





Global analysis of RNA structures and their dynamics in the adaptative response of *Staphylococcus aureus*.

AZEDE Alan

PARIS-SACLAY UNIVERSITY ED SDSV- PH.D Bacteriology/Bioinformatic 39th TBI Winterseminar I2BC-SRRB / UMR9198

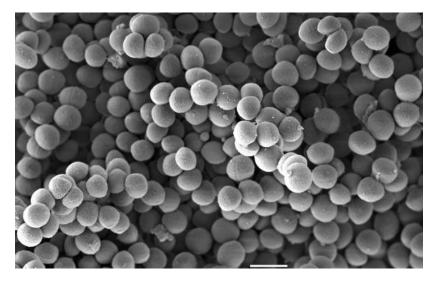
Supervisor : Philippe BOULOC Co-tutors : Yann PONTY and Sebastian WILL(CNRS/LIX), Bruno SARGUEIL (Pharma Paris)

ÉCOLE DOCTORALE

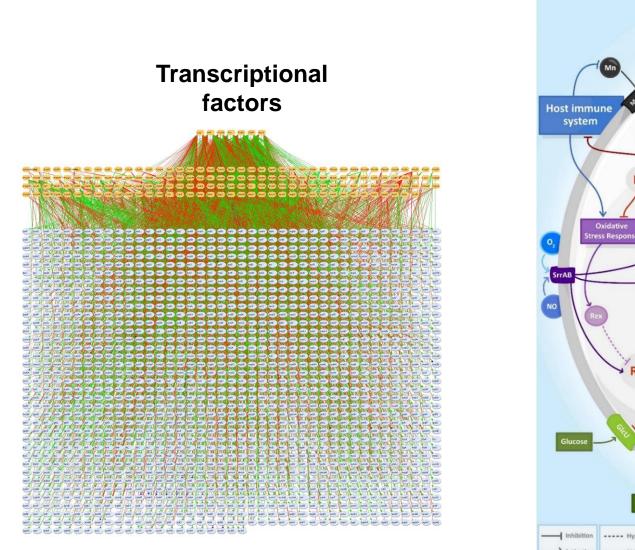
Structure et dynamique des systèmes vivants (SDSV)

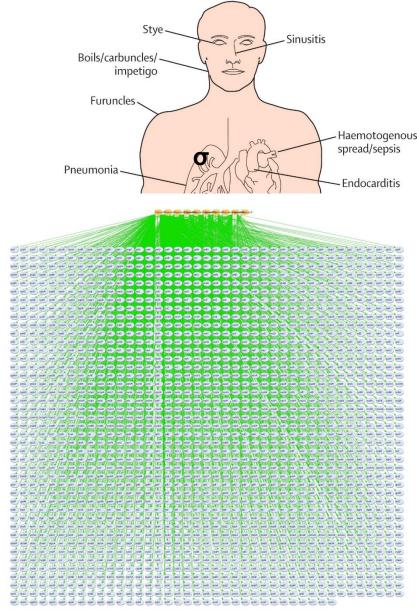


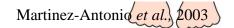
Introduction to the 80prime CNRS project

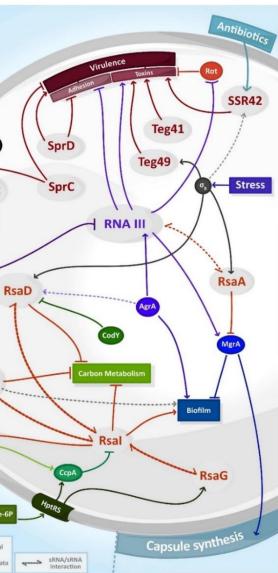


- Major Gram positive coagulase + pathogen
- Hospital/Community-acquired infections associated with antibiotic resistants strains (ESKAPE)
- \rightarrow Bone and/or joint infection, toxin-related infection, whitlow, furonculosis, ...
- Numerous virulence factors, adaption to various environmental conditions, persistence ulletwithin the host, **biofilm** formation...









Barrientos et al, 2021

But also RNA...

Decipher RNA structures dynamic in adaption and global ulletphysiology

Classify RNA structures/motifs into families based on position/similarities + structure function analysis

- Find or validate novel RNA regulatory motifs

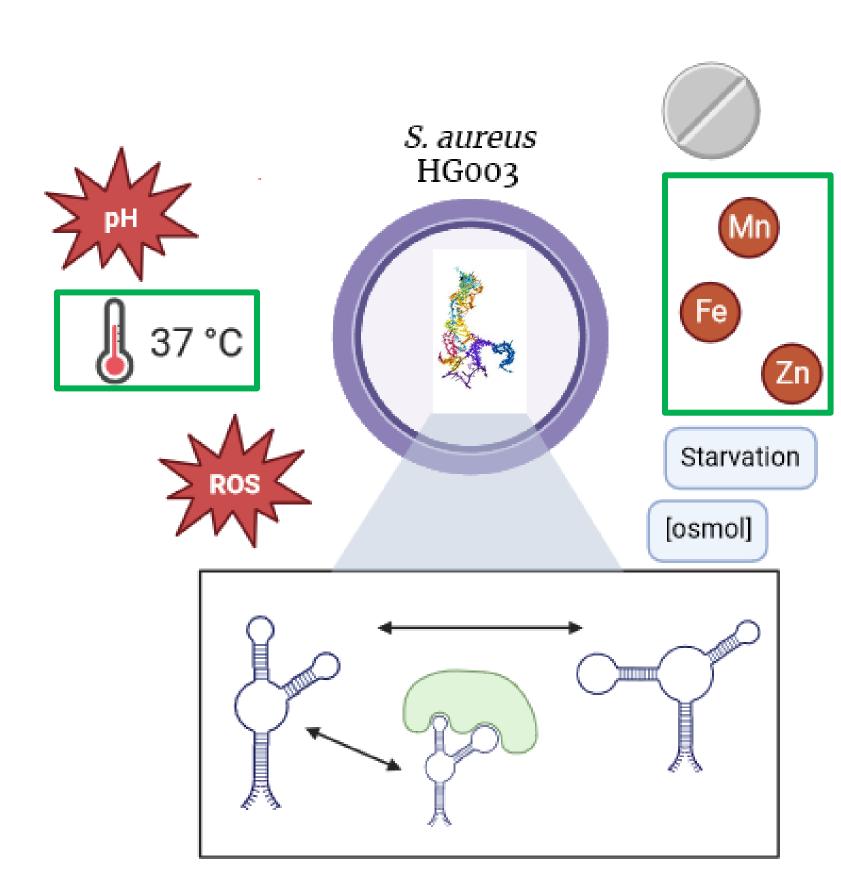
 \rightarrow Look at the RBS/TE + translational coupling between ORFs

- Study the effect of temperature on structures linked to pathogenicity

- Contribution of **RNA chaperones** on these structures
- Effect of **sRNA's induction** on mRNA targets ?
- Explore new potentiel targets for drug design

Mapping a « druggable transcriptome » in *S. aureus* ?

