

HU Binding Coupled Bending of DNA

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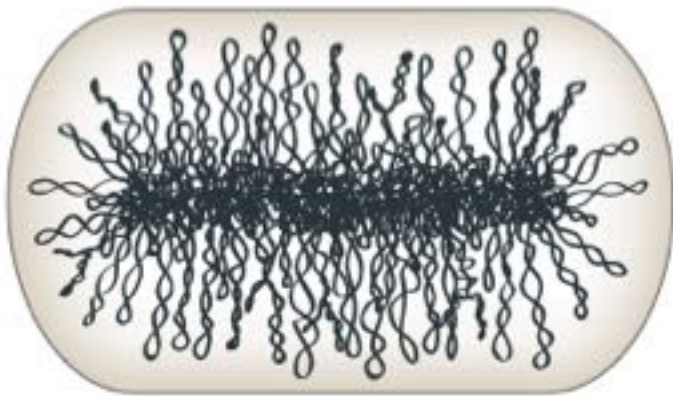
Kyoto University

2015-09-13

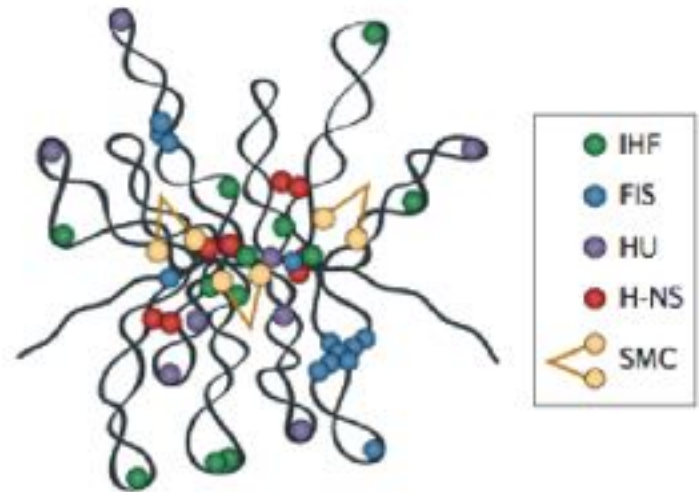
Tan, C.; Terakawa, T.; Takada, S. *J. Am. Chem. Soc.* **2016**, *138* (27), 8512.

Introduction

- Double stranded DNA: one of the stiffest biomolecules (Persistence length $\sim 50\text{nm} \sim 150\text{bp}$)



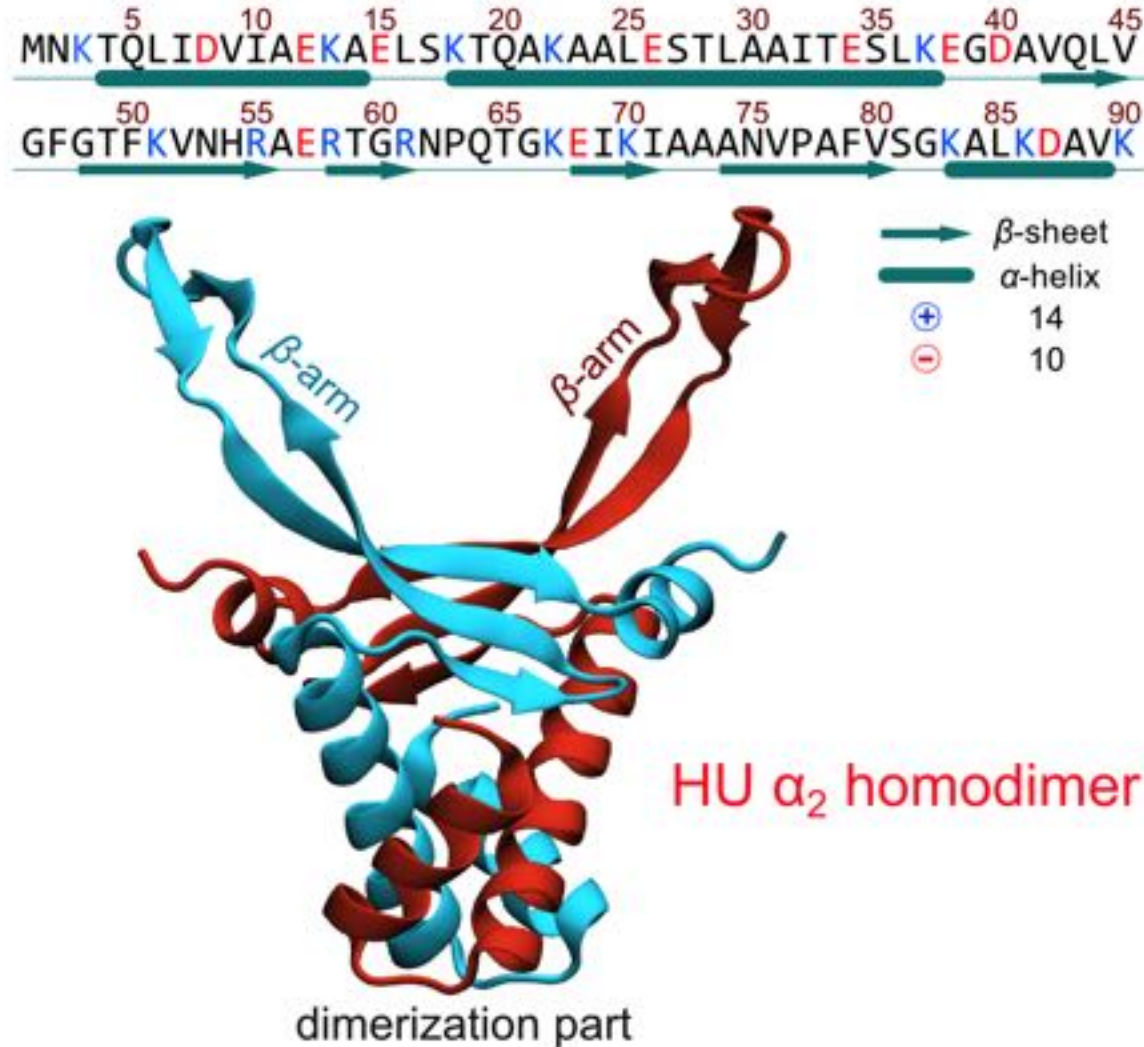
Packaging of DNA into cells (prokaryotic)



“Architectural” DNA-binding proteins

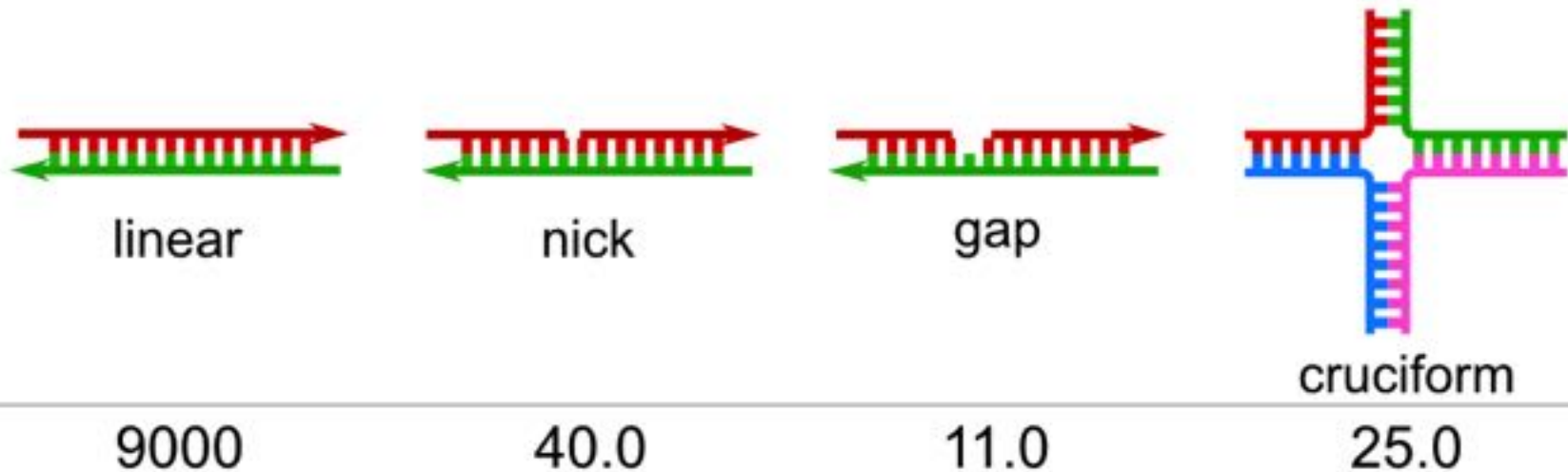
Introduction

- HU: one of the most abundant "architectural" proteins



Introduction

- HU-DNA binding specificity:
Sequence: Slight preference for A/T-rich DNA.
Structure: Strong preference for **cruciform** or **gap/nick**.

