

The Kei-ichiro Maeda  
Memorial T&C Award



# Transcriptome-wide studies on mRNA tailing and investigation of stress responses in immune cells

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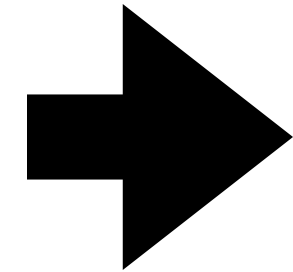
# My academic journey from veterinary medicine to basic science



**B.S./D.V.M.**

**Seoul National University  
College of Veterinary Medicine**

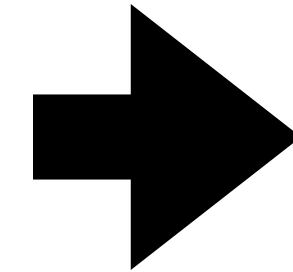
**2005-2011**



**Ph.D.**

**Seoul National University  
School of Biological Sciences**

**2011-2017**

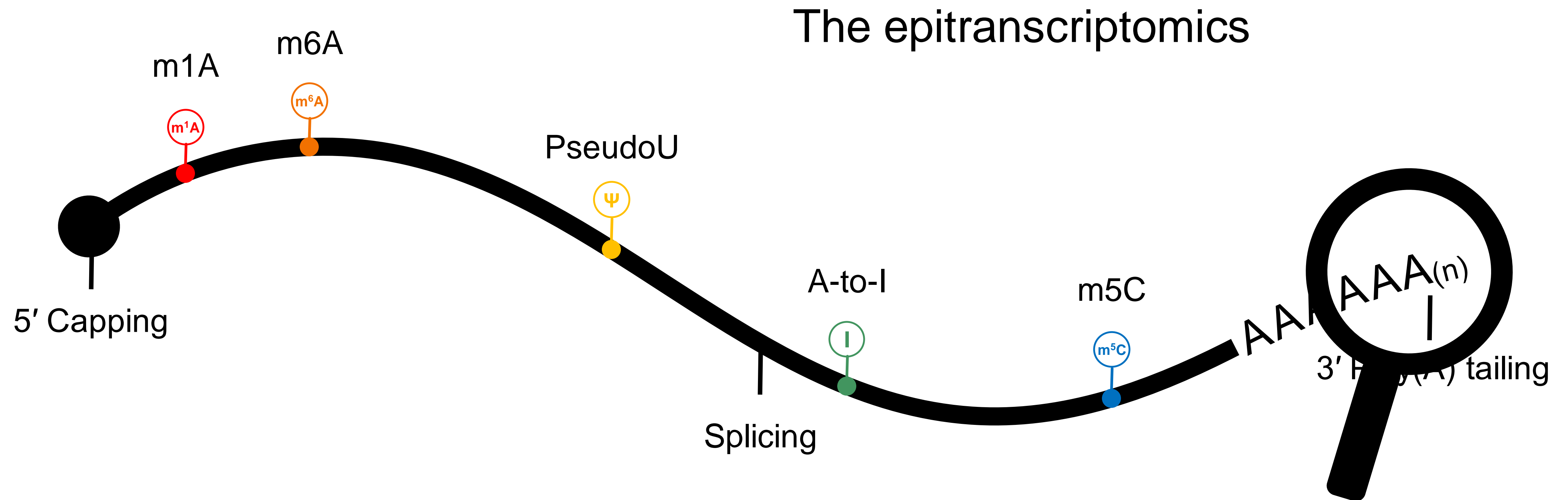


**Postdoc**

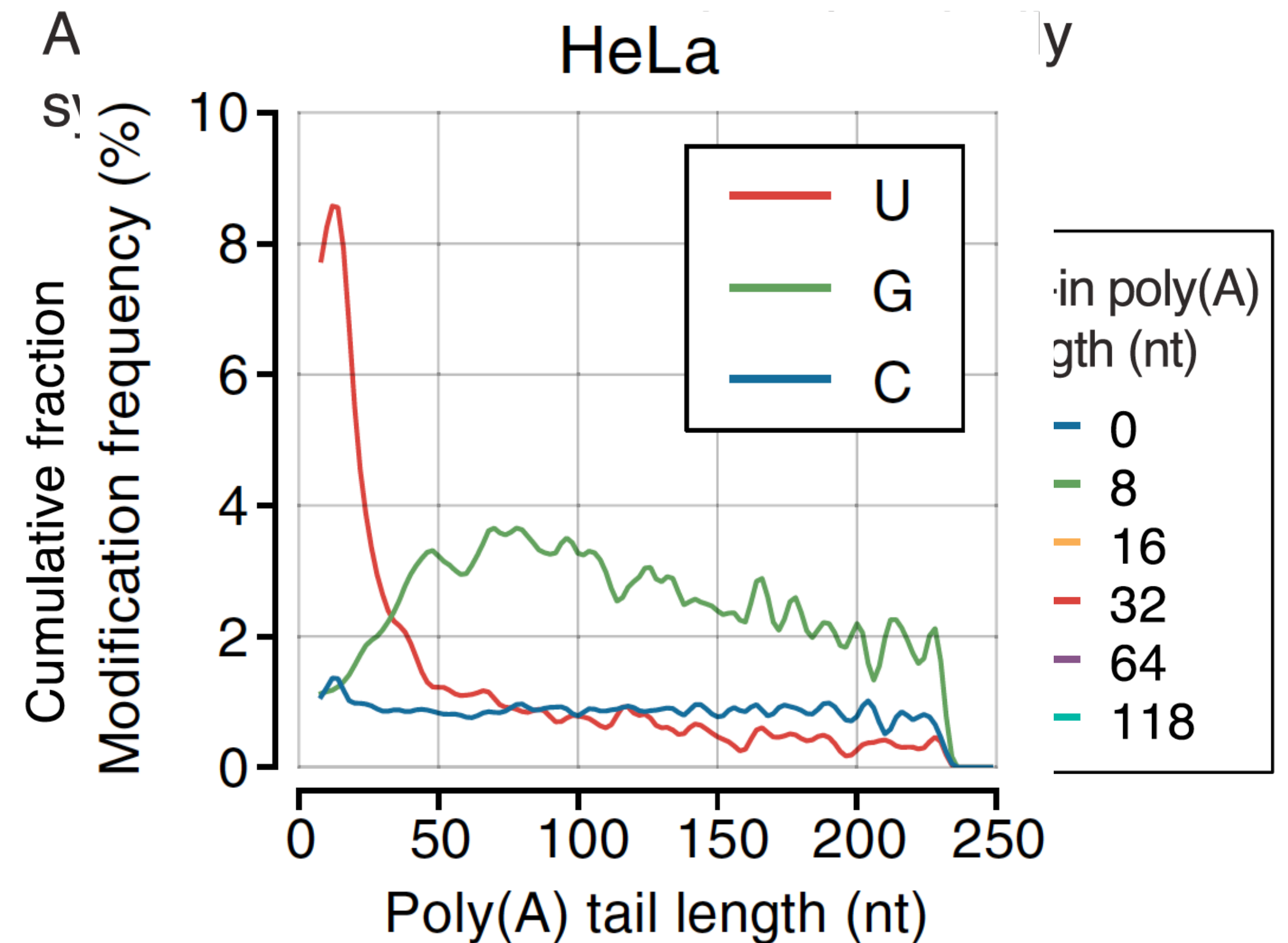
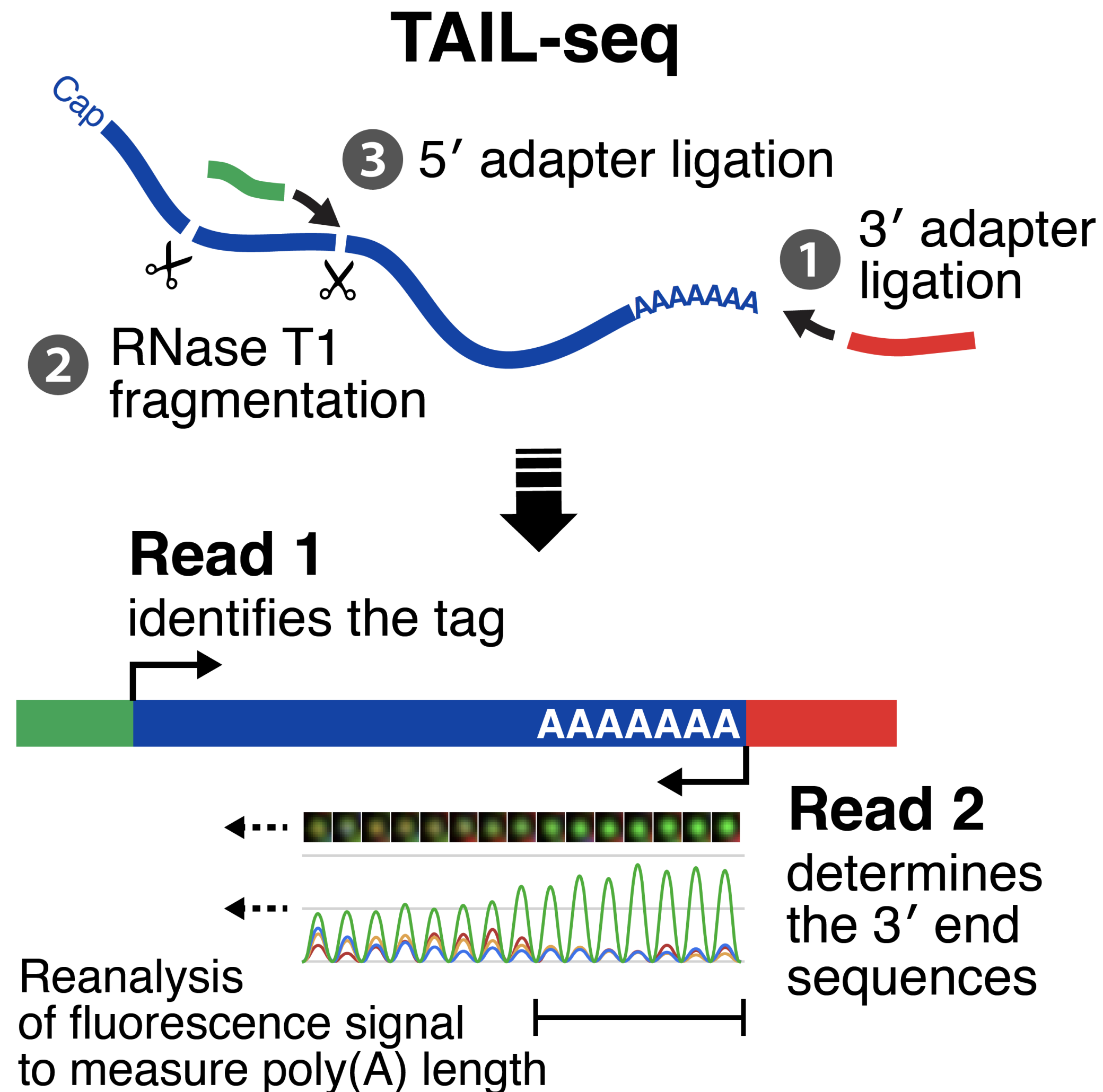
**Yale School of Medicine  
Department of Immunobiology**

