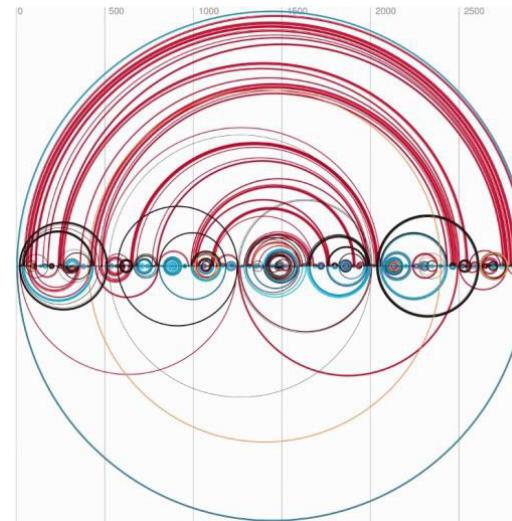


Graduate Student Seminar

Revisiting the Central Dogma The role of **Small RNA** in **Bacteria**



The Chinese University of Hong Kong
Faculty of Medicine
Department of Microbiology

Supervisor : Prof. Margaret Ip
Student : Helen Ma (PhD student)
Date : 2014-12-15

Content

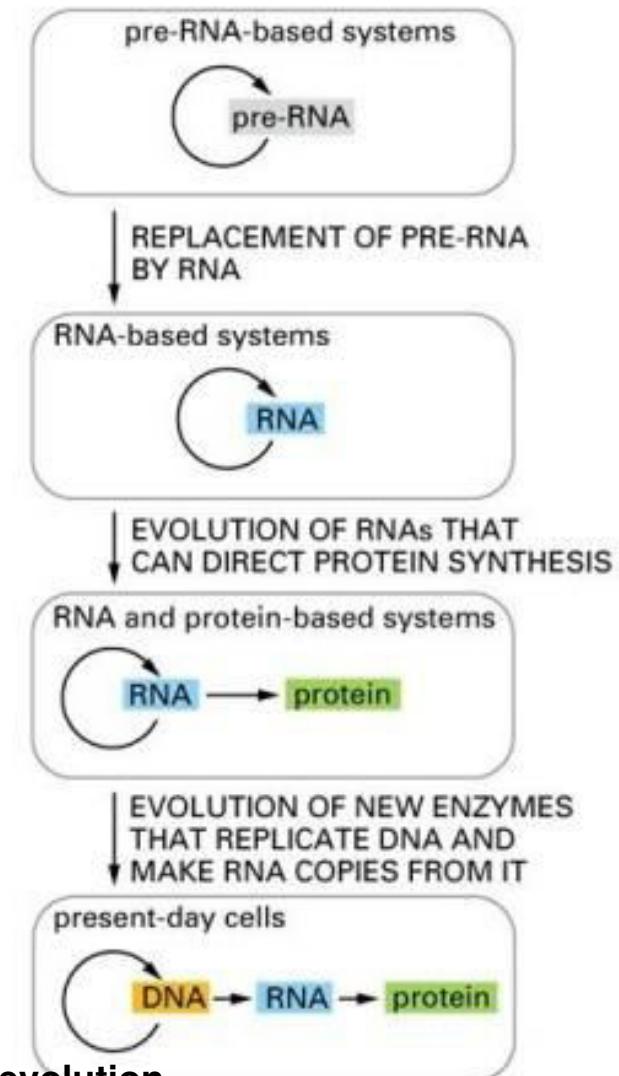
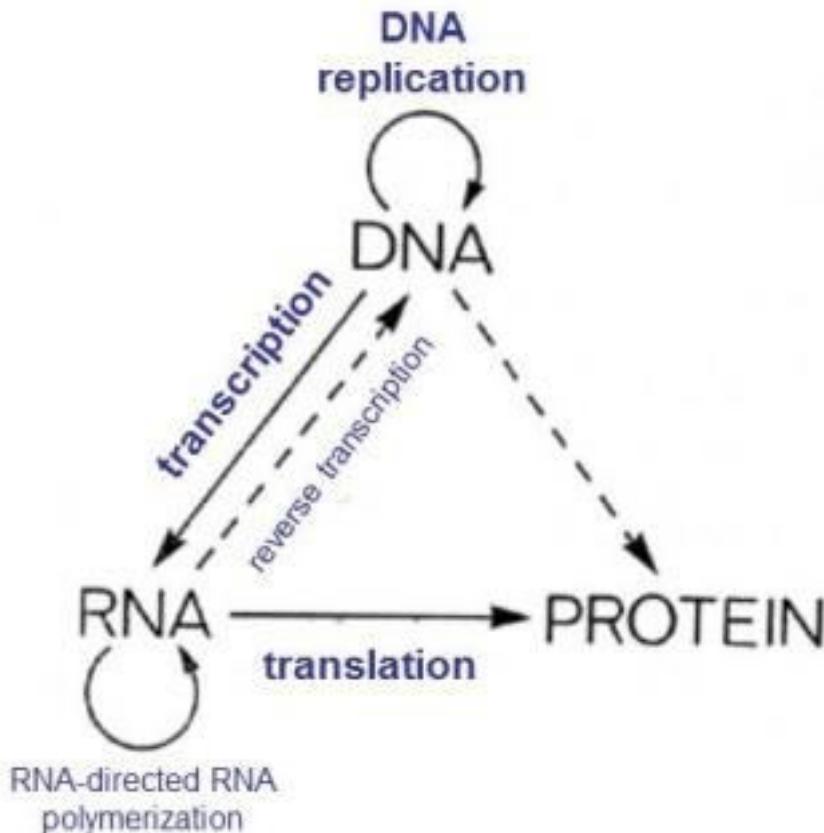
- (I) Introduciton
 - Revisiting the Central Dogma
 - Types of RNA / Small RNAs in Bacteria
- (II) Functions and Mechanisms of Small RNA
 - (A) Antisense RNAs
 - (B) Riboswitches
 - (C) Intergenic RNAs
- (III) Small RNA Prediction Softwares and Databases
 - RNAfold vs. CoFold
 - BSDR - Bacterial Small Regulatory RNA Database
- (IV) Future Perspectives
 - Hijacking nature's design - Artificial small RNAs

