2	ATM, ATR	2	32	583.97	2.841e-6	1.904e-4
positive regulation of transcription by RNA polymerase II	GO:0045944	11	TP53, ATM, IKZF3, RB1, SMARCA4, TNF, CDKN2A, WNT7A, OGG1, VEGFA, WWOX	1208	32	5.32	2.871e-6	1.921e-4