

DNA replication, GO:0006260

nuclear chromosome, GO:0000784
regulation of signal transduction by p53 class mediator, GO:1901796
chromatin, GO:0000785
nucleic acid phosphodiester bond hydrolysis, GO:0090305
nuclease activity, GO:0004518
G1/S transition of mitotic cell cycle, GO:0000082
DNA recombination, GO:0006310
transcription-coupled nucleotide-excision repair, GO:0006283
single-stranded DNA binding, GO:0003697
regulation of cellular response to heat, GO:1900034
peptidyl-serine phosphorylation, GO:0018105
double-strand break repair via nonhomologous end joining, GO:0006303
double-strand break repair via homologous recombination, GO:0000724
PML body, GO:0016605
double-stranded DNA binding, GO:0003690
iron-sulfur cluster binding, GO:0051536
nucleotidyltransferase activity, GO:0016779
double-strand break repair, GO:0006302
damaged DNA binding, GO:0003684
exonuclease activity, GO:0004527
interstrand cross-link repair, GO:0036297
DNA duplex unwinding, GO:0032508
DNA damage response, GO:0006977
endonuclease activity, GO:0004519
chromosome, GO:0000781
mitochondrial nucleoid, GO:0042645
4 iron, GO:0051539
telomere maintenance, GO:0000723
response to ionizing radiation, GO:0010212
response to UV, GO:0009411
meiotic cell cycle, GO:0051321
nucleobase-containing compound metabolic process, GO:0006139
DNA-dependent ATPase activity, GO:0008094
nucleotide-excision repair, GO:0006289
DNA replication-dependent nucleosome assembly, GO:0006335
histone H3 acetylation, GO:0043966
intrinsic apoptotic signaling pathway in response to DNA damage, GO:0008630
replication fork processing, GO:0031297
nucleotide-excision repair, GO:0033683
nucleotide-excision repair, GO:0006296
histone deacetylation, GO:0016575
site of double-strand break, GO:0035861
histone deacetylase activity, GO:0004407
DNA synthesis involved in DNA repair, GO:0000731
ATP-dependent DNA helicase activity, GO:0004003
DNA damage checkpoint, GO:0000077
DNA replication initiation, GO:0006270
translesion synthesis, GO:0019985
cellular response to ionizing radiation, GO:0071479
cellular response to UV, GO:0034644
centrosome cycle, GO:0007098
base-excision repair, GO:0006284
DNA biosynthetic process, GO:0071897
histone acetylation, GO:0016573
mismatch repair, GO:0006298
telomere maintenance via semi-conservative replication, GO:0032201
regulation of transcription involved in G1/S transition of mitotic cell cycle, GO:0000083
DNA-directed DNA polymerase activity, GO:0003887
condensed nuclear chromosome, GO:0000794
strand displacement, GO:0000732
nucleotide-excision repair, GO:0006294
condensed chromosome, GO:0000793
mitotic cell cycle checkpoint, GO:0007093
cell aging, GO:0007569
replication fork, GO:0005657
DNA helicase activity, GO:0003678
neuron apoptotic process, GO:0051402
regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, GO:0051439
nucleobase-containing small molecule interconversion, GO:0015949
nucleotide-excision repair, GO:0006293
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regulation of cyclin-dependent protein serine/threonine kinase activity, GO:0000079
endodeoxyribonuclease activity, GO:0004520
cyclin-dependent protein serine/threonine kinase activity, GO:0004693
nucleotide-excision repair, GO:0006295
embryo development, GO:0009790
ATP-dependent helicase activity, GO:0008026
hydrolase activity, GO:0016788
embryonic organ development, GO:0048568
DNA-dependent DNA replication, GO:0006261
G2 DNA damage checkpoint, GO:0031572
DNA metabolic process, GO:0006259
reciprocal meiotic recombination, GO:0007131
positive regulation of DNA repair, GO:0045739
telomere maintenance via telomerase, GO:0007004
cellular response to gamma radiation, GO:0071480
DNA double-strand break processing, GO:0000729
positive regulation of G2/M transition of mitotic cell cycle, GO:0010971
ESC/E(Z) complex, GO:0035098
positive regulation of DNA replication, GO:0045740
negative regulation of DNA replication, GO:0008156
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core promoter sequence-specific DNA binding, GO:0001046
cyclin binding, GO:0030332
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t-circle formation, GO:0090656
response to X-ray, GO:0010165
DNA replication origin binding, GO:0003688
Sin3 complex, GO:0016580
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histone H4-K8 acetylation, GO:0043982
5'-3' exonuclease activity, GO:0008409
nucleotide metabolic process, GO:0009117
histone mRNA catabolic process, GO:0071044
hydrolase activity, GO:0016818
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RNA polymerase II transcription corepressor activity, GO:0001106
positive regulation of DNA binding, GO:0043388
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positive regulation of protein localization to nucleus, GO:1900182
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MOZ/MORF histone acetyltransferase complex, GO:0070776
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DNA replication checkpoint, GO:0000076
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positive regulation of telomere maintenance, GO:0032206
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NuRD complex, GO:0016581
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protein deacetylase activity, GO:0033558
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regulation of mitotic metaphase/anaphase transition, GO:0030071
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DNA strand elongation involved in DNA replication, GO:0006271
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positive regulation of fibroblast proliferation, GO:0048146
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positive regulation of protein import into nucleus, GO:0033160
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negative regulation of Rho protein signal transduction, GO:0035024
positive regulation of cholesterol efflux, GO:0010875
telomeric D-loop disassembly, GO:0061820
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determination of adult lifespan, GO:0008340
response to organonitrogen compound, GO:0010243
Ctf18 RFC-like complex, GO:0031390
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Y-form DNA binding, GO:0000403
regulation of telomere maintenance, GO:0032204
UV-damage excision repair, GO:0070914
macrophage differentiation, GO:0030225
positive regulation of calcineurin-NFAT signaling cascade, GO:0070886
Swr1 complex, GO:0000812
3'-5' DNA helicase activity, GO:0043138
RNA-DNA hybrid ribonuclease activity, GO:0004523
G-quadruplex DNA binding, GO:0051880
chromosome organization involved in meiotic cell cycle, GO:0070192
cellular glucose homeostasis, GO:0001678
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DNA clamp loader activity, GO:0003689
GTP-Rho binding, GO:0017049
3'-UTR-mediated mRNA destabilization, GO:0061158
peptidyl-lysine deacetylation, GO:0034983
four-way junction helicase activity, GO:0009378
peptidyl-lysine acetylation, GO:0018394
MutSalpha complex binding, GO:0032407
epsilon DNA polymerase complex, GO:0008622
positive regulation of nuclear cell cycle DNA replication, GO:0010571
5'-deoxyribose-5-phosphate lyase activity, GO:0051575
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chiasma assembly, GO:0051026
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protein acetylation, GO:0006473
DNA-directed RNA polymerase II, GO:0016591
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positive regulation of DNA-directed DNA polymerase activity, GO:1900264
DNA topoisomerase activity, GO:0003916
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neurotransmitter catabolic process, GO:0042135
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negative regulation of TORC1 signaling, GO:1904262
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transmembrane receptor protein tyrosine kinase activator activity, GO:0030297
Mre11 complex, GO:0030870
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