(I) Introduction

Revisiting the Central Dogma

RNA World Hypothesis

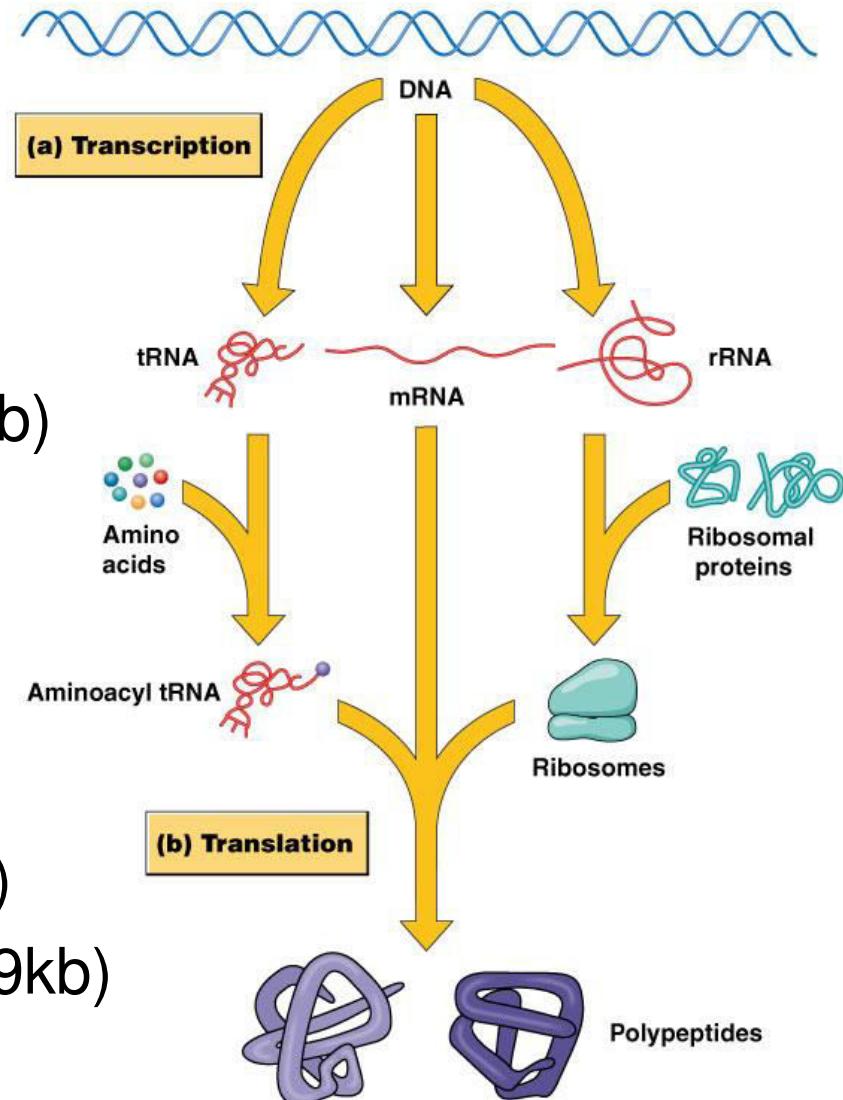
Flow of information



(I) Introduction

Types of RNA in Bacteria

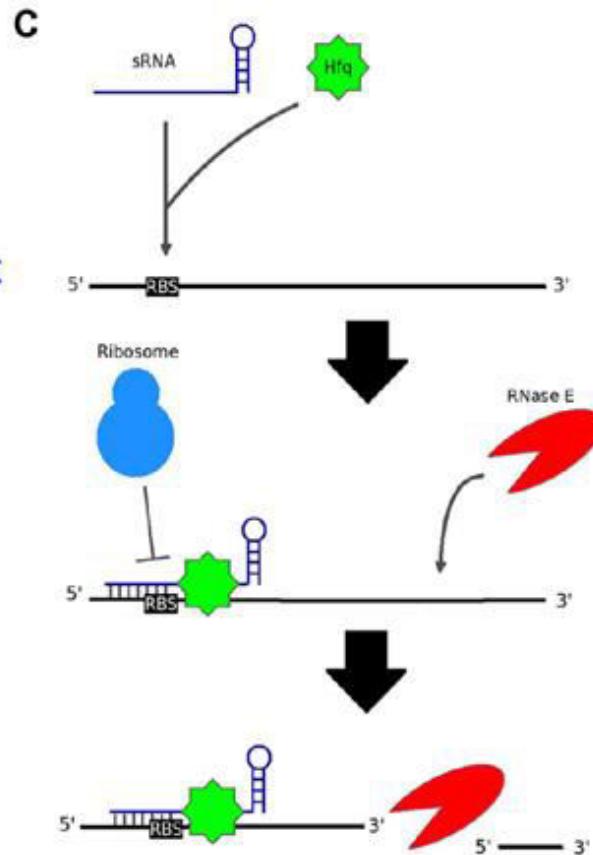
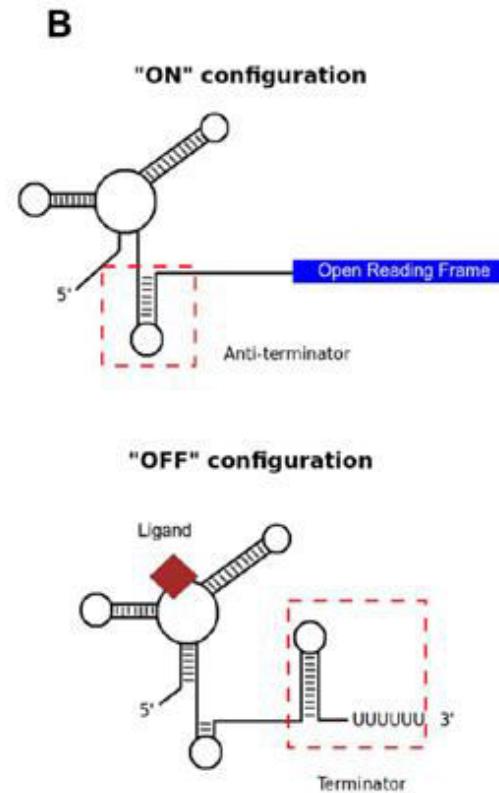
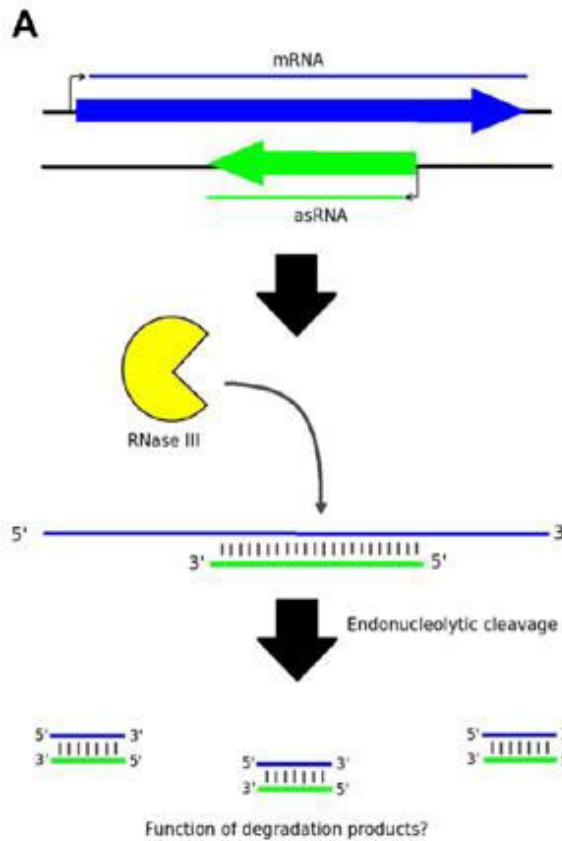
- **Coding RNA**
 - code for / translated to a protein
- Messenger RNA (mRNA, ~1-2kb)
- **Non-coding RNA (ncRNA)**
 - does not code for / translated to a protein
- Transfer RNA (tRNA, ~60-95bp)
- Ribosomal RNA (rRNA, ~1.5-2.9kb)
- **Small RNAs (~30-500nts)**



(I) Introduction

Types of Small RNA in Bacteria

(A) Antisense RNAs (asRNA) (B) Riboswitches (C) Intergenic Small RNAs

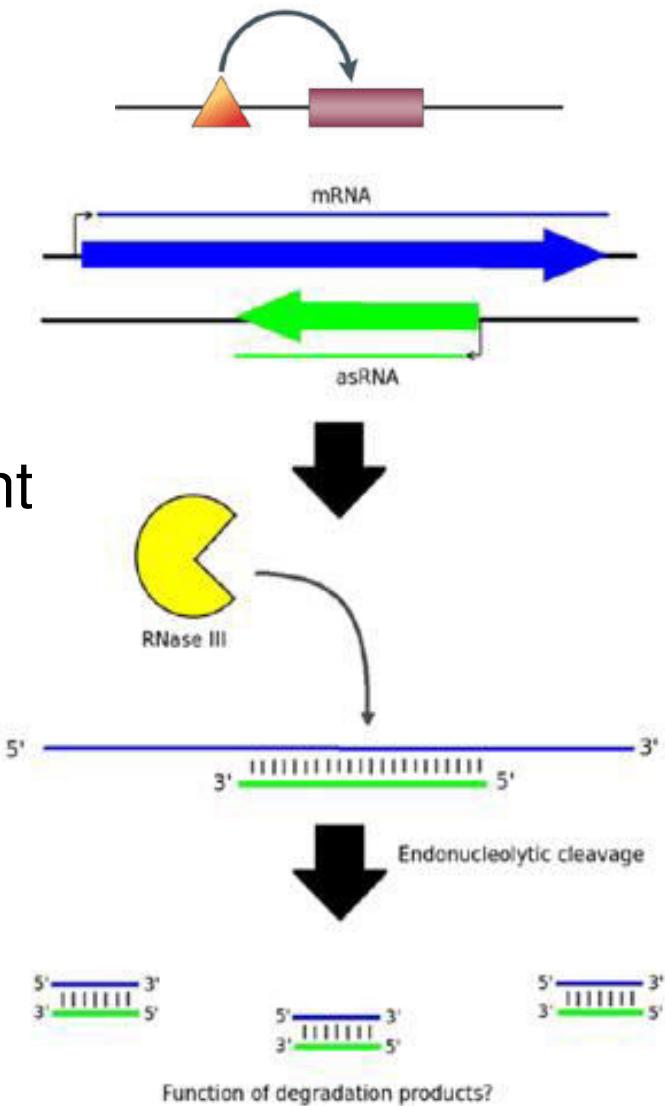


(II) Functions and Mechanisms

(A) Antisense RNAs

- Study in *E. coli* since 1960s
- Transcribed from opposite strand
- Maintain plasmid number
- Against bacteriophage development
- Blocks ribosome for protein expression
- Down-regulate gene expression
e.g. outer membrane proteins
OmpF(efflux pump),
DicF (cell division), etc.

a Cis (local)

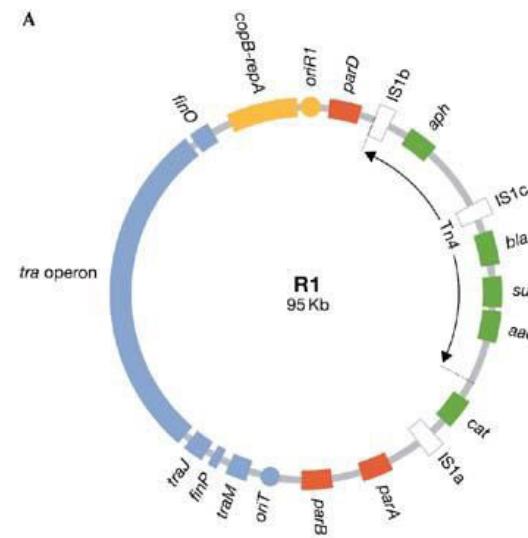


Wager E.G.H. and Simons R.W. ANTISENSE RNA CONTROL IN BACTERIA, PHAGES, AND PLASMIDS.
Annu. Rev. Microbiol. 1994. 48.'713-4

