

TABLE 11-1 Half-Lives of Messenger RNAs

| Cell | Cell Generation Time | mRNA Half-Lives* | |
|-----------------------------------------|----------------------|------------------|------------------------------------------------------------------------------------------------|
| | | Average | Range Known for Individual Cases |
| <i>Escherichia coli</i> | 20–60 min | 3–5 min | 2–10 min |
| <i>Saccharomyces cerevisiae</i> (yeast) | 3 h | 22 min | 4–40 min |
| Cultured human or rodent cells | 16–24 h | 10 h | 30 min or less (histone and <i>c-myc</i> mRNAs) 0.3–24 h (specific mRNAs of cultured cells) |

*For information on specific mRNA half-lives for *E. coli*, see A. Hirashima, G. Childs, and M. Inouye, 1973, *J. Mol. Biol.* **119**: 373; for yeast, see L.-L. Chia and C. McLaughlin, 1979, *Mol. Gen. Genet.* **170**:137; and for mammalian cells, see M. M. Harpold, M. Wilson, and J. E. Darnell, 1981, *Mol. Cell Biol.* **1**:188.

Protein-RNA complex structures involved in pre-mRNA processing

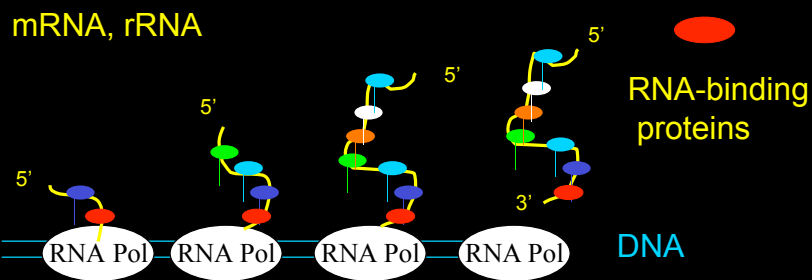
Gene expression and regulation

DNA → RNA → protein

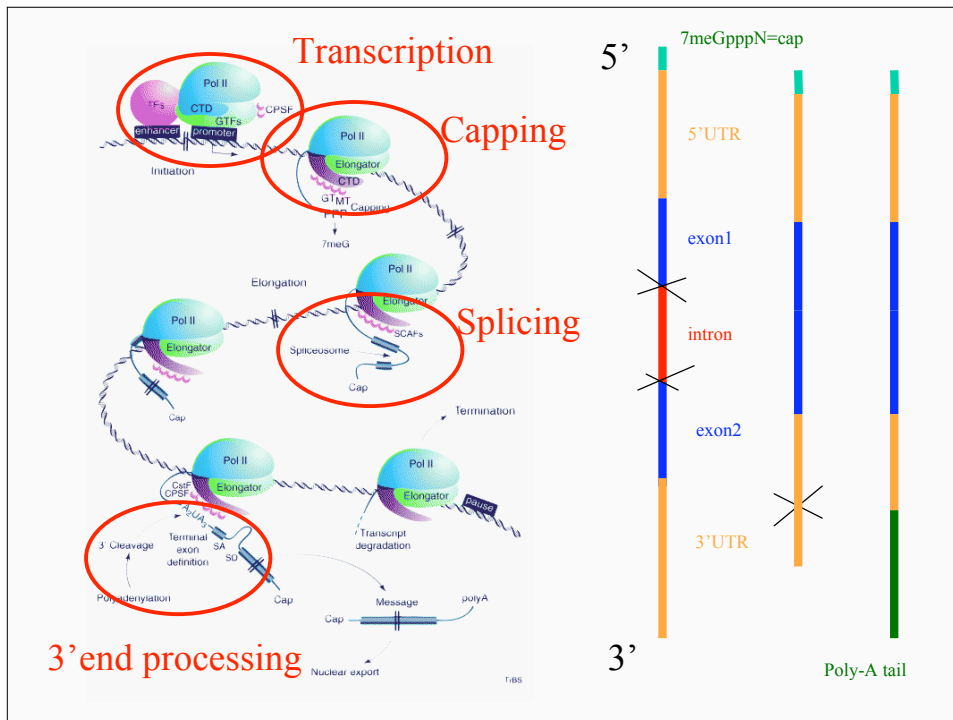
Transcription factors
Methylation

?

Phosphorylation
Modification



- RNA packaging, stability
- 5' capping
- splicing **Alternative-splicing**
- 3' end processing (cleavage and polyadenylation)
- RNA editing**
- export
- translation



Biophysical, chemical approach

RNA binding **proteins** of two types:

- **enzymes**

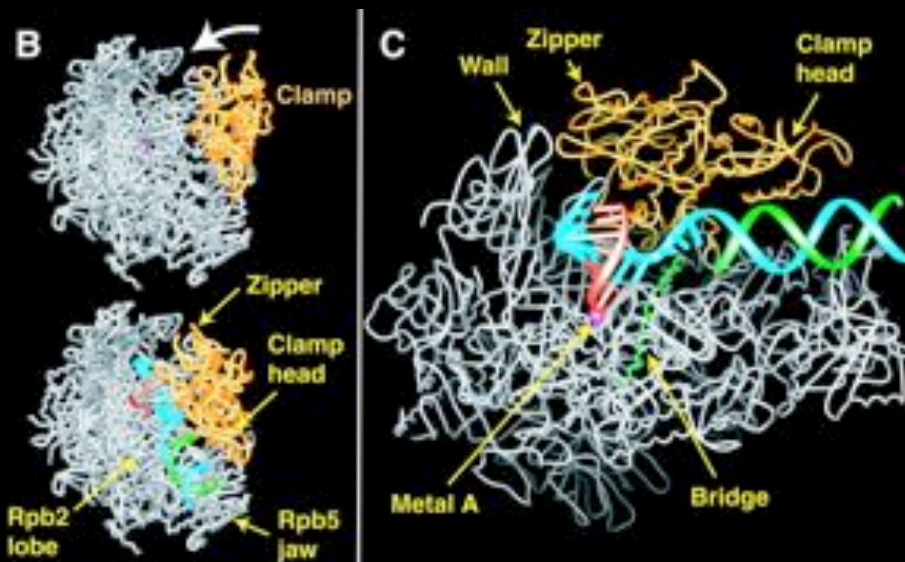
polymerase, nuclease, modifying enzymes

- **binding proteins**

protection, folding (chaperone), **gene regulation**

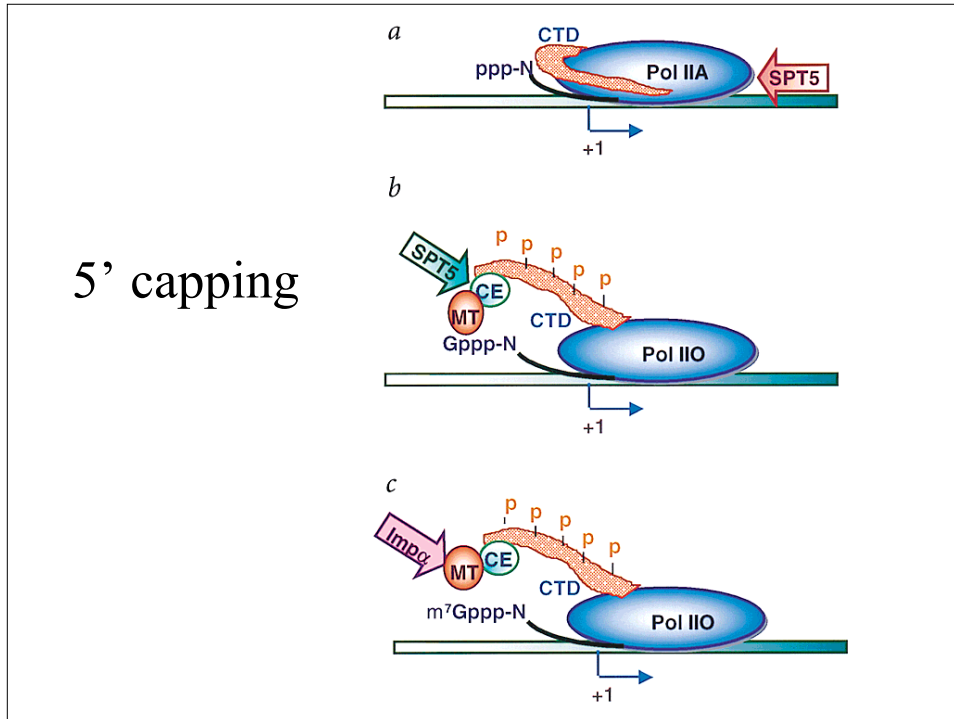
Protein-RNA structure of the
constitutive mRNA
processing machinery

Yeast Pol II-mRNA-DNA complex

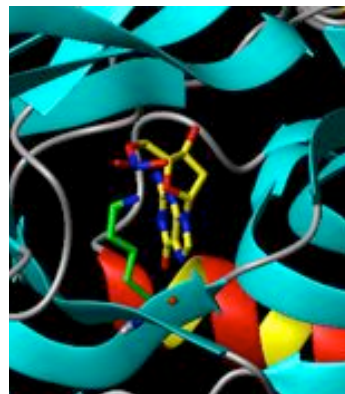
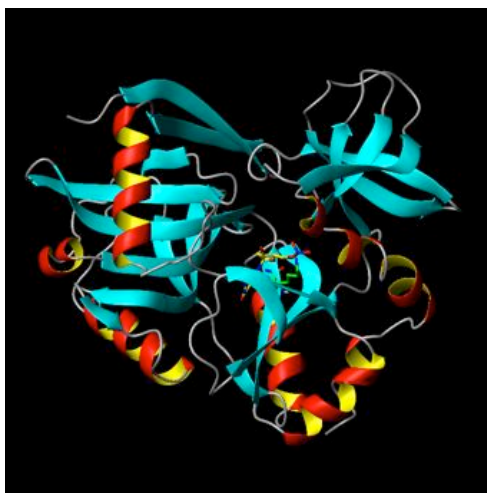
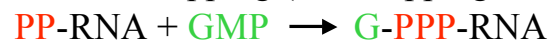


Gnatt et al and Kornberg, Science 2001

5' capping

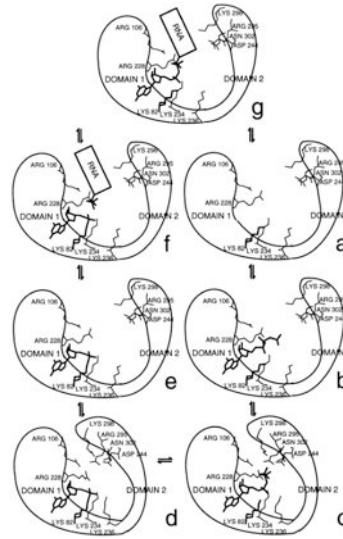
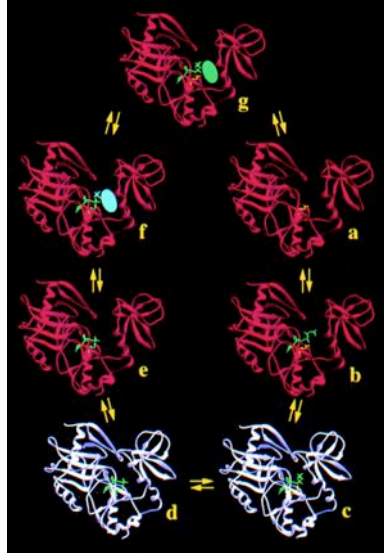
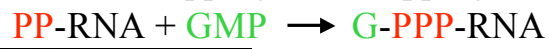


