CSEP 590 B
Computational Biology

RNA: Function, Secondary Structure
Prediction, Search, Discovery

GENOME 541 Syllabus

"… *protein* and *DNA* sequence analysis … to determine the "periodic table of biology," i.e., the list of *proteins* …, which can be regarded as the first stage in…"

No mention of RNA…

The Message

Cells make lots of ~~RNA~~ *noncoding* RNA

Functionally important, functionally diverse

Structurally complex

New tools required

alignment, discovery, search, scoring, etc.

Rough Outline

Today

- Noncoding RNA Examples
- RNA structure prediction

Next Time

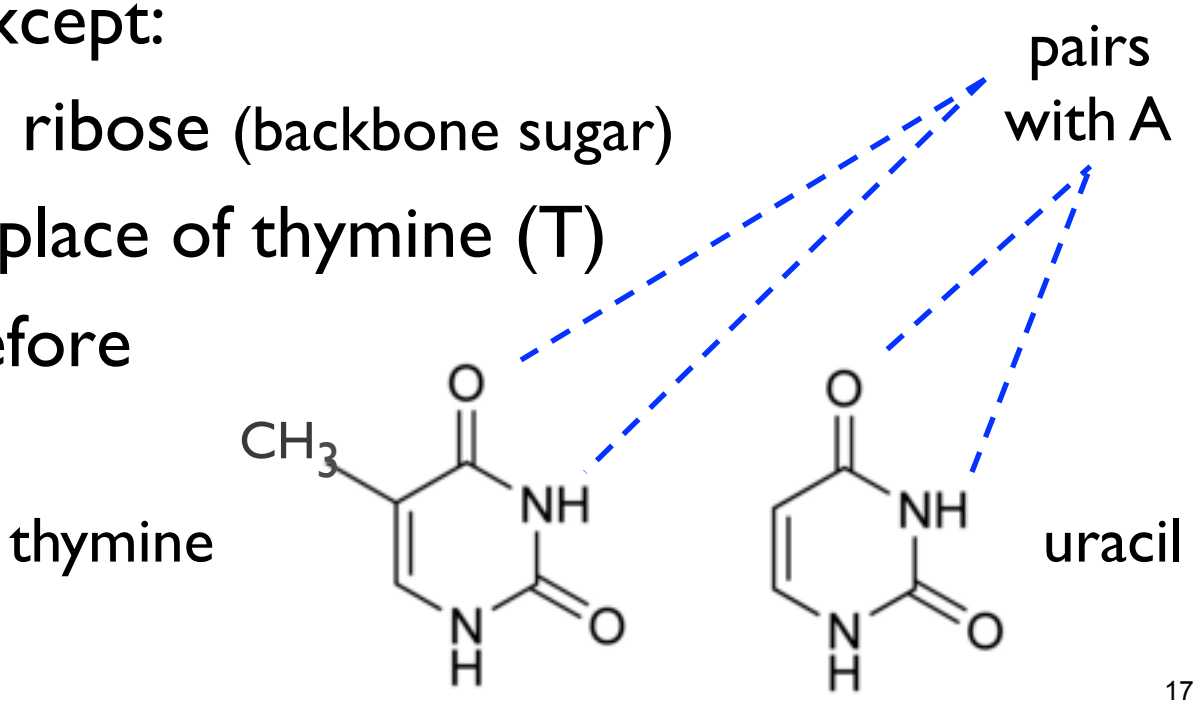
- RNA "motif" models
- Search
- Motif discovery

RNA

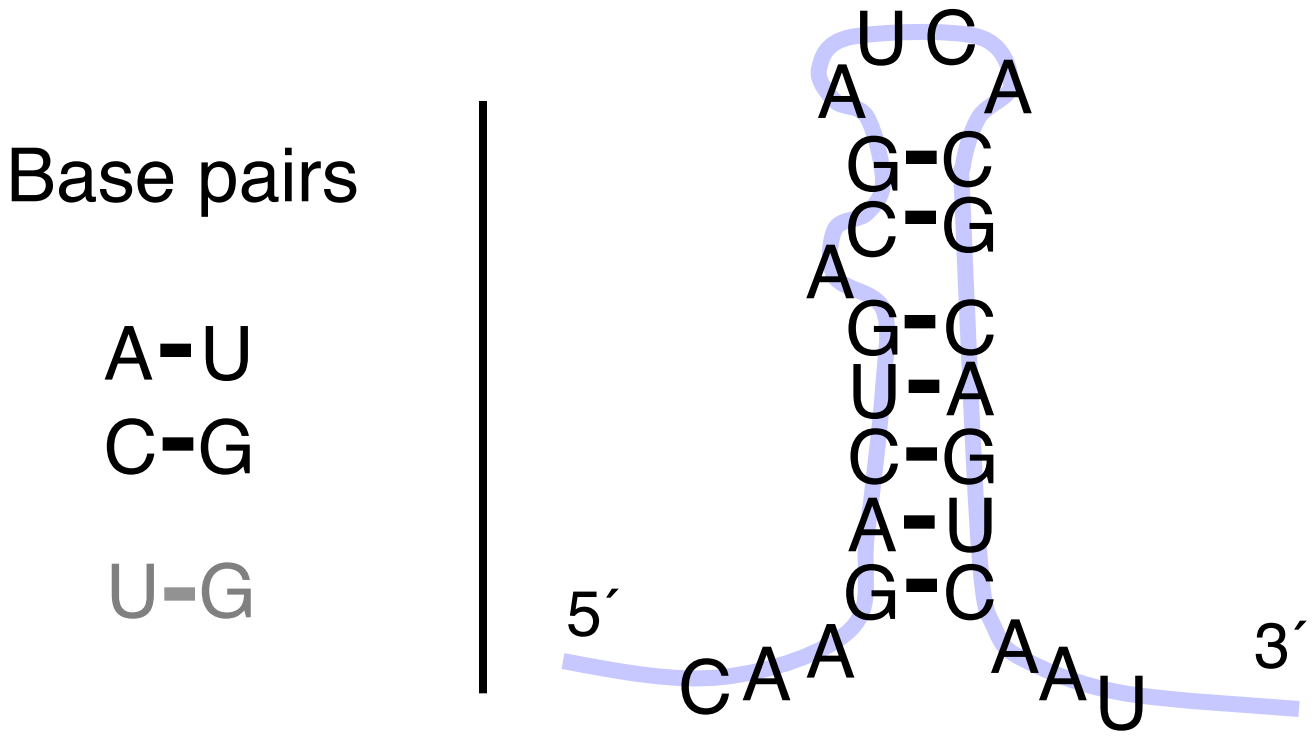
DNA: DeoxyriboNucleic Acid

RNA: RiboNucleic Acid

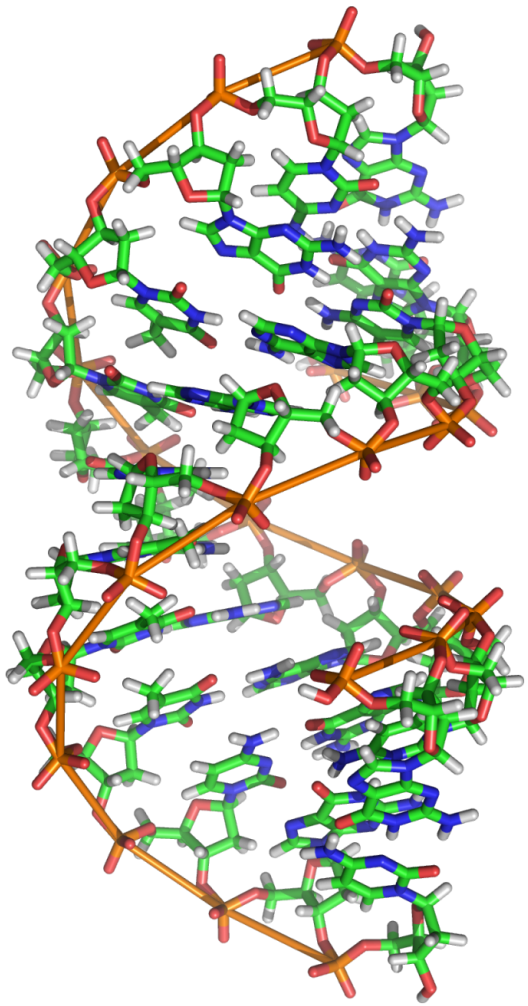
- Like DNA, except:
- Lacks OH on ribose (backbone sugar)
- Uracil (U) in place of thymine (T)
- A, G, C as before



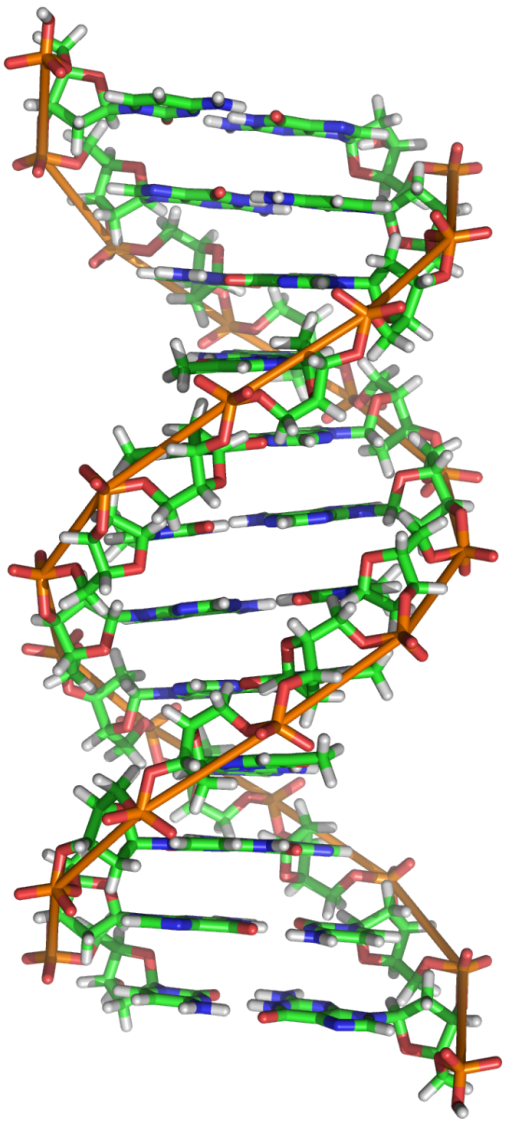
RNA Secondary Structure:
RNA makes helices too



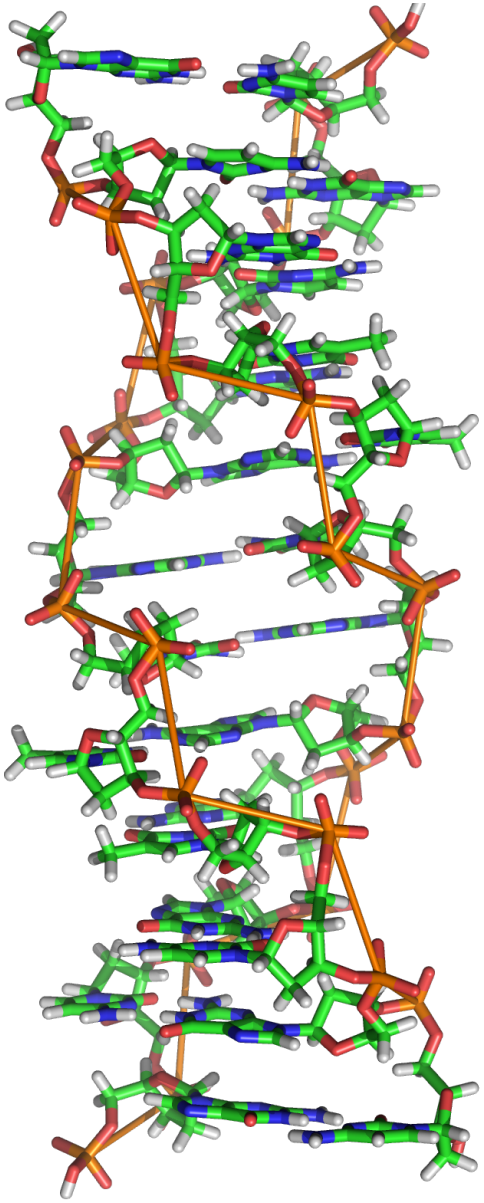
Usually *single* stranded



A
(norm for RNA)



B
(norm for DNA)



Z

http://en.wikipedia.org/wiki/File:A-DNA,_B-DNA_and_Z-DNA.png

NATURE VOL. 227 AUGUST 8 1970

Central Dogma of Molecular Biology

by
FRANCIS CRICK
MRC Laboratory
Hills Road,
Cambridge CB2 2QH

The central dogma of molecular biology deals with the detailed residue-by-residue transfer of sequential information. It states that such information cannot be transferred from protein to either protein or nucleic acid.

"The central dogma, enunciated by Crick in 1958 and the keystone of molecular biology ever since, is likely to prove a considerable over-simplification."

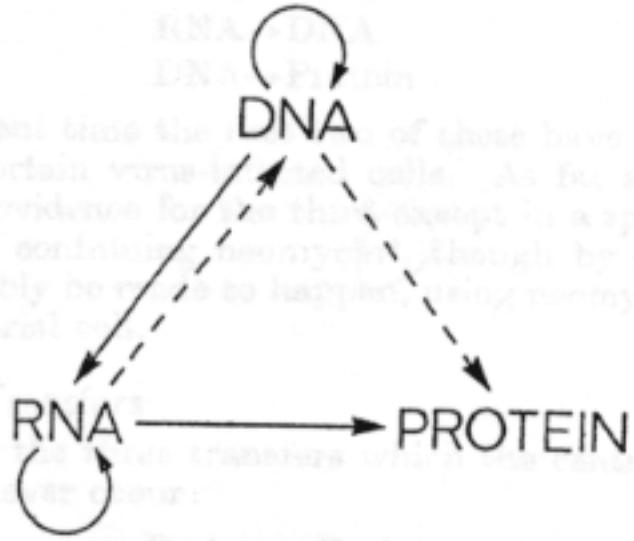


Fig. 2. The arrows show the situation as it seemed in 1958. Solid arrows represent probable transfers, dotted arrows possible transfers. The absent arrows (compare Fig. 1) represent the impossible transfers postulated by the central dogma. They are the three possible arrows starting from protein.

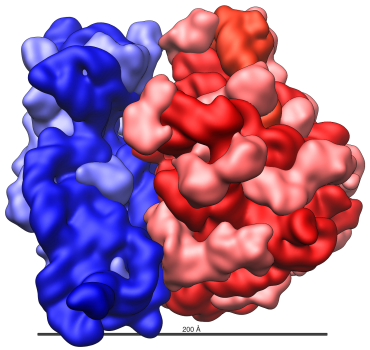
“Classical” RNAs

rRNA - ribosomal RNA (~4 kinds, 120-5k nt)

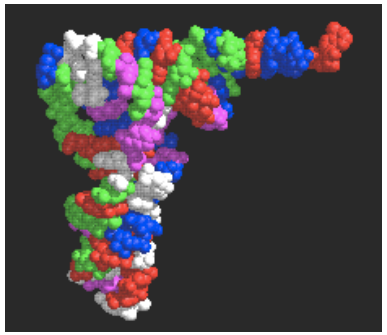
tRNA - transfer RNA (~61 kinds, ~ 75 nt)

RNaseP - tRNA processing (~300 nt)

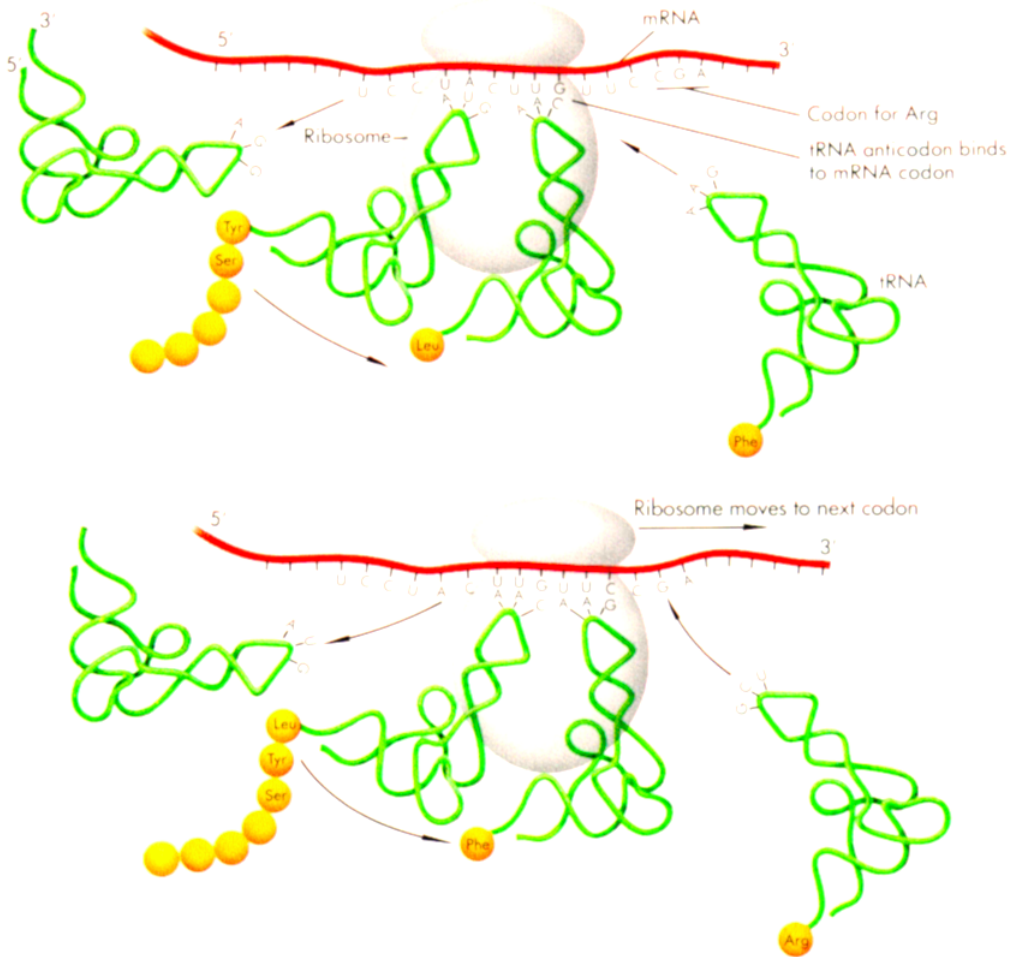
snRNA - small nuclear RNA (splicing: U1, etc, 60-300nt)



a handful of others



Ribosomes



Watson, Gilman, Witkowski, & Zoller, 1992

Ribosomes

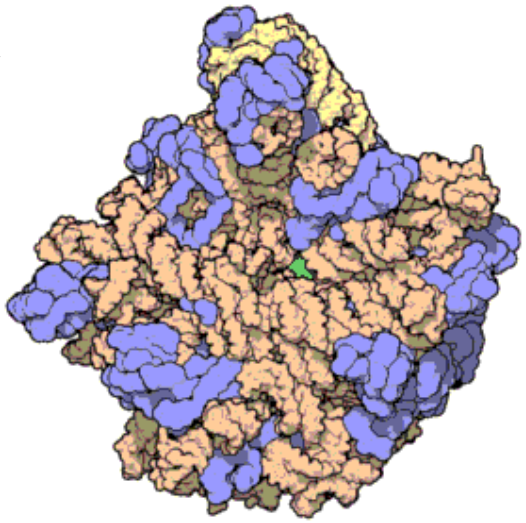
1974 Nobel prize to Romanian biologist George Palade (1912-2008) for discovery in mid 50's

50-80 proteins

3-4 RNAs (half the mass)

Catalytic core is RNA

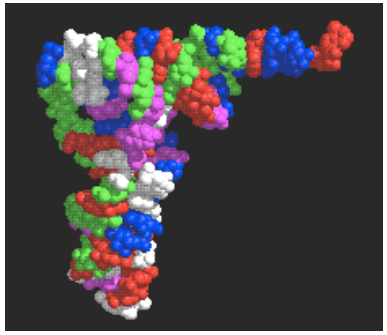
Of course, mRNAs and tRNAs (messenger & transfer RNAs) are critical too



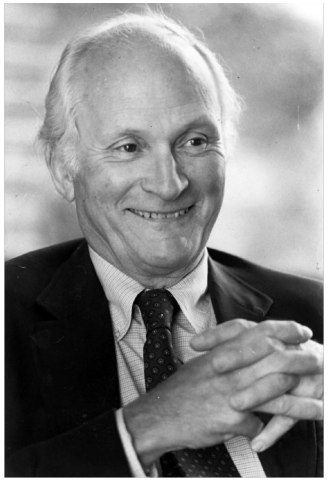
Atomic structure of the 50S Subunit from *Haloarcula marismortui*. Proteins are shown in blue and the two RNA strands in orange and yellow. The small patch of green in the center of the subunit is the active site.
- Wikipedia

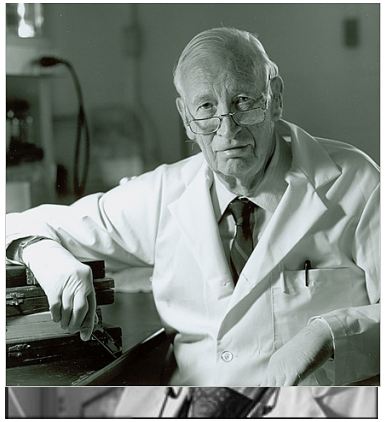
Transfer RNA

The "adapter" coupling mRNA to protein synthesis.