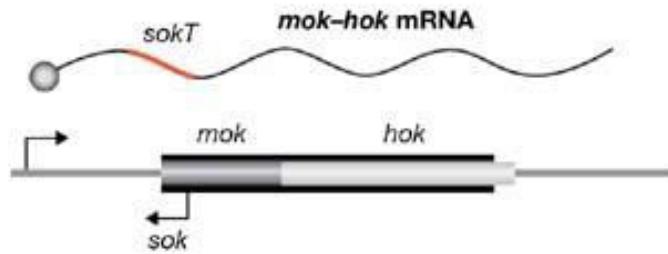
(II) Functions and Mechanisms

(A) Antisense RNAs

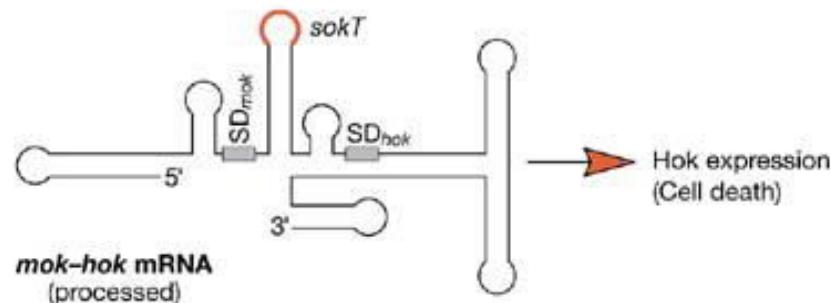
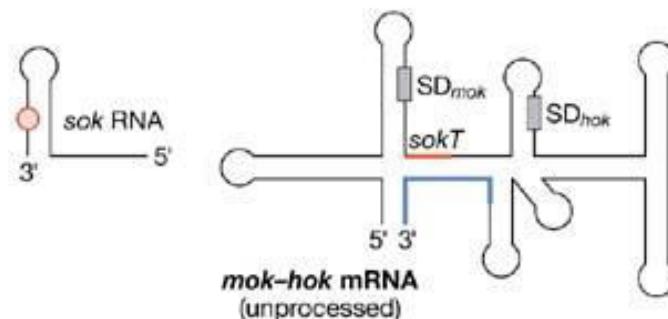
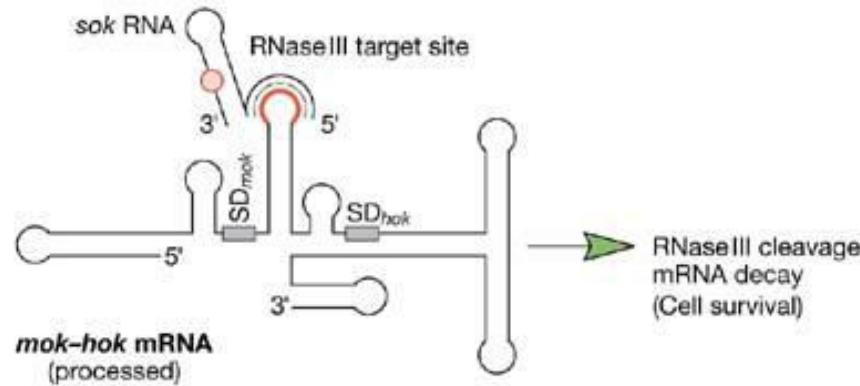
- Post-segregation killing system in plasmid R1
- **Stem-loop structures** of translated **parB** gene
- **hok** : host killing
- **mok** : mediator of killing
- **sok / sokT** : suppression of killing



A

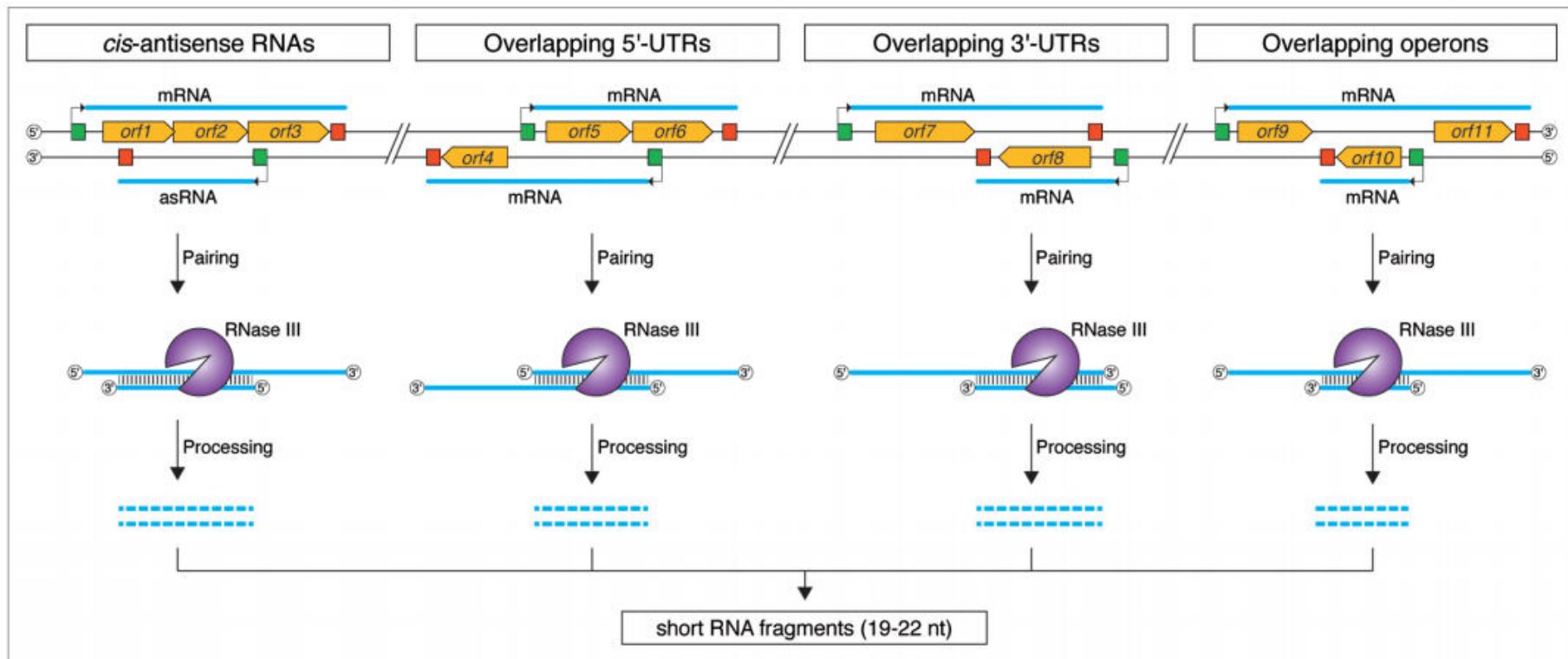


B



(II) Functions and Mechanisms

(A) Antisense RNAs



Hypothesis :

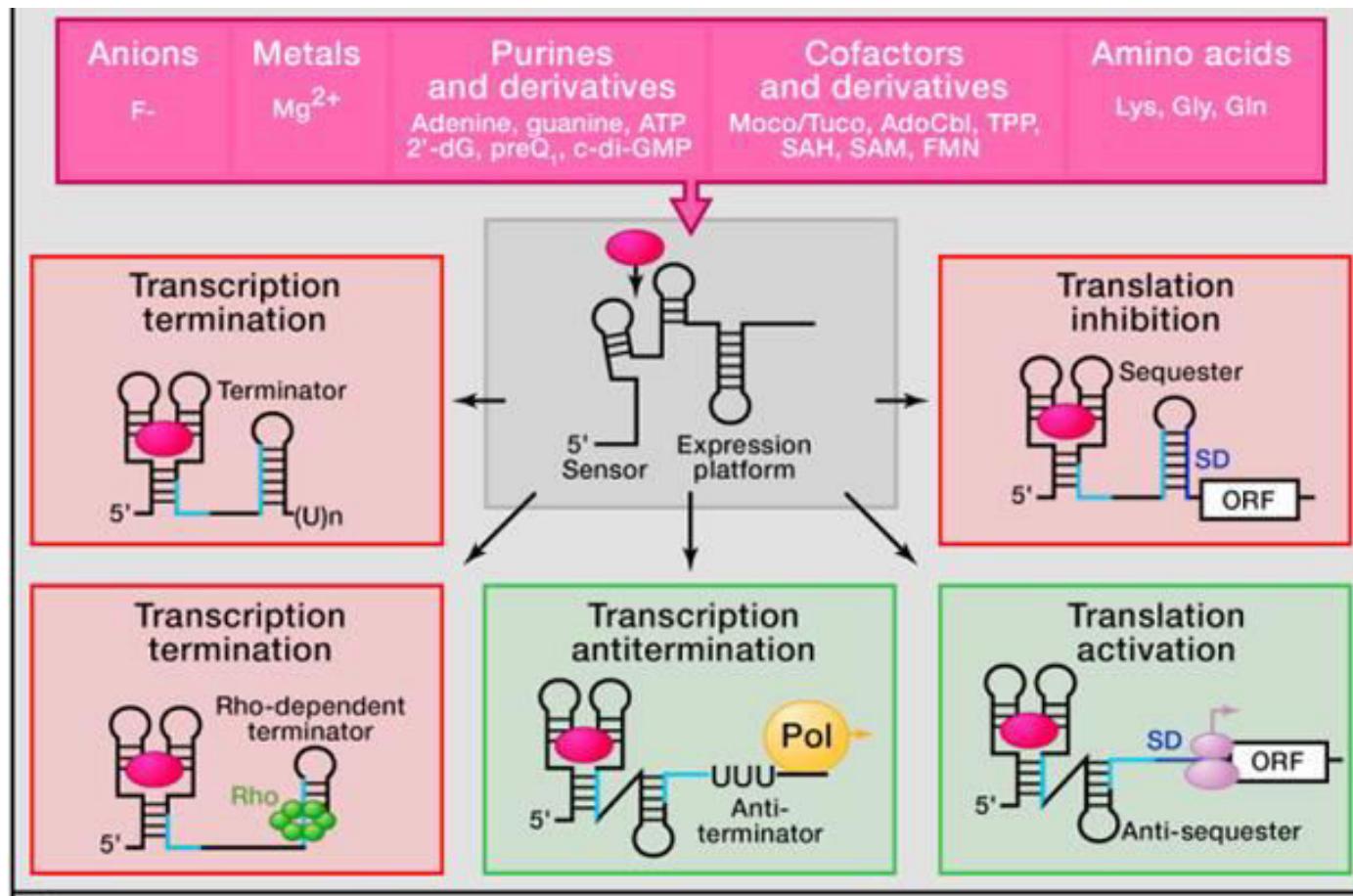
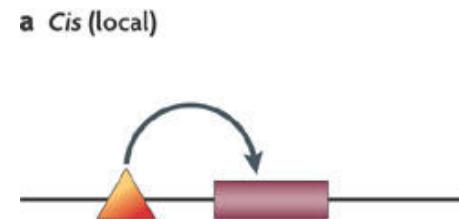
- (1) Antisense RNA acts as a threshold level to control level of sense RNA, to prevent over reaction to environmental stimuli
- (2) Control over genes in the same operon by one antisense RNA molecule
- (3) Potential role of short RNA fragments on target gene expression

Lasa S. et. al., An effort to make sense of antisense transcription in bacteria.
RNA Biology 9:8, 1039-1044; August 2012; © 2012 Landes Bioscience