Mechanism of capping (viral capping enzyme)



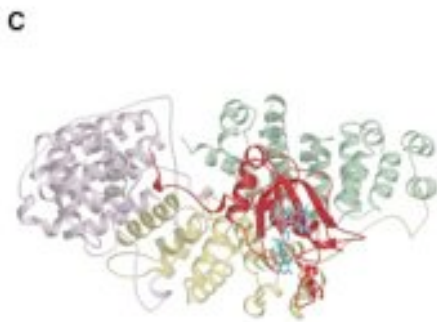
Hakansson et al et Wigley, Cell 1997

Mechanism of capping (viral capping enzyme)

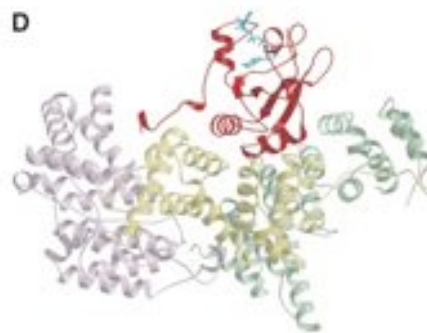


Hakansson et al et Wigley, Cell 1997

5' cap binding protein, CBP20-CBP80

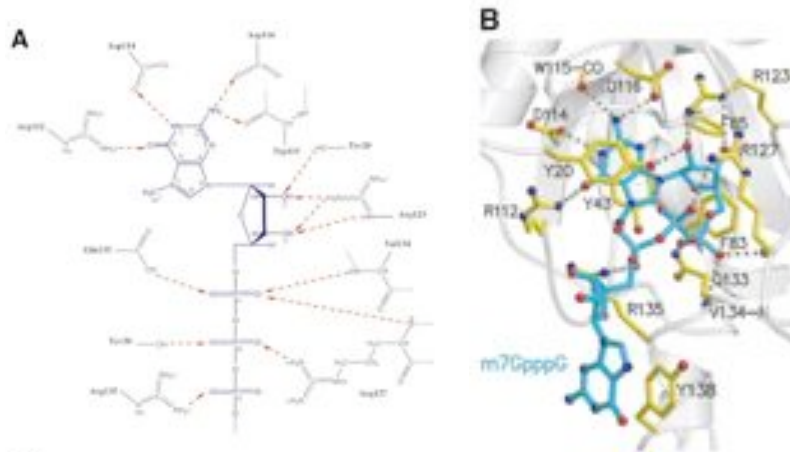


CBP20-CBP80

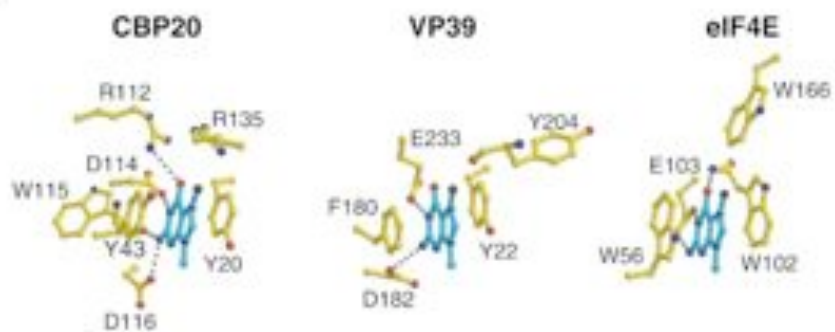


Mazza et al, EMBO J (2002)

