



Epigenetics

... tweaking your genetic destiny



Tim Herman

What is Epigenetics?

Epigenetics is the study of how your behaviors and environment can cause ***changes that affect the way your genes work***. Unlike genetic changes, epigenetic changes are reversible and do not change your DNA sequence, but they can change how your body reads a DNA sequence.

**NO MORE
EXCUSES**
Don't blame it on genes

Workshop Outline

Epigenetics...chemical modifications of your genome

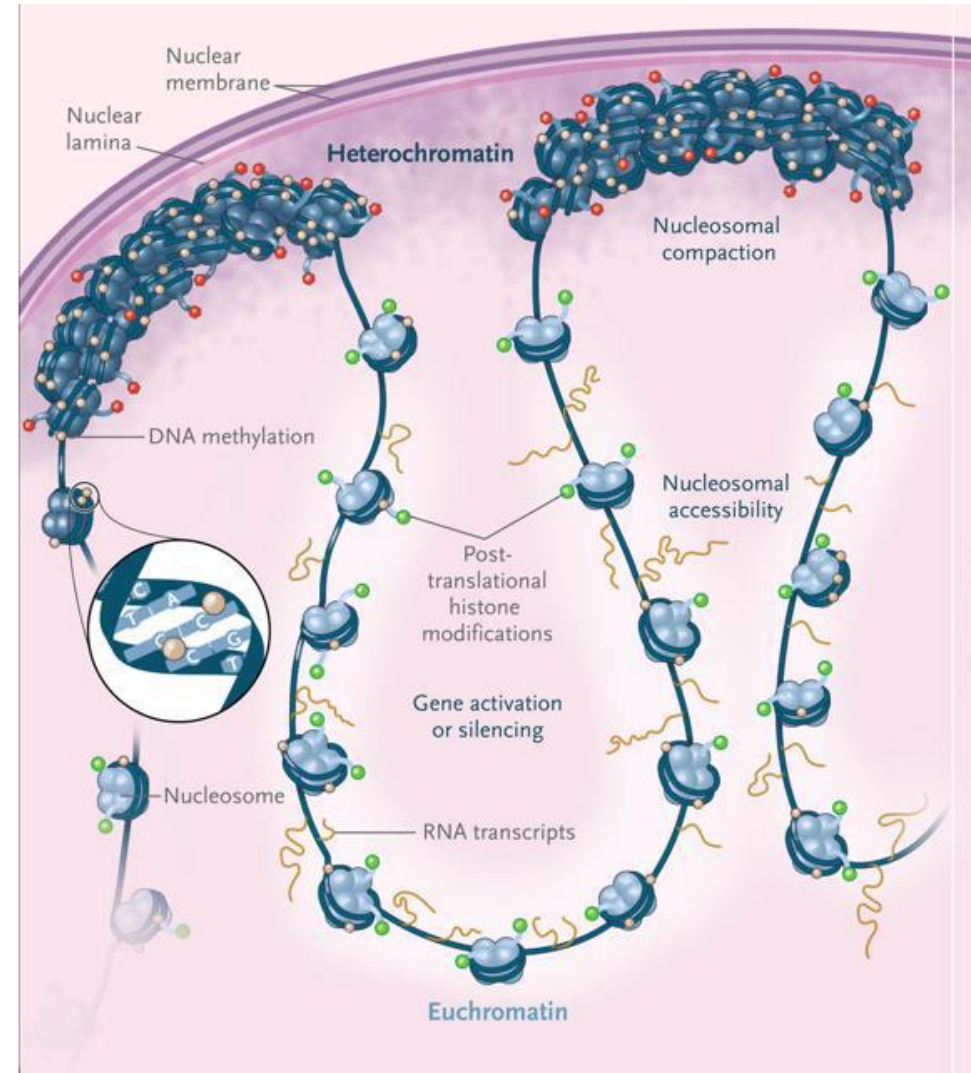
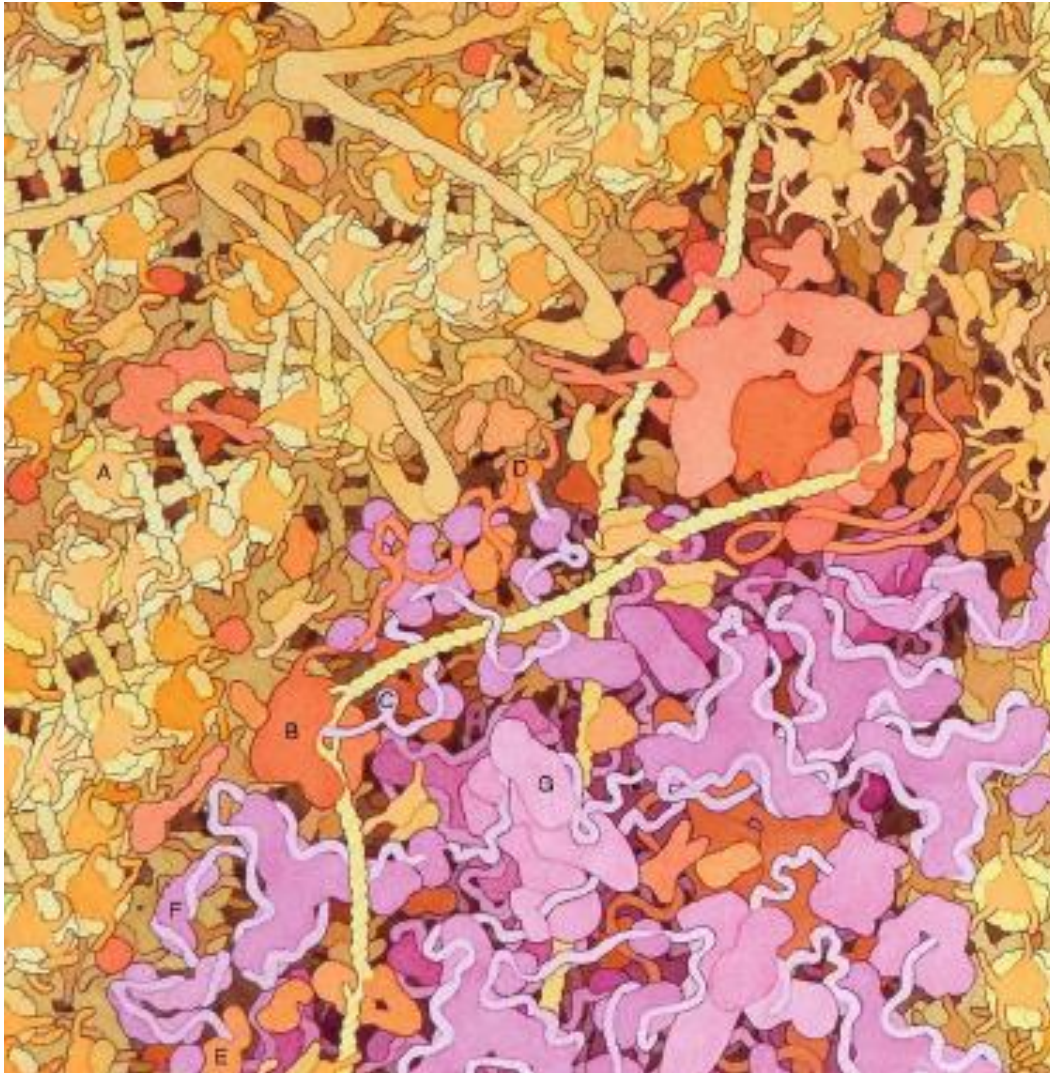
Writers / Erasers / Readers

