

DNA replication, GO:0006260

regulation of signal transduction by p53 class mediator, GO:1901796
nuclear chromosome, GO:0000784
histone binding, GO:0042393
chromatin, GO:0000785
transcription-coupled nucleotide-excision repair, GO:0006283
nuclease activity, GO:0004518
DNA recombination, GO:0006310
G1/S transition of mitotic cell cycle, GO:0000082
single-stranded DNA binding, GO:0003697
nucleic acid phosphodiester bond hydrolysis, GO:0090305
peptidyl-serine phosphorylation, GO:0018105
double-strand break repair via homologous recombination, GO:0000724
regulation of cellular response to heat, GO:1900034
iron-sulfur cluster binding, GO:0051536
double-stranded DNA binding, GO:0003690
damaged DNA binding, GO:0003684
nucleotidyltransferase activity, GO:0016779
DNA duplex unwinding, GO:0032508
PML body, GO:0016605
double-strand break repair via nonhomologous end joining, GO:0006303
interstrand cross-link repair, GO:0036297
endonuclease activity, GO:0004519
4 iron, GO:0051539
DNA replication-dependent nucleosome assembly, GO:0006335
nucleotide-excision repair, GO:0033683
double-strand break repair, GO:0006302
nucleotide-excision repair, GO:0006296
DNA damage response, GO:0006977
DNA replication initiation, GO:0006270
response to ionizing radiation, GO:0010212
exonuclease activity, GO:0004527
site of double-strand break, GO:0035861
chromosome, GO:0000781
DNA-dependent ATPase activity, GO:0008094
mitochondrial nucleoid, GO:0042645
histone deacetylation, GO:0016575
telomere maintenance via semi-conservative replication, GO:0032201
DNA damage checkpoint, GO:0000077
meiotic cell cycle, GO:0051321
telomere maintenance, GO:0000723
response to UV, GO:0009411
translesion synthesis, GO:0019985
ATP-dependent DNA helicase activity, GO:0004003
nucleobase-containing compound metabolic process, GO:0006139
condensed chromosome, GO:0000793
mismatch repair, GO:0006298
histone H3 acetylation, GO:0043966
DNA synthesis involved in DNA repair, GO:0000731
nucleotide-excision repair, GO:0006294
cellular response to UV, GO:0003464
histone acetylation, GO:0016573
centrosome cycle, GO:0007098
nucleotide-excision repair, GO:0006289
DNA biosynthetic process, GO:0071897
strand displacement, GO:0000732
condensed nuclear chromosome, GO:0000794
base-excision repair, GO:0006284
nucleobase-containing small molecule interconversion, GO:0015949
cellular response to hydrogen peroxide, GO:0070301
DNA helicase activity, GO:0003678
regulation of transcription involved in G1/S transition of mitotic cell cycle, GO:0000083
intrinsic apoptotic signaling pathway in response to DNA damage, GO:0008630
histone deacetylase activity, GO:0004407
replication fork processing, GO:0031297
nucleotide-excision repair, GO:0006293
cellular response to ionizing radiation, GO:0071479
nucleotide-excision repair, GO:0006295
nucleocytoplasmic transport, GO:0006913
RNA polymerase II repressing transcription factor binding, GO:0001103
regulation of cyclin-dependent protein serine/threonine kinase activity, GO:0000079
positive regulation of catalytic activity, GO:0043085
DNA replication origin binding, GO:0003688
DNA-directed DNA polymerase activity, GO:0003887
cell aging, GO:0007569
neuron apoptotic process, GO:0051402
histone H4-K5 acetylation, GO:0043981
histone H4-K8 acetylation, GO:0043982
replication fork, GO:0005657
cyclin binding, GO:0030332
four-way junction DNA binding, GO:0000400
single-stranded DNA-dependent ATPase activity, GO:0043142
telomere maintenance via telomerase, GO:0007004
response to organonitrogen compound, GO:0010243
mitochondrion morphogenesis, GO:0070584
cellular response to gamma radiation, GO:0071480
reciprocal meiotic recombination, GO:0007131
positive regulation of G2/M transition of mitotic cell cycle, GO:0010971
MCM complex, GO:0042555
regulation of double-strand break repair via homologous recombination, GO:0010569
response to gamma radiation, GO:0010332
isotype switching, GO:0045190
cyclin-dependent protein kinase holoenzyme complex, GO:0000307
ESC/E(Z) complex, GO:0035098
regulation of DNA replication, GO:0006275
endodeoxyribonuclease activity, GO:0004520