CBP20-m7GpppG contacts

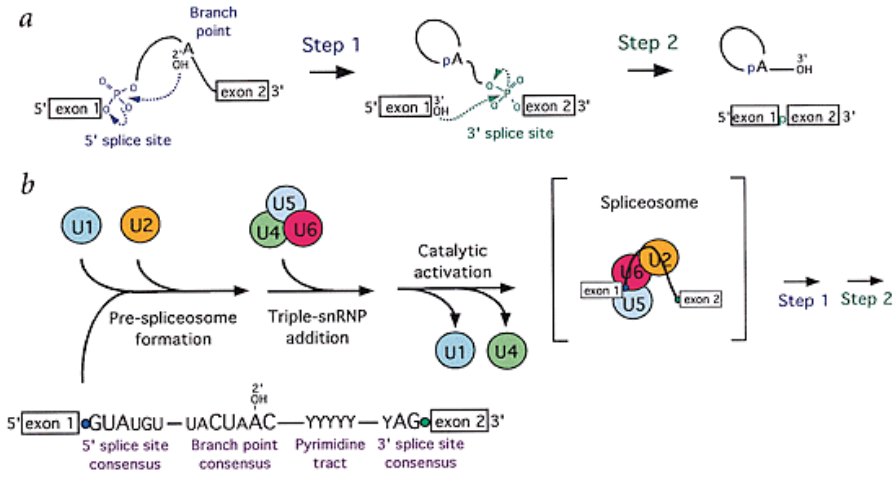


Comparison with other 5' cap binding proteins



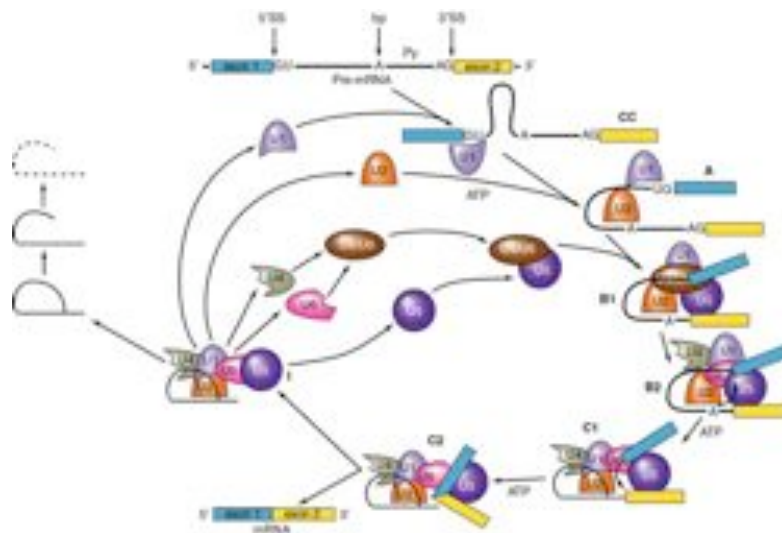
vaccinia virus

Constitutive splicing

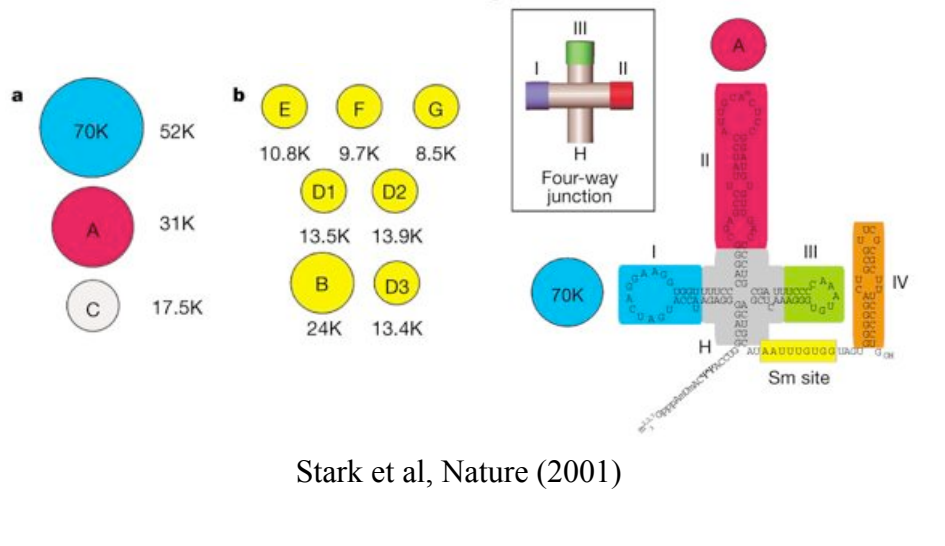


Collins & Guthrie, Nat.Struct.Biol 2000

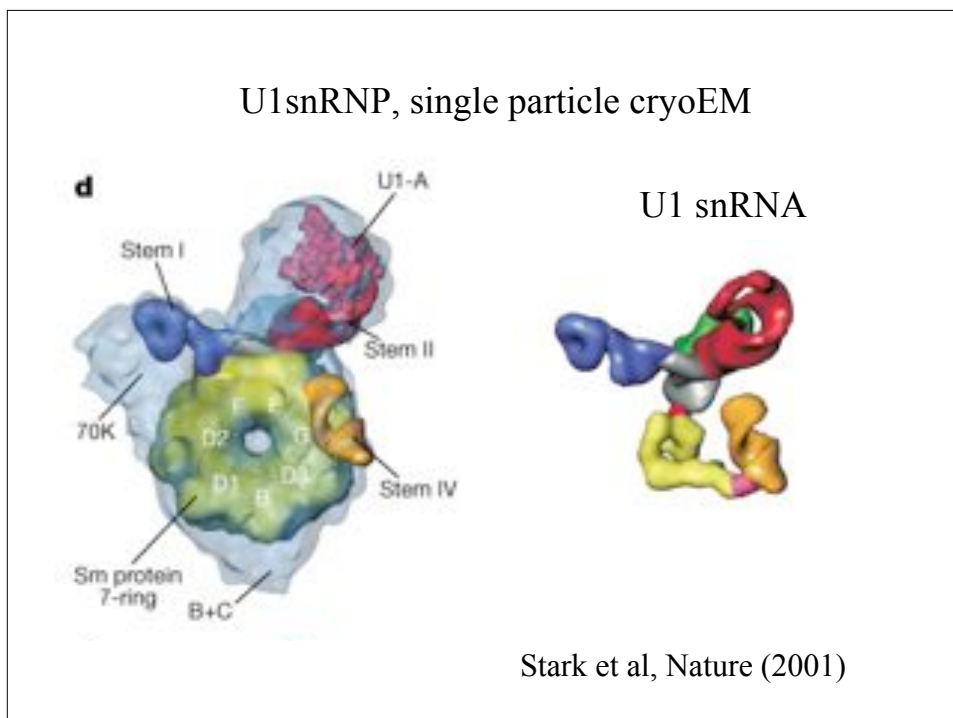
Pre-mRNA splicing



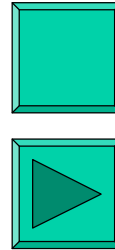
U1snRNP, single particle cryoEM



U1snRNP, single particle cryoEM

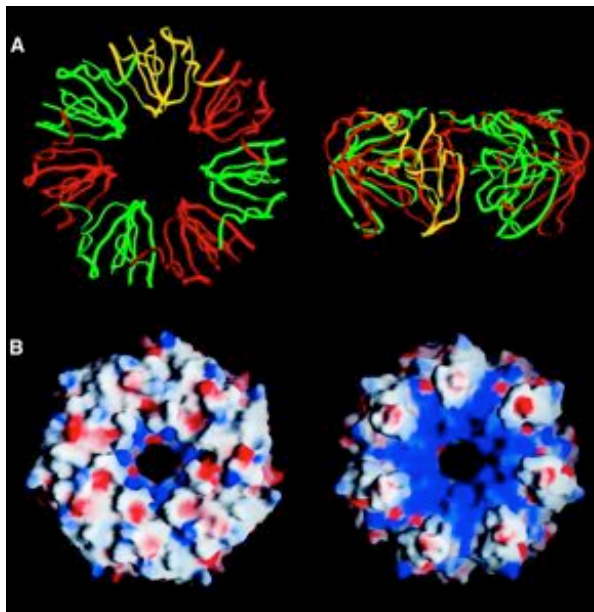


U1A-U1snRNA SLII

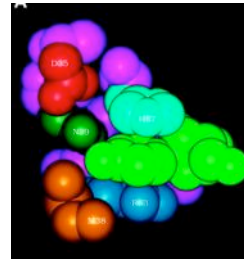
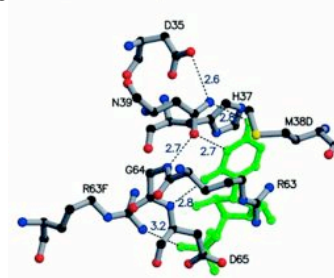
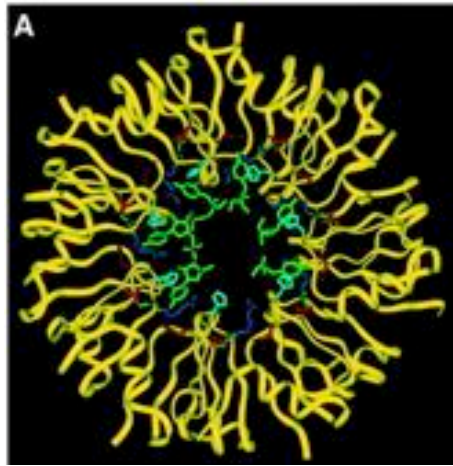


Oubridge et al, Nature (1994)

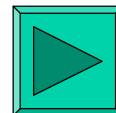
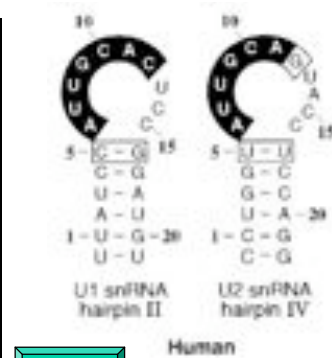
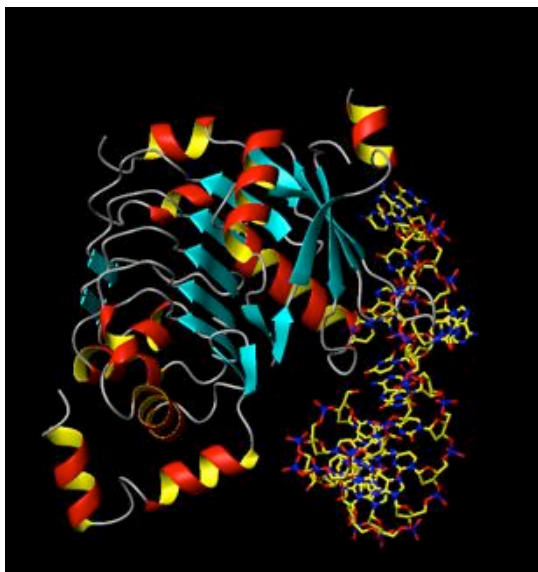
SM proteins-RNA complex, Archaea, Toro et al, EMBO J (2001)



SM protein-RNA complex

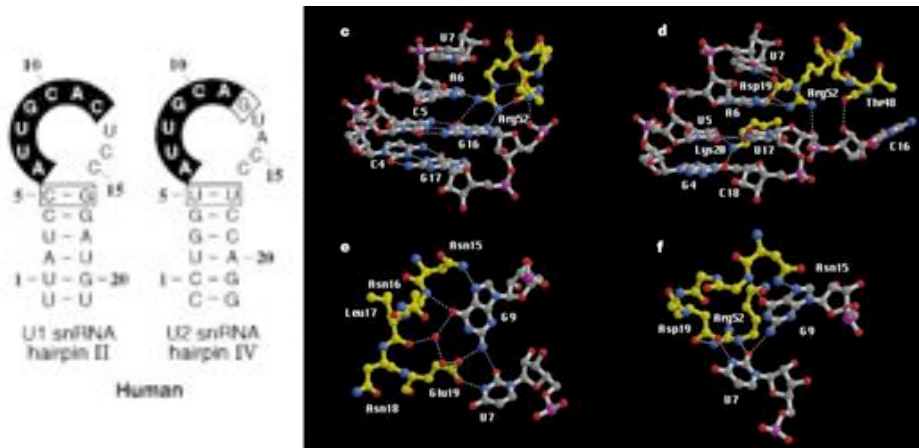


U2A-U2B''-U2snRNA stem-loop IV



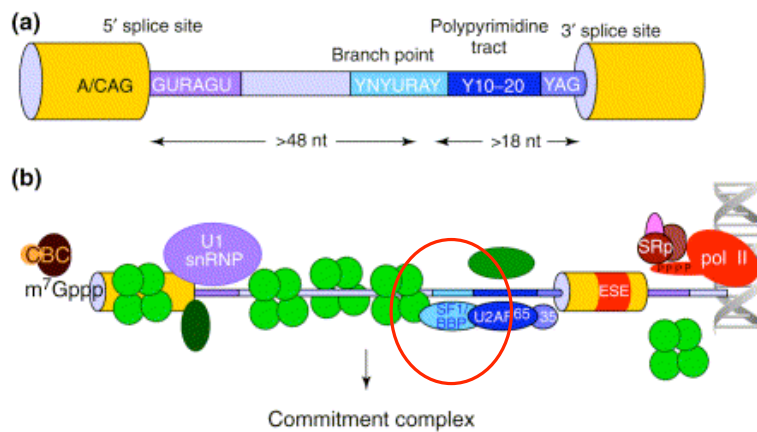
Price et al, Nature (1998)

U2A-U2B''-U2snRNA stem-loop IV

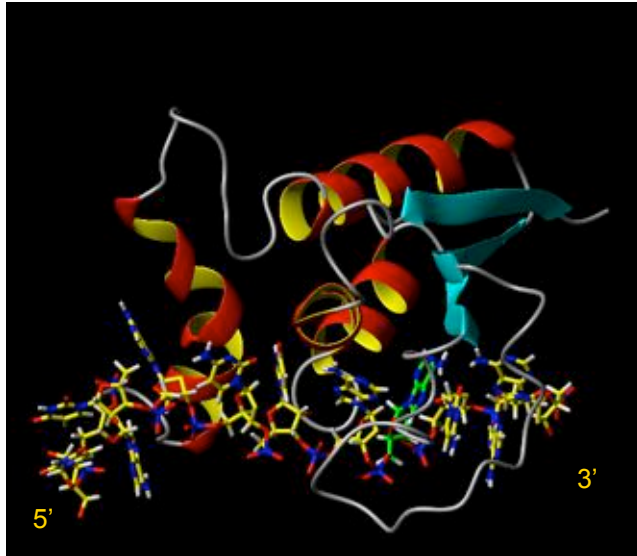


Price et al, Nature (1998)

The commitment complex

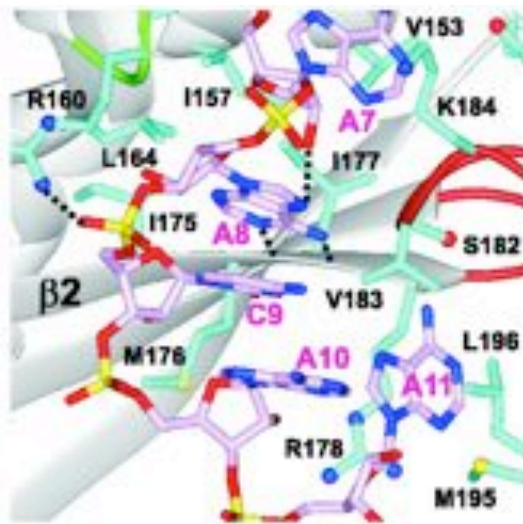


SF1-branch point complex

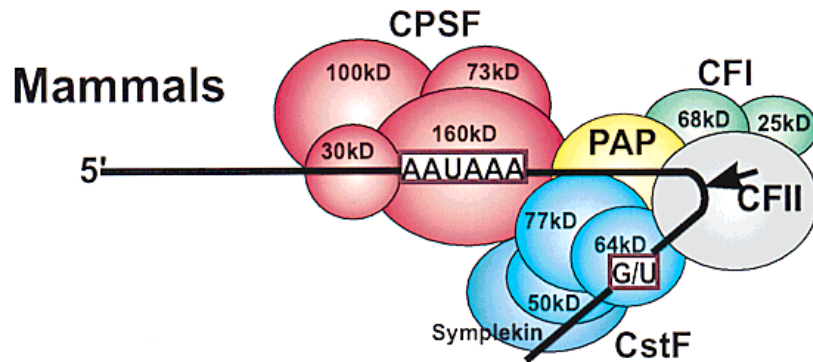


Liu et al, Science (2001)

