

DNA replication, GO:0006260

regulation of signal transduction by p53 class mediator, GO:1901796  
nuclear chromosome, GO:0000784  
chromatin, GO:0000785  
transcription-coupled nucleotide-excision repair, GO:0006283  
DNA recombination, GO:0006310  
histone binding, GO:0042393  
single-stranded DNA binding, GO:0003697  
nuclease activity, GO:0004518  
nucleic acid phosphodiester bond hydrolysis, GO:0090305  
double-strand break repair via homologous recombination, GO:0000724  
G1/S transition of mitotic cell cycle, GO:0000082  
regulation of cellular response to heat, GO:1900034  
PML body, GO:0016605  
double-strand break repair, GO:0006302  
regulation of cell cycle, GO:0051726  
damaged DNA binding, GO:0003684  
double-strand break repair via nonhomologous end joining, GO:0006303  
DNA duplex unwinding, GO:0032508  
interstrand cross-link repair, GO:0036297  
iron-sulfur cluster binding, GO:0051536  
DNA damage response, GO:0042769  
double-stranded DNA binding, GO:0003690  
DNA damage response, GO:0006977  
nucleotidyltransferase activity, GO:0016779  
exonuclease activity, GO:0004527  
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nucleotide-excision repair, GO:0006296  
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endonuclease activity, GO:0004519  
telomere maintenance, GO:0000723  
intrinsic apoptotic signaling pathway in response to DNA damage, GO:0008630  
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meiotic cell cycle, GO:0051321  
nucleobase-containing compound metabolic process, GO:0006139  
nucleotide-excision repair, GO:0006297  
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DNA damage checkpoint, GO:0000077  
DNA replication-dependent nucleosome assembly, GO:0006335  
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cellular response to UV, GO:0034644  
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site of double-strand break, GO:0035861  
telomere maintenance via semi-conservative replication, GO:0032201  
ATP-dependent DNA helicase activity, GO:0004003  
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condensed nuclear chromosome, GO:0000794  
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telomeric DNA binding, GO:0042162  
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DNA-dependent ATPase activity, GO:0008094  
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positive regulation of catalytic activity, GO:0043085  
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histone acetyltransferase complex, GO:0000123  
histone deacetylation, GO:0016575  
DNA biosynthetic process, GO:0071897  
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regulation of transcription involved in G1/S transition of mitotic cell cycle, GO:0000083  
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negative regulation of ERBB signaling pathway, GO:1901185  
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