LECTURE 4

HISTONE METHYALTION

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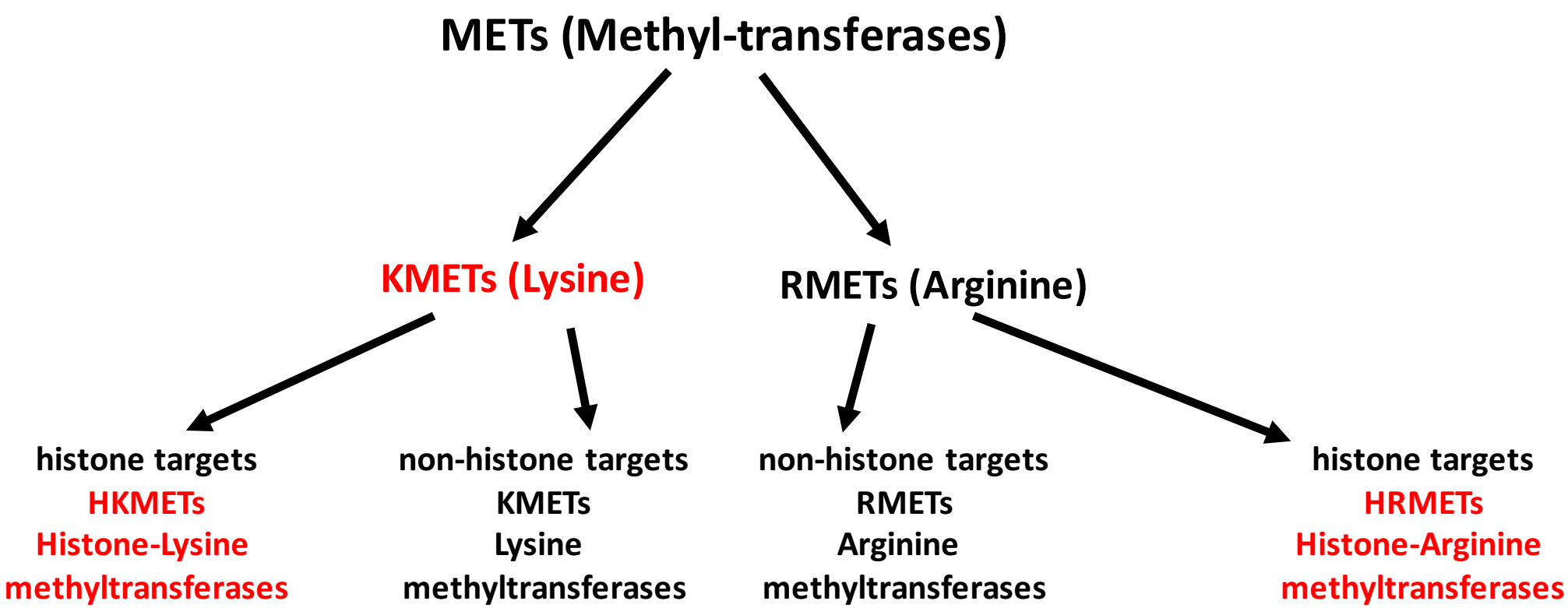
HISTONE METHYALTION MECHANISMS

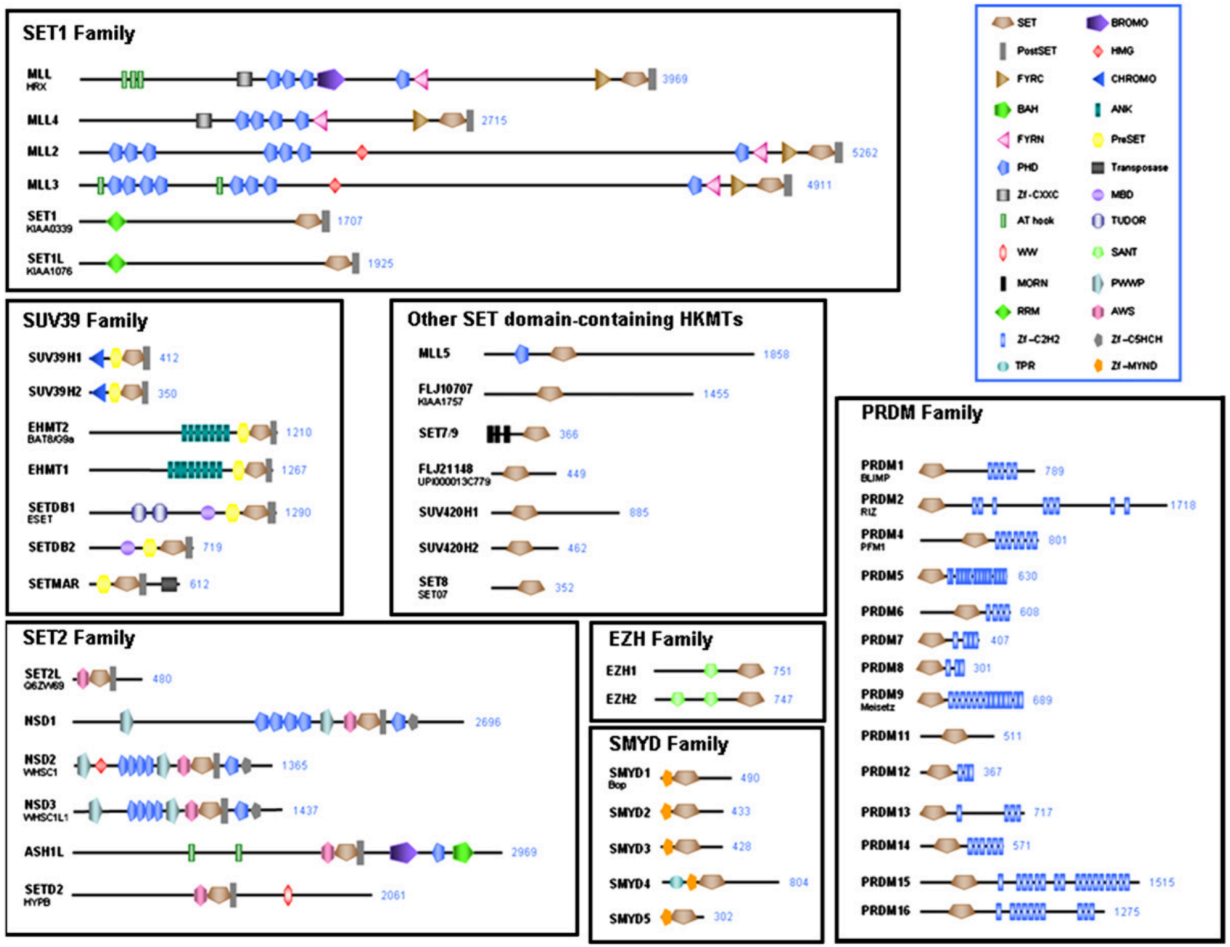
HISTONE LYSINE AND ARGININE METHYL TRANSFERASES (HKMETs and HRMETs))



HISTONE LYSINE METHYL TRANSFERASES (HKMETs)

all HKMETs contain a conserved SET domain that catalyzes the methylation of Lysines (K)

(exception Dot1 – no SET domain)



50 SET domain proteins are categorized according to sequence homology into 6 HKMET subfamilies

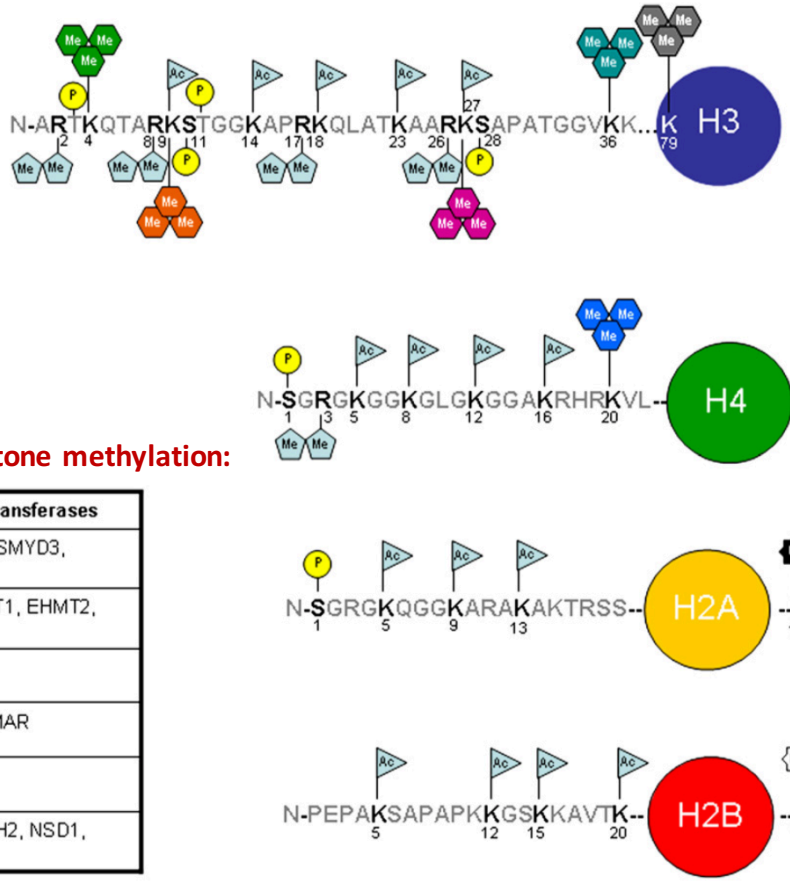
1. SET1 family
2. SET2 family
3. SUV39 family
4. EZH family
5. SMYD family
6. PRDM family
7. other SET domain HKMETs

50 SET domain proteins contain many other protein domains

→ Interaction with other proteins or DNA

HKMET HRMET SUBSTRATES ON HUMAN HISTONES

A



Effect on gene activity: **Best studied examples of histone methylation:**

	Substrate	Histone lysine methyltransferases
activation	H3K4	SET9, SET1, MLL, ASH1L, SMYD3, PRDM9, SETMAR
repression	H3K9	SUV39H1, SUV39H2, EHMT1, EHMT2, SETDB1, PRDM2, ASH1L
repression	H3K27	EZH2, EHMT2
activation	H3K36	NSD1, SETD2/HYPB, SETMAR
activation	H3K79	DOT1L
repression	H4K20	SET8, SUV420H1, SUV420H2, NSD1, ASH1L

HKMETS epigenetic writers are substrate specific and can result in gene repression but also gene activation
→→→
The epigenetic reader that binds to the modified histone K residue at the individual histone tail makes the difference

Fig. 1. Histone modifications. (A) The modifications on human histones include methylation (Me) on arginine and lysine residues, acetylation (Ac) on lysine residues, phosphorylation (P) on serine and threonine residues and ubiquitination (Ub) on lysine residues. (B) The enzymes responsible for methylation of human histone lysine residues are listed according to their target sites. Histone lysine methyltransferases (HKMTs) are very specific but redundant in several cases.