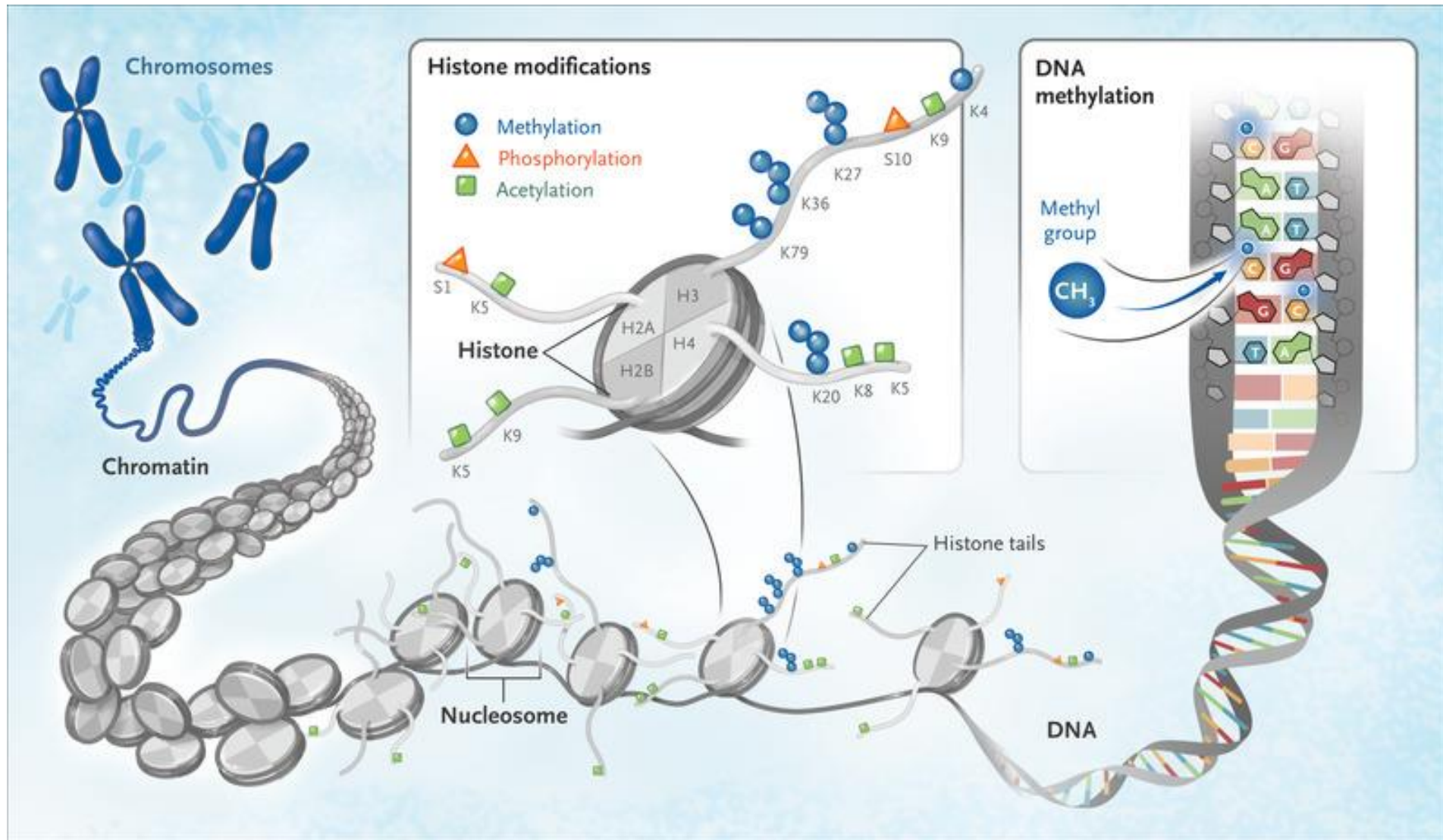
1. Histone modifications

2. DNA modifications

... methylation of CpG

... a 3-D structure/function story





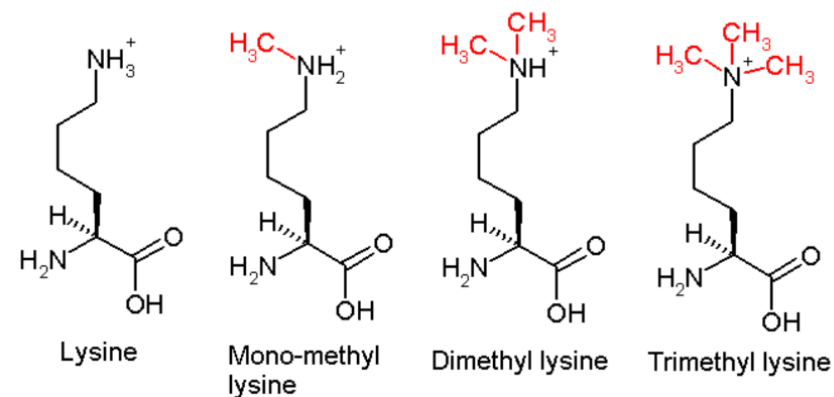
Lysine (K) #4 of histone H3 is tri-methylated....

H3K4me3 regulates RNA polymerase II promoter-proximal pause-release

- <https://doi.org/10.1038/s41586-023-05780->

“Trimethylation of histone H3 lysine 4 (H3K4me3) is associated with transcriptional start sites and has been proposed to regulate transcription initiation^{1,2}.”

Lysine methylation [edit]



Modeling chromatin....



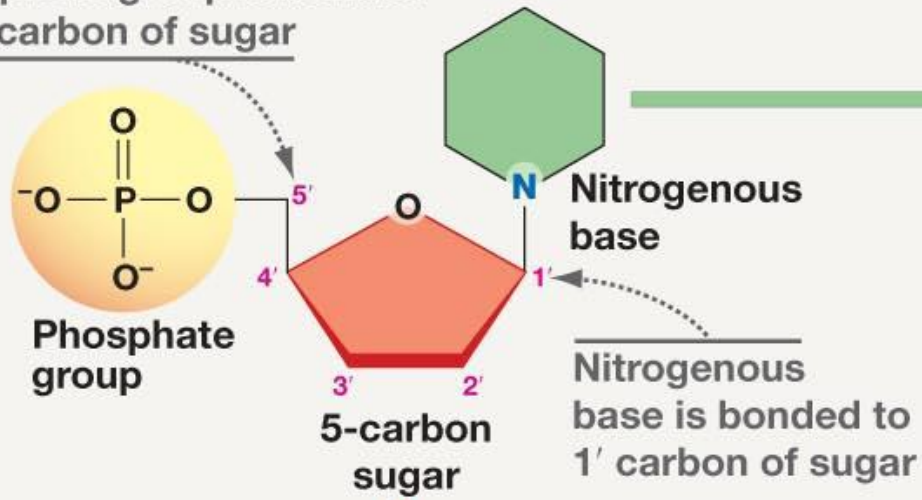
Post-transcriptional modification of DNA

Methylation of CpG to C^{Me}pG

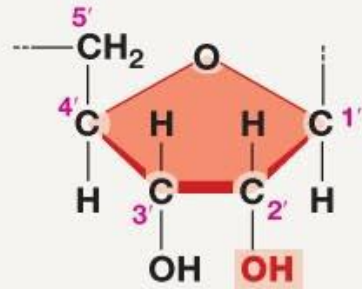


(a) Nucleotide

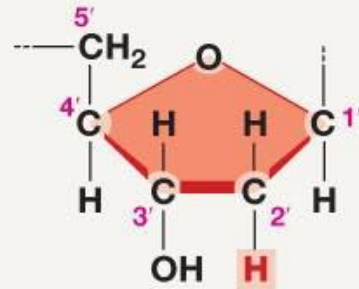
Phosphate group is bonded to 5' carbon of sugar



(b) Sugars

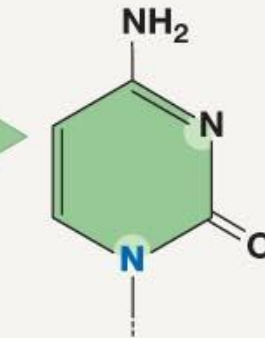


Ribose in RNA

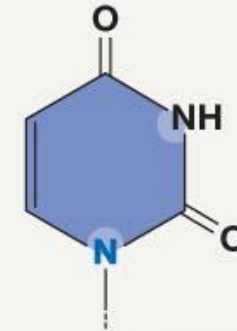


Deoxyribose in DNA

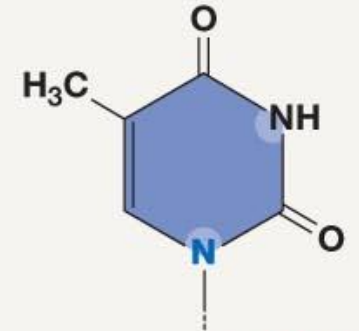
(c) Nitrogenous bases



Cytosine (C)