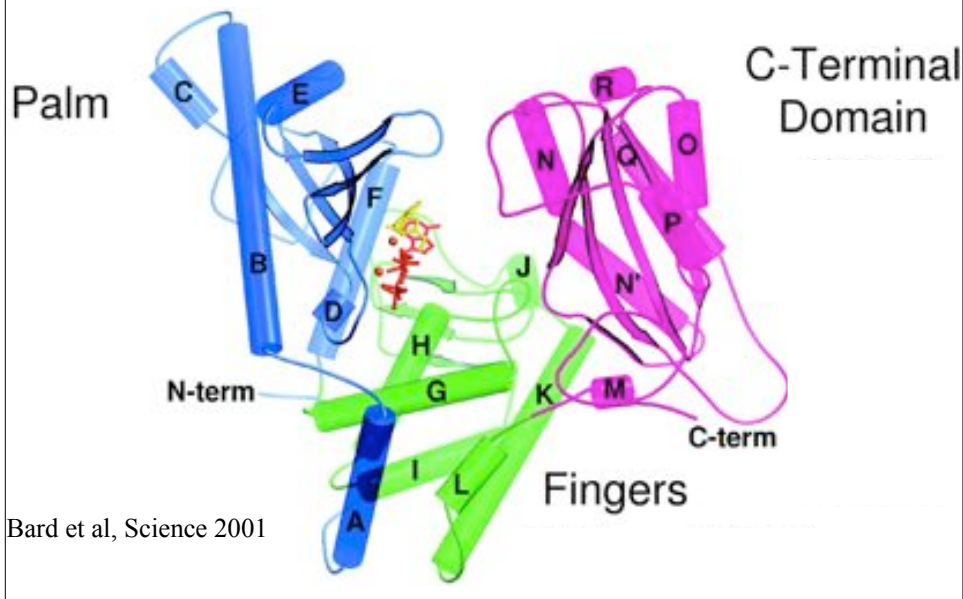
SF1-branch point (A8) complex

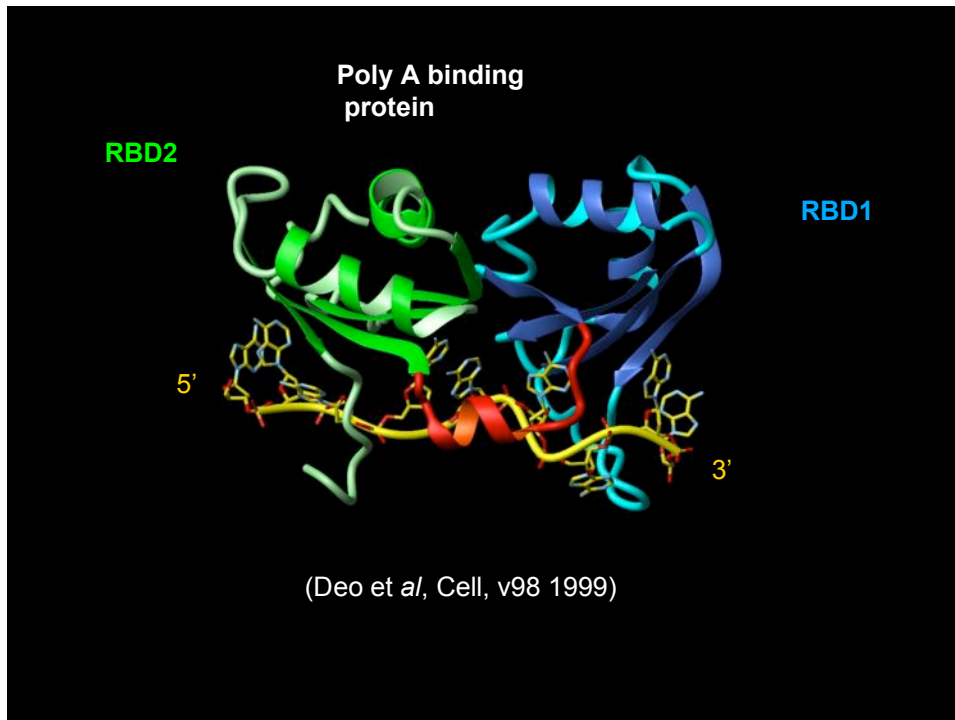


3' end processing Cleavage and polyadenylation



Yeast PolyA Polymerase-dATP-dATP complex



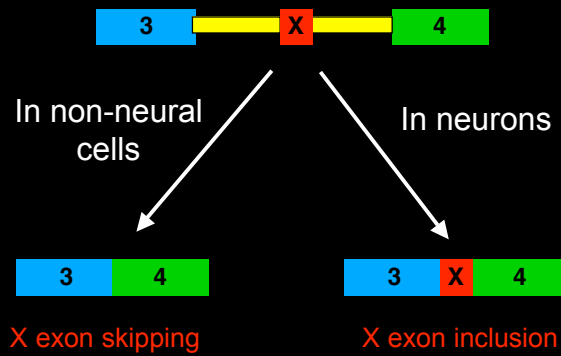


Protein-RNA structures of the regulated mRNA processing machinery

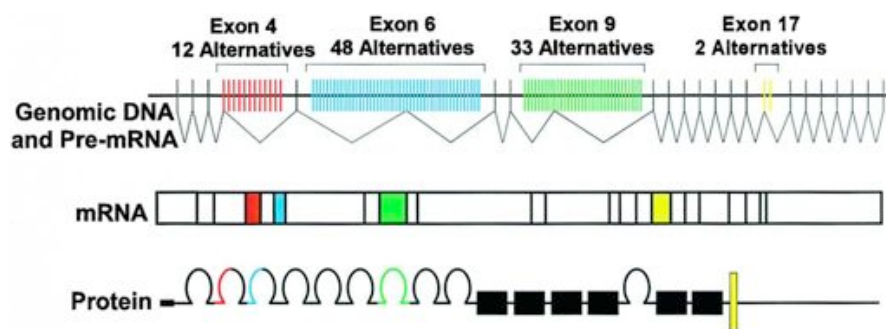
Post-transcriptional gene regulation

Unique to each gene

Alternative splicing

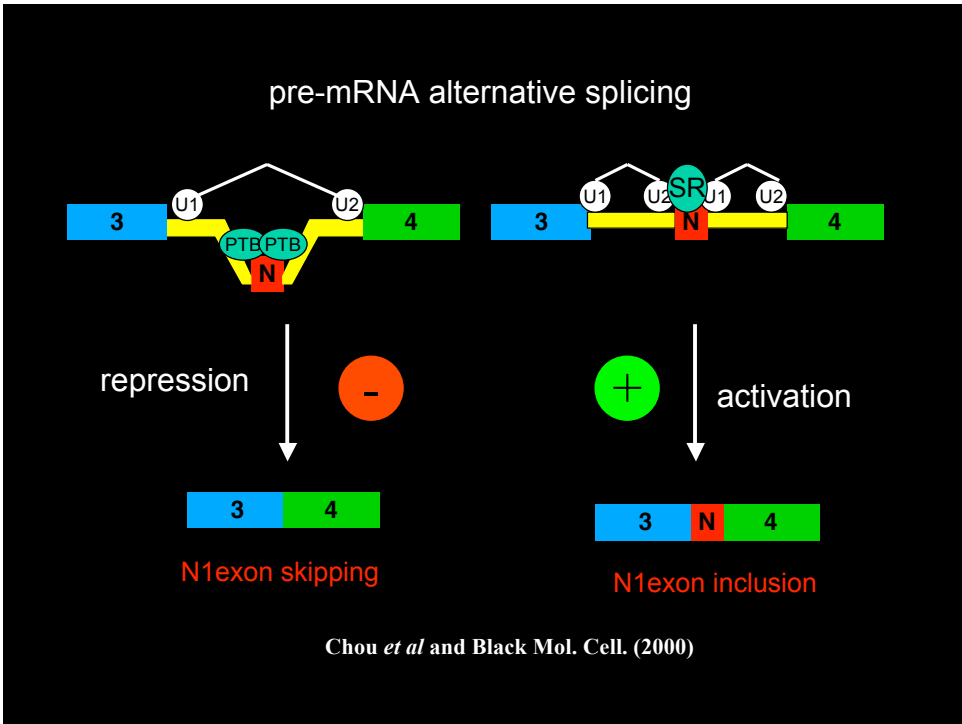
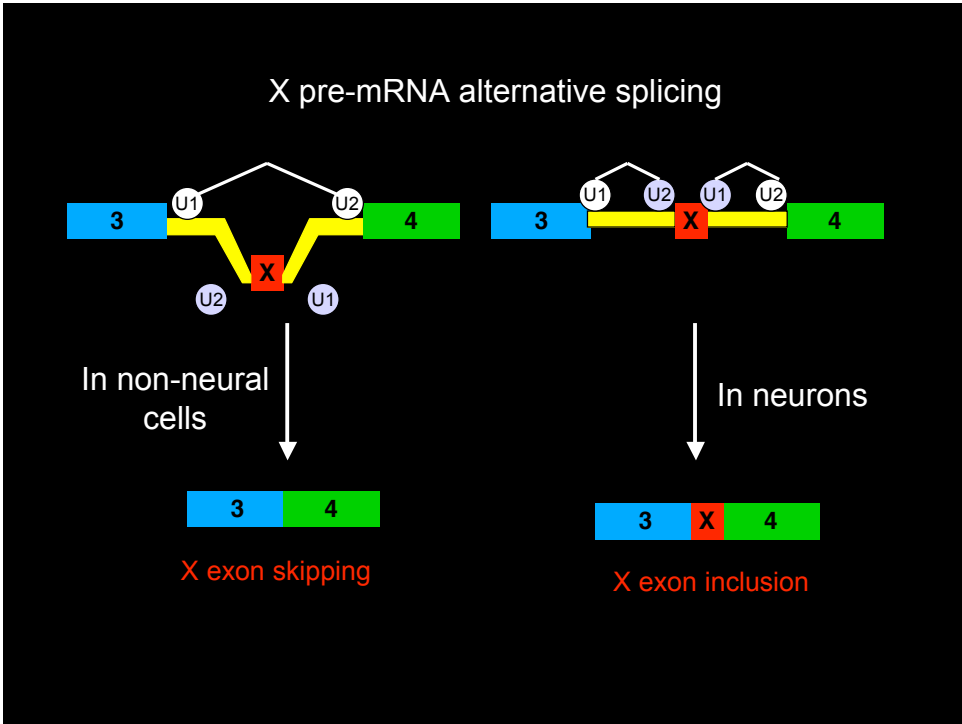


Alternative-splicing of the DSCAM gene

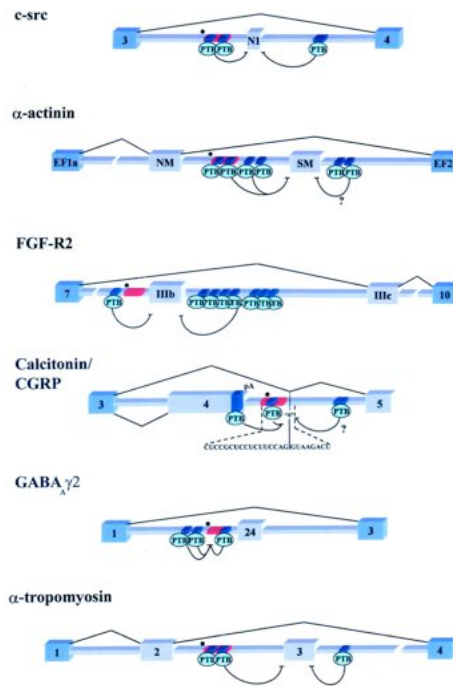
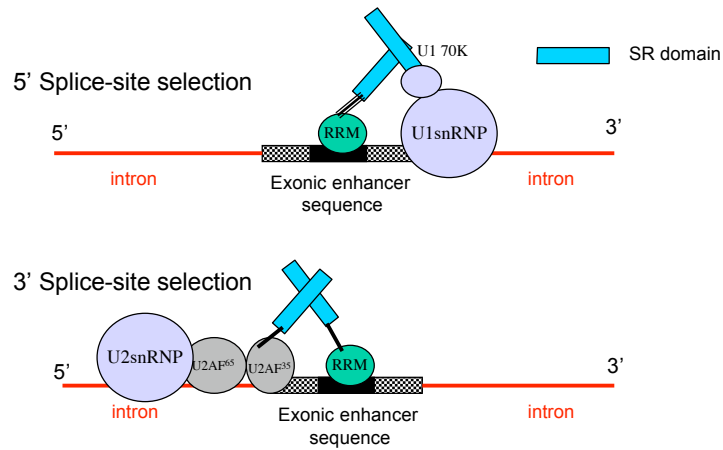


