

methyltransferase activity, GO:0008168

- tRNA processing, GO:0008033
- regulation of megakaryocyte differentiation, GO:0045652
- tRNA binding, GO:0000049
- p53 binding, GO:0002039
- tRNA methylation, GO:0030488
- response to toxic substance, GO:0009636
- 7-methylguanosine mRNA capping, GO:0006370
- tRNA modification, GO:0006400
- stem cell population maintenance, GO:0019827
- histone-lysine N-methyltransferase activity, GO:0018024
- RNA polymerase II core promoter sequence-specific DNA binding, GO:0000979
- response to ethanol, GO:0045471
- regulation of protein binding, GO:0043393
- histone methylation, GO:0016571
- germ cell development, GO:0007281
- oxidoreductase activity, GO:0016706
- histone methyltransferase complex, GO:0035097
- RNA methyltransferase activity, GO:0008173
- RNA methylation, GO:0001510
- positive regulation of histone H3-K4 methylation, GO:0051571
- histone H3-K4 methylation, GO:0051568
- ferrous iron binding, GO:0008198
- protein-lysine N-methyltransferase activity, GO:0016279
- histone methyltransferase activity (H3-K4 specific), GO:0042800
- rRNA methylation, GO:0031167
- positive regulation of mitochondrial translation, GO:0070131
- methionine biosynthetic process, GO:0009086
- retinoic acid receptor binding, GO:0042974
- homeostasis of number of cells within a tissue, GO:0048873
- ubiquinone biosynthetic process, GO:0006744
- Set1C/COMPASS complex, GO:0048188
- regulation of DNA methylation, GO:0044030
- TFIID-class transcription factor binding, GO:0001094
- neurogenesis, GO:0022008
- histone methyltransferase activity (H3-K36 specific), GO:0046975
- rRNA modification, GO:0000154
- response to vitamin A, GO:0033189
- morphogenesis of a branching structure, GO:0001763
- protein-arginine N-methyltransferase activity, GO:0016274
- promoter-specific chromatin binding, GO:1990841
- fertilization, GO:0009566
- methyl-CpG binding, GO:0008327
- tRNA wobble uridine modification, GO:0002098
- histone H3-K36 methylation, GO:0010452
- histone H3-K4 trimethylation, GO:0080182
- response to nutrient levels, GO:0031667
- folic acid binding, GO:0005542
- histone H3-K27 methylation, GO:0070734
- peptidyl-arginine N-methylation, GO:0035246
- peptidyl-diphthamide biosynthetic process from peptidyl-histidine, GO:0017183
- chromatin silencing at telomere, GO:0006348
- pyrimidine nucleobase metabolic process, GO:0006206
- regulation of peptidyl-serine phosphorylation, GO:0033135
- DNA methylation involved in gamete generation, GO:0043046
- tetrahydrofolate metabolic process, GO:0046653
- MLL3/4 complex, GO:0044666
- response to folic acid, GO:0051593
- rRNA base methylation, GO:0070475
- glycine decarboxylation via glycine cleavage system, GO:0019464
- BRISC complex, GO:0070552
- glycerophospholipid metabolic process, GO:0006650
- extrinsic component of mitochondrial inner membrane, GO:0031314
- mammary gland epithelial cell differentiation, GO:0060644
- protein methyltransferase activity, GO:0008276
- maternal placenta development, GO:0001893
- cellular response to dexamethasone stimulus, GO:0071549
- negative regulation of retinoic acid receptor signaling pathway, GO:0048387
- endothelial cell activation, GO:0042118
- nucleoside-triphosphate diphosphatase activity, GO:0047429
- mRNA methylation, GO:0080009
- protein repair, GO:0030091
- regulation of mRNA export from nucleus, GO:0010793
- tetrahydrofolate interconversion, GO:0035999
- peroxisome proliferator activated receptor binding, GO:0042975
- translation repressor activity, GO:0000900
- sulfur amino acid metabolic process, GO:0000096
- glycerol metabolic process, GO:0006071
- histone methyltransferase activity (H3-K27 specific), GO:0046976