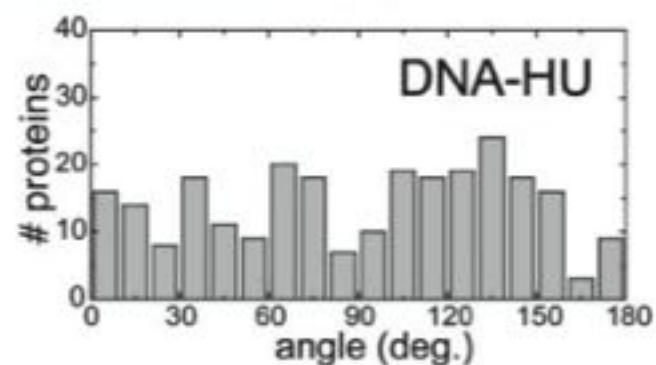
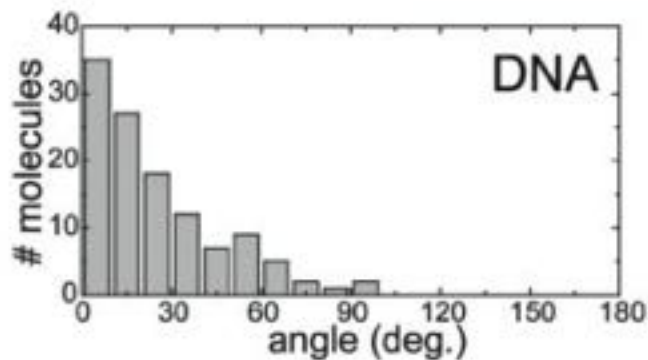
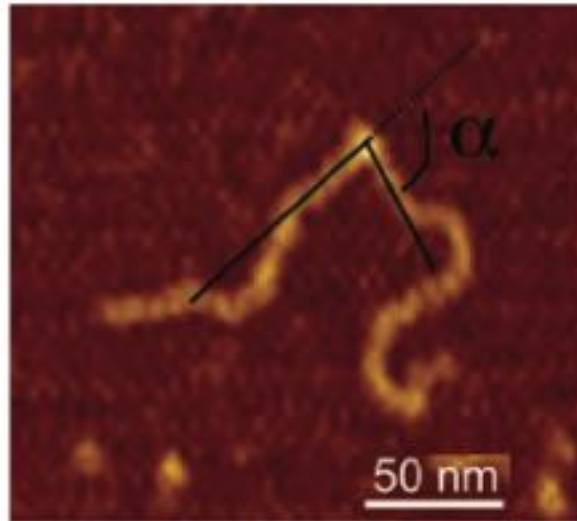


Prieto, A. I. *et al.* (2012) *Nucleic Acids Res.* **40**, 3524.

Pinson, V. *et al.* (1999) *J. Mol. Biol.* **287**, 485.

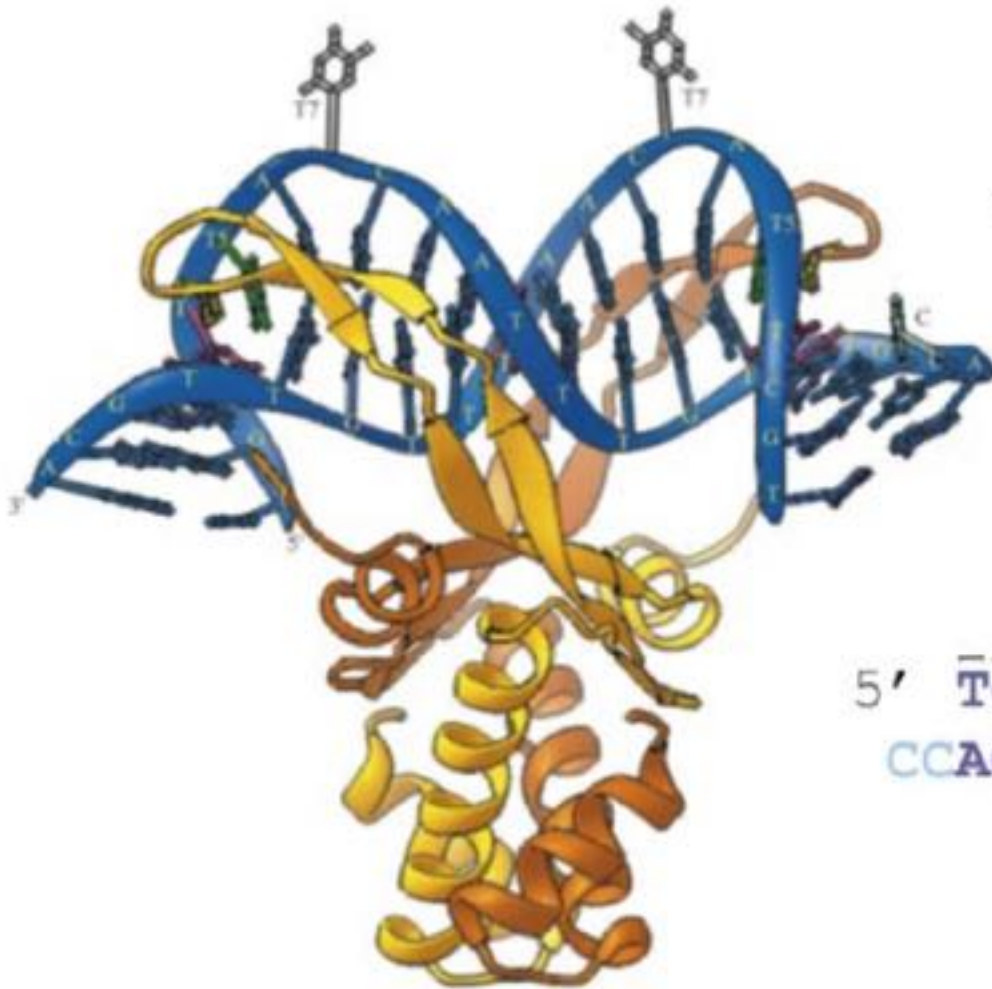
Introduction

- HU enhances DNA bending (AFM experiment)



Introduction

- HU-DNA complex structure:



crystal structure of
Anabaena HU bound to DNA

PDB: 1P71

5' 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21
TGCTTATCAATTG-T-TGCACC
CCACGT-T-GTTAACTATTCGT

Motivation

- How does HU bind to and slide on DNA?
- How does DNA conformation change in response to HU binding?
- What's the relationship between HU binding and DNA conformational change?

