
methyltransferase activity, GO:0008168
tRNA processing, GO:0008033
tRNA binding, GO:0000049
negative regulation of gene expression, GO:0045814
p53 binding, GO:0002039
regulation of megakaryocyte differentiation, GO:0045652
stem cell population maintenance, GO:0019827
histone-lysine N-methyltransferase activity, GO:0018024
tRNA modification, GO:0006400
heat shock protein binding, GO:0031072
7-methylguanosine mRNA capping, GO:0006370
response to toxic substance, GO:0009636
histone methyltransferase complex, GO:0035097
tRNA methylation, GO:0030488
histone lysine methylation, GO:0034968
RNA polymerase II core promoter sequence-specific DNA binding, GO:0000979
response to ethanol, GO:0045471
histone H3-K4 methylation, GO:0051568
histone methylation, GO:0016571
lysine-acetylated histone binding, GO:0070577
protein-lysine N-methyltransferase activity, GO:0016279
histone methyltransferase activity (H3-K4 specific), GO:0042800
germ cell development, GO:0007281
Set1C/COMPASS complex, GO:0048188
regulation of protein binding, GO:0043393
ubiquinone biosynthetic process, GO:0006744
protein methyltransferase activity, GO:0008276
MLL3/4 complex, GO:0044666
DNA methylation involved in gamete generation, GO:0043046
response to cocaine, GO:0042220
histone methyltransferase activity, GO:0042054
S-adenosylmethionine-dependent methyltransferase activity, GO:0008757
oxidoreductase activity, GO:0016706
retinoic acid receptor binding, GO:0042974
positive regulation of histone H3-K4 methylation, GO:0051571
positive regulation of mitochondrial translation, GO:0070131
RNA methylation, GO:0001510
homeostasis of number of cells within a tissue, GO:0048873
rRNA methylation, GO:0031167
ferrous iron binding, GO:0008198
neurogenesis, GO:0022008
promoter-specific chromatin binding, GO:1990841
fertilization, GO:0009566
RNA methyltransferase activity, GO:0008173
histone H3-K4 trimethylation, GO:0080182
negative regulation of G1/S transition of mitotic cell cycle, GO:2000134
extrinsic component of mitochondrial inner membrane, GO:0031314
response to vitamin A, GO:0033189
endothelial cell activation, GO:0042118
peptidyl-lysine methylation, GO:0018022
phosphatidylethanolamine binding, GO:0008429
L-serine metabolic process, GO:0006563
regulation of mitochondrial translation, GO:0070129
left/right axis specification, GO:0070986
tetrahydrofolate interconversion, GO:0035999
histone H3-K27 methylation, GO:0070734
mitogen-activated protein kinase p38 binding, GO:0048273
one-carbon metabolic process, GO:0006730
peptidyl-arginine N-methylation, GO:0035246
rRNA modification, GO:0000154
methionine biosynthetic process, GO:0009086
methyl-CpG binding, GO:0008327
skeletal muscle tissue development, GO:0007519
response to nutrient levels, GO:0031667
regulation of mitotic cell cycle spindle assembly checkpoint, GO:0090266
glycerophospholipid metabolic process, GO:0006650
tetrahydrofolate metabolic process, GO:0046653
protein-arginine N-methyltransferase activity, GO:0016274
chromatin silencing at telomere, GO:0006348
mRNA methylation, GO:0080009
histone H3-K27 trimethylation, GO:0098532
L-serine biosynthetic process, GO:0006564
peptidyl-lysine trimethylation, GO:0018023
tRNA wobble uridine modification, GO:0002098
regulation of peptidyl-serine phosphorylation, GO:0033135
peptidyl-diphthamide biosynthetic process from peptidyl-histidine, GO:0017183
response to type I interferon, GO:0034340
histone methyltransferase activity (H3-K27 specific), GO:0046976
histidine catabolic process, GO:0006548
peptidyl-lysine monomethylation, GO:0018026
peroxisome proliferator activated receptor binding, GO:0042975
cobalamin binding, GO:0031419
auditory receptor cell development, GO:0060117
histone H3-K36 methylation, GO:0010452
regulation of mRNA export from nucleus, GO:0010793
histone methyltransferase activity (H3-K36 specific), GO:0046975
translation repressor activity, GO:0000900
O-methyltransferase activity, GO:0008171