 \rightarrow Design/improve small molecules/analogs for riboswitches

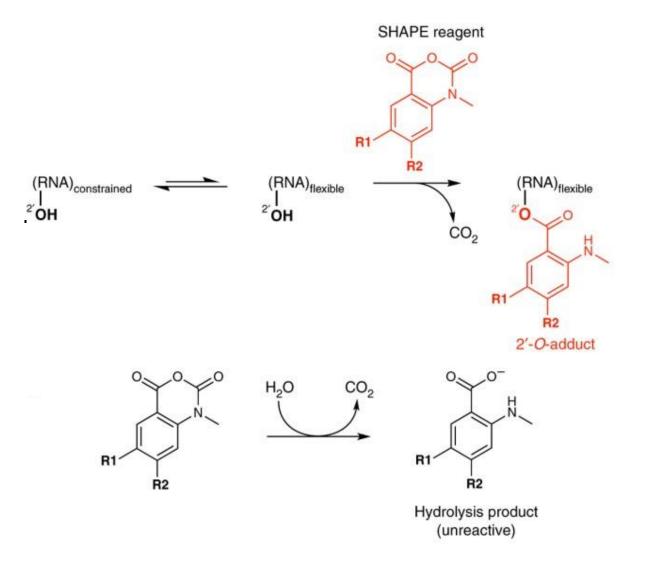


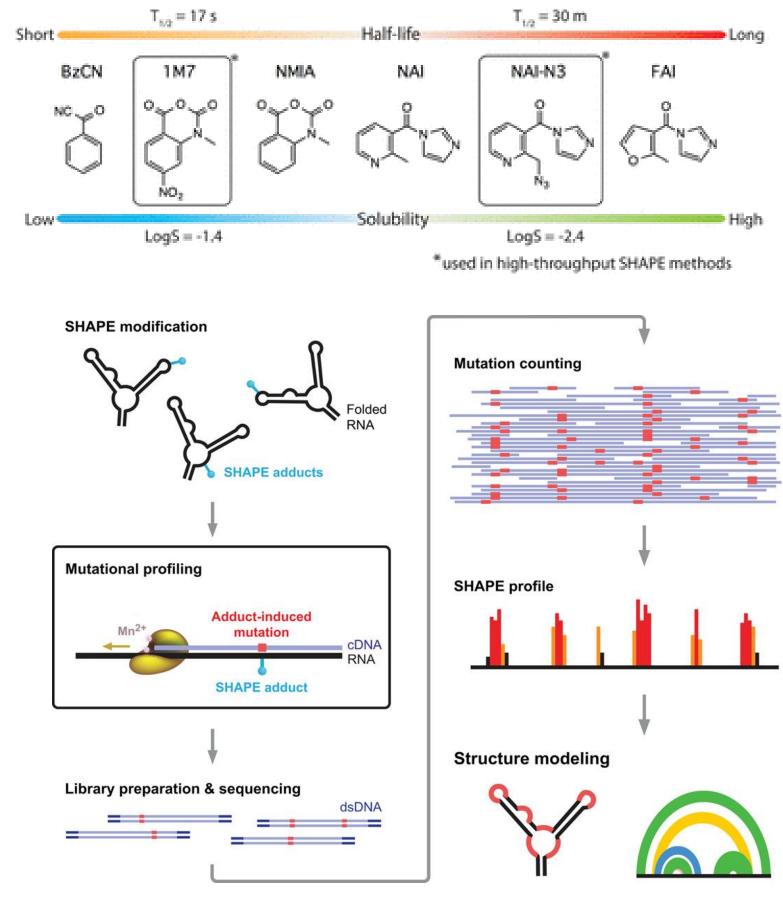
Deciphering RNA structures with the SHAPE chemistry

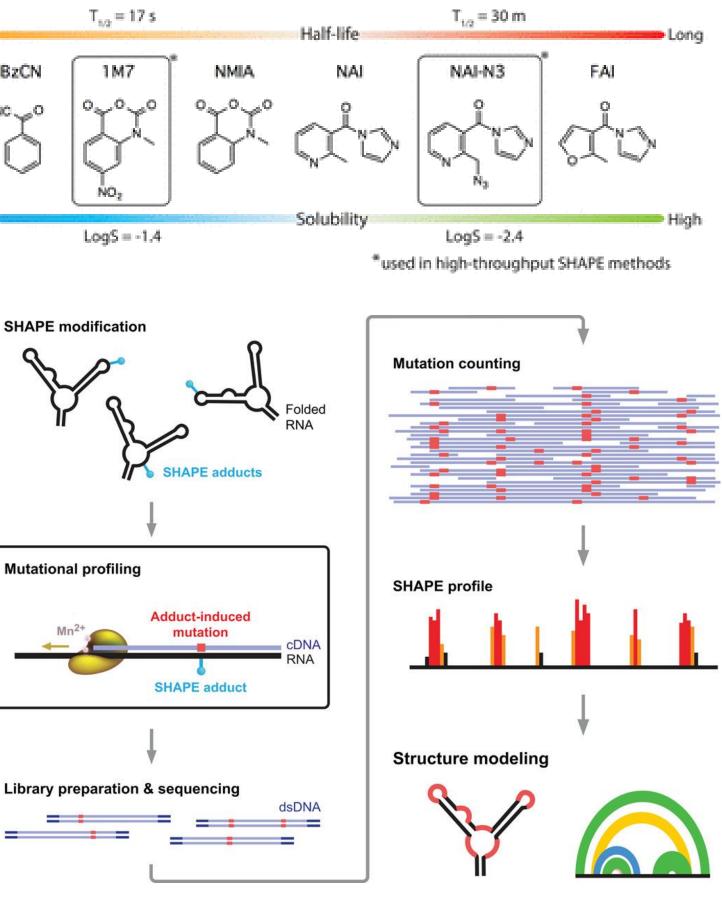
SHAPE = **Selective 2'-hydroxyl acylation** analyzed by primer extension;

Acylation of 2'OH for a **structurally "flexible" nucleotide**;

Solving secondary RNAs structures in vitro, ex vivo and in vivo





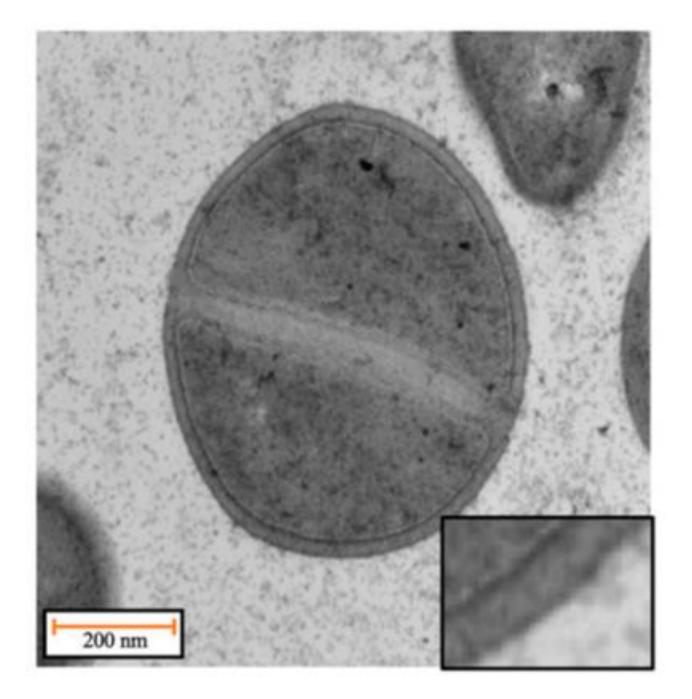


Matthew J Smola et al, 2015

Sigfried et al, 2014

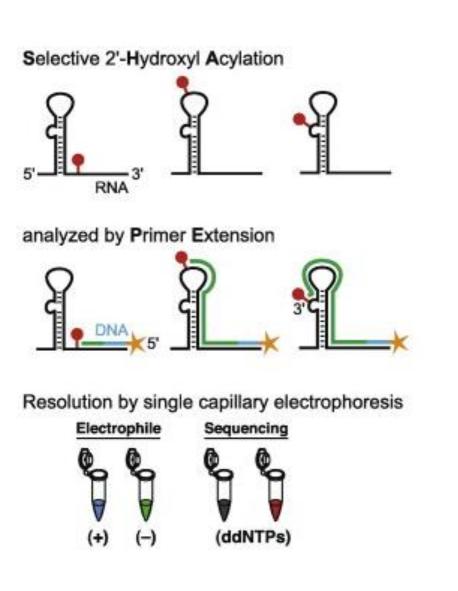
- \rightarrow Gram positive = thick **PG**
- → Cellular environment
- \rightarrow Conditions, probes, ... \rightarrow reproductibility + robustness
- \rightarrow Modelling/predict methodologies to **detect** precise conformational changes
- → Various species of RNA in cellulo
- \rightarrow Reactivity profiles at the transcriptomic level = huge volumes of data
- \rightarrow RNA interactome and folding dynamics