Coarse-Grained Models and Methods

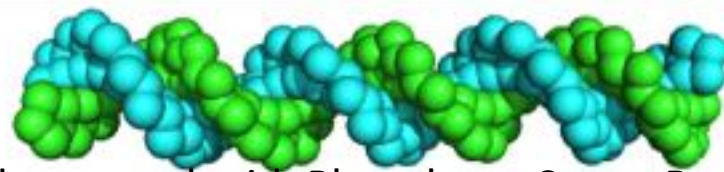
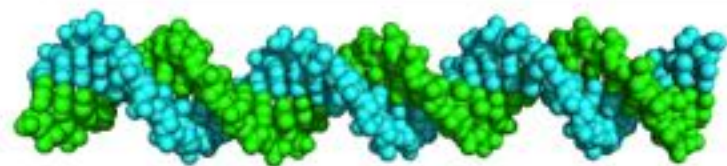
- CG Protein: **AICG2+**

W. Li *et al.* (2014) *PNAS*.

- DNA: **3SPN.2C**

Sequence dependent properties

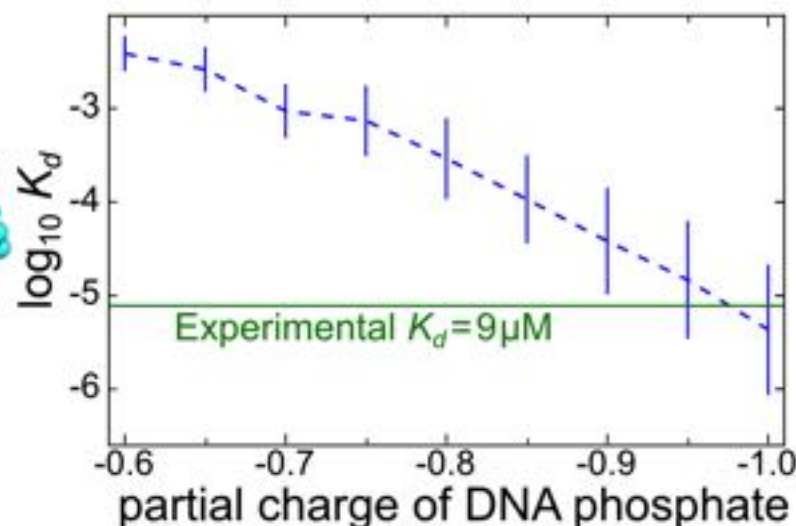
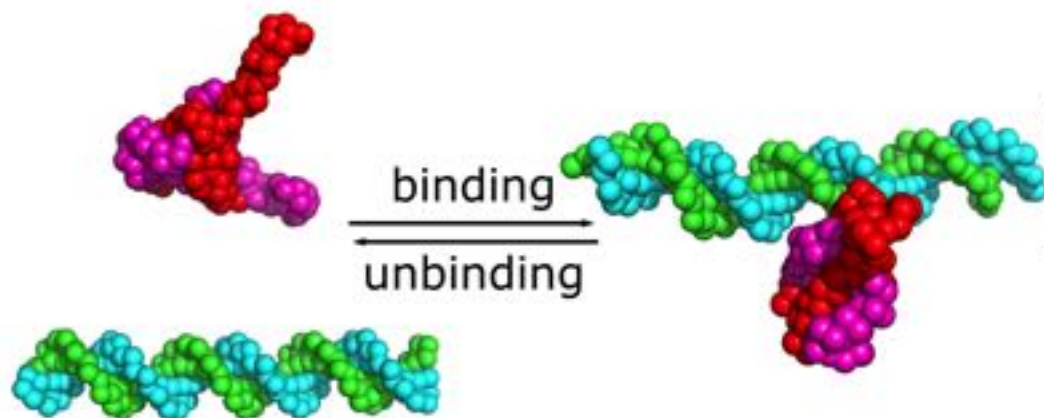
G. Freeman *et al.* (2014) *JCP*.



1 bead per residue

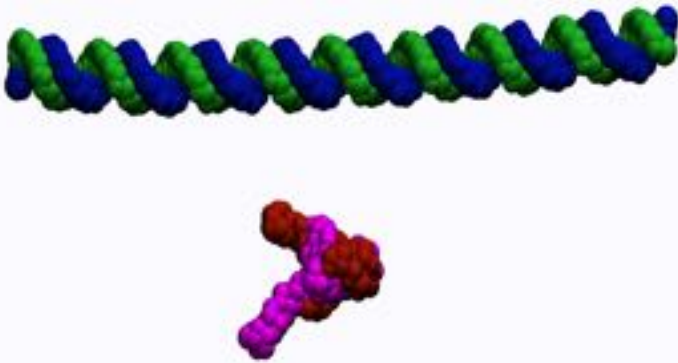
3 beads per nucleoid: Phosphate, Sugar, Base

- Intermolecular interactions:
electrostatic + excluded volume

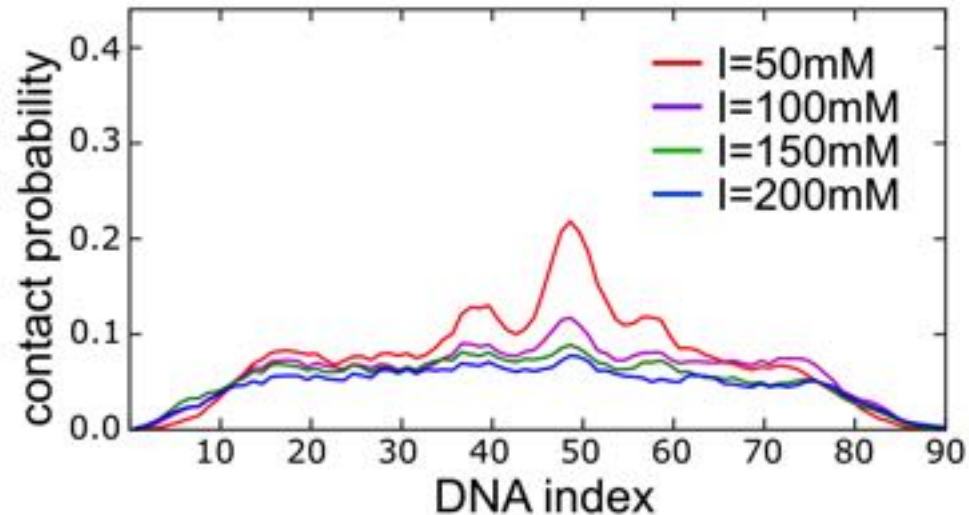
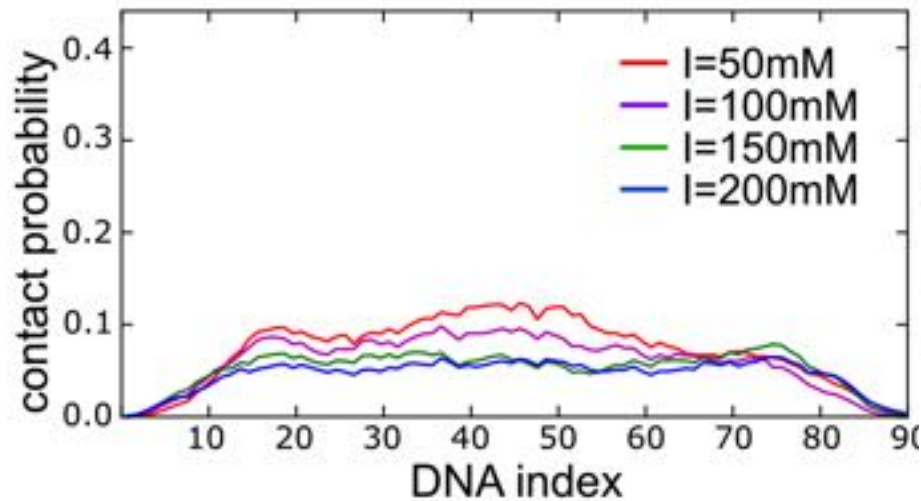
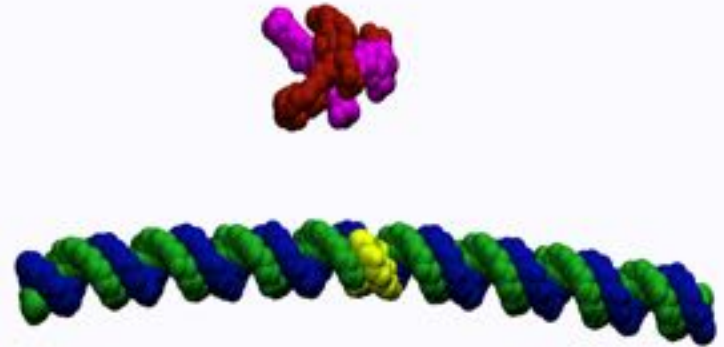