HISTONE MODIFICATIONS AND EPIGENTIC READERS

Protein domains that bind to histone modifications

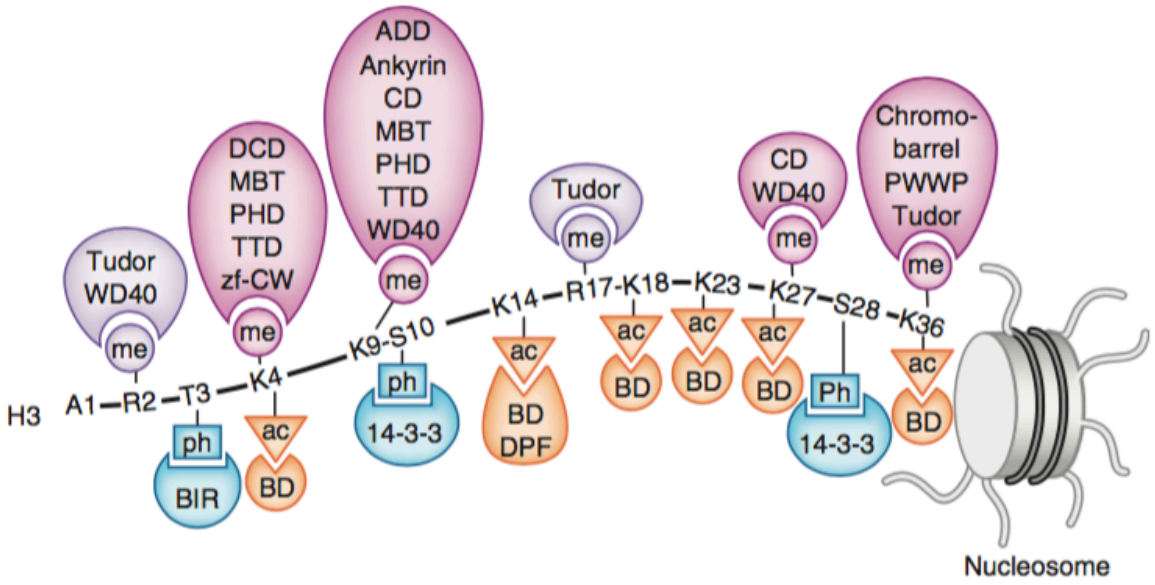


Figure 1 Readers of histone PTMs. Recognition of the methylated (me) lysine, methylated (me) arginine, acetylated (ac) lysine and phosphorylated (ph) serine and threonine residues of the N-terminal histone H3 tail by indicated readers.

Table 1 Histone readers and their target PTMs

Recognition of	Reader	Histone PTM
Methyllysine	ADD	H3K9me3
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	PWWP	H3K36me3, H4K20me1, H4K20me3, H3K79me3
	TTD	H3K4me3, H3K9me3, H4K20me2
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Acetyllysine	Bromodomain	H3Kac, H4Kac, H2AKac, H2BKac
	DBD	H3KacKac, H4KacKac
	DPF	H3Kac
	Double PH	H3K56ac
Phosphoserine or phosphothreonine	14-3-3	H3S10ph, H3S28ph
	BIR	H3T3ph
	Tandem BRCT	H2AXS139ph
Unmodified histone	ADD	H3un
	PHD	H3un
	WD40	H3un

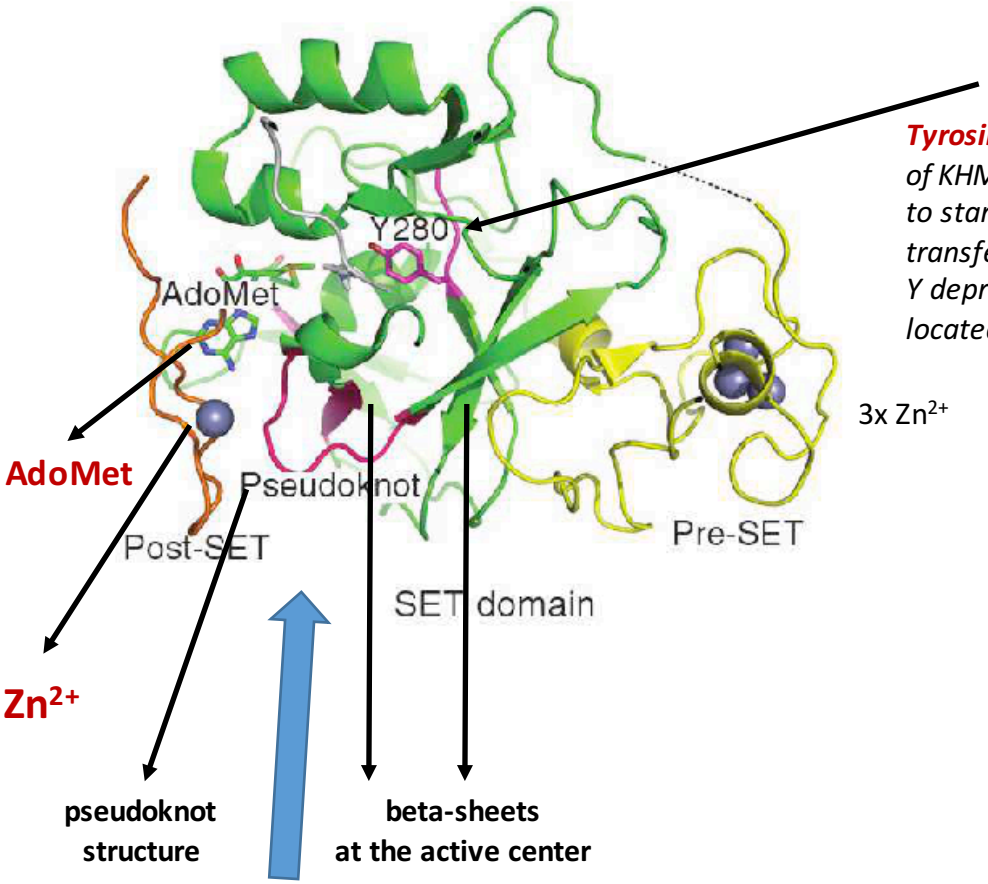
A large number of proteins contain these protein domains:

→ High complexity in gene regulation that

→ Creation of large numbers of EPIGENOMES

THE SET DOMAIN – EXCLUSIVELY IN KMETS

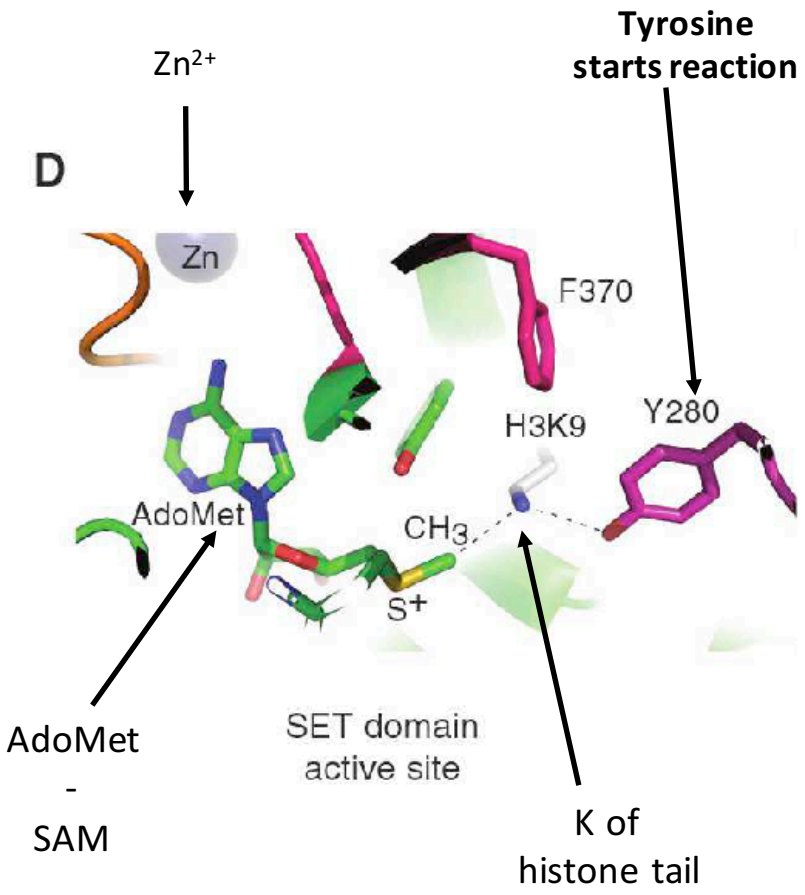
THE SET DOMAIN



Tyrosine residue *of KHMTs is required to start the methyl-transferase reaction. Y deprotonates K residue located in the histone tail.*

3x Zn^{2+}

THE ACTIVE SITE IN THE SET DOMAIN

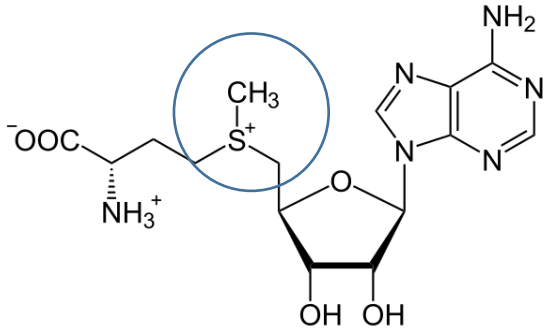


THE BIOCHEMISTRY OF HISTONE LYSINE METHYLATION

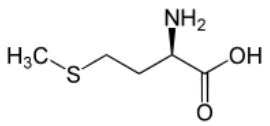
The source of the methyl group is S-adenosyl-l-methionine (AdoMet) or (SAM), which is converted to S-adenosyl-l-homocysteine (AdoHcy) in the reaction.

S-Adenosyl methionine is a common cosubstrate involved in methyl group transfers, transsulfuration, and aminopropylation.
SAM = enzymatic cofactor
<u>SAM is after ATP the most commonly used cofactor used by the cell</u>
Although these anabolic reactions occur throughout the body, most **SAM is produced and consumed in the liver**. More than 40 methyl transfers from SAM are known, to various substrates such as nucleic acids, proteins, lipids and secondary metabolites. It is made from adenosine triphosphate (ATP) and methionine by methionine adenosyltransferase. SAM was first discovered in Italy by Giulio Cantoni in 1952.