(II) Functions and Mechanisms

(B) Riboswitches

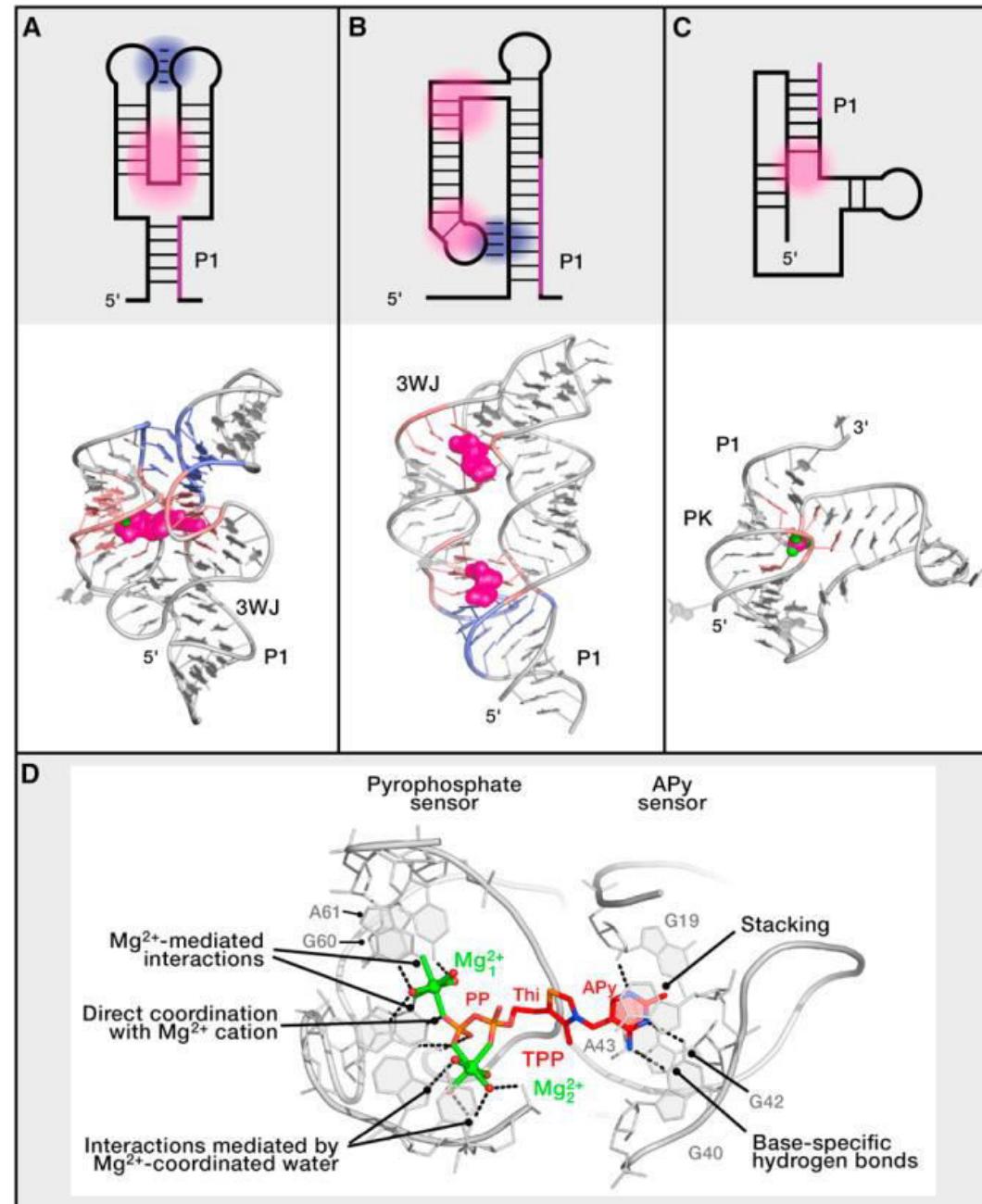
- Discovered in 2000s
- RNA-based intracellular sensors
- Stem-loop structures



(II) Functions and Mechanisms

(B) Riboswitches

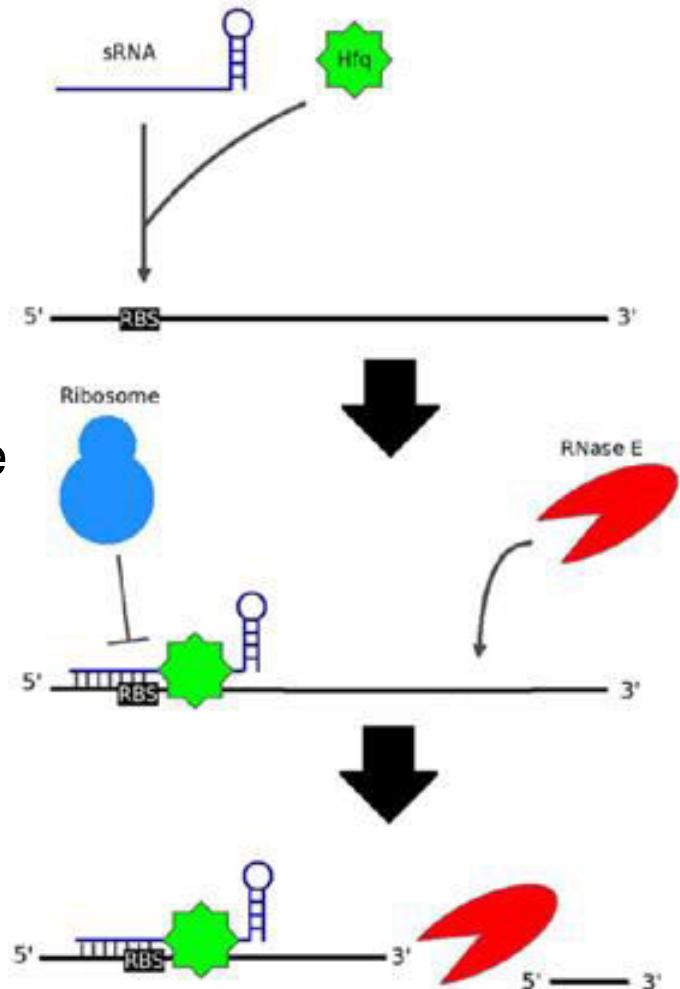
- "Junctional" riboswitches
- Position of metabolic sensors
- Stability of **stem-loop structures**
- Class Ia (A) e.g. purines
- Class Ib (B) e.g. vitamine derivatives
- Class II (C) e.g. Mg²⁺



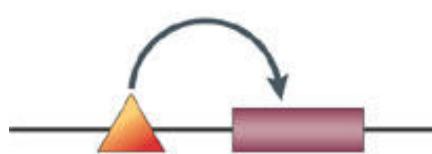
(II) Functions and Mechanisms

(C) Intergenic small RNAs

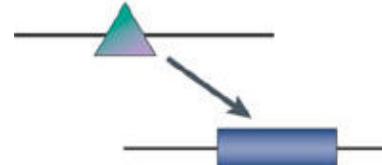
- Binds to target mRNA in short stretches (7-12nt)
- generally overlapping with / close to ribosomal binding site (RBS)
- **Stem-loop structures** block 70S ribosome formation and translation initiation



a *Cis* (local)

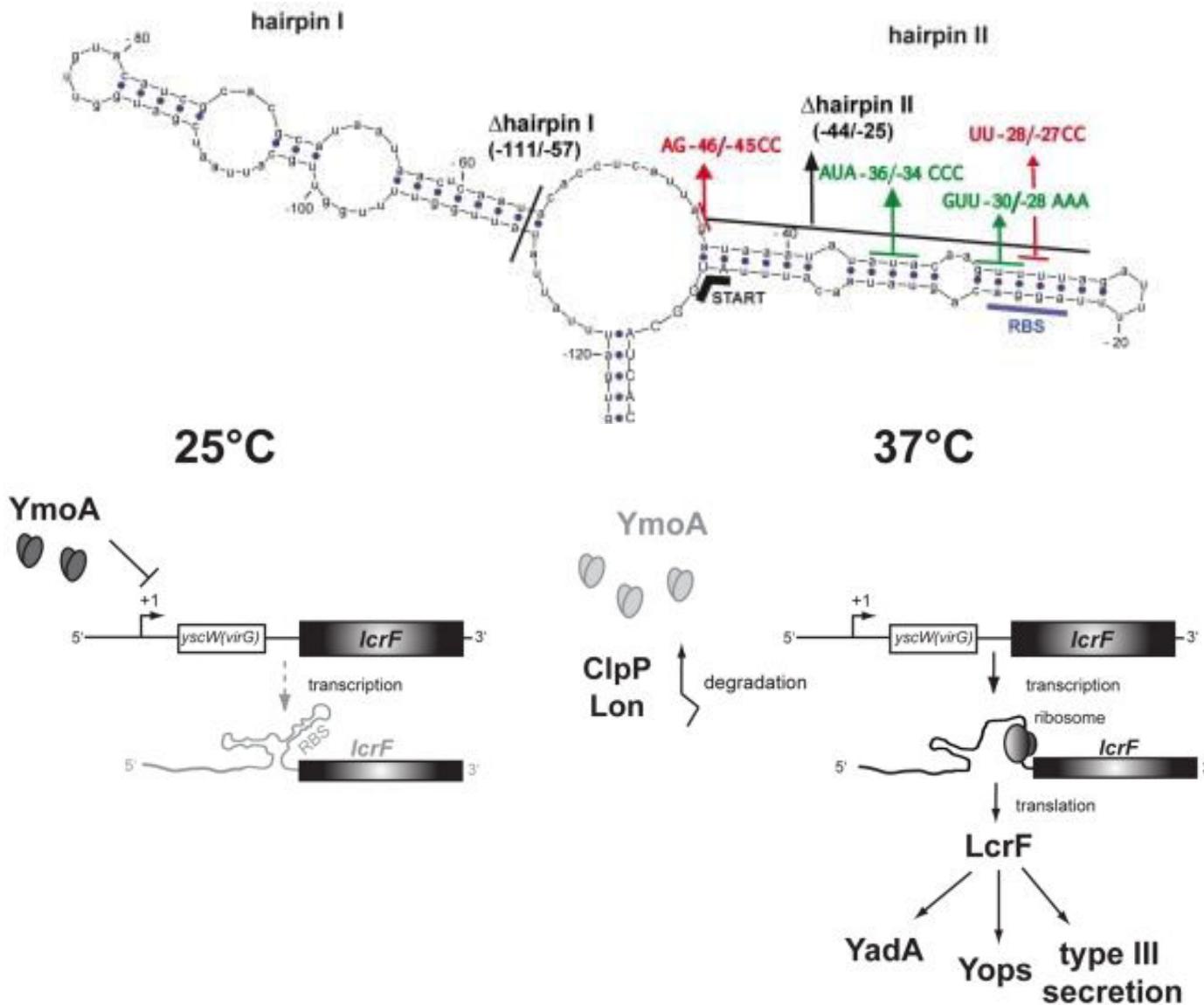


b *Trans* (distal)