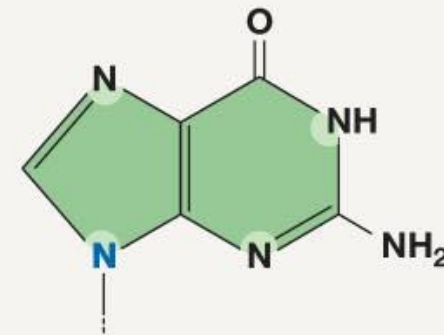


Uracil (U) in RNA

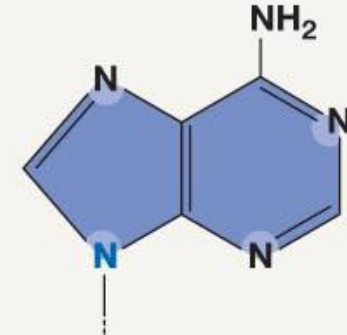


Thymine (T) in DNA

Pyrimidines



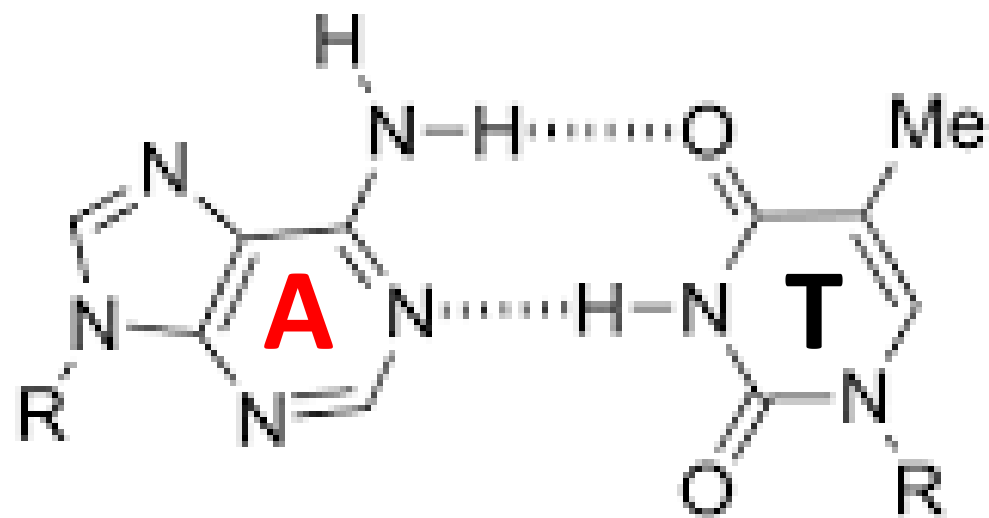
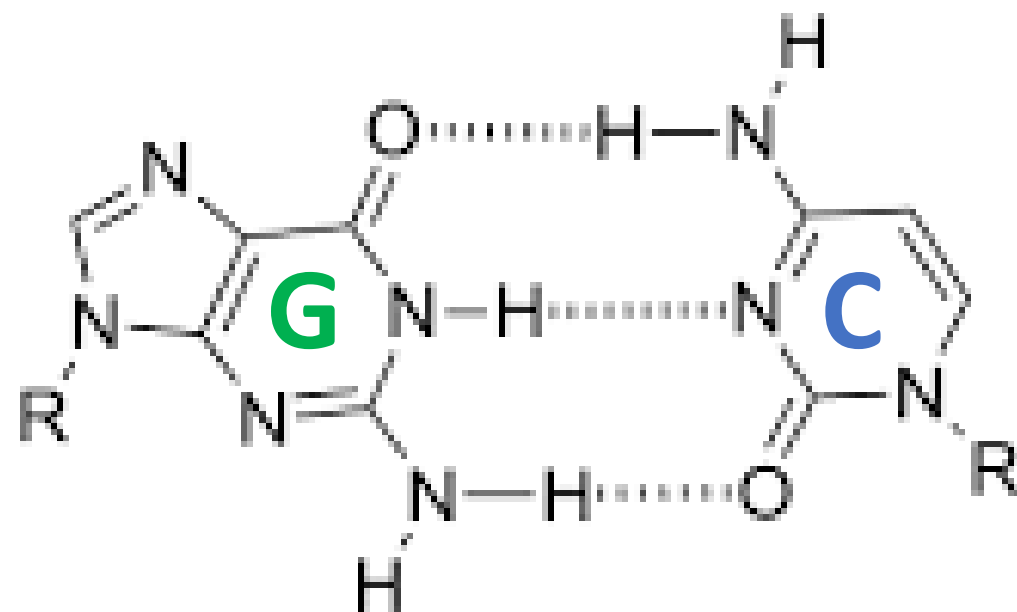
Guanine (G)



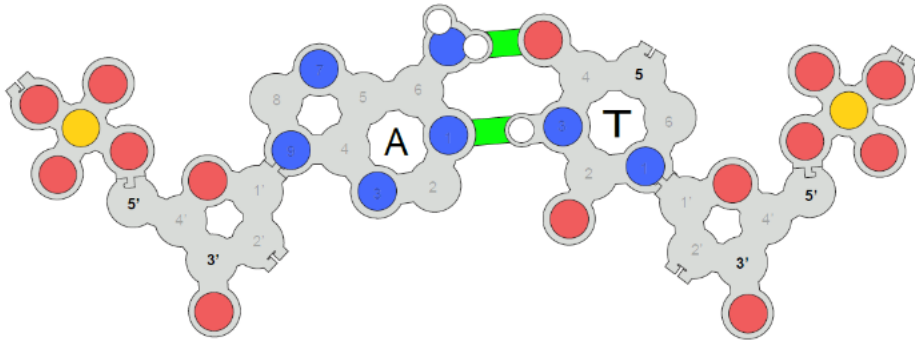
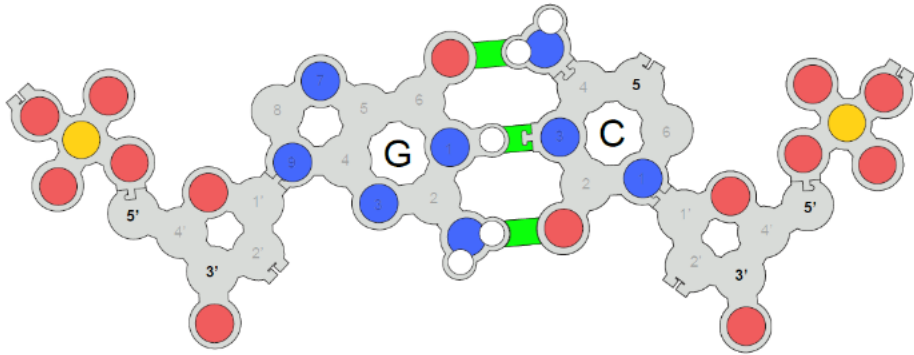
Adenine (A)

Purines are larger than pyrimidines

Purines

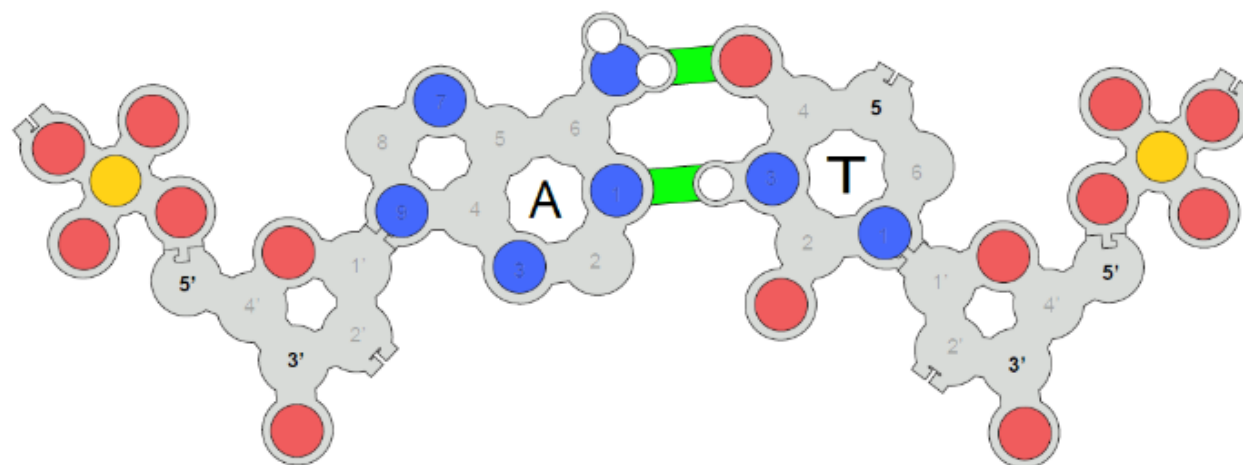
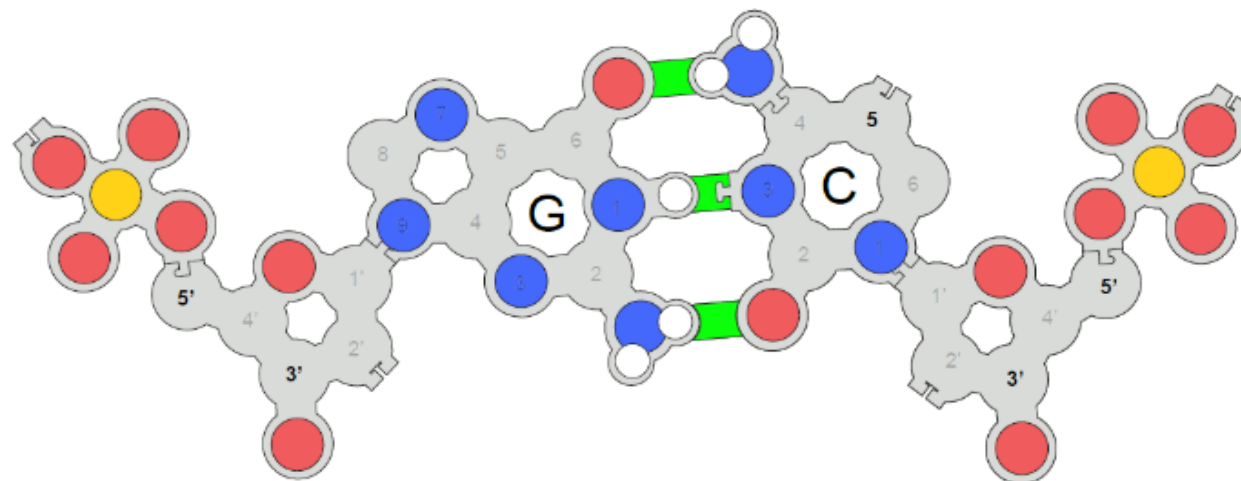


