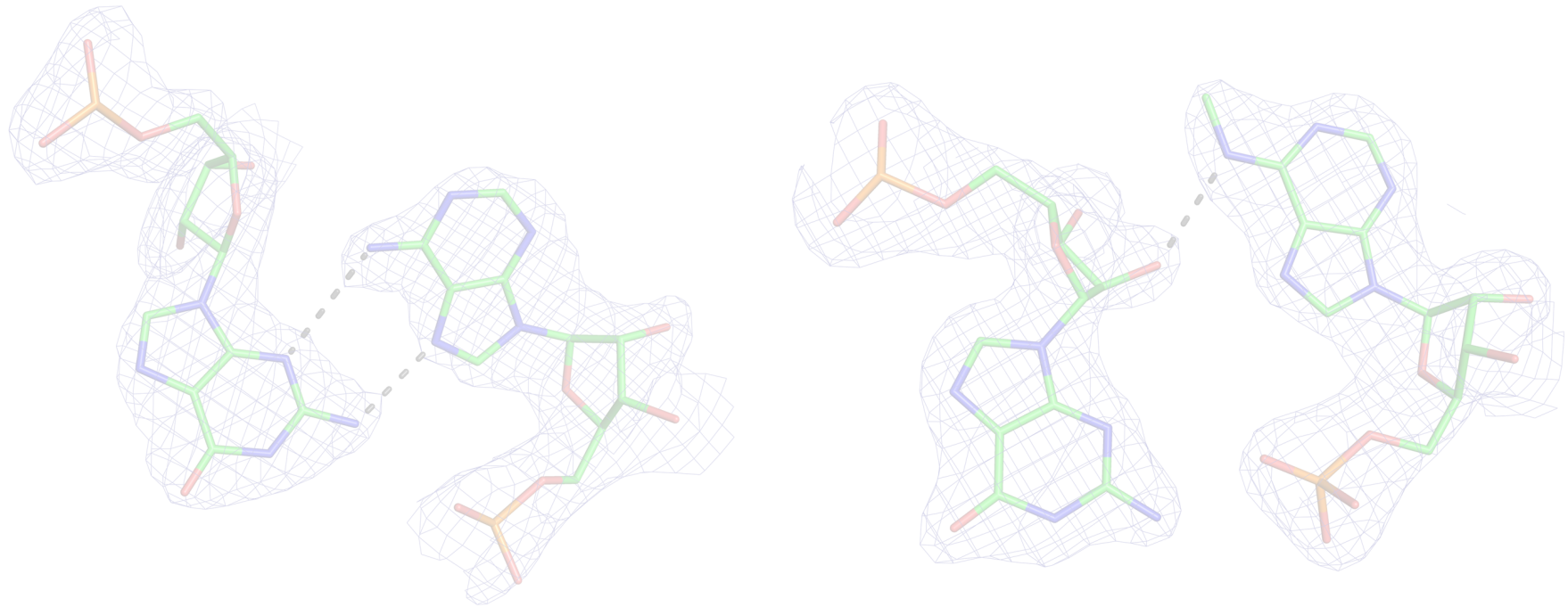


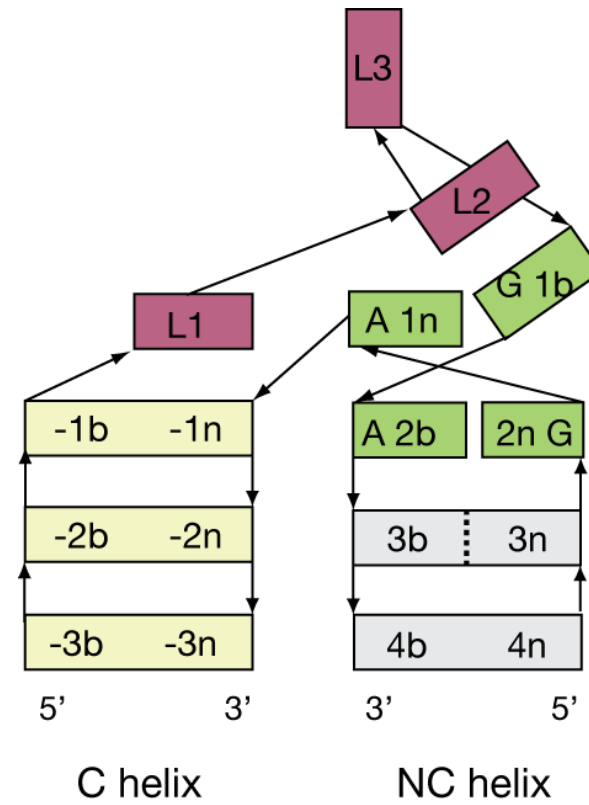
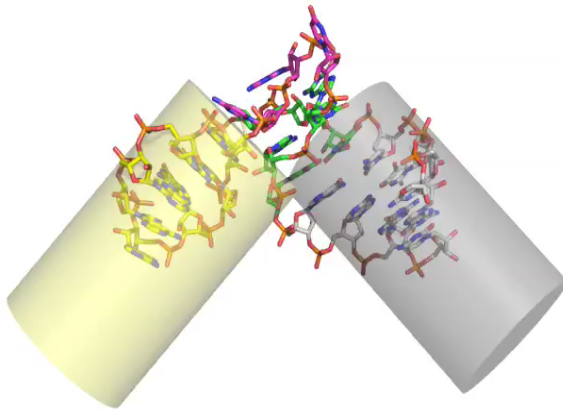
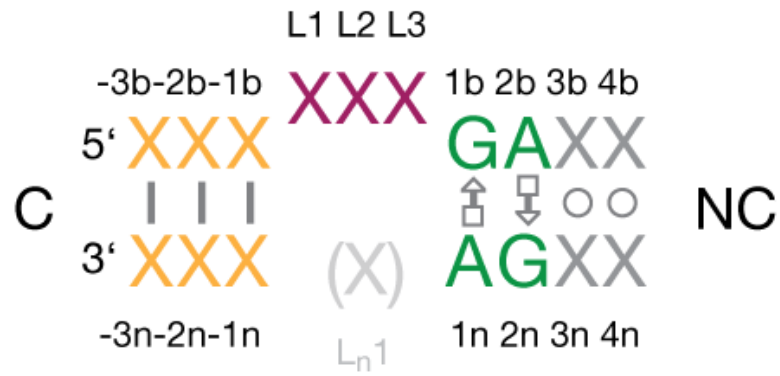
N⁶-methylation of adenine in box C/D snoRNA :
regulation of RNP assembly



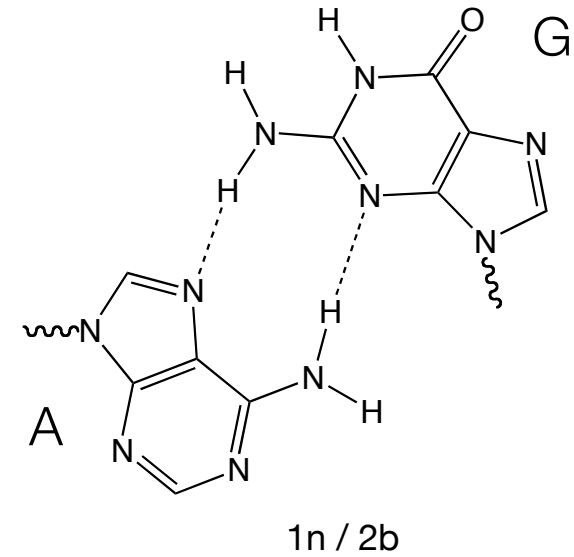
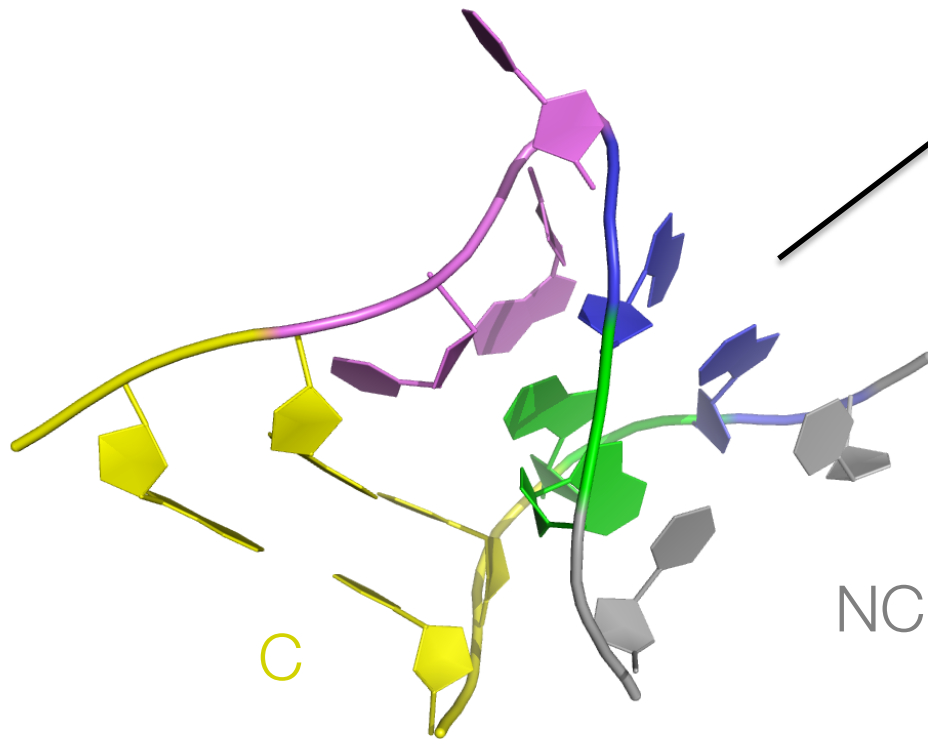
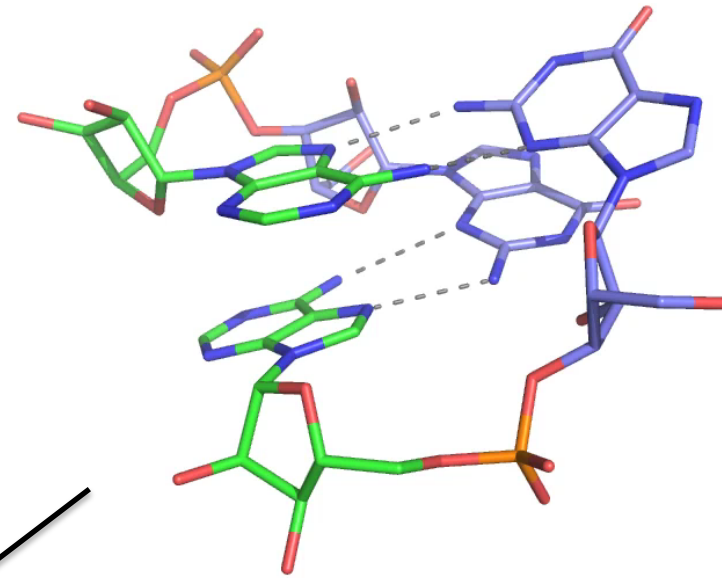
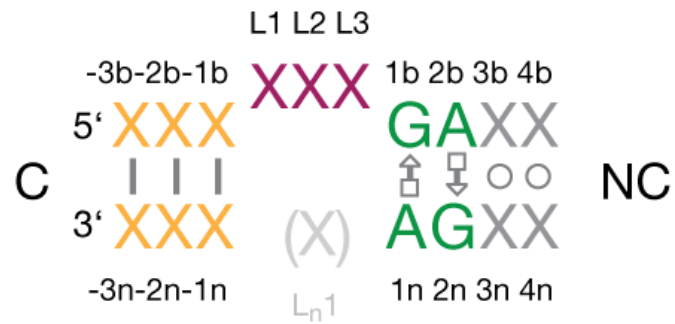
Lin Huang
David MJ Lilley Lab
Dundee University, UK

The k-turn motif - structure

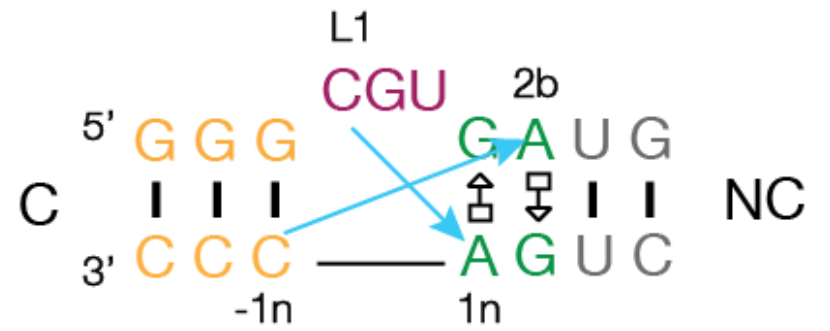
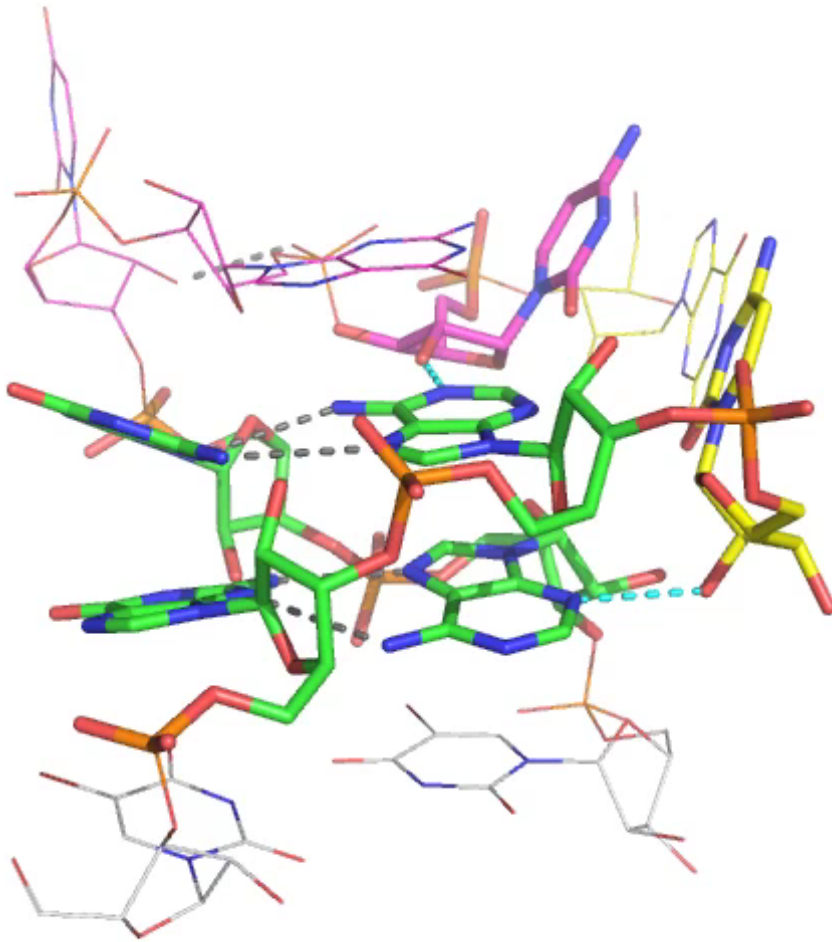
generic k-turn