HU Prefers A/T Rich Region

- Purely CG

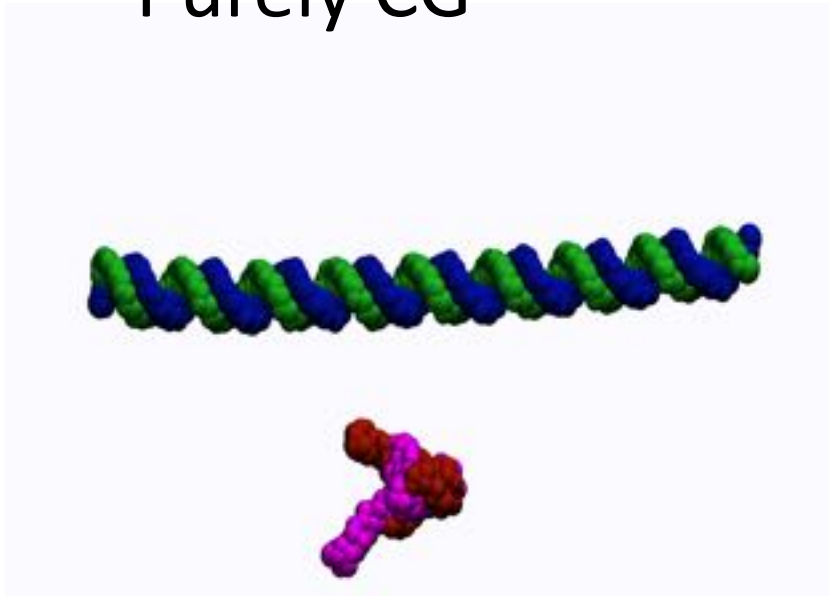


- A/T region at center

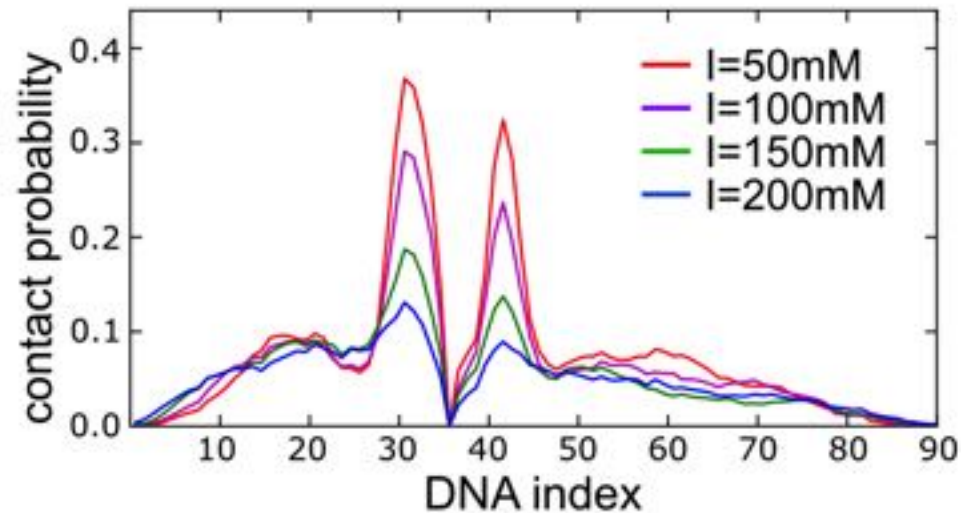
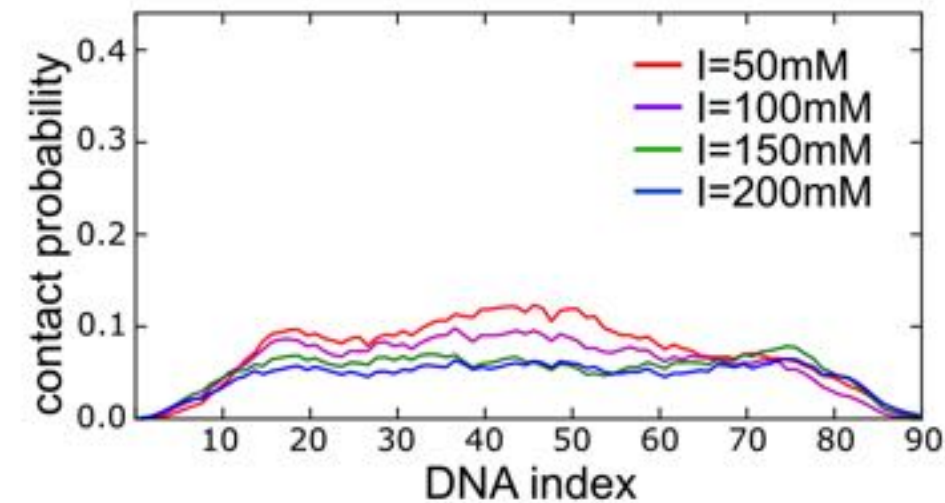
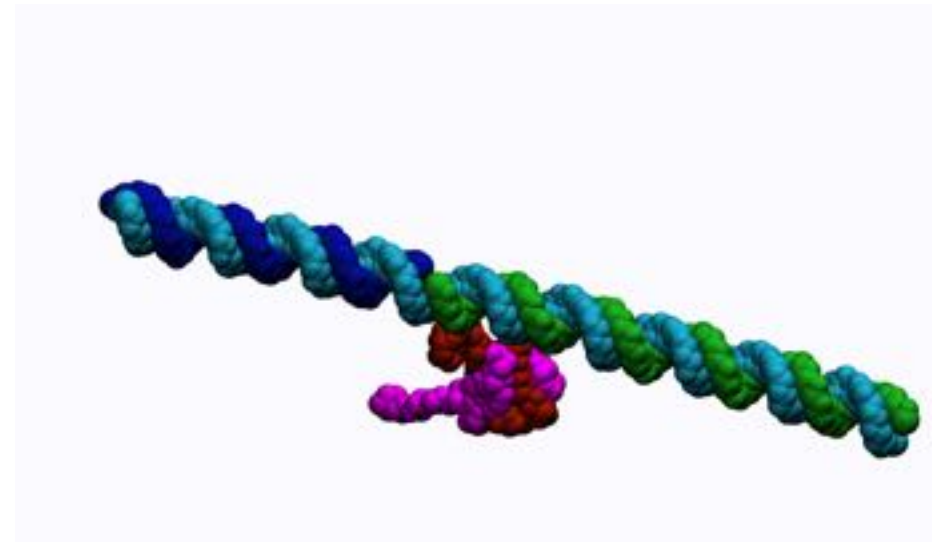