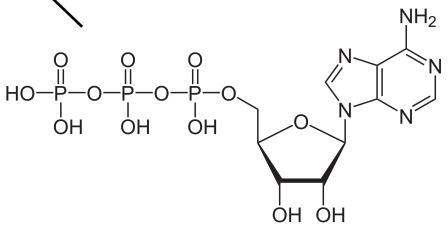
S-adenosyl-l-methionine (AdoMet) or (SAM),



Methionine Adenosyltransferase

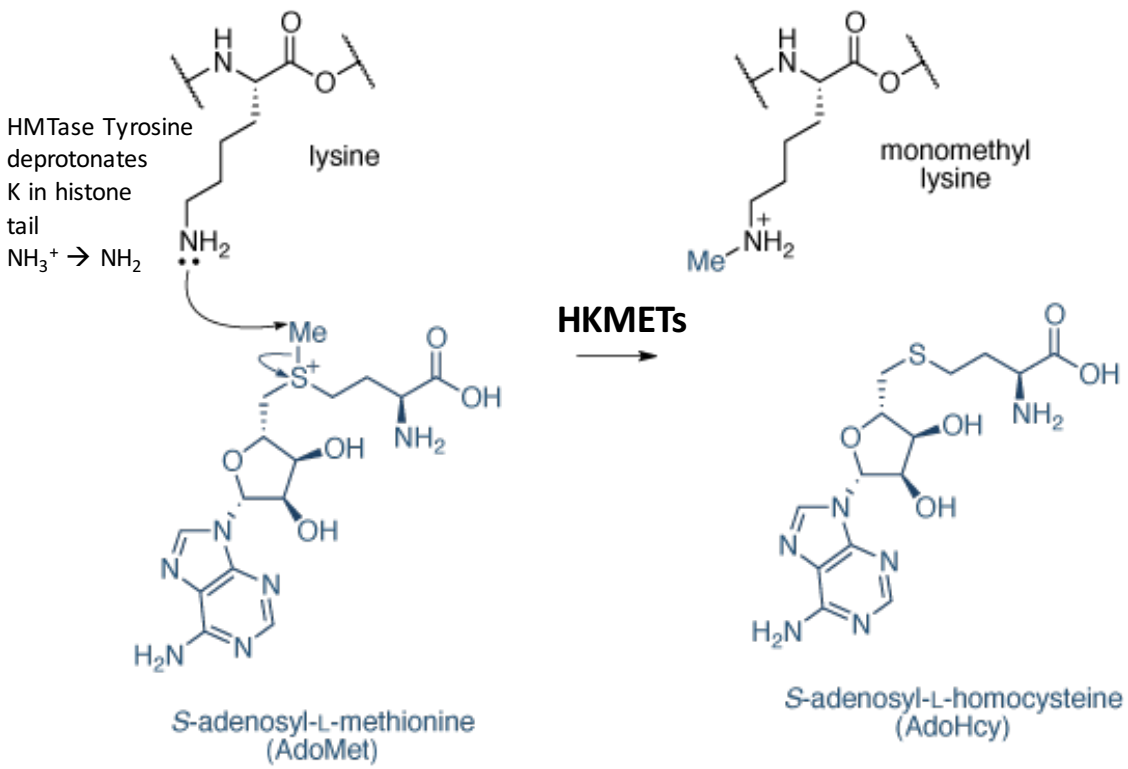


methionin



Adenosin triphosphate (ATP)

THE BIOCHEMISTRY OF HISTONE LYSINE METHYLATION



Catalytic mechanism

In order for the reaction to proceed, S-Adenosyl methionine (SAM) and the lysine residue of the substrate histone tail must first be bound and properly oriented in the catalytic pocket of the SET domain. Next, **a nearby tyrosine residue deprotonates the ε-amino group of the lysine residue.**
The lysine chain then makes a nucleophilic attack on the methyl group on the sulfur atom of the SAM molecule, transferring the methyl group to the lysine side chain.

ENZYMATIC ASSAY TO DETECT KMTase ACTIVITY

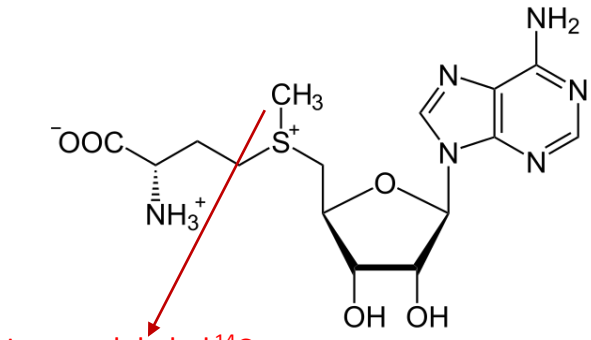
Experiment:

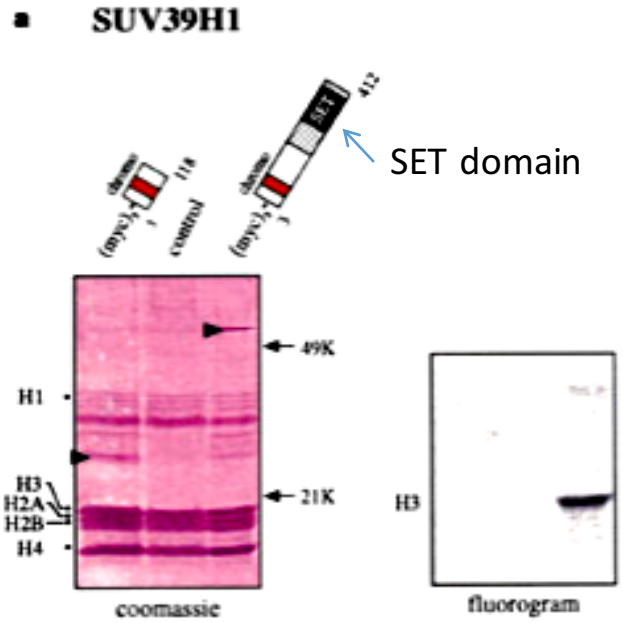
Overexpression of **myc-tagged-SUV39H1 KMT** in Hela cells

Use an antibody to immunoprecipitate SUV39H1 → high concentration of SUV39H1

Incubate Immunopreciptate with purified histones and S-adenosyl-[methyl-^{14}C]-$_L$-methionin as methyl donor

S-adenosyl-l-methionine (AdoMet) or (SAM),



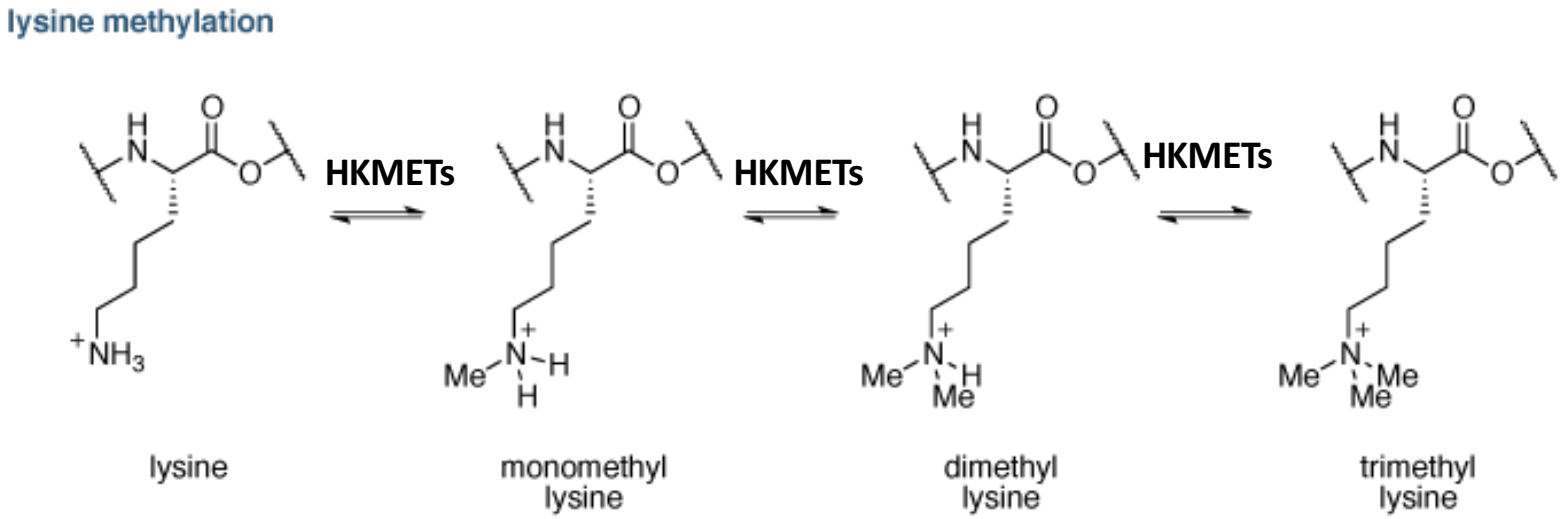


SET – domain is required for histone methyl transferases activity

- The SET domain of the SUV39H1 is required for histone methyltransferase activity and this enzyme methylates H3 at Lys9

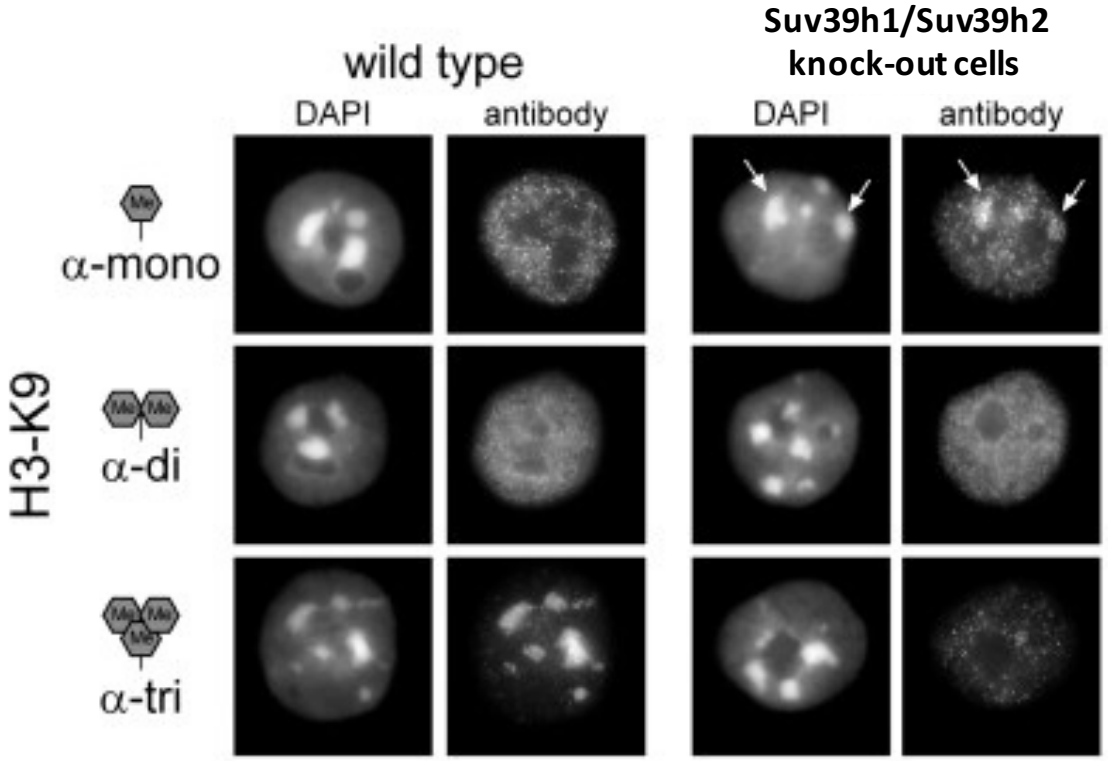
Rea et al, Nature, 2000

HISTONE LYSINES CAN BE MONO- DI- AND TRI-METHYALTED



ARE THERE KMTs THAT CREATE SPECIFIC METHYLATION LEVELS (mono-methylation, di-methylation, tri-methylation?