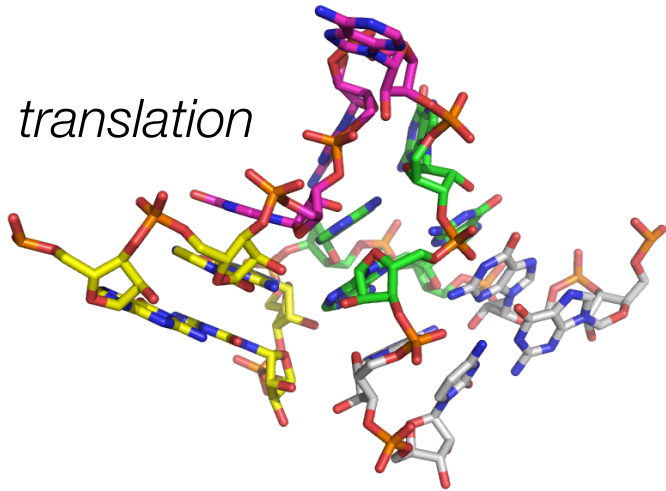
The G•A pairs



The key hydrogen bonds of a standard k-turn

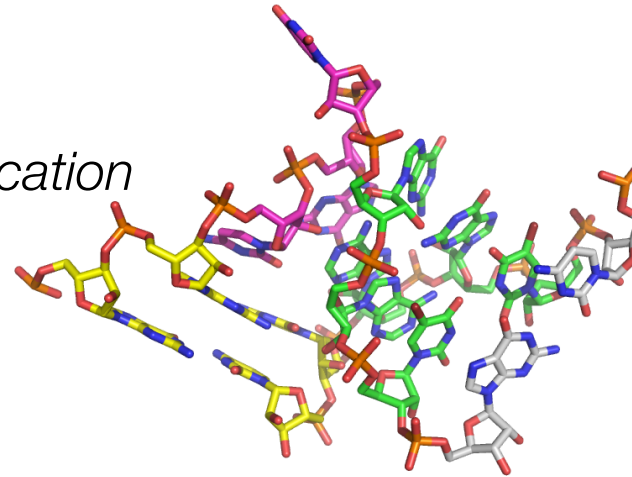


The ubiquitous functions of k-turns



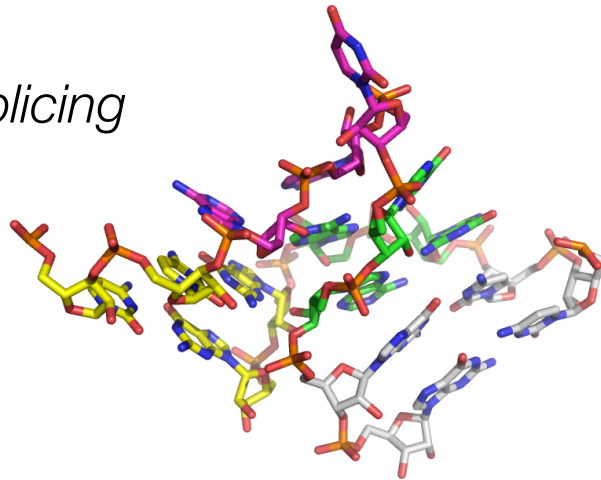
ribosome 50S Kt-7

*RNA
modification*



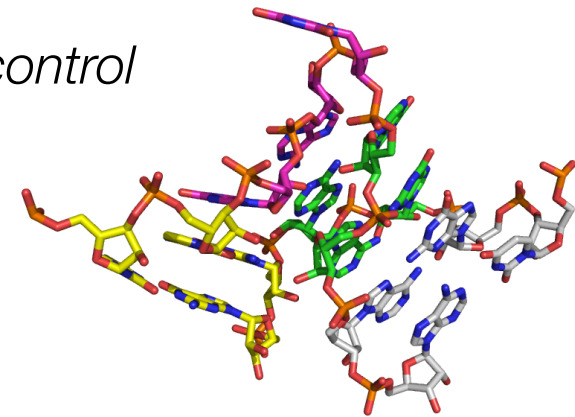
box C/D snoRNA

RNA splicing



U4 snRNA

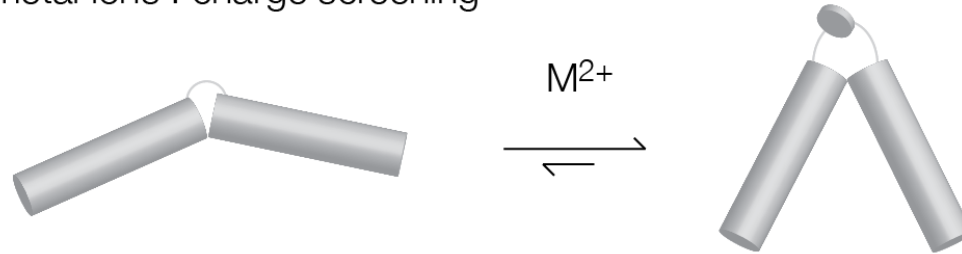
genetic control



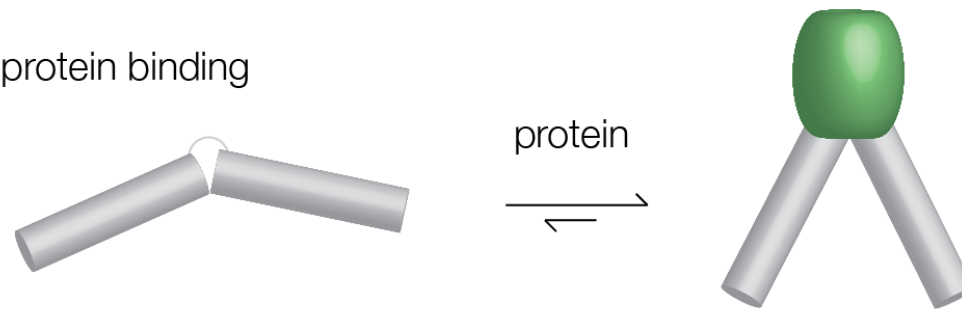
SAM riboswitch

The k-turn folding : three processes

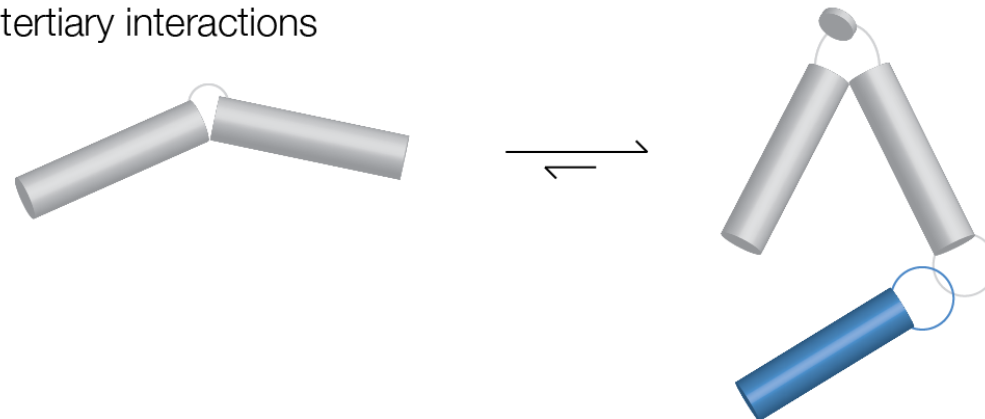
metal ions : charge screening



protein binding

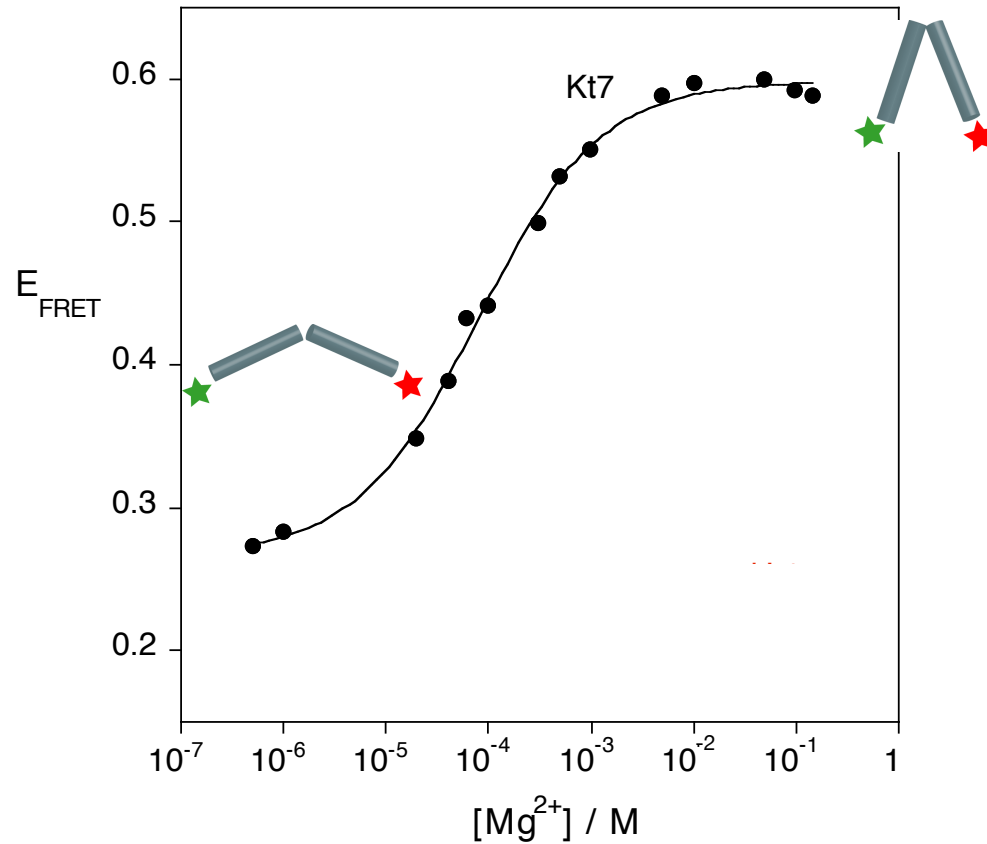


tertiary interactions



Folding of k-turns is induced by metal ions

steady-state FRET

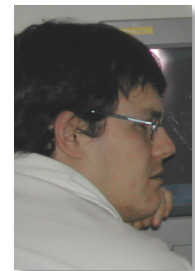


$[\text{Mg}^{2+}]_{1/2} \sim 80 \mu\text{M}$

$[\text{Na}^+]_{1/2} \sim 30 \text{mM}$

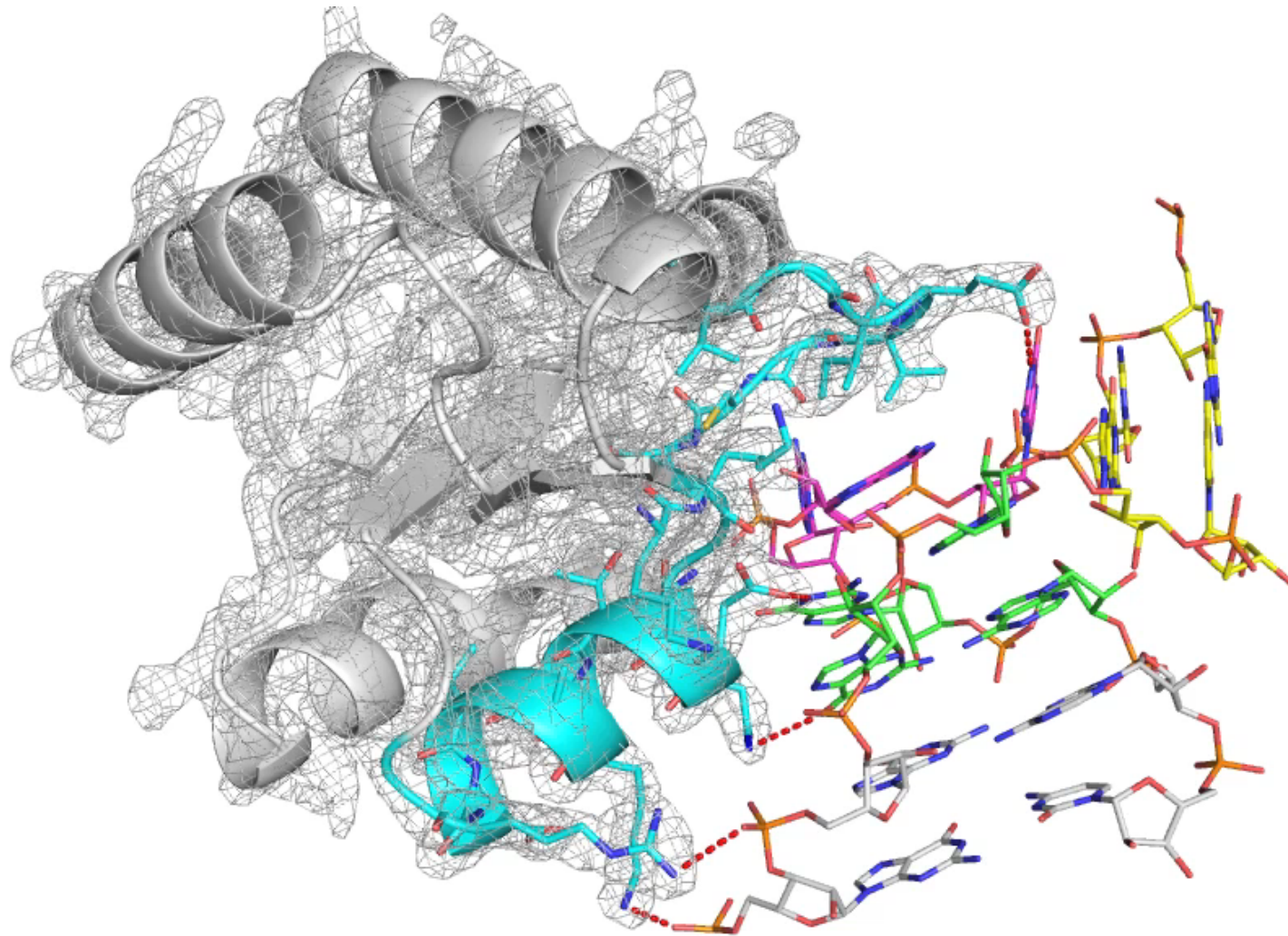
Kinking of K-turn RNA induced by binding of Mg^{2+} ions

Transition fits two-state behavior

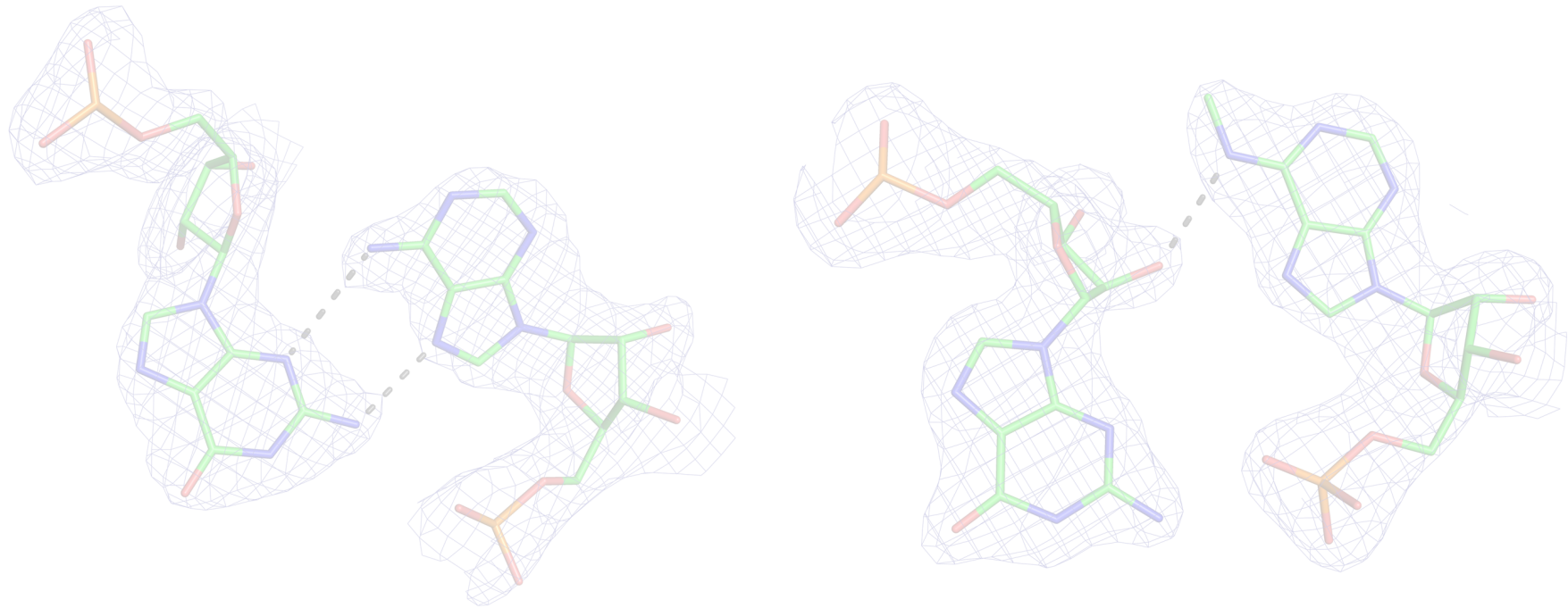


Terry Goody

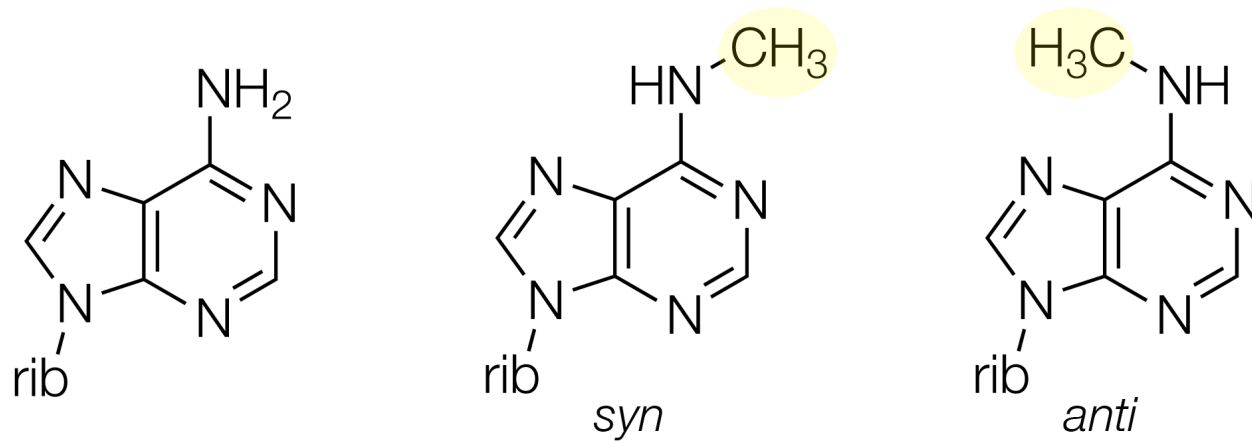
The structure of the complex of L7Ae bound to Kt-7



N⁶-methylation of adenine in box C/D snoRNA :
regulation of RNP assembly



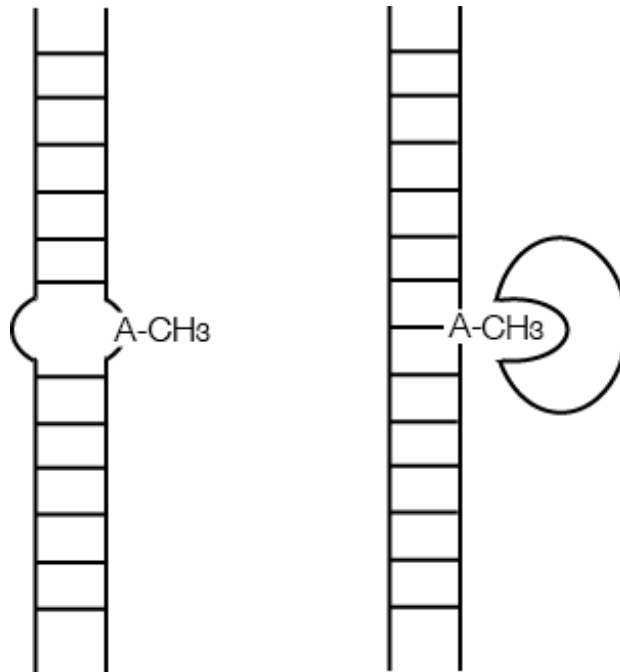
N⁶-methylation of adenine in RNA



N⁶-methylation of adenine is the most common modification in RNA

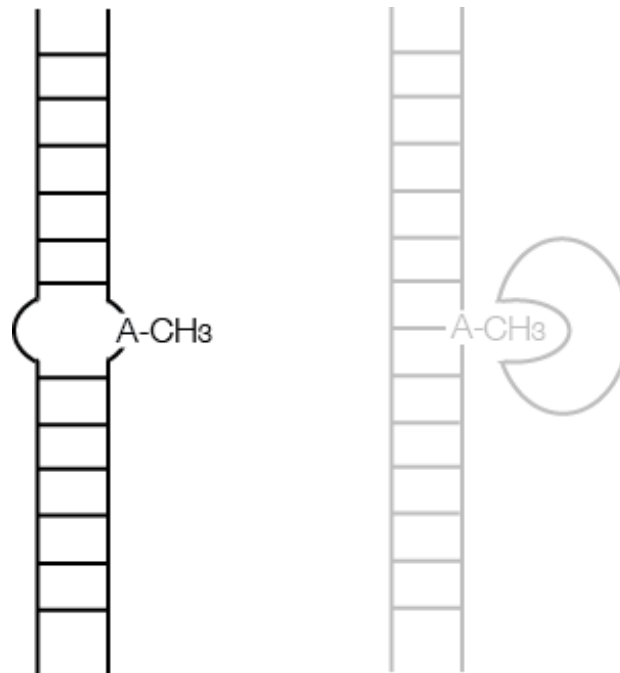
How is N⁶mA expressed ?