Discovered in the mid-1950s by Mahlon Hoagland (1921-2009, left), Mary Stephenson, and Paul Zamecnik (1912-2009; Lasker award winner, right).





Bacteria

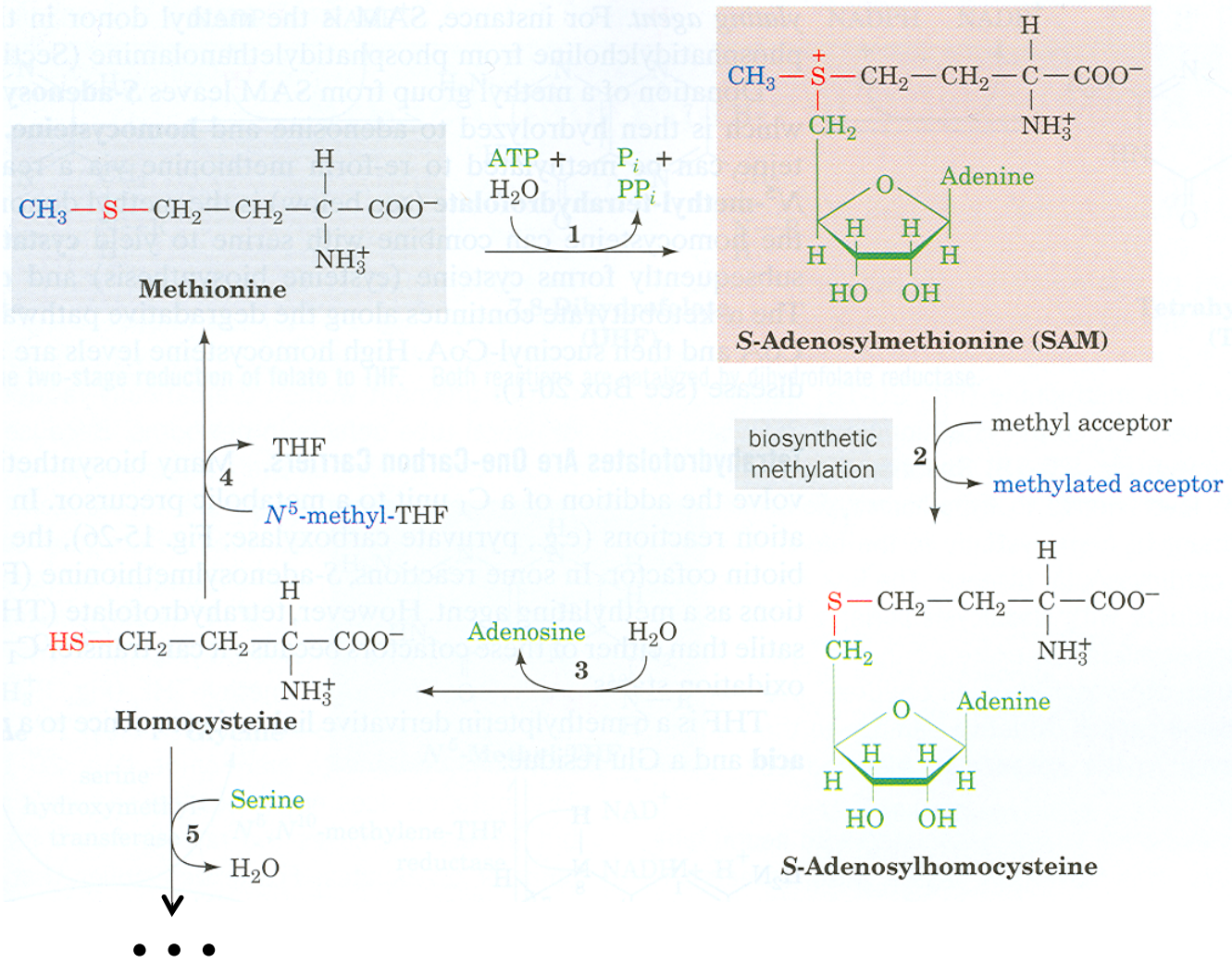
Triumph of proteins

80% of genome is coding DNA

Functionally diverse

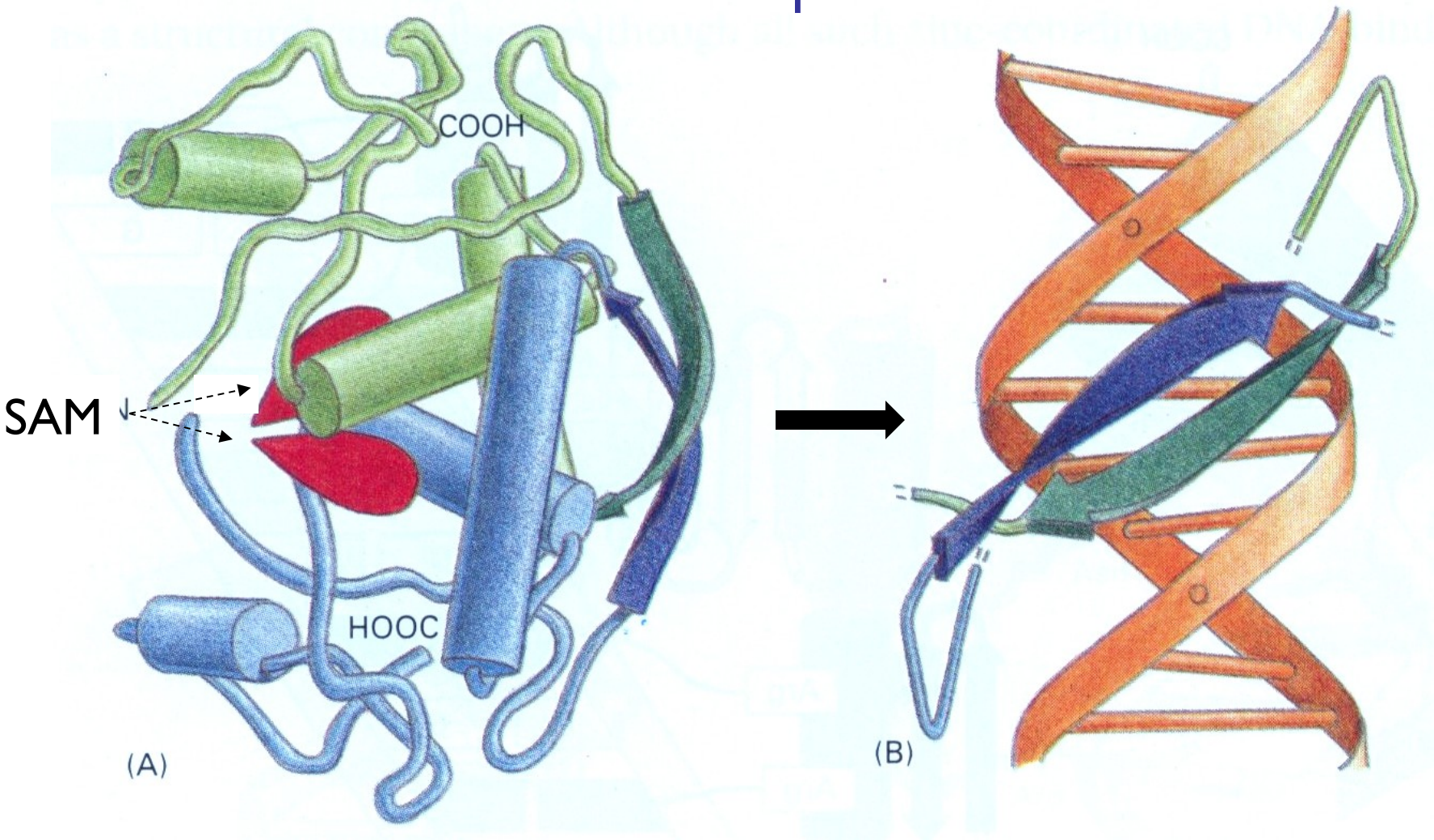
- receptors
- motors
- catalysts
- regulators (Monod & Jakob, Nobel prize 1965)
- …

Proteins Catalyze Biochemistry: Met Pathways



Proteins Regulate Biochemistry:

The MET Repressor



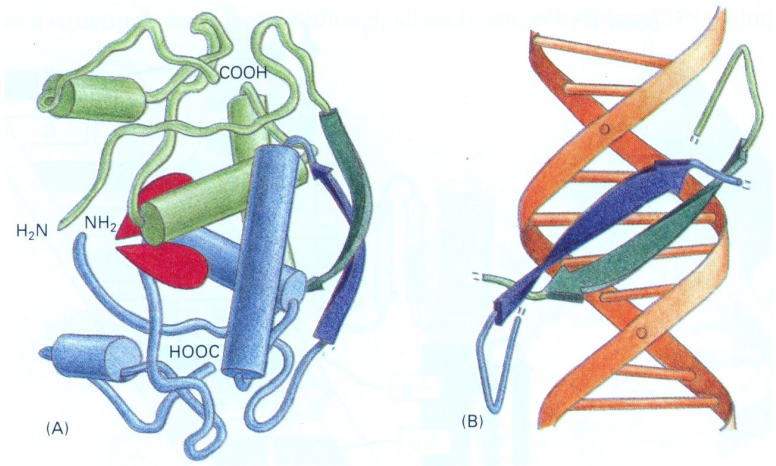
Protein

Alberts, et al, 3e.

DNA

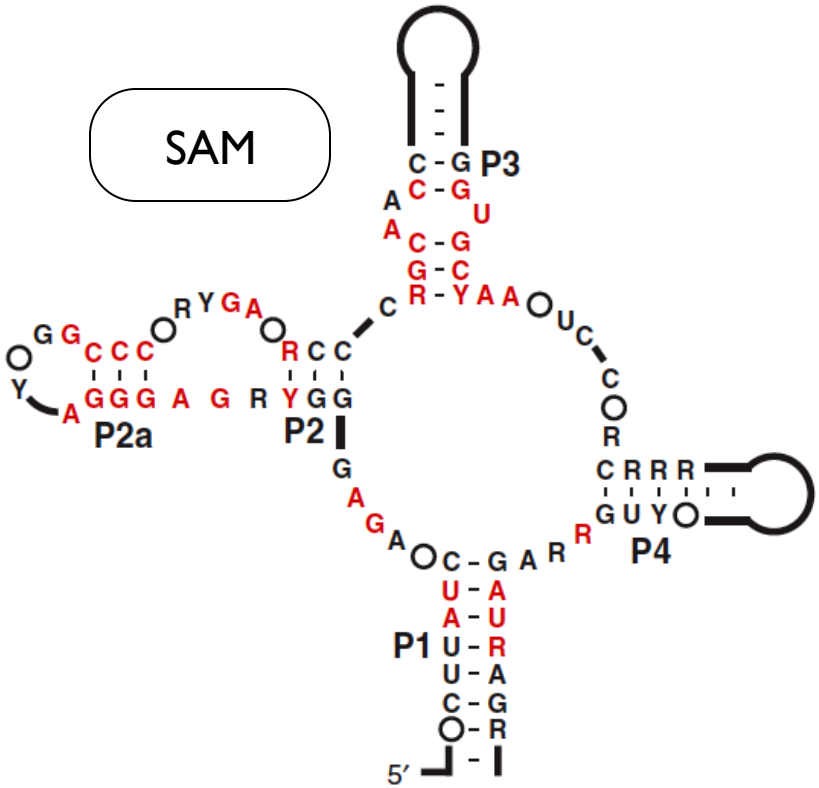
Not the only way!

Alberts, et al, 3e.



Protein way

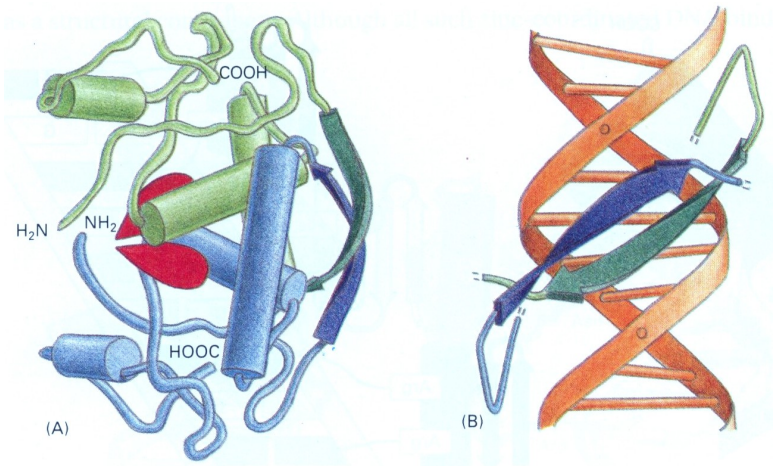
Riboswitch alternative



Grundy & Henkin, Mol. Microbiol 1998
Epshtein, et al., PNAS 2003
Winkler et al., Nat. Struct. Biol. 2003

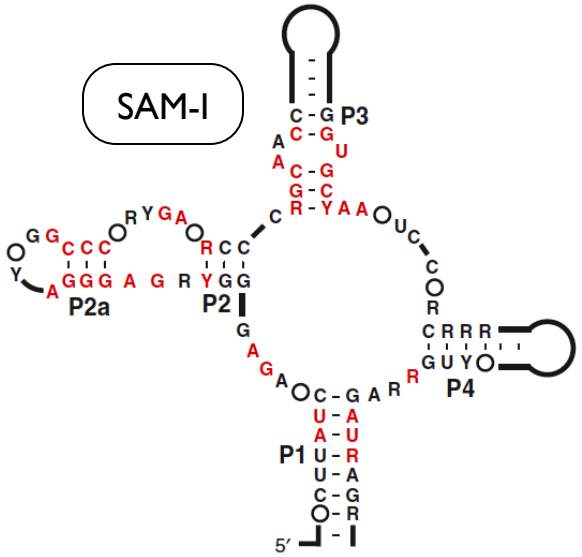
Not the only way!

Alberts, et al, 3e.

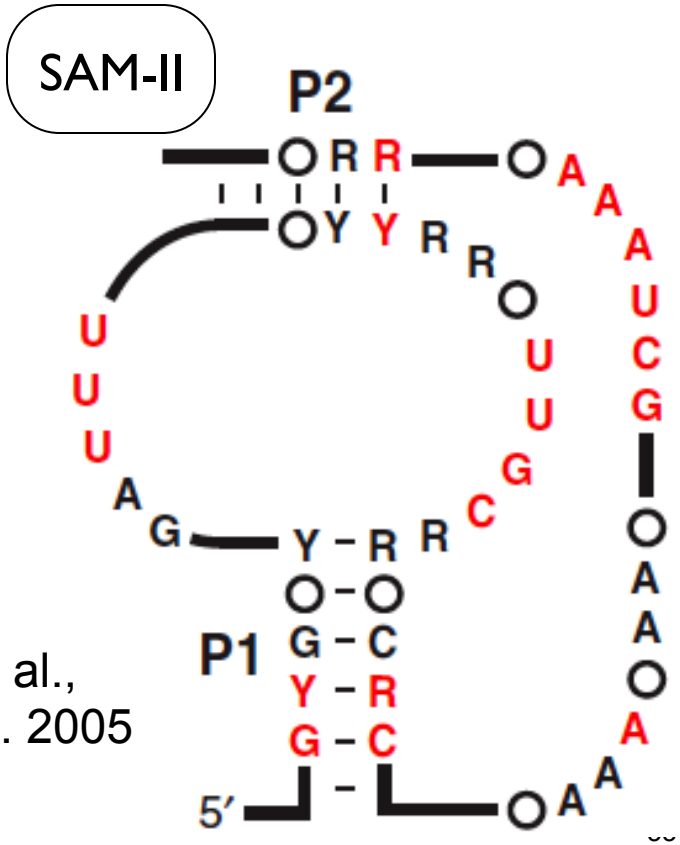


Protein way

Riboswitch alternatives



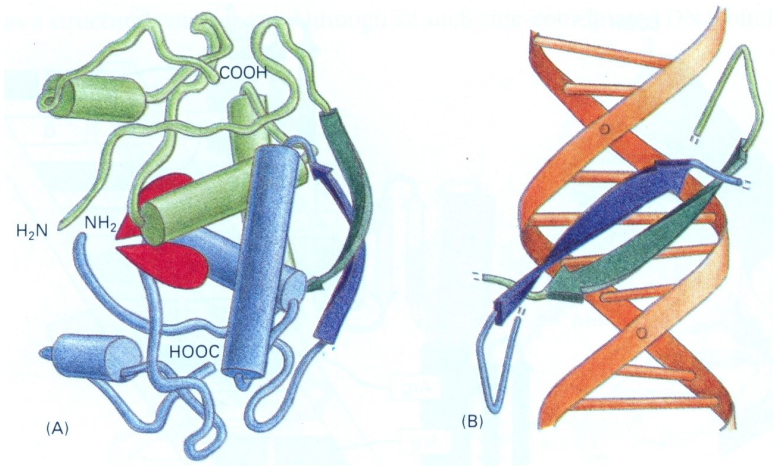
Grundy, Epshtein, Winkler et al., 1998, 2003



Corbino et al., Genome Biol. 2005

Not the only way!