How can we believe that our probing by **SHAPE reagents will work in vivo?**

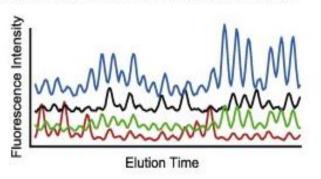


Ideas and benchmark experiments

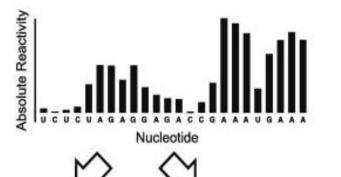
- \rightarrow Use an « inert » RNA as a template for SHAPE-CE
- → Known structure or at least predicted
- → **Stable** and fold independently
- → Perform a SHAPE-CE experiment in vivo



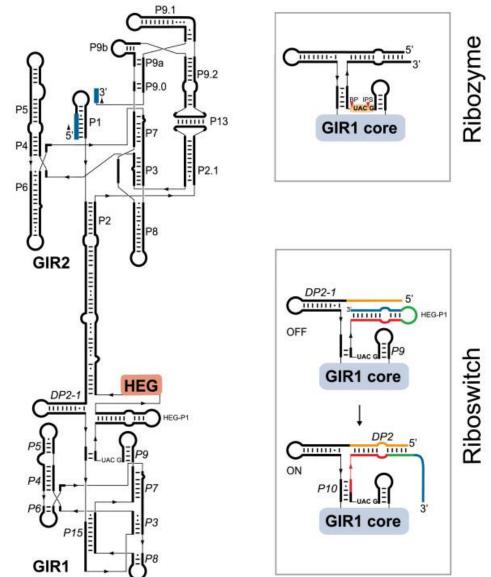
Raw capillary electrophoresis electropherogram



SHAPE reactivities (integrated peak areas)



- Direct applications:
- confirm/refine structures
- monitor RNA folding
- observe ligand binding
- Constrain RNAstructure folding:
- propose new structures
- detect alternative conformations



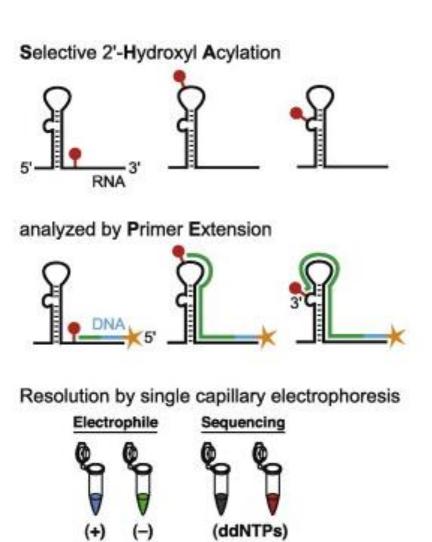




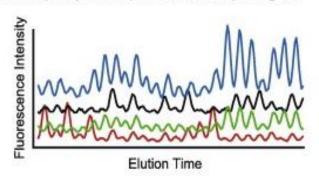
Didymium iridis

Ideas and benchmark experiments

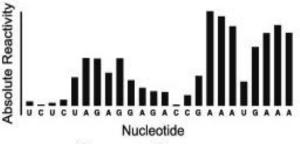
- \rightarrow Use an « inert » RNA as a template for SHAPE-CE
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Raw capillary electrophoresis electropherogram



SHAPE reactivities (integrated peak areas)

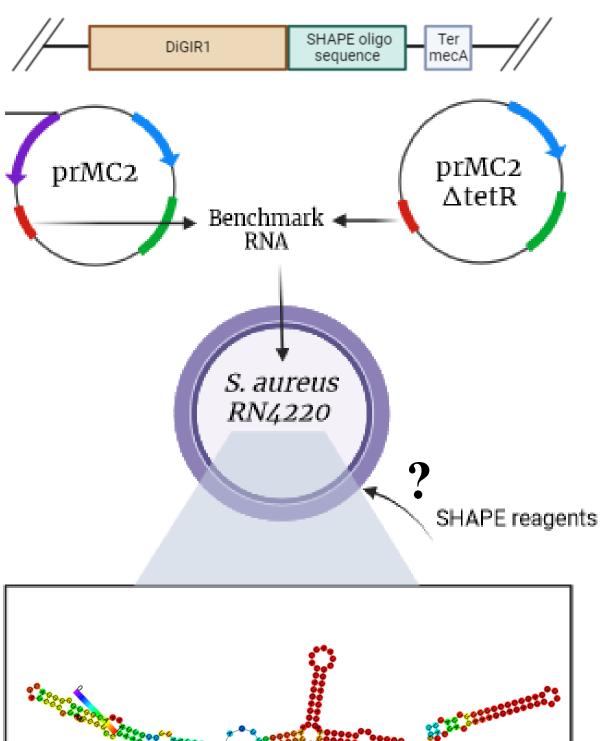




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tetR

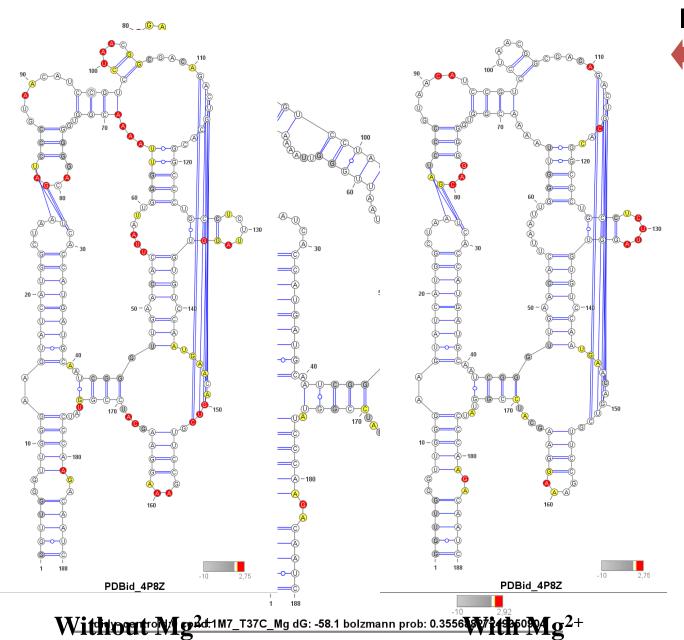




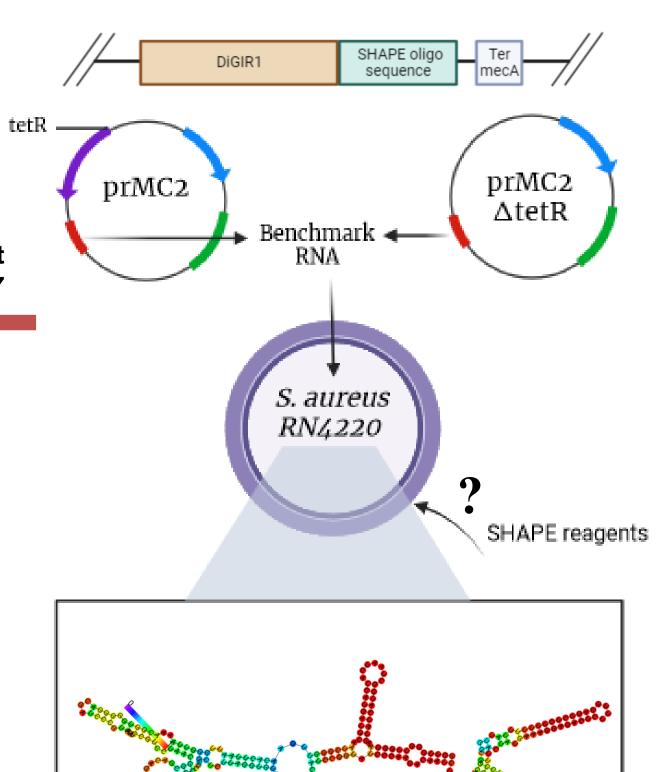
Ideas and benchmark experiments

- \rightarrow Use an « inert » RNA as a template for SHAPE-CE
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SHAPE-CE on the construct In vitro Transcription + 1M7







- Cloning the intron in pJET1.2 and pRMC2 \rightarrow **Done**
- Transformation in *E. coli* IMO8B \rightarrow **Done**
- Transformation in S. aureus RN4220 and HG003 strains -> Done and checked but...
- Test few probes in vivo/in vitro (5NIA, 2A3...) \rightarrow on going
- SHAPE-CE in vivo \rightarrow **Done** and on going



• RNA III in vivo ???