**2017-2023**

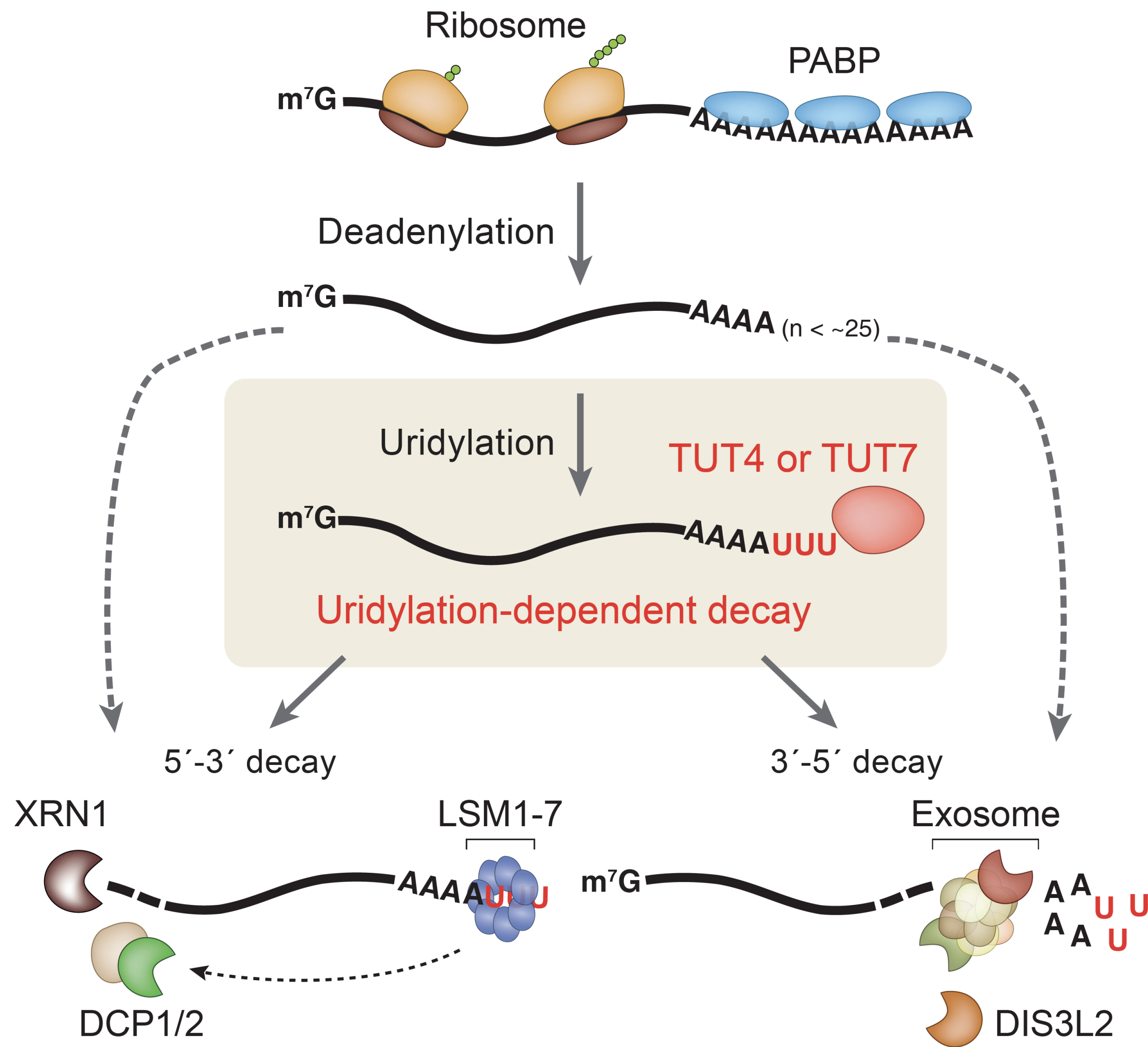
# Post-transcriptional modifications of messenger RNA