SUBSTRATE SPECIFICITY OF HISTOME METHYL TRANSFERASES: AN EXAMPLE: THE HKMT SUV39H1

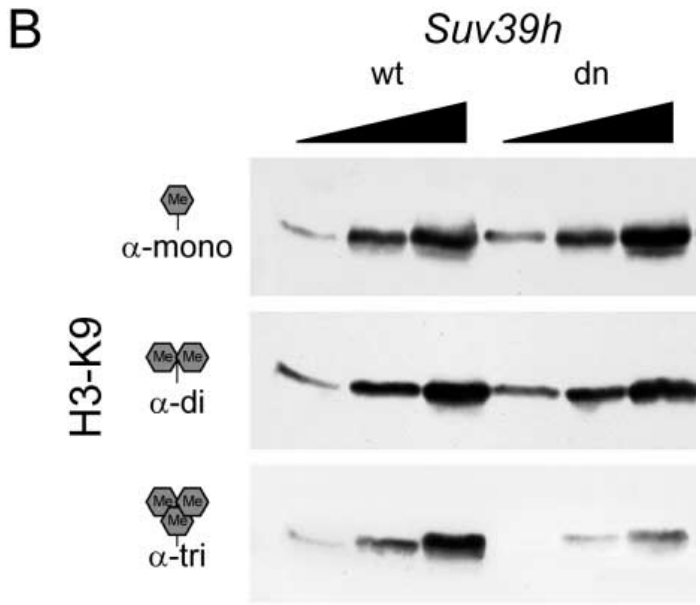


Suv39dn cells

H3K9me1: increased and pattern similar to wt H3K9me3 (chromocenter)

H3K9me2: similar to wt

H3K9me3: strongly reduced; lost at chromocenters



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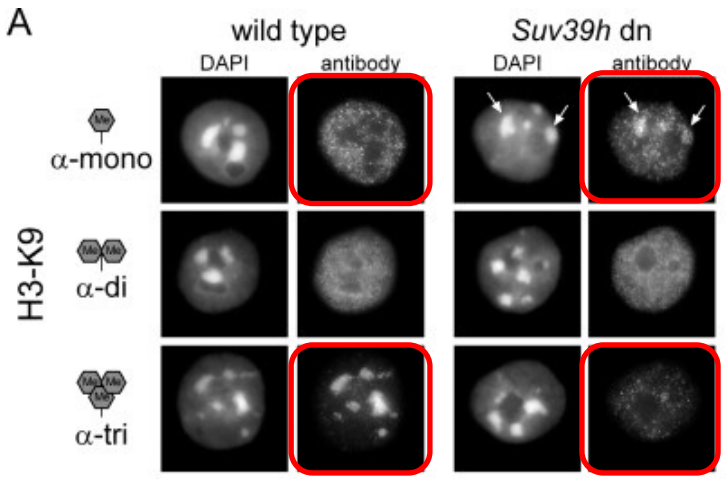
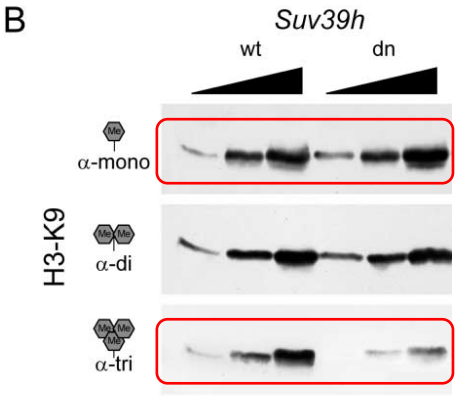


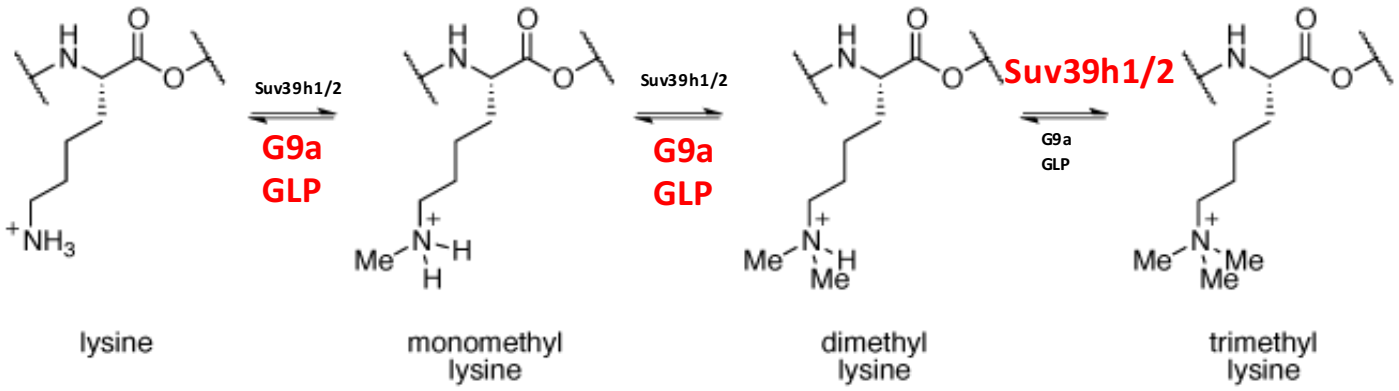


The H3K9 specific KMTs G9a and GLP are the major H3K9me1 and H3K9me2 methyltransferases

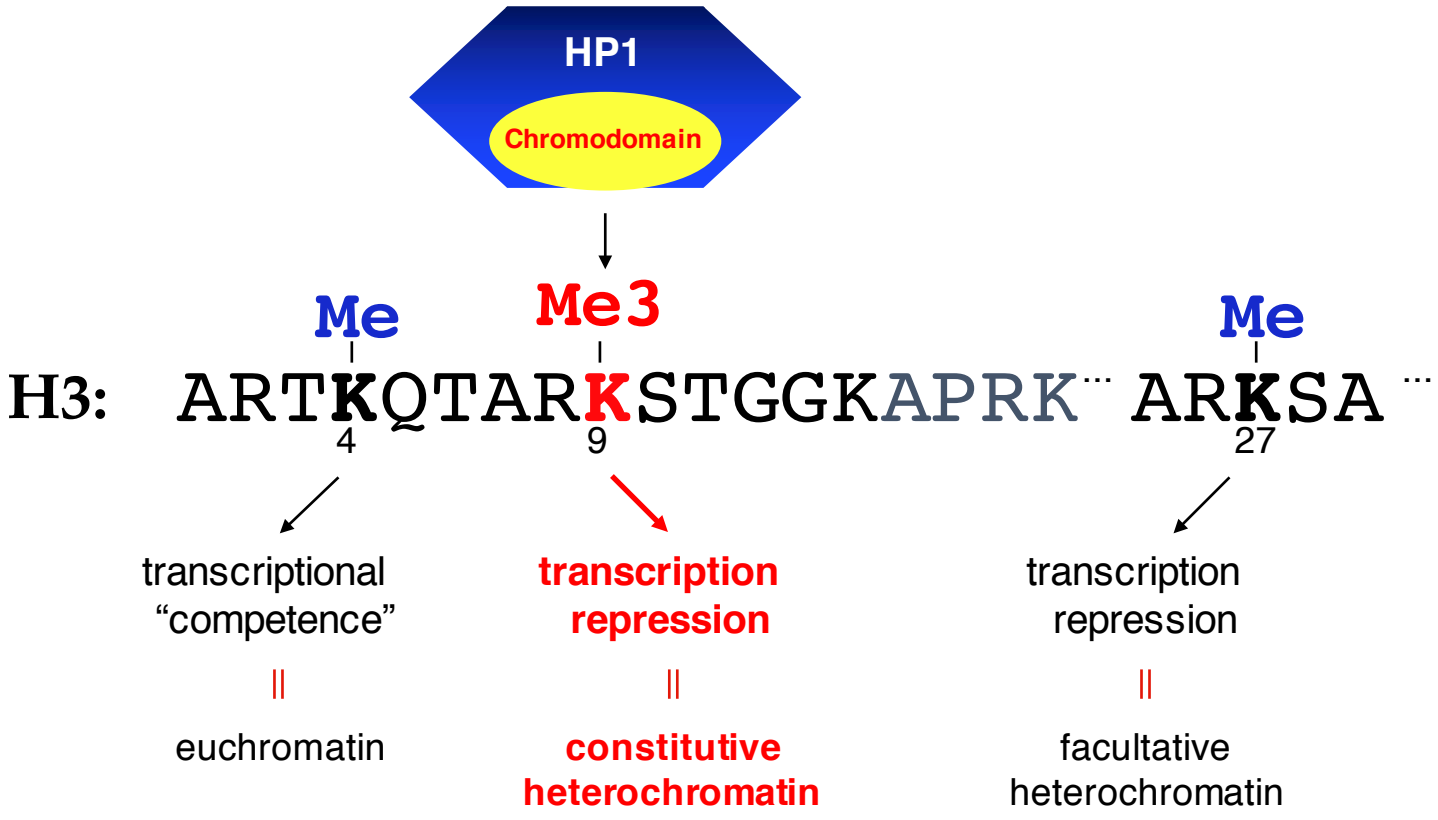
The H3K9 specific KMTases Suv39h1 and Suv39h2 are the major H3K9me3 methyltransferases