3DMD Base Pair Models



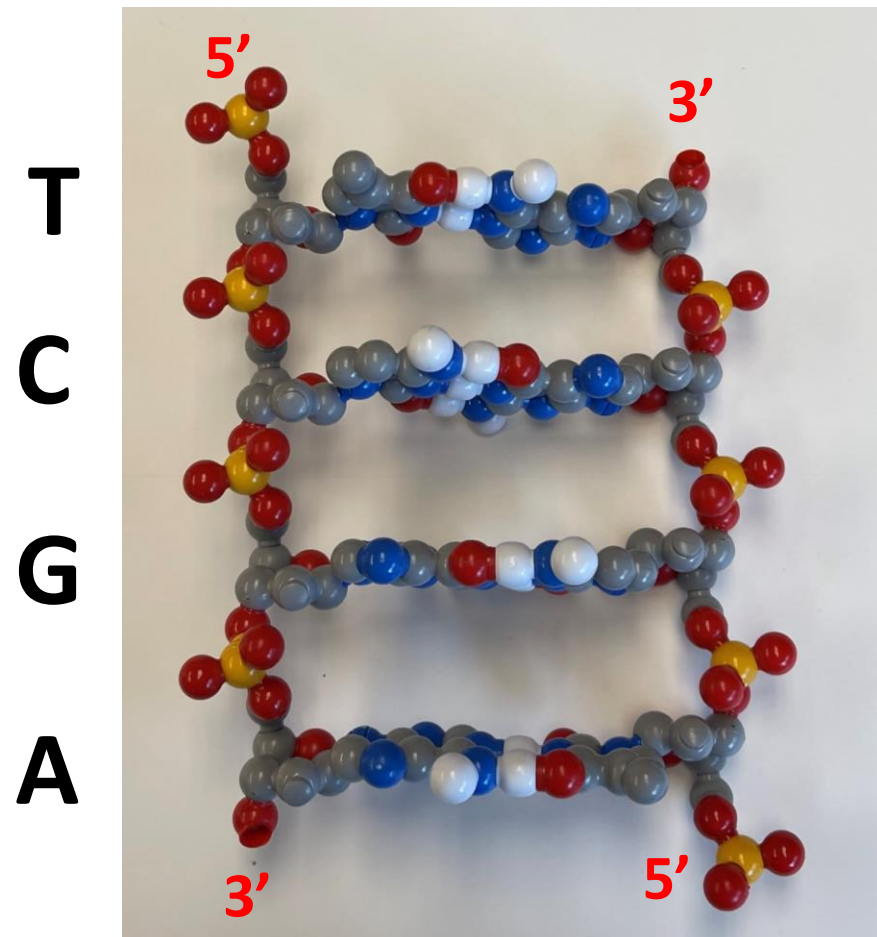
What can you teach?

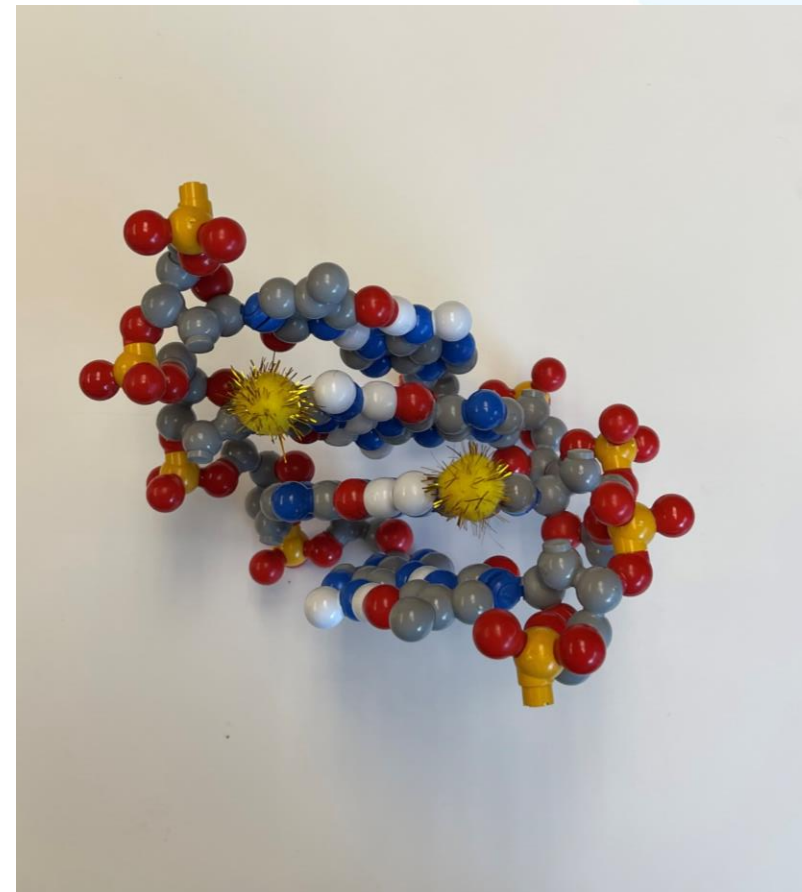
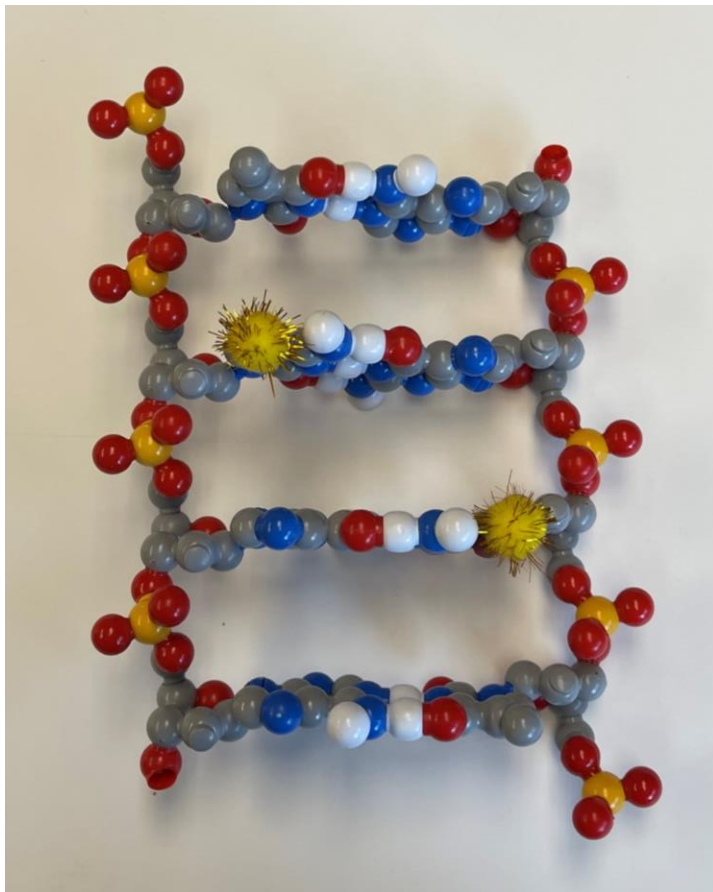
- *Why does RNA use U's... and DNA T's?*
- *What is pseudouridine?,... and why should I care?*
- *How does methylation of C regulate gene expression?*
- *Why are there surprisingly few CpG dinucleotides in our genes?*



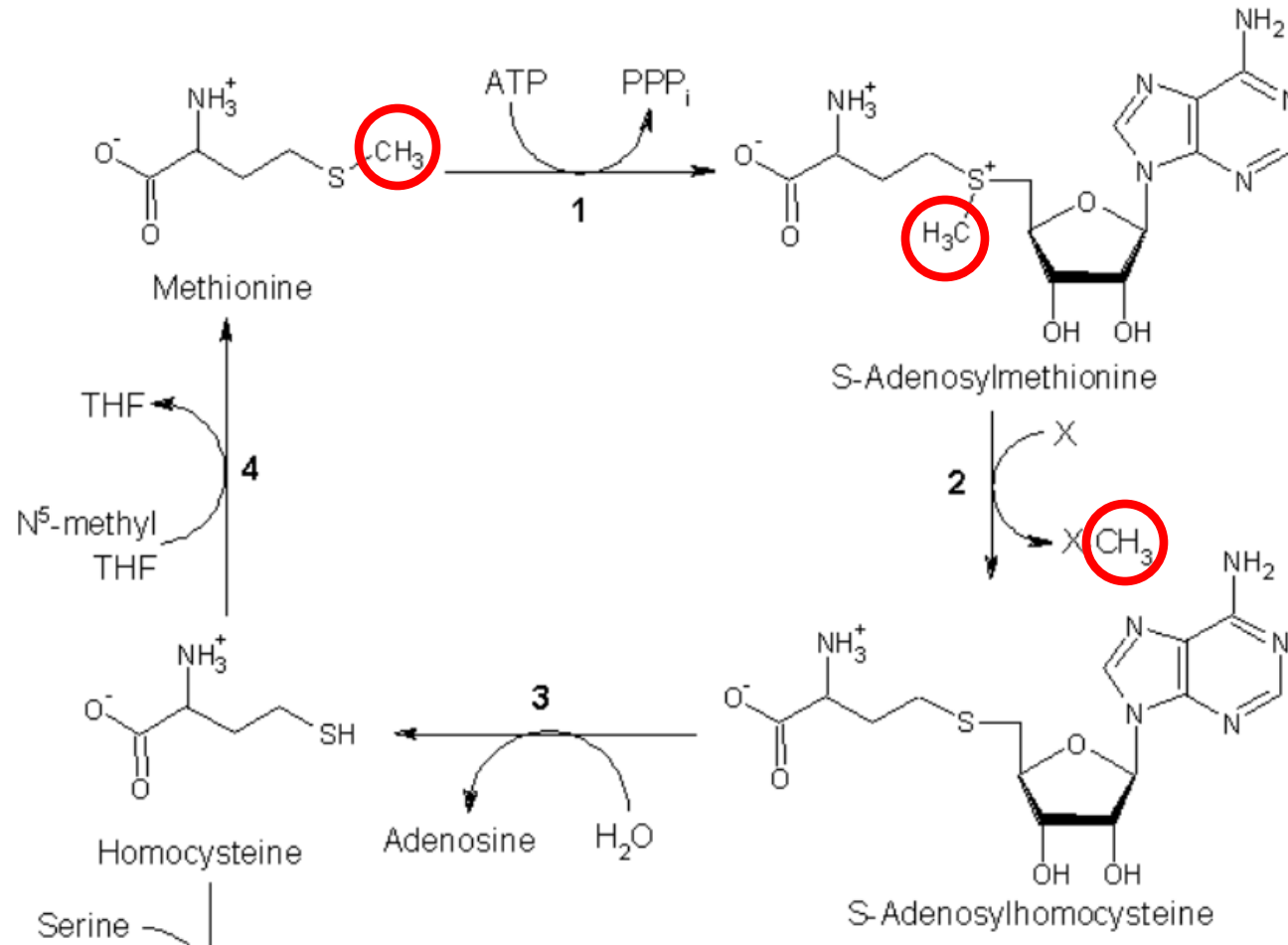
Looking for CpG's....