Gupta et al., 2015

Aknowledgement





SRRB team :

Philippe Bouloc

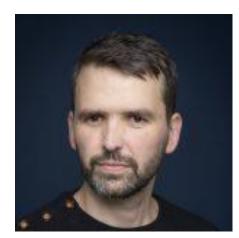
Nara Figueroa-Bossi

Lionello Bossi

Maxime Barrault

Etornam Kofi Kumeko

Patricia Kerboriou









AMIB(io) team : Yann Ponty **Sebastian Will** Sarah J. Berkemer Théo Boury Nan Pan







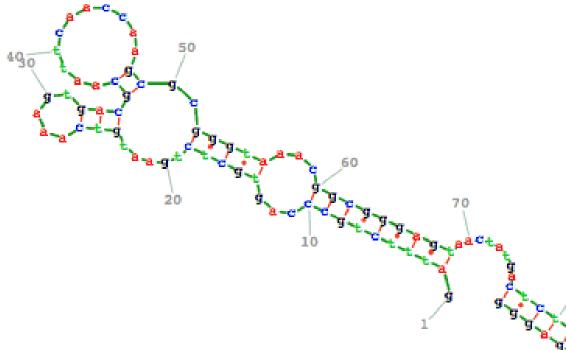
<u>CiTCoM team :</u>

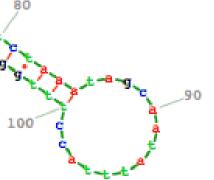
Bruno Sargueil

Pierre Hardouin

Christelle Vasnier

Thank you for your attention





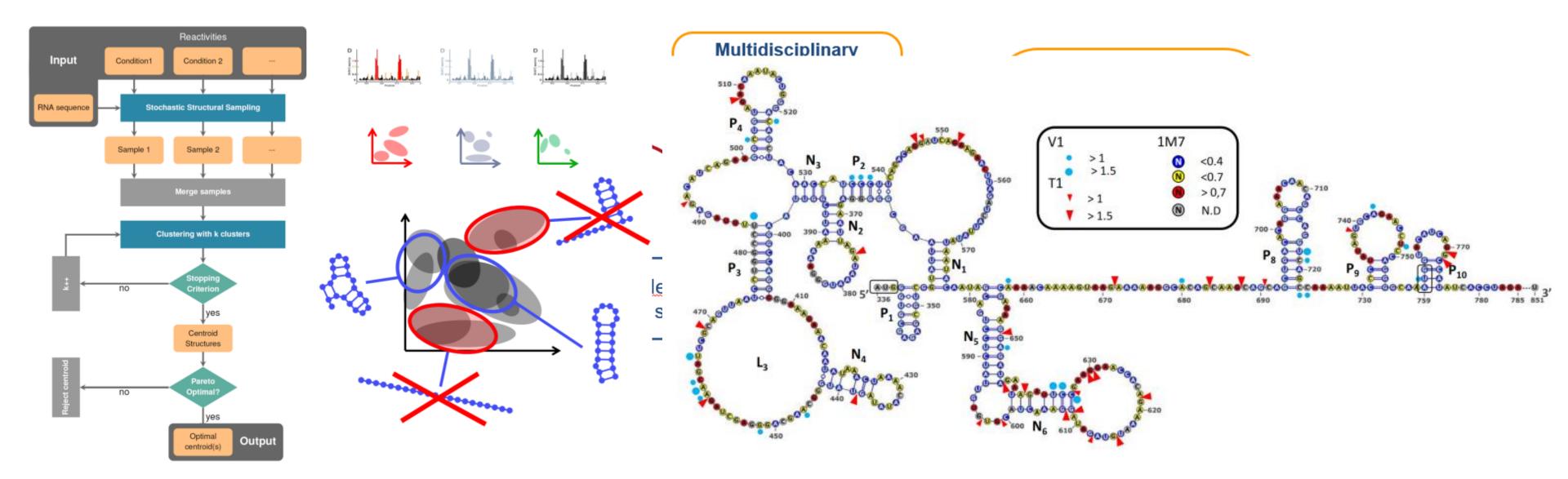
Introduction to the 80prime CNRS project



