

**methyltransferase activity, GO:0008168**

- tRNA processing, GO:0008033
- rhythmic process, GO:0048511
- regulation of megakaryocyte differentiation, GO:0045652
- p53 binding, GO:0002039
- stem cell population maintenance, GO:0019827
- heat shock protein binding, GO:0031072
- 7-methylguanosine mRNA capping, GO:0006370
- chromatin organization, GO:0006325
- response to toxic substance, GO:0009636
- negative regulation of gene expression, GO:0045814
- histone-lysine N-methyltransferase activity, GO:0018024
- tRNA binding, GO:0000049
- response to ethanol, GO:0045471
- tRNA modification, GO:0006400
- histone lysine methylation, GO:0034968
- histone methyltransferase complex, GO:0035097
- tRNA methylation, GO:0030488
- protein-lysine N-methyltransferase activity, GO:0016279
- RNA polymerase II core promoter sequence-specific DNA binding, GO:0000979
- S-adenosylmethionine-dependent methyltransferase activity, GO:0008757
- thyroid hormone receptor binding, GO:0046966
- histone methyltransferase activity (H3-K4 specific), GO:0042800
- histone H3-K4 methylation, GO:0051568
- histone methylation, GO:0016571
- germ cell development, GO:0007281
- RNA methyltransferase activity, GO:0008173
- histone H3-K4 trimethylation, GO:0080182
- RNA methylation, GO:0001510
- Set1C/COMPASS complex, GO:0048188
- ferrous iron binding, GO:0008198
- promoter-specific chromatin binding, GO:1990841
- peptidyl-lysine methylation, GO:0018022
- lysine-acetylated histone binding, GO:0070577
- homeostasis of number of cells within a tissue, GO:0048873
- methionine biosynthetic process, GO:0009086
- rRNA methylation, GO:0031167
- one-carbon metabolic process, GO:0006730
- regulation of DNA methylation, GO:0044030
- sulfur amino acid metabolic process, GO:0000096
- neurogenesis, GO:0022008
- histidine catabolic process, GO:0006548
- TFIID-class transcription factor binding, GO:0001094
- ubiquinone biosynthetic process, GO:0006744
- positive regulation of histone H3-K4 methylation, GO:0051571
- DNA methylation involved in gamete generation, GO:0043046
- regulation of response to DNA damage stimulus, GO:2001020
- regulation of gluconeogenesis, GO:0006111
- Golgi ribbon formation, GO:0090161
- glycerophospholipid metabolic process, GO:0006650
- MLL3/4 complex, GO:0044666
- peptidyl-lysine monomethylation, GO:0018026
- regulation of erythrocyte differentiation, GO:0045646
- regulation of protein binding, GO:0043393
- regulation of histone H3-K4 methylation, GO:0051569
- tetrahydrofolate interconversion, GO:0035999
- regulation of cysteine-type endopeptidase activity involved in apoptotic process, GO:0043281
- regulation of mRNA export from nucleus, GO:0010793
- cardiac muscle hypertrophy in response to stress, GO:0014898
- positive regulation of mitochondrial translation, GO:0070131
- chromatin silencing at telomere, GO:0006348
- estrogen metabolic process, GO:0008210
- skeletal muscle tissue development, GO:0007519
- definitive hemopoiesis, GO:0060216
- nucleoside-triphosphate diphosphatase activity, GO:0047429
- glycerol metabolic process, GO:0006071
- protein methyltransferase activity, GO:0008276
- mitochondrial tRNA methylation, GO:0070901
- fertilization, GO:0009566
- amine metabolic process, GO:0009308
- mammary gland epithelial cell differentiation, GO:0060644
- cofactor binding, GO:0048037
- peroxisome proliferator activated receptor binding, GO:0042975
- peptidyl-diphthamide biosynthetic process from peptidyl-histidine, GO:0017183
- catecholamine biosynthetic process, GO:0042423
- L-serine metabolic process, GO:0006563
- peptidyl-lysine trimethylation, GO:0018023
- histone H3-K36 methylation, GO:0010452
- histone methyltransferase activity (H3-K36 specific), GO:0046975
- extrinsic component of mitochondrial inner membrane, GO:0031314
- catecholamine metabolic process, GO:0006584
- negative regulation of ATPase activity, GO:0032780
- tetrahydrofolate metabolic process, GO:0046653
- rRNA base methylation, GO:0070475
- phosphatidylethanolamine binding, GO:0008429
- O-methyltransferase activity, GO:0008171
- folic acid metabolic process, GO:0046655
- response to cocaine, GO:0042220
- endothelial cell activation, GO:0042118
- protein-arginine N-methyltransferase activity, GO:0016274
- negative regulation of autophagosome assembly, GO:1902902
- histone H3-K27 trimethylation, GO:0098532
- mRNA methylation, GO:0080009
- S-adenosylmethionine metabolic process, GO:0046500
- choline catabolic process, GO:0042426
- positive regulation of neural precursor cell proliferation, GO:2000179