

Multiscale Structuring of the *E. coli* Chromosome by Nucleoid-Associated and Condensin Proteins

Vicky Lioy

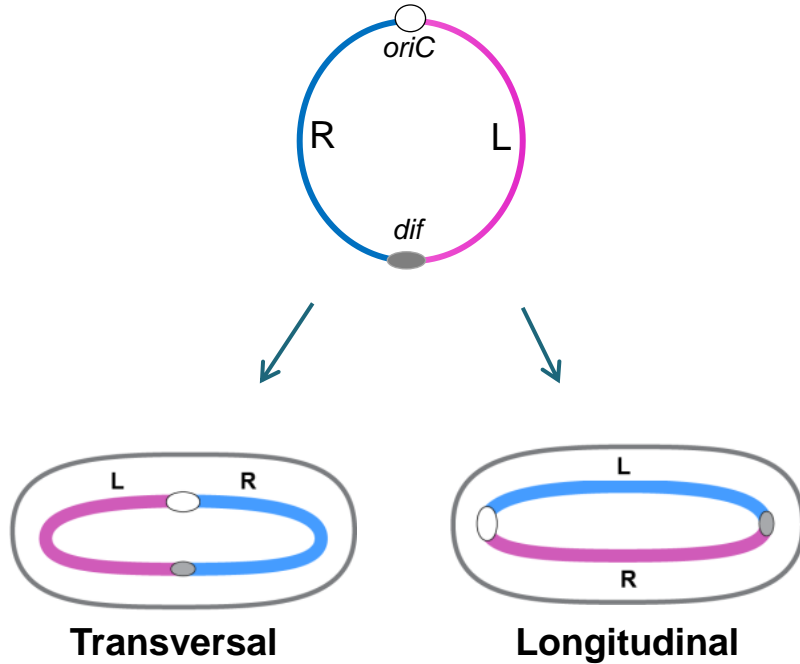


Frédéric Boccard's lab

Réunion annuelle du GdR ADN
10th April 2018



Chromosome organization in bacteria



- One origin of replication *oriC*
- One *dif* site

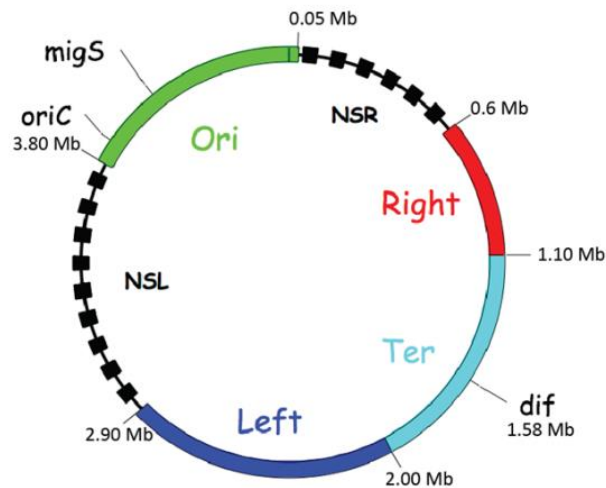
➔ Different chromosome disposition inside the cell

- Segregation and replication occurs concomitantly
- Coordination of cell division with chromosome segregation