Suv39h1 and Suv39h1 work best on H3K9me2

H3K9 methylation



EPIGENTIC READERS
AN EXAMPLE: H3K9me3 and HP1



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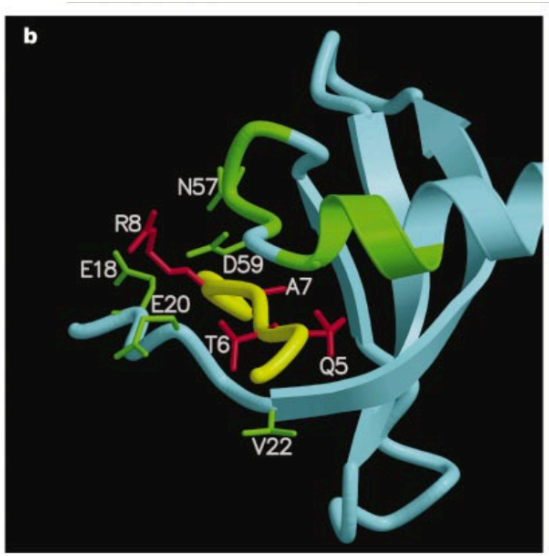
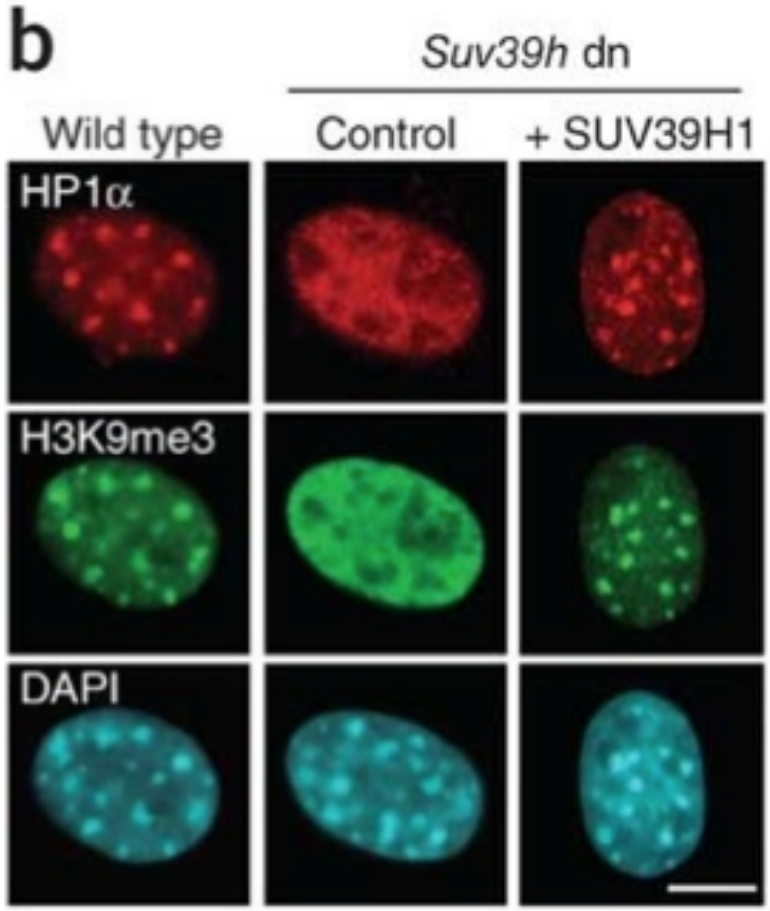
	BIR	H3T3ph
	Tandem BRCT	H2AXS139ph
Unmodified histone	ADD	H3un
	PHD	H3un
	WD40	H3un

EPIGENTIC READERS – IN VIVO EVIDENCE
AN EXAMPLE: HP1 has high affinity for H3K9me3



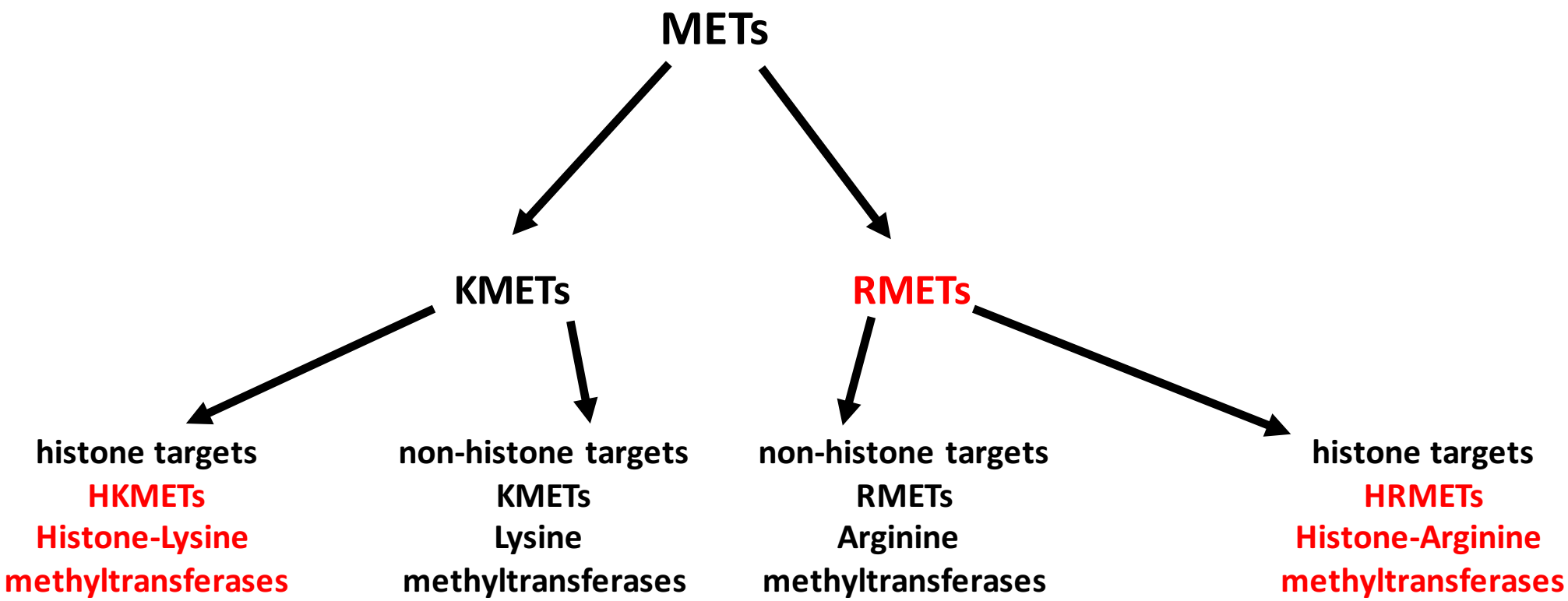
A chromodomain (chromatin organization modifier) is a protein structural domain of about 40-50 amino acid residues commonly found in proteins associated with the remodeling and manipulation of chromatin. The domain is highly conserved among both plants and animals, and is represented in a large number of different proteins in many genomes, such as that of the mouse. Chromodomain-containing proteins also bind methylated histones and appear in the RNA-induced transcriptional silencing complex.
YELLOW: histone tail
RODs: Interacting aminoacids of HP1



Loss of Suv39h1/2: reduced (2 slides earlier) **and delocalized** (this slide) **H3K9me3**.

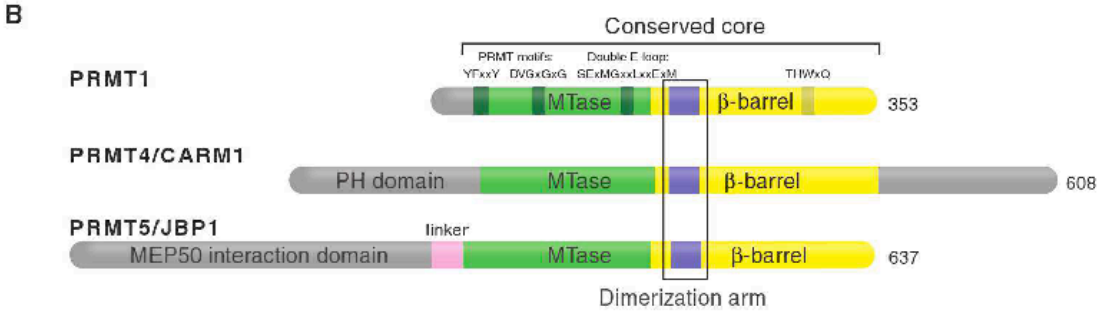
Consequence:
HP1 is also delocalized!!!!
= binding to low-affinity targets

HISTONE LYSINE AND ARGININE METHYL TRANSFERASES (HKMETs and HRMETs))



HISTONE ARGININE METHYL TRANSFERASES (HRMETs)

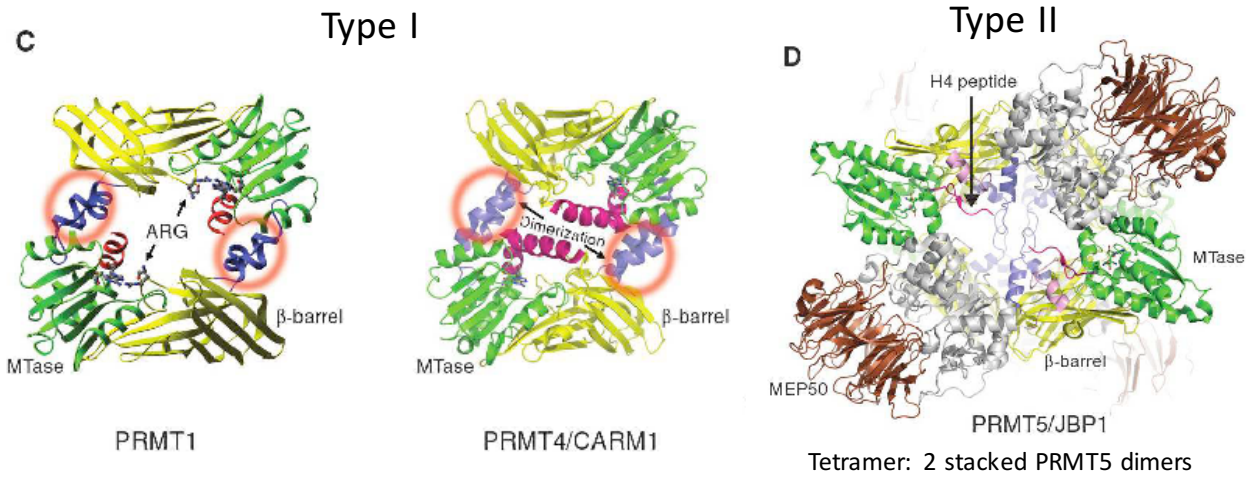
Family if PRMTs: Protein Arginine (R) methyl-transferases



PRMTs have a MTase domain that is Different from the SET domain!!!

Conserved core:

- MTase domain: catalyzes methylation of R
- Beta barrel domain: Important for dimerization of PRMTs