- 1) A direct effect on local RNA structure
- 2) Recognition by specific binding proteins

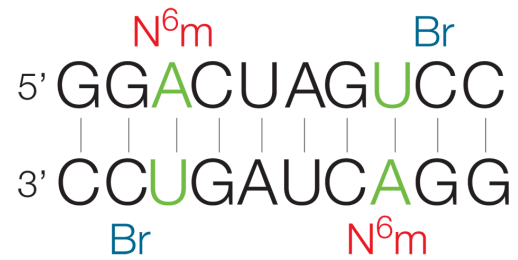


How is N⁶mA expressed ?

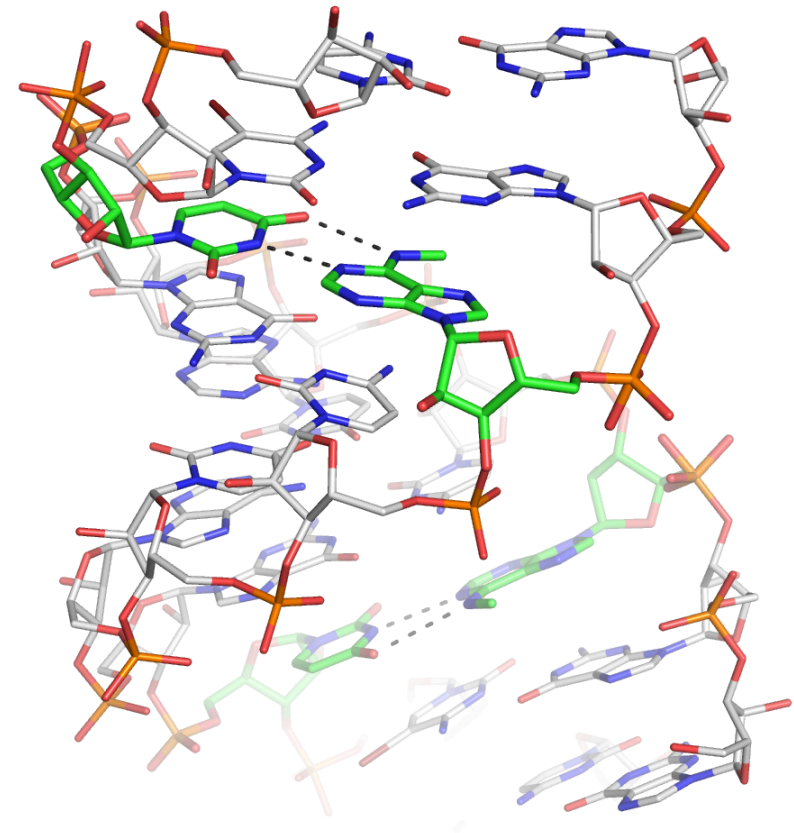
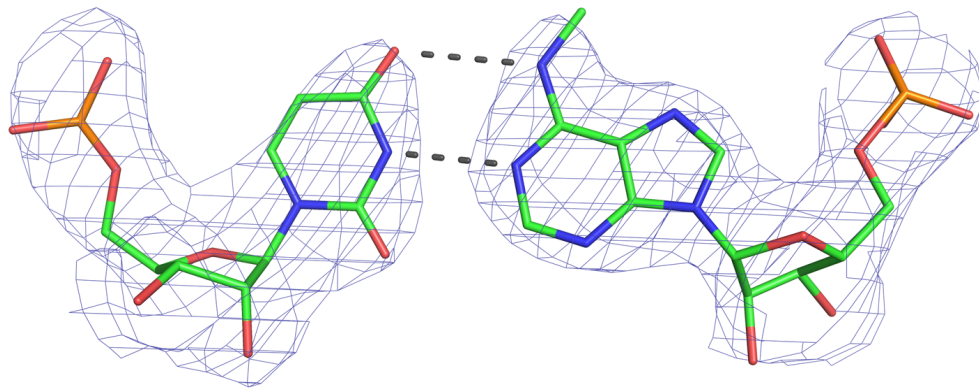
- 1) A direct effect on local RNA structure
- 2) Recognition by specific binding proteins



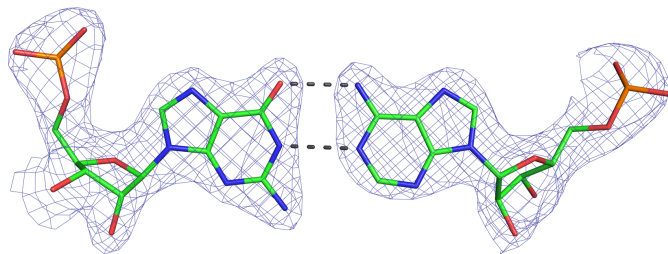
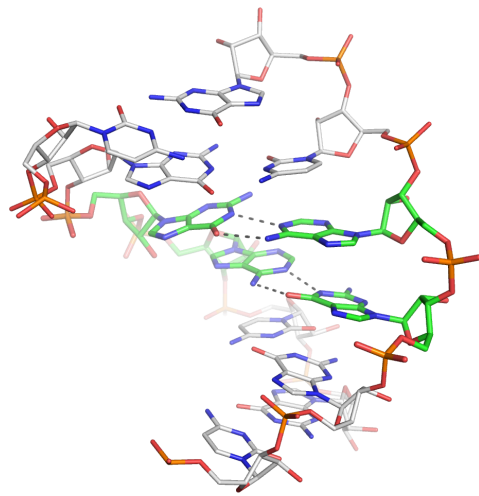
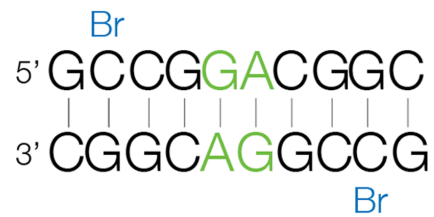
N⁶-methylation of adenine is tolerated in Watson-Crick A-U basepair



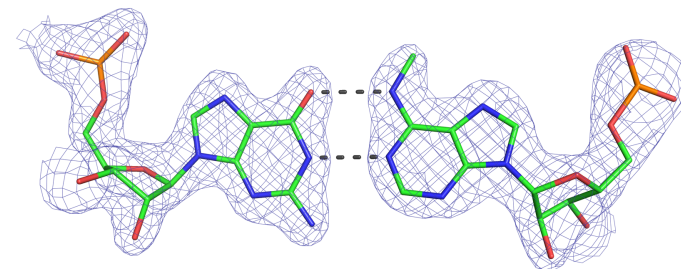
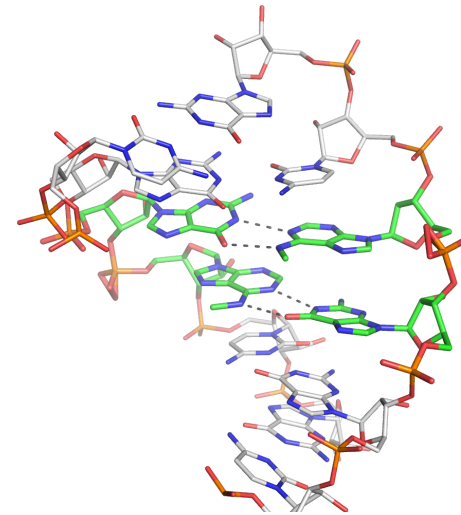
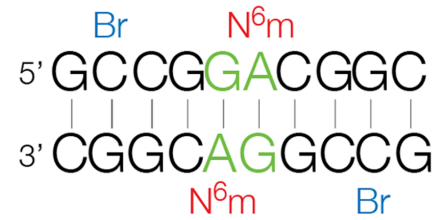
P6₅ 2.27 Å resolution



N⁶-methylation of adenine is tolerated in Watson-Crick G-A basepair

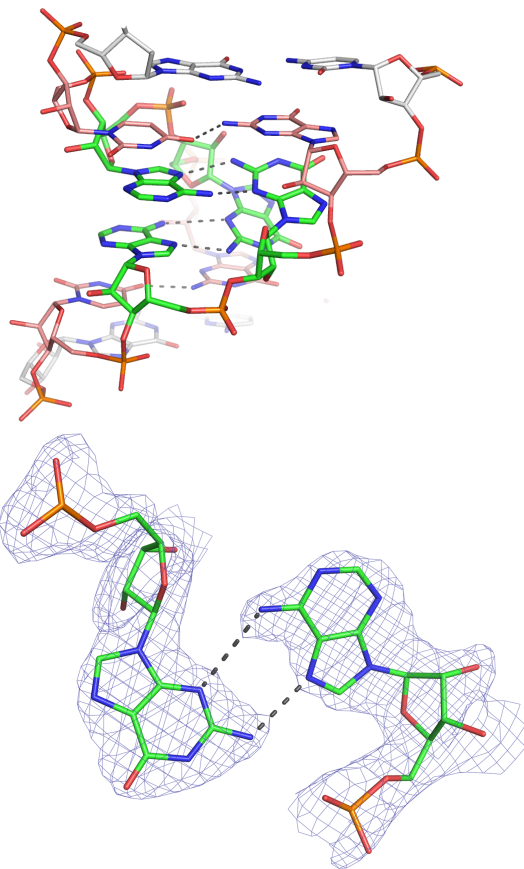


P4₃2₁2 1.87 Å resolution



P4₃2₁2 1.50 Å resolution

N⁶-methylation of adenine is NOT tolerated in sugar-Hoogsteen G-A basepair



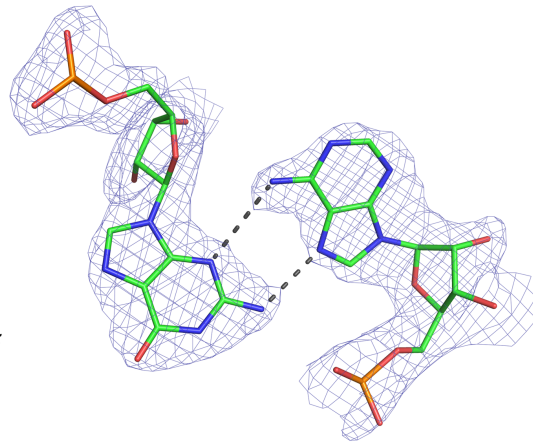
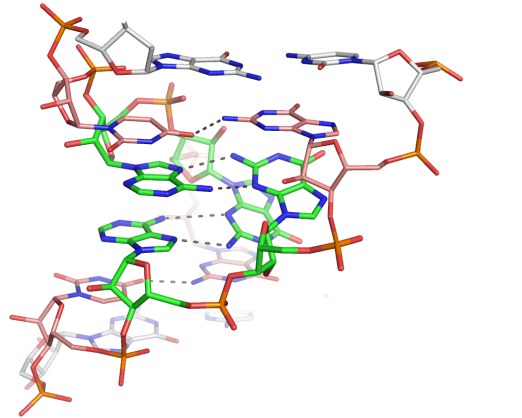
2F_o-F_c
contoured at 1.2σ

P4₃2₁2 1.65 Å resolution

Huang, Ashraf & Lilley *EMBO rep* **18**, 1631-1645 (2017)

2F_o-F_c contoured at 1.2σ

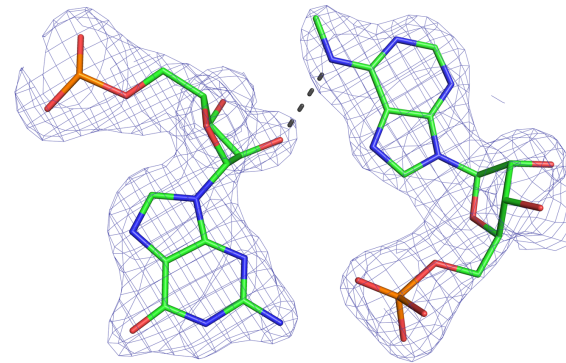
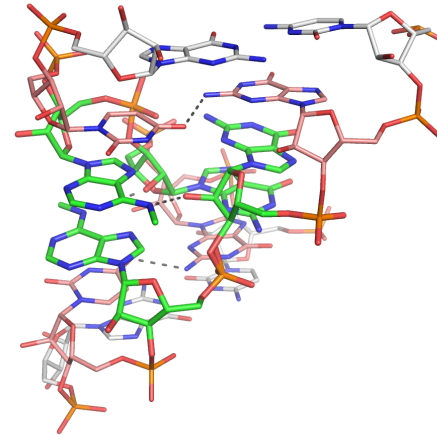
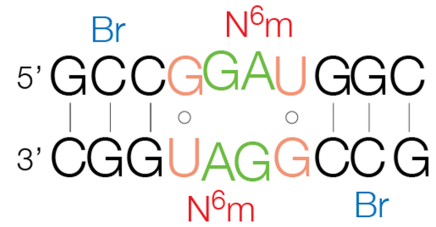
N⁶-methylation of adenine is NOT tolerated in sugar-Hoogsteen G-A basepair



2F_o-F_c
 contoured at 1.2σ

P4₃2₁2 1.65 Å resolution

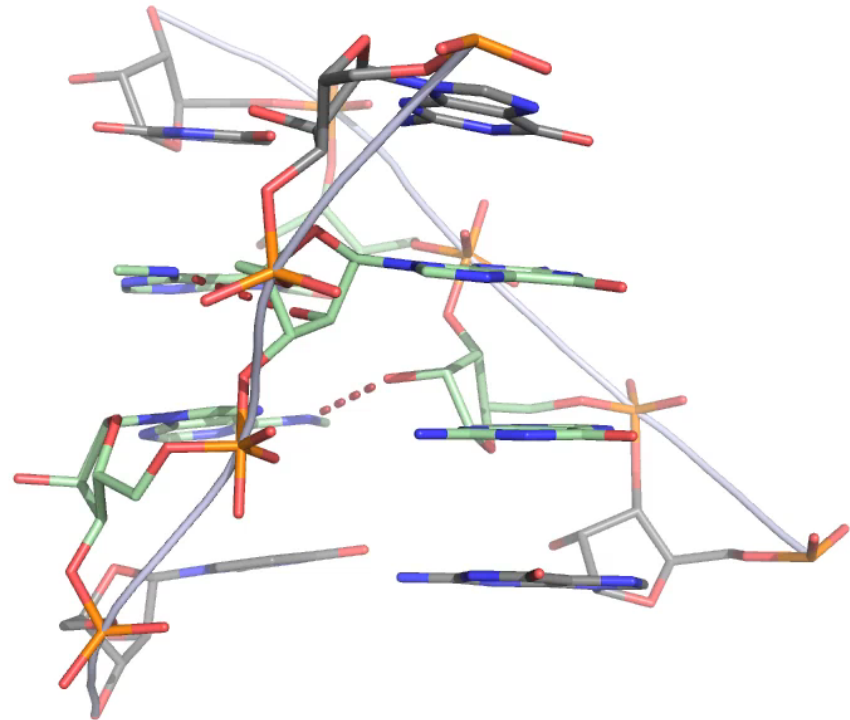
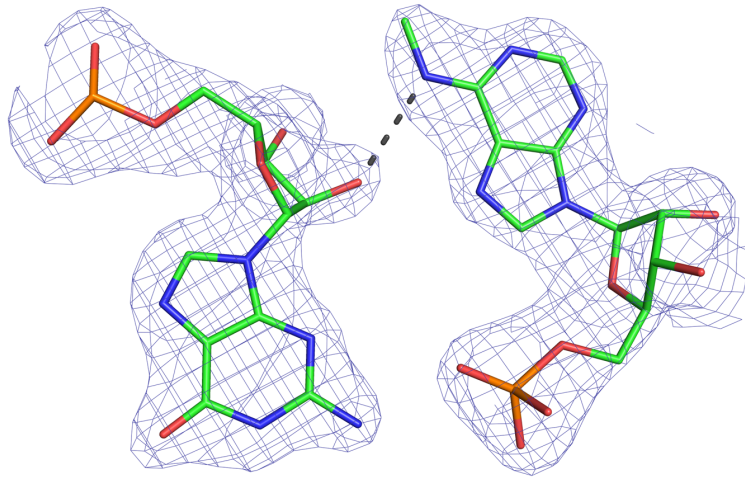
Huang, Ashraf & Lilley *EMBO rep* 18, 1631-1645 (2017)