➔ Different chromosome choreography during the cell cycle

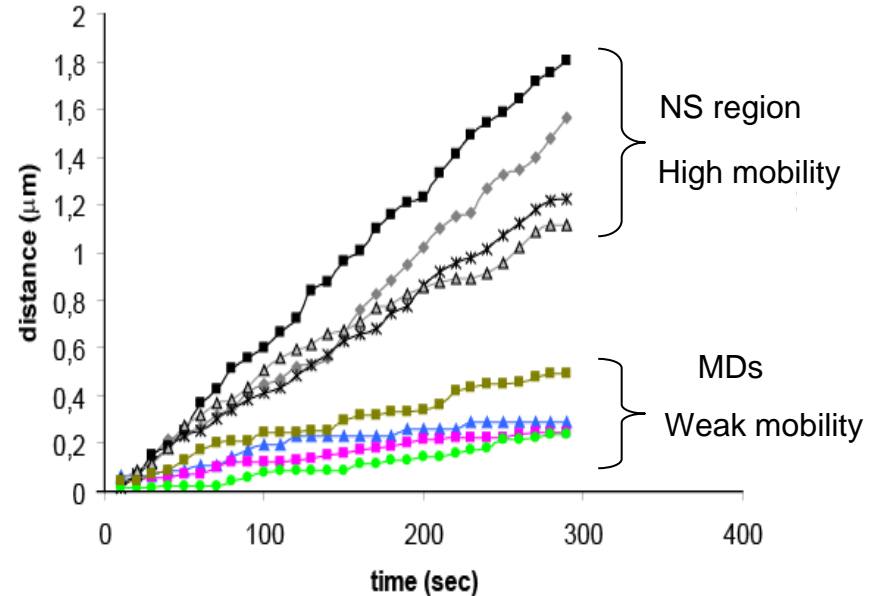
Chromosome organization in *E. coli*

- Genetic analysis: Site-specific recombination to probe DNA collisions



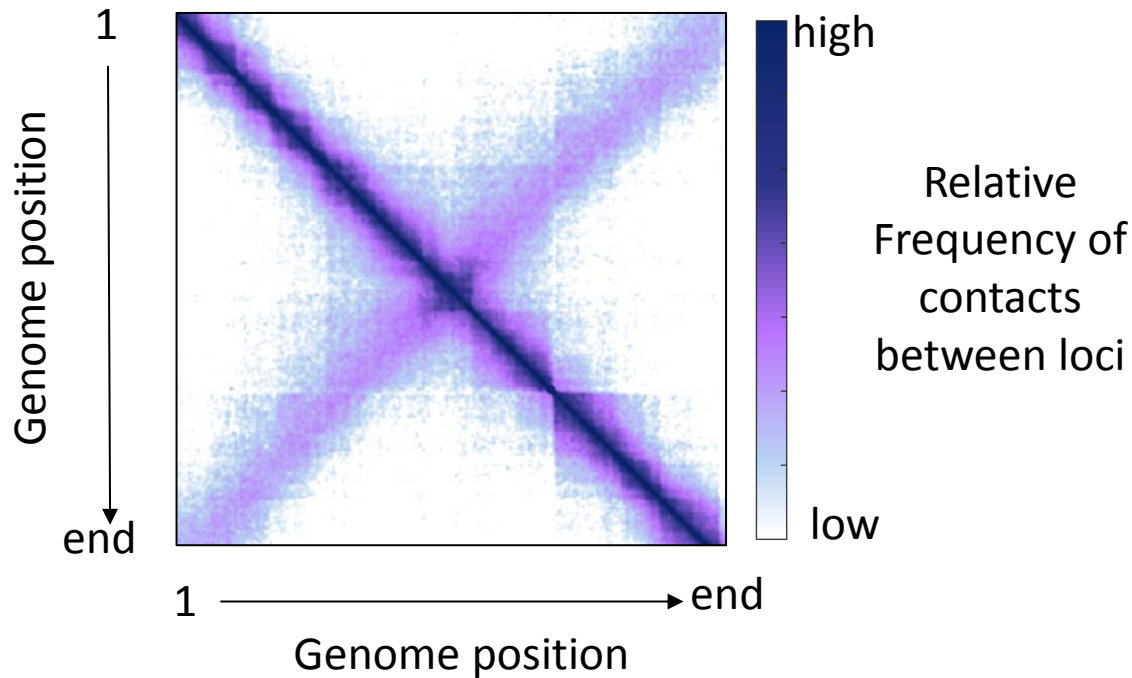
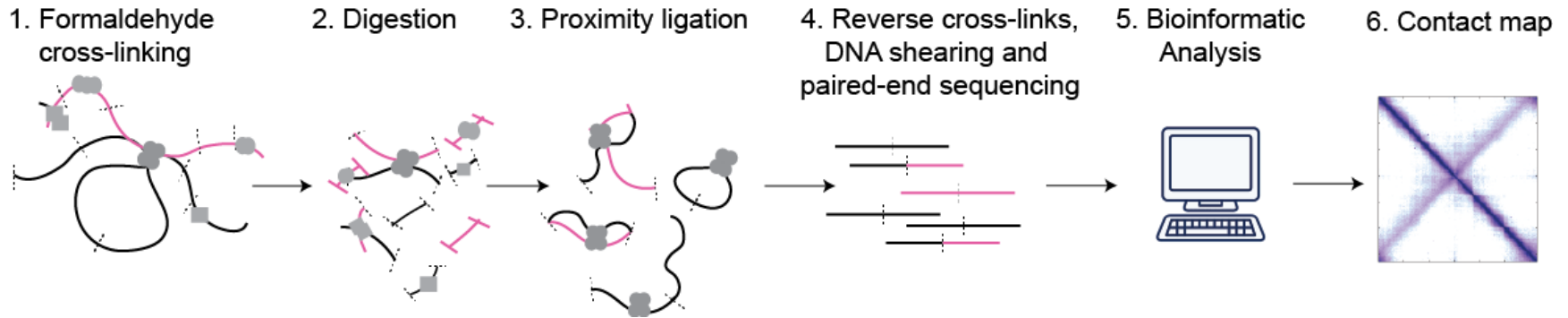
➔ MD and NSR regions