Can produce up to **38016** different protein isoforms

From Black D.L. *Cell* (2000), v103 p367



Exon definition by SR proteins +



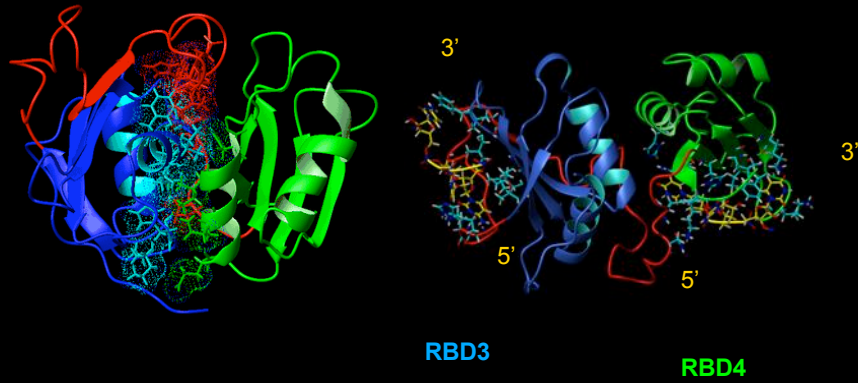
PTB is a general Splicing repressor



■ Pyr tract
■ Pyr tract near Branch point

Wagner et al (2001)
Mol Cell Biol **21**, 3281 - 3288

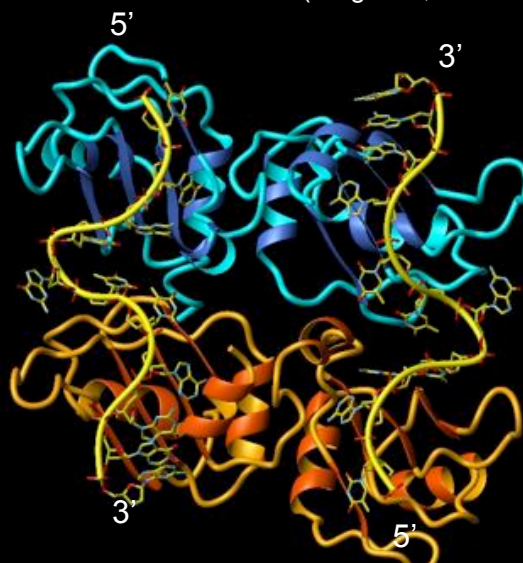
Model for splicing repression by PTB



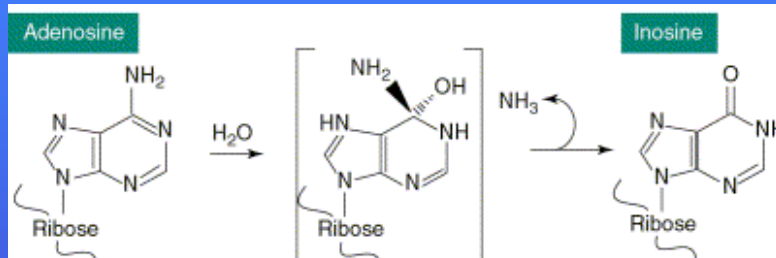
Splicing repression

hnRNPA1- DNA

(Ding et al, Gene & Dev, 1999)



RNA editing by adenine deamination



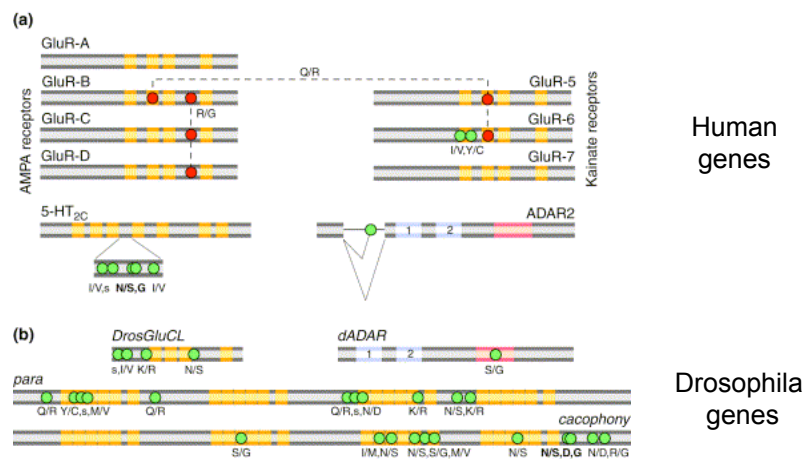
A



I

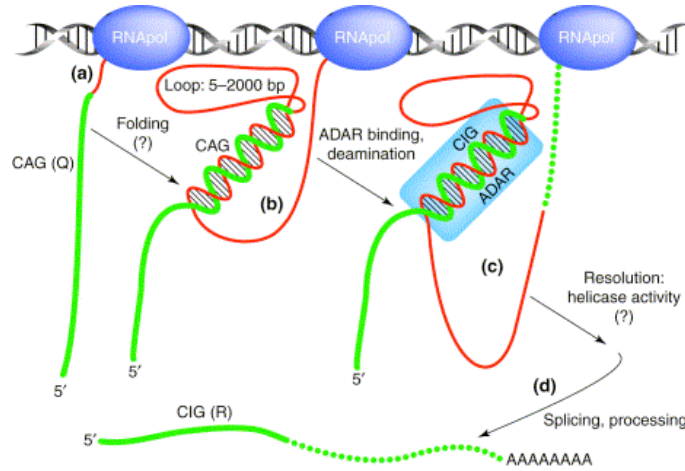
read as G

Pre-mRNA editing by Adenosine deamination



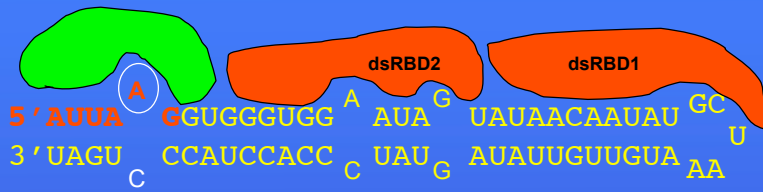
From Reenan *Trends in Genetics* (2001), v17 p53

Editing mechanism by ADAR



From Reenan *Trends in Genetics* (2001), v17 p53

GluR-B pre-mRNA



Arg (**AGG**) to Gly (**GGG**)

ADAR2



RNA binding domain

Deaminase domain

Drosophila Paralytic gene

13 alternative exons

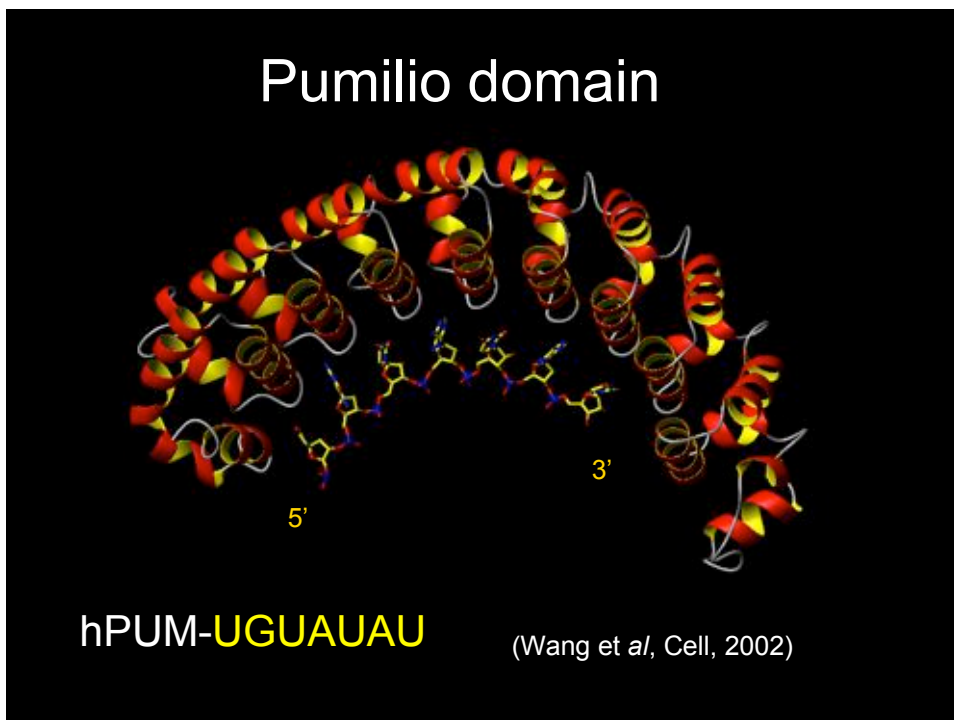
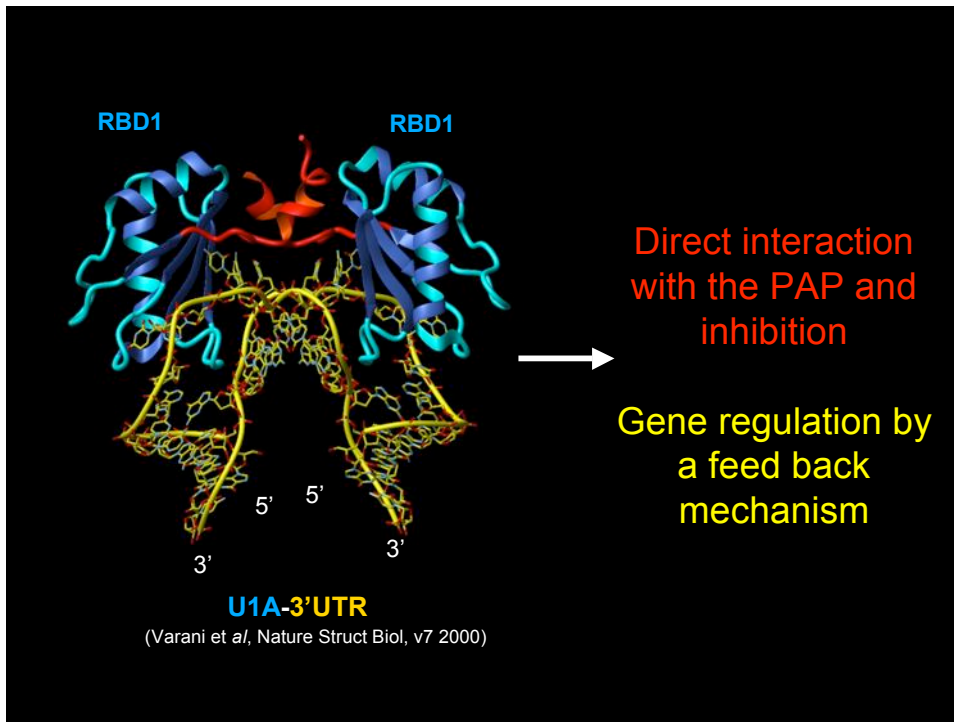
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11 RNA editing sites