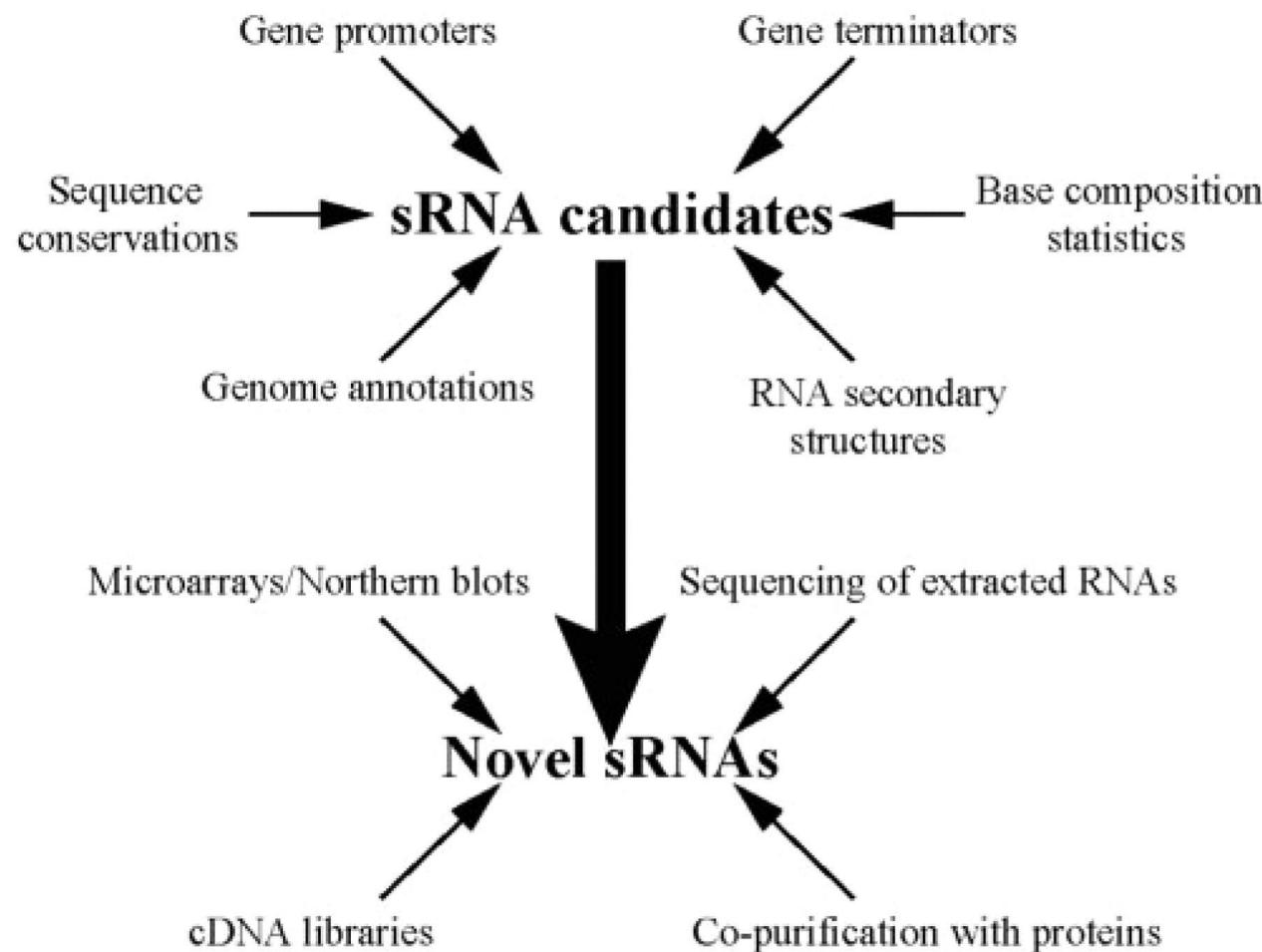
(II) Functions and Mechanisms

- Virulence regulation by thermosensor in *Yersinia*



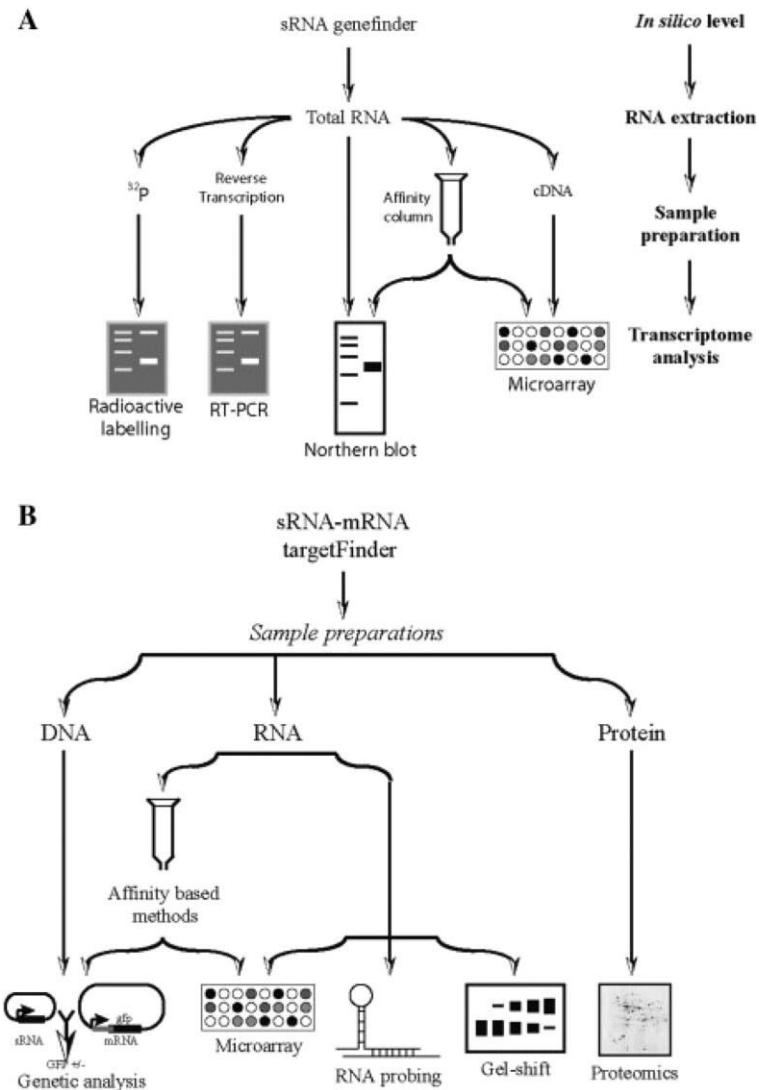
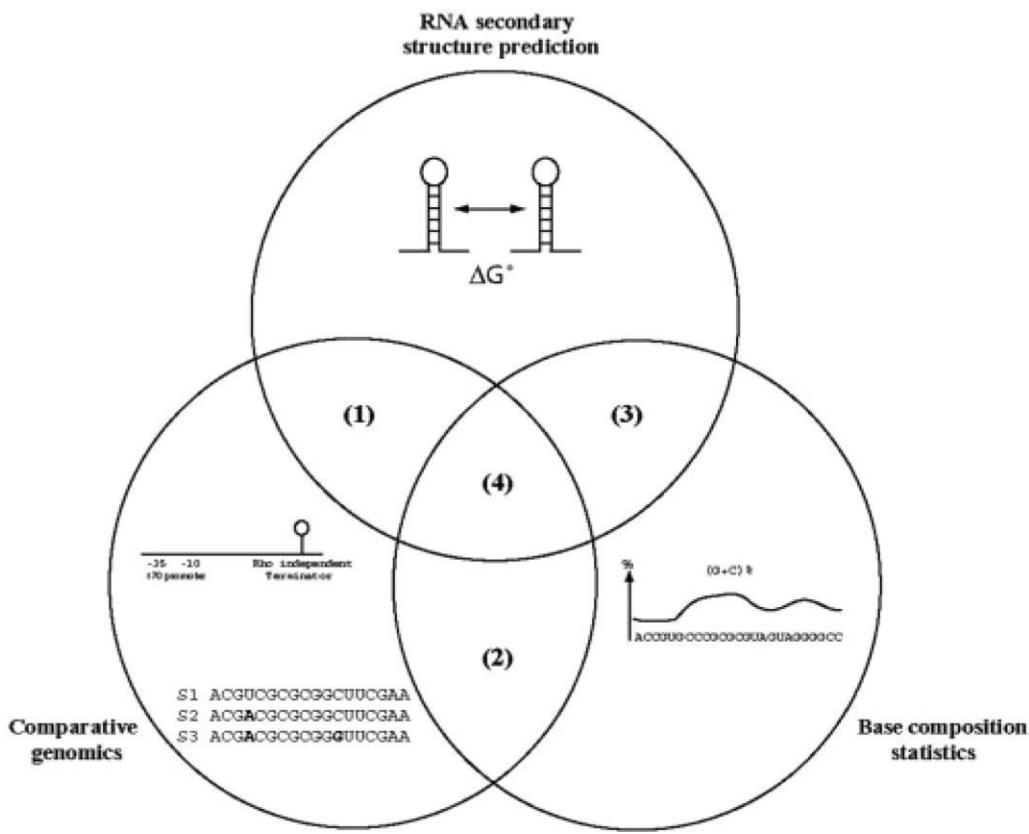
(III) Softwares and Databases