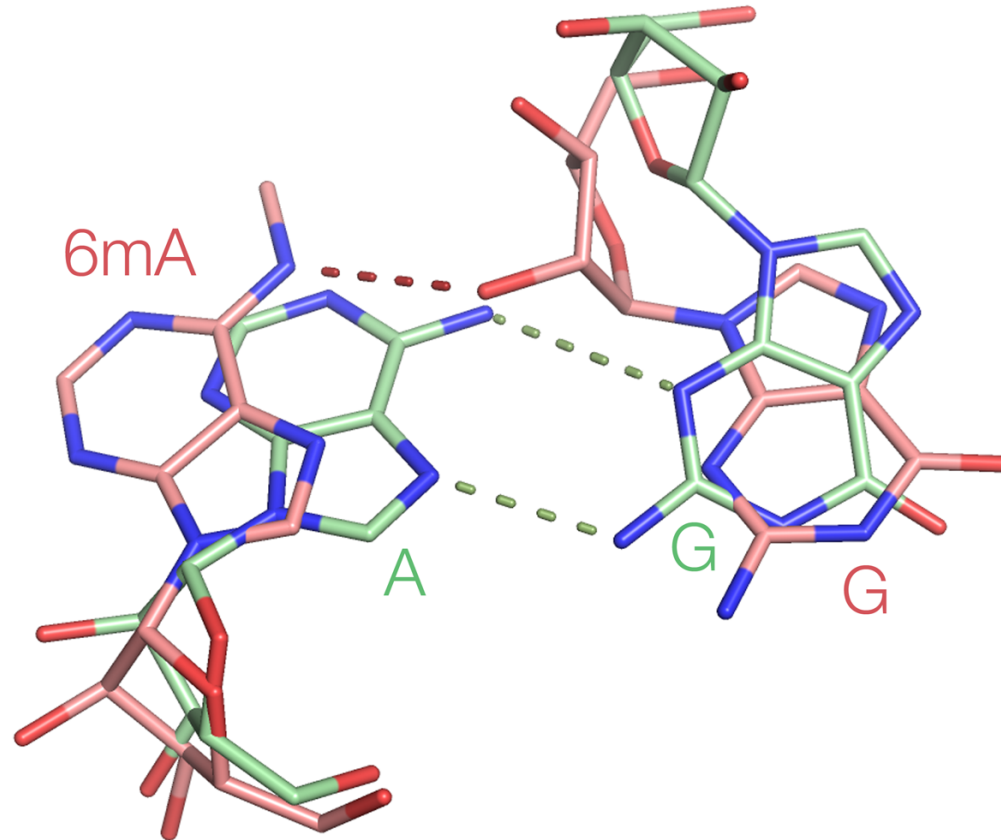
2F_o-F_c contoured at 1.2σ

P4₃2₁2 1.72 Å resolution

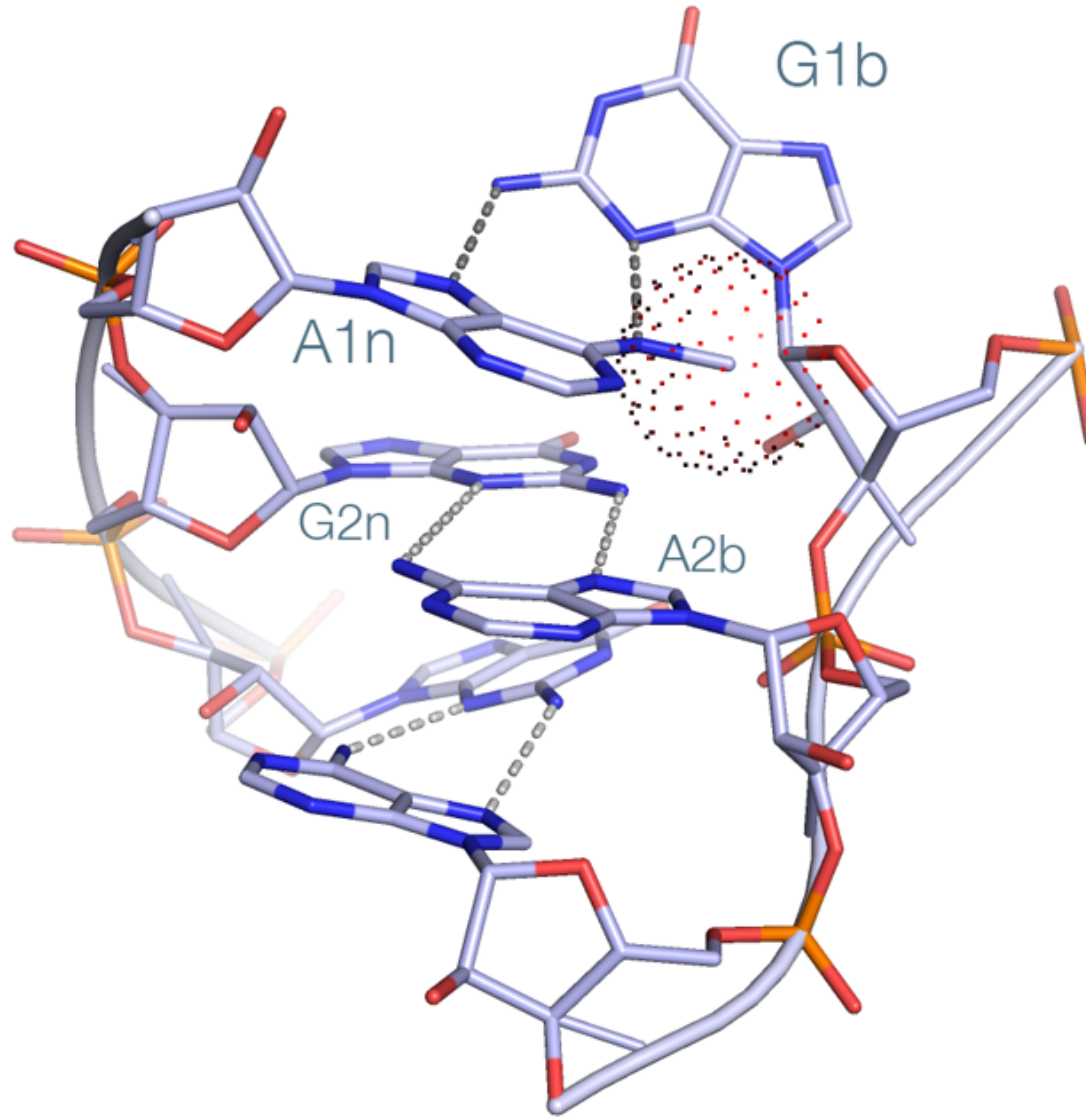
N^6 -methylation of adenine disrupts sugar-Hoogsteen G-A basepair



N^6 -methylation of adenine disrupts sugar-Hoogsteen G-A basepair

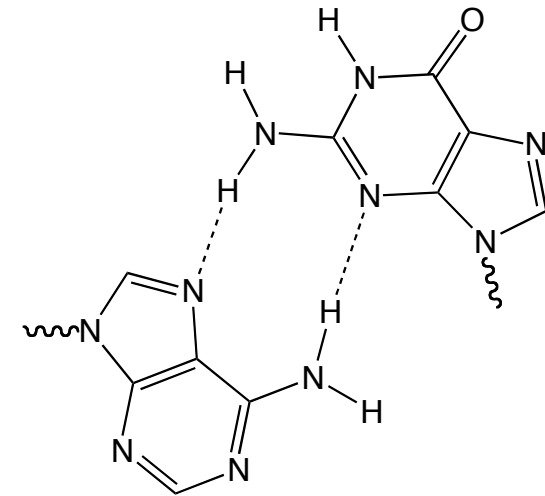
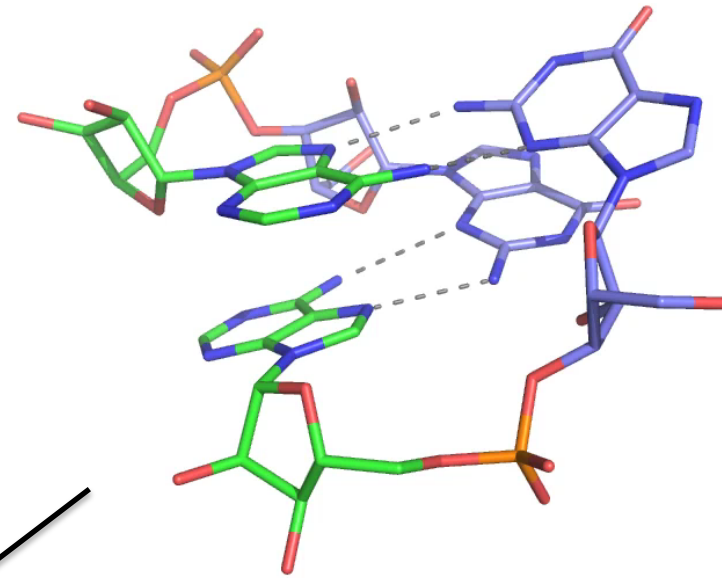
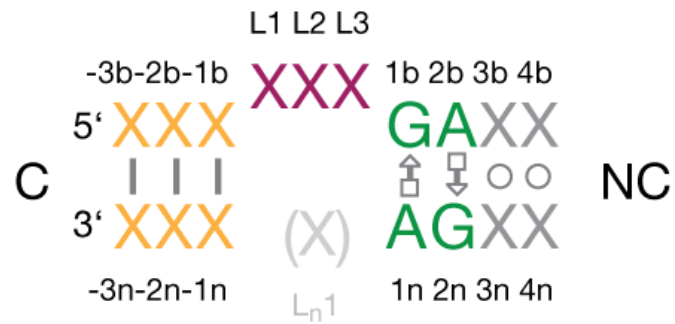


N⁶-methylation of adenine causes steric clash in sugar-Hoogsteen G-A basepair



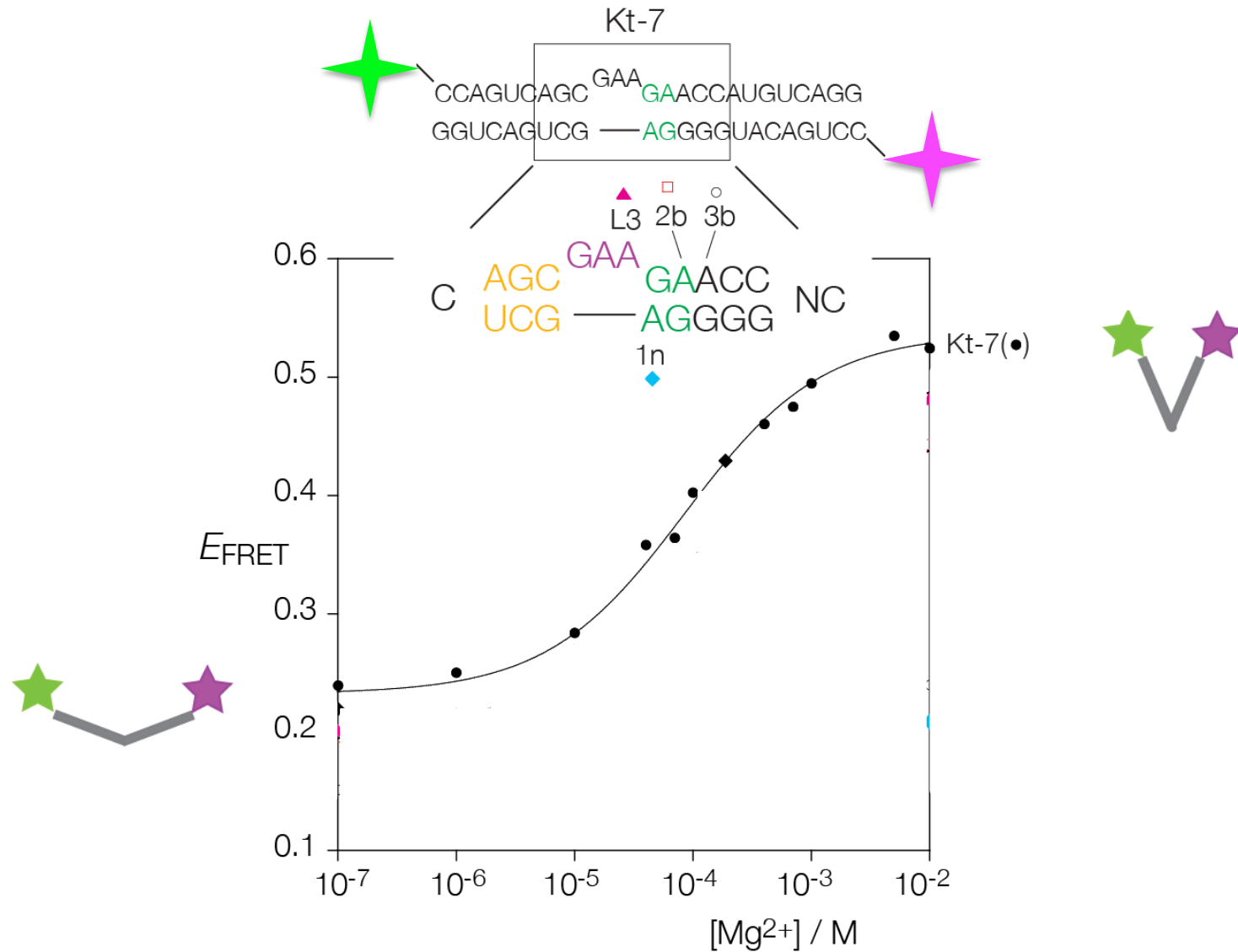
Conclusion : N⁶-methylation of adenine is tolerated in Watson-Crick pairs
but disrupts sugar-Hoogsteen sheared G•A pairs