Methionine... *is a methyl-group donor*



After all these years,... a kick in the pants.

FOOD

- Folate
- EGCG from green tea
- Selenium

PHYSICAL ACTIVITY

TOBACCO SMOKE

INTRAUTERINE LIFE

- Maternal diet
- Tobacco smoke

ALCOHOL

- High intake

POLLUTANTS

- Arsenic
- Chromate
- PM
- Benzene
- PAHs
- POPs

AGING

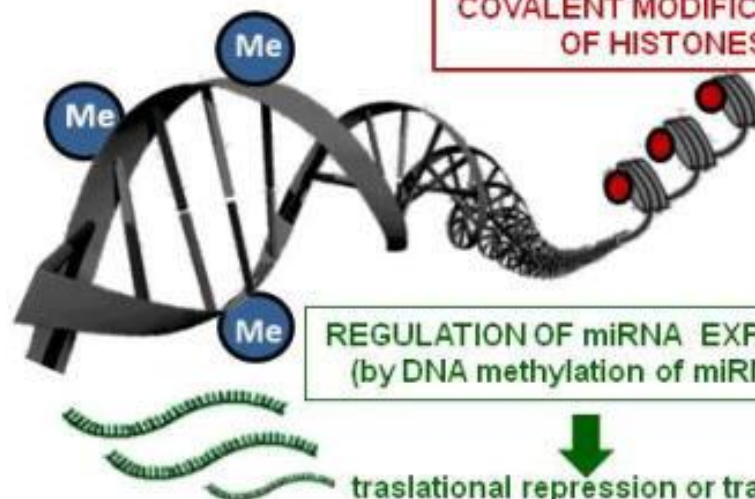
STRESS CONDITIONS

SHIFTWORK

silencing expression

↑ ↑
HYPER HYPO
gene expression
regulation

DNA METHYLATION



relaxed/compact chromatin
structure associated with
differential transcriptional activity

COVALENT MODIFICATIONS
OF HISTONES

FOOD

- Polyphenols from vegetables
- Selenium

PHYSICAL ACTIVITY

PHYSICAL ACTIVITY
CIGARETTE SMOKE
INTRAUTERINE LIFE

- Tobacco smoke

Fragile X Syndrome *a genetic/epigenetic disorder??*

X linked triplet repeat (**CGG**) expansion disorder

Fragile X patients do not express FMR1 and have cognitive/autism spectrum disabilities

All human genomes have CGG repeats in FMR1 5' untranslated region

Cytosines tend to become methylated at high repeat number (epigenetic modification!)

Methylation of cytosines inhibits transcription of FMR1

CAUTION...*rabbit hole ahead!*

Histone / DNA cross-talk?

YES...

What's CRISPR got to do with it??

Epigenome editing: targeted manipulation of epigenetic modifications in plants.

Shin H, Choi WL, Lim JY, Huh JH (March 2022).
Genes & Genomics. 44 (3): 307–315.

Review

CRISPR/Cas-Based Epigenome Editing: Advances, Applications, and Clinical Utility

Jacob H. Goell ¹ and Isaac B. Hilton ^{1,2,3,*,@}

The epigenome dynamically regulates gene expression and guides cellular differentiation throughout the lifespan of eukaryotic organisms. Recent advances in clustered regularly interspaced palindromic repeats (CRISPR)/Cas-based epigenome editing technologies have enabled researchers to site-specifically program epigenetic modifications to endogenous DNA and histones and to manipulate the architecture of native chromatin. As a result, epigenome editing has helped to uncover the causal relationships between epigenetic marks and gene expression. As epigenome editing tools have continued to develop, researchers have applied them in new ways to explore the function of the epigenome in human health and disease. In this review, we discuss the recent technical improvements in CRISPR/Cas-based epigenome editing that have advanced clinical research and examine how these technologies could be improved for greater future utility.

Highlights

Epigenome editing enables researchers to activate and repress endogenous gene expression and can provide graded control over gene regulation.

Recruitment of epigenome editing effector domains using CRISPR/Cas systems allows site-specific control over modifications to DNA, histones, and chromatin architecture.

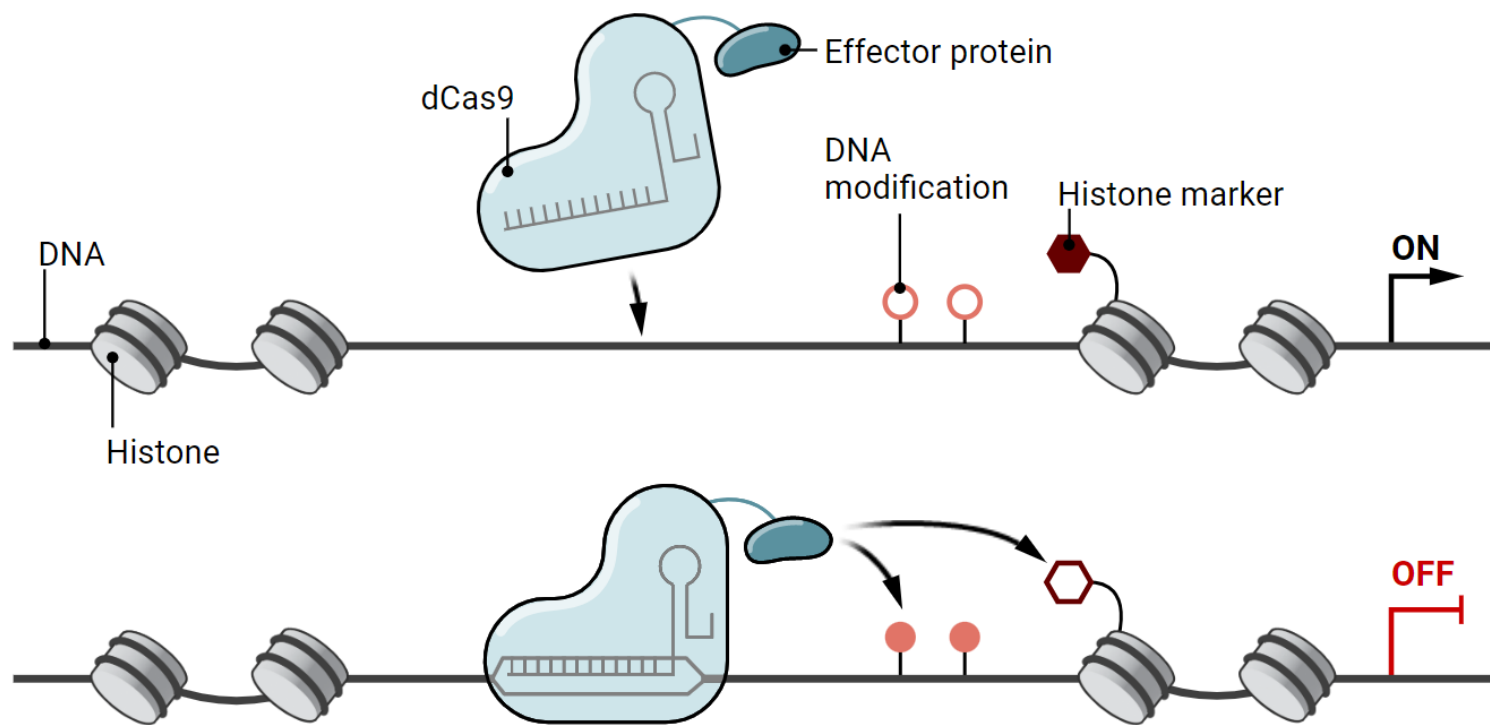
The combined use of patient-derived induced pluripotent stem cells and epigenome editing permits precision disease

Trends in Biotechnology, July 2021, Vol. 39, No. 7
<https://doi.org/10.1016/j.tibtech.2020.10.012>

Regulation of Gene Expression and the Elucidative Role of CRISPR-Based Epigenetic Modifiers and CRISPR-Induced Chromosome Conformational Changes

Abstract

In complex multicellular systems, gene expression is regulated at multiple stages through interconnected complex molecular pathways and regulatory networks. Transcription is the first step in gene expression and is subject to multiple layers of regulation in which epigenetic mechanisms such as DNA methylation, histone tail modifications, and chromosomal conformation play an essential role. In recent years, CRISPR-Cas9 systems have been employed to unearth this complexity and provide new insights on the contribution of chromatin dysregulation in the development of genetic diseases, as well as new tools to prevent or reverse this dysregulation. In this review, we outline the recent development of a variety of CRISPR-based epigenetic editors for targeted DNA methylation/demethylation, histone modification, and three-dimensional DNA conformational change, highlighting their relative performance and impact on gene regulation. Finally, we provide insights on the future developments aimed to accelerate our understanding of the causal relationship between epigenetic marks, genome organization, and gene regulation.