HU Favors Gap in DNA

- Purely CG



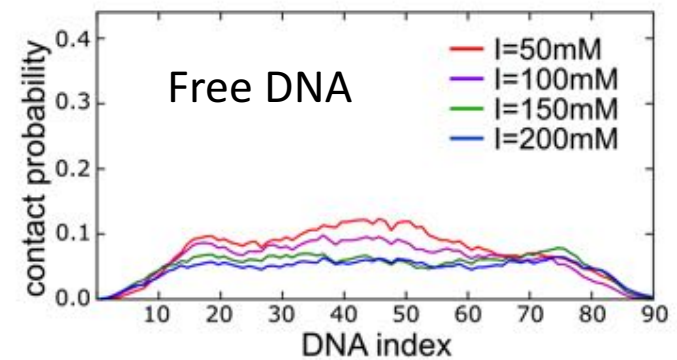
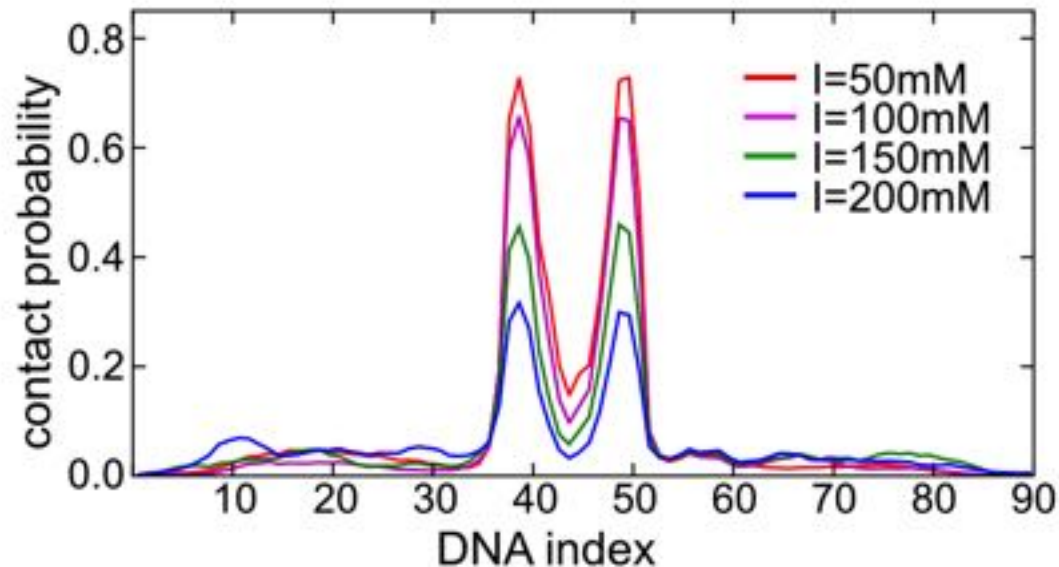
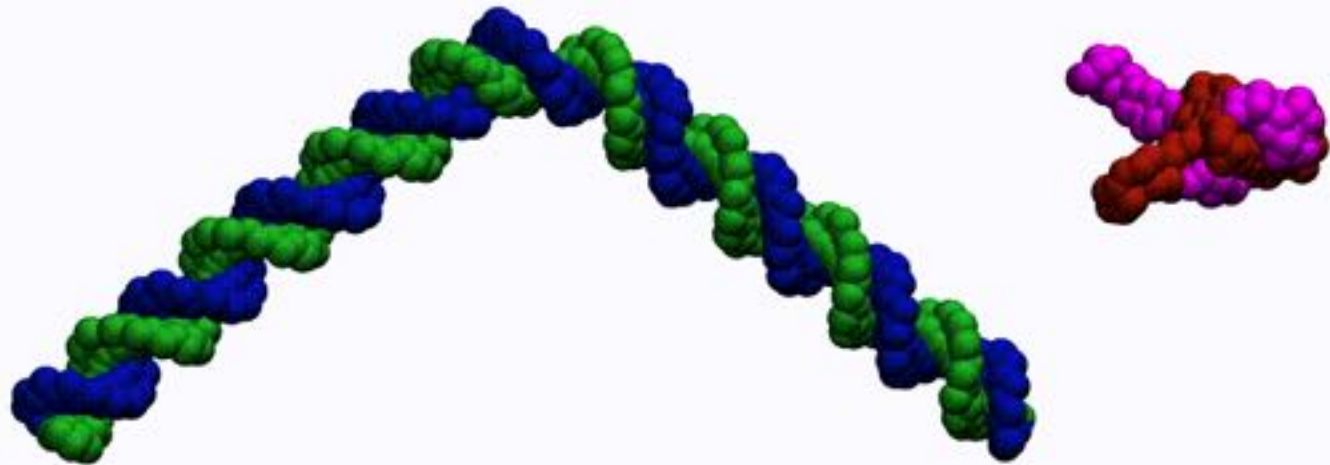
- Gap at index 36



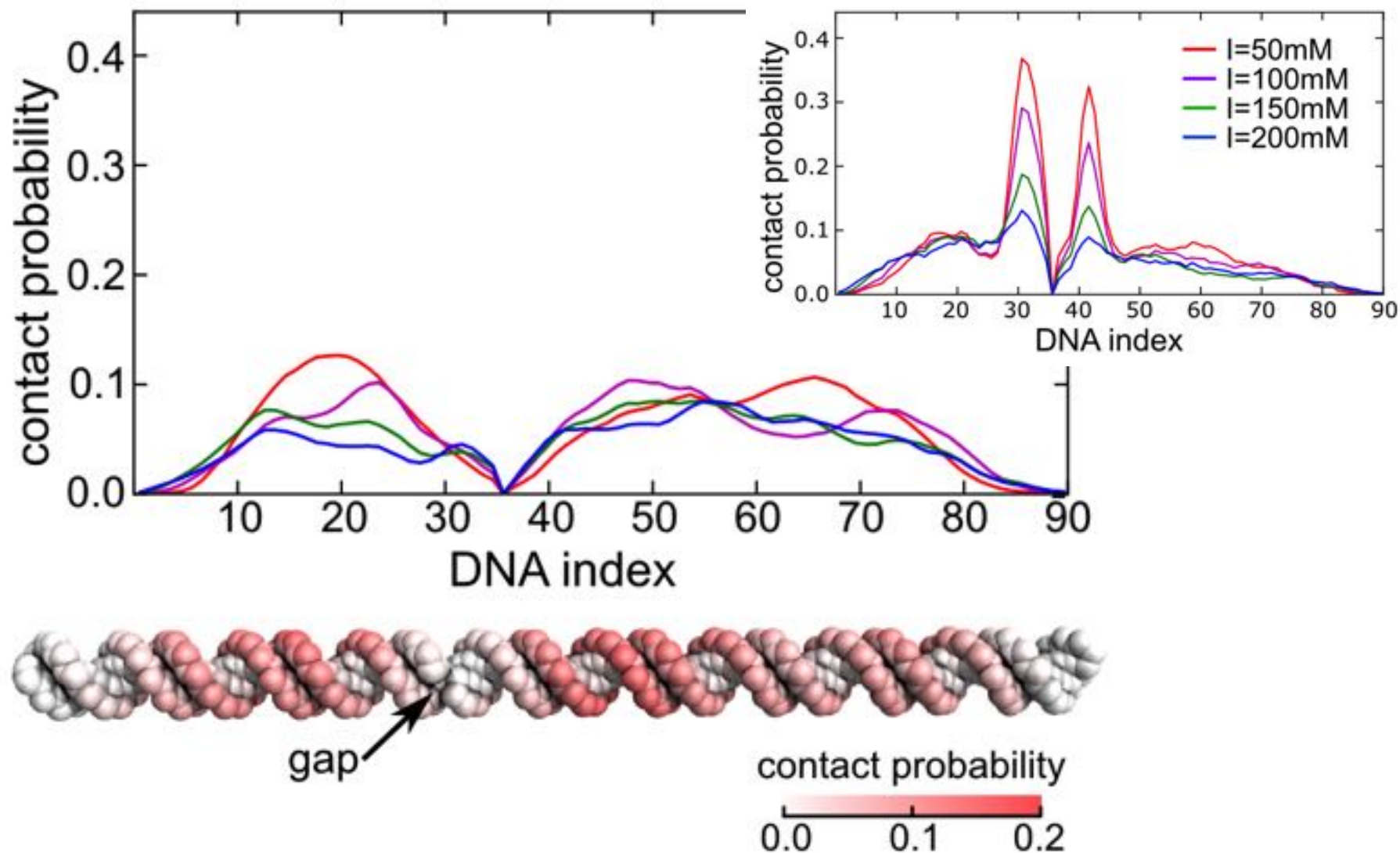
Summary of HU Binding Specificity

- Slight preference for A/T rich sequence
- Strong preference for gap/nick
- New questions:
 - Origin of A/T specificity: sequence or structure?
 - Origin of gap preference: topology or flexibility?

