

DNA replication, GO:0006260

regulation of signal transduction by p53 class mediator, GO:1901796
nuclear chromosome, GO:0000784
chromatin, GO:0000785
single-stranded DNA binding, GO:0003697
histone binding, GO:0042393
PML body, GO:0016605
DNA recombination, GO:0006310
transcription-coupled nucleotide-excision repair, GO:0006283
nuclease activity, GO:0004518
double-stranded DNA binding, GO:0003690
nucleic acid phosphodiester bond hydrolysis, GO:0090305
G1/S transition of mitotic cell cycle, GO:0000082
double-strand break repair via homologous recombination, GO:0000724
peptidyl-serine phosphorylation, GO:0018105
regulation of cell cycle, GO:0051726
meiotic cell cycle, GO:0051321
nucleotidyltransferase activity, GO:0016779
double-strand break repair via nonhomologous end joining, GO:0006303
iron-sulfur cluster binding, GO:0051536
histone deacetylation, GO:0016575
damaged DNA binding, GO:0003684
mitochondrial nucleoid, GO:0042645
endonuclease activity, GO:0004519
DNA damage response, GO:0006977
histone deacetylase activity, GO:0004407
double-strand break repair, GO:0006302
chromosome, GO:0000781
interstrand cross-link repair, GO:0036297
mismatch repair, GO:0006298
nucleotide-excision repair, GO:0033683
DNA duplex unwinding, GO:0032508
4 iron, GO:0051539
site of double-strand break, GO:0035861
response to ionizing radiation, GO:0010212
nucleotide-excision repair, GO:0006296
base-excision repair, GO:0006284
condensed nuclear chromosome, GO:0000794
exonuclease activity, GO:0004527
intrinsic apoptotic signaling pathway in response to DNA damage, GO:0008630
DNA replication initiation, GO:0006270
nucleobase-containing compound metabolic process, GO:0006139
nucleotide-excision repair, GO:0006289
DNA-dependent ATPase activity, GO:0008094
mitotic cell cycle checkpoint, GO:0007093
DNA damage checkpoint, GO:0000077
telomere maintenance, GO:0000723
cellular response to ionizing radiation, GO:0071479
translesion synthesis, GO:0019985
telomere maintenance via semi-conservative replication, GO:0032201
DNA biosynthetic process, GO:0071897
nucleotide-excision repair, GO:0006294
cellular response to hydrogen peroxide, GO:0070301
reciprocal meiotic recombination, GO:0007131
nucleobase-containing small molecule interconversion, GO:0015949
condensed chromosome, GO:0000793
positive regulation of fibroblast proliferation, GO:0048146
methylated histone binding, GO:0035064
response to UV, GO:0009411
ATP-dependent DNA helicase activity, GO:0004003
regulation of transcription involved in G1/S transition of mitotic cell cycle, GO:0000083
RNA polymerase II repressing transcription factor binding, GO:0001103
cellular response to gamma radiation, GO:0071480
nucleotide-excision repair, GO:0006293
replication fork, GO:0005657
nucleotide-excision repair, GO:0006295
histone H3 acetylation, GO:0043966
histone acetylation, GO:0016573
DNA replication-dependent nucleosome assembly, GO:0006335
centrosome cycle, GO:0007098
neuron apoptotic process, GO:0051402
RNA polymerase II transcription corepressor activity, GO:0001106
mitochondrion morphogenesis, GO:0070584
G2 DNA damage checkpoint, GO:0031572
cyclin-dependent protein serine/threonine kinase activity, GO:0004693
replication fork processing, GO:0031297
DNA synthesis involved in DNA repair, GO:0000731
embryo development, GO:0009790
DNA-directed DNA polymerase activity, GO:0003887
regulation of DNA replication, GO:0006275
regulation of cyclin-dependent protein serine/threonine kinase activity, GO:0000079
DNA helicase activity, GO:0003678
DNA replication origin binding, GO:0003688
positive regulation of DNA repair, GO:0045739
four-way junction DNA binding, GO:0000400