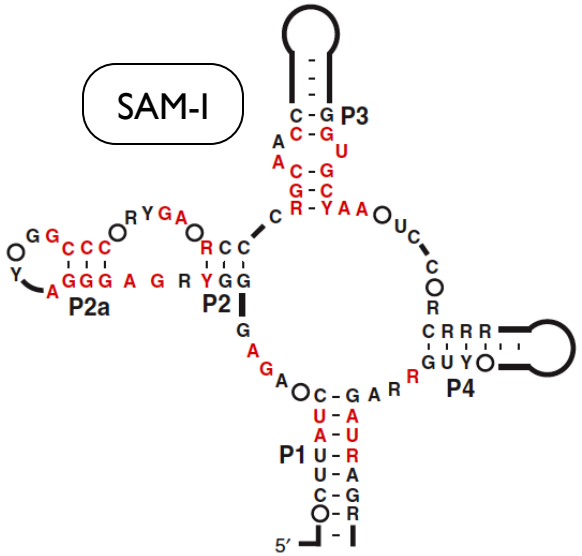
Alberts, et al, 3e.



Protein way

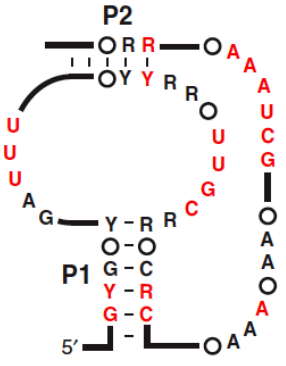
Riboswitch alternatives

SAM-I



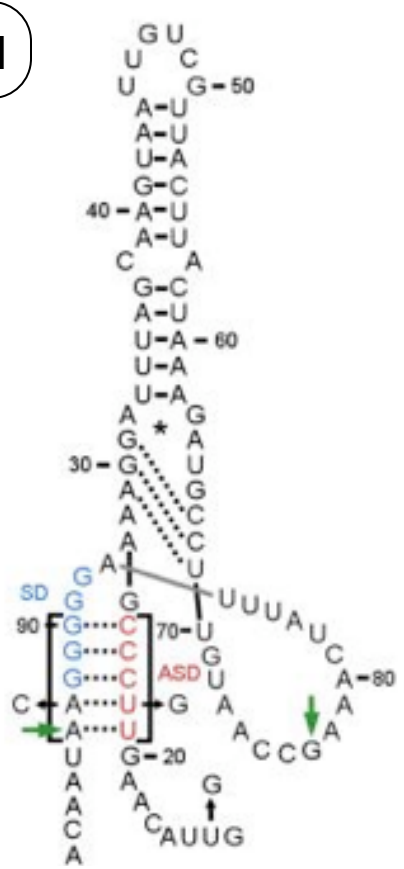
Grundy, Epshtein, Winkler et al., 1998, 2003

SAM-II



Corbino et al., Genome Biol. 2005

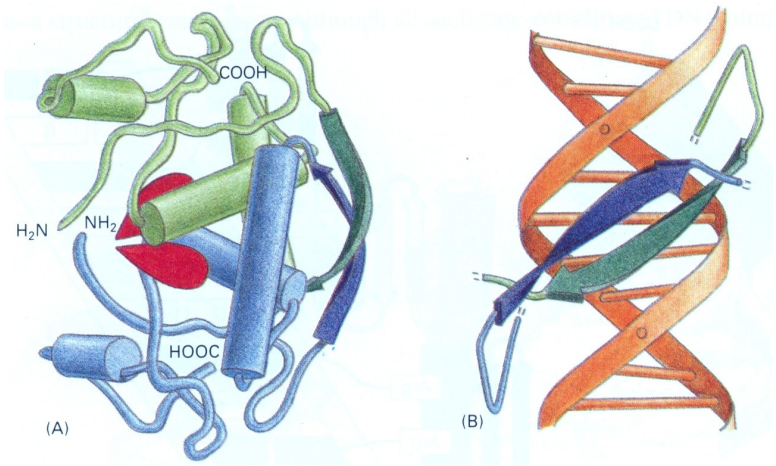
SAM-III



Fuchs et al., NSMB 2006

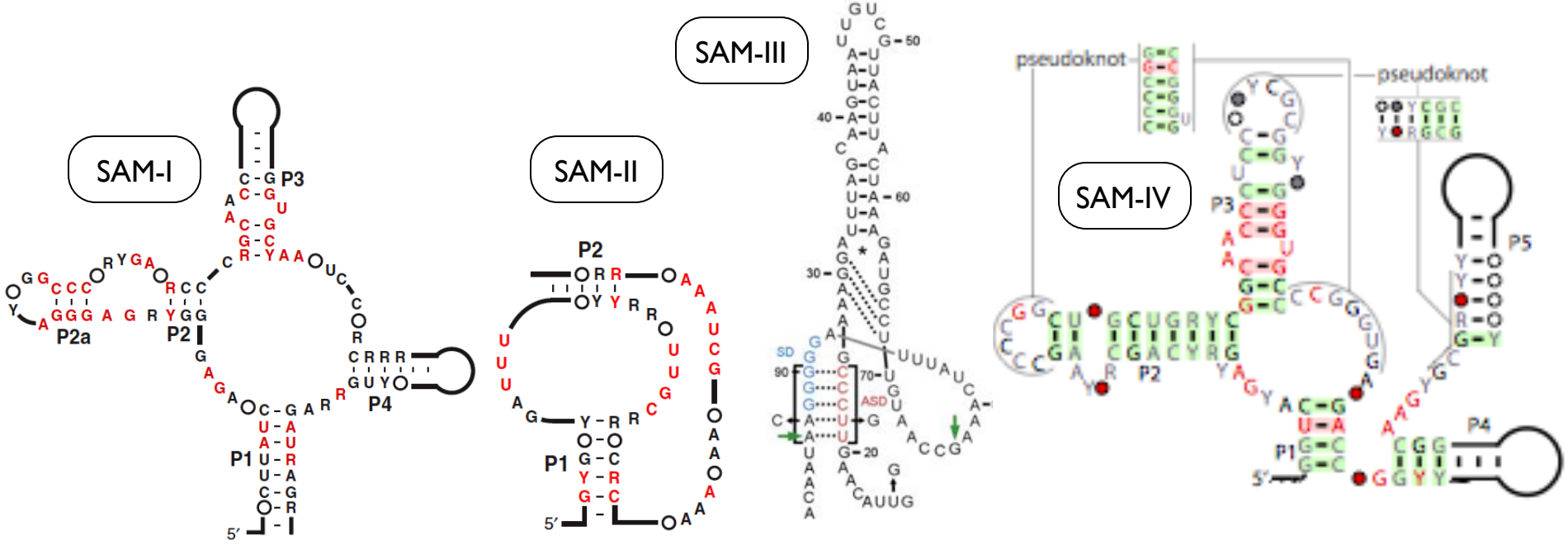
Not the only way!

Alberts, et al, 3e.



← Protein way

Riboswitch alternatives ↓



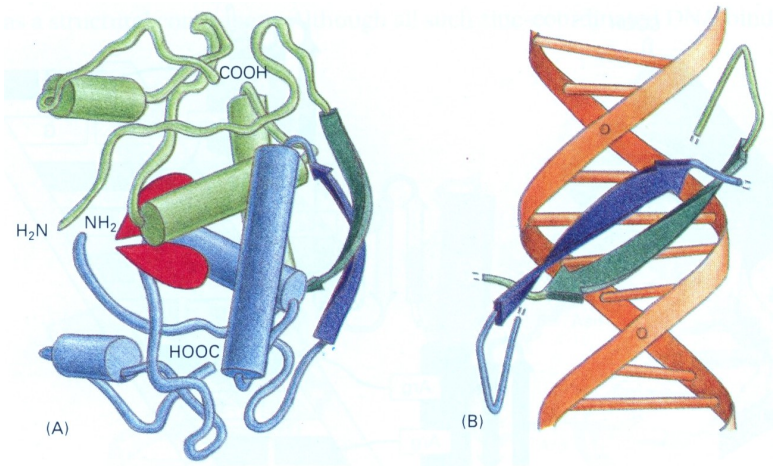
Grundy, Epshtein, Winkler et al., 1998, 2003

Corbino et al., Genome Biol. 2005

Fuchs et al., NSMB 2006

Weinberg et al., RNA 2008

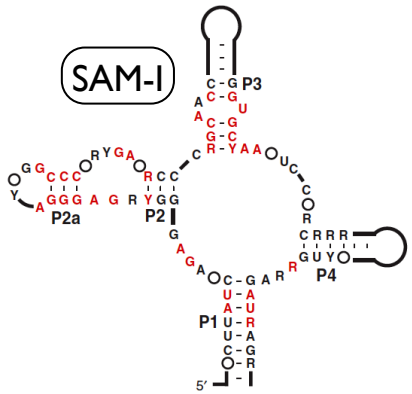
Not the only way!



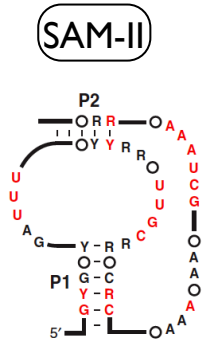
Alberts, et al, 3e.

← Protein way

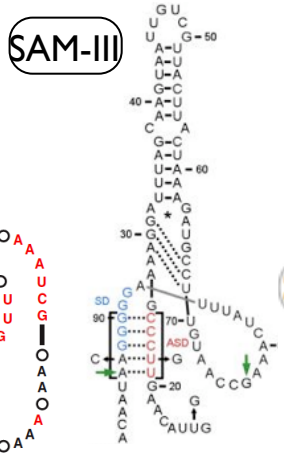
Riboswitch alternatives ↓



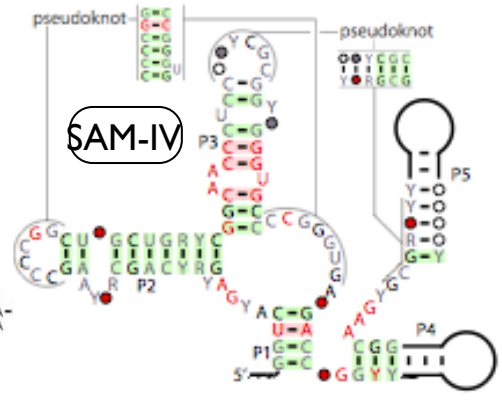
Grundy, Epshtein, Winkler et al., 1998, 2003



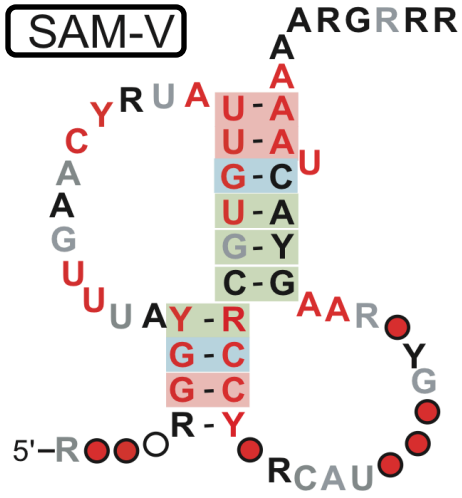
Corbino et al., Genome Biol. 2005



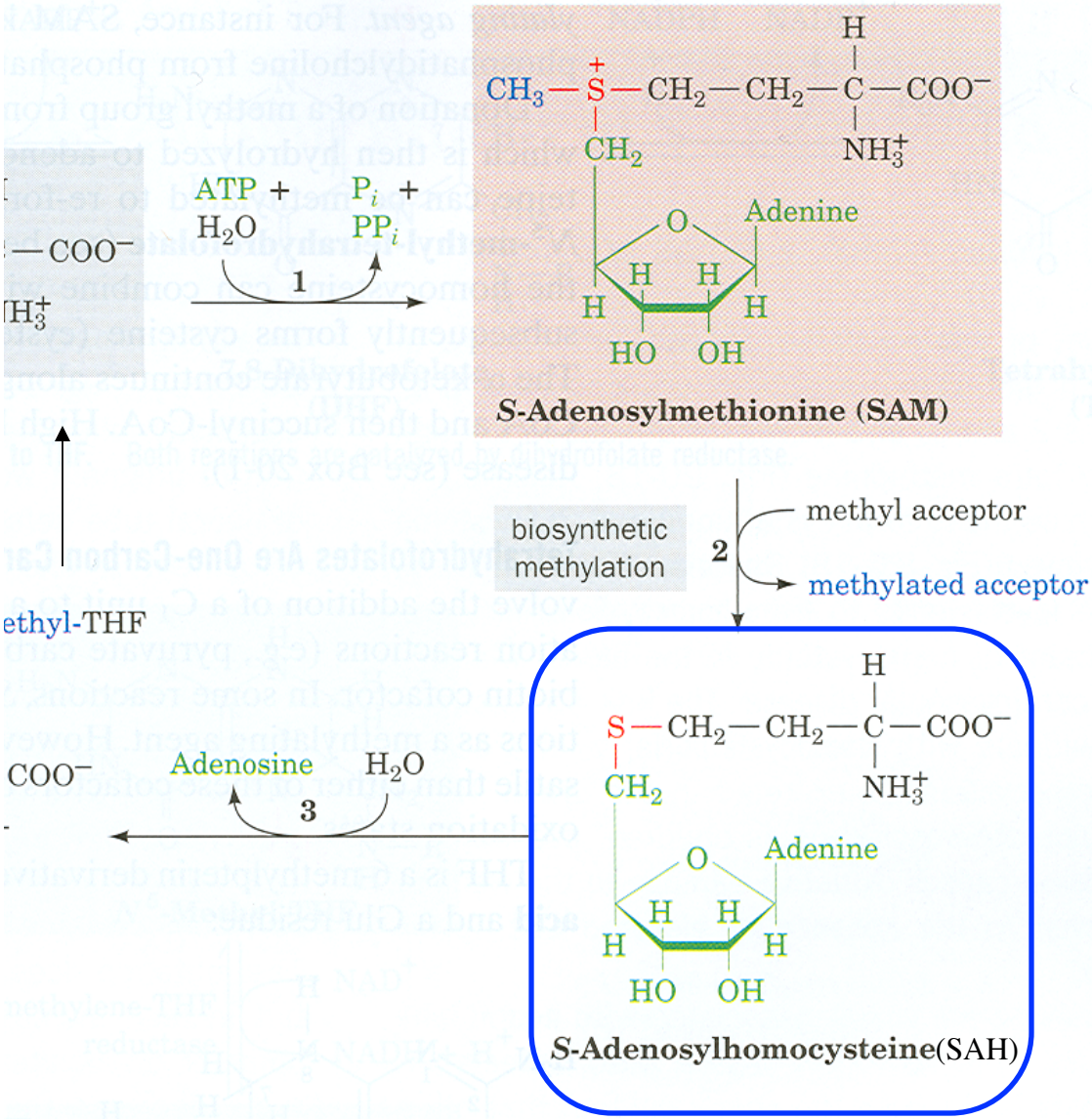
Fuchs et al., NSMB 2006



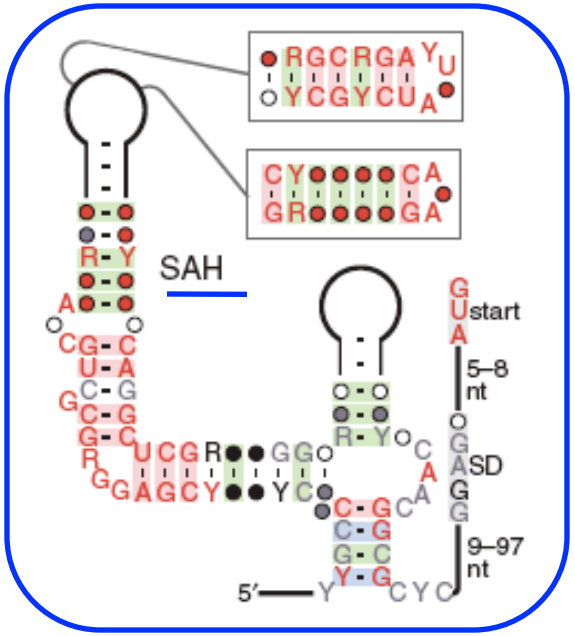
Weinberg et al., RNA 2008



Meyer, etal., BMC Genomics 2009



And in other bacteria, a riboswitch senses SAH



Example: Glycine Regulation

Glycine: 1 of 20 amino acids

EITHER used to make proteins

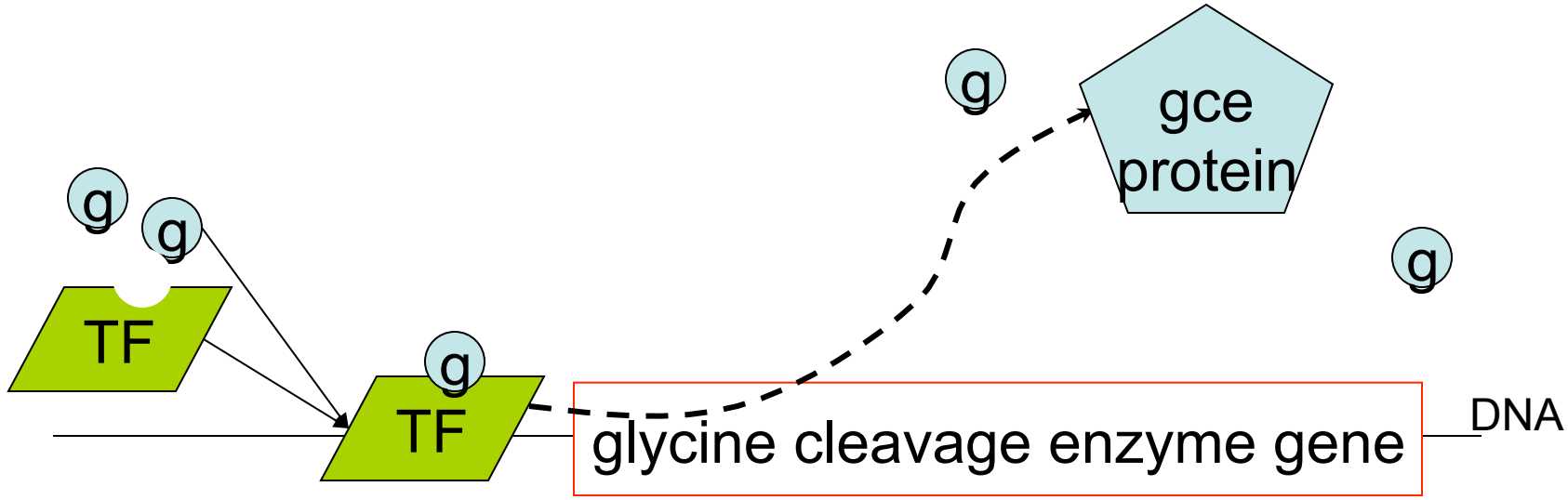
OR used as an energy source

Cells need to *measure* glycine levels and *respond* to changes by turning genes on/off

Example: Glycine Regulation

How is glycine level regulated?