(III) Small RNA Prediction Softwares and Databases



(III) Softwares and Databases

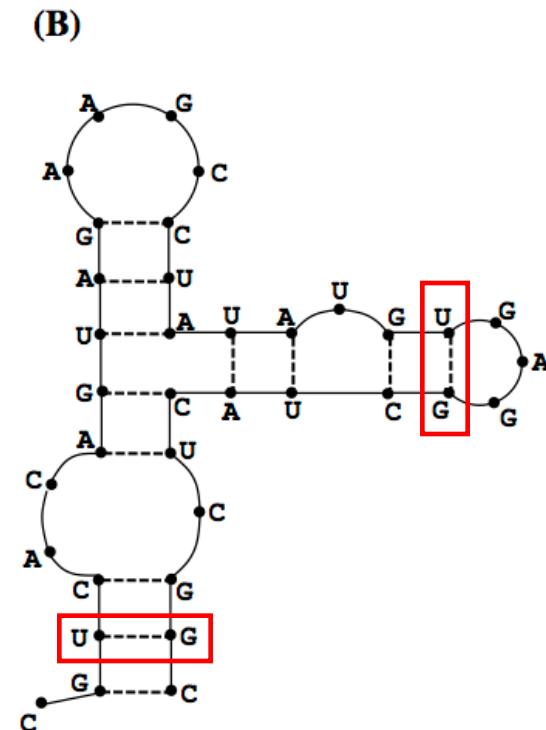
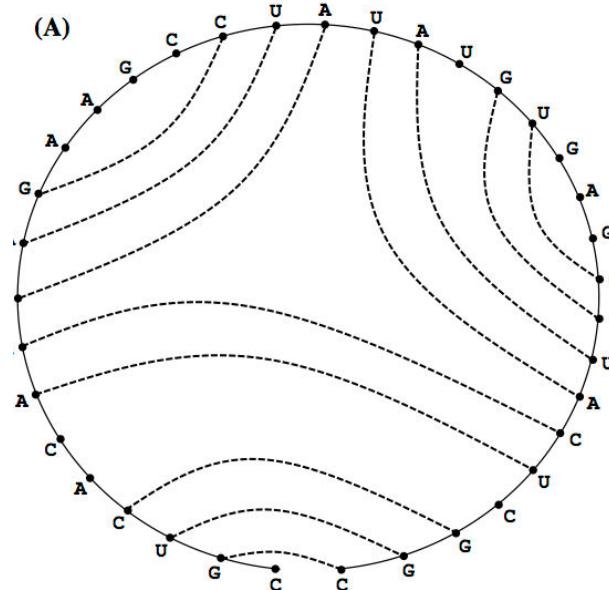
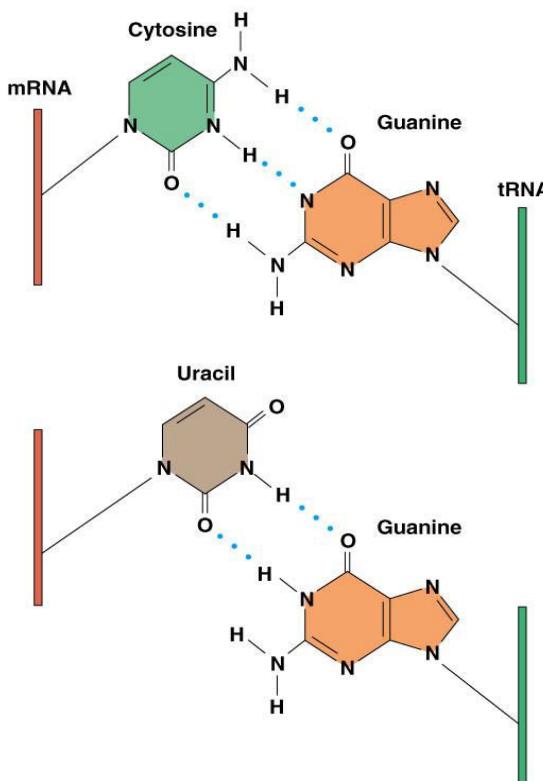
(III) Small RNA Prediction Softwares and Databases



(III) Softwares and Databases

- DNA base pairing : A-T , G-C
- RNA base pairing : A-U , G-C, **G-U...**
- Sample RNA string:

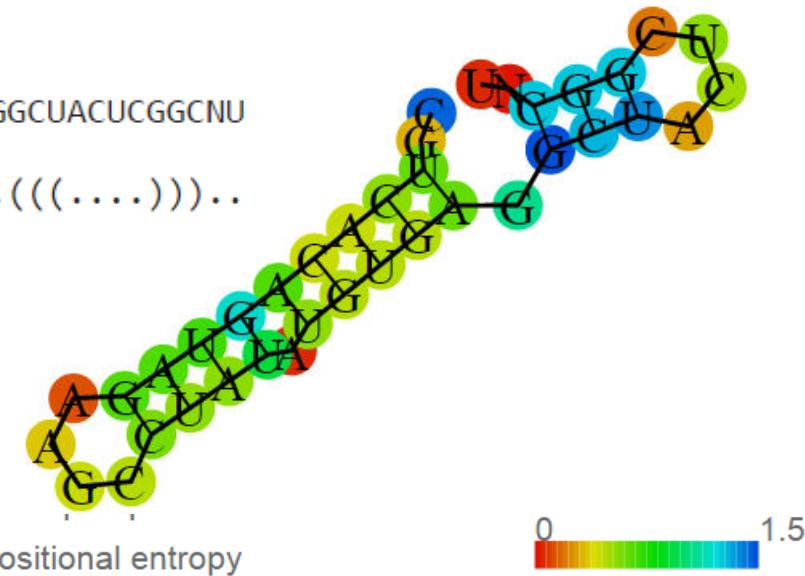
CGUCACAGUAGAAGCCUAUAUGUGAGGCUACUCGGC (36nt)



(III) Softwares and Databases

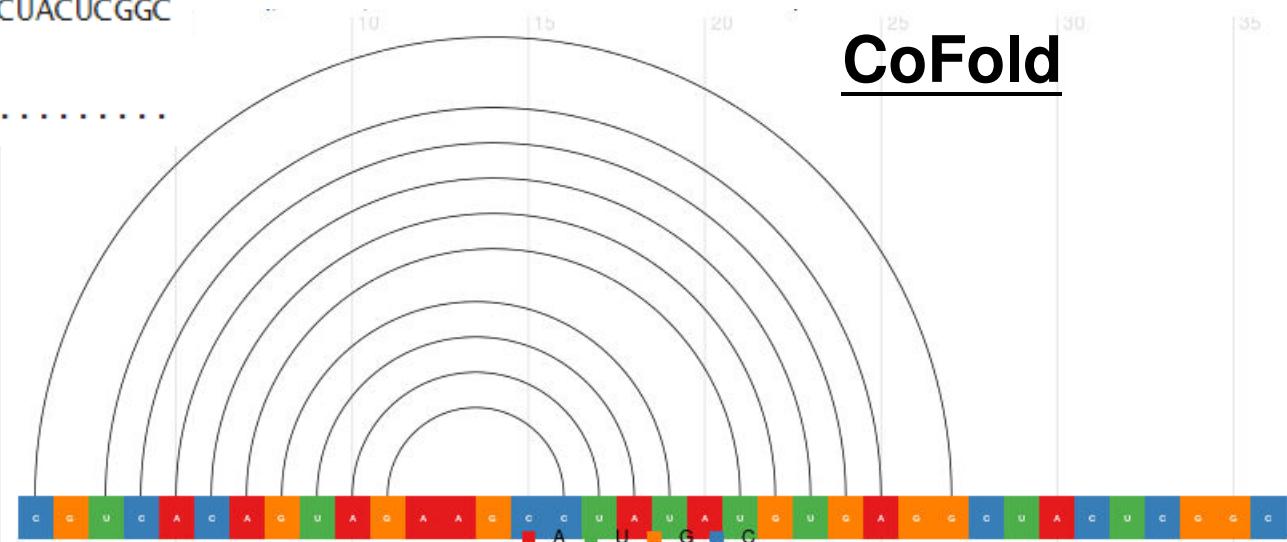
RNAfold

CGUCACAGUAGAAGCCUAUAUGUGAGGCUACUCGGCNU
..(((((((((....))))).))).((((....)))..



CGUCACAGUAGAAGCCUAUAUGUGAGGCUACUCGGC
.(((((((((....))))).))).((((....)))..)