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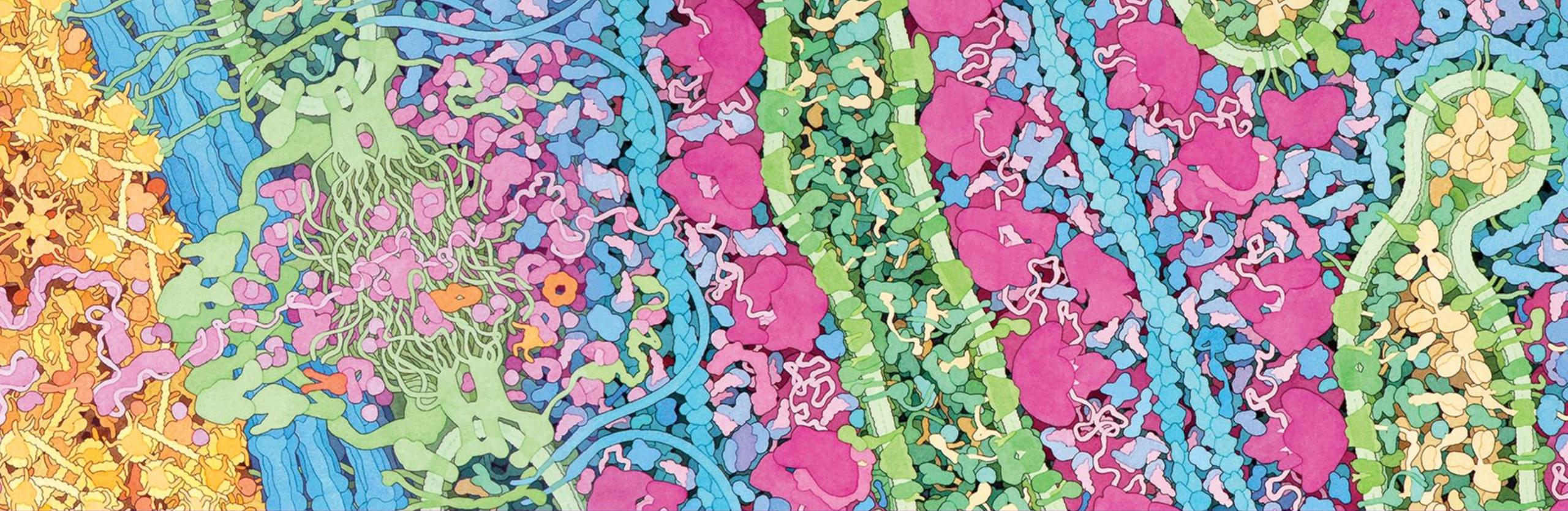
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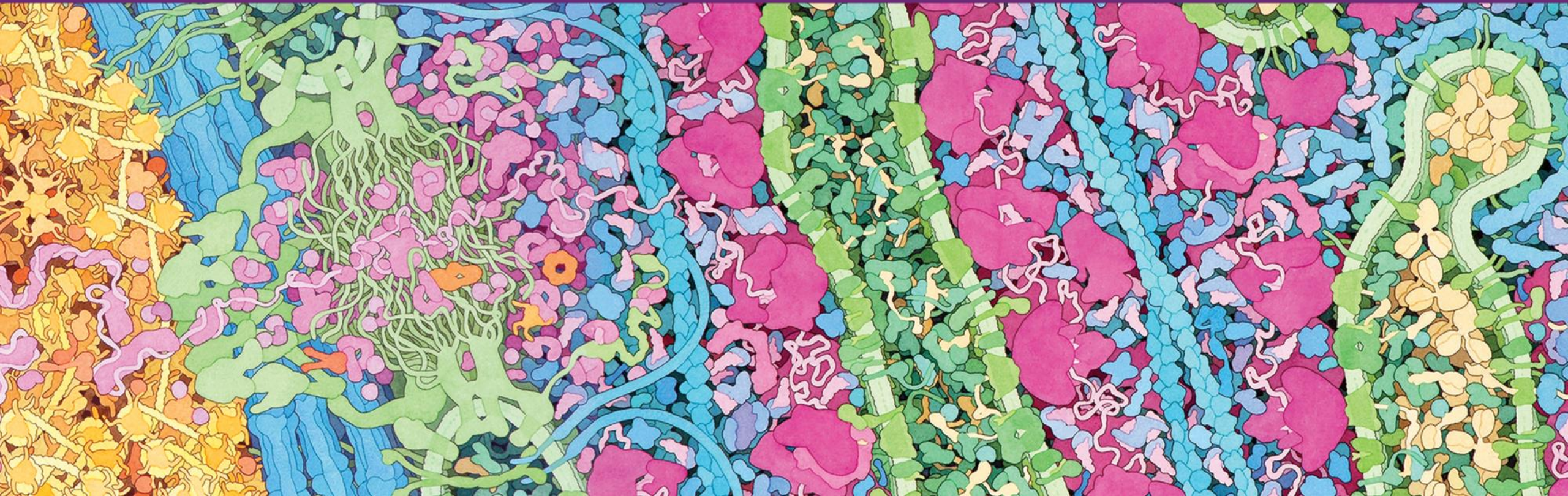
Session 1 -- June 26–30, or

Session 2 -- July 17 – 21



3d molecular
designs

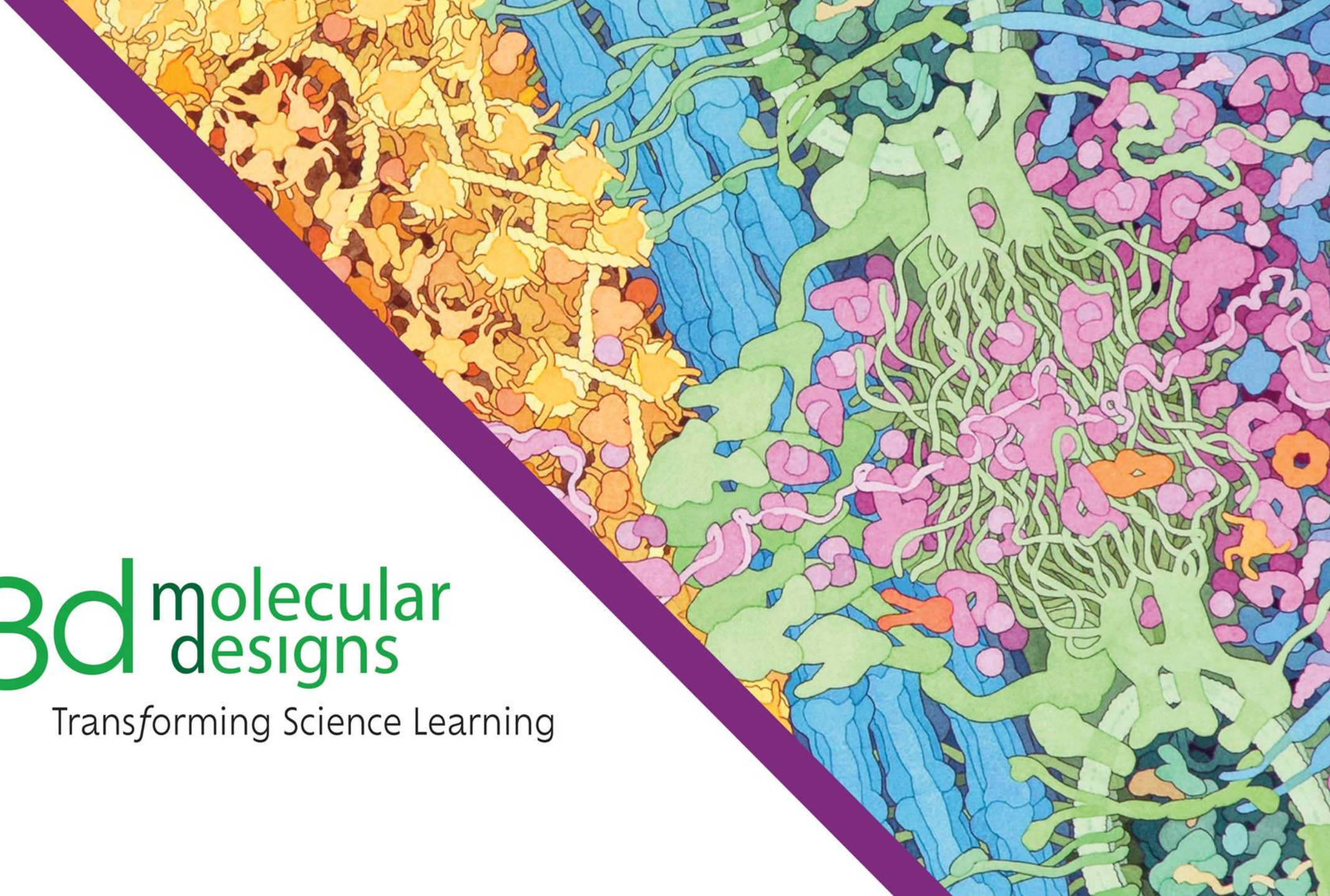
Transforming Science Learning

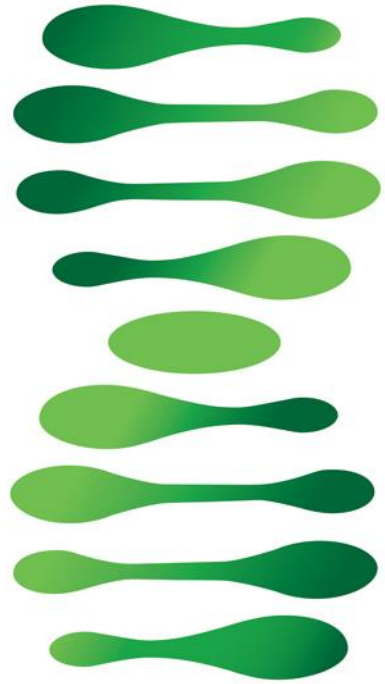




3d molecular
designs

Transforming Science Learning





Transforming Science Learning



WHY...did T replace U in DNA?