Tetramer: 2 stacked PRMT5 dimers

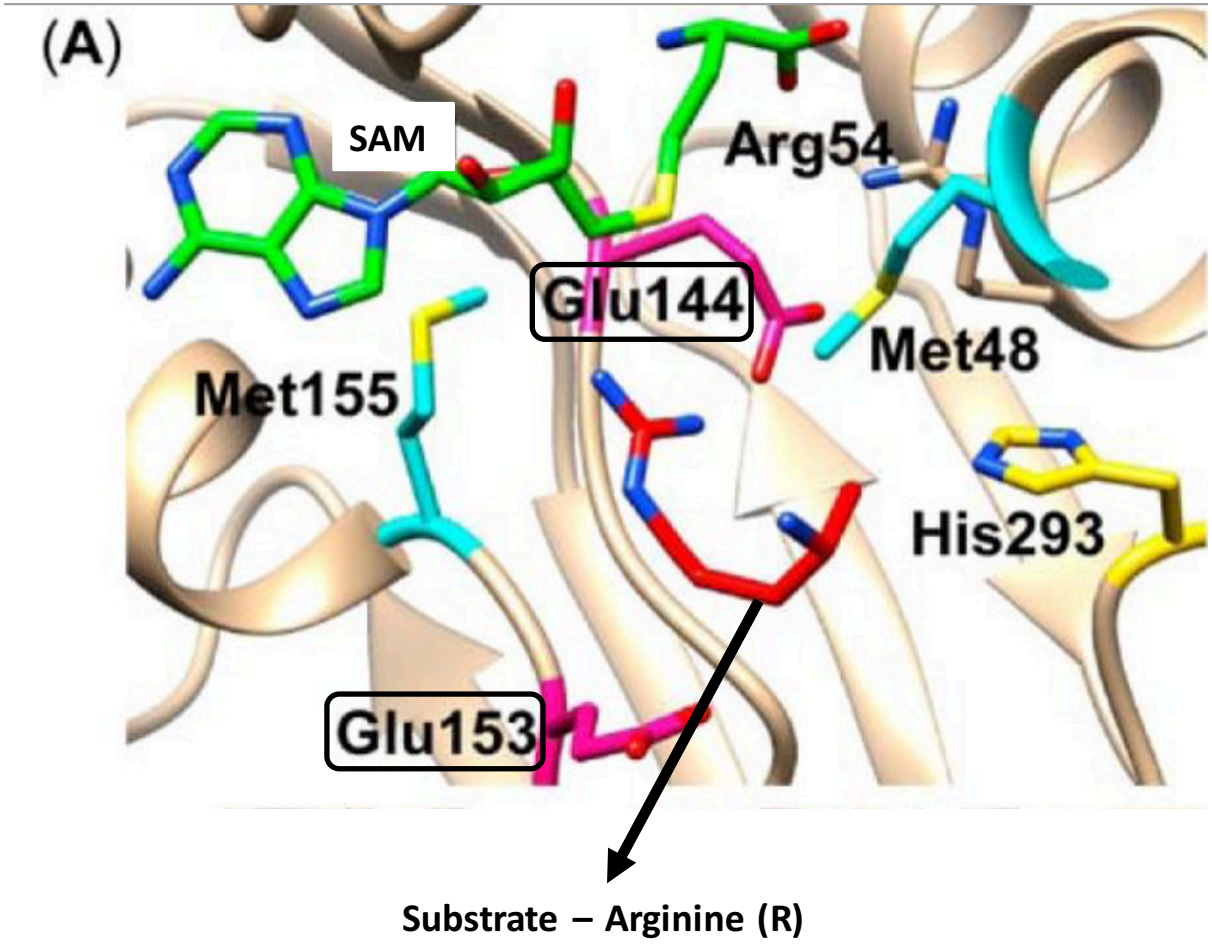
PRMTs

- Type I PRMTs: need to dimerize to be functional
- Type II PRMTs: form larger complexes – dimers interact to form tetramers, other proteins can interact

THE BIOCHEMISTRY OF HISTONE ARGININE METHYLATION

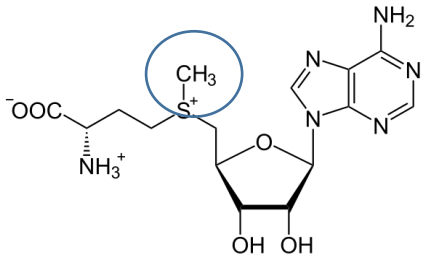
Methyl transfer reactions catalyzed by AdoMet-dependent PRMTs.
Example: PRMT1
The reacting arginine substrate acts by nucleophil attacking the methyl group present on SAM (S-AdoMet).
The reaction has been proposed to involve 3 key conserved residues in the active site of PRMT1:
Arg-54, Glu-144, and Glu-153.

Arg-54 and **Glu-144** help to properly position the substrates for the nucleophilic attack
Glu-153 is hypothesized to play a role in increasing the nucleophilicity of the guanidinium moiety of the substrate via enhanced electronic effects.
Glu-144 has also been postulated to act as the active site base, abstracting a proton from the reacting arginine.

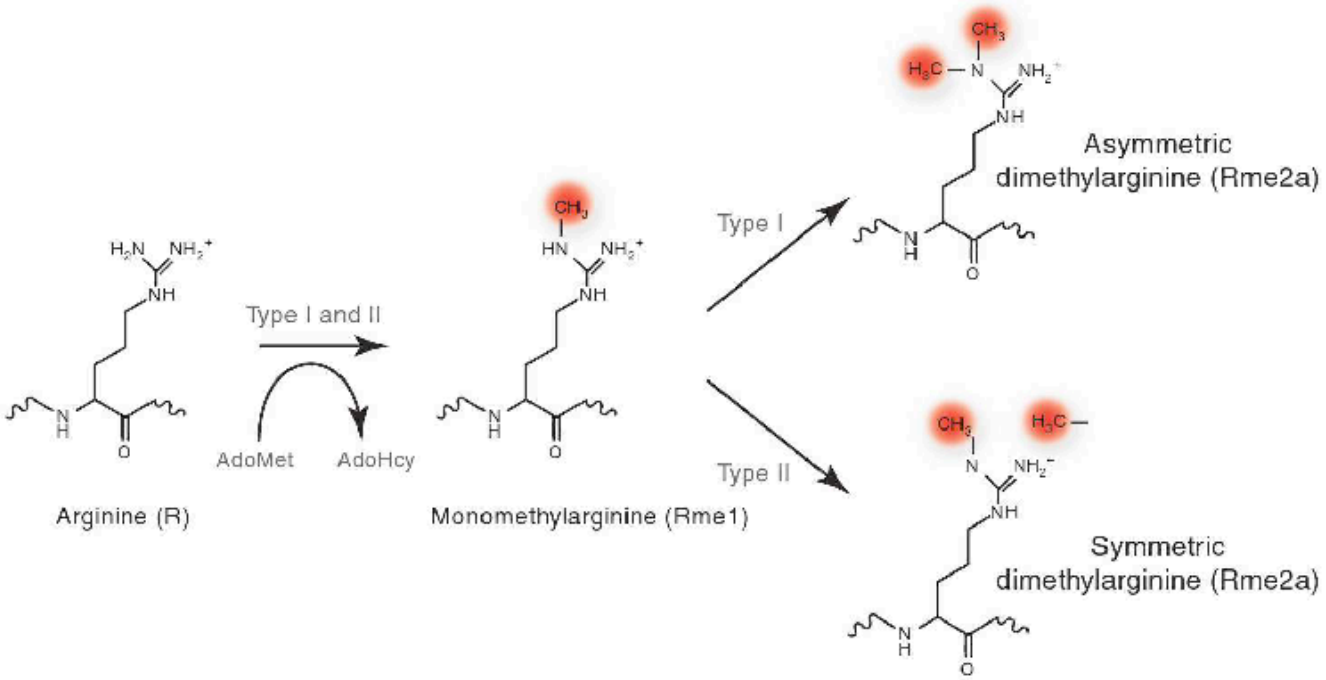


THE BIOCHEMISTRY OF HISTONE ARGININE METHYLATION

PRMT activity requires :
substrate containing R,
AdoMet (SAM) as enzymatic cofactor
PRMT



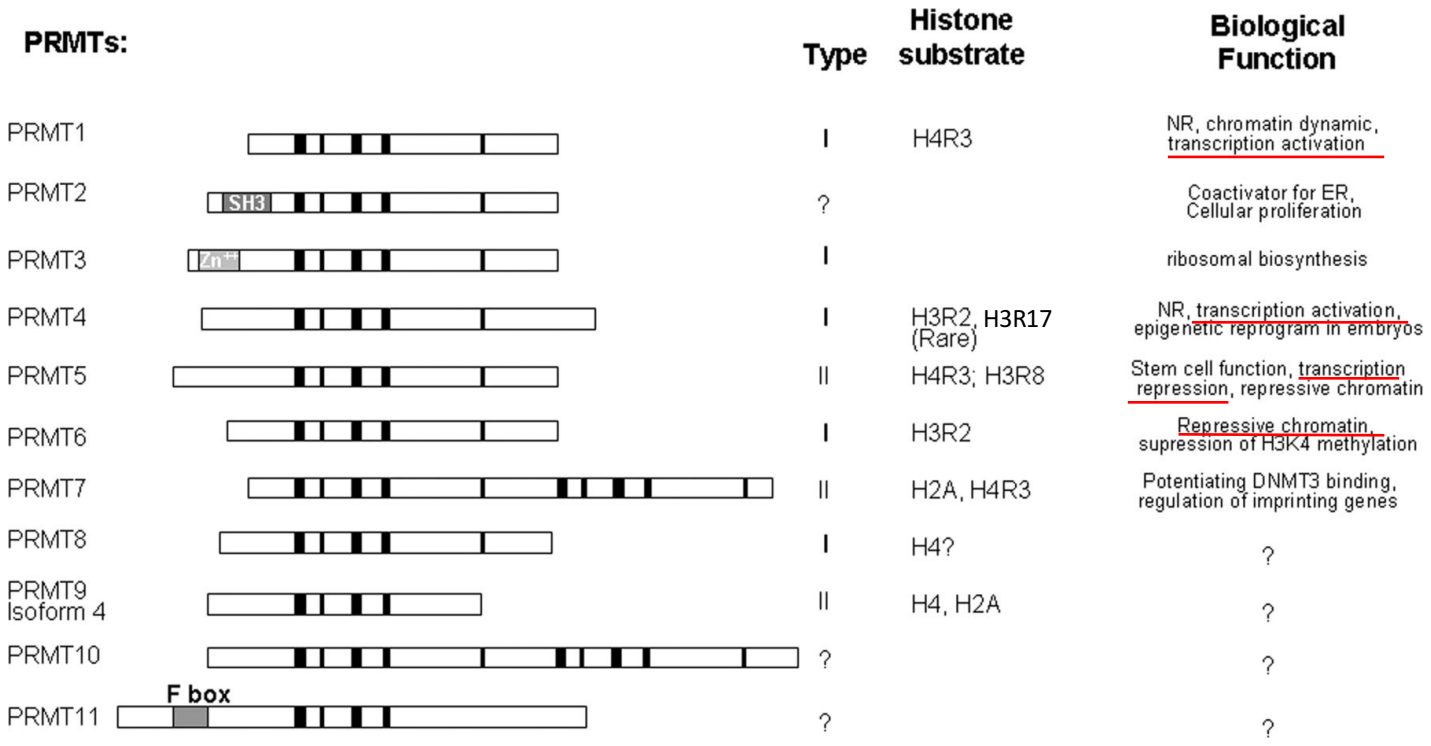
S-adenosyl-l-methionine (AdoMet) or (SAM),