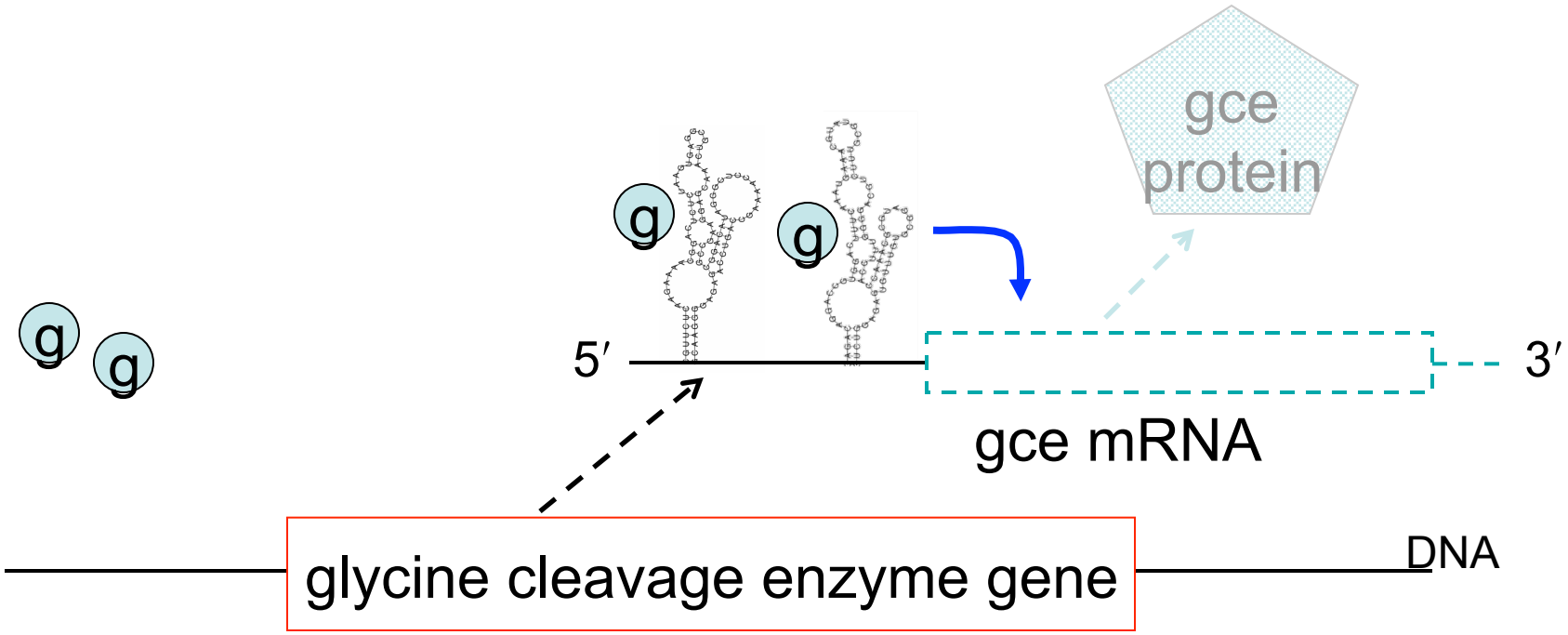
Plausible answer:



transcription factors (proteins) bind to DNA to turn nearby genes on or off

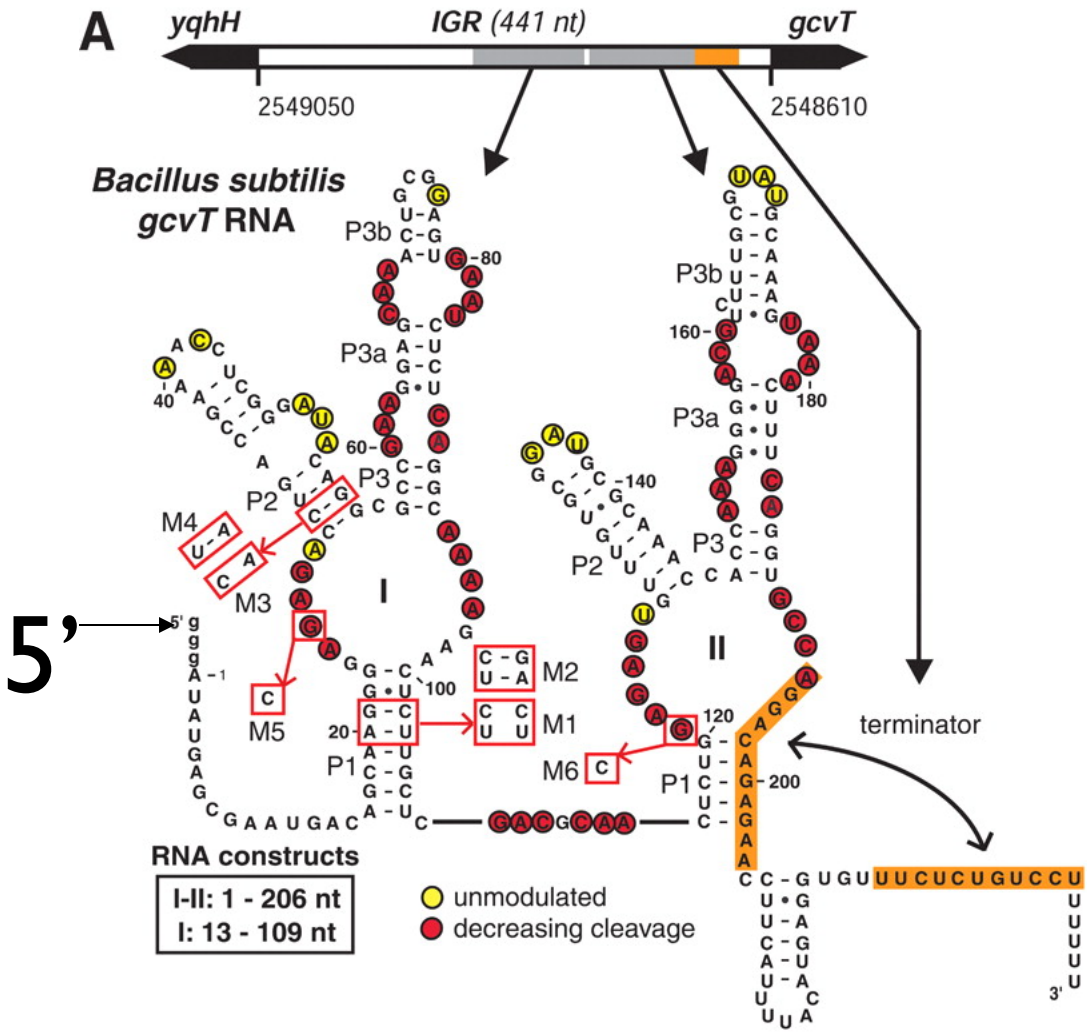
The Glycine Riboswitch

Actual answer (in many bacteria):



Mandal et al. Science 2004

The Glycine Riboswitch



(Mandal, Lee, Barrick, Weinberg, Emilsson, Ruzzo, Breaker, *Science* 2004)

5'

gcvT ORF

3'

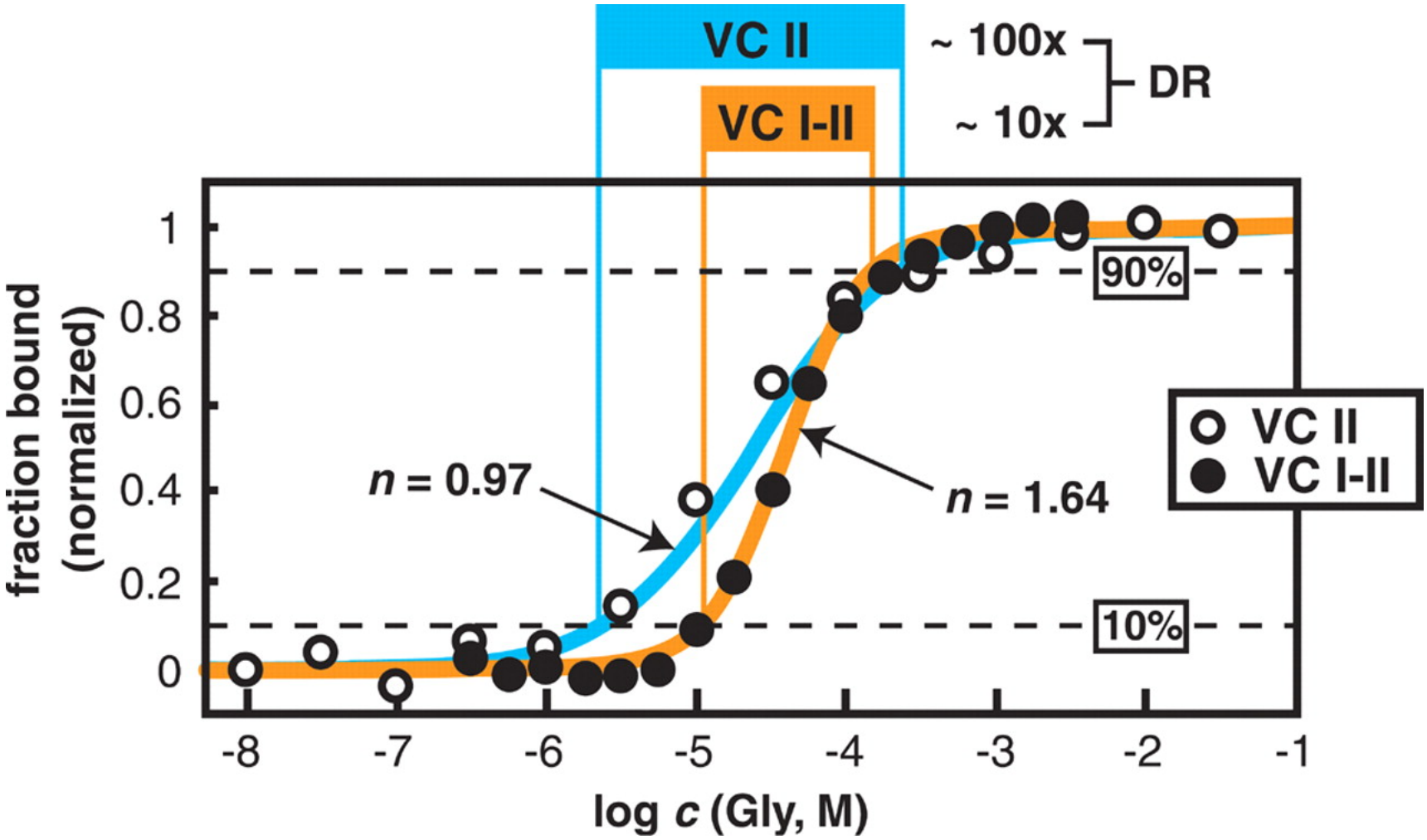


Fig. 3. Cooperative binding of two glycine molecules by the VC I-II RNA. Plot depicts the fraction of VC II (open) and VC I-II (solid) bound to ligand versus the concentration of glycine. The constant, n, is the Hill coefficient for the lines as indicated that best fit the aggregate data from four different regions (fig. S3). Shaded boxes demark the dynamic range (DR) of glycine concentrations needed by the RNAs to progress from 10%- to 90%-bound states.

Riboswitches

~ 20 ligands known; multiple nonhomologous solutions for some

dozens to hundreds of instances of each

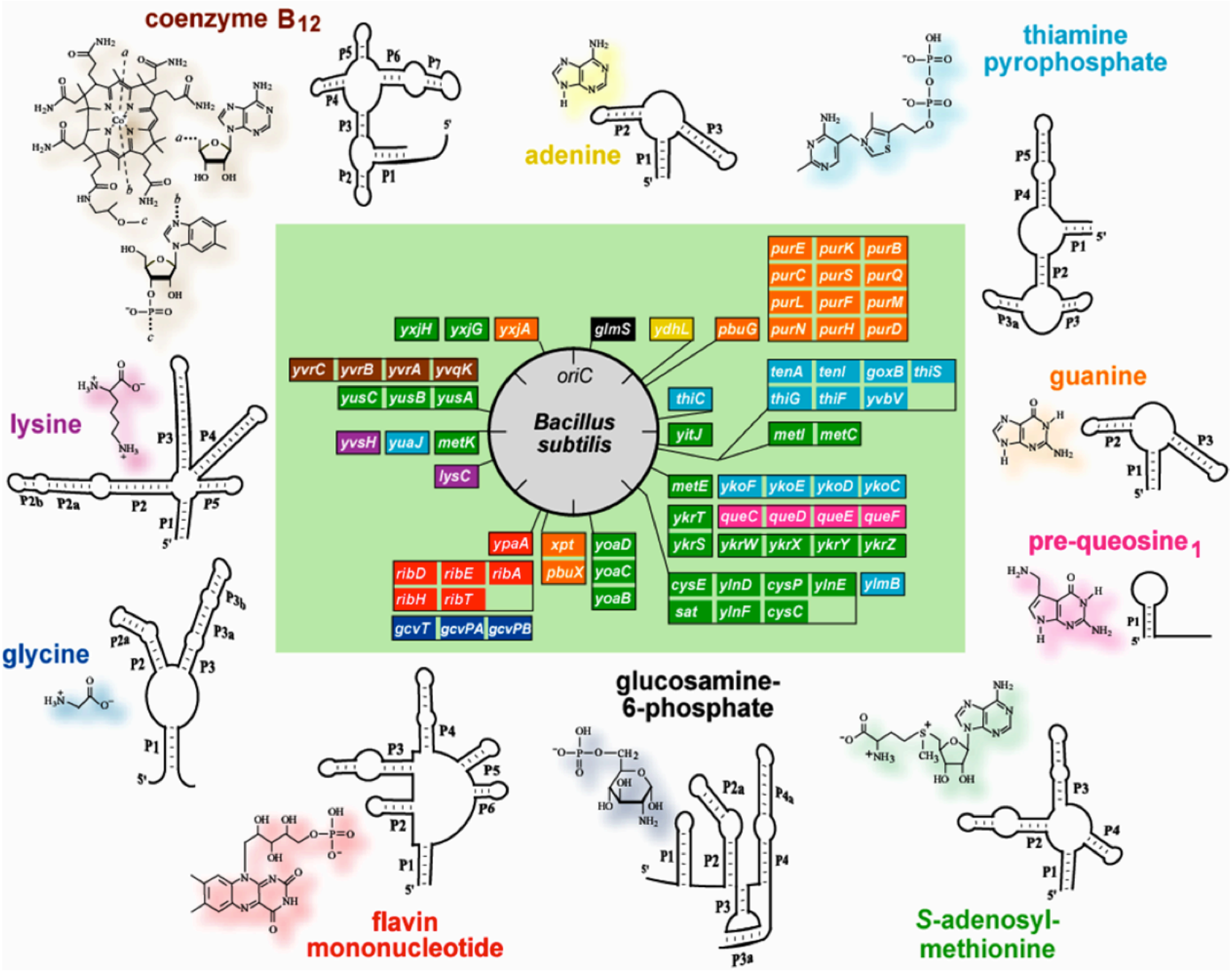
TPP known in archaea & eukaryotes

one known in bacteriophage

on/off; transcription/translation; splicing; combinatorial control

In some bacteria, more riboregulators identified than protein TFs

all found since ~2003


coenzyme B12
adenine
thiamine pyrophosphate
guanine
lysine
glycine
pre-queosine1
glucosamine-6-phosphate
flavin mononucleotide
S-adenosyl-methionine
oriC
Bacillus subtilis
yxjH yxjG yxjA
glmS
ydhL
pbuG
purE purK purB
purC purS purQ
purL purF purM
purN purH purD
yvrC yvrB yvrA yvqK
yusC yusB yusA
yvsH yuaJ metK
lysC
thiC
yitJ
tenA tenI goxB thiS
thiG thiF yvbV
metI metC
metE ykoF ykoE ykoD ykoC
ykrT queC queD queE queF
ykrS ykrW ykrX ykrY ykrZ
ypaA xpt yoaD
pbuX yoaC
yoaB
ribD ribE ribA
ribH ribT
gcvT gcvPA gcvPB
cysE ylnD cysP ylnE ylmB
sat ylnF cysC

Antibiotics?

Old drugs, new understanding:

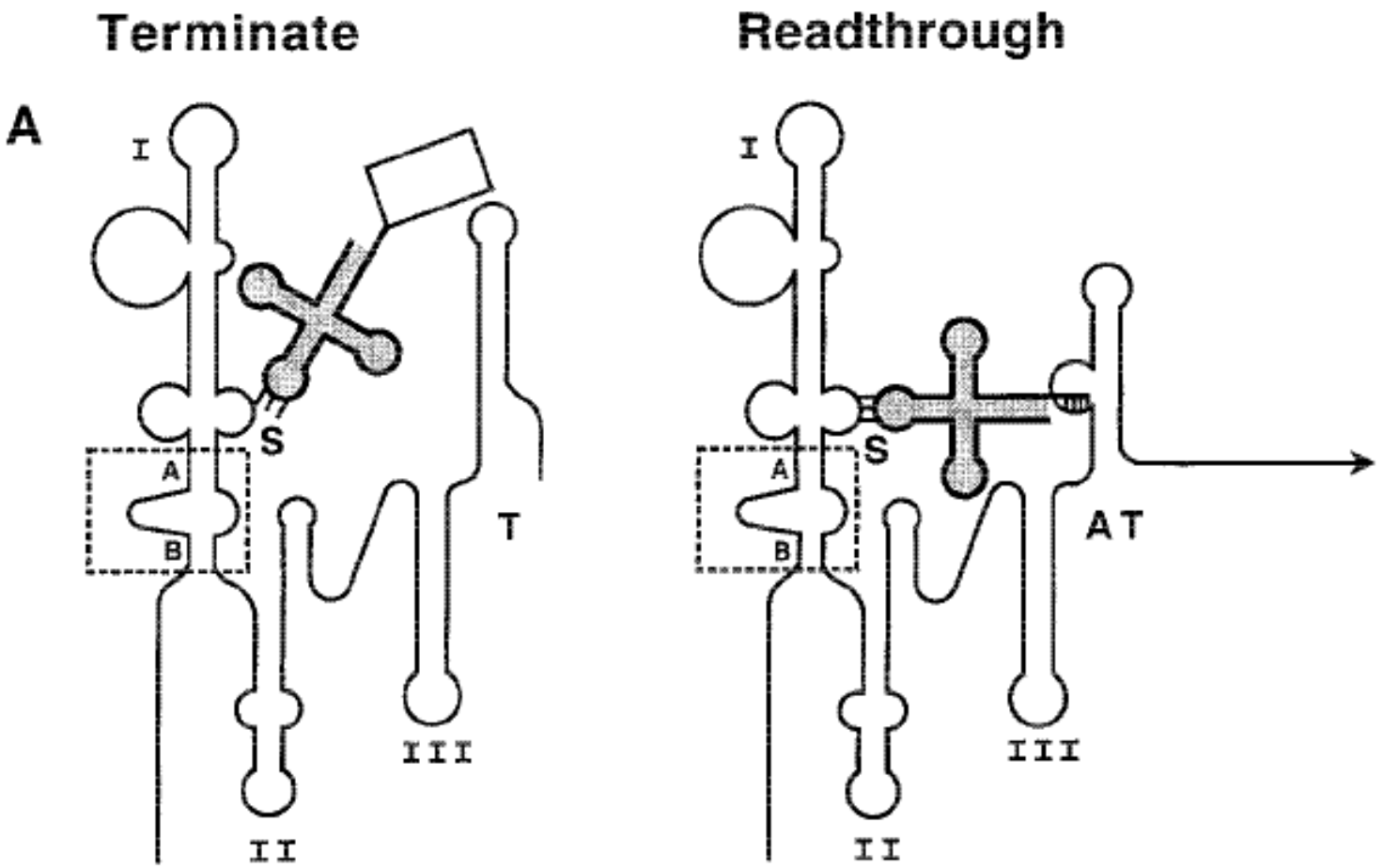
TPP ~ pyrithiamine

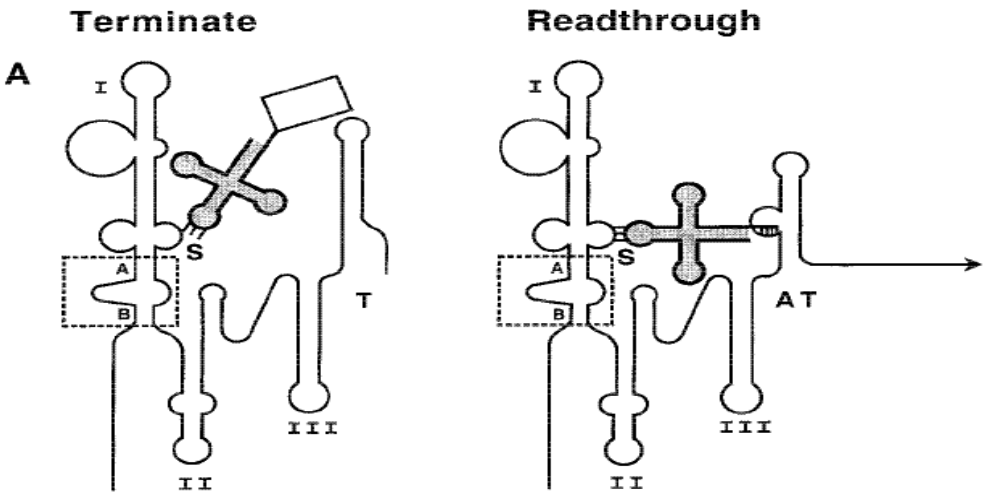
lysine ~ L-aminoethylcysteine, DL-4-oxalysine