Philippe BOULOC Signaling and Regulatory Network in Bacteria - SRRB



Bruno SARGUEIL Molecular Mecanisms of viral RNA translation - CitCoM

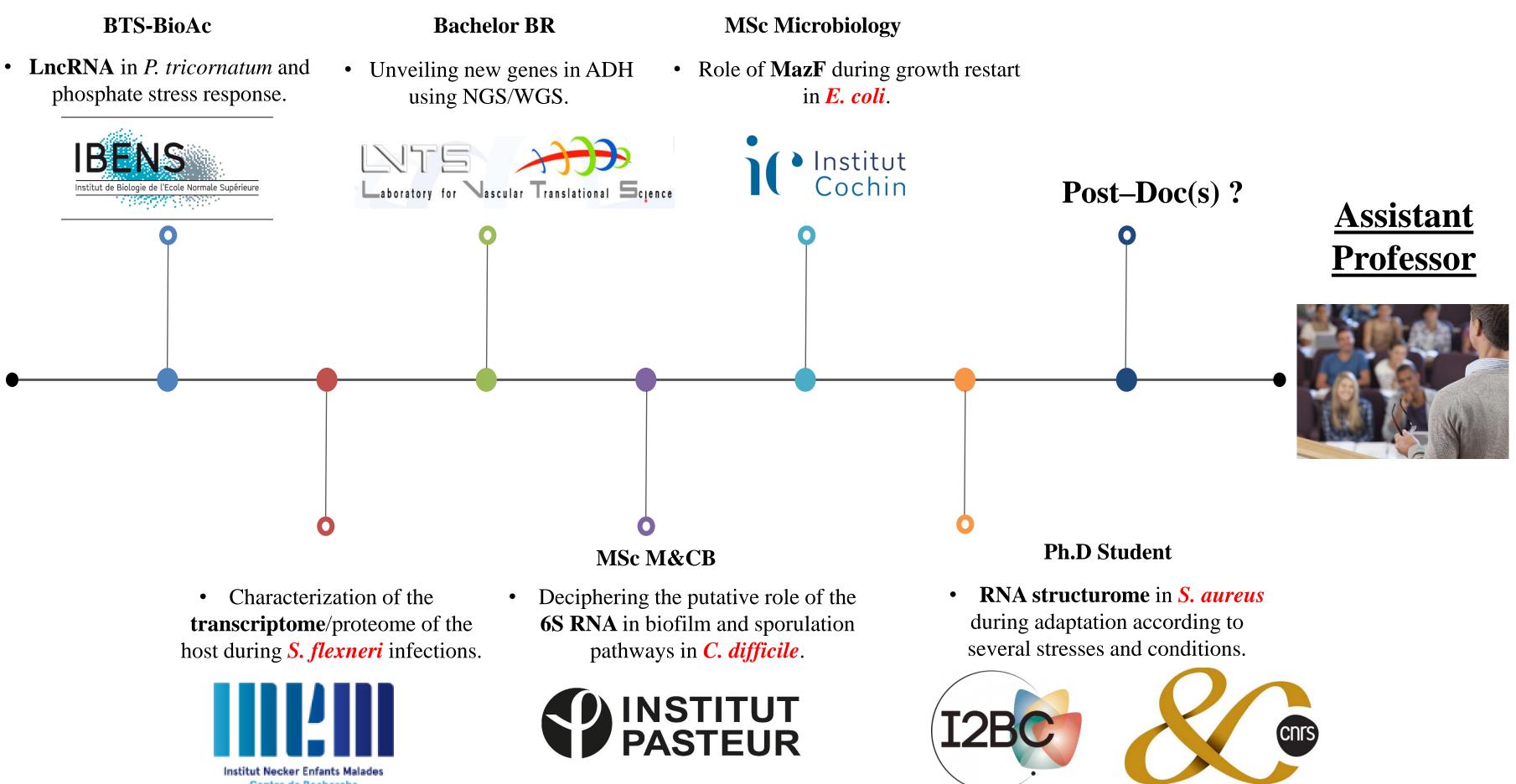






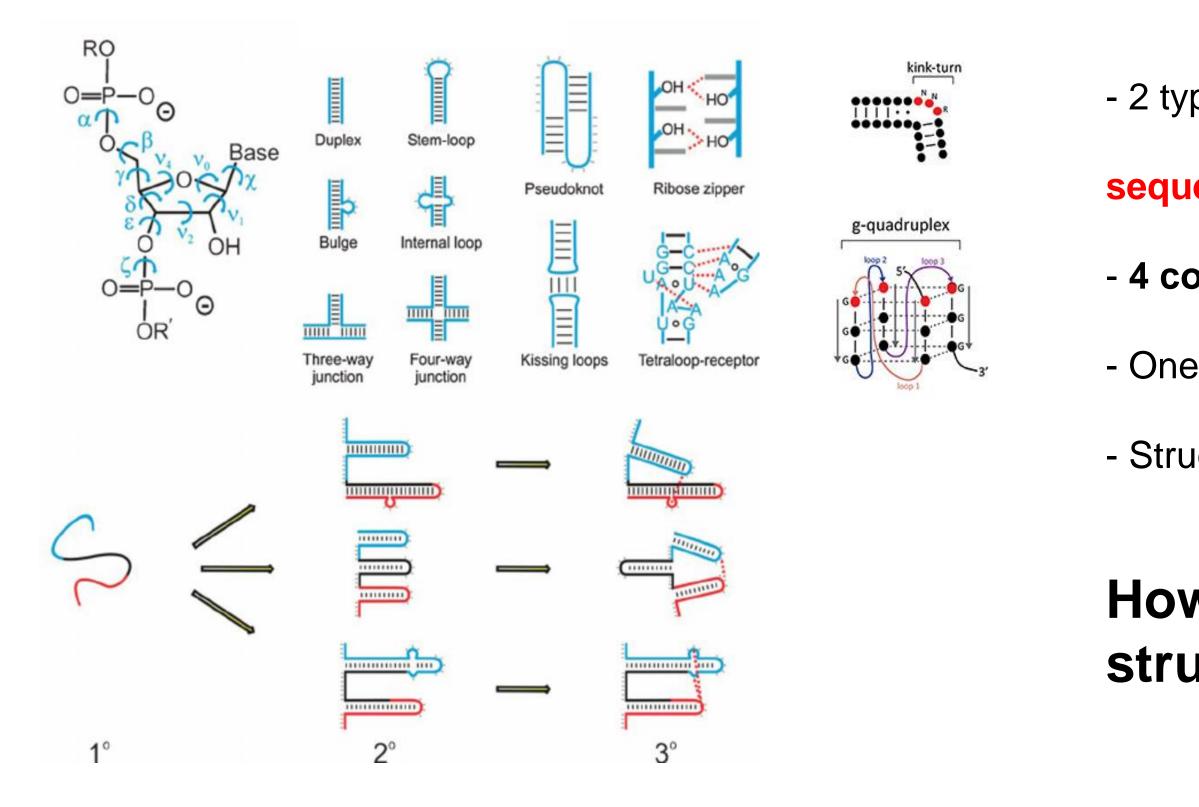
Yann PONTY et Sebastian WILL Algorithms and Models for Integrative Biology – AMIB(IO)

My research and academic related experience



Centre de Recherche

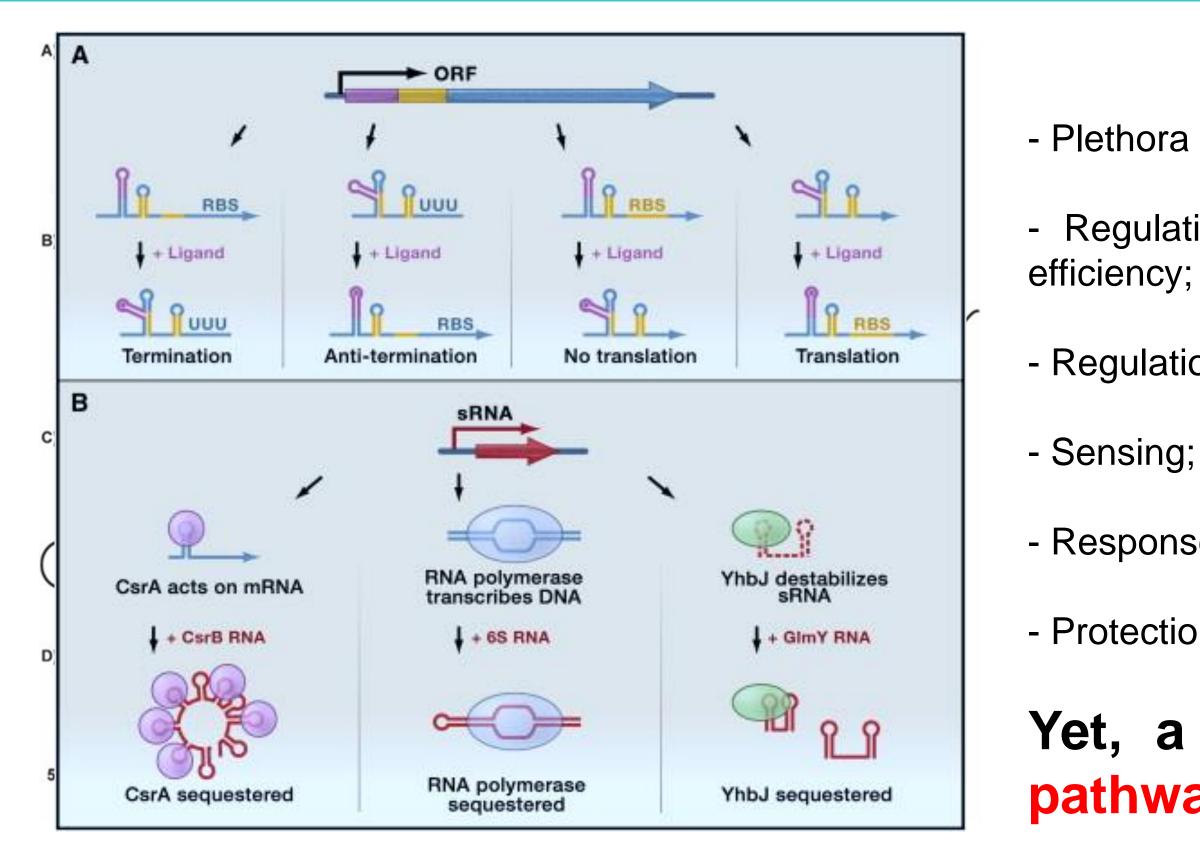
Dual properties of RNA chemistry



- 2 types of information :
- sequence and structure
- 4 conformational structures;
- One given sequence \rightarrow several structures;
- Structure ⇔ function;

How can we determine these structures ?