The G•A pairs are the core of k-turn structure



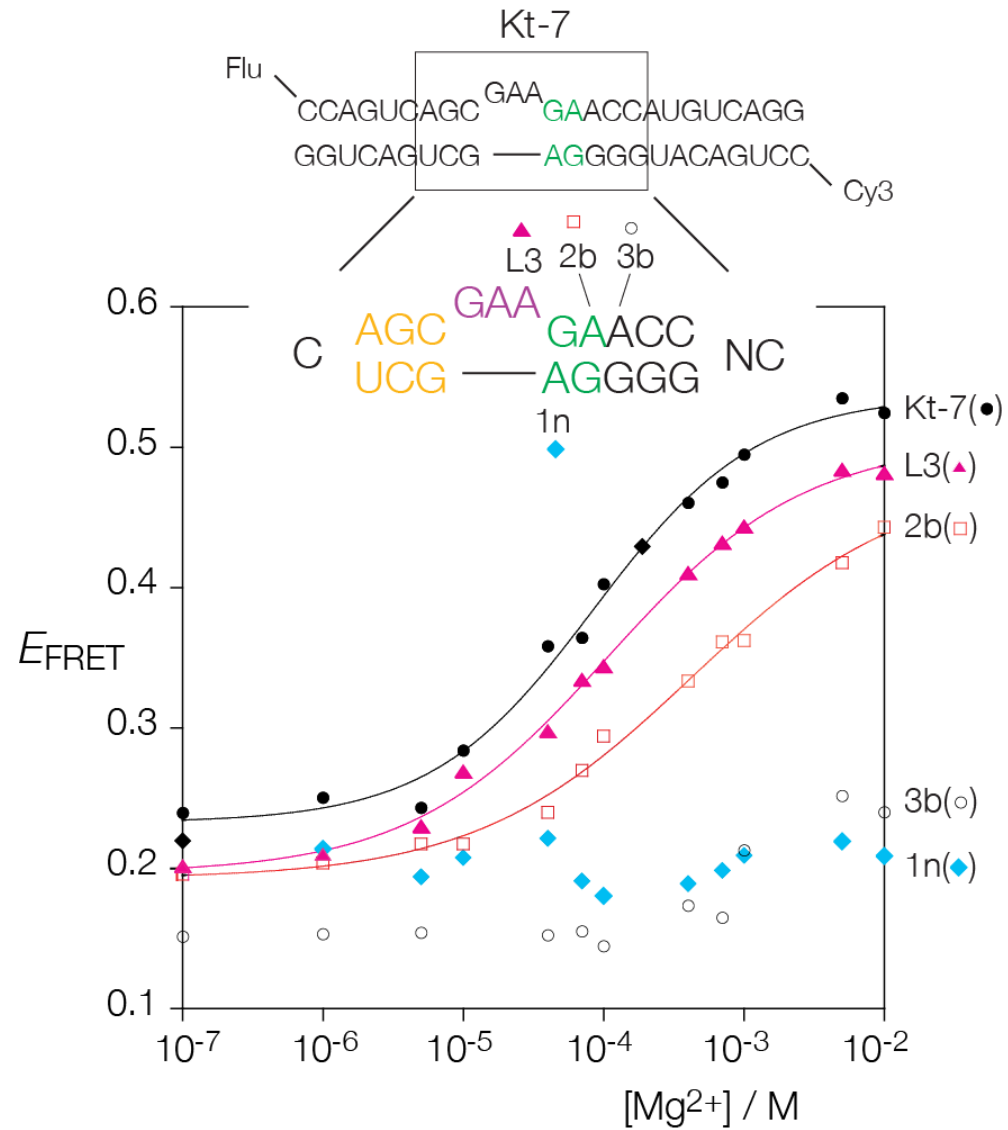
1n / 2b

Effect of N⁶-methylation of adenine on the ion-induced folding of Kt-7



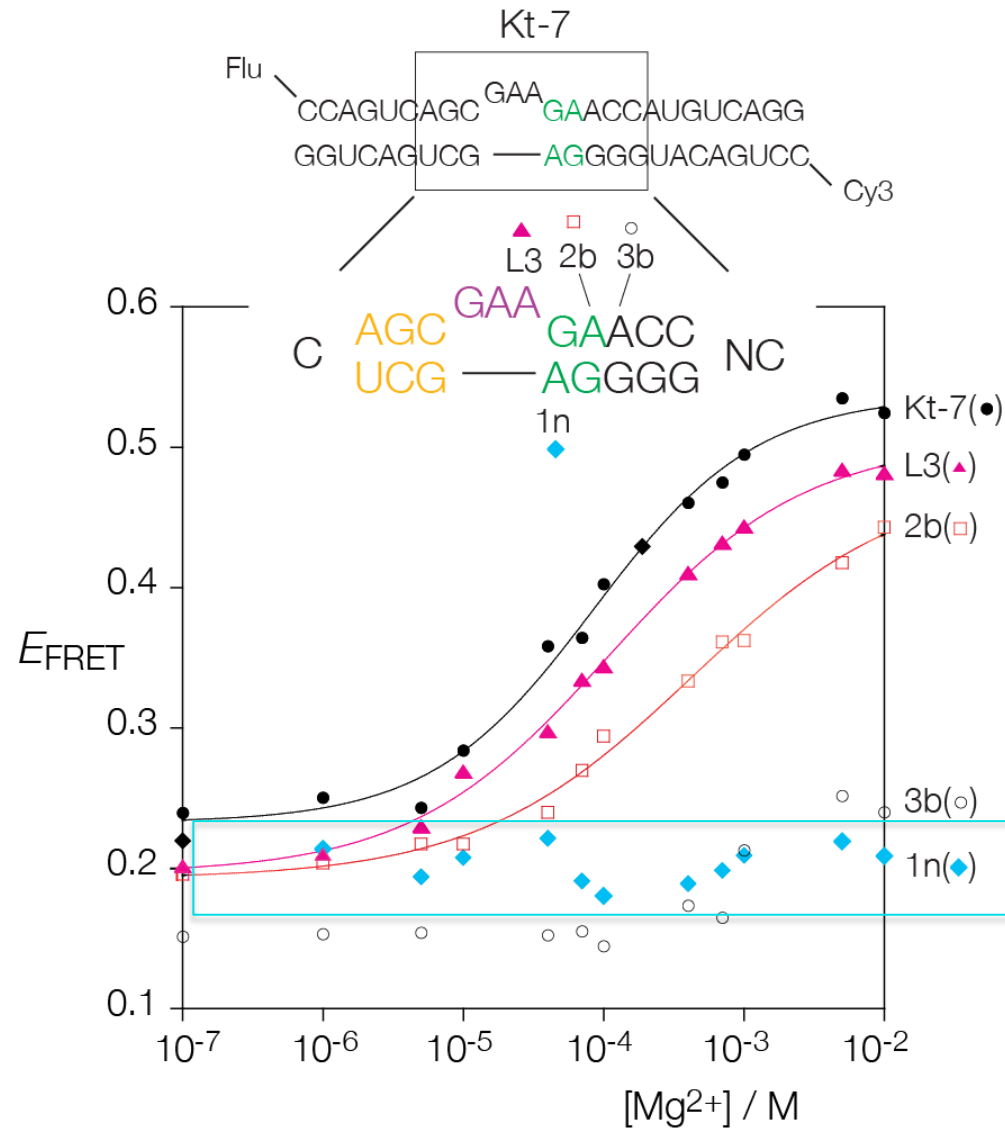
Saira Ashraf

Effect of N⁶-methylation of adenine on the ion-induced folding of Kt-7



Saira Ashraf

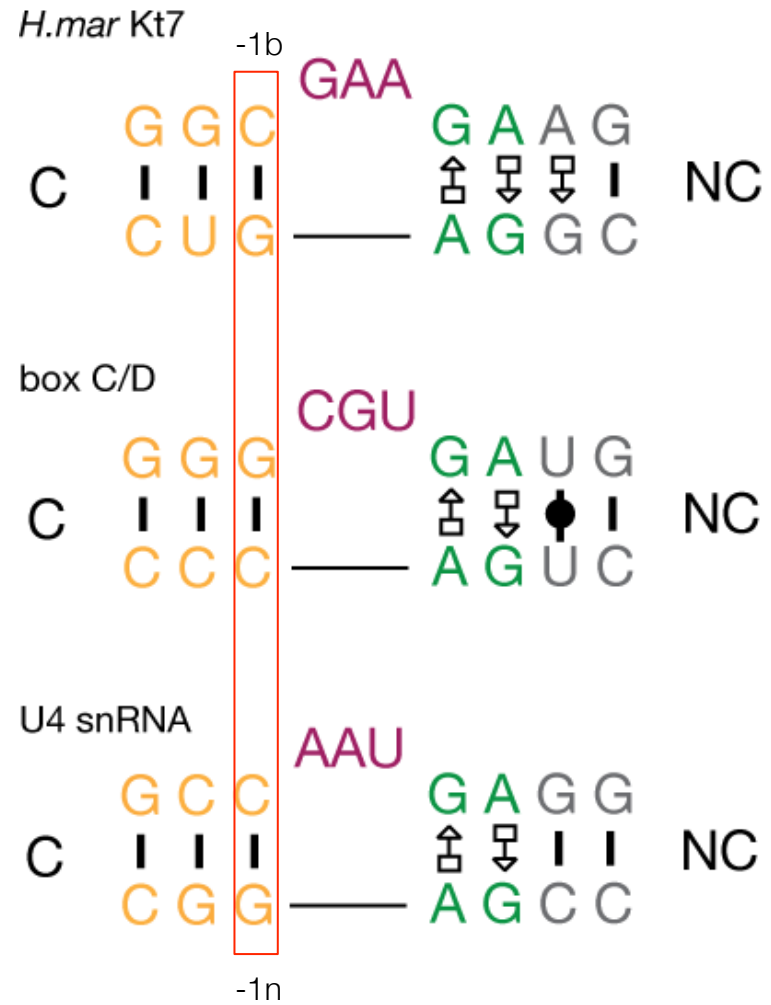
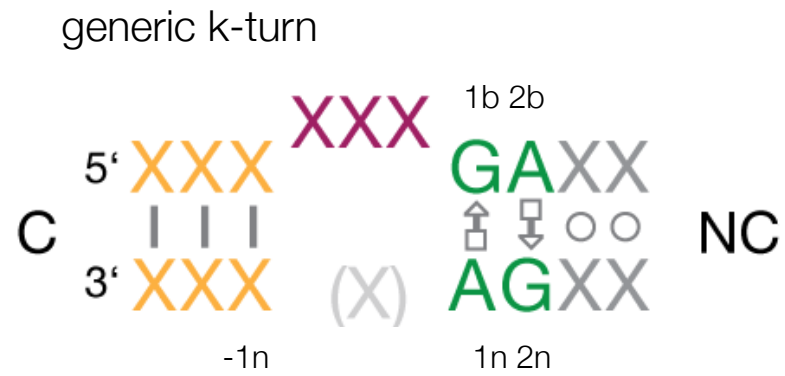
Effect of N⁶-methylation of adenine on the ion-induced folding of Kt-7



Saira Ashraf

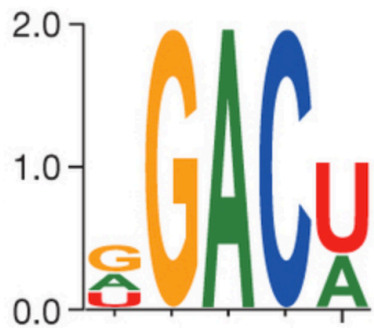
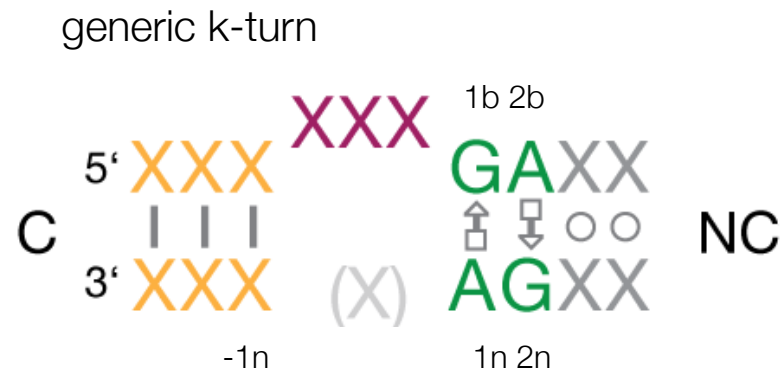
1n methylation prevents folding

The k-turn motif

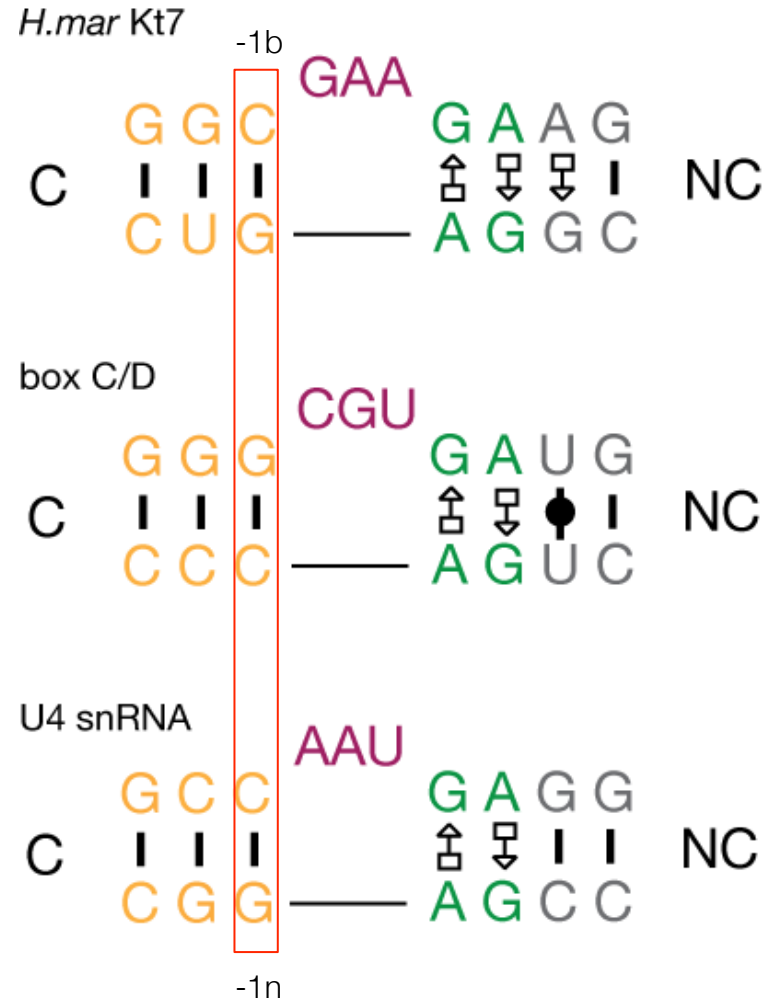


The k-turn motif

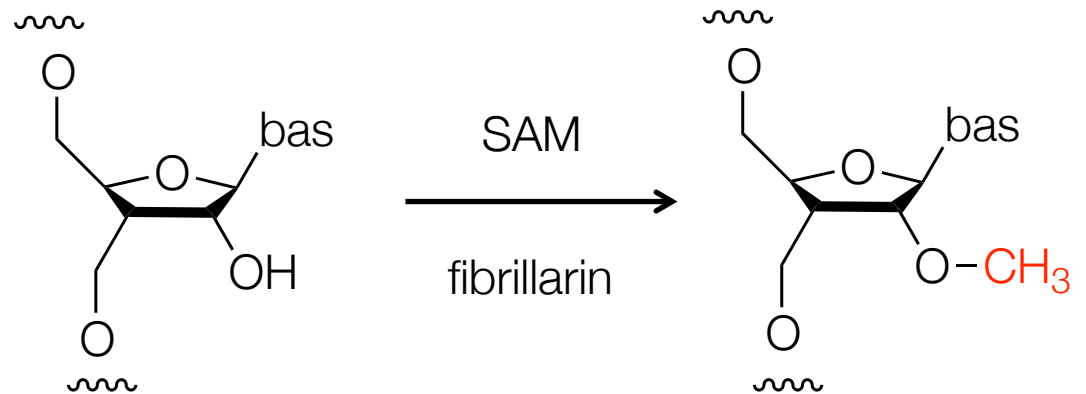
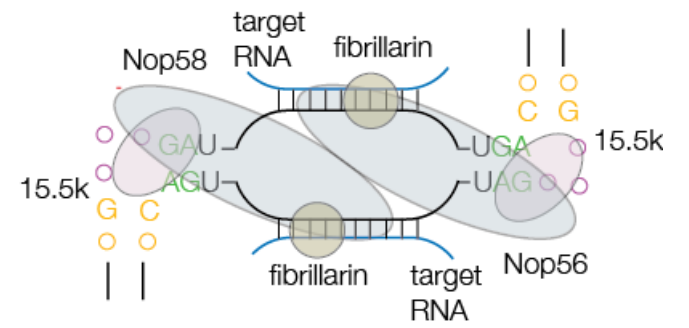
《kturn》结构基序



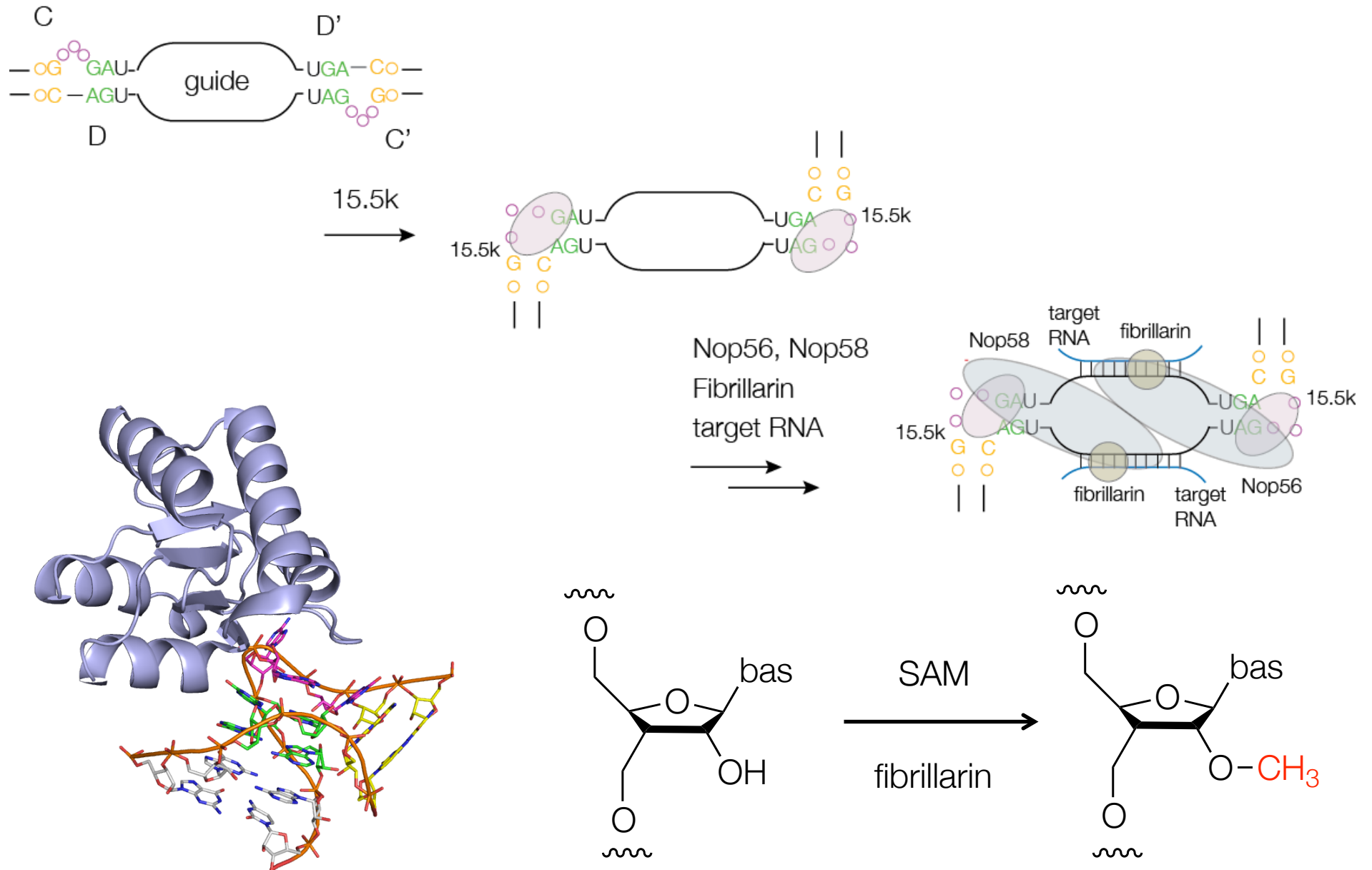
N6mA methyl transferase
 consensus sequence



Box C/D snoRNP : site-specific O^{2'} methylation

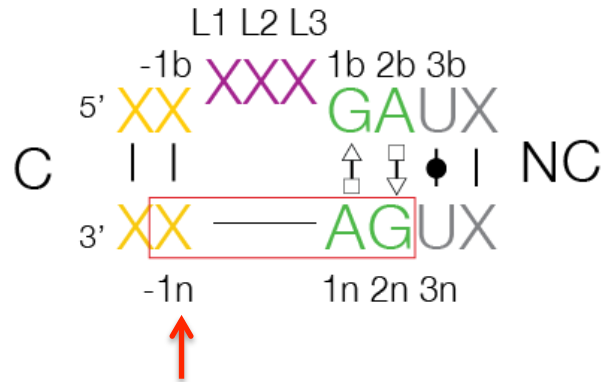


Box C/D snoRNP assembly



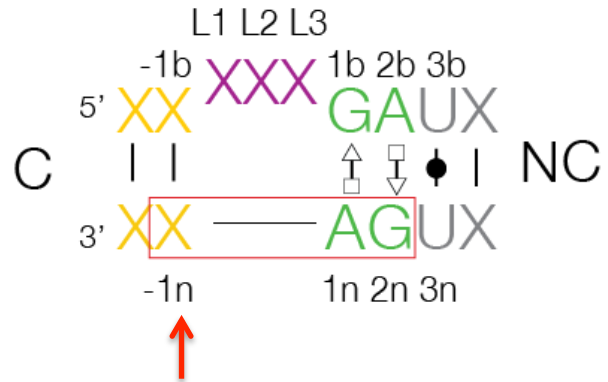
Some snoRNP sequences have a N⁶A methylation sequence

Potential methylation sites in box C/D k-turn sequences



If -1n = C, it creates GAC methylation target on lower strand

Potential methylation sites in box C/D k-turn sequences



If $-1n = C$, it creates GAC methylation target on lower strand

In humans, how frequently is this C ?

