

DNA replication, GO:0006260

helicase activity, GO:0004386
regulation of signal transduction by p53 class mediator, GO:1901796
nuclear chromosome, GO:0000784
histone binding, GO:0042393
chromatin, GO:0000785
G1/S transition of mitotic cell cycle, GO:0000082
DNA recombination, GO:0006310
regulation of cellular response to heat, GO:1900034
PML body, GO:0016605
regulation of cell cycle, GO:0051726
double-strand break repair via homologous recombination, GO:0000724
transcription-coupled nucleotide-excision repair, GO:0006283
single-stranded DNA binding, GO:0003697
nucleotidyltransferase activity, GO:0016779
double-stranded DNA binding, GO:0003690
nuclease activity, GO:0004518
nucleic acid phosphodiester bond hydrolysis, GO:0090305
double-strand break repair via nonhomologous end joining, GO:0006303
double-strand break repair, GO:0006302
damaged DNA binding, GO:0003684
DNA duplex unwinding, GO:0032508
interstrand cross-link repair, GO:0036297
iron-sulfur cluster binding, GO:0051536
DNA replication initiation, GO:0006270
DNA damage response, GO:0042769
histone H3 acetylation, GO:0043966
mitochondrial nucleoid, GO:0042645
site of double-strand break, GO:0035861
chromosome, GO:0000781
DNA damage response, GO:0006977
exonuclease activity, GO:0004527
endonuclease activity, GO:0004519
translesion synthesis, GO:0019985
intrinsic apoptotic signaling pathway in response to DNA damage, GO:0008630
telomere maintenance, GO:0000723
4 iron, GO:0051539
meiotic cell cycle, GO:0051321
nucleobase-containing compound metabolic process, GO:0006139
nucleotide-excision repair, GO:0006296
histone deacetylation, GO:0016575
replication fork processing, GO:0031297
nucleotide-excision repair, GO:0033683
DNA helicase activity, GO:0003678
DNA damage checkpoint, GO:0000077
RNA phosphodiester bond hydrolysis, GO:0090502
response to UV, GO:0009411
DNA synthesis involved in DNA repair, GO:0000731
ATP-dependent DNA helicase activity, GO:0004003
DNA biosynthetic process, GO:0071897
cellular response to UV, GO:0034644
nucleotide-excision repair, GO:0006289
response to ionizing radiation, GO:0010212
condensed chromosome, GO:0000793
histone deacetylase activity, GO:0004407
cellular response to ionizing radiation, GO:0071479
telomere maintenance via semi-conservative replication, GO:0032201
DNA-directed DNA polymerase activity, GO:0003887
nucleocytoplasmic transport, GO:0006913
cell aging, GO:0007569
regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle, GO:0051439
strand displacement, GO:0000732
mismatch repair, GO:0006298
error-prone translesion synthesis, GO:0042276
regulation of cyclin-dependent protein serine/threonine kinase activity, GO:0000079
neuron apoptotic process, GO:0051402
nucleotide-excision repair, GO:0006294
nucleotide-excision repair, GO:0006297
DNA-dependent ATPase activity, GO:0008094
DNA replication-dependent nucleosome assembly, GO:0006335
base-excision repair, GO:0006284
nucleobase-containing small molecule interconversion, GO:0015949
mitotic cell cycle checkpoint, GO:0007093
error-free translesion synthesis, GO:0070987
regulation of transcription involved in G1/S transition of mitotic cell cycle, GO:0000083
positive regulation of fibroblast proliferation, GO:0048146
cellular response to gamma radiation, GO:0071480
condensed nuclear chromosome, GO:0000794
telomeric DNA binding, GO:0042162
RNA polymerase II transcription corepressor activity, GO:0001106
G2 DNA damage checkpoint, GO:0031572
DNA-dependent DNA replication, GO:0006261
positive regulation of DNA repair, GO:0045739
histone H4-K5 acetylation, GO:0043981
histone H4-K8 acetylation, GO:0043982
DNA replication-independent nucleosome assembly, GO:0006336
mitochondrion morphogenesis, GO:0070584
reciprocal meiotic recombination, GO:0007131
isotype switching, GO:0045190
histone acetylation, GO:0016573
enzyme activator activity, GO:0008047
response to X-ray, GO:0010165
3'-5' exonuclease activity, GO:0008408
chromosome organization, GO:0051276
endodeoxyribonuclease activity, GO:0004520
telomere maintenance via telomerase, GO:0007004
ATP-dependent helicase activity, GO:0008026
