

GeDiPNet Cluster 459 -- 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: 2026-10-19 23:18:22

GO Term	GO ID	Overlap Genes	Overlap Gene Names	Term Gene Count	Cluster Gene Count	Fold Enrichment	P-value	FDR Q-value
double-strand break repair	GO:0006302	4	ATM, TP53, NSD2, BRCA2	87	7	122.74	1.517e-8	2.535e-6
DNA damage response, signal transduction by p53 class mediator	GO:0030330	3	ATM, TP53, BRCA2	48	7	166.85	5.527e-7	5.293e-5
cellular senescence	GO:0090398	3	ATM, TP53, BRCA2	57	7	140.50	9.336e-7	8.133e-5
cell population proliferation	GO:0008283	4	TP53, NOTCH2, KRAS, BRCA2	263	7	40.60	1.298e-6	1.065e-4
regulation of telomere maintenance via telomerase	GO:0032210	2	ATM, POT1	6	7	889.86	1.803e-6	1.394e-4
establishment of protein localization to telomere	GO:0070200	2	POT1, BRCA2	7	7	762.73	2.524e-6	1.827e-4
regulation of double-strand break repair via nonhomologous end joining	GO:2001032	2	POT1, NSD2	8	7	667.39	3.364e-6	2.299e-4
neuron apoptotic process	GO:0051402	3	ATM, TP53, KRAS	98	7	81.72	4.821e-6	3.083e-4
multicellular organism growth	GO:0035264	3	ATM, TP53, NOTCH2	115	7	69.64	7.805e-6	4.506e-4
replicative senescence	GO:0090399	2	ATM, TP53	16	7	333.70	1.440e-5	7.220e-4
cardiac septum morphogenesis	GO:0060411	2	TP53, NOTCH2	16	7	333.70	1.440e-5	7.220e-4
glial cell proliferation	GO:0014009	2	TP53, KRAS	18	7	296.62	1.835e-5	8.673e-4
response to X-ray	GO:0010165	2	TP53, BRCA2	19	7	281.01	2.051e-5	9.419e-4
positive regulation of cellular senescence	GO:2000774	2	TP53, KRAS	20	7	266.96	2.278e-5	1.019e-3
negative regulation of telomere maintenance via telomerase	GO:0032211	2	TP53, POT1	22	7	242.69	2.769e-5	1.178e-3