And how often is it the A_{1n} methylated ?

Data base mining

snoRNA box C/D, C'/D'



snoRNABase and snOPY

27 have GAC methylation sequence

Data base mining

snoRNA box C/D, C'/D'



snoRNABase and snOPY

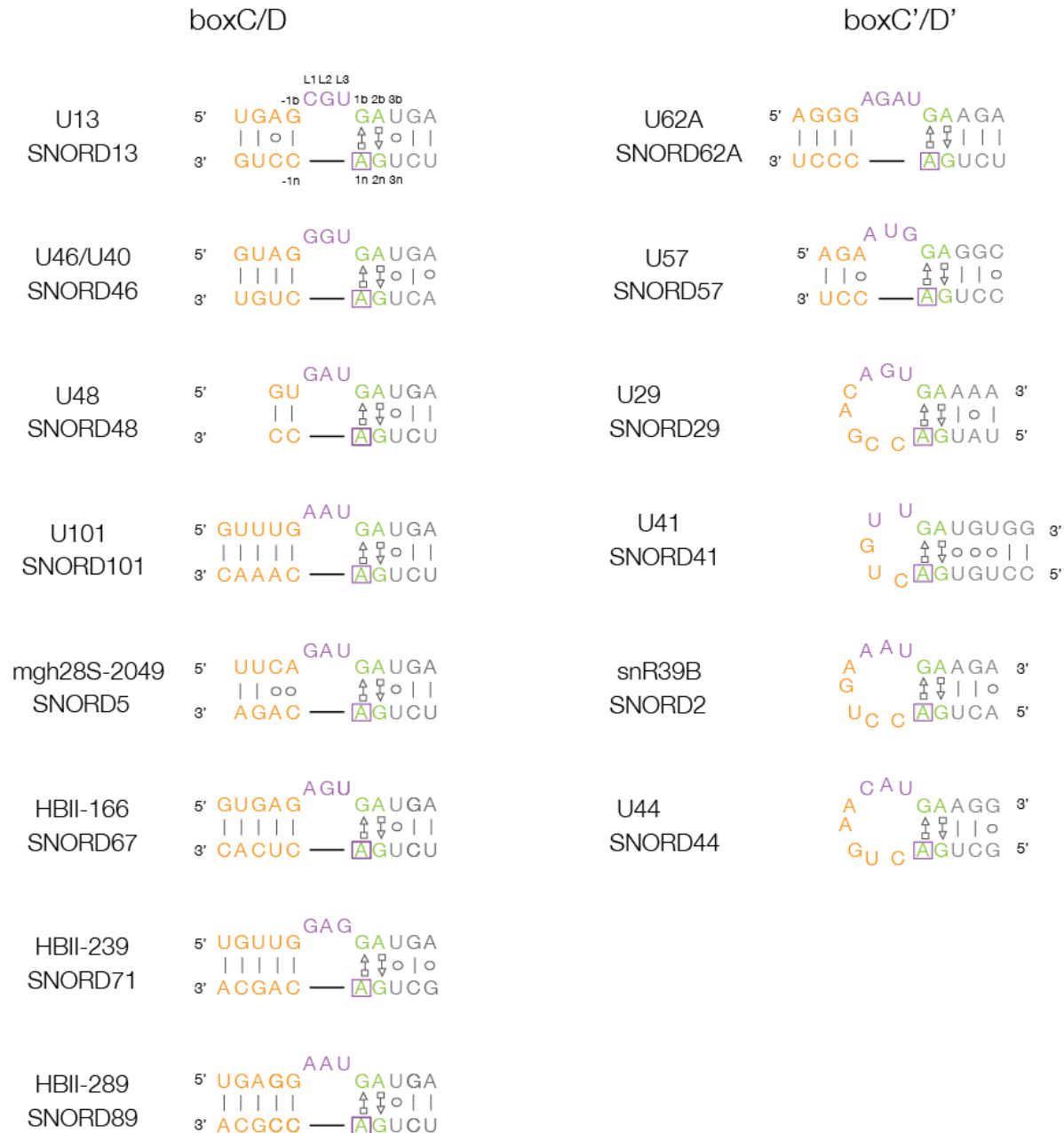
27 have GAC methylation sequence



RMBase

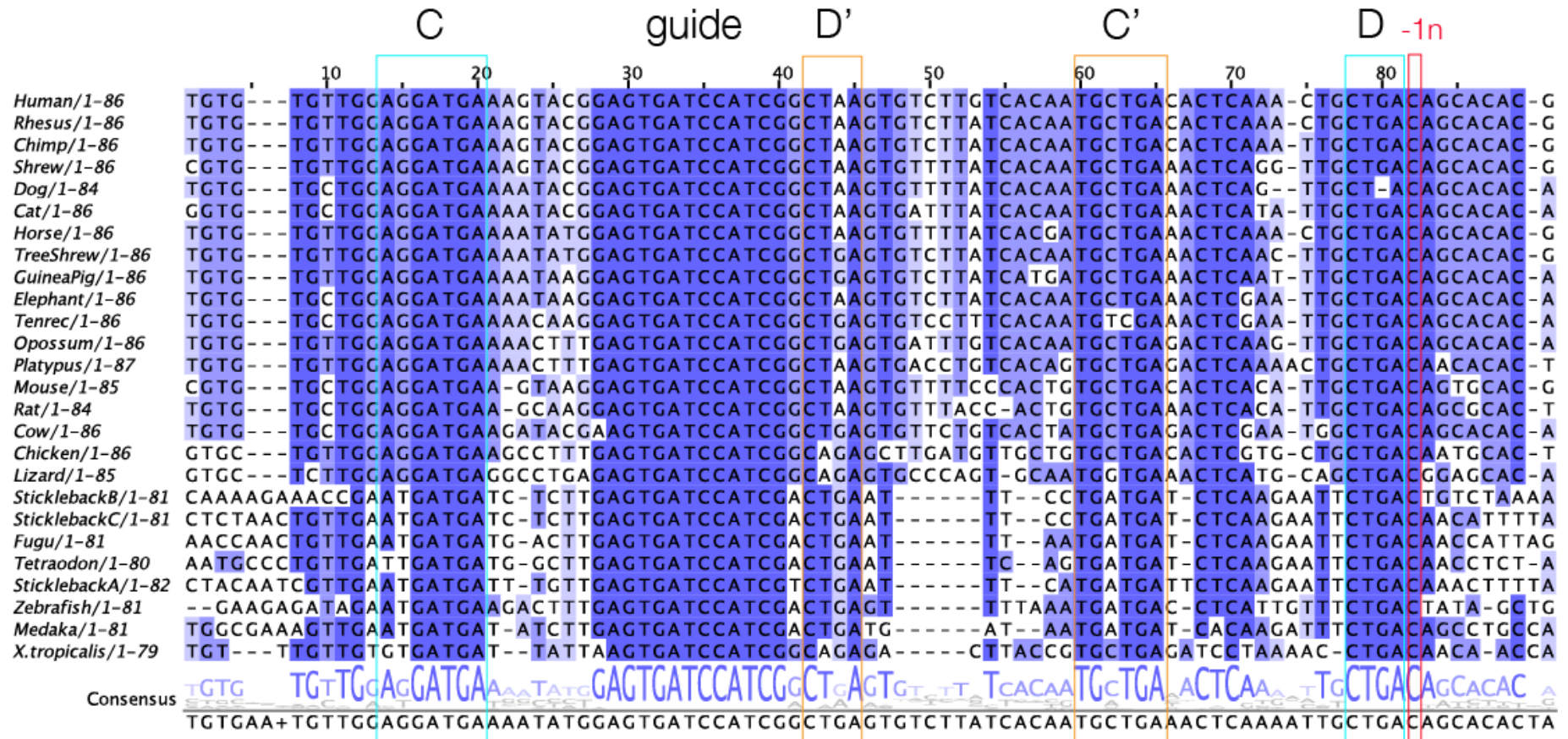
14 are methylated *in vivo*

Human box C/D RNA subject to A1N N⁶-methylation identified in RMBase

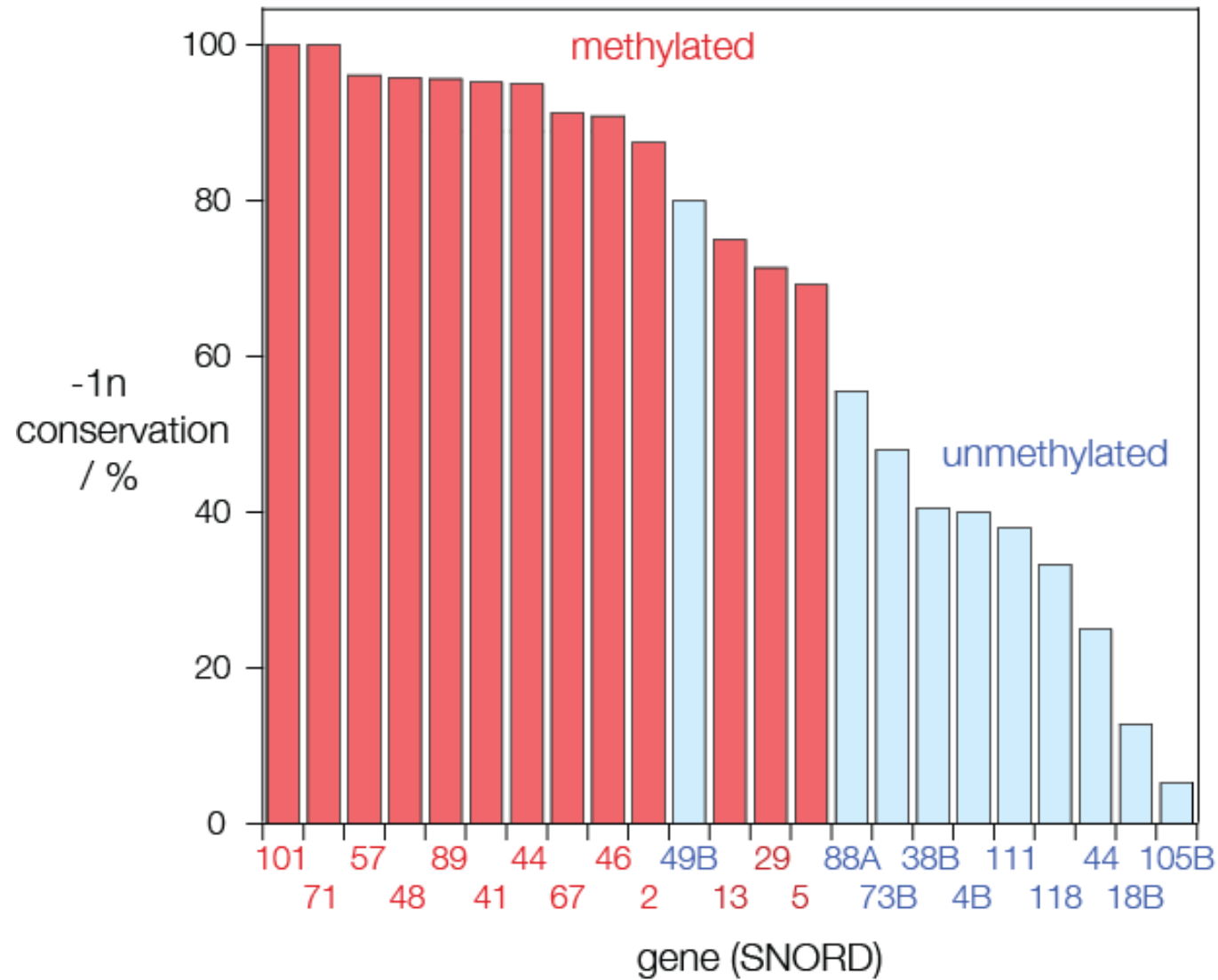


The methylation signals are conserved

Sequence alignment for SNORD71

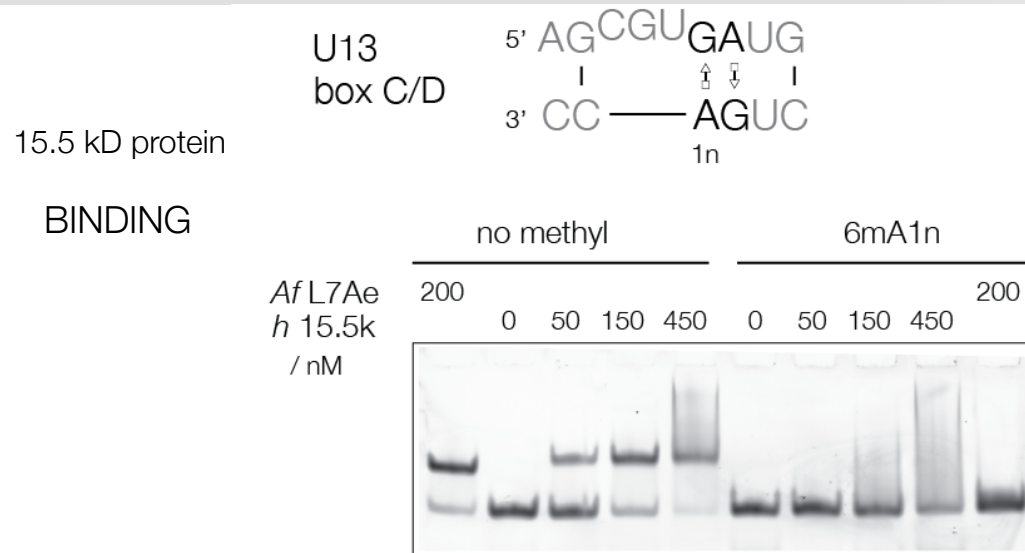


Conservation of -1n sequences (% C) for box C/D where -1n = C in humans

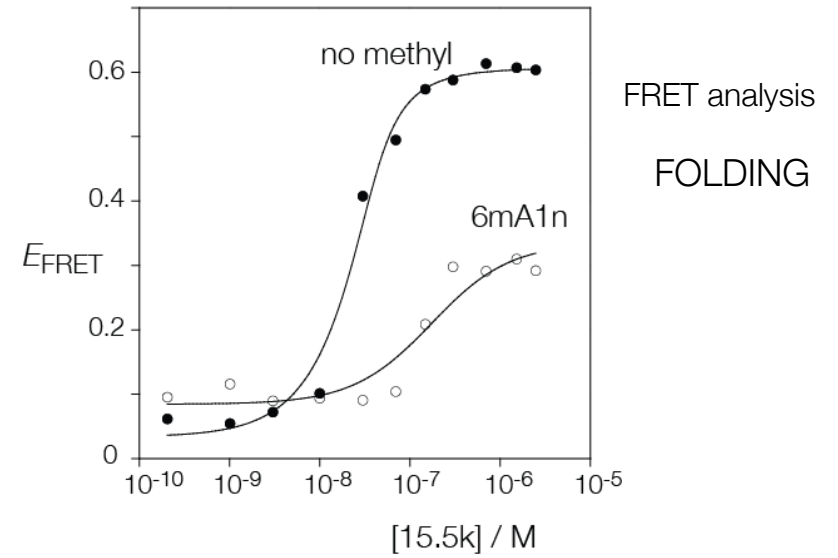
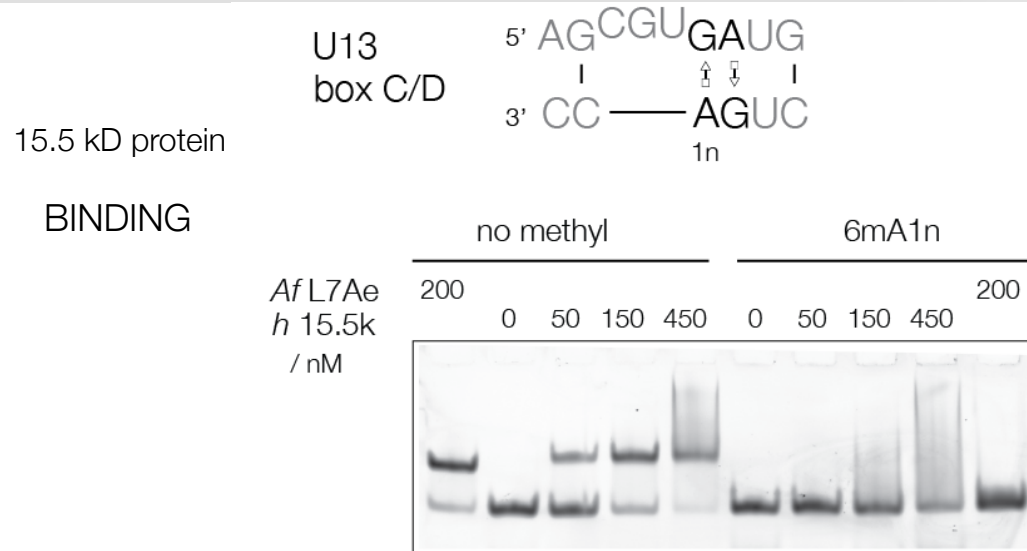