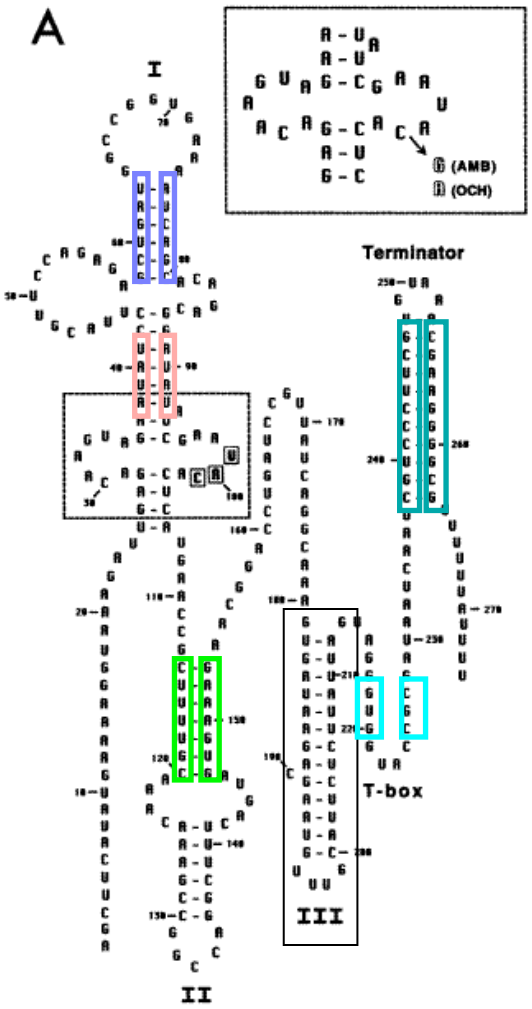
FMN ~roseoflavin

Potential advantages - no (known) human riboswitches, but often multiple copies in bacteria

ncRNA Example: T-boxes








```
NC_000964.1 AUAUC.CUUACGU..UCCAGAGAGCUGAUGGCCGGUGAAA.AUCAGCACAGACGGAUAUAU
NC_004722.1 CAAAU.GUCGUUUcUUAUAGAGAGUCGAUGGUUGGUGGAA.AUCGAUAG..AAACAGUUUG
NC_004193.1 AAAAGUAGAACCG.AUCUAGCGAAUUGAGGAU.GGUGUGAGCUCAGUGC.GGAAAGCUUUU
NC_003997.3 CAAAU.GUCGUUUcUUAUAGAGAGUCGAUGGUUGGUGGAA.AUCGAUAG..AAACAGUUUG

NC_000964.1 CGAA..UACACUCAUGAACCGCUUUUGCAAACAAAGccggccaggcuuucAGUA.GUGAAAG
NC_004722.1 UGAA..UCCAUCCUGGAAU..GGAAUGUGGAAUAUCUuuuggauu.....AGUAAGCAUUCC
NC_004193.1 AGAAAAUC.ACUCUUGAGUU.UUCAUUACGAAA..CA............AGUAGUAAUGGA
NC_003997.3 UGAA..UCCAUCCUGGAAU..GGAAUGUGGAAUAUCUuuaugauu.....AGUAAACAUUCC

NC_000964.1 aCGGAC.CUGAUCCGUUAUCAGGCAAAGUGGUACCGCGAUAAUCAAUCGUCCCUUCGUGUAAaCGAAGGGGCGUUU
NC_004722.1 .CGGUG.AAGAGCCGUUAUU...UCuAGUGGCAACGCGG..GUUAACUCCCGUCCCUUUAUAUaAGGGACGGGAGUU
NC_004193.1 .CGGUUcAUC.UCCGUUAUCGAUCUUAGUGGUACCGCGA.....GUCUUCUCGUCCCUUUU..GGGAUUAGAAGGC
NC_003997.3 .CGGUG.AAGAGCCGUUAUU...UCuAGUGGCAACGCGG..GUUAACUCCCGUCCCUUUAUAUaAGGGACGGGAGUU
```

ncRNA Example: 6S

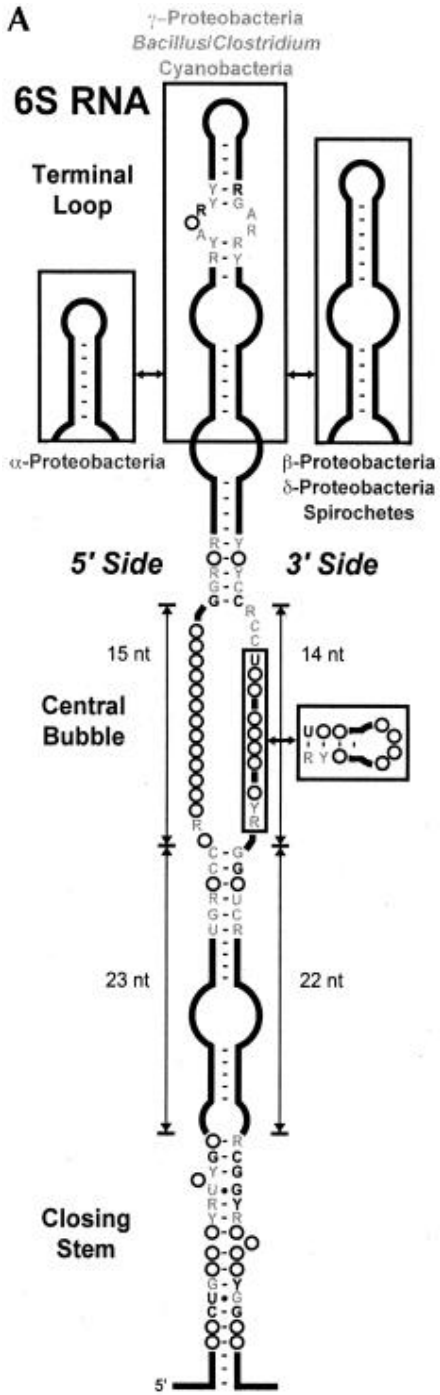
medium size (175nt)

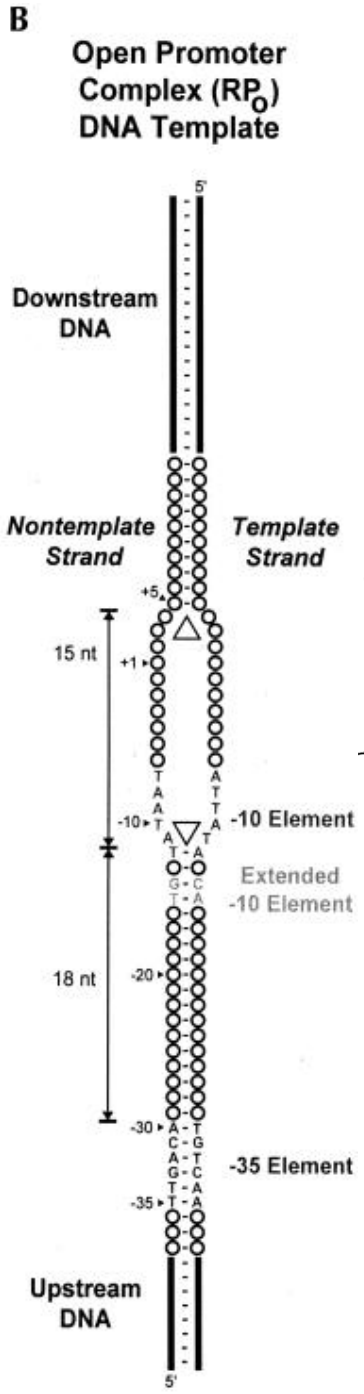
structured

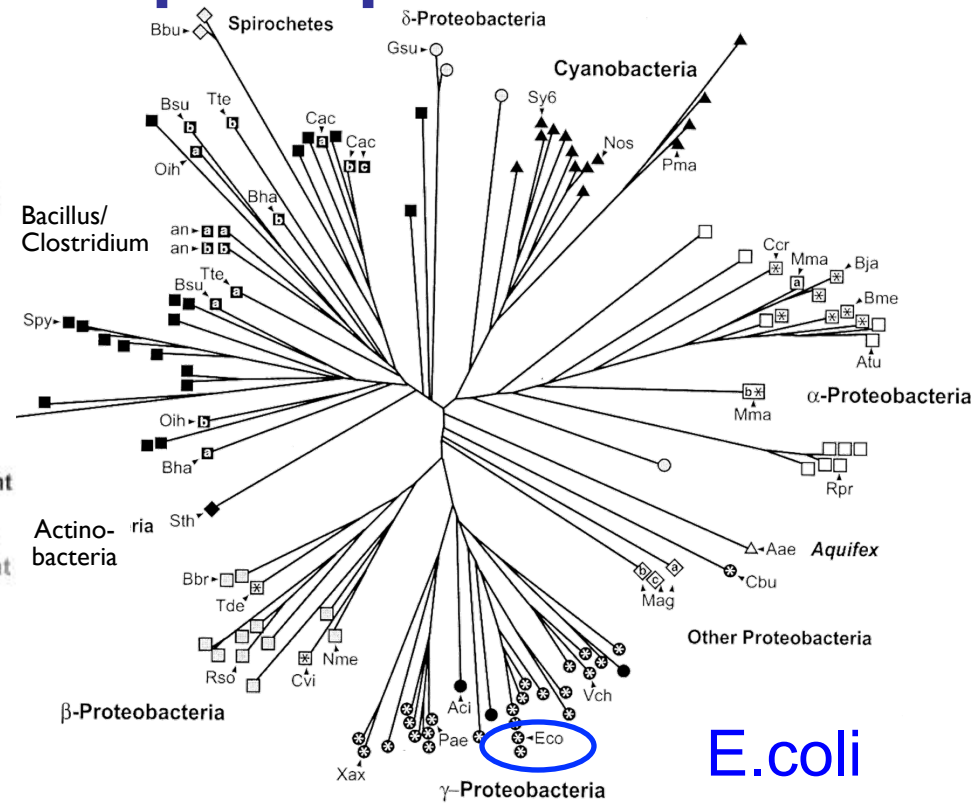
highly expressed in E. coli in certain growth conditions

sequenced in 1971; function unknown for 30 years

6S mimics an open promoter







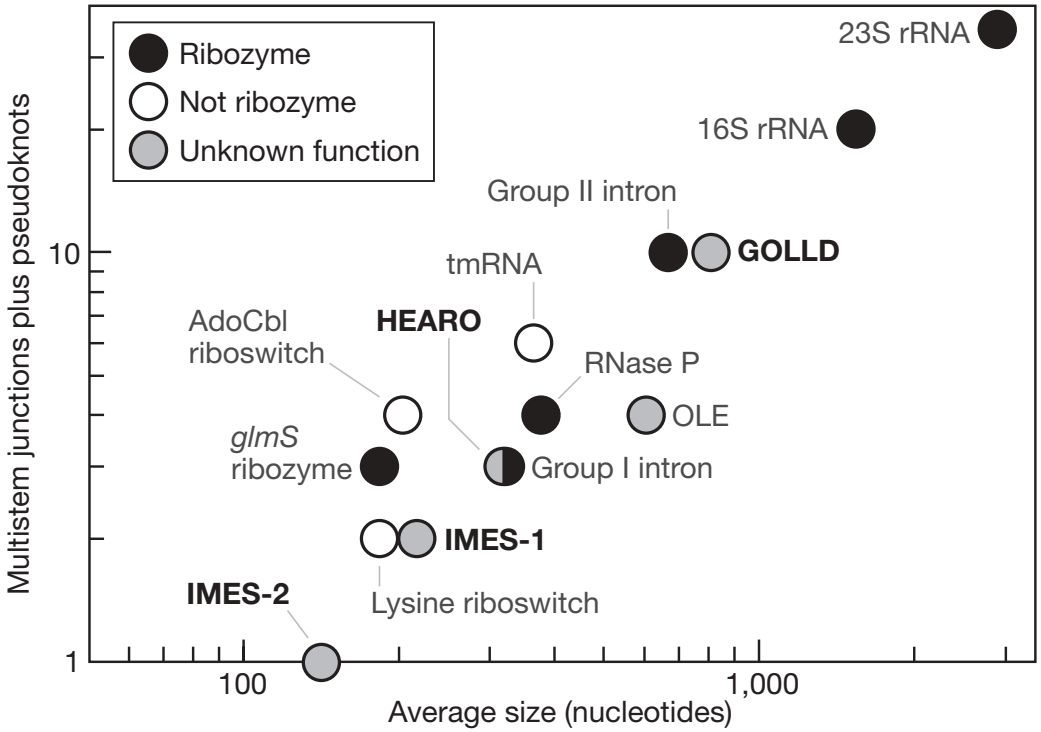
Barrick et al. *RNA* 2005
Trotochaud et al. *NSMB* 2005
Willkomm et al. NAR 2005

nature Vol 462|3 December 2009|doi:10.1038/nature08586

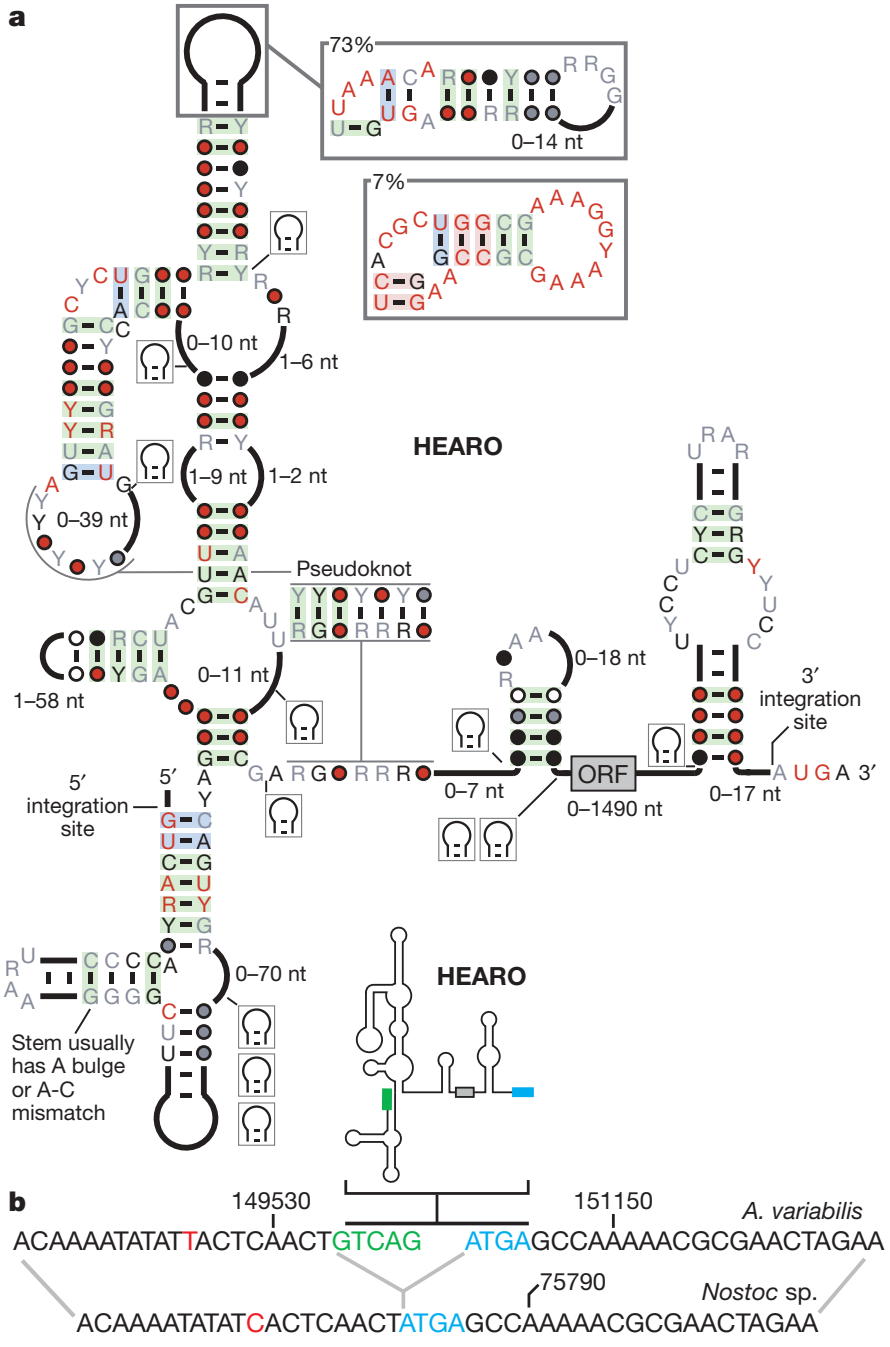
LETTERS

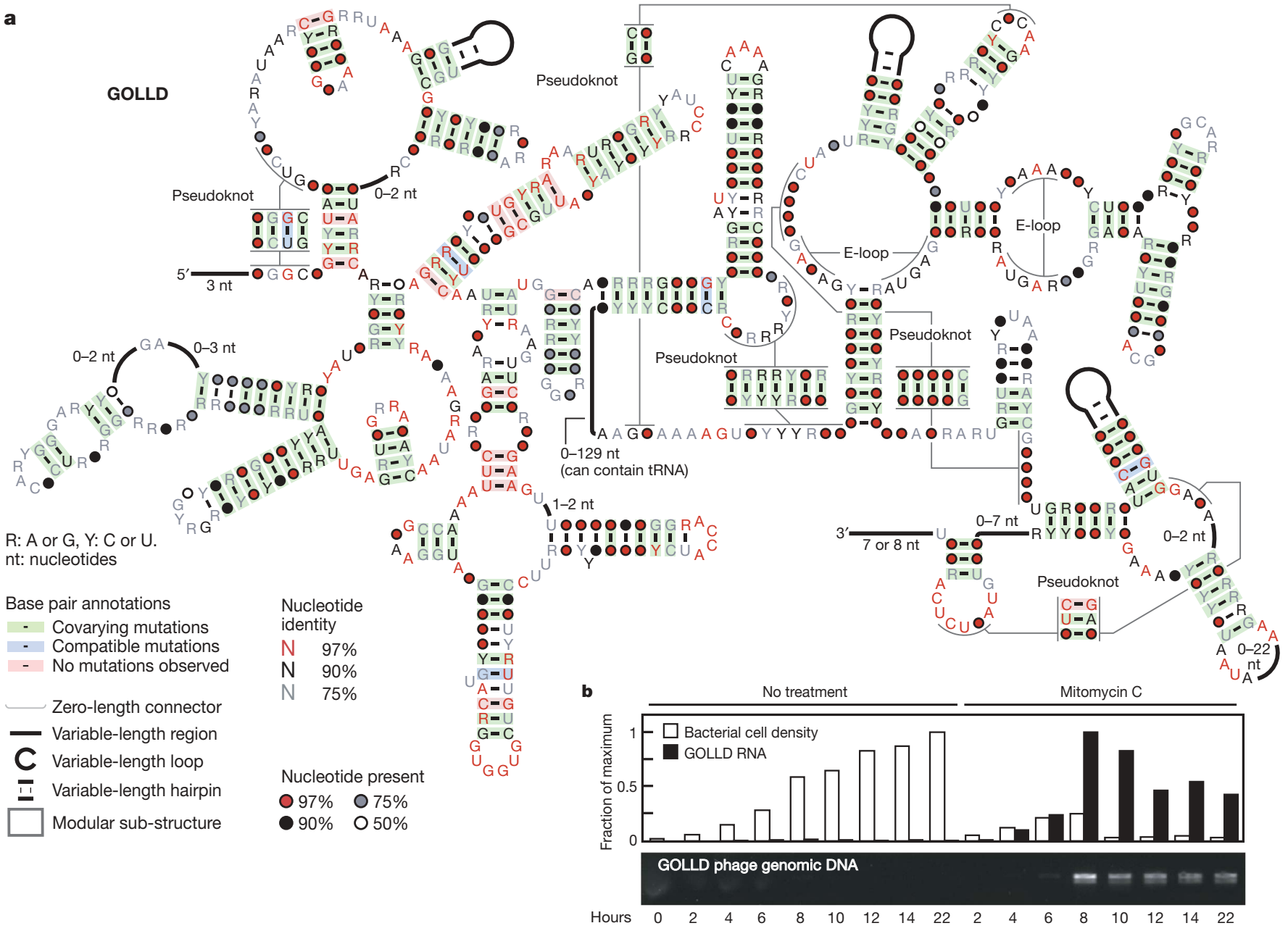
Exceptional structured noncoding RNAs revealed by bacterial metagenome analysis