PRMTs CATALYZE MONO and DIMETHYLATION
- Not trimethylation -

PRMT SUBSTRATES AND BIOLOGICAL ACTIVITY

PRMTs can act as activators and repressors of gene expression



PRMTs epigenetic writers, are substrate specific and can result in gene repression but also gene activation
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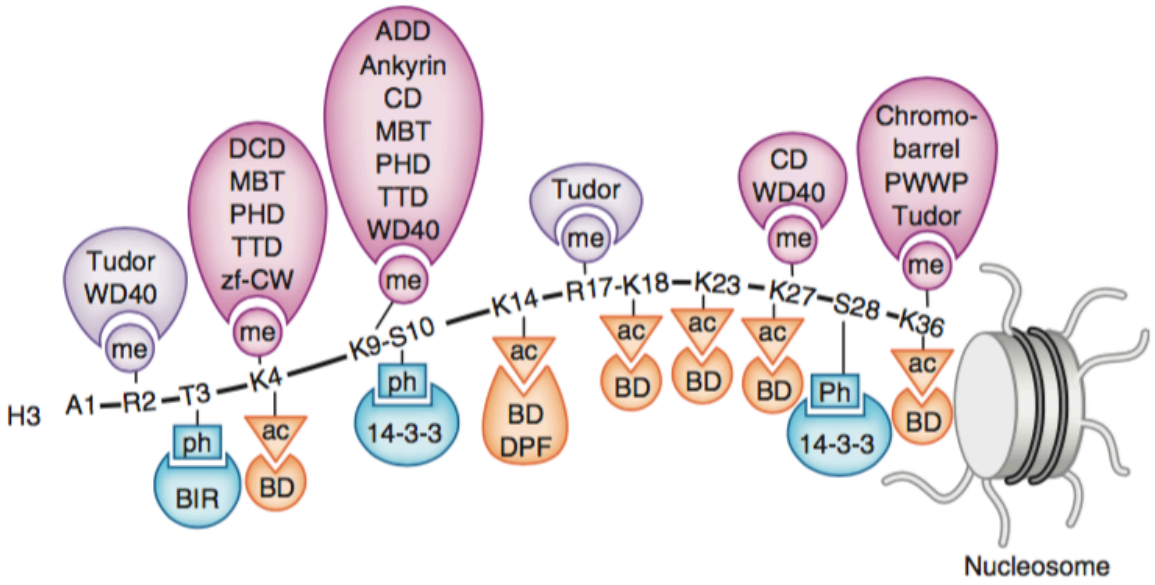
The epigenetic reader that binds to the modified histone R residue at the individual histone tail makes the difference

HISTONE MODIFICATIONS AND EPIGENTIC READERS

Protein domains that bind to histone modifications



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	DPF	H3Kac
	Double PH	H3K56ac
Phosphoserine or phosphothreonine	14-3-3	H3S10ph, H3S28ph
	BIR	H3T3ph
	Tandem BRCT	H2AXS139ph
Unmodified histone	ADD	H3un
	PHD	H3un
	WD40	H3un

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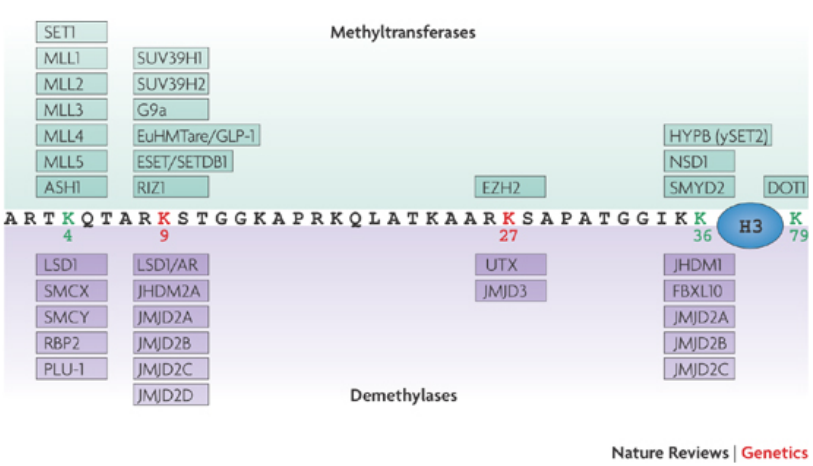
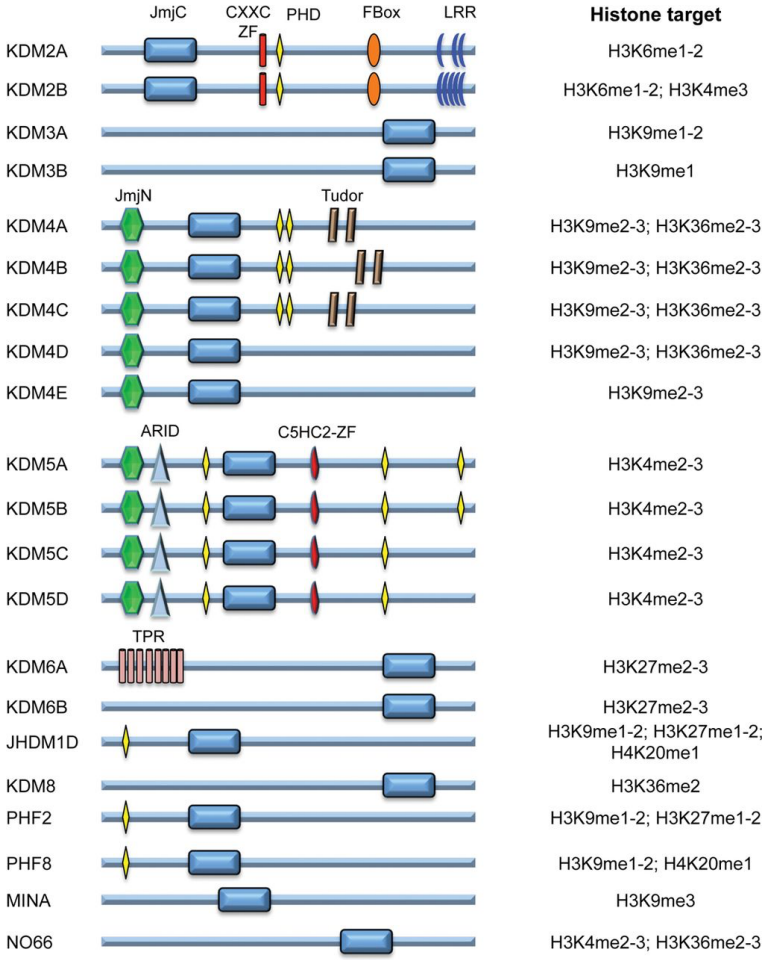
→ Creation of large numbers of EPIGENOMES

LYSINE AND ARGININE METHYLATION IN HISTONES IS REVERSIBLE



The **Jumonji N (JmjN) and Jumonji C (JmjC)** domains are two non-adjacent domains which have been identified in the jumonji family of transcription factors. Although it was originally suggested that the JmjN and JmjC domains always co-occur and might form a single functional unit within the folded protein, the JmjC domain was latter found without the JmjN domain in organisms from bacteria to human. The JmjC domain is the best studied domain that mediated histone demethylation - is conserved from yeast to human



1. **LSD1 (KDM1A): demethylation by <u>oxidation</u>**
2. **Big family of Jumonji domain containing proteins: <u>hydroxylation</u>**

Histone: unmethylated

RMETs
KMETs

R-demethylases
K-demethylases (KDMs)

Histone: methylated

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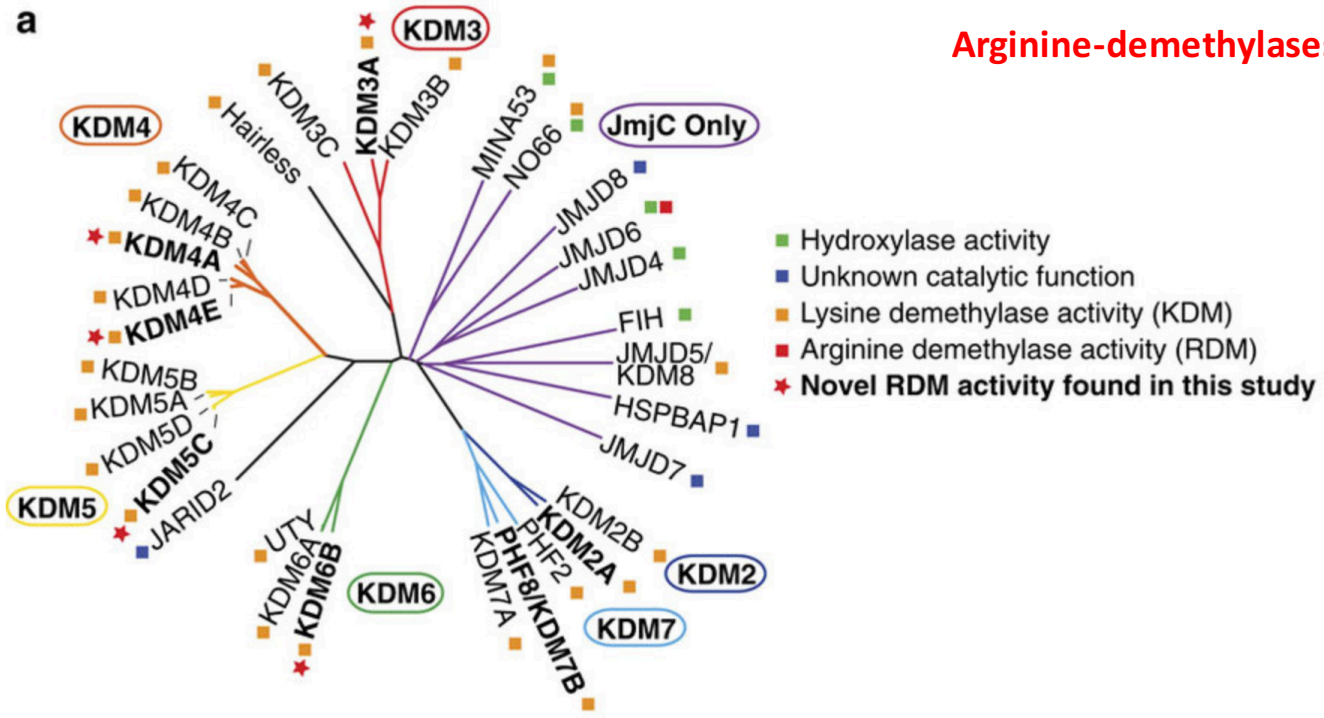

Arginine-demethylases are less well studied

Histone: unmethylated

RMETs
KMETs

R-demethylases
K-demethylases

Histone: methylated

nature COMMUNICATIONS

ARTICLE

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Arginine demethylation is catalysed by a subset of JmjC histone lysine demethylases

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LECTURE 4

DNA METHYLATION

DNA METHYLATION CONTROLS GENE EXPRESSION

FACTS:

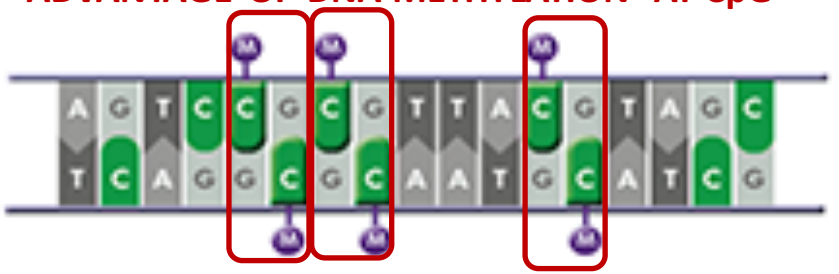
1. DNA methylation is created at CpG di-nucleotide motifs

2. An accumulation of CpG is called "CpG island" (CGI)

3. CpG islands are enriched at promotes and sequence elements that are important for gene expression control. In some cases, CpG islands can be also located in distant locations.