# TAIL-seq revealed the transcriptome-wide landscape of RNA 3' ends

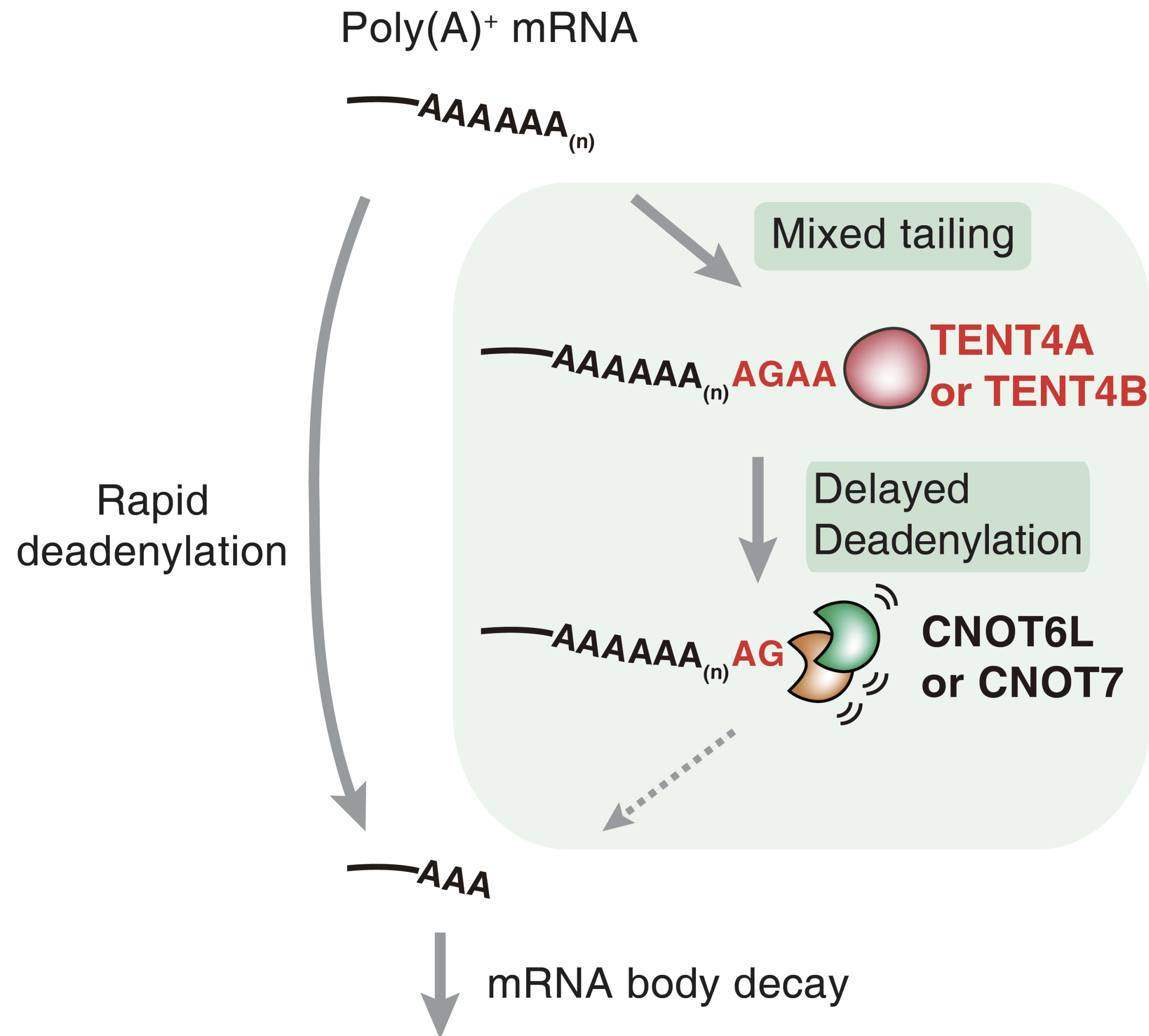


# Uridylation facilitates global mRNA degradation



1. TUT4 and TUT7 specifically uridylate deadenylated mRNAs and thereby facilitate global mRNA decay.
2. mRNAs with short A tails (<~25 nt) lose PABP and instead gain a U-tail.
3. The oligo-U tail triggers mRNA decay by serving as a general mark that is recognized by downstream decay factors.

# Mixed tailing shields mRNA from deadenylation



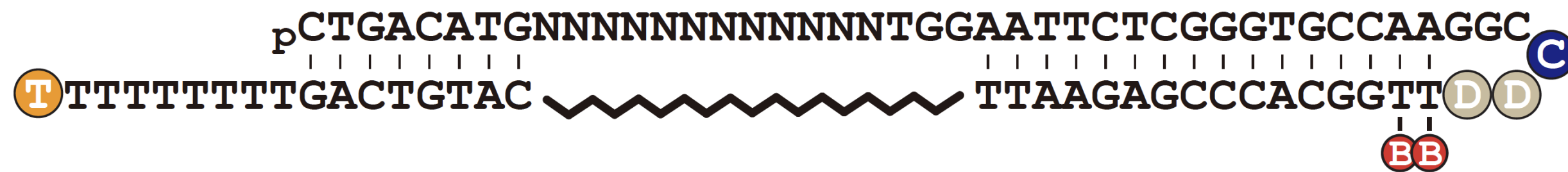
1. TENT4A/B add mixed tails (A  $\gg$  G > C, U) to poly(A) mRNAs.
2. Non-adenosine residues slow down CNOT6L/7 deadenylases.
3. The mixed tail protects and stabilizes mRNAs from deadenylation.