cyclin-dependent protein kinase holoenzyme complex, GO:0000307
DNA replication origin binding, GO:0003688
DNA double-strand break processing, GO:0000729
DNA metabolic process, GO:0006259
cyclin binding, GO:0030332
regulation of DNA replication, GO:0006275
transferase activity, GO:0016747
embryonic organ development, GO:0048568
response to cadmium ion, GO:0046686
intracellular estrogen receptor signaling pathway, GO:0030520
mitotic sister chromatid cohesion, GO:0007064
embryo development, GO:0009790
MCM complex, GO:0042555
replication fork, GO:0005657
regulation of double-strand break repair via homologous recombination, GO:0010569
mitotic DNA replication checkpoint, GO:0033314
ESC/E(Z) complex, GO:0035098
response to gamma radiation, GO:0010332
nucleotide-excision repair, GO:0006293
single-stranded DNA-dependent ATPase activity, GO:0043142
intra-S DNA damage checkpoint, GO:0031573
DNA unwinding involved in DNA replication, GO:0006268
postreplication repair, GO:0006301
nuclear pore organization, GO:0006999
four-way junction DNA binding, GO:0000400
nuclear origin of replication recognition complex, GO:0005664
crossover junction endodeoxyribonuclease activity, GO:0008821
nucleosome disassembly, GO:0006337
mitotic G1 DNA damage checkpoint, GO:0031571
nucleotide metabolic process, GO:0009117
nucleotide-excision repair, GO:0006295
nuclear pore outer ring, GO:0031080
positive regulation of chromatin binding, GO:0035563
GTP-Rho binding, GO:0017049
DNA damage response, GO:0006978
response to UV-C, GO:0010225
DNA replication factor A complex, GO:0005662
circadian rhythm, GO:0007623
response to hormone, GO:0009725
positive regulation of DNA replication, GO:0045740
positive regulation of telomere maintenance, GO:0032206
inner cell mass cell proliferation, GO:0001833
positive regulation of protein localization to nucleus, GO:1900182
t-circle formation, GO:0090656
cellular response to glucose stimulus, GO:0071333
core promoter sequence-specific DNA binding, GO:0001046
protein deacetylase activity, GO:0033558
regulation of telomere maintenance, GO:0032204
cell cycle checkpoint, GO:0000075
DNA strand elongation involved in DNA replication, GO:0006271
Ctf18 RFC-like complex, GO:0031390
cellular response to hydroxyurea, GO:0072711
female gamete generation, GO:0007292
negative regulation of telomere maintenance via telomere lengthening, GO:1904357
ovarian follicle development, GO:0001541
mitotic G2 DNA damage checkpoint, GO:0007095
hydrolase activity, GO:0016818
DNA double-strand break processing involved in repair via single-strand annealing, GO:0010792
chromo shadow domain binding, GO:0070087
DNA ligation, GO:0006266
NURF complex, GO:0016589
negative regulation of double-strand break repair via homologous recombination, GO:2000042
positive regulation of double-strand break repair, GO:2000781
nuclear inclusion body, GO:0042405
positive regulation of G2/M transition of mitotic cell cycle, GO:0010971
positive regulation of transcription elongation from RNA polymerase II promoter, GO:0032968
negative regulation of growth, GO:0045926
telomere maintenance via recombination, GO:0000722
DNA clamp loader activity, GO:0003689
attachment of mitotic spindle microtubules to kinetochore, GO:0051315
histone H4-K12 acetylation, GO:0043983
histone mRNA catabolic process, GO:0071044
nuclear pore complex assembly, GO:0051292
protein localization to chromosome, GO:0070198
5'-3' exonuclease activity, GO:0008409
protein localization to kinetochore, GO:0034501
DNA ligation involved in DNA repair, GO:0051103
activation of innate immune response, GO:0002218
male germ cell nucleus, GO:0001673
histone phosphorylation, GO:0016572
protein hexamerization, GO:0034214
cellular metabolic process, GO:0044237
regulation of transcription from RNA polymerase III promoter, GO:0006359
chromatin assembly, GO:0031497
DNA replication factor C complex, GO:0005663
nuclear pore nuclear basket, GO:0044615
alpha DNA polymerase:primase complex, GO:0005658
Sin3 complex, GO:0016580
telomeric D-loop disassembly, GO:0061820
negative regulation of DNA replication, GO:0008156
cAMP response element binding, GO:0035497