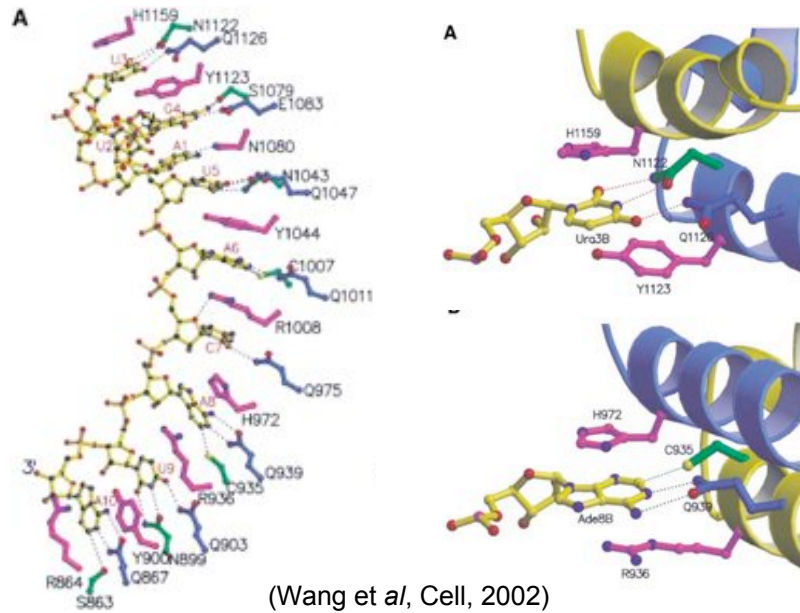
=

> 1 000 000 potential isoforms

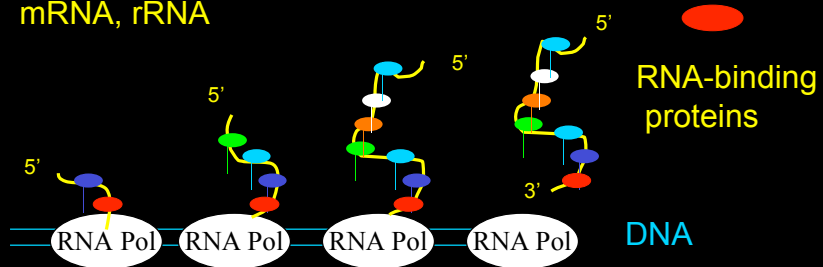
Gene regulation at the 3'end



Pumilio domain



mRNA, rRNA



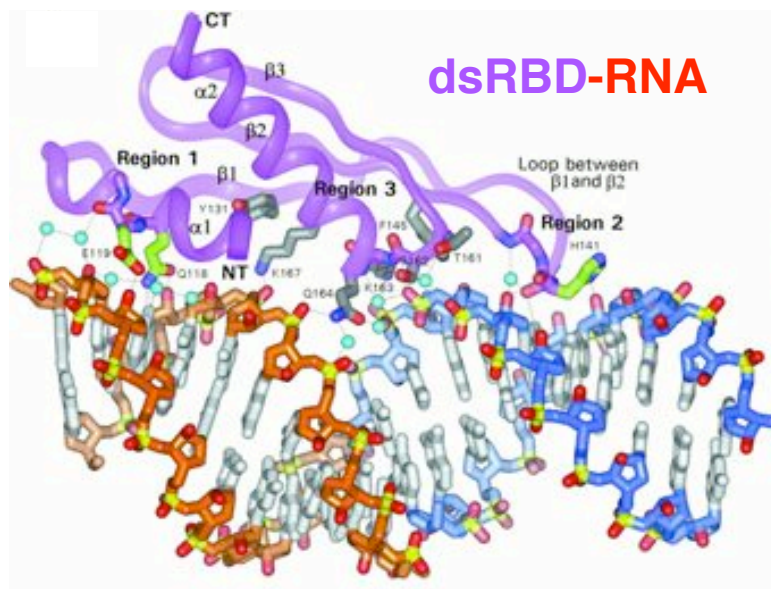
protection, folding (chaperone), gene regulation

RNA binding specificity

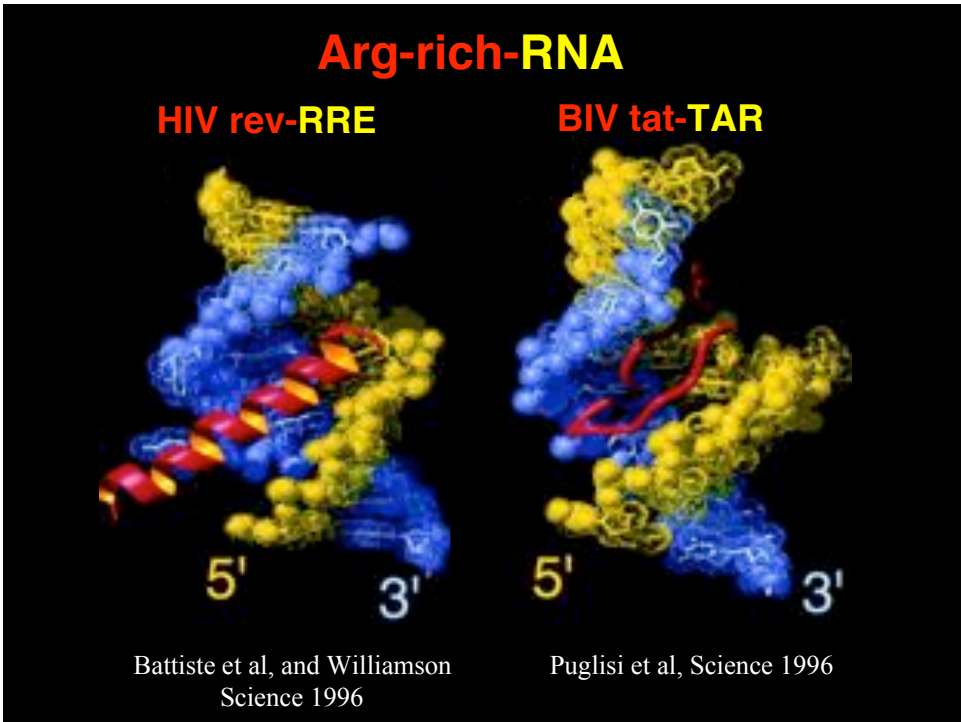
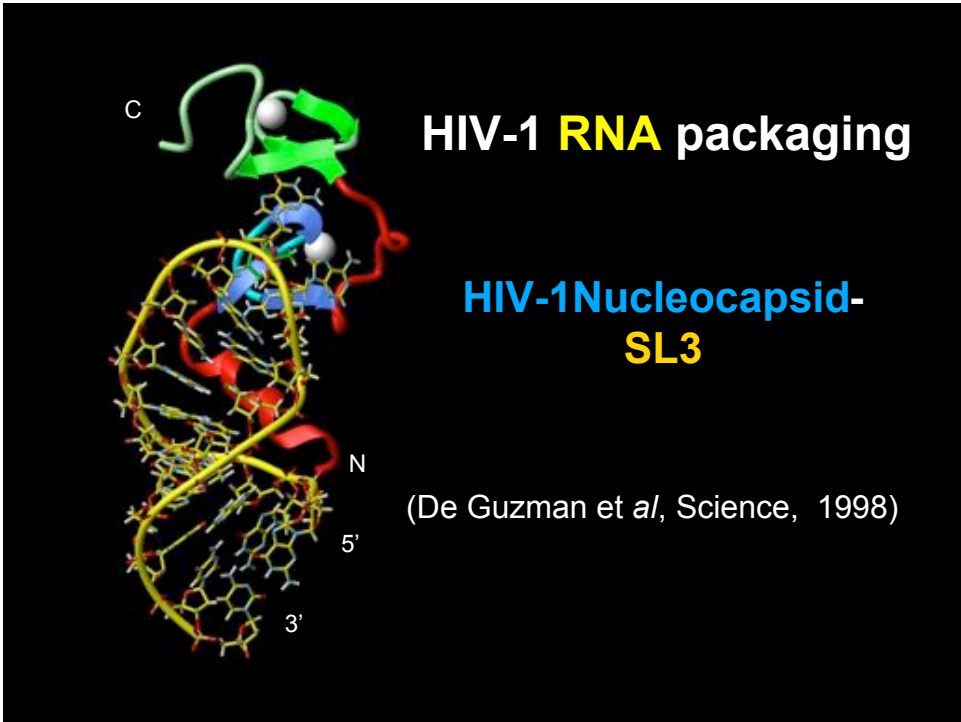
RNA binding proteins: multidomain protein



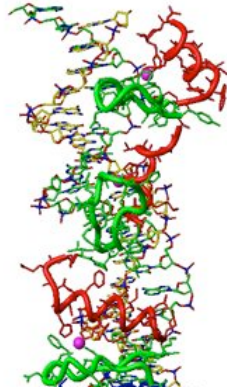
| | |
|--------------|--------------|
| RGG | RBD/RRM/RNP |
| (Gar) | KH, Sam |
| SR | dsRBD |
| Dimerisation | Arg-rich |
| | Zinc knuckle |
| | Zinc finger |



Ryter and Schultz, Embo J, 1998

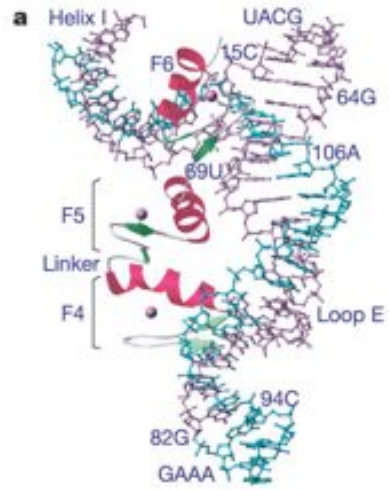


Zinc finger-DNA



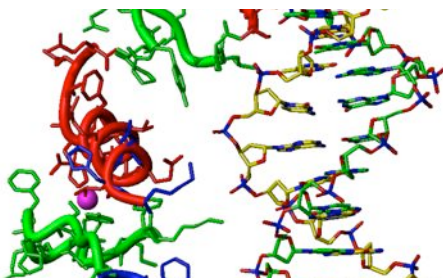
(Nolte et al, PNAS , 1998)