# mTAIL-seq accurately measures poly(A) tail length with low input samples

TAIL-seq 3' adaptor

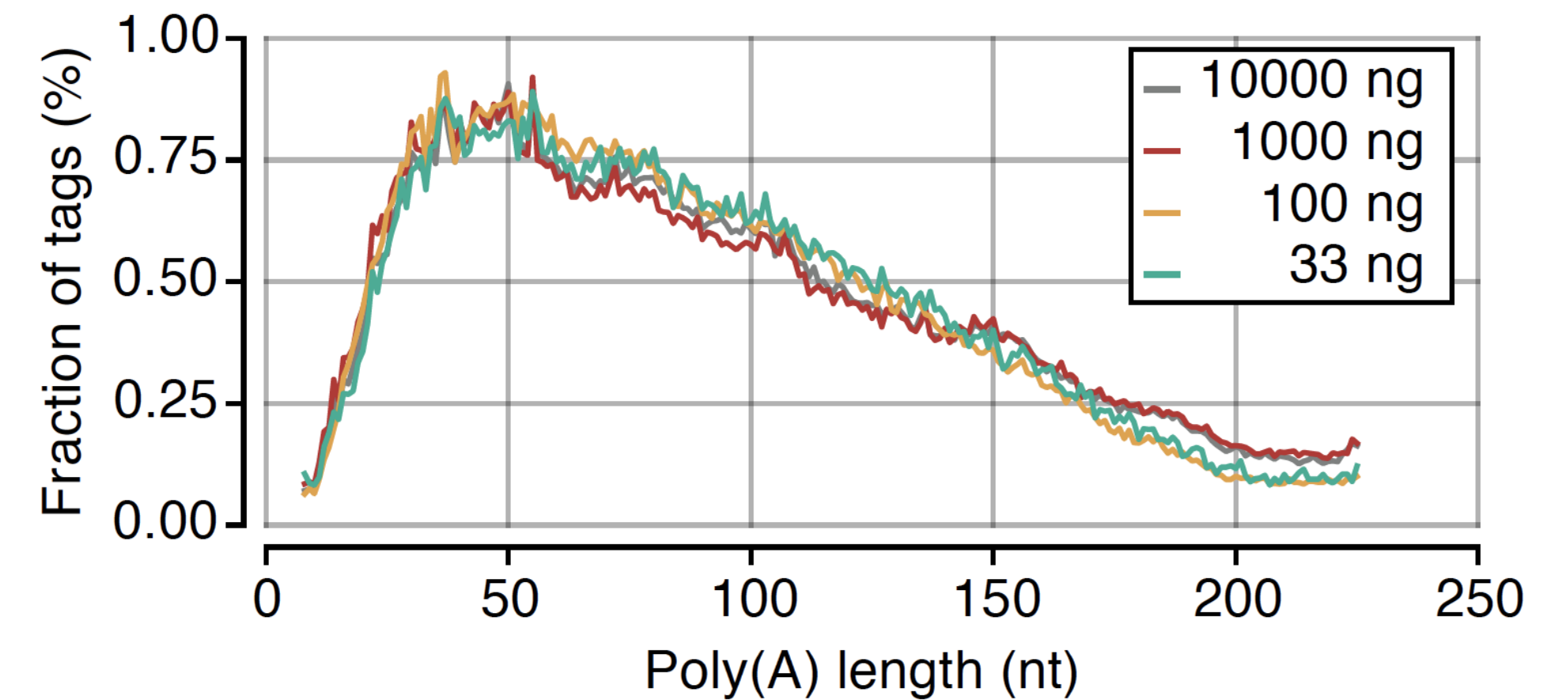


mTAIL-seq 3' adaptor (hairpin)



- B Biotin       Spacer      T Inverted dT (3'-3' linkage)
- C C3 spacer phosphoramidite      D 1', 2' -Dideoxyribose (abasic site)

Global poly(A) distribution



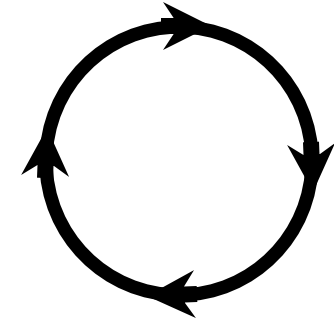
→ Fly oocytes and embryos  
 → Dynamic poly(A) tail regulation in oocyte-to-embryo development

# TAIL-seq and mTAIL-seq have been applied to various biological studies



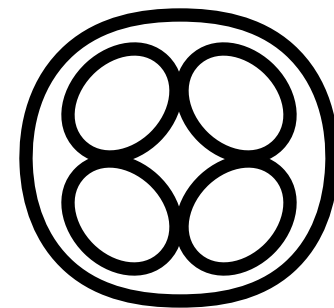
mRNA metabolism  
(Deadenylation, decay, and translation)

Lima et al., *Nat Str Mol Biol*, 2017  
Yi\*, Park\* et al., *Mol Cell*, 2018  
Eisen\*, Eichhorn\*, Subtelny\* et al., *Mol Cell*, 2020  
Xiang and Bartel, *eLife*, 2021



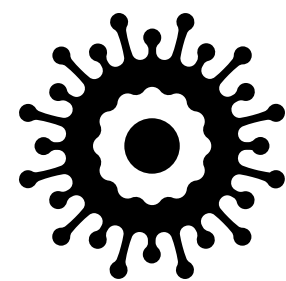
Cell cycle regulation

Park\*, Yi\*, Kim\* et al., *Mol Cell*, 2016  
Liu et al., *iScience*, 2020



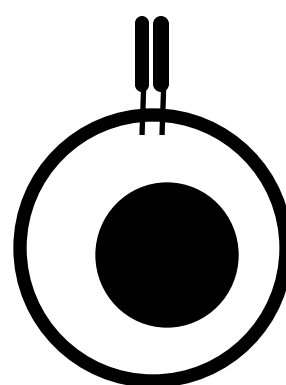
Development  
(Oogenesis and embryogenesis)