Zasha Weinberg[1,2], Jonathan Perreault[2], Michelle M. Meyer[2] & Ronald R. Breaker[1,2,3]



RNAs of unusual size and complexity

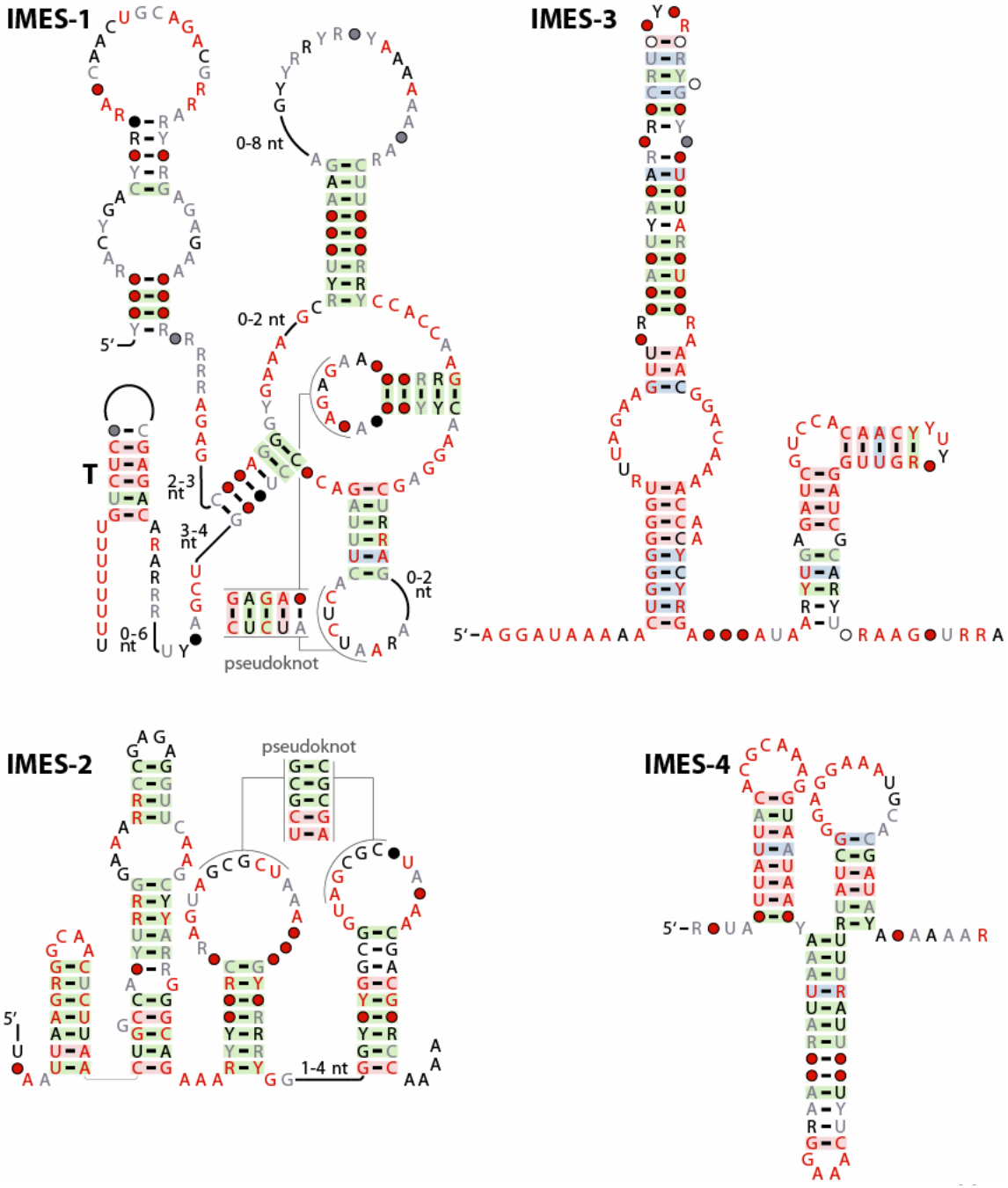



a
GOLLD
Pseudoknot
0–2 nt
5′
3 nt
0–2 nt
0–3 nt
Pseudoknot
Pseudoknot
0–129 nt
(can contain tRNA)
E-loop
E-loop
Pseudoknot
1–2 nt
3′
7 or 8 nt
0–7 nt
Pseudoknot
0–2 nt
0–22
nt
R: A or G, Y: C or U.
nt: nucleotides
Base pair annotations
Covarying mutations
Compatible mutations
No mutations observed
Zero-length connector
Variable-length region
Variable-length loop
Variable-length hairpin
Modular sub-structure
Nucleotide identity
N 97%
N 90%
N 75%
Nucleotide present
97%
75%
90%
50%
b
No treatment
Mitomycin C
Fraction of maximum
1
0.5
0
Bacterial cell density
GOLLD RNA
GOLLD phage genomic DNA
Hours
0 2 4 6 8 10 12 14 22 2 4 6 8 10 12 14 22

RNAs of unusual abundance

More abundant than 5S rRNA

From unknown marine organisms



Summary: RNA in Bacteria

- Widespread, deeply conserved, structurally sophisticated, functionally diverse, biologically important uses for ncRNA throughout prokaryotic world.
- Regulation of MANY genes involves RNA
  - In some species, we know identities of more ribo-regulators than protein regulators
- Dozens of classes & thousands of new examples in just last 5 years

Vertebrates

Bigger, more complex genomes

<2% coding

But >5% conserved in sequence?

And 50-90% transcribed?

And *structural* conservation, if any, invisible

(without proper alignments, etc.)

What's going on?

RNA In Humans

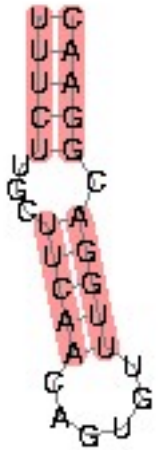
More RNA- than DNA-binding proteins?

Much more conserved DNA than coding

MUCH more transcribed DNA than coding

Structural conservation (as opposed to sequence conservation) is only now beginning to be explored

ncRNA Example: IRE

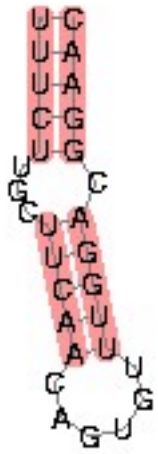


Iron Response Element: a short conserved stem-loop, bound by iron response proteins (IRPs). Found in UTRs of various mRNAs whose products are involved in iron metabolism. E.g., the mRNA of ferritin (an iron storage protein) contains one IRE in its 5' UTR. When iron concentration is low, IRPs bind the ferritin mRNA IRE, repressing translation. Binding of multiple IREs in the 3' and 5' UTRs of the transferrin receptor (involved in iron acquisition) leads to increased mRNA stability. These two activities form the basis of iron homeostasis in the vertebrate cell.

Iron Response Element

IRE (partial seed alignment):

```
Hom.sap.   GUUCCUGCUUCAACAGUGUUUGGAUGGAAC
Hom.sap.   UUUCUUC.UUCAACAGUGUUUGGAUGGAAC
Hom.sap.   UUUCCUGUUUCAACAGUGCUUGGA.GGAAC
Hom.sap.   UUUAUC..AGUGACAGAGUUCACU.AUAAA
Hom.sap.   UCUCUUGCUUCAACAGUGUUUGGAUGGAAC
Hom.sap.   AUUAUC..GGGAACAGUGUUUCCC.AUAAU
Hom.sap.   UCUUGC..UUCAACAGUGUUUGGACGGAAG
Hom.sap.   UGUAUC..GGAGACAGUGAUCUCC.AUAUG
Hom.sap.   AUUAUC..GGAAGCAGUGCCUUCC.AUAAU
Cav.por.   UCUCCUGCUUCAACAGUGCUUGGACGGAGC
Mus.mus.   UAUAUC..GGAGACAGUGAUCUCC.AUAUG
Mus.mus.   UUUCCUGCUUCAACAGUGCUUGAACGGAAC
Mus.mus.   GUACUUGCUUCAACAGUGUUUGAACGGAAC
Rat.nor.   UAUAUC..GGAGACAGUGACCUCC.AUAUG
Rat.nor.   UAUCUUGCUUCAACAGUGUUUGGACGGAAC
SS_cons    <<<<<...<<<<<......>>>>>.>>>>>
```



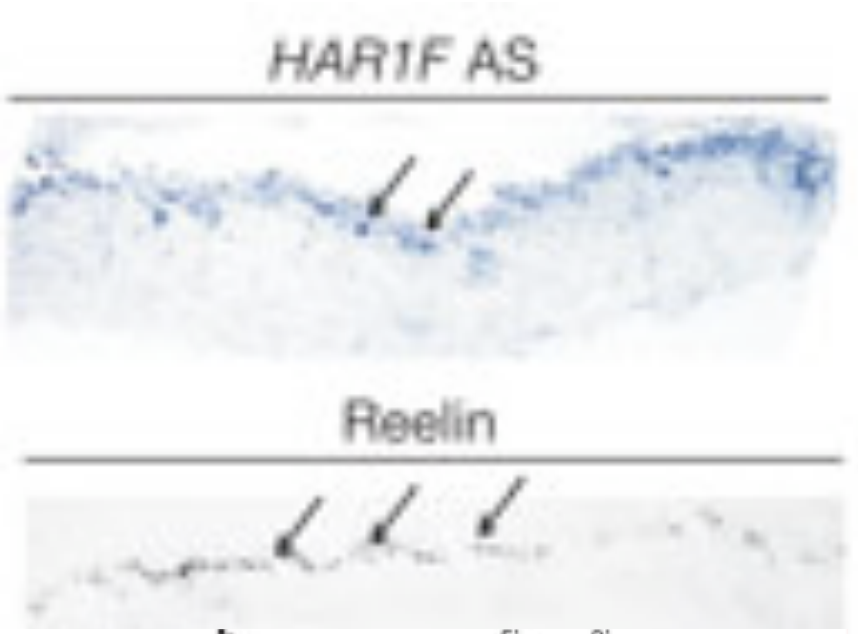
ncRNA Example: Xist

large (12kb?)

largely unstructured RNA

required for X-inactivation in mammals

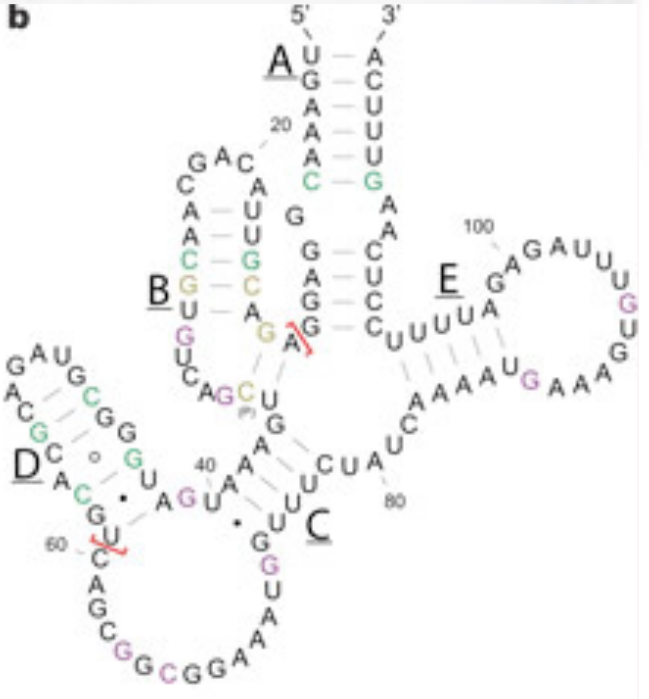
Fastest Human Gene?



a

Position	20	30	40	50
Human	AGACGTTACAGCAACGTGTCAGCTGAAATGATGGGCGTAGACGCACGT			
Chimpanzee	AGAAATTACAGCAATTTATCAACTGAAATTATAGGTGTAGACACATGT			
Gorilla	AGAAATTACAGCAATTTATCAACTGAAATTATAGGTGTAGACACATGT			
Orang-utan	AGAAATTACAGCAATTTATCAACTGAAATTATAGGTGTAGACACATGT			
Macaque	AGAAATTACAGCAATTTATCAGCTGAAATTATAGGTGTAGACACATGT			
Mouse	AGAAATTACAGCAATTTATCAGCTGAAATTATAGGTGTAGACACATGT			
Dog	AGAAATTACAGCAATTTATCAACTGAAATTATAGGTGTAGACACATGT			
Cow	AGAAATTACAGCAATTCATCAGCTGAAATTATAGGTGTAGACACATGT			
Platypus	ATAAATTACAGCAATTTATCAAATGAAATTATAGGTGTAGACACATGT			
Opossum	AGAAATTACAGCAATTTATCAACTGAAATTATAGGTGTAGACACATGT			
Chicken	AGAAATTACAGCAATTTATCAACTGAAATTATAGGTGTAGACACATGT			
Fold	((((((((.....)))))).....))[[[[[.((((.(((....)))).))))			
Pair symbol	lmnopqr rqpon ml rstuvwx xwvutsr			

b



MicroRNA

1st discovered 1992 in C. elegans

2nd discovered 2000, also C. elegans

- *and* human, fly, everything between

21-23 nucleotides

- literally fell off ends of gels

Hundreds now known in human

- may regulate 1/3-1/2 of all genes
- development, stem cells, cancer, infectious diseases,…

siRNA

2006 Nobel Prize
Fire & Mello

"Short Interfering RNA"

Also discovered in *C. elegans*

Possibly an antiviral defense, shares machinery with miRNA pathways

Allows artificial repression of most genes in most higher organisms

Huge tool for biology & biotech

Human Predictions

Evofold

S Pedersen, G Bejerano, A Siepel, K Rosenbloom, K Lindblad-Toh, ES Lander, J Kent, W Miller, D Haussler, "Identification and classification of conserved RNA secondary structures in the human genome." PLoS Comput. Biol., 2, #4 (2006) e33.

48,479 candidates (~70% FDR?)

RNAz

S Washietl, IL Hofacker, M Lukasser, A Hüttenhofer, PF Stadler, "Mapping of conserved RNA secondary structures predicts thousands of functional noncoding RNAs in the human genome." Nat. Biotechnol., 23, #11 (2005) 1383-90.

30,000 structured RNA elements

1,000 conserved across all vertebrates.

~1/3 in introns of known genes, ~1/6 in UTRs

~1/2 located far from any known gene

FOLDALIGN

E Torarinsson, M Sawera, JH Havgaard, M Fredholm, J Gorodkin, "Thousands of corresponding human and mouse genomic regions unalignable in primary sequence contain common RNA structure." *Genome Res.*, 16, #7 (2006) 885-9.

1800 candidates from 36970 (of 100,000) pairs

CMfinder

Torarinsson, Yao, Wiklund, Bramsen, Hansen, Kjems, Tommerup, Ruzzo and Gorodkin. Comparative genomics beyond sequence based alignments: RNA structures in the ENCODE regions.

Genome Research, Feb 2008, 18(2):242-251 PMID: 18096747

6500 candidates in ENCODE alone (better FDR, but still high)

Thousands of Predictions

Bottom line?