CoFold

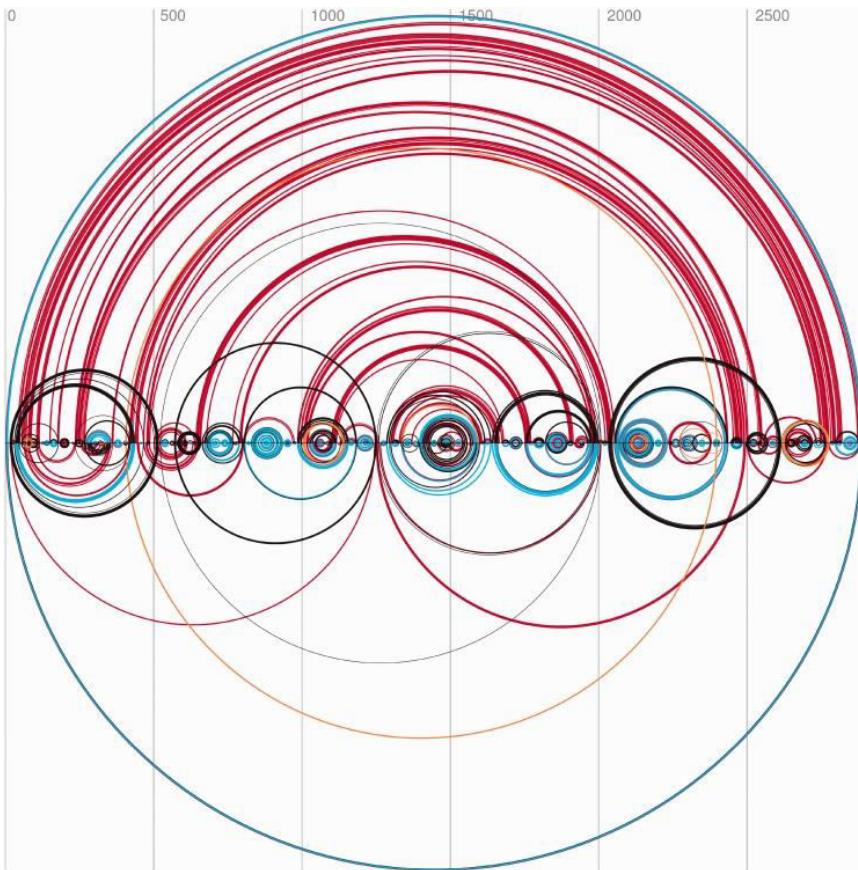


RNAfold <http://rna.tbi.univie.ac.at/cgi-bin/RNAfold.cgi>

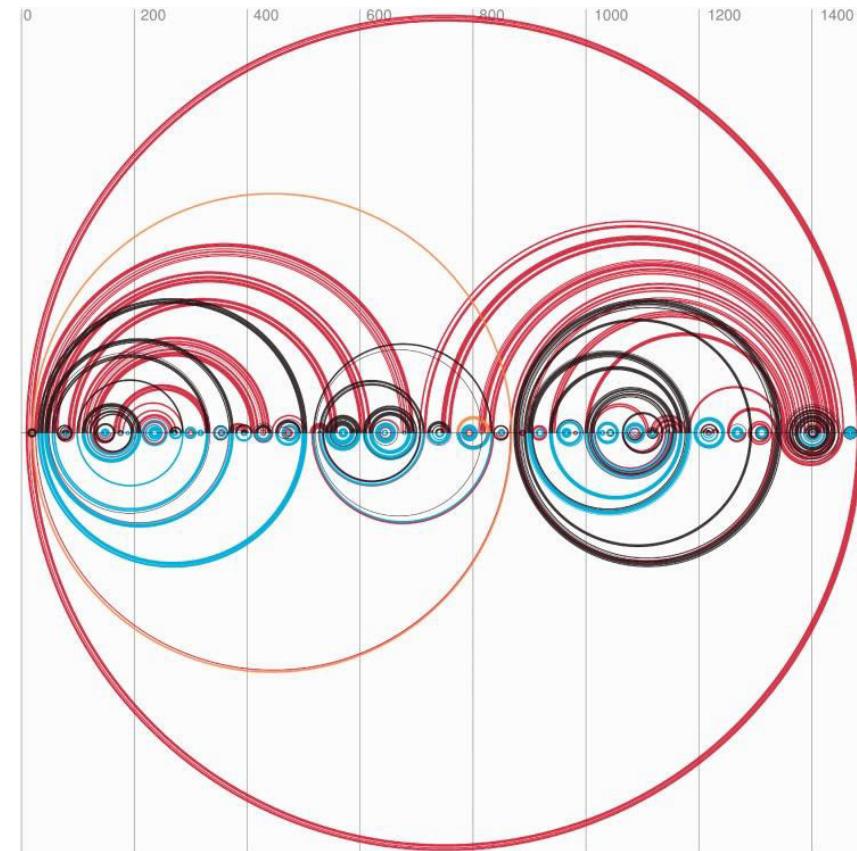
CoFold <http://www.e-rna.org/cofold/>

(III) Softwares and Databases

- RNAfold vs. CoFold



23S rRNA of *P. aeruginosa* (2893nt)

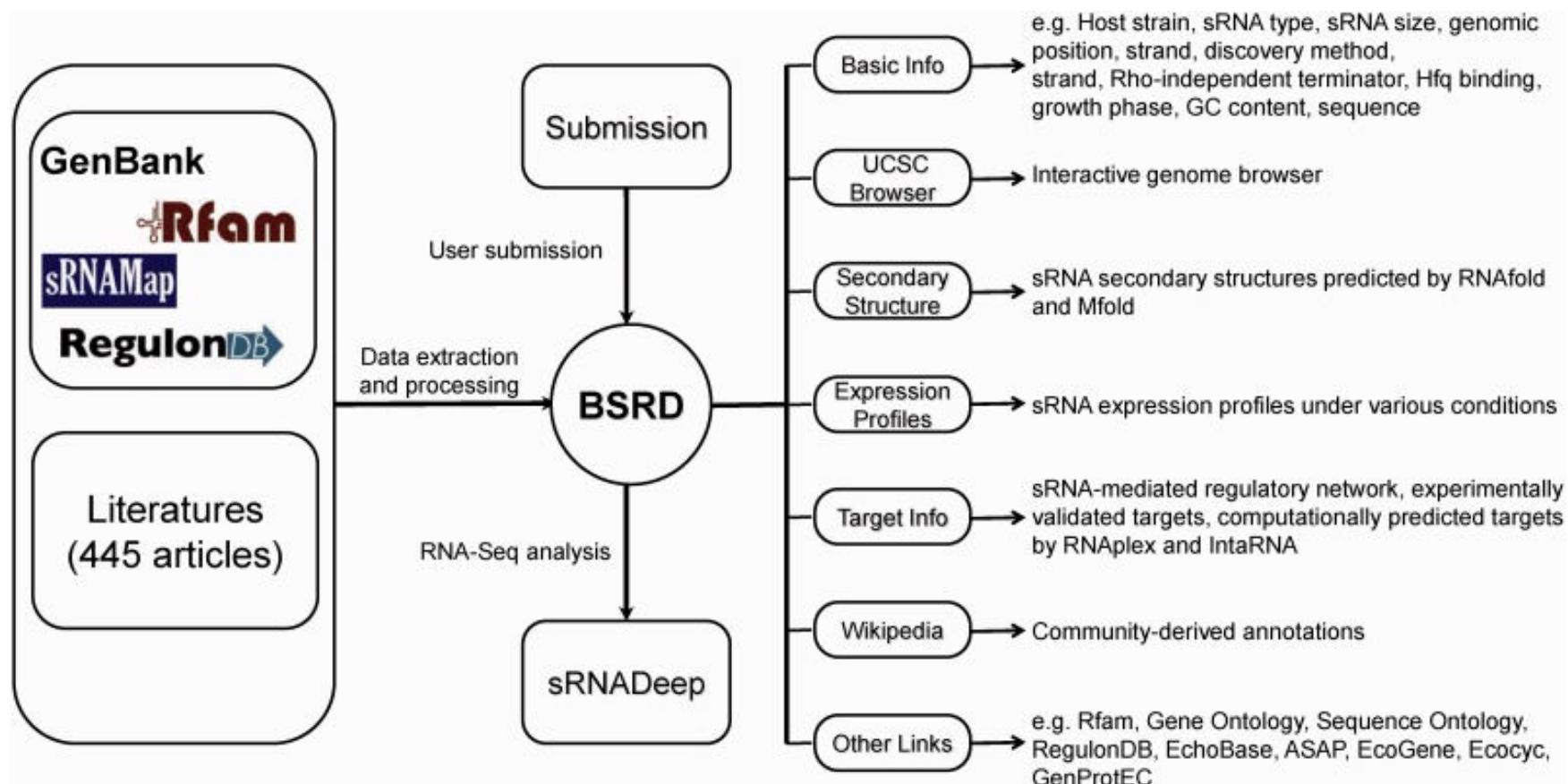


16S rRNA fresh water algae
Cryptomonas sp. (1493bp)

Proctor J. R. and Meyer I. M. CoFold: an RNA secondary structure prediction method that takes co-transcriptional folding into account. Nucleic Acids Res. May 2013; 41(9): e102.

(III) Small RNA Prediction Softwares and Databases

- BSRD: a repository for bacterial small regulatory RNA



(III) Small RNA Prediction Softwares and Databases

- BSRD: a repository for bacterial small regulatory RNA

(a)

• Menu

- Home
- Search BSRD
- Hierarchical taxonomy
- **Regulatory network**
- BLAST BSRD
- Download
- sRNADeep
- Submission
- Latest publications

• Regulatory network

Regulatory network ⓘ

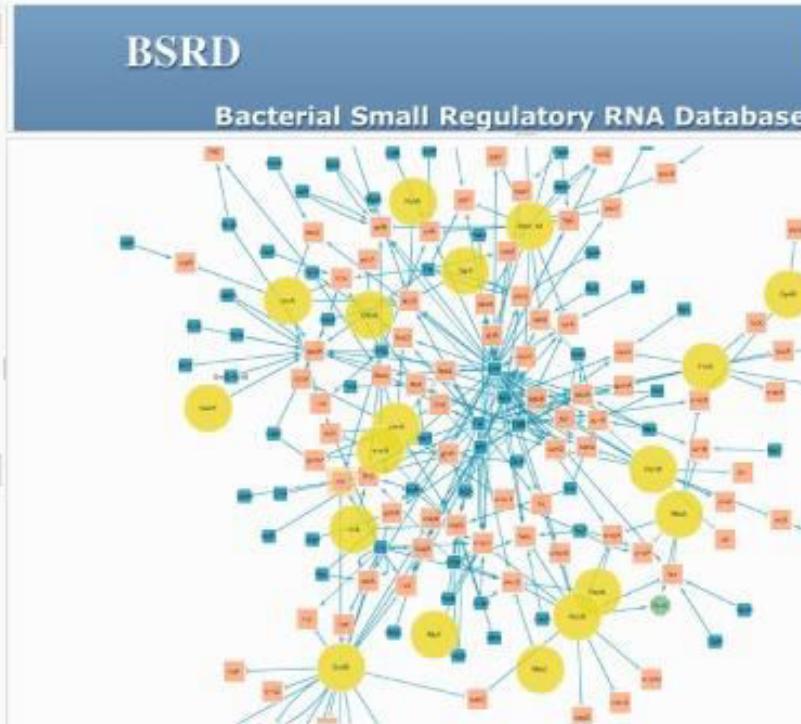
Select organism:
Escherichia coli K12 MG1655

Select Layout: ForceDirected

Submit

Filter by name: (Case sensitive)

Submit Clear Filter



(C) Interaction info

Strain name	Escherichia coli K12 MG1655
Target gene	btuB
Regulation effect	repression
Pubmed ID	16359331

(b)

Phosphoglucomutase - Escherichia coli (strain K12)

UniProt Downloads Contact Documentation Help

Documents Clusters Order Search Blast+ Align Retrieve

Search in Query Protein Knowledgebase (UniProtKB)

P31120 (GLMM_ECOLI) Reviewed, UniProtKB/Swiss-Prot Last modified July 11, 2012. Version 108. History...