A1n N⁶-methylation blocks folding/binding of the k-turn

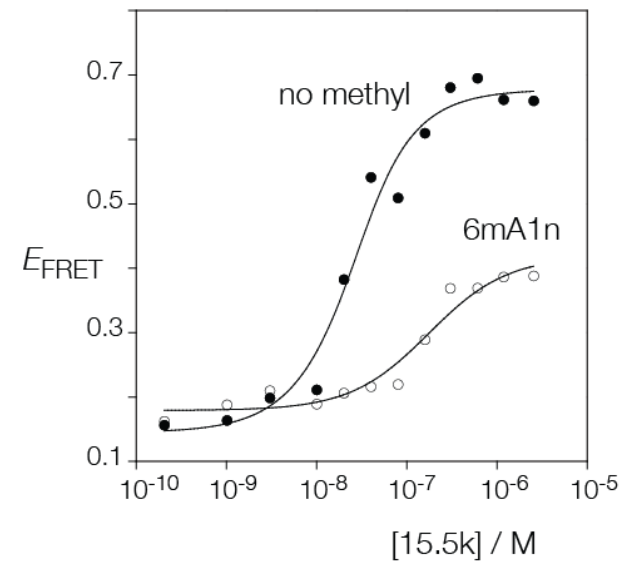
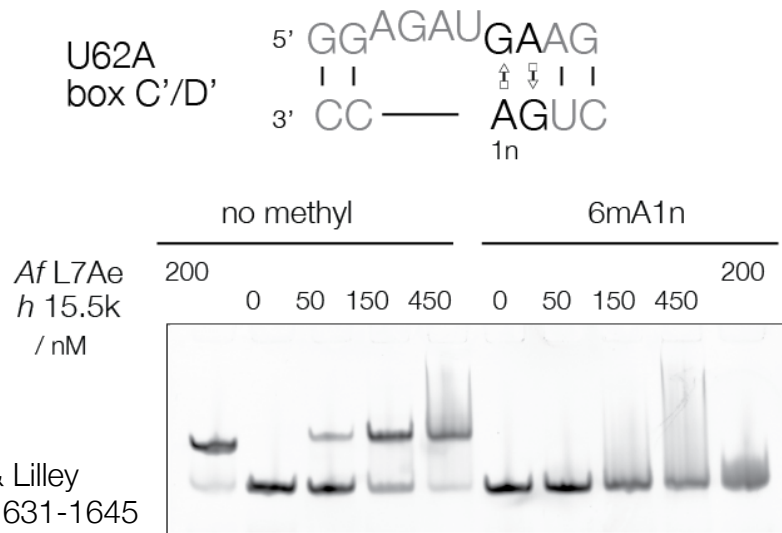
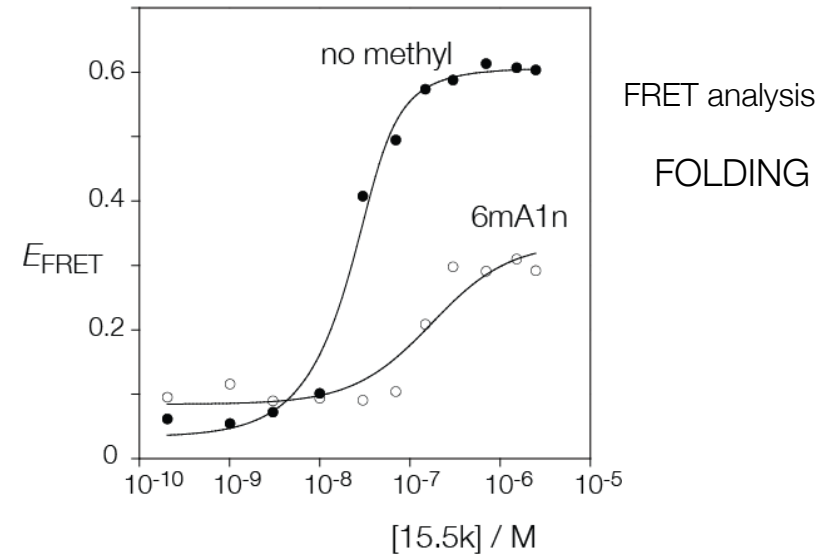
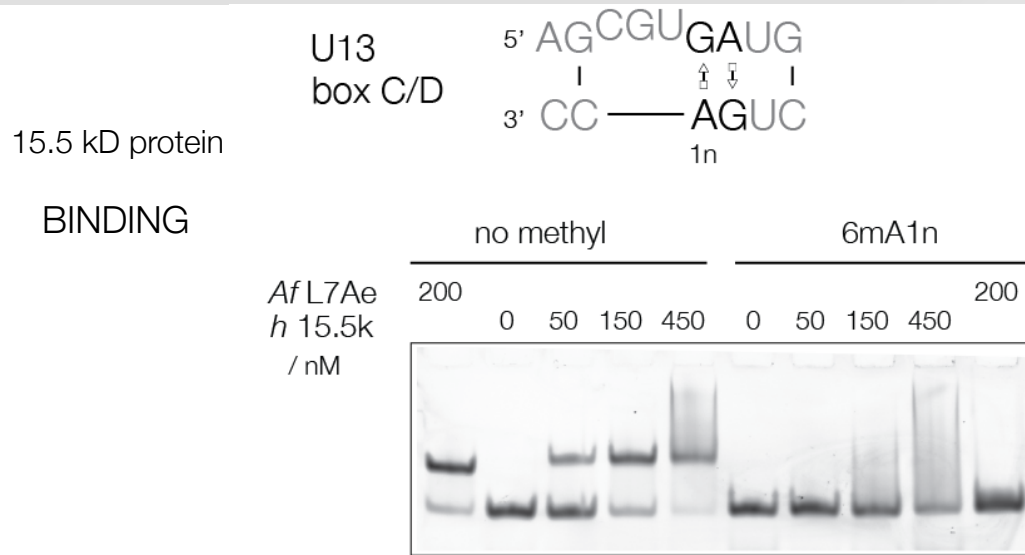
Effect of N⁶A-methylation on 15.5 kD protein binding to box C/D



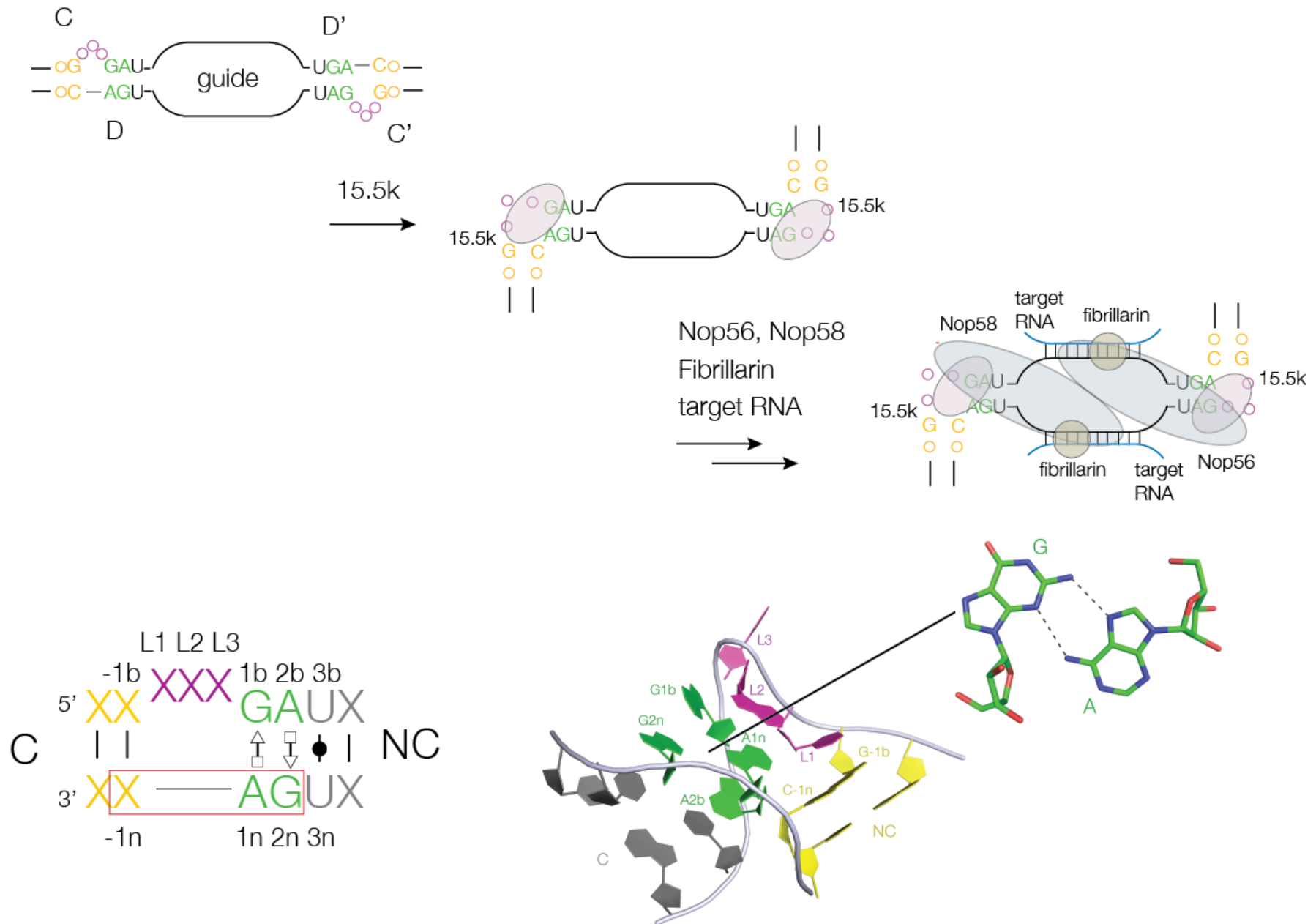
Effect of N⁶A-methylation on 15.5 kD protein binding to box C/D



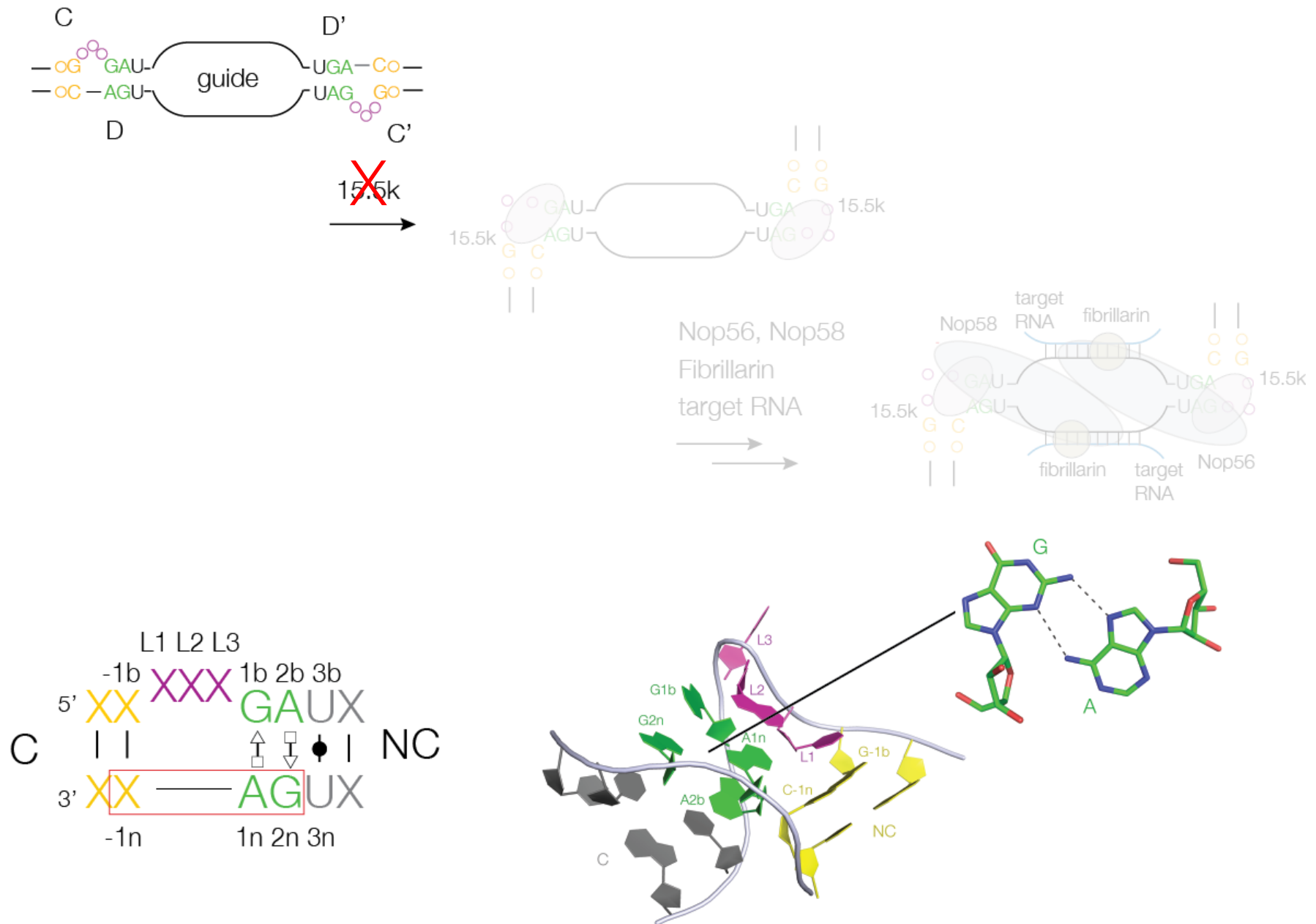
Effect of N⁶A-methylation on 15.5 kD protein binding to box C/D