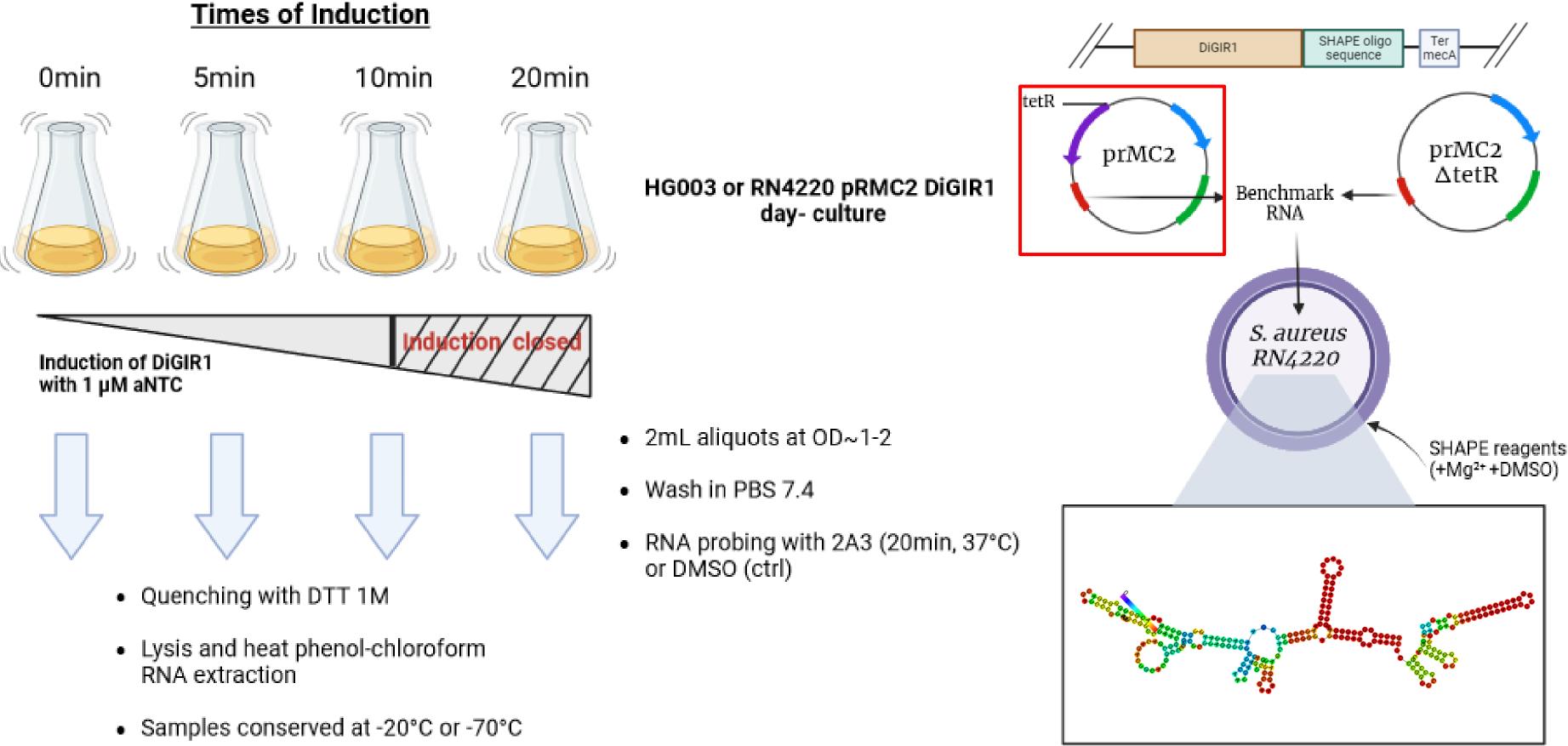
RNA-mediated regulation in bacteria



- Plethora of basic cellular processes;
- Regulation of gene expression and translation
- Regulation of effector proteins;
- Response to stimuli;
- Protection against MGE

Yet, a lot of these regulatory pathways need to be uncover !

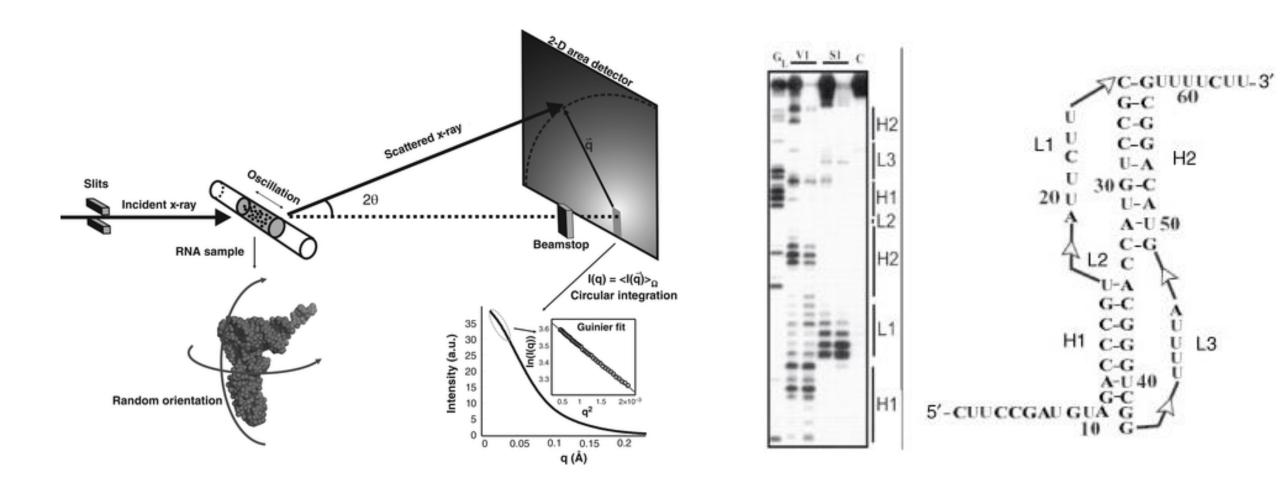
2A3 probing *in vivo* experiment (adapted)

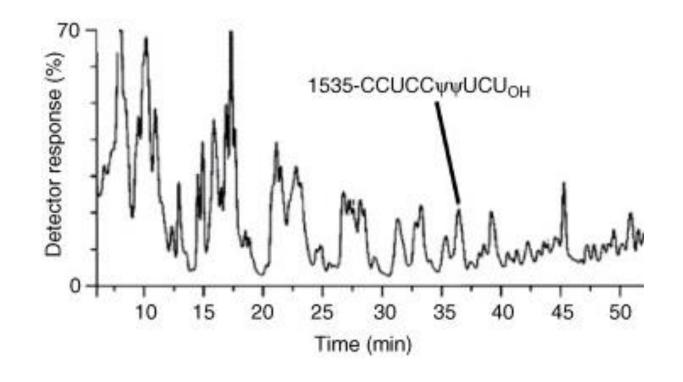




Accessing the RNA structure

- Biophysic methods :
- Cristallography
- SAXS;
- NMR;
- LC-MS;
- Cryo-EM;
- FRET...
- **Structure-specific chemicals+ enzymes :** •
- Nucleases;
- Rnases-mimics;
- Base-specific probes;
- Ribose-specific probes...