A significant number of "one-off" examples

Extremely wise-spread ncRNA expression

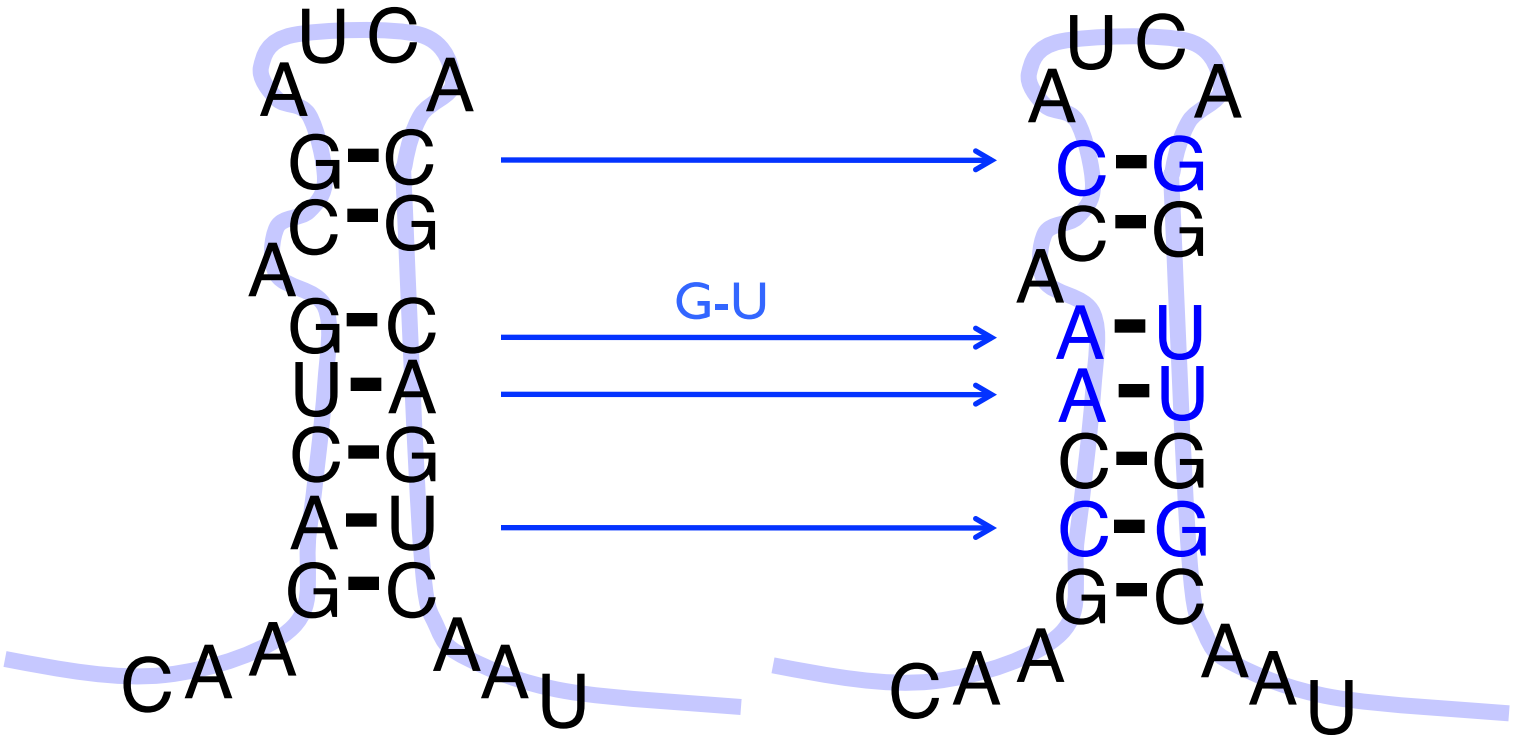
At a minimum, a vast evolutionary substrate

New technology (e.g. RNAseq) exposing more

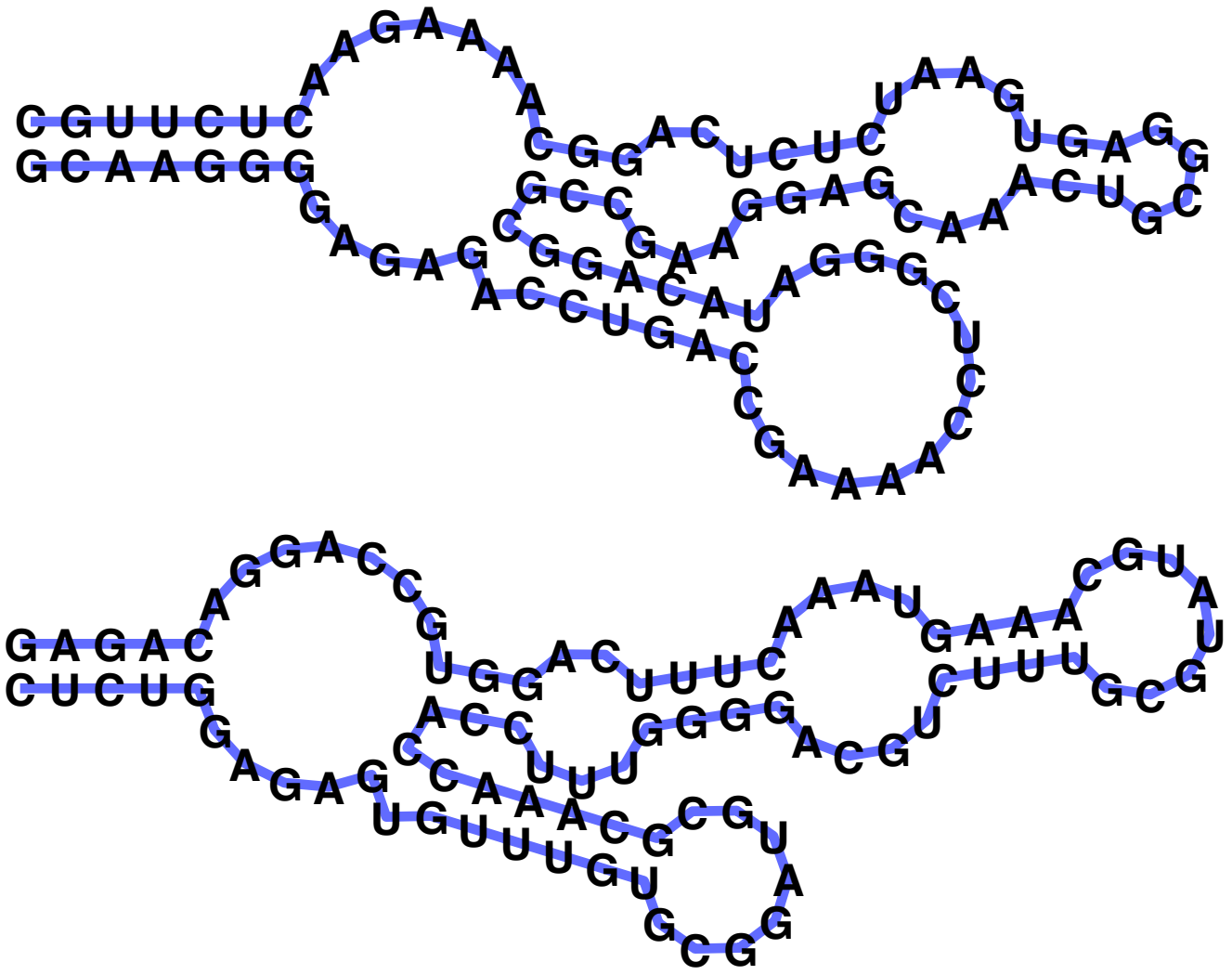
How do you recognize an interesting one?

Conserved secondary structure

RNA Secondary Structure: can be fixed while sequence evolves



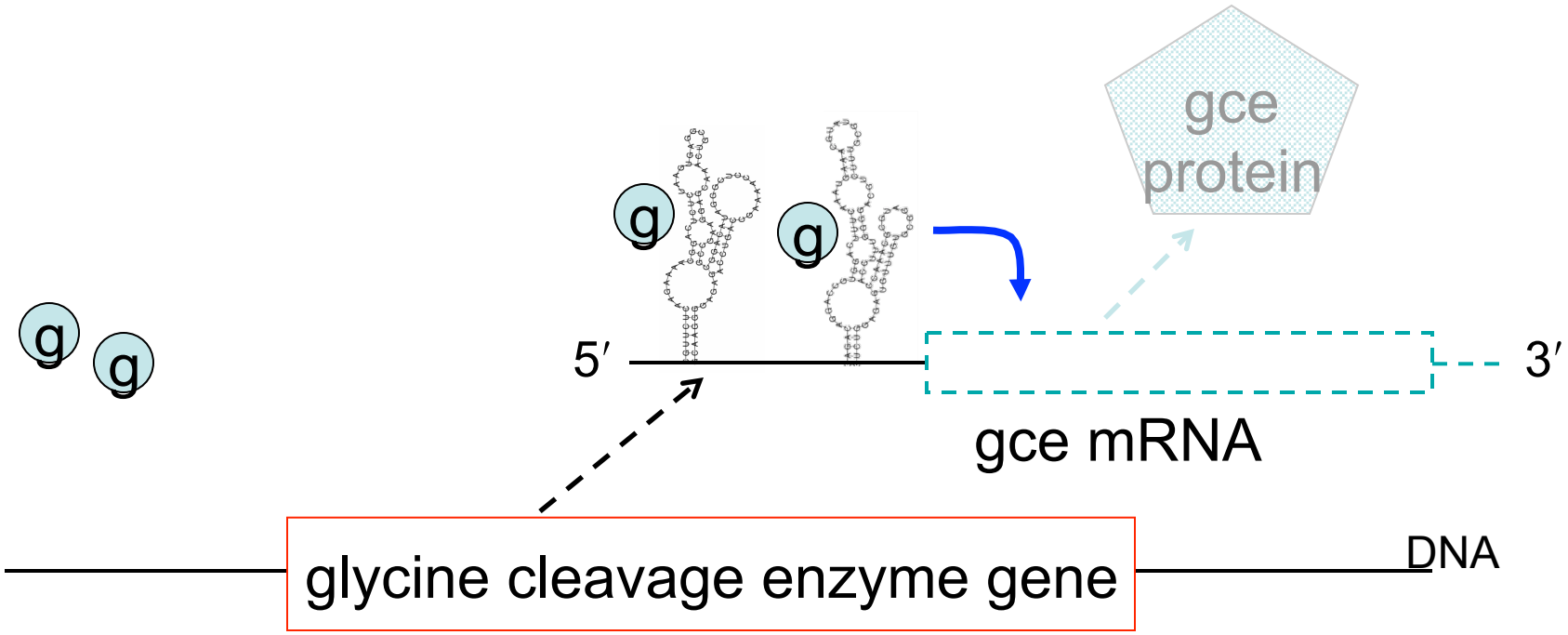
Why is RNA hard to deal with?



A: *Structure* often more important than *sequence*

The Glycine Riboswitch

Actual answer (in many bacteria):



Mandal et al. Science 2004

Wanted

Good structure prediction tools

Good motif descriptions/models

Good, fast search tools

("RNA BLAST", etc.)

Good, fast motif discovery tools

("RNA MEME", etc.)

Importance of structure makes last 3 hard

Structure Prediction

RNA Structure

Primary Structure: Sequence

Secondary Structure: Pairing

Tertiary Structure: 3D shape

RNA Pairing

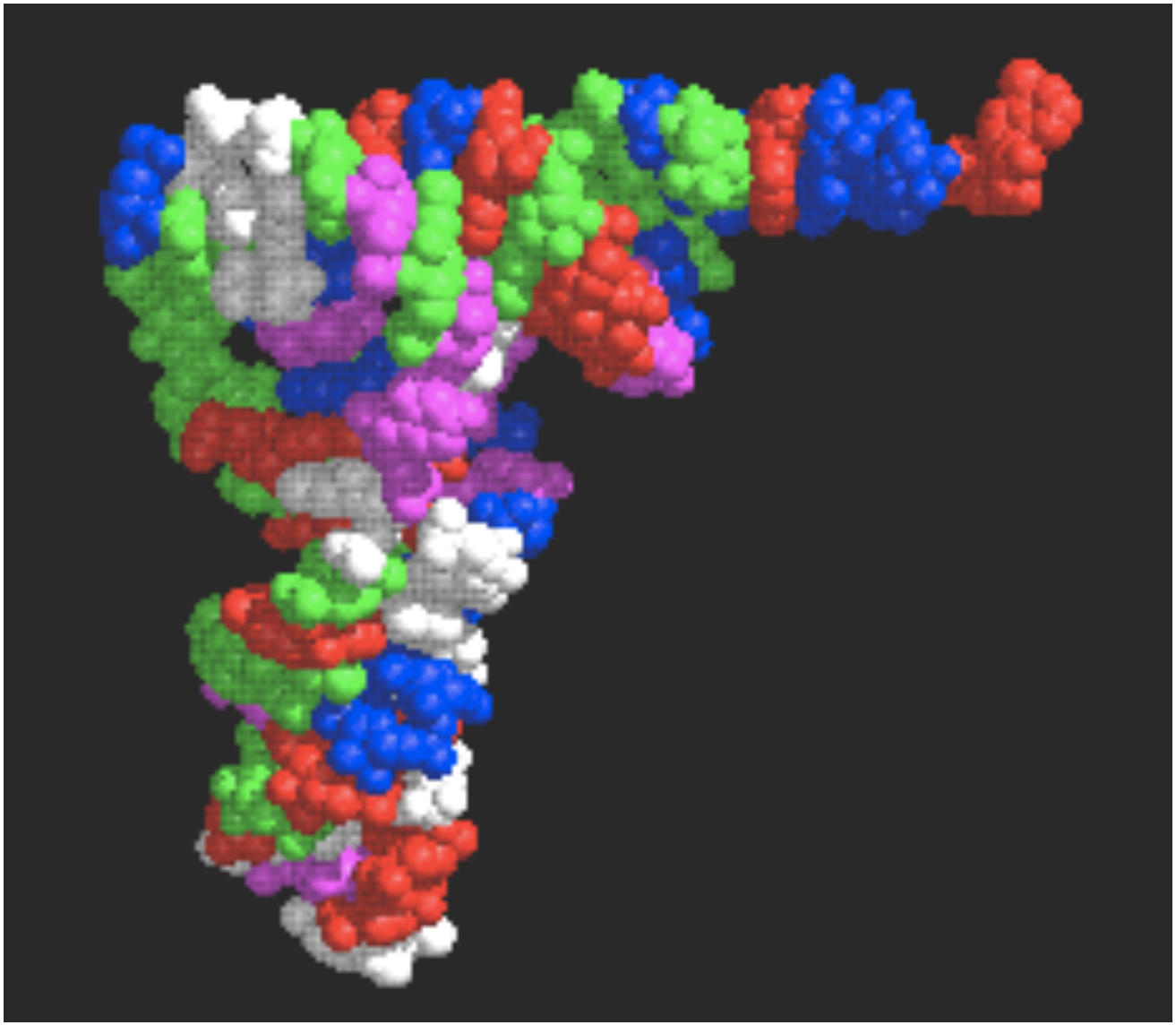
Watson-Crick Pairing

- C - G ~ 3 kcal/mole
- A - U ~ 2 kcal/mole

"Wobble Pair" G - U ~1 kcal/mole

Non-canonical Pairs (esp. if modified)

tRNA 3d Structure



tRNA - Alt. Representations

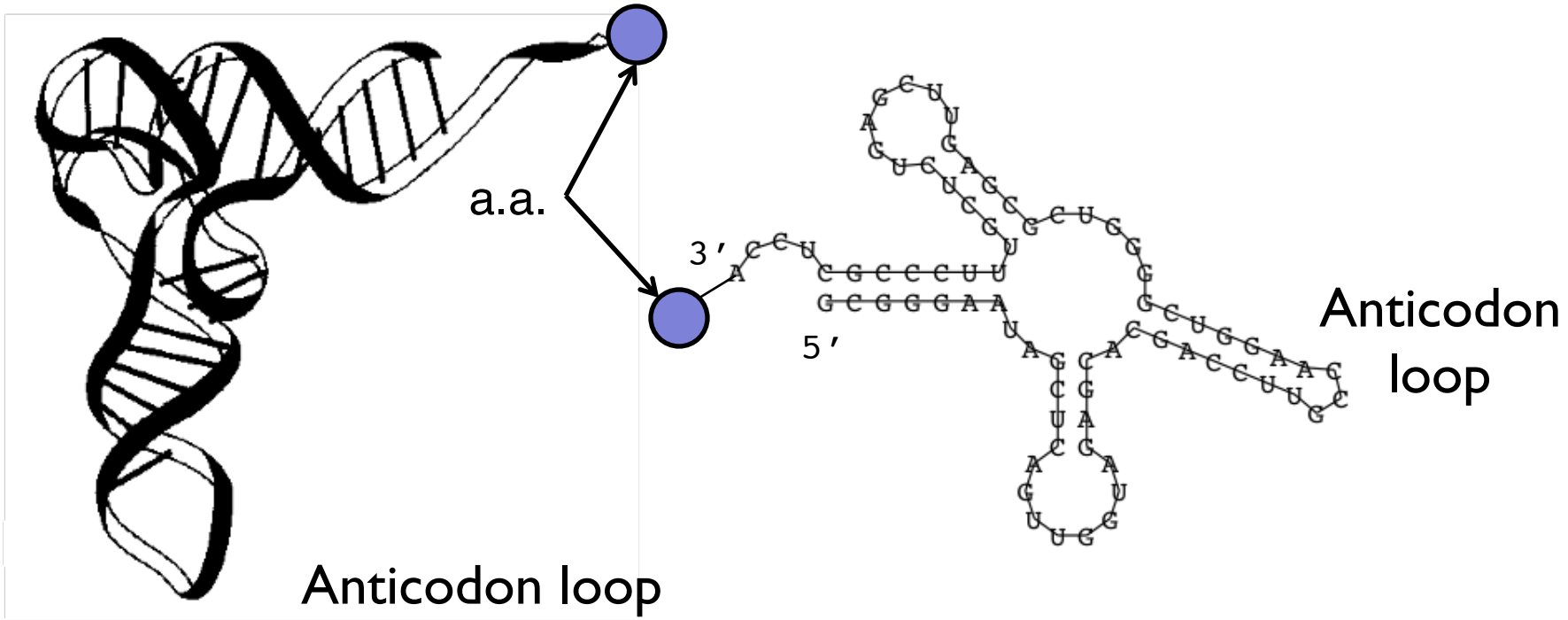
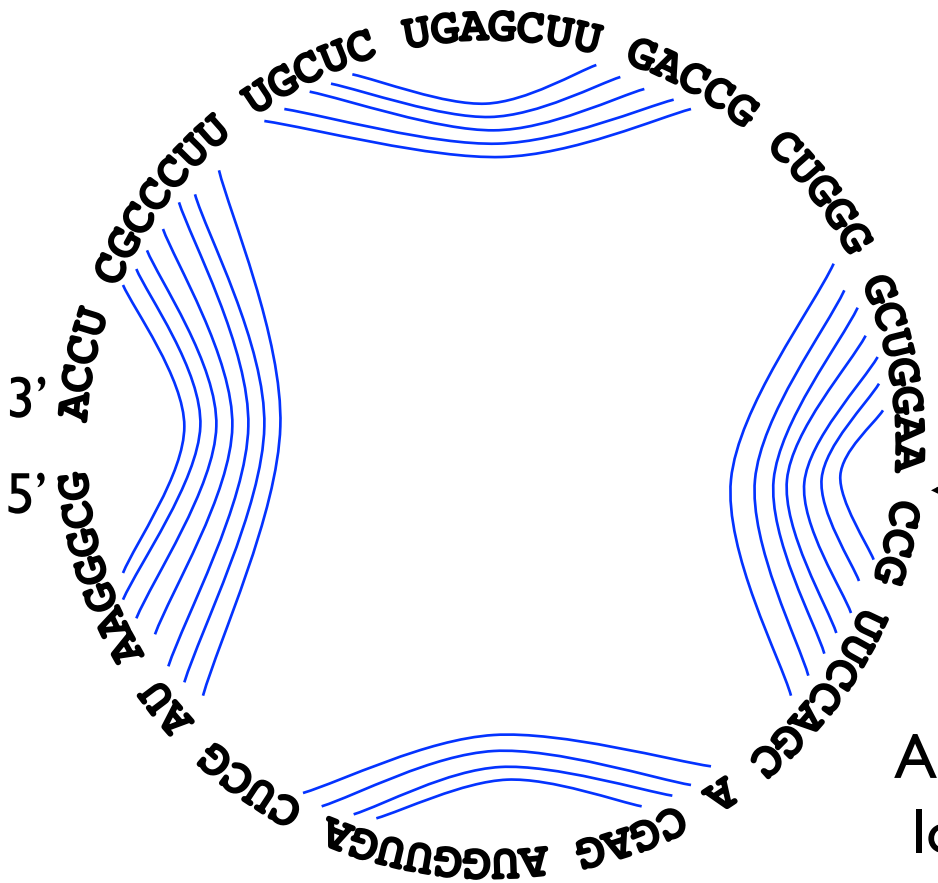