telomeric DNA binding, GO:0042162
strand displacement, GO:0000732
DNA metabolic process, GO:0006259
3'-5' exonuclease activity, GO:0008408
regulation of double-strand break repair via homologous recombination, GO:0010569
mitotic G2 DNA damage checkpoint, GO:0007095
protein deacetylase activity, GO:0033558
DNA-dependent DNA replication, GO:0006261
cyclin-dependent protein kinase holoenzyme complex, GO:0000307
chromosome organization, GO:0051276
embryonic organ development, GO:0048568
cellular response to glucose stimulus, GO:0071333
protein deacetylation, GO:0006476
positive regulation of protein localization to nucleus, GO:1900182
cell aging, GO:0007569
endodeoxyribonuclease activity, GO:0004520
synapsis, GO:0007129
ESC/E(Z) complex, GO:0035098
branching morphogenesis of an epithelial tube, GO:0048754
DNA replication-independent nucleosome assembly, GO:0006336
histone acetyltransferase complex, GO:0000123
cellular response to hydroxyurea, GO:0072711
response to X-ray, GO:0010165
DNA double-strand break processing, GO:0000729
inner cell mass cell proliferation, GO:0001833
response to gamma radiation, GO:0010332
positive regulation of DNA replication, GO:0045740
nuclear inclusion body, GO:0042405
positive regulation of protein autophosphorylation, GO:0031954
DNA-directed RNA polymerase II, GO:0016591
NuRD complex, GO:0016581
intra-S DNA damage checkpoint, GO:0031573
chromatin silencing complex, GO:0005677
regulation of gene silencing, GO:0060968
positive regulation of cilium assembly, GO:0045724
t-circle formation, GO:0090656
postreplication repair, GO:0006301
intracellular estrogen receptor signaling pathway, GO:0030520
mitotic G1 DNA damage checkpoint, GO:0031571
protein localization to kinetochore, GO:0034501
nucleocytoplasmic transport, GO:0006913
nuclear origin of replication recognition complex, GO:0005664
GTP-Rho binding, GO:0017049
positive regulation of transcription of nuclear large rRNA transcript from RNA polymerase I promoter, GO:1901838
DNA unwinding involved in DNA replication, GO:0006268
Sin3 complex, GO:0016580
glucocorticoid receptor signaling pathway, GO:0042921
mitotic sister chromatid cohesion, GO:0007064
lateral element, GO:0000800
DNA clamp loader activity, GO:0003689
positive regulation of telomere maintenance, GO:0032206
histone mRNA catabolic process, GO:0071044
Cul4A-RING E3 ubiquitin ligase complex, GO:0031464
isotype switching, GO:0045190
3'-UTR-mediated mRNA destabilization, GO:0061158
negative regulation of telomere maintenance via telomere lengthening, GO:1904357
regulation of telomere maintenance, GO:0032204
cyclin binding, GO:0030332
insulin-like growth factor receptor signaling pathway, GO:0048009
negative regulation of intracellular estrogen receptor signaling pathway, GO:0033147
regulation of mitotic metaphase/anaphase transition, GO:0030071
telomere maintenance via recombination, GO:0000722
regulation of DNA damage checkpoint, GO:2000001
negative regulation of histone H3-K9 trimethylation, GO:1900113
cAMP response element binding, GO:0035497
positive regulation of epidermal growth factor-activated receptor activity, GO:0045741
response to UV-C, GO:0010225
histone H4-K5 acetylation, GO:0043981
histone H4-K8 acetylation, GO:0043982
negative regulation of DNA recombination, GO:0045910
negative regulation of interleukin-2 production, GO:0032703
negative regulation of Rho protein signal transduction, GO:0035024
positive regulation of cholesterol efflux, GO:0010875
regulation of protein localization to cell surface, GO:2000008
MCM complex, GO:0042555
MOZ/MORF histone acetyltransferase complex, GO:0070776
G-quadruplex DNA binding, GO:0051880