Zinc finger-RNA



(Lu et al, Nature , 2003)

Zinc finger4-DNA



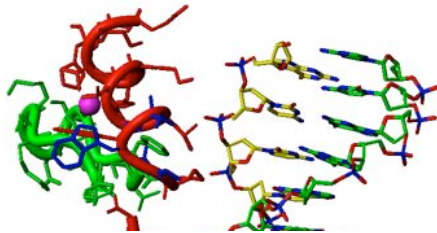
(Nolte et al, PNAS , 1998)

Zinc finger4-RNA



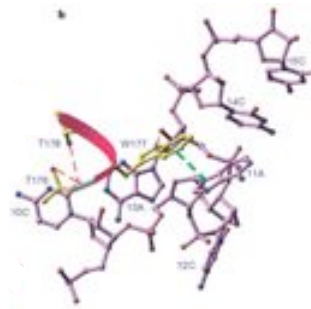
(Lu et al, Nature , 2003)

Zinc finger6-DNA



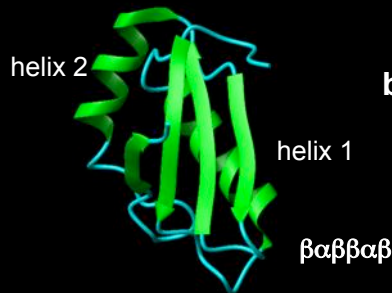
(Nolte et al, PNAS , 1998)

Zinc finger6-RNA

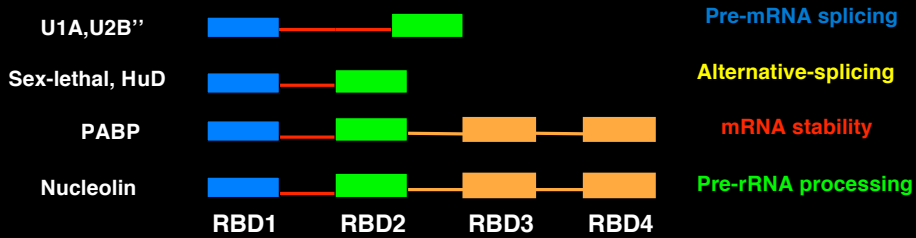


(Lu et al, Nature , 2003)

RNA Binding Domain or RNP domain



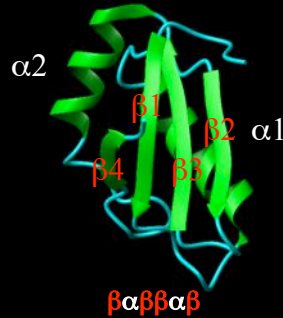
The most common RNA binding modules found in **224** proteins (**324** modules) (**0.5-1%** of the genes)



RNA Binding Domain or RNP domain

75-85 residue long

- $\beta 1$ U (F/Y) U * N L
- $\alpha 1$ * * * L * * * F
- $\beta 2$ G * U * * Z * U
- $\beta 3$ (R/K) G (F/Y) (A/G) (F/Y) V * F
- $\alpha 2$ Z * * A U * *
- $\beta 4$ G * U * U * *



U hydrophobic
Z non charged
* any residue

Nucleolin, the most abundant nucleolar protein

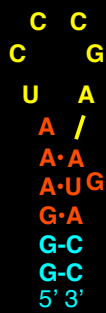
Interaction with U3snoRNA
and ribosomal proteins

NRE RNA binding

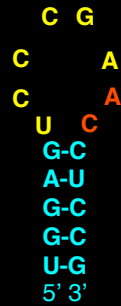
Interaction with
ribosomal proteins



Nucleolin RNA Targets



sNRE
5-20nM



B1
10-50nM
(5'ETS)
Mouse

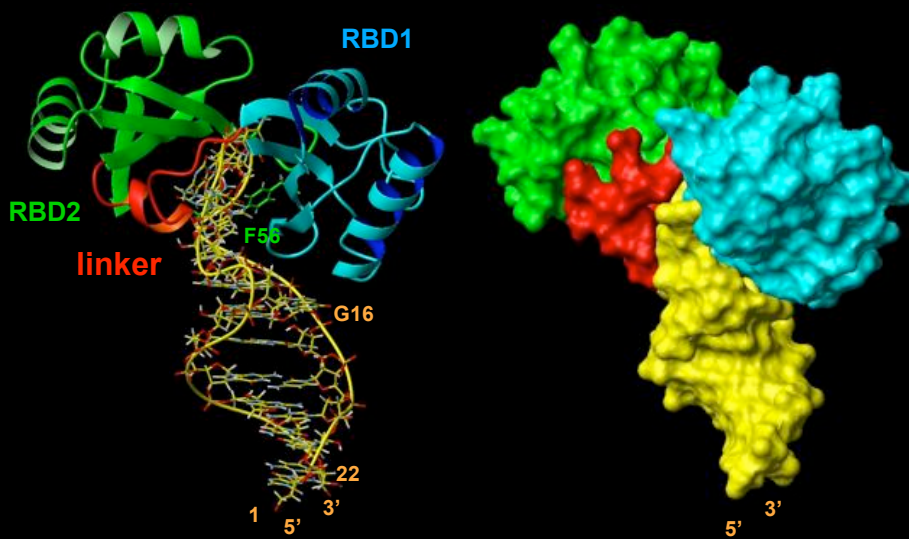


B2
50-100nM
(5'ETS)
Mouse

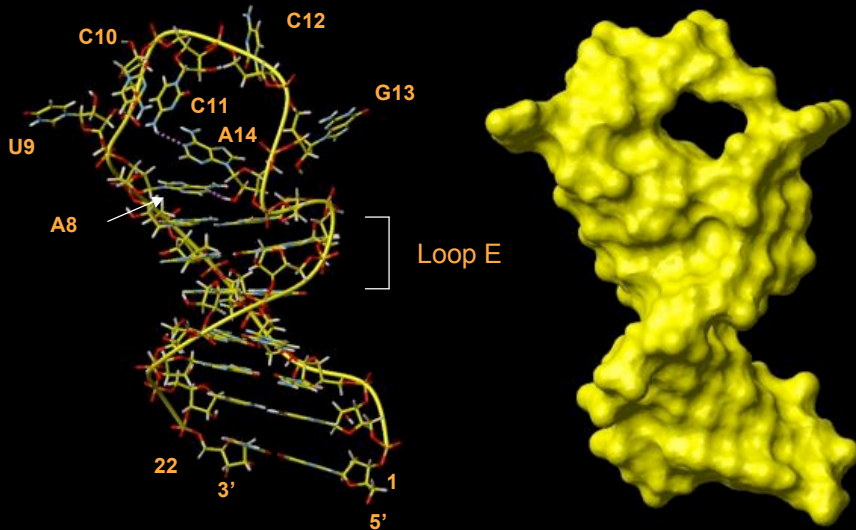


Consensus NRE

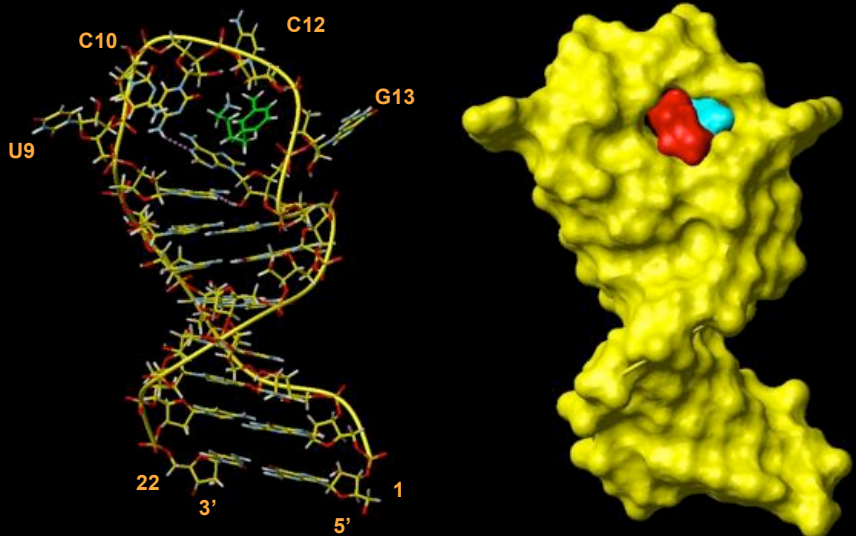
RBD2-RNA-RBD1 "sandwich"