Lim\*, Lee\* et al., *Genes Dev*, 2016  
Morgan\*, Much\* et al., *Nature*, 2017  
Chang\*, Yeo\* et al., *Mol Cell*, 2018



Viral infection

Batra\*, Stark\* et al., *Nat Str Mol Biol*, 2016  
Kim\*, Lee\*, Jung\*, Yeo\* et al., *Nat Str Mol Biol*, 2020

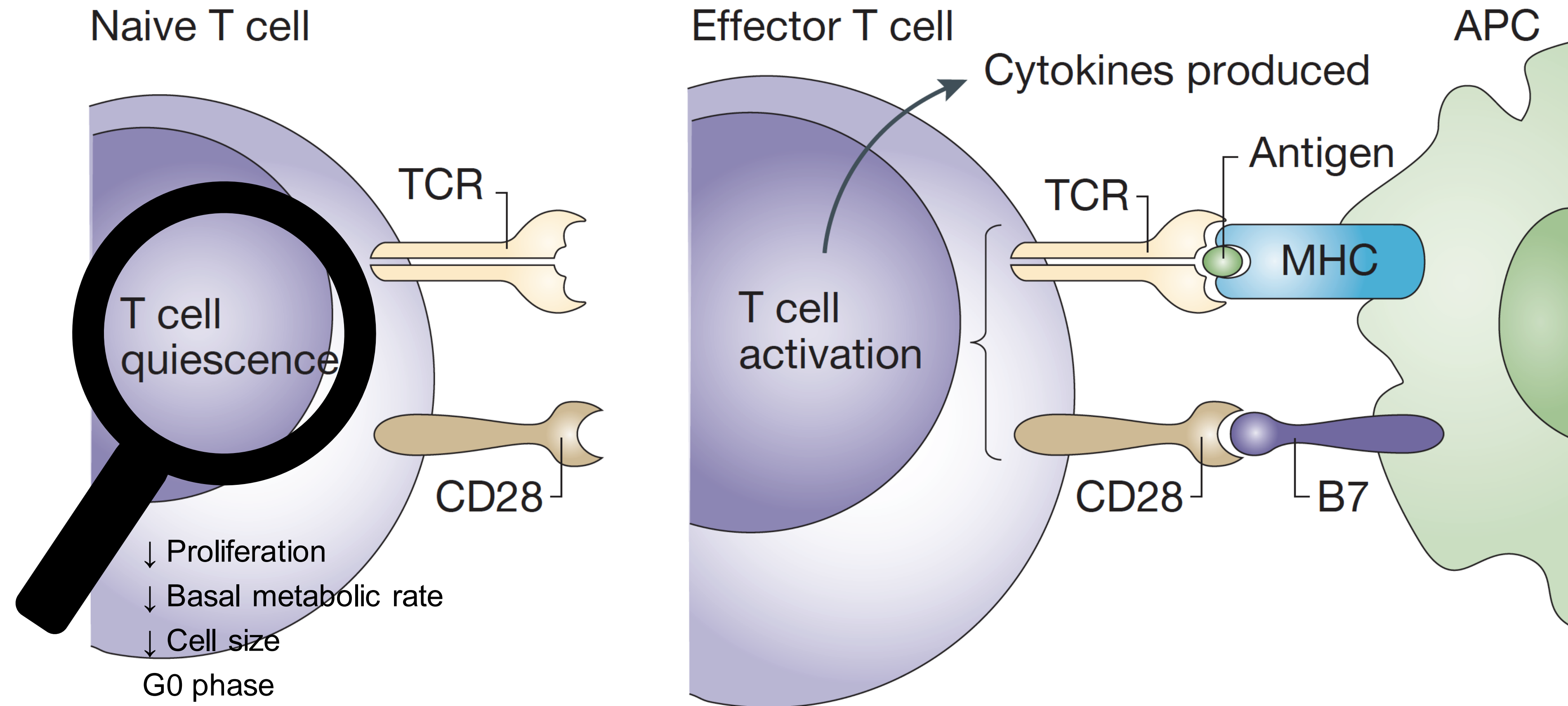


T cell quiescence

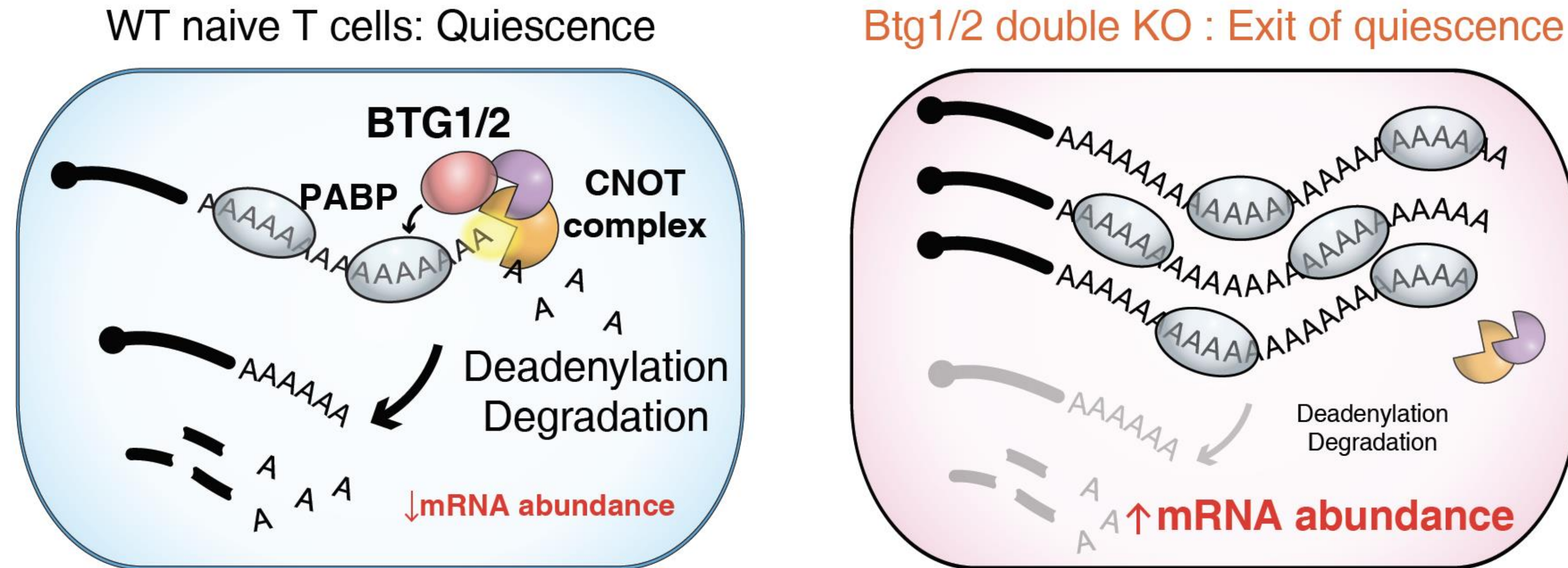
Hwang\*, Lim\* et al., *Science*, 2020



# T cells maintain quiescence in the absence of activation stimuli

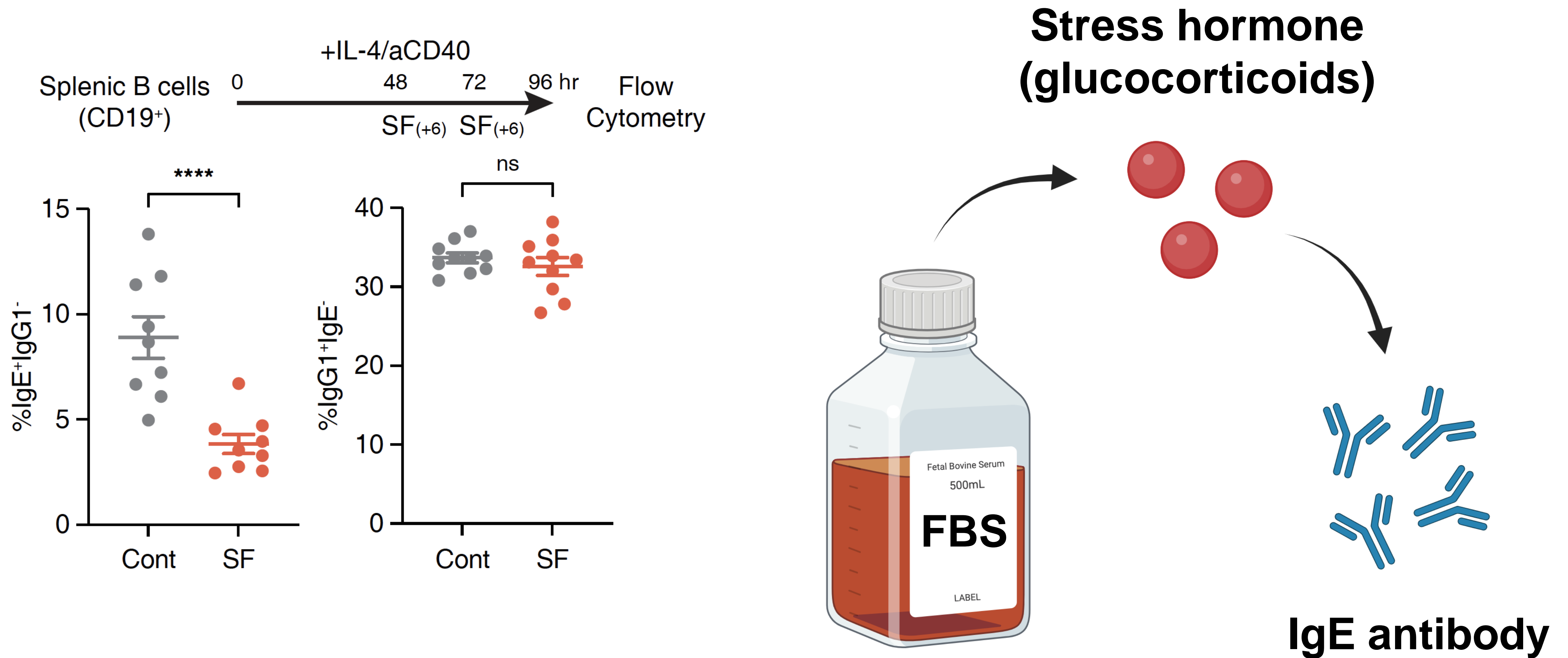


# mRNA destabilization by BTG1/2 maintains T cell quiescence

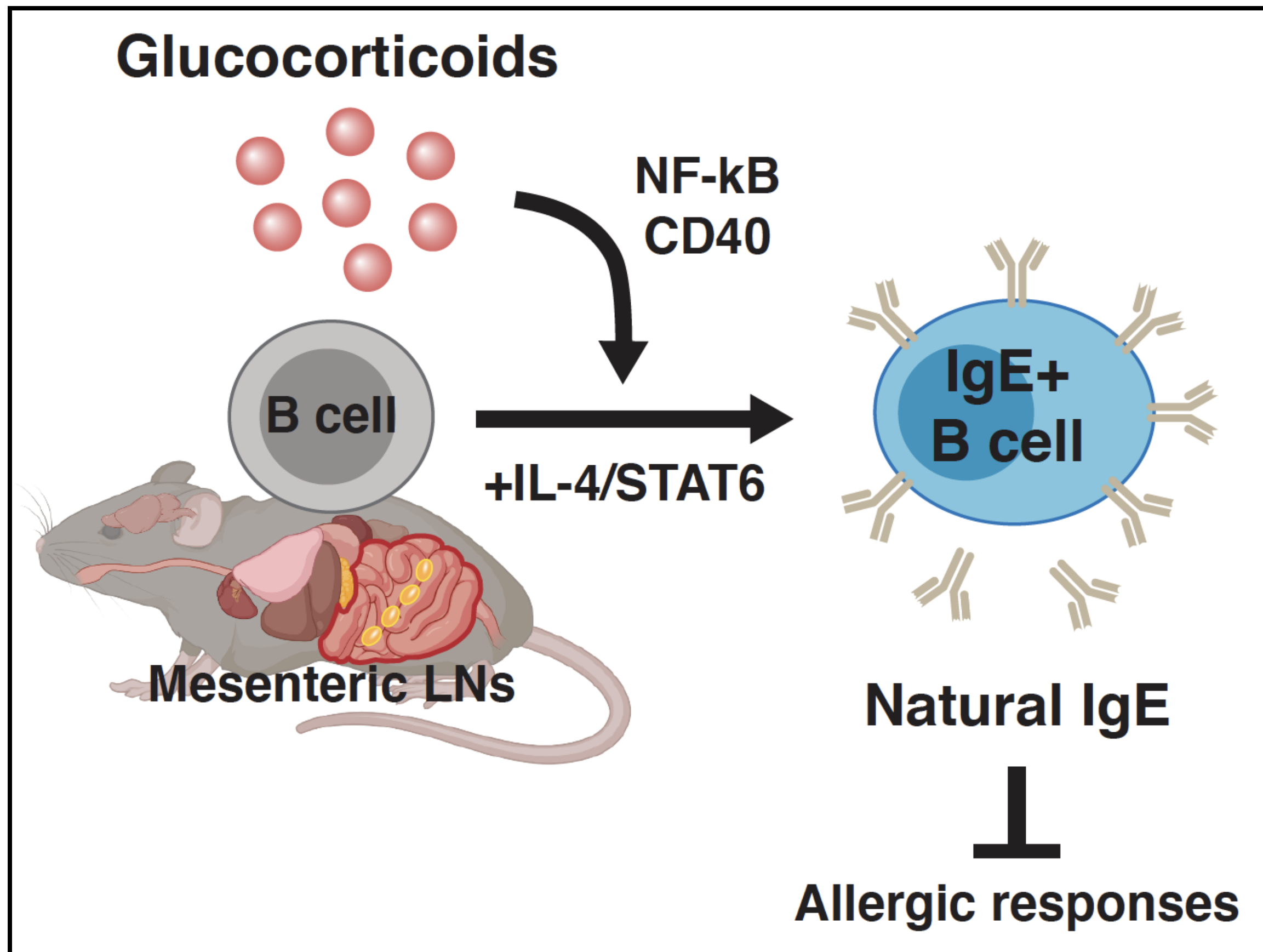


1. BTG1/2 promote global mRNA deadenylation and degradation in naive T cells.
2. Loss of Btg1/2 results in exit of T cell quiescence by increasing global mRNA levels.
