

methyltransferase activity, GO:0008168

- tRNA processing, GO:0008033
- tRNA binding, GO:0000049
- negative regulation of gene expression, GO:0045814
- regulation of megakaryocyte differentiation, GO:0045652
- p53 binding, GO:0002039
- heat shock protein binding, GO:0031072
- stem cell population maintenance, GO:0019827
- tRNA modification, GO:0006400
- small-subunit processome, GO:0032040
- histone methyltransferase complex, GO:0035097
- histone-lysine N-methyltransferase activity, GO:0018024
- promoter-specific chromatin binding, GO:1990841
- tRNA methylation, GO:0030488
- thyroid hormone receptor binding, GO:0046966
- lysine-acetylated histone binding, GO:0070577
- histone H3-K4 methylation, GO:0051568
- response to ethanol, GO:0045471
- germ cell development, GO:0007281
- positive regulation of histone H3-K4 methylation, GO:0051571
- histone methyltransferase activity (H3-K4 specific), GO:0042800
- rRNA modification, GO:0000154
- neurogenesis, GO:0022008
- methyl-CpG binding, GO:0008327
- histone H3-K4 trimethylation, GO:0080182
- positive regulation of mitochondrial translation, GO:0070131
- ubiquinone biosynthetic process, GO:0006744
- S-adenosylmethionine-dependent methyltransferase activity, GO:0008757
- oxidoreductase activity, GO:0016706
- Set1C/COMPASS complex, GO:0048188
- histone methylation, GO:0016571
- cognition, GO:0050890
- RNA methylation, GO:0001510
- skeletal muscle tissue development, GO:0007519
- RNA methyltransferase activity, GO:0008173
- protein-lysine N-methyltransferase activity, GO:0016279
- rRNA methylation, GO:0031167
- histone H3-K36 methylation, GO:0010452
- histone methyltransferase activity (H3-K36 specific), GO:0046975
- tetrahydrofolate metabolic process, GO:0046653
- DNA methylation involved in gamete generation, GO:0043046
- tRNA wobble uridine modification, GO:0002098
- fertilization, GO:0009566
- regulation of mitochondrial translation, GO:0070129
- ferrous iron binding, GO:0008198
- glycerophospholipid metabolic process, GO:0006650
- homeostasis of number of cells within a tissue, GO:0048873
- MLL3/4 complex, GO:0044666
- dopamine metabolic process, GO:0042417
- morphogenesis of a branching structure, GO:0001763
- neutrophil mediated immunity, GO:0002446
- membranous septum morphogenesis, GO:0003149
- glycerol metabolic process, GO:0006071
- regulation of cysteine-type endopeptidase activity involved in apoptotic process, GO:0043281
- mitochondrial tRNA processing, GO:0090646
- maternal placenta development, GO:0001893
- negative regulation of retinoic acid receptor signaling pathway, GO:0048387
- DNA integration, GO:0015074
- peroxisome proliferator activated receptor binding, GO:0042975
- peptidyl-diphthamide biosynthetic process from peptidyl-histidine, GO:0017183
- peptidyl-lysine methylation, GO:0018022
- cofactor binding, GO:0048037
- TFIID-class transcription factor binding, GO:0001094
- methionine biosynthetic process, GO:0009086
- regulation of short-term neuronal synaptic plasticity, GO:0048172
- translation repressor activity, GO:0000900
- O-methyltransferase activity, GO:0008171
- response to nutrient levels, GO:0031667
- negative regulation of MAPK cascade, GO:0043409
- protein-arginine N-methyltransferase activity, GO:0016274
- pericardium development, GO:0060039
- S-adenosylmethionine metabolic process, GO:0046500
- histone H3-K27 trimethylation, GO:0098532
- DNA packaging, GO:0006323
- negative regulation of renal sodium excretion, GO:0035814
- peptidyl-lysine trimethylation, GO:0018023
- regulation of mRNA export from nucleus, GO:0010793
- toxin metabolic process, GO:0009404
- amine metabolic process, GO:0009308
- extrinsic component of mitochondrial inner membrane, GO:0031314