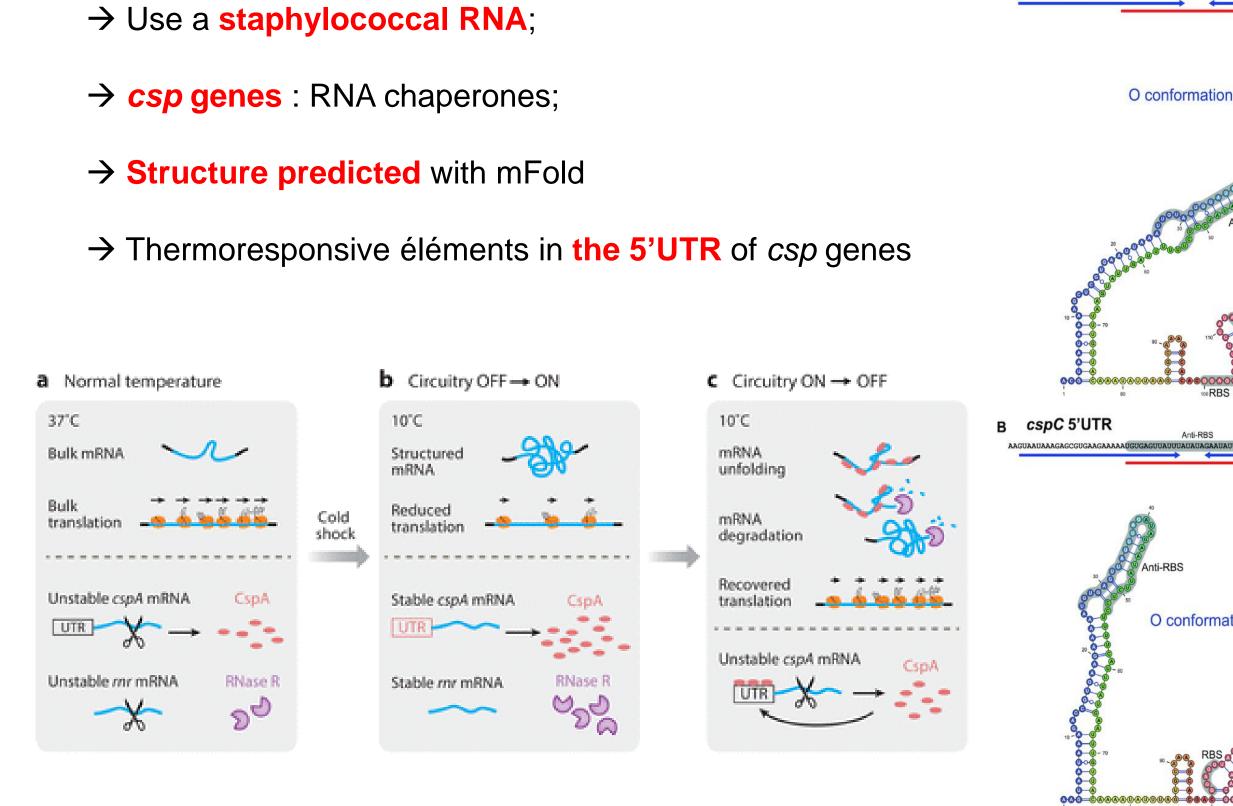


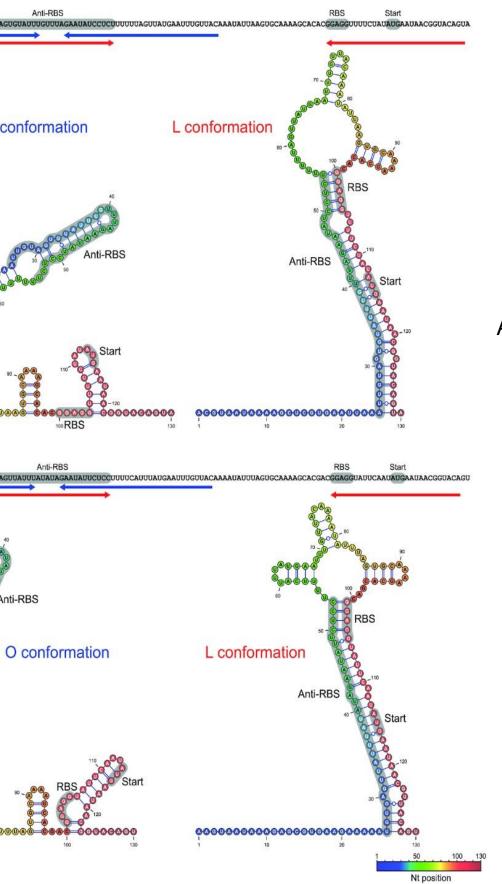


Testing temperature with thermoresponsive sequences ?

A cspB 5'UTR

CGUAAUAAAACCUCGUGAAUUA







Arancha Catalan-Moreno Ph.D



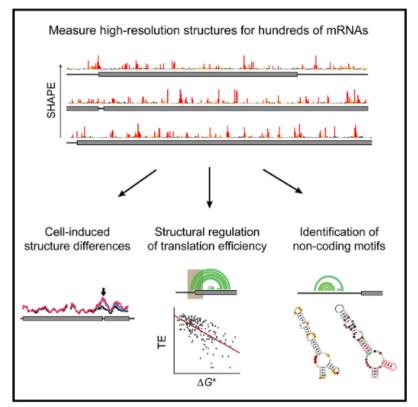
Alejandro Toledo-Arana

Relationship between TE and mRNA's structure/regulation in *E. coli*

Cell

Pervasive Regulatory Functions of mRNA Structure Revealed by High-Resolution SHAPE Probing

Graphical Abstract



Authors

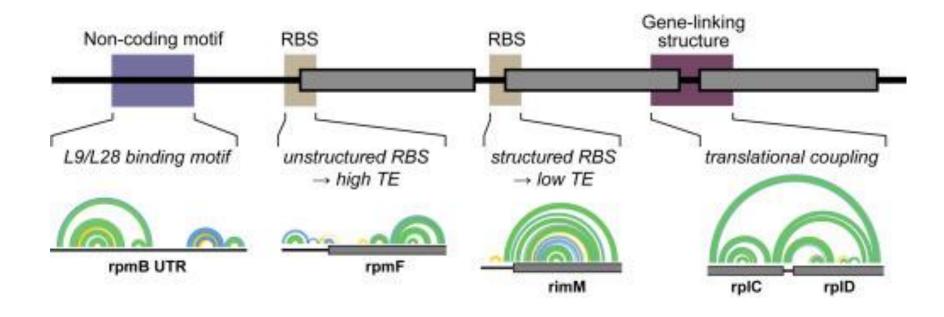
Anthony M. Mustoe, Steven Busan, Greggory M. Rice, ..., Razvan Nutiu, Jeremy L. Baryza, Kevin M. Weeks