3. Active mRNA turnover might be a crucial feature for maintaining quiescence.

# Transient serum starvation selectively decreases IgE switching



# Stress hormones, glucocorticoids, induce natural IgE



- 1) Glucocorticoids induce natural IgE both *in vivo* and *ex vivo* without antigenic challenge.
- 2) Glucocorticoids reinforce CD40 signaling and are dependent on IL-4/STAT6.
- 3) Natural IgE-producing B cells are localized in mLNs *in vivo*.
- 4) Natural IgE induced by glucocorticoids may have a protective role in preventing allergic reactions.

# Future plans in the college of veterinary medicine

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I will investigate how cells or animals adapt to stress conditions.

1. Animals have a variety of digestive systems. I aim to understand how immune cells maintain homeostasis, especially in the gut. I am interested in the role of immune cells when gut homeostasis is perturbed, such as dysbiosis or food poisoning.
2. In response to stress, some animals exhibit a highly stress-resistant state, like hibernation or dormancy. I am interested in the molecular mechanisms how cells or animals cope with extreme environmental conditions.

# Acknowledgements

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Erica Lin  
Jun Young Hong

## Collaborators

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Yale Center for Genome Analysis

Cold Spring Harbor Lab

Amazon Web Service

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Sergei Mekhedov

**RAS** Andrew Goodkov  
Alexander Kudryavtsev



*Thank you!*