HU Binding to Fixed Bent DNA



HU Binding to Fixed Straight Gapped DNA



Summary of HU Binding Specificity

Answers to the questions:

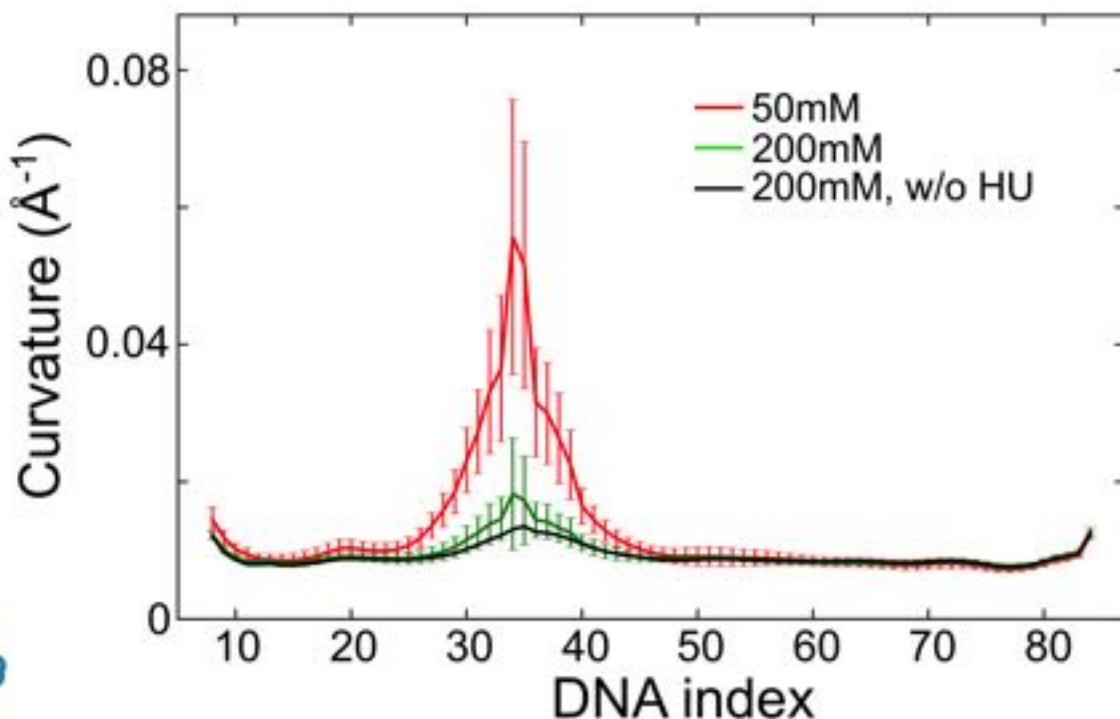
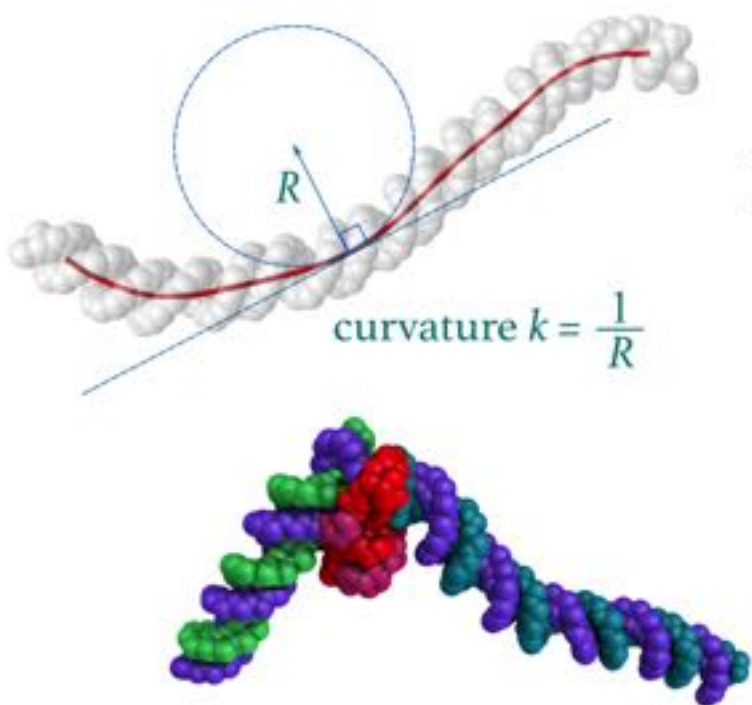
- Origin of sequence specificity: structure properties.
- Origin of gap preference: flexibility.

“Bendability”

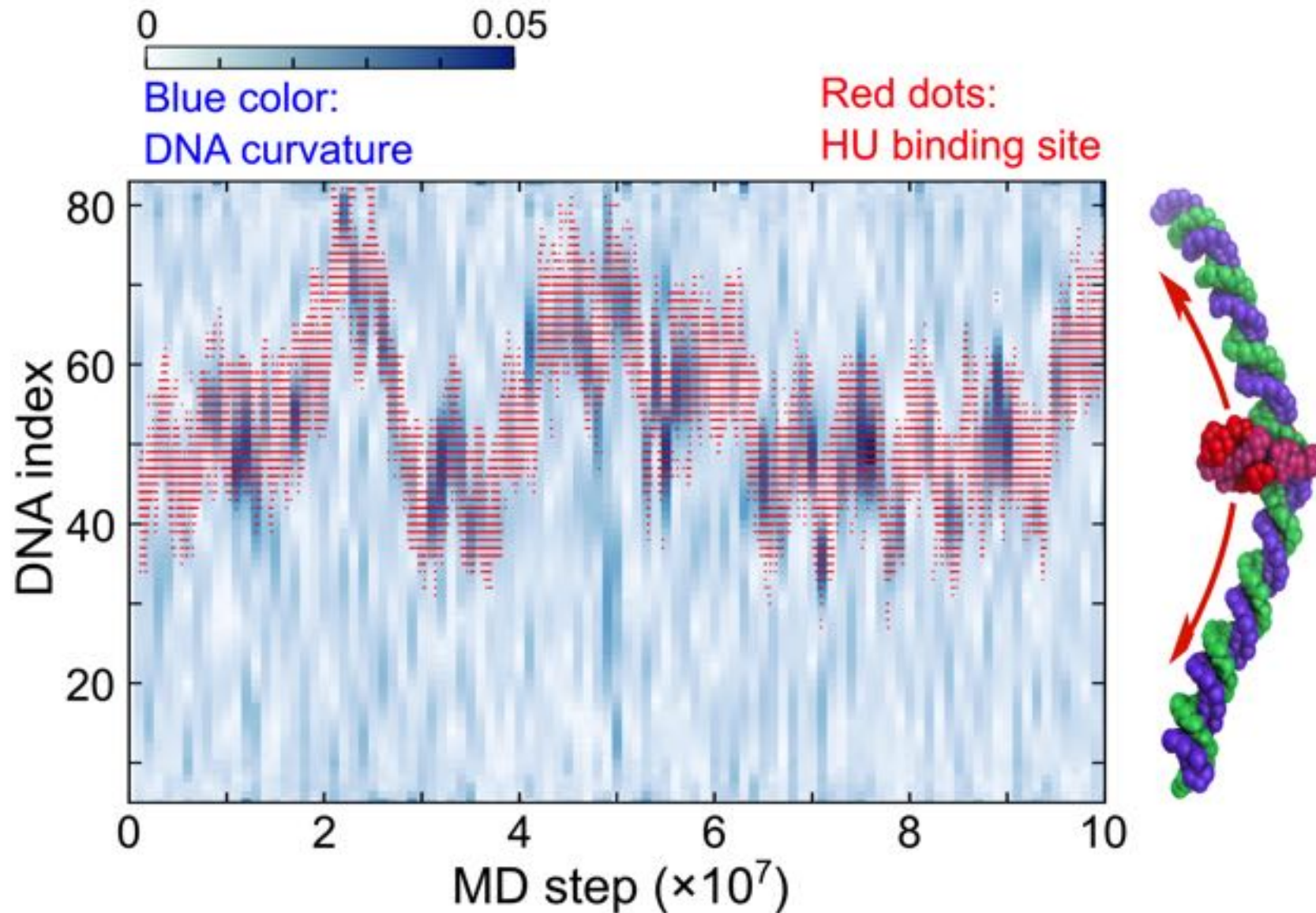
New question:

How does HU affect conformation of DNA?