resolution of meiotic recombination intermediates, GO:0000712
positive regulation of DNA damage response, GO:0043517
response to growth hormone, GO:0060416
cellular response to dopamine, GO:1903351
negative regulation of TORC1 signaling, GO:1904262
nuclear replication fork, GO:0043596
negative regulation of telomerase activity, GO:0051974
positive regulation of protein secretion, GO:0050714
positive regulation of DNA-directed DNA polymerase activity, GO:1900264
BRCA1-A complex, GO:0070531
ERK1 and ERK2 cascade, GO:0070371
oocyte development, GO:0048599
positive regulation of mRNA catabolic process, GO:0061014
somatic hypermutation of immunoglobulin genes, GO:0016446
regulation of gene silencing, GO:0060968
Swr1 complex, GO:0000812
transcription from mitochondrial promoter, GO:0006390
regulation of phosphorylation, GO:0042325
positive regulation of protein import into nucleus, GO:0033160
mitochondrial genome maintenance, GO:0000002
MOZ/MORF histone acetyltransferase complex, GO:0070776
positive regulation of kinase activity, GO:0033674
negative regulation of transcription elongation from RNA polymerase II promoter, GO:0034244
positive regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway, GO:1902237
viral genome replication, GO:0019079
response to hyperoxia, GO:0055093
regulation of gene expression by genetic imprinting, GO:0006349
cellular response to xenobiotic stimulus, GO:0071466
positive regulation of transcription of nuclear large rRNA transcript from RNA polymerase I promoter, GO:1901838
nonhomologous end joining complex, GO:0070419
glucocorticoid receptor signaling pathway, GO:0042921
positive regulation of insulin-like growth factor receptor signaling pathway, GO:0043568
pyrimidine nucleoside catabolic process, GO:0046135
negative regulation of Rho protein signal transduction, GO:0035024
positive regulation of protein autophosphorylation, GO:0031954
positive regulation of DNA-templated transcription, GO:0032786
chromatin-mediated maintenance of transcription, GO:0048096
G-rich strand telomeric DNA binding, GO:0098505
salivary gland morphogenesis, GO:0007435
nucleotide phosphorylation, GO:0046939
annealing helicase activity, GO:0036310
response to L-glutamate, GO:1902065
basal lamina, GO:0005605
protein deacetylation, GO:0006476
regulation of cell cycle process, GO:0010564
Y-form DNA binding, GO:0000403
fatty acid homeostasis, GO:0055089
negative regulation of circadian rhythm, GO:0042754
leptin-mediated signaling pathway, GO:0033210
regulation of DNA damage checkpoint, GO:2000001
regulation of mitotic metaphase/anaphase transition, GO:0030071
gamma-tubulin ring complex, GO:0008274
negative regulation of DNA biosynthetic process, GO:2000279
negative regulation of protein localization to nucleus, GO:1900181
multicellular organism aging, GO:0010259
STAT protein import into nucleus, GO:0007262
chromosome separation, GO:0051304
positive regulation of nuclear cell cycle DNA replication, GO:0010571
DNA replication, GO:0006269
5'-deoxyribose-5-phosphate lyase activity, GO:0051575
kinetochore organization, GO:0051383
DNA strand renaturation, GO:0000733
myoblast differentiation, GO:0045445
response to amine, GO:0014075
regulation of protein localization to cell surface, GO:2000008
DNA topological change, GO:0006265
cell activation, GO:0001775
activation of protein kinase B activity, GO:0032148
3'-UTR-mediated mRNA destabilization, GO:0061158
regulation of transcription from RNA polymerase II promoter in response to oxidative stress, GO:0043619
meiotic chromosome condensation, GO:0010032
checkpoint clamp complex, GO:0030896
origin recognition complex, GO:0000808
replication fork protection, GO:0048478
protein localization to chromosome, GO:0034502
ATP-dependent 3'-5' DNA helicase activity, GO:0043140
regulation of telomere maintenance via telomerase, GO:0032210
positive regulation of adaptive immune response, GO:0002821
DNA ligase (ATP) activity, GO:0003910
regulation of DNA methylation, GO:0044030
response to copper ion, GO:0046688
negative regulation of mitotic nuclear division, GO:0045839
positive regulation of histone phosphorylation, GO:0033129