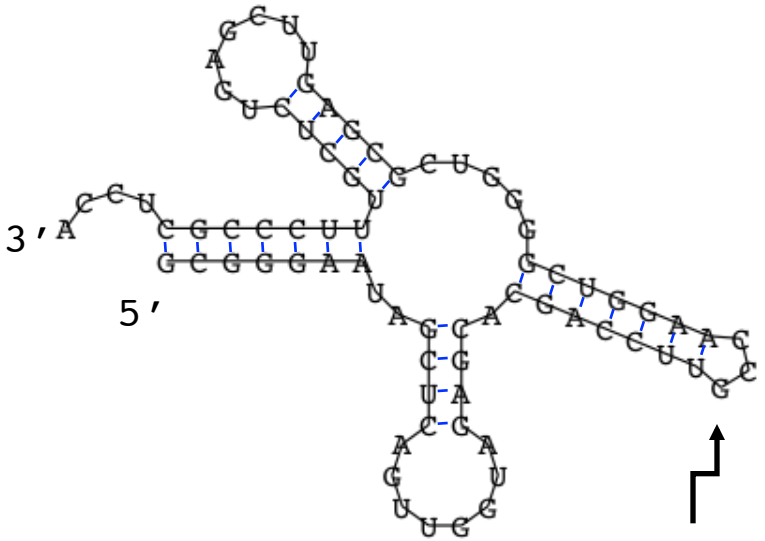
Figure 1: a) The spatial structure of the phenylalanine tRNA form yeast

b) The secondary structure extracts the most important information about the structure, namely the pattern of base pairings.

tRNA - Alt. Representations



Anticodon loop



Anticodon loop

Definitions

Sequence $^{5'}$ $r_1\ r_2\ r_3 \ldots r_n$ $^{3'}$ in {A, C, G, T/U}

A Secondary Structure is a set of pairs i•j s.t.

i < j-4, and } no sharp turns

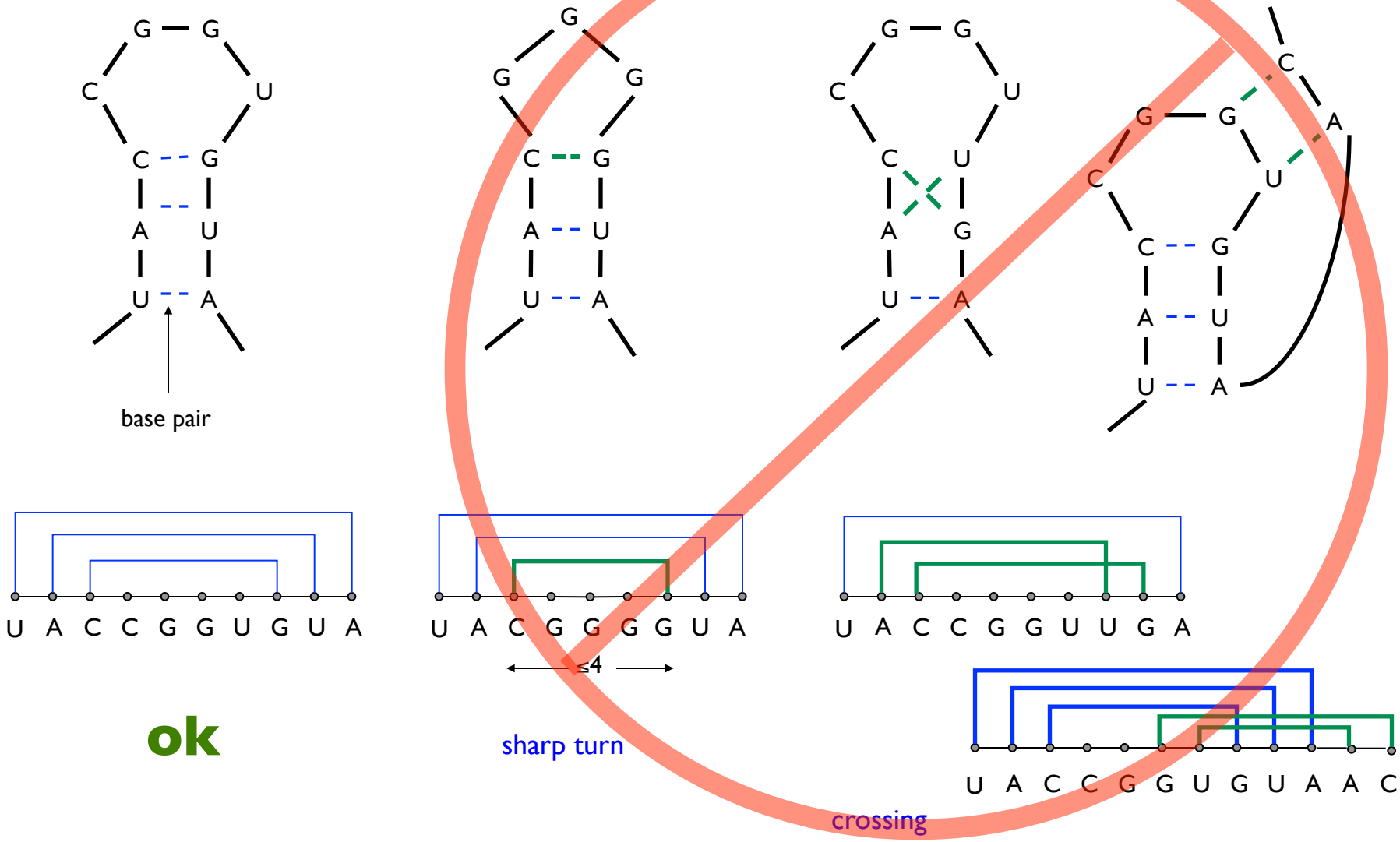
if i•j & i'•j' are two different pairs with i ≤ i', then

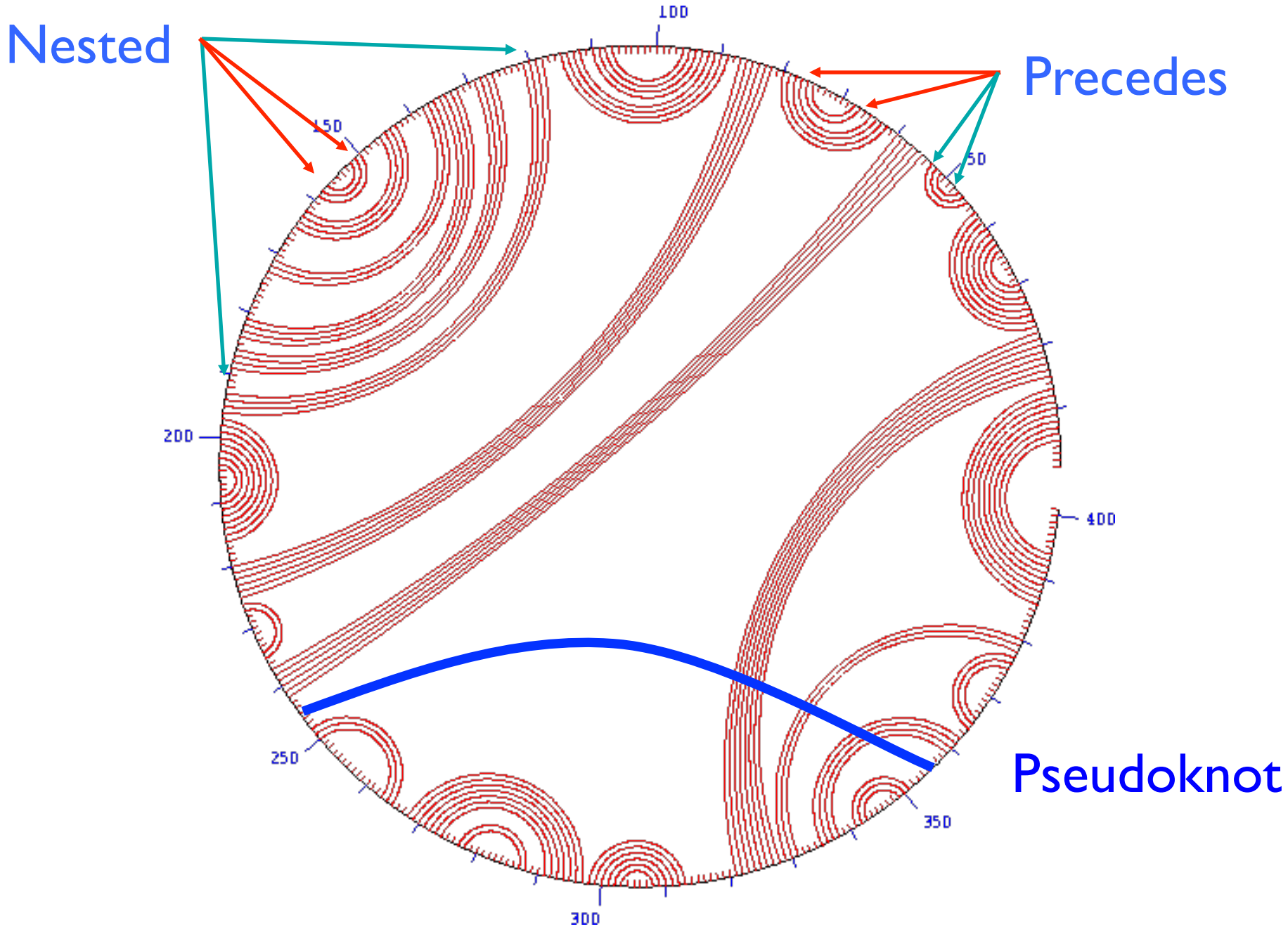
j < i', or

i < i' < j' < j

} 2nd pair follows 1st, or is nested within it; no "pseudoknots."

RNA Secondary Structure: Examples




Nested
Precedes
Pseudoknot
100
150
50
200
400
250
350
300

Approaches to Structure Prediction

Maximum Pairing
- + works on single sequences
- + simple
- - too inaccurate

Minimum Energy
- + works on single sequences
- - ignores pseudoknots
- - only finds “optimal” fold

Partition Function
- + finds all folds
- - ignores pseudoknots

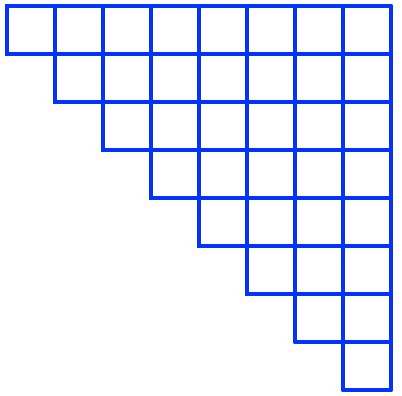
Nussinov: Max Pairing

$B(i,j)$ = # pairs in optimal pairing of r_i ... r_j

$B(i,j) = 0$ for all i, j with $i \geq j-4$; otherwise

$B(i,j)$ = max of:

$$\begin{cases} B(i,j-1) \\ \max \{ B(i,k-1)+1+B(k+1,j-1) \mid \\ \quad i \leq k < j-4 \text{ and } r_k\text{-}r_j \text{ may pair} \} \end{cases}$$

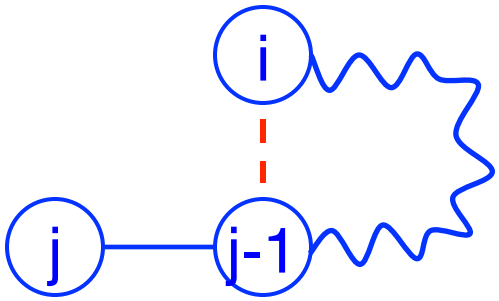


R Nussinov, AB Jacobson, "Fast algorithm for predicting the secondary structure of single-stranded RNA." PNAS 1980.

"Optimal pairing of r_i ... r_j"
Two possibilities

j Unpaired:

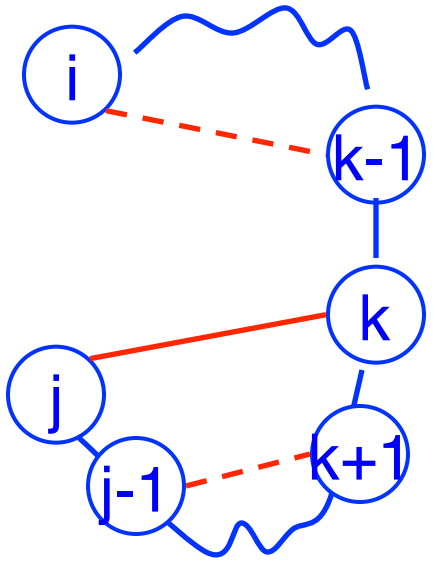
Find best pairing of r_i ... r_{j-1}



j Paired (with some k):

Find best r_i ... r_{k-1} +

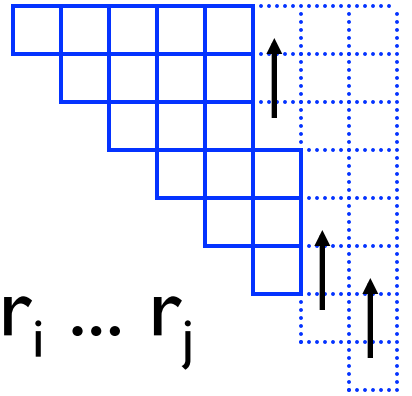
best r_{k+1} ... r_{j-1} plus 1



Why is it slow?

Why do pseudoknots matter?

Nussinov:
A Computation Order

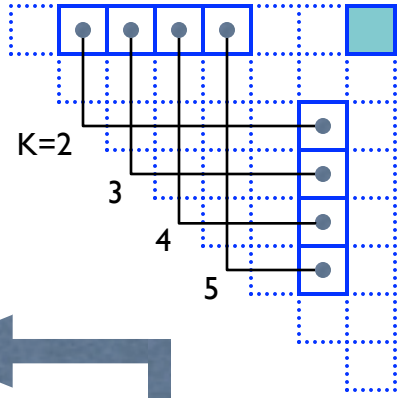


B(i,j) = # pairs in optimal pairing of r_i ... r_j

B(i,j) = 0 for all i, j with i ≥ j-4; otherwise

B(i,j) = max of:

$$\begin{cases} B(i,j-1) \\ \max \{ B(i,k-1)+1+B(k+1,j-1) \mid \\ \quad i \le k < j-4 \text{ and } r_k\text{-}r_j \text{ may pair} \} \end{cases}$$



Time: $O(n^3)$

Which Pairs?

Usual dynamic programming "trace-back" tells you *which* base pairs are in the optimal solution, not just how many

Approaches to Structure Prediction

Maximum Pairing
- + works on single sequences
- + simple
- - too inaccurate

Minimum Energy
- + works on single sequences
- - ignores pseudoknots
- - only finds “optimal” fold

Partition Function
- + finds all folds
- - ignores pseudoknots

Pair-based Energy Minimization

E(i,j) = energy of *pairs* in optimal pairing of r_i ... r_j

E(i,j) = ∞ for all i, j with $i \geq j-4$; otherwise

E(i,j) = min of:

$$\begin{cases} E(i,j-1) \\ \min \{ E(i,k-1) + e(r_k, r_j) + E(k+1,j-1) \mid i \leq k < j-4 \} \end{cases}$$

energy of k-j *pair*

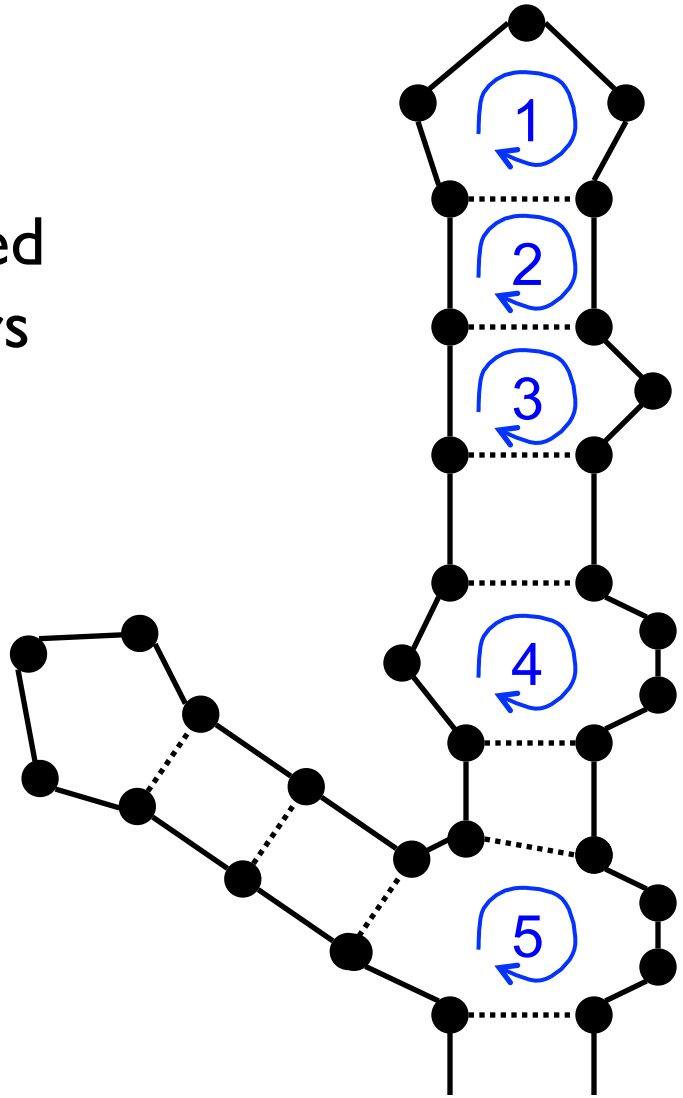
Time: $O(n^3)$

Loop-based Energy Minimization

Detailed experiments show it's more accurate to model based on *loops*, rather than just pairs

Loop types

1. Hairpin loop
2. Stack
3. Bulge
4. Interior loop
5. Multiloop



Zuker: Loop-based Energy, I

W(i,j) = energy of optimal pairing of r_i ... r_j

V(i,j) = as above, but forcing pair i•j

W(i,j) = V(i,j) = ∞ for all i, j with i ≥ j-4

W(i,j) = min(W(i,j-1),

min { W(i,k-1)+V(k,j) | i ≤ k < j-4 }

)

Zuker: Loop-based Energy, II

hairpin stack bulge/ interior multi- loop

$$V(i,j) = \min(eh(i,j),\ es(i,j)+V(i+1,j-1),\ VBI(i,j),\ VM(i,j))$$

$$VM(i,j) = \min \{\ W(i,k)+W(k+1,j) \mid i < k < j\ \}$$

$$VBI(i,j) = \min \{\ ebi(i,j,i',j') + V(i', j') \mid i < i' < j' < j \ \&\ i'-i+j-j' > 2\ \}$$

bulge/ interior

Time: $O(n^4)$

$O(n^3)$ possible if ebi(.) is "nice"

Energy Parameters

Q. Where do they come from?

A1. Experiments with carefully selected synthetic RNAs

A2. Learned algorithmically from trusted alignments/structures [Andronescu et al., 2007]

Single Seq Prediction Accuracy

Mfold, Vienna,... [Nussinov, Zuker, Hofacker, McCaskill]

Latest estimates suggest ~50-75% of base pairs predicted correctly in sequences of up to ~300nt

Definitely useful, but obviously imperfect

Approaches to Structure Prediction

Maximum Pairing
- \+ works on single sequences
- \+ simple
- \- too inaccurate

Minimum Energy
- \+ works on single sequences
- \- ignores pseudoknots
- \- only finds “optimal” fold

Partition Function
- \+ finds all folds
- \- ignores pseudoknots

Approaches, II

Comparative sequence analysis

+ handles all pairings (potentially incl. pseudoknots)
- requires several (many?) aligned, appropriately diverged sequences

Stochastic Context-free Grammars

Roughly combines min energy & comparative, but no pseudoknots

Physical experiments (x-ray crystalography, NMR)

Next Lecture

Summary

RNA has important roles beyond mRNA

- Many unexpected recent discoveries

Structure is critical to function

- True of proteins, too, but they're easier to find from sequence alone due, e.g., to codon structure, which RNAs lack

RNA secondary structure can be predicted (to useful accuracy) by dynamic programming

Next: RNA "motifs" (seq + 2-ary struct) well-captured by "covariance models"