

### Reconstructing the Parallel Folding Pathways of Intercalating Motifs by Thermo Hysteresis

### Introduction

Intercalating motifs (i-motifs) are four-stranded, cytosine-rich nucleic acid structures that regulate many biological processes such as transcription. The i-motifs are structurally heterogeneous, which exist as interconvertible conformers. The coexistence of multiple folded conformations suggests that there may be multiple folding pathways. We aim to use a method that developed by our lab called thermal hysteresis that quantitatively measures the rates of individual pathways for the i-motif and applied it to the i-motif found in the human c-myc promoter region.

### The c-myc intercalating motif

- quadruplex regulate c-myc expression<sup>(1)</sup>
- Protonated cytosine making hydrogen bonds with cytosine to stabilize the i-motif structure
- The wildtype c-myc i-motif could adopt multiple isomers
- Selectively mutating cytosine residue to thymine traps species in certain conformation





### **Two-State Model**

• The fully trapped i-motif sequence can be modelled as two states: the folded state and unfolded state

fully trapped i-motif sequence

Fully trapped	$\mathbf{k}_{\mathbf{F}}$	k <sub>U</sub>	E <sub>F</sub>	E <sub>U</sub>
55	1.58	$-5.1 \times 10^{-3}$	6.19	332.70
53	1.16	$1.51 \times 10^{-2}$	61.8	359.49
35	1.22	$1.27 \times 10^{-2}$	30.4	310.13
33	2.44	6.66×10 <sup>-2</sup>	69.5	273.39



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# Introduction

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# The c-myc intercalating motif

The c-myc oncogene is one of the most upregulated oncogenes in cancer, the i-motif and G-quadruplex regulate c-myc expression

Protonated cytosine making hydrogen bonds with cytosine to stabilize the i-motif structure

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Selectively mutating cytosine residue to thymine traps species in certain conformation



Yellow: Cytosine

**Blue**: Thymine

Red: Adenine

 $C \longrightarrow T$  mutation

Orange Bonds: hydrogen















# **Two-State Model**

# unfolded state

k	k	Er
1.58	$-5.1 \times 10^{-3}$	6.19
1.16	$1.51 \times 10^{-2}$	61.8
1.22	$1.27 \times 10^{-2}$	30.4
2.44	$6.66 \times 10^{-2}$	69.5

• The fully trapped i-motif sequence can be modelled as two states: the folded state and

• Using the MATLAB, we can find the kinetic parameters for the fully trapped i-motif sequence

## ET

332.70

359.49

310.13

273.39



# WT









• To develop a global model, which accurately represents the folding dynamics of the wild type imotif.

• Understanding the i-motif folding pathway could help with the development of i-motif specific targeting drugs that might treat the cancer

## Future Work

• For the thermal hysteresis experiment, we want to apply multiple scan rates in the future.