...if we had not switched...

spontaneous oxidative
deamination of C



AGUCGAAGUCAACCGAGGCUGCGCUAC
UCAGCUUUCAGUUGGCUCCGACGCGAUG



AGUCGAAGU^U_xAACCGAGGCUGCGCUAC
UCAGCUUUCAG_GUUGGCUCCGACGCGAUG

A DNA repair system can remove “U” from DNA.
But,...how can we distinguish between a
“deaminated C” and a normal U?

ANSWER: We can't.

WHY...did T replace U in DNA?

...but after we switched...

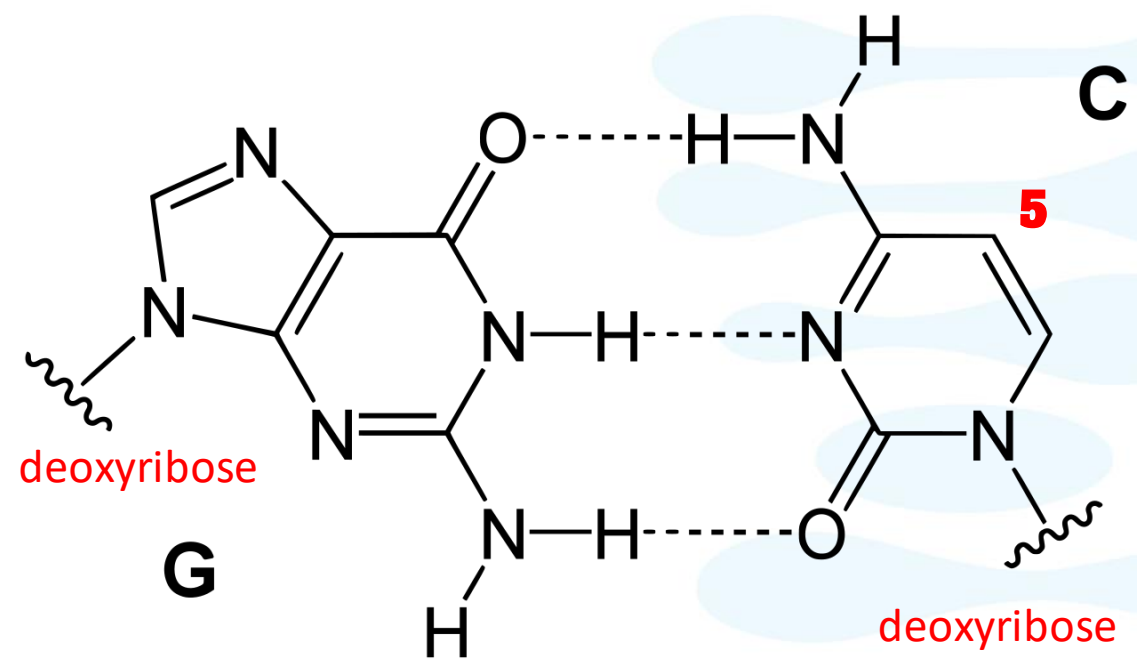
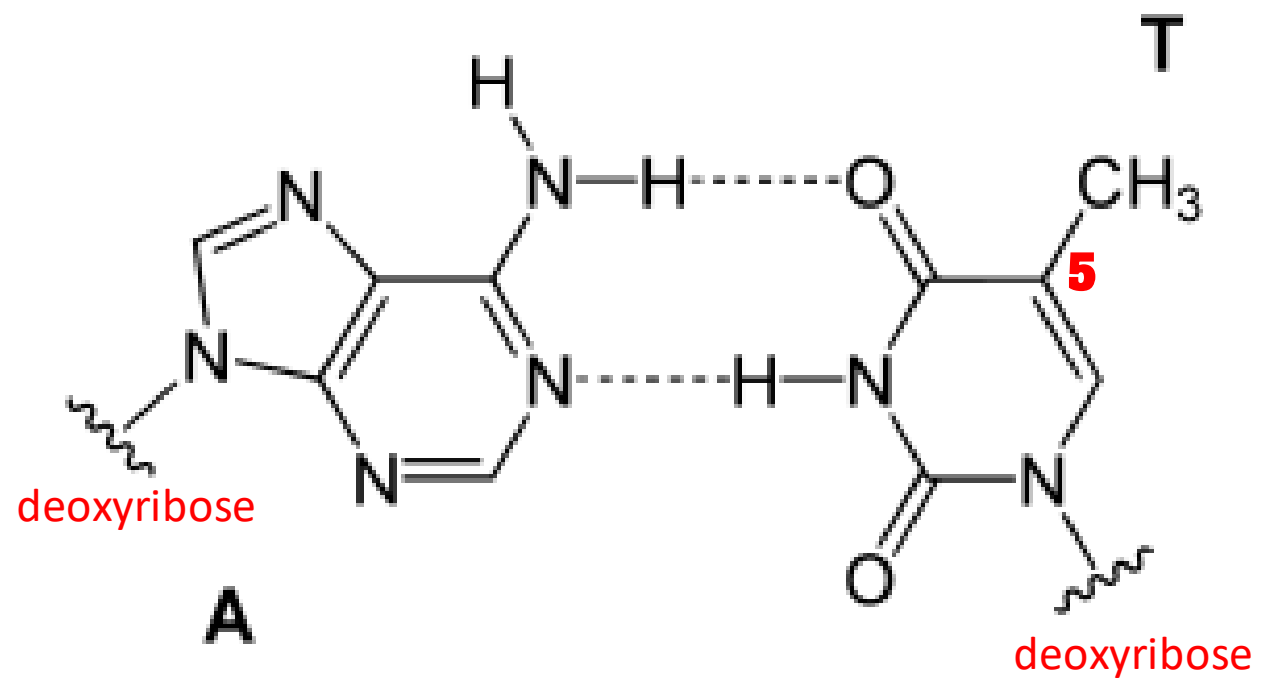
spontaneous oxidative
deamination of C