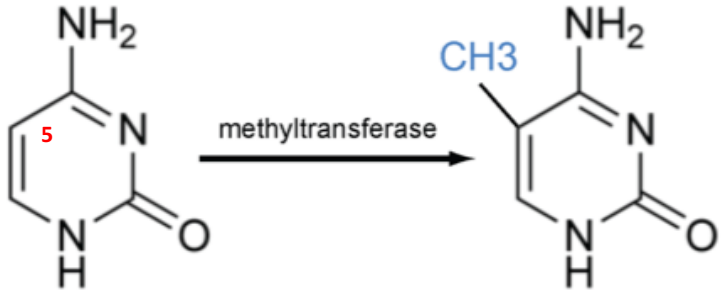
4. *CpG methylation (="DNA methylation") is directly linked with stable, inheritable gene silencing*

ADVANTAGE OF DNA METHYLATION AT CpG



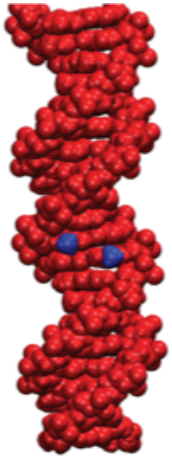
CpGs are self-complementary
Di-nucleotide in paired stand also contains methylation
Methylation patterns can be maintained during DNA replication

Epigenetic modification that is imposed on genomic DNA



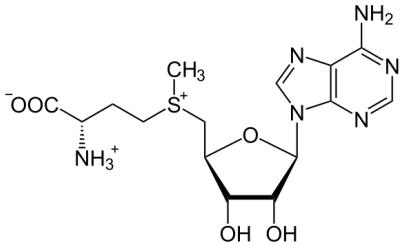
CYTOSINE

METHYL-CYTOSINE



DNA METHYLTRANSFERASES CATALYZE DNA METHYLATION

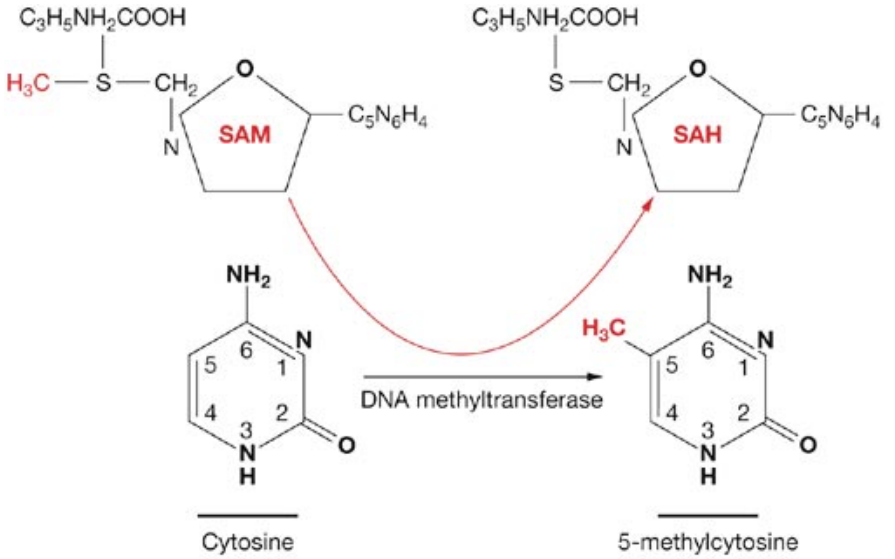
DNA methyltransferases (DNMTs) transfer a methyl-group from AdoMet (SAM) to Cytosine located in a CpG dinucleotide

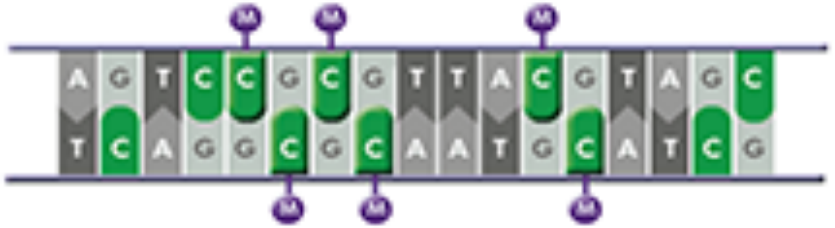


S-adenosyl-l-methionine (AdoMet) or (SAM),

The source of the methyl group is S-adenosyl-l-methionine (AdoMet) or (SAM), which is converted to S-adenosyl-l-homocysteine (AdoHcy) in the reaction.

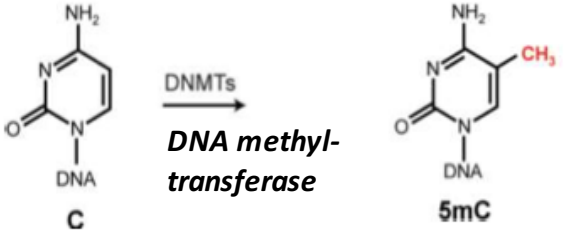
S-Adenosyl methionine is a common cosubstrate involved in methyl group transfers, transsulfuration, and aminopropylation.
SAM = enzymatic cofactor
<u>SAM is after ATP the most commonly used cofactor used by the cell</u>
Although these anabolic reactions occur throughout the body, most **SAM-e is produced and consumed in the liver**. More than 40 methyl transfers from SAM-e are known, to various substrates such as nucleic acids, proteins, lipids and secondary metabolites. It is made from adenosine triphosphate (ATP) and methionine by methionine adenosyltransferase. SAM was first discovered in Italy by Giulio Cantoni in 1952.





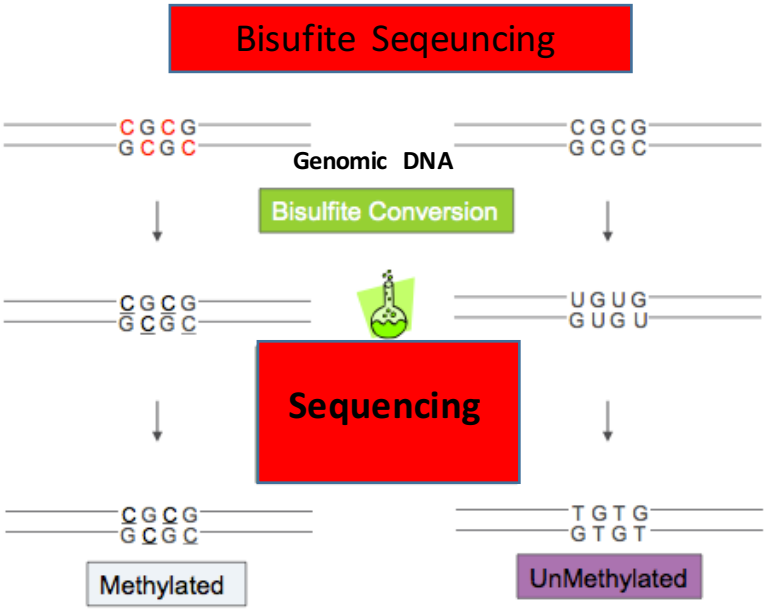
Mapping DNA methylation at CpG islands
BISULFITE SEQUENCING

Methylation of cytosine at CpG dinucleotides is an important epigenetic regulatory modification in many eukaryotic genomes.
DNA methylation was found to be located genome-wide with a pattern of low methylation in proximity to promoters and high gene body-methylation in highly-expressed genes → methylation pattern can identify transcribed DNA (gene)

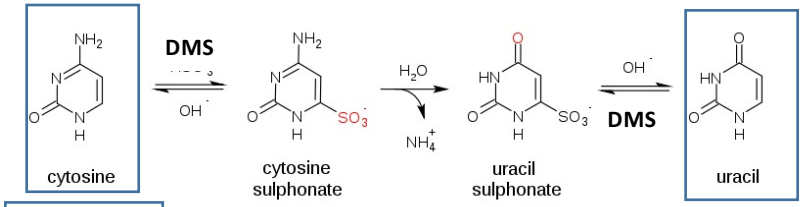


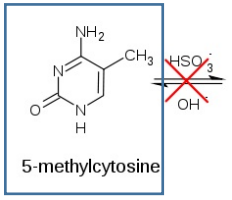
active gene

silenced gene



Bisulfite conversion: C→U conversion using dimethyl sulfate





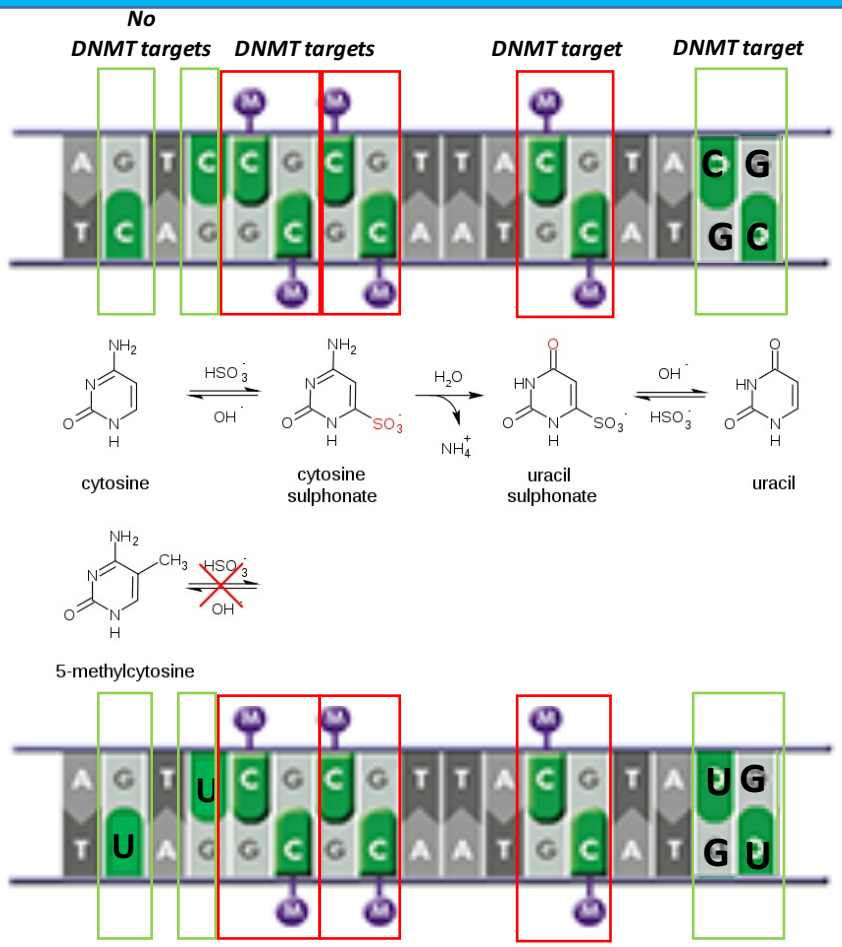
methylated C cannot be converted!!

DMS = Dimethyl sulfate

Treatment of DNA with bisulfite converts cytosine residues to uracil, but leaves 5-methylcytosine residues unaffected. Thus, bisulfite treatment introduces specific changes in the DNA sequence that depend on the methylation status of individual cytosine residues, yielding single-nucleotide resolution information about the methylation status of a segment of DNA.

Mapping DNA methylation at CpG islands
BISULFITE SEQUENCING

Genomic DNA



Bisulfite conversion

DNA for Sequencing

Seqeuncing of both strands reveals C → U (T) transition

Compare with genomic sequence
C→U sequence change = DNA methylation
C→C no sequence change = no DNA methylation