Contribute Send feedback Read comments (0) or add your own

Clusters with 100%, 90%, 50% identity | Documents (2) | Next and previous entry

Third-party data

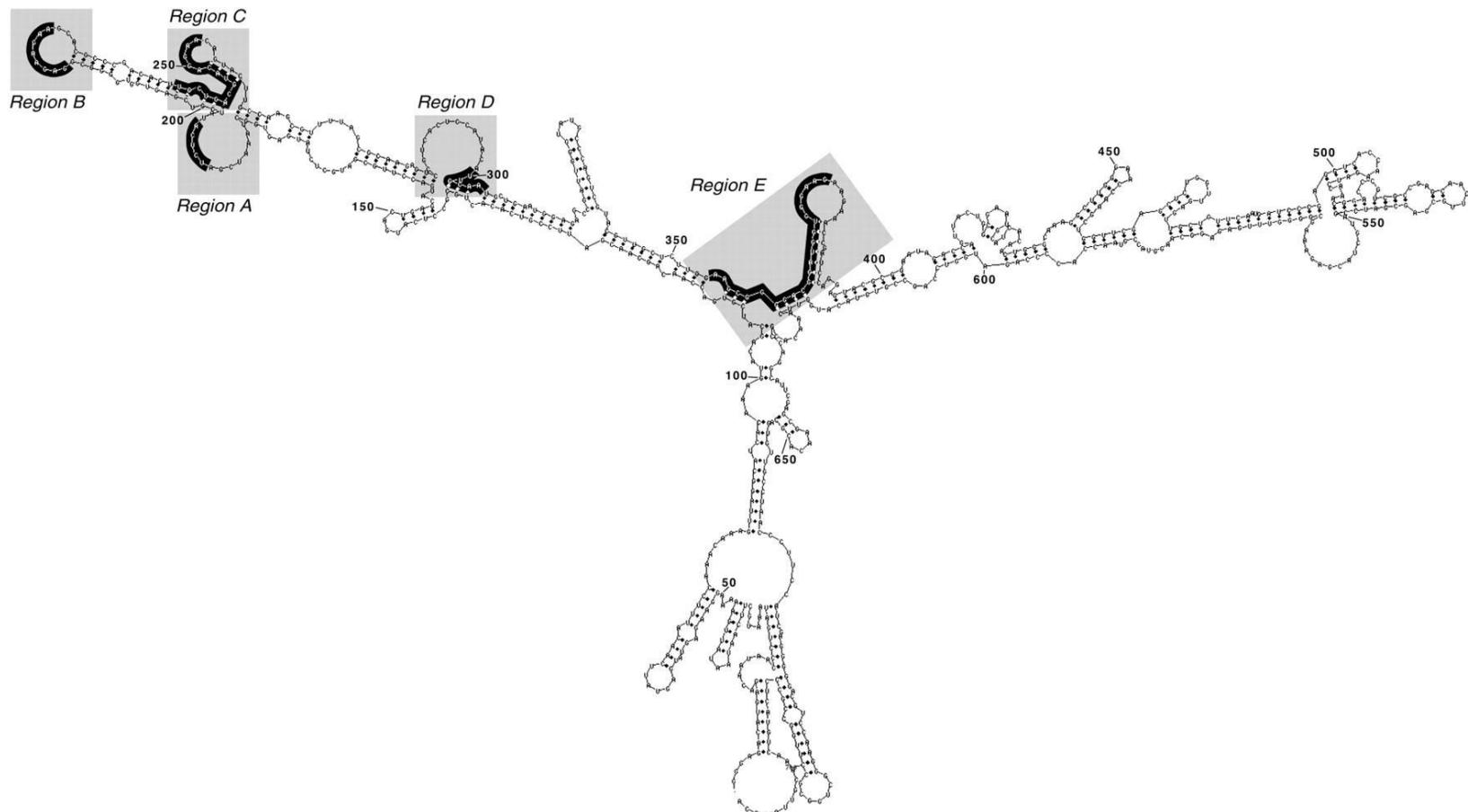
Names Attributes General annotation Ontologies Interactions Sequence annotation Sequences References Cross-refs Entry info Documents Customize order

Names and origin

Protein names	Recommended name: Phosphoglucomutase EC:5.4.2.10
Gene names	Name: glmM Synonyms: msA, ytbF Ordered Locus Names:b3176, JW3143
Organism	Escherichia coli (strain K12) [Reference proteome] [HAMP]
Taxonomic identifier	83333 [NCBI]
Taxonomic lineage	Bacteria - Proteobacteria - Gammaproteobacteria - Enterobacterales - Enterobacteriaceae - Escherichia

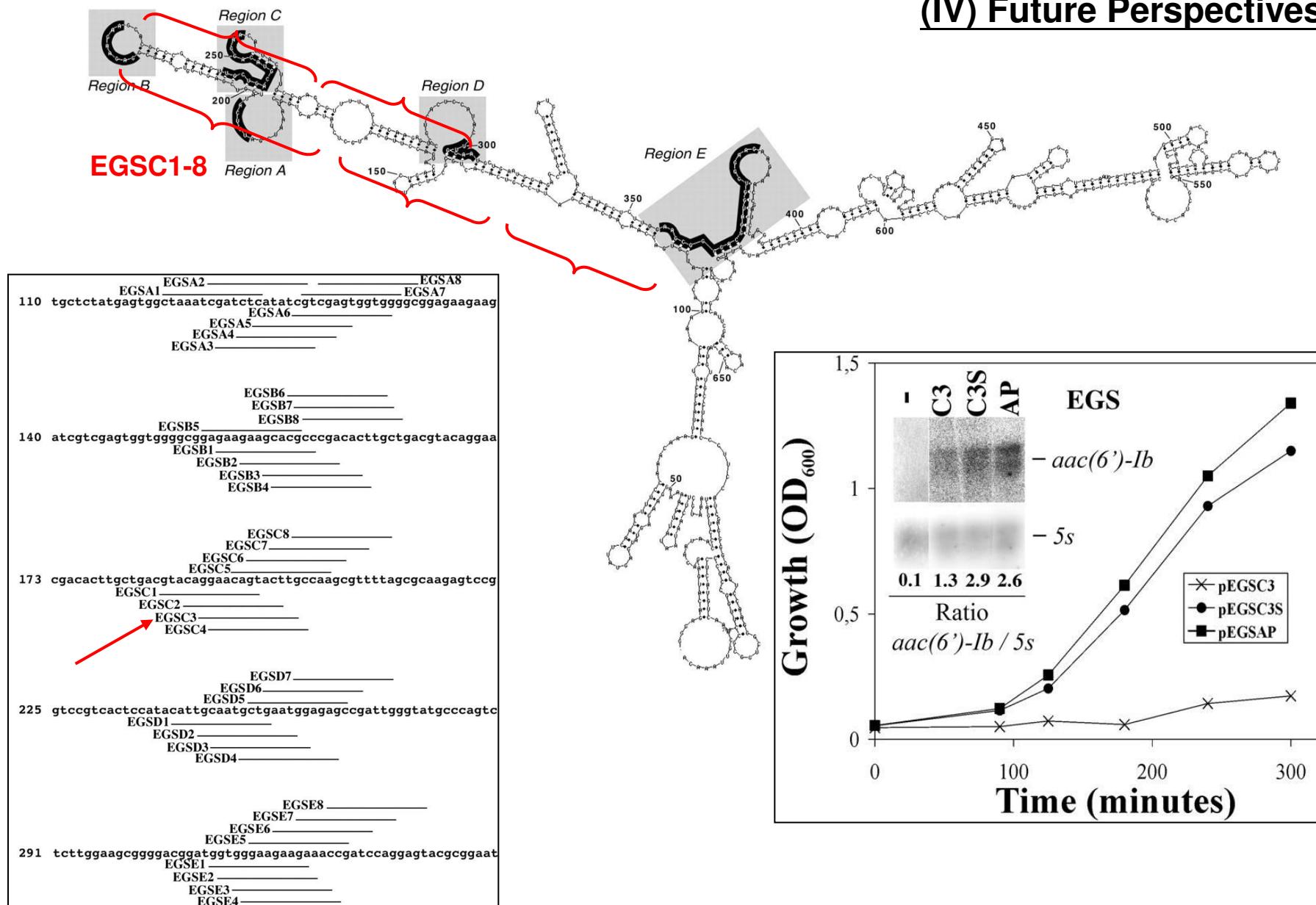
(IV) Future Perspectives

- **Hijacking nature's design - Artificial small RNAs**
- Switching off the aminoglycoside resistance gene, *aac(6')-Ib*



Sarno R. et. al. Inhibition of Aminoglycoside 6'-N-Acetyltransferase Type Ib-Mediated Amikacin Resistance by Antisense Oligodeoxynucleotides *Antimicrob. Agents Chemother.* October 2003 vol. 47 no. 10 3296-3304
Ramirez M. S. et. al. Rise and dissemination of aminoglycoside resistance: the *aac(6')-Ib* paradigm. *Front. Microbiol.*, 17 May 2013 | doi: 10.3389/fmicb.2013.00121

(IV) Future Perspectives



Solar Bistue A. J. C. et. al. External Guide Sequences Targeting the *aac(6')*-Ib mRNA Induce Inhibition of Amikacin Resistance. *Antimicrob. Agents Chemother.* June 2007 vol. 51 no. 6 1918-1925
 Ramirez M. S. et. al. Rise and dissemination of aminoglycoside resistance: the *aac(6')*-Ib paradigm. *Front. Microbiol.*, 17 May 2013 | doi: 10.3389/fmicb.2013.00121