Box C/D snoRNP assembly

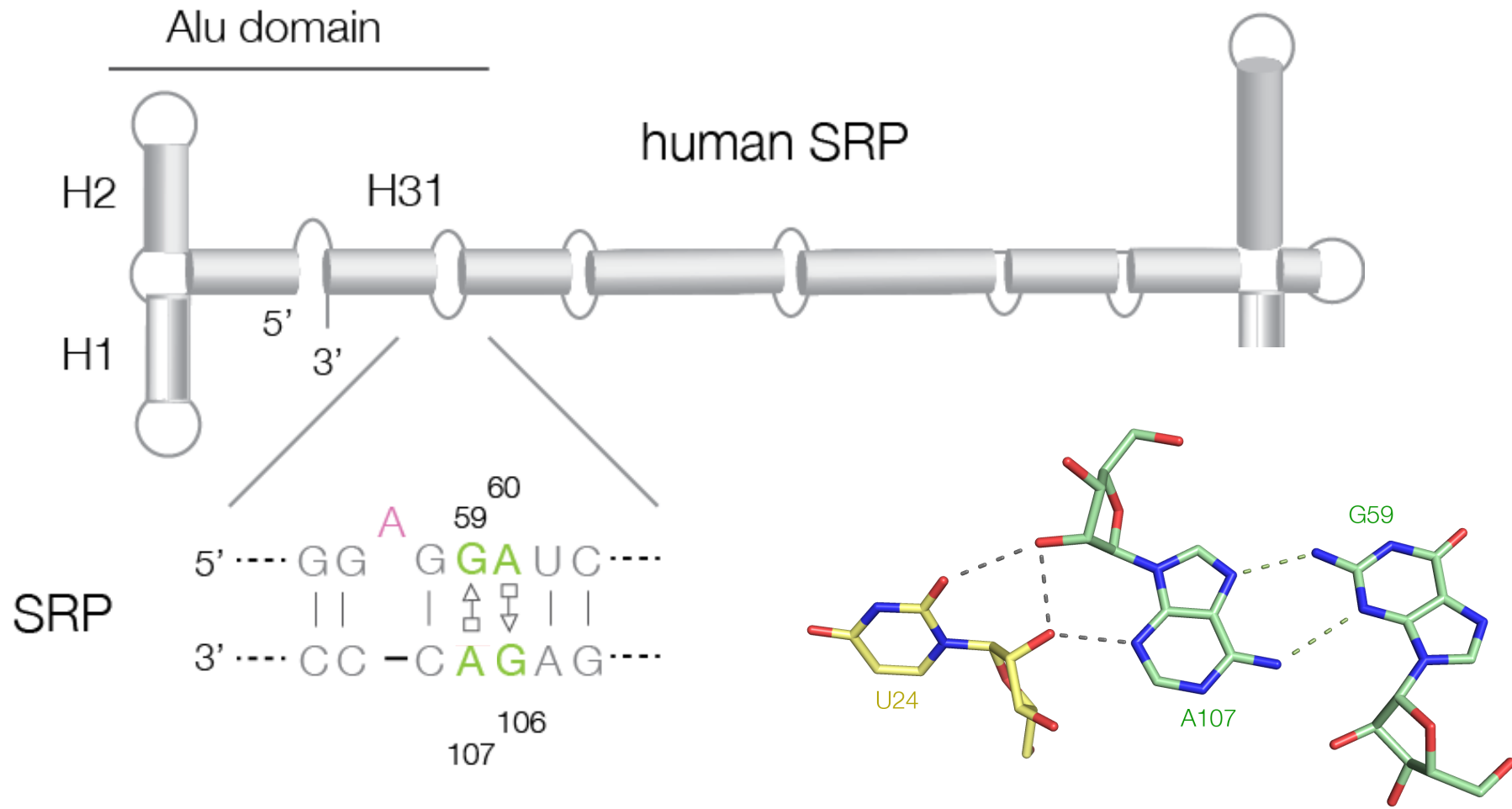


Box C/D snoRNP assembly

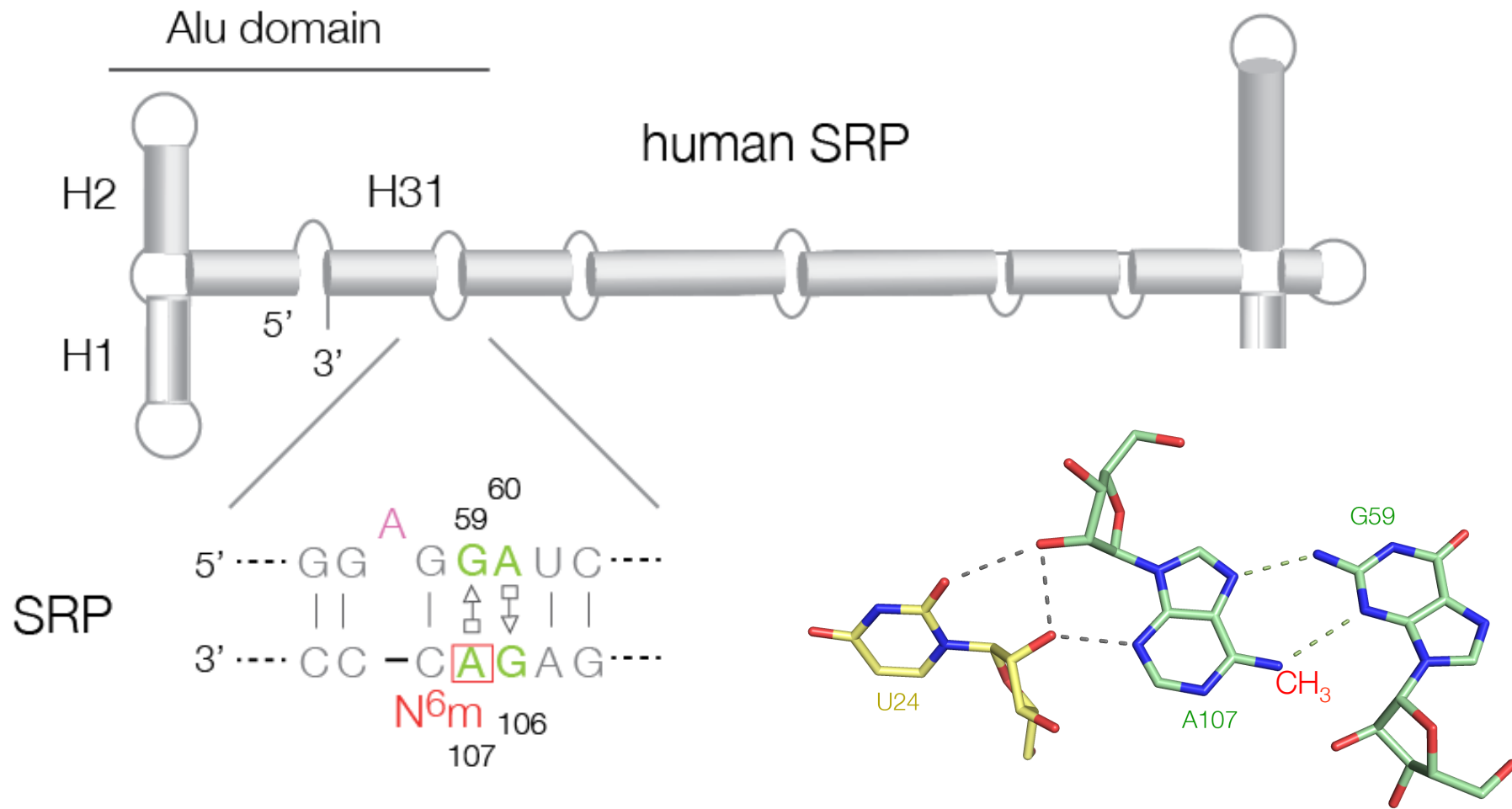


N⁶A methylation in the human signal recognition particle Alu domain

Methylation in the human signal recognition particle RNA

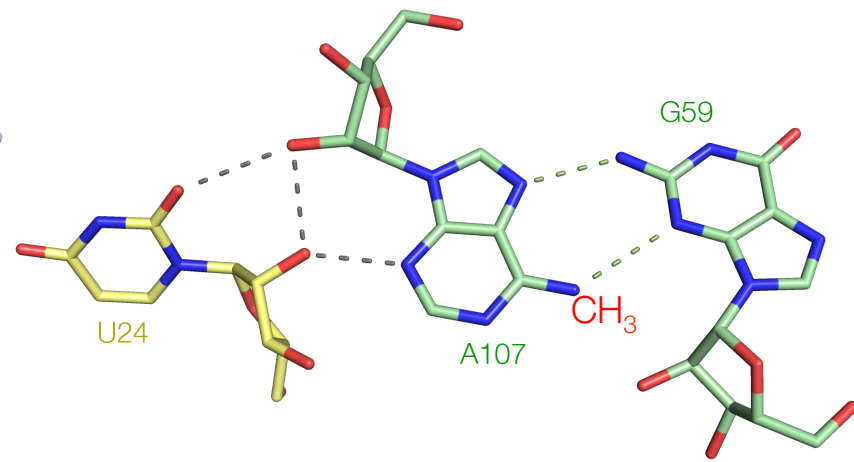
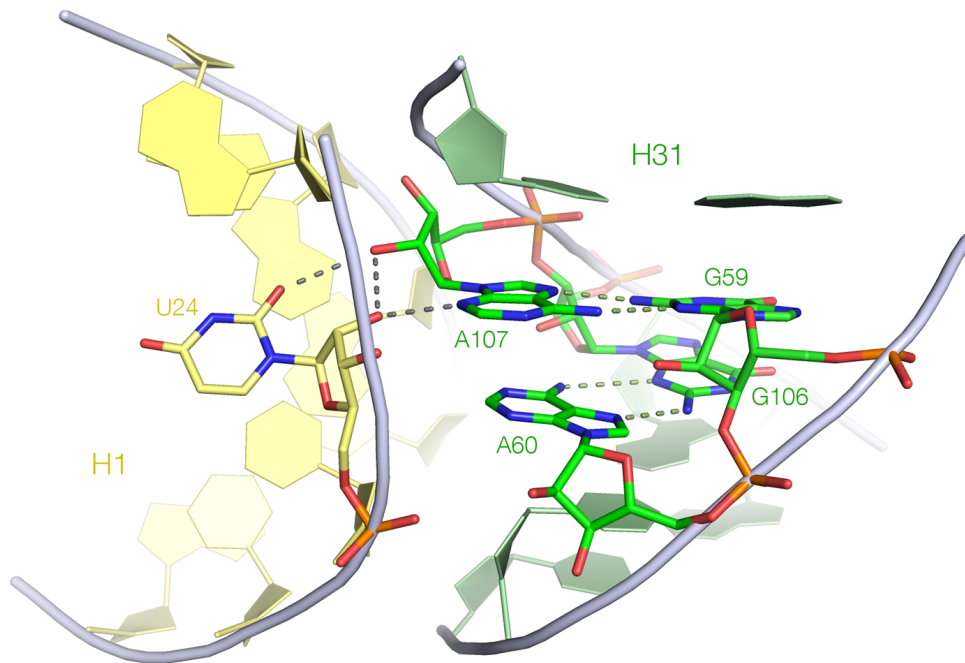
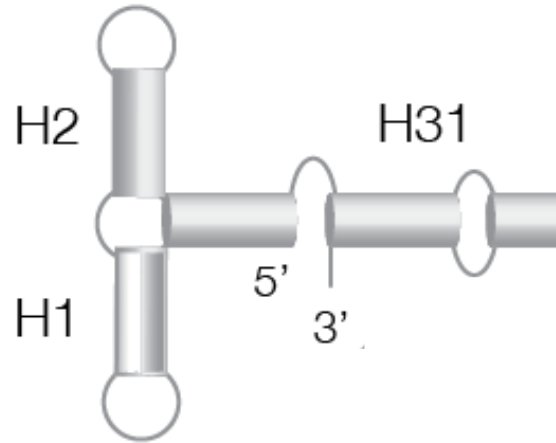


Methylation in the human signal recognition particle RNA



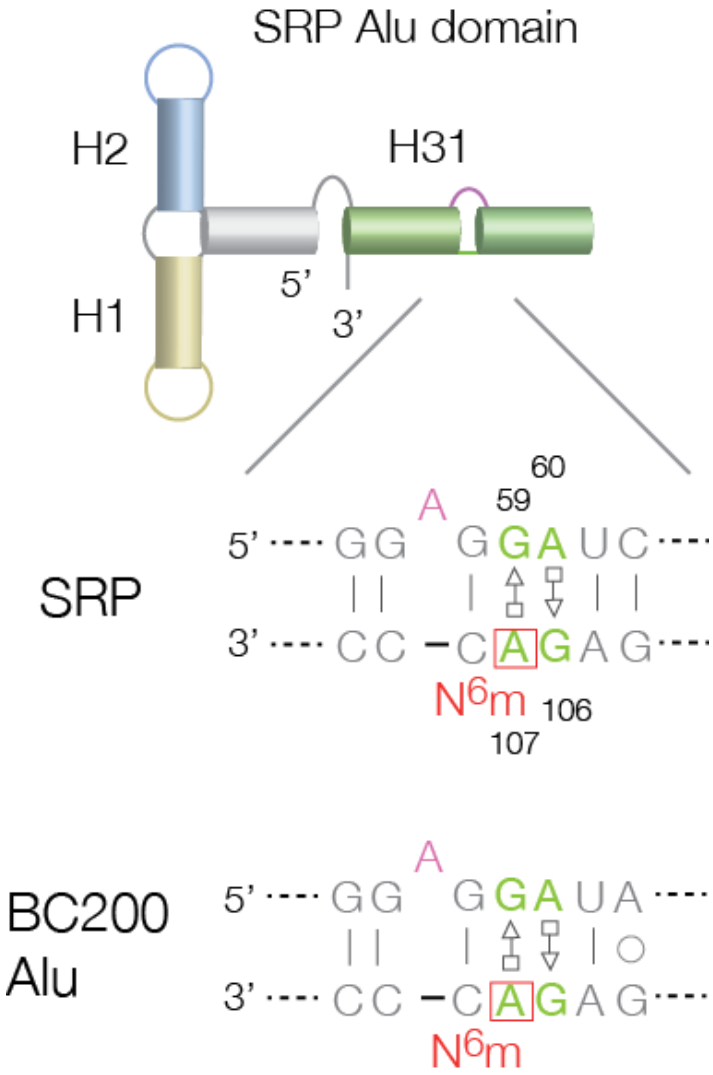
Methylation in the human signal recognition particle RNA

Alu domain



N⁶A methylation in human Alu elements

N⁶-methylation of Alu sequences



N⁶-methylation of Alu sequences ; RMBase data

gene	mod ID	xsome	position	support no	sequence (N ⁶ meA)
srpRNA	m6A_site_38024	chr14	50329278	14	AGCCTGAGCAACATAGCGAGACCCCGTCTCTTTTGCCCCC
AluJo	m6A_site_12507	chr1	214372362	5	GCCTGAGCAACATAGCGAGACCCCGTCTCTAAAACAAAA
AluSp	m6A_site_9026	chr1	154184358	4	GCCTGGGCAACAAAAGTGAAACTCTGTCTCAAAAAAAAAA
FAM	m6A_site_31320	chr12	76858065	4	AGCCTGAGCAACATAGTGAGACCCGTCTCTAAAAGCAAC
AluJb	m6A_site_32596	chr12	112742257	4	AGCCTGGGCAACATAGCGAGACCCCGTCTCTGCAAAAAAAT
AluJr	m6A_site_119490	chr7	70342837	4	AGCCTGAGCAACATAGCGAGACCCCGTCTCTACAAAAACTA
AluSc	m6A_site_134766	chr9	139728960	4	TCCAGCCTGGACAGAGTGAGACTCCGTCTCCAAAAAAAAGA
AluJr	m6A_site_30705	chr12	58271974	3	AGCCTGAGCAACATAGCGAGACCCCGTCTCTACAAAAAAA
AluSx3	m6A_site_30910	chr12	66517102	3	AGCCTGGCTAATACAGTGAAACCCCATCTCTACTAAAATA
AluSz6	m6A_site_40909	chr14	104057184	3	AGCCTGGAAGACCAAACGAGACTCTGTATCAAAAAATAATA
AluSz	m6A_site_62849	chr19	2342640	3	AGCCTGGGTGACAGAGTGAGACTCCATCTCAAAAACAAAAT
AluSz	m6A_site_64656	chr19	12986232	3	AGCCTGGGTGACAGAATGAGACTCTGTGTCAAAAAATAAA
BC200	m6A_site_139606	chrX	138802845	1	TGCCTGGGCAATATAGCGAGACCCCGTTCTCCAGAAAAAGG

RMBase : Sun et al *Nucleic Acids res* **44**, D259 (2016).

Huang, Ashraf & Lilley *EMBO rep* **18**, 1631-1645 (2017)

Summary

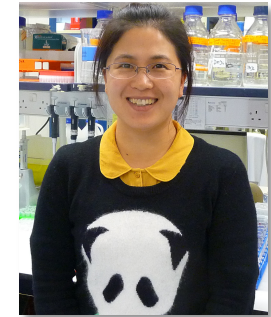
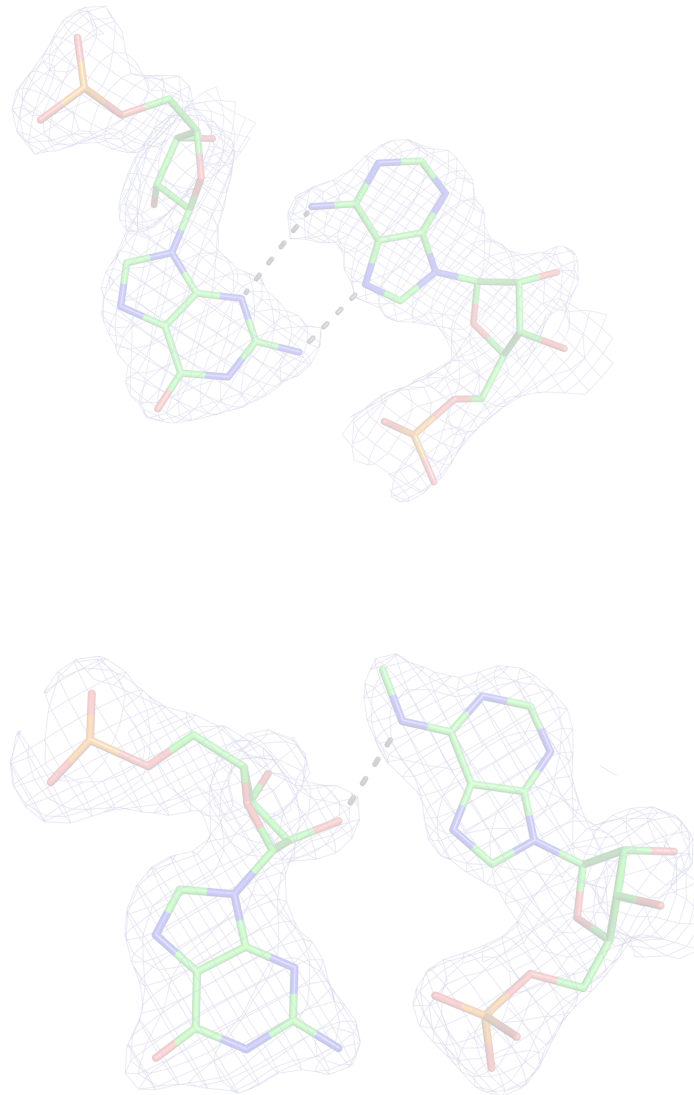
- N⁶mA is tolerated in Watson-Crick basepairs, but prevents the formation of *trans* Hoogsteen-sugar A•G basepairs.
- A sub-set of human box C/D snoRNA species have target GAC sequences that result in the formation of N⁶-methyladenine at a key *trans* Hoogsteen-sugar A•G basepair, of which half are methylated *in vivo*.
- The GAC target is conserved only in those that are methylated. Methylation prevents binding of the 15.5 kDa protein and the induced folding of the RNA. Thus the assembly of the box C/D snoRNP can be regulated by RNA methylation at its critical first stage.
- More generally, N⁶-methylation of adenine occurs at sheared A•G basepairs involved in tertiary contacts in the human signal recognition particle RNA and related Alu retrotransposon RNA species.
- N⁶-methylation at A•G basepairs is probably a general method of controlling conformation and RNP assembly in cellular RNA.



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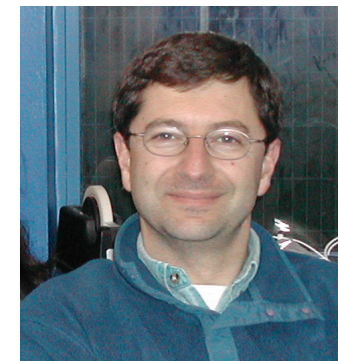
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<http://www.dundee.ac.uk/biocentre/nasg/index.php>

Thanks !