HU Enhances Bending of Gapped DNA



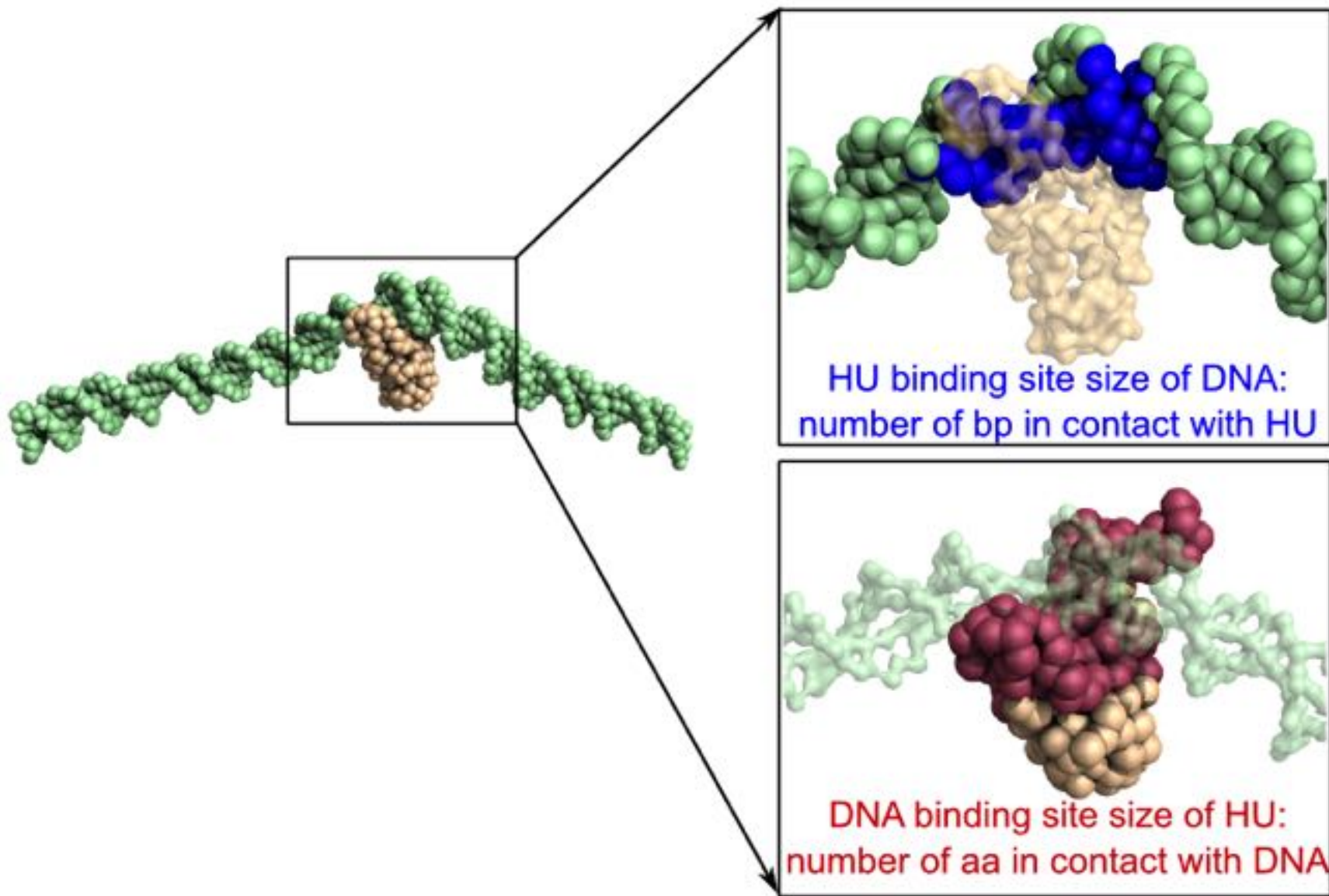
Coupling of Binding and Bending



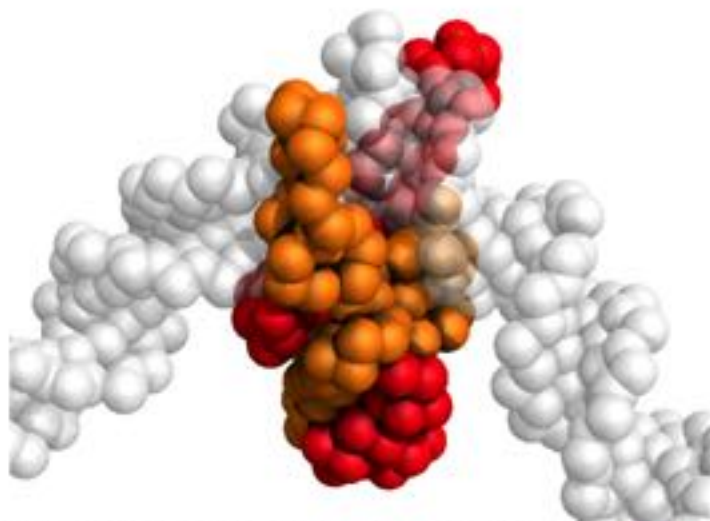
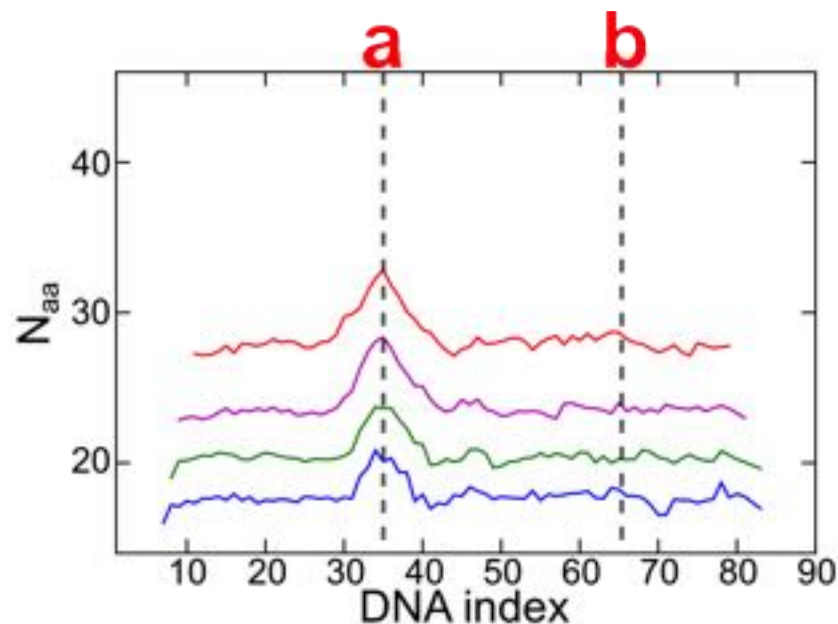
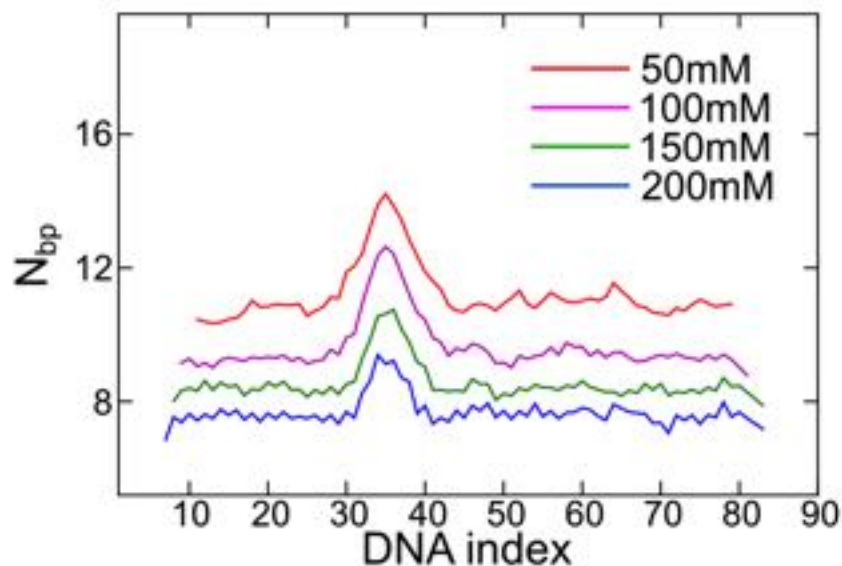
HU Binding & DNA Bending