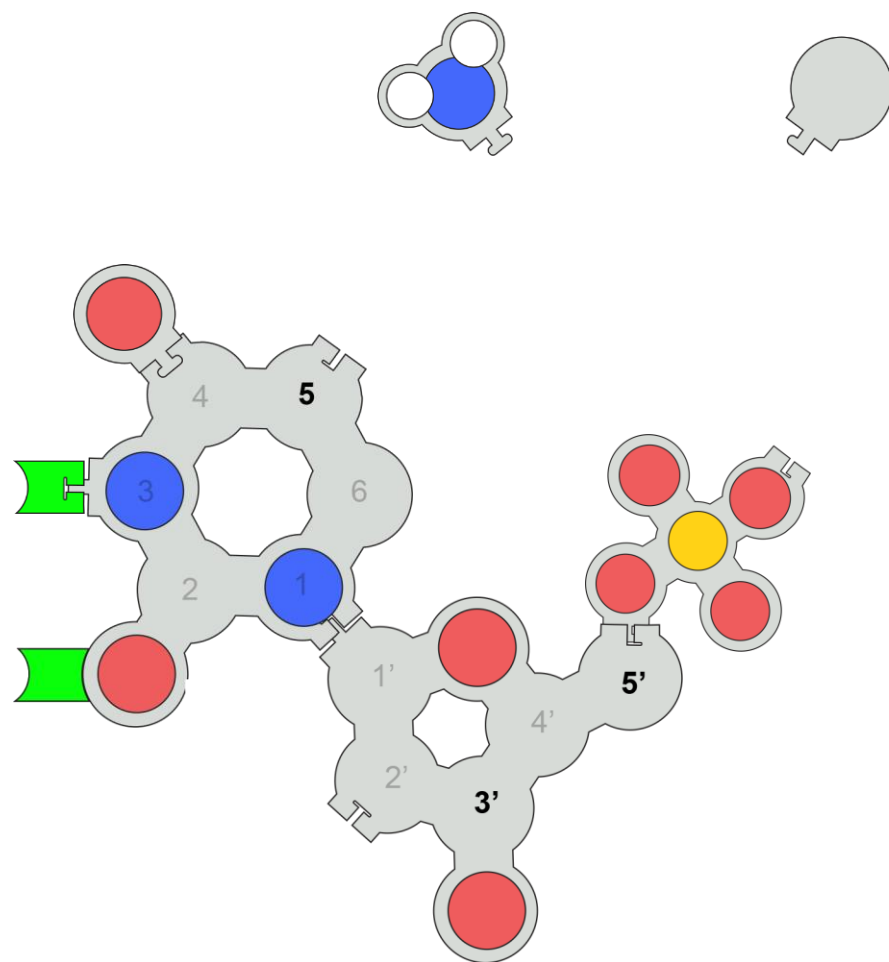
AGTCGAAGTCAACCGAGGCTGCGCTAC
TCAGCTTCA GTTGGCTCCGACGCGATG



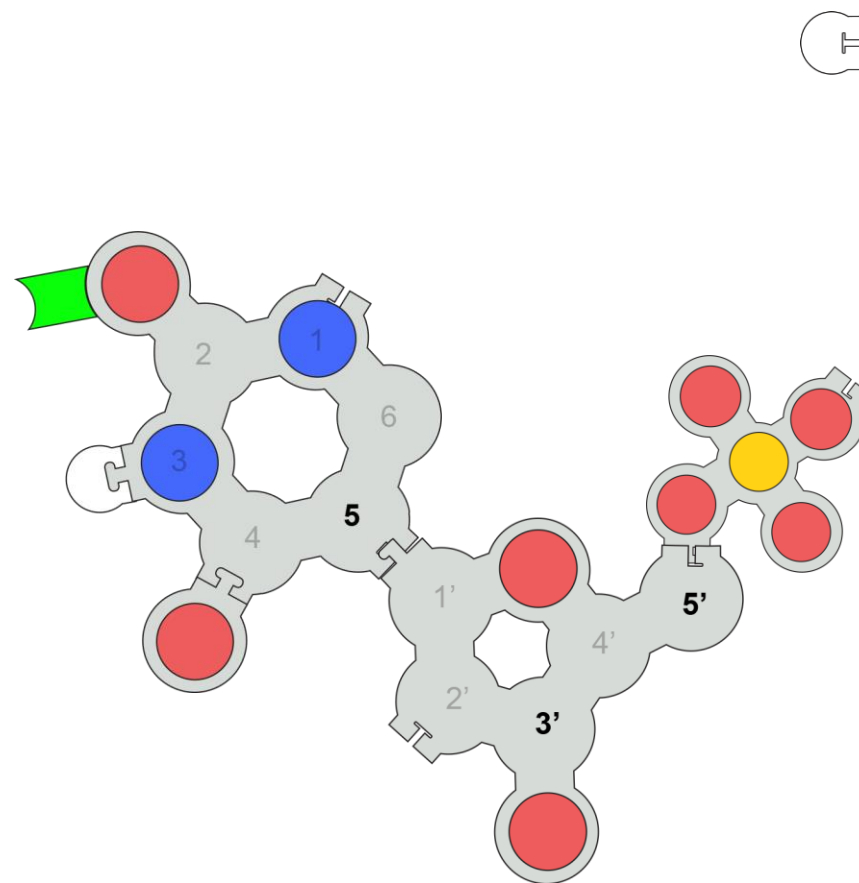
AGTCGAAGT^U_xAACCGAGGCTGCGCTAC
TCAGCTTCA_GTTGGCTCCGACGCGATG

Uracil glycosidase constantly scans the DNA....looking for U's.
Any U ... is a bad U...and should be repaired.

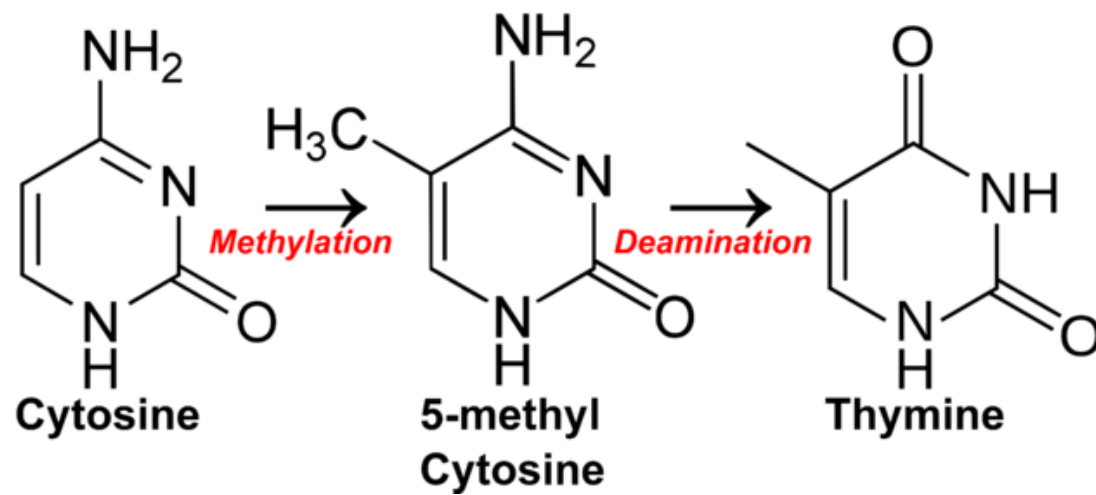


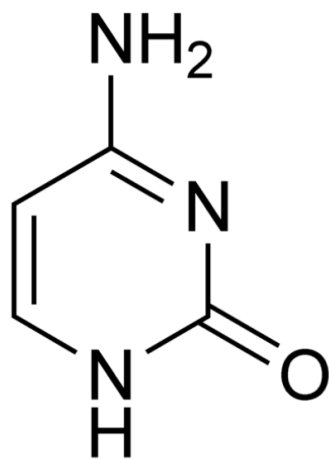


Uridine

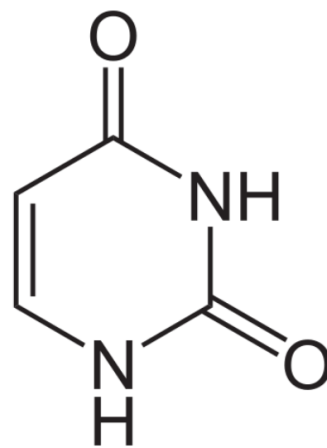


Pseudo-Uridine

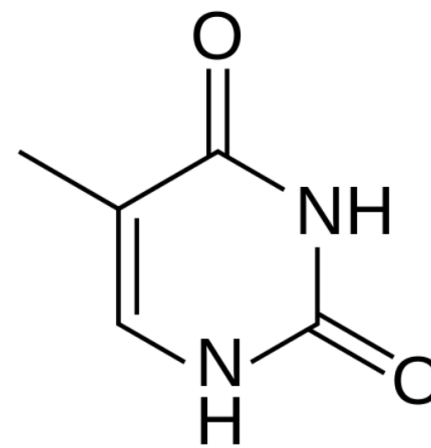




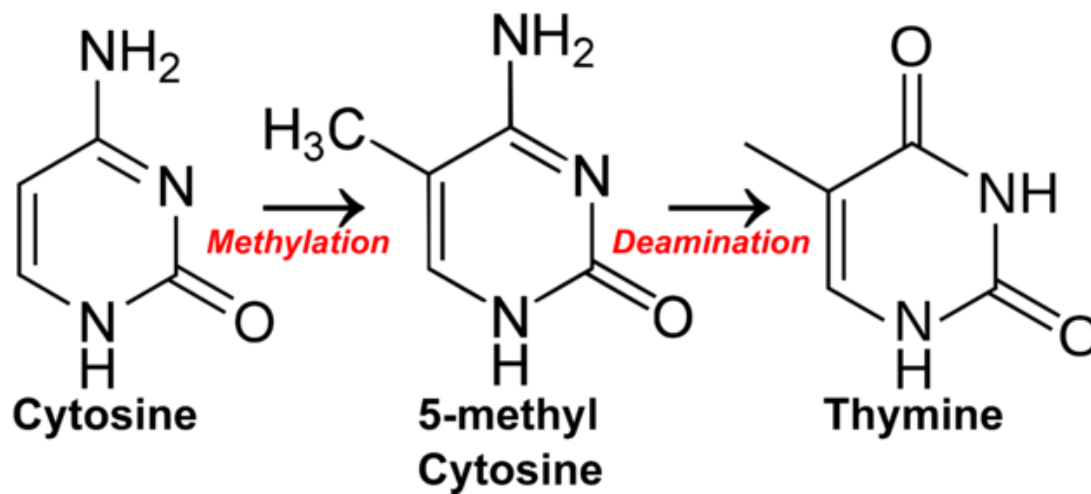
Cytosine

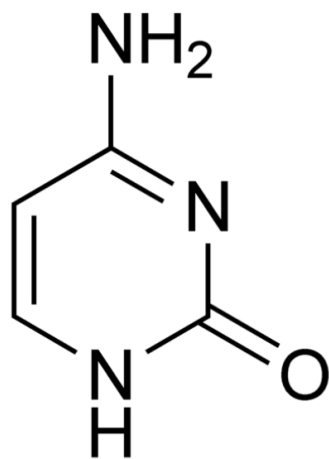


Uracil

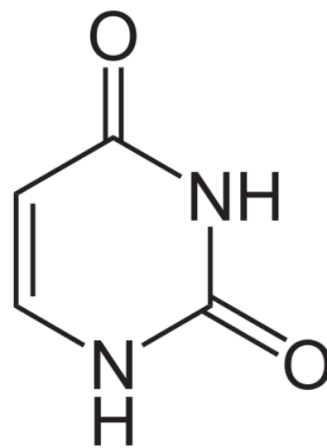


Thymine

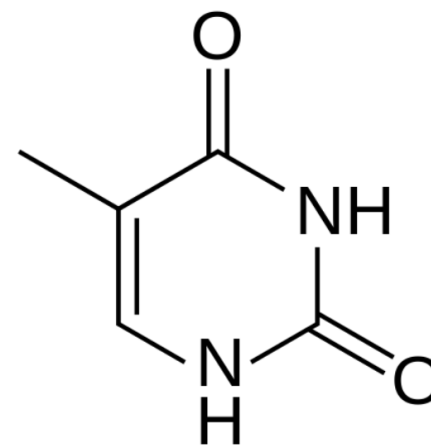




Cytosine



Uracil



Thymine