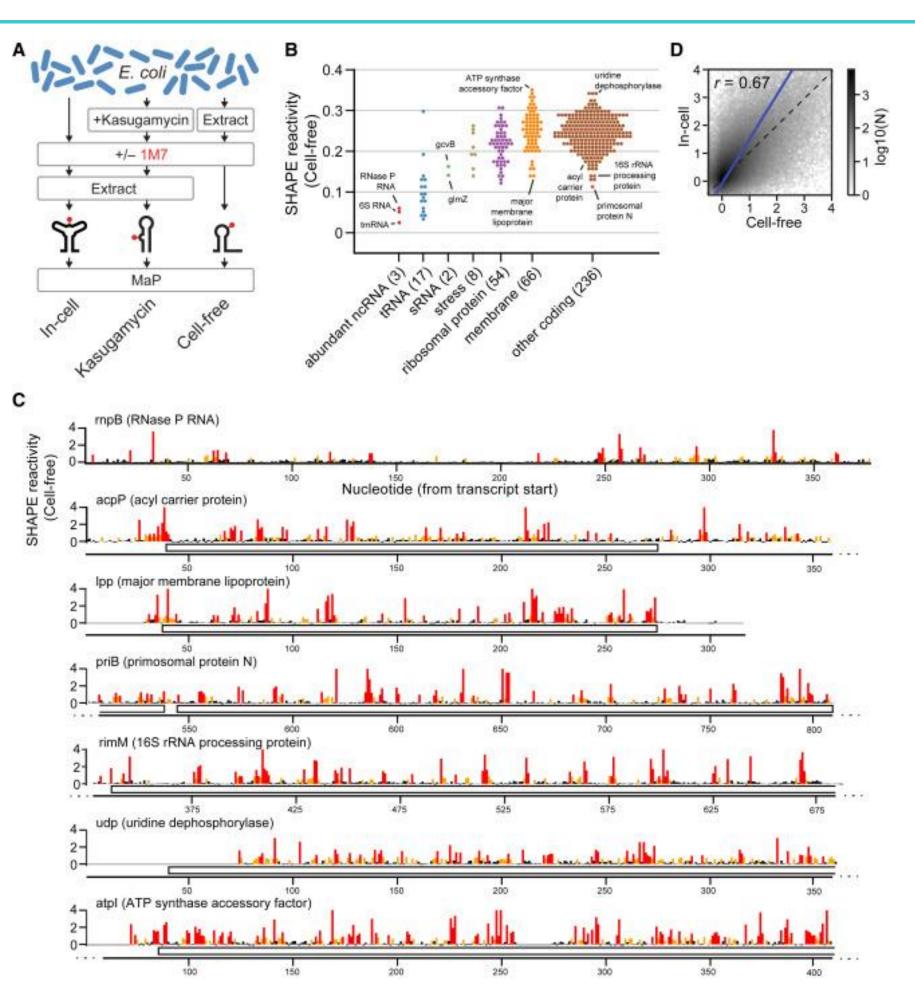
Correspondence

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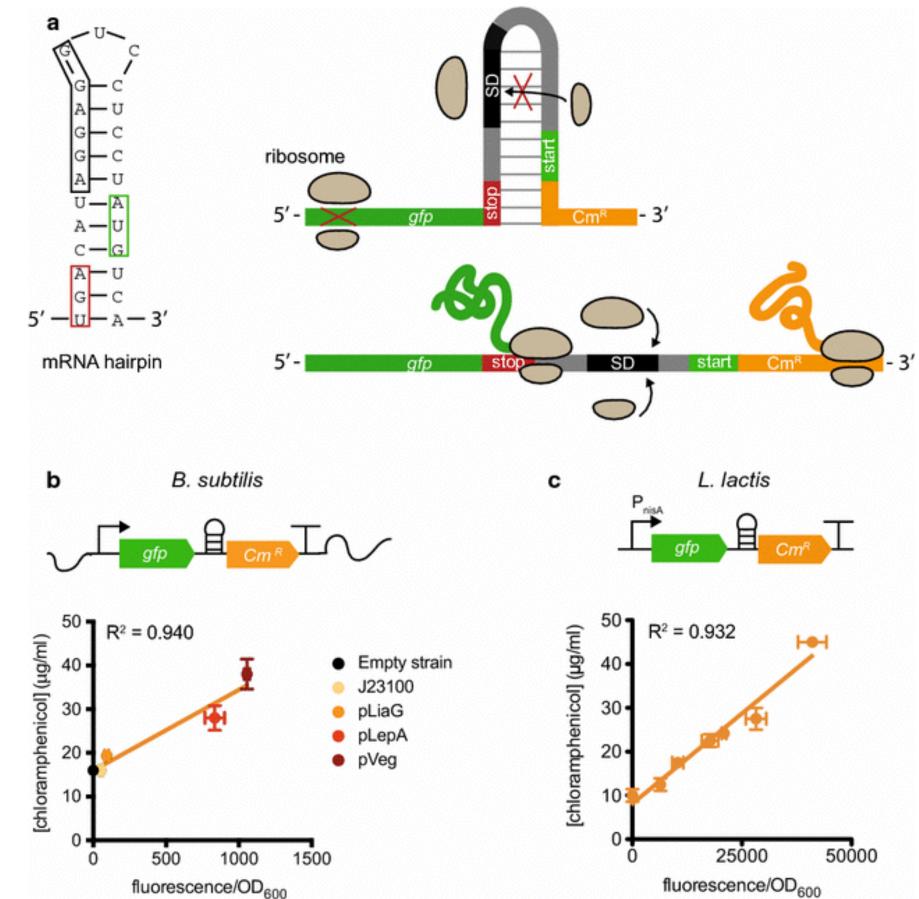
In Brief

High-resolution probing of hundreds of genes in living *E. coli* cells reveals that bacterial mRNAs fold into highly diverse and complex structures and that these structures have widespread regulatory functions.

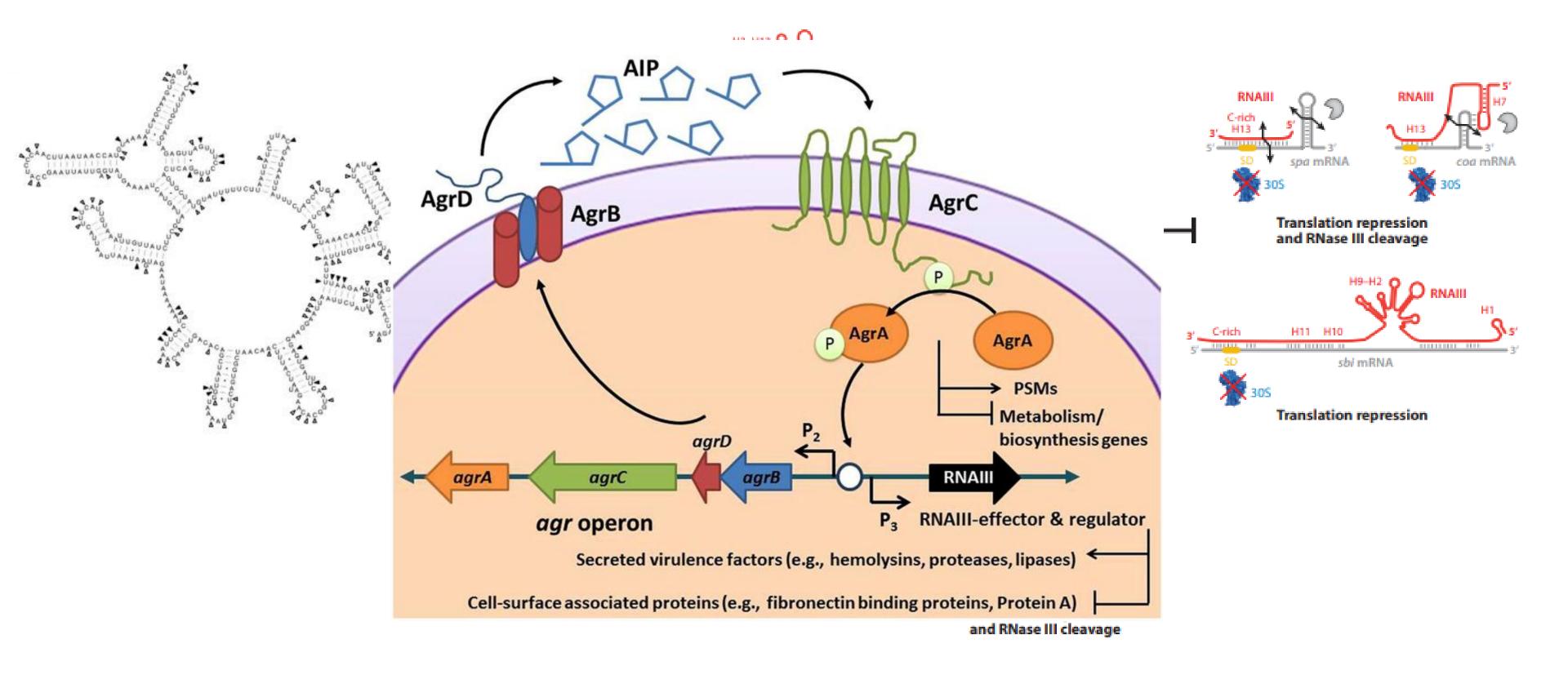




Translational coupling in bacteria



RNAIII



2A3



Danny Incarnato



Tycho Marinus