- HU binding statistically facilitates DNA bending
- HU binding is dynamically coupled to DNA bending

HU-DNA Binding Site Size



Binding site of HU-Gaped DNA

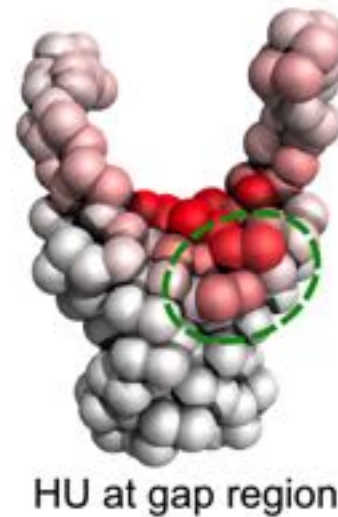
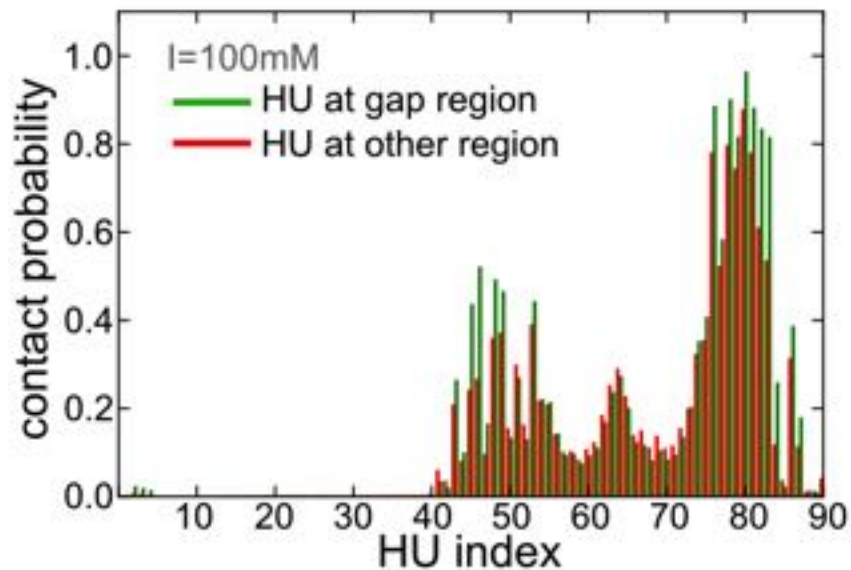
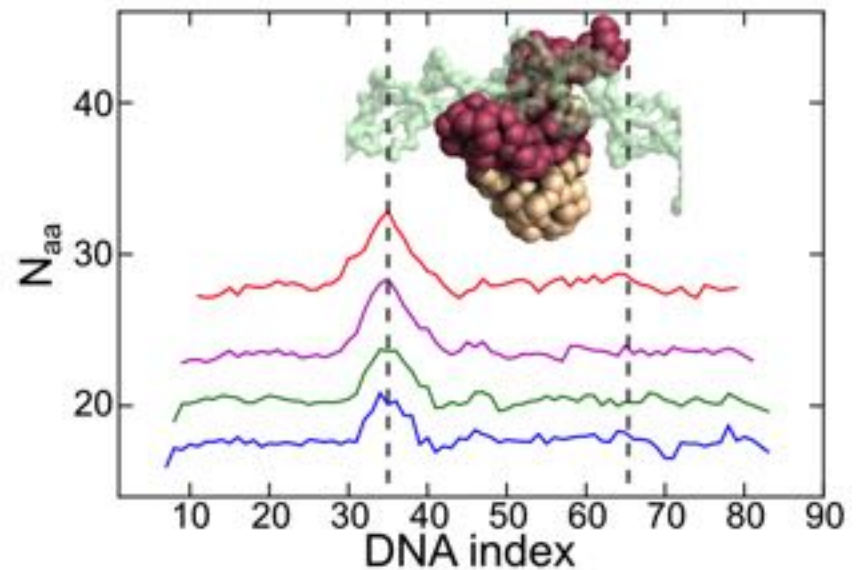
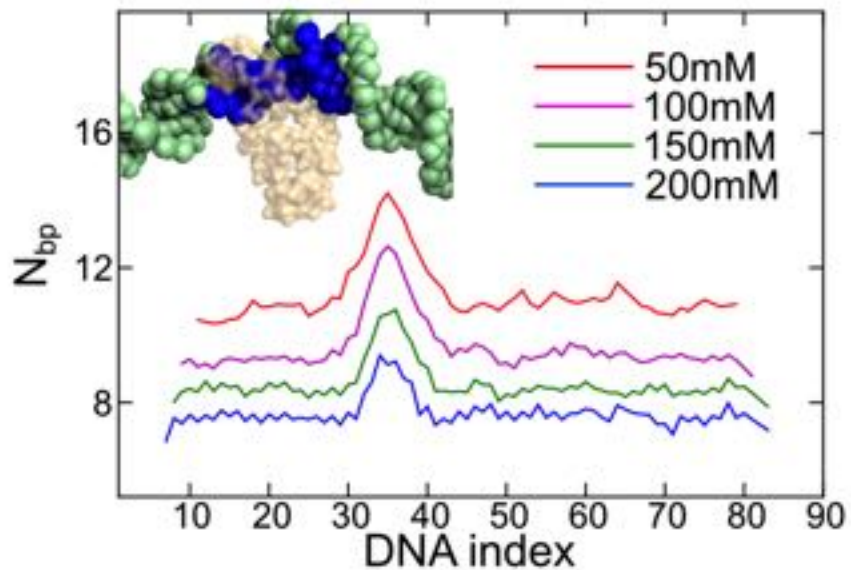


HU binds to position **a**

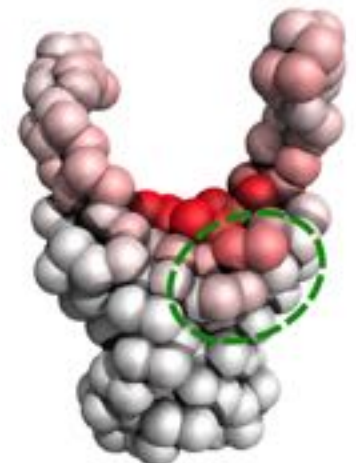


HU binds to position **b**

Binding Site of HU-Gaped DNA



HU at gap region



HU at other region

Conclusions

- HU selects “bendable” DNA structures;
- HU **binding** is highly **coupled** to DNA **bending**;
- HU facilitated DNA bending by contributing larger contact interface.