histone mRNA catabolic process, GO:0071044
DNA-dependent DNA replication, GO:0006261
DNA metabolic process, GO:0006259
branching morphogenesis of an epithelial tube, GO:0048754
nucleotide metabolic process, GO:0009117
3'-5' exonuclease activity, GO:0008408
embryo development, GO:0009790
circadian rhythm, GO:0007623
cellular response to glucose stimulus, GO:0071333
DNA double-strand break processing, GO:0000729
mitotic sister chromatid cohesion, GO:0007064
mitotic DNA replication checkpoint, GO:0033314
positive regulation of DNA binding, GO:0043388
ATP-dependent helicase activity, GO:0008026
somatic hypermutation of immunoglobulin genes, GO:0016446
DNA strand elongation involved in DNA replication, GO:0006271
DNA unwinding involved in DNA replication, GO:0006268
inner cell mass cell proliferation, GO:0001833
positive regulation of chromatin binding, GO:0035563
DNA damage response, GO:0006978
mitotic G2 DNA damage checkpoint, GO:0007095
negative regulation of DNA replication, GO:0008156
nuclear replication fork, GO:00043596
DNA clamp loader activity, GO:0003689
cellular response to hydroxyurea, GO:0072711
enzyme activator activity, GO:0008047
response to hormone, GO:0009725
response to X-ray, GO:0010165
positive regulation of DNA repair, GO:0045739
Ctf18 RFC-like complex, GO:0031390
double-stranded telomeric DNA binding, GO:0003691
transcription from mitochondrial promoter, GO:0006390
intra-S DNA damage checkpoint, GO:0031573
hydrolase activity, GO:0016818
t-circle formation, GO:0090656
RNA polymerase II transcription corepressor activity, GO:0001106
positive regulation of protein localization to nucleus, GO:1900182
DNA topological change, GO:0006265
Swr1 complex, GO:0000812
regulation of DNA damage checkpoint, GO:2000001
RNA-DNA hybrid ribonuclease activity, GO:0004523
protein deacetylation, GO:0006476
postreplication repair, GO:0006301
positive regulation of protein secretion, GO:0050714
response to cadmium ion, GO:0046686
DNA ligation involved in DNA repair, GO:0051103
Sin3 complex, GO:0016580
negative regulation of growth, GO:0045926
histone phosphorylation, GO:0016572
protein localization to chromosome, GO:0070198
positive regulation of mitotic nuclear division, GO:0045840
positive regulation of telomere maintenance, GO:0032206
positive regulation of DNA replication, GO:0045740
5'-3' exonuclease activity, GO:0008409
crossover junction endodeoxyribonuclease activity, GO:0008821
negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator, GO:1902166
Cul4A-RING E3 ubiquitin ligase complex, GO:0031464
replication fork protection complex, GO:0031298
DNA replication factor C complex, GO:0005663
alpha DNA polymerase:primase complex, GO:0005658
negative regulation of DNA recombination, GO:0045910
G2 DNA damage checkpoint, GO:0031572
positive regulation of fibroblast proliferation, GO:0048146
DNA ligation, GO:0006266
glucocorticoid receptor signaling pathway, GO:0042921
positive regulation of cholesterol efflux, GO:0010875
nuclear origin of replication recognition complex, GO:0005664
regulation of gene silencing, GO:0060968
regulation of mitotic metaphase/anaphase transition, GO:0030071
positive regulation of DNA-directed DNA polymerase activity, GO:1900264
histone H4-K12 acetylation, GO:0043983
hydrolase activity, GO:0016788
neural precursor cell proliferation, GO:0061351
DNA-directed RNA polymerase II, GO:0016591
positive regulation of kinase activity, GO:0033674
histone exchange, GO:0043486
negative regulation of Rho protein signal transduction, GO:0035024
protein acetylation, GO:0006473
nucleosome disassembly, GO:0006337
negative regulation of circadian rhythm, GO:0042754
positive regulation of protein autophosphorylation, GO:0031954
DNA replication checkpoint, GO:0000076
positive regulation of cilium assembly, GO:0045724
replicative senescence, GO:0090399
origin recognition complex, GO:0000808
cellular response to lithium ion, GO:0071285
establishment of integrated proviral latency, GO:0075713
nucleotide phosphorylation, GO:0046939
response to copper ion, GO:0046688
stress fiber assembly, GO:0043149
white fat cell differentiation, GO:0050872
negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway, GO:1902176
telomere maintenance via recombination, GO:0000722
chromatin assembly, GO:0031497
3'-5' DNA helicase activity, GO:0043138
positive regulation of histone H3-K9 methylation, GO:0051574
activation of innate immune response, GO:0002218
NuRD complex, GO:0016581
transferase activity, GO:0016747
protein hexamerization, GO:0034214
single strand break repair, GO:0000012
regulation of phosphorylation, GO:0042325
chromosome organization involved in meiotic cell cycle, GO:0070192
gamma-tubulin ring complex, GO:0008274
positive regulation of sister chromatid cohesion, GO:0045876
negative regulation of peptidyl-lysine acetylation, GO:2000757
cellular response to xenobiotic stimulus, GO:0071466
MutLalpha complex binding, GO:0032405
Cul4B-RING E3 ubiquitin ligase complex, GO:0031465
DNA repair complex, GO:1990391
NURF complex, GO:0016589
embryonic retina morphogenesis in camera-type eye, GO:0060059
positive regulation of transcription of nuclear large rRNA transcript from RNA polymerase I promoter, GO:1901838
embryonic cleavage, GO:0040016
female meiotic nuclear division, GO:0007143
negative regulation of cellular senescence, GO:2000773
nuclear inclusion body, GO:0042405
protein deacetylase activity, GO:0033558
negative regulation of intracellular estrogen receptor signaling pathway, GO:0033147
regulation of embryonic development, GO:0045995
negative regulation of TORC1 signaling, GO:1904262
amyloid precursor protein metabolic process, GO:0042982
response to leptin, GO:0044321
MOZ/MORF histone acetyltransferase complex, GO:0070776
G-quadruplex DNA binding, GO:0051880
meiotic chromosome condensation, GO:0010032
5'-flap endonuclease activity, GO:0017108
cell cycle phase transition, GO:0044770
DNA ligase (ATP) activity, GO:0003910
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positive regulation of histone phosphorylation, GO:0033129
positive regulation of double-strand break repair, GO:2000781
nonhomologous end joining complex, GO:0070419
negative regulation of transcription regulatory region DNA binding, GO:2000678
synaptic cleft, GO:0043083
regulation of organ growth, GO:0046620
response to UV-C, GO:0010225
cell cycle checkpoint, GO:0000075
negative regulation of DNA damage response, GO:0043518
response to lipid, GO:0033993
pyrimidine nucleoside catabolic process, GO:0046135
ERK1 and ERK2 cascade, GO:0070371
renal system process, GO:0003014
seminiferous tubule development, GO:0072520
negative regulation of transcription elongation from RNA polymerase II promoter, GO:0034244
cellular response to dopamine, GO:1903351
5'-nucleotidase activity, GO:0008253
lateral element, GO:0000800
negative regulation of ERBB signaling pathway, GO:1901185
aminoacyl-tRNA editing activity, GO:0002161
regulation of translational termination, GO:0006449
double-strand break repair via break-induced replication, GO:0000727
positive regulation of histone H4 acetylation, GO:0090240
kinetochore organization, GO:0051383
chiasma assembly, GO:0051026
negative regulation of double-strand break repair via homologous recombination, GO:2000042
positive regulation of epidermal growth factor-activated receptor activity, GO:0045741
mitotic G1 DNA damage checkpoint, GO:0031571
deacetylase activity, GO:0019213
DNA double-strand break processing involved in repair via single-strand annealing, GO:0010792
replication fork protection, GO:0048478
DNA topoisomerase activity, GO:00003916
nuclear pore organization, GO:0006999
Y-form DNA binding, GO:0000403
negative regulation of histone H3-K9 trimethylation, GO:1900113
positive regulation of helicase activity, GO:0051096
regulation of telomere maintenance, GO:0032204
negative regulation of pri-miRNA transcription from RNA polymerase II promoter, GO:1902894
synapsis, GO:0007129
exocytic vesicle, GO:0070382
viral genome replication, GO:0019079
negative regulation of mitotic nuclear division, GO:0045839
protein K6-linked ubiquitination, GO:0085020
response to hyperoxia, GO:0055093
negative regulation of interleukin-2 production, GO:0032703