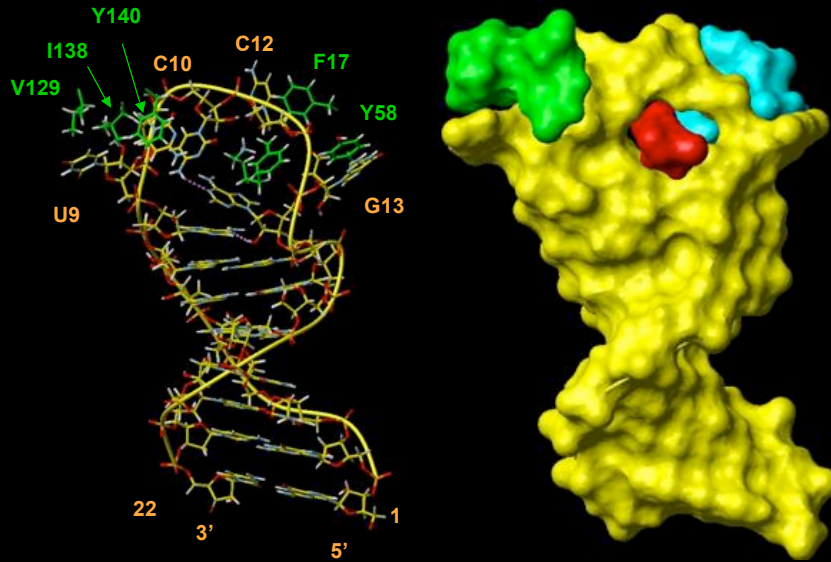
Structure of the RNA in complex



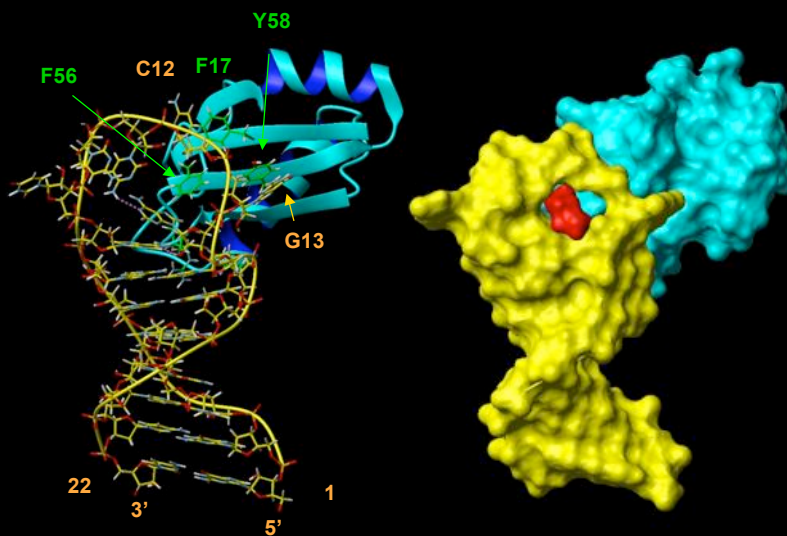
F56 and K94 insert in the loop



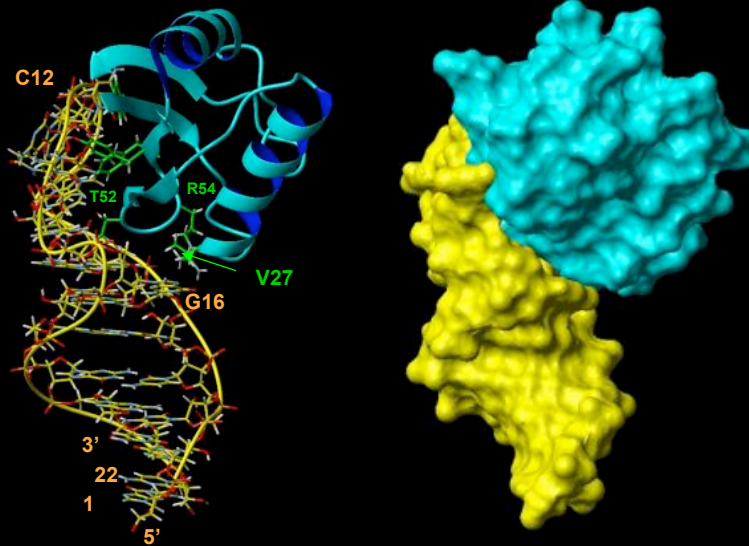
Protein side-chain-RNA base stacking



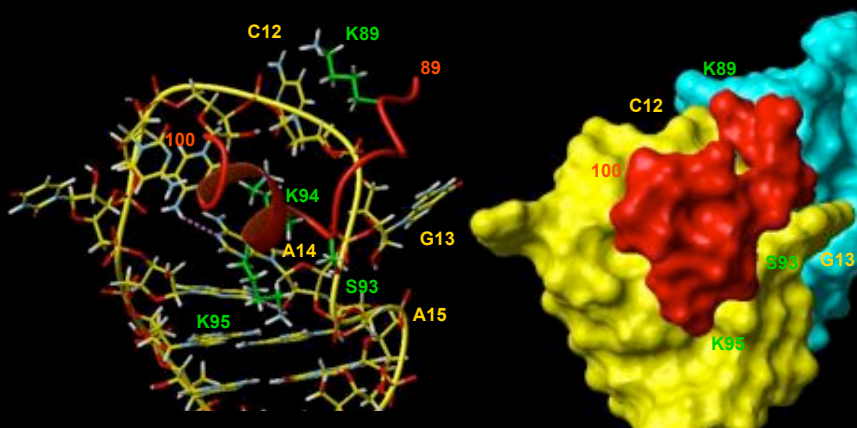
RBD1-RNA interactions



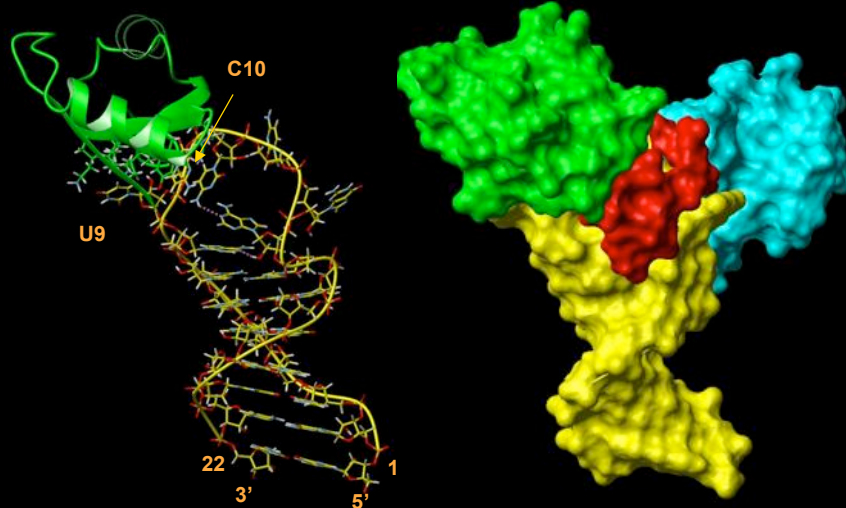
RBD1-RNA stem interactions



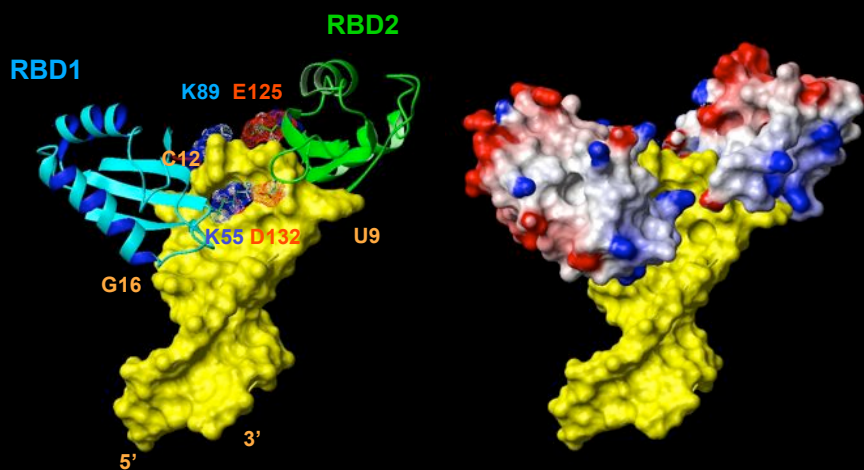
linker-RNA interactions



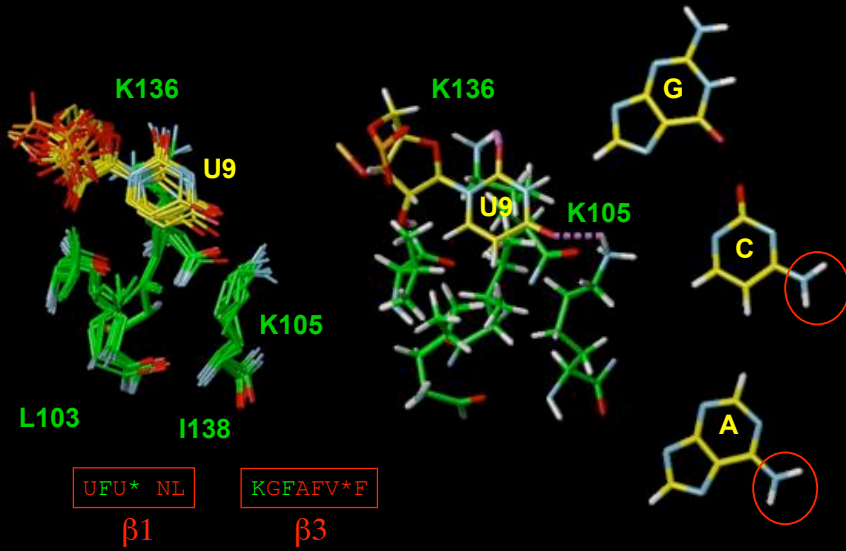
RBD2-RNA interactions



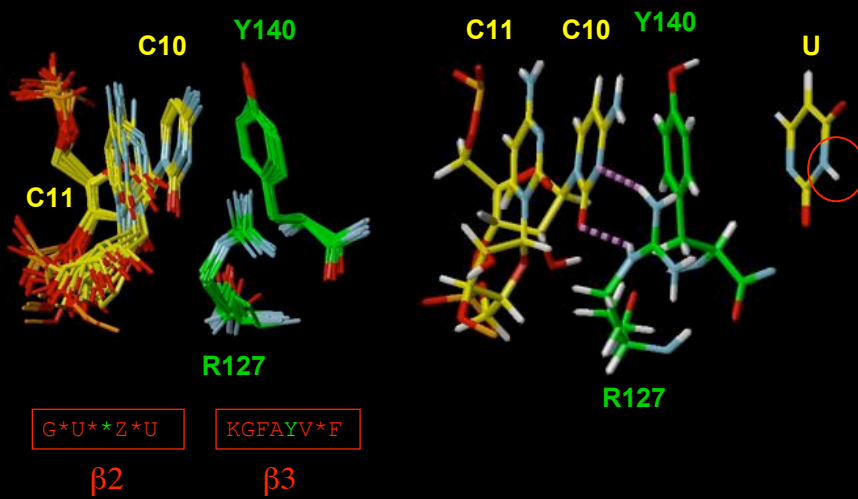
RBD1-RBD2 interactions



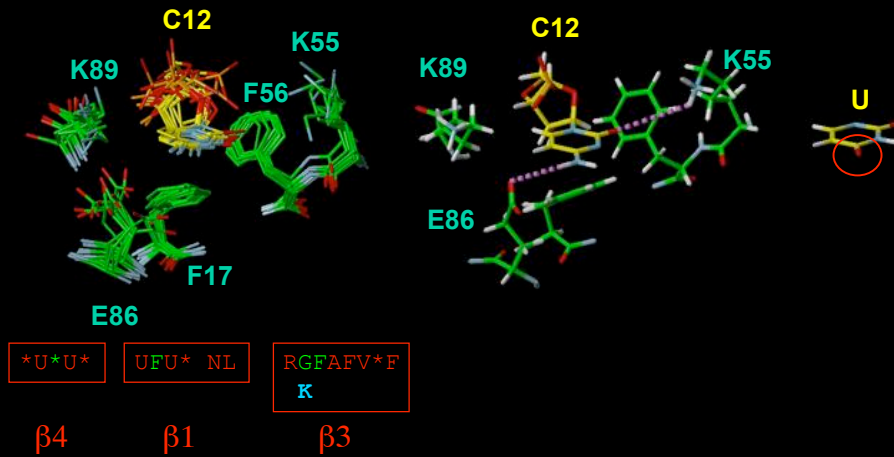
Sequence specificity: **U/G**CCCCGA



Sequence specificity: **U**CCCGA



Sequence specificity: UCCCGA



Sequence specificity: UCCCGA