- Chromosome dynamics: FROS analysis

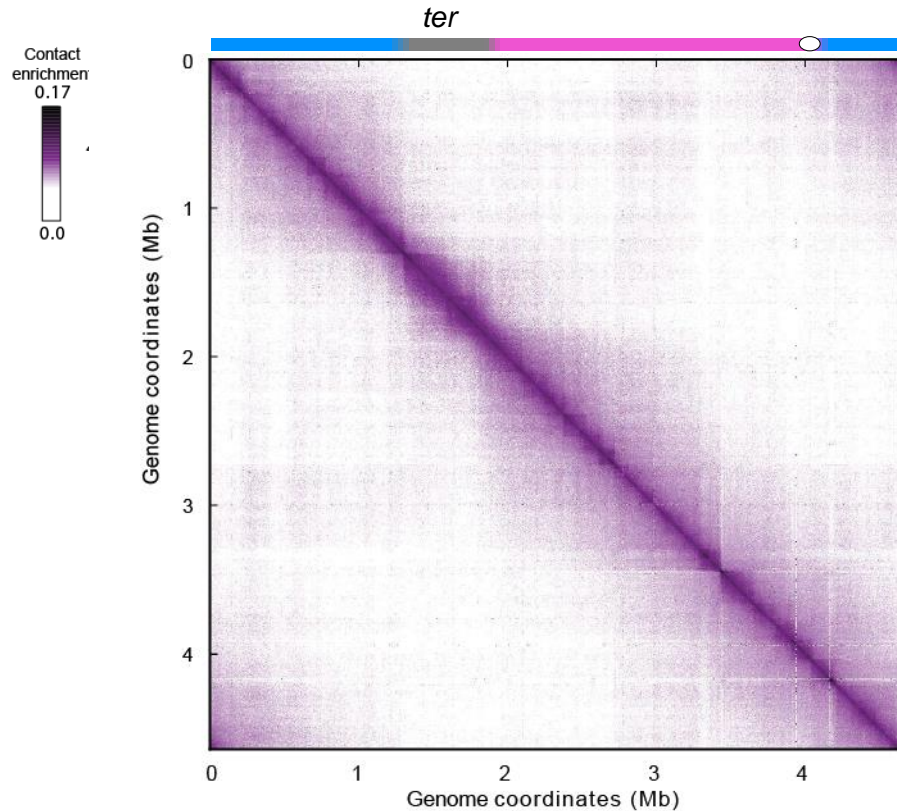


➔ DNA dynamics correlate with MD topography

Chromosome conformation capture (3C-seq)

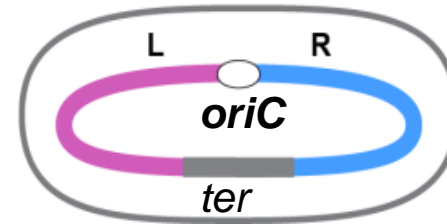


A high resolution contact map of the *E. coli* chromosome

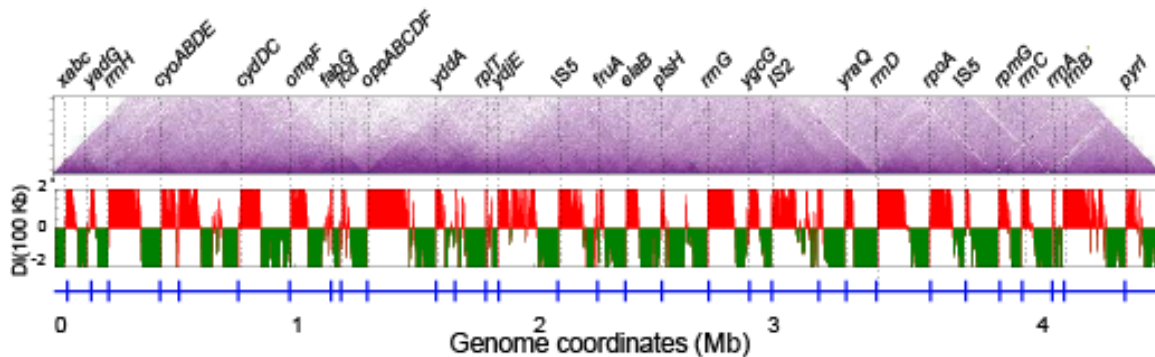


One main diagonal:

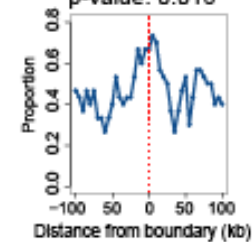
✓ TRANSVERSAL Disposition



✓ 31 CIDs (size: from 40 to ~300 kb)

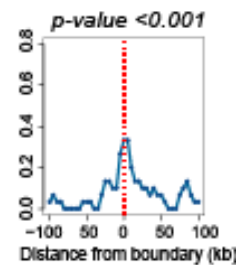


Highly expressed genes (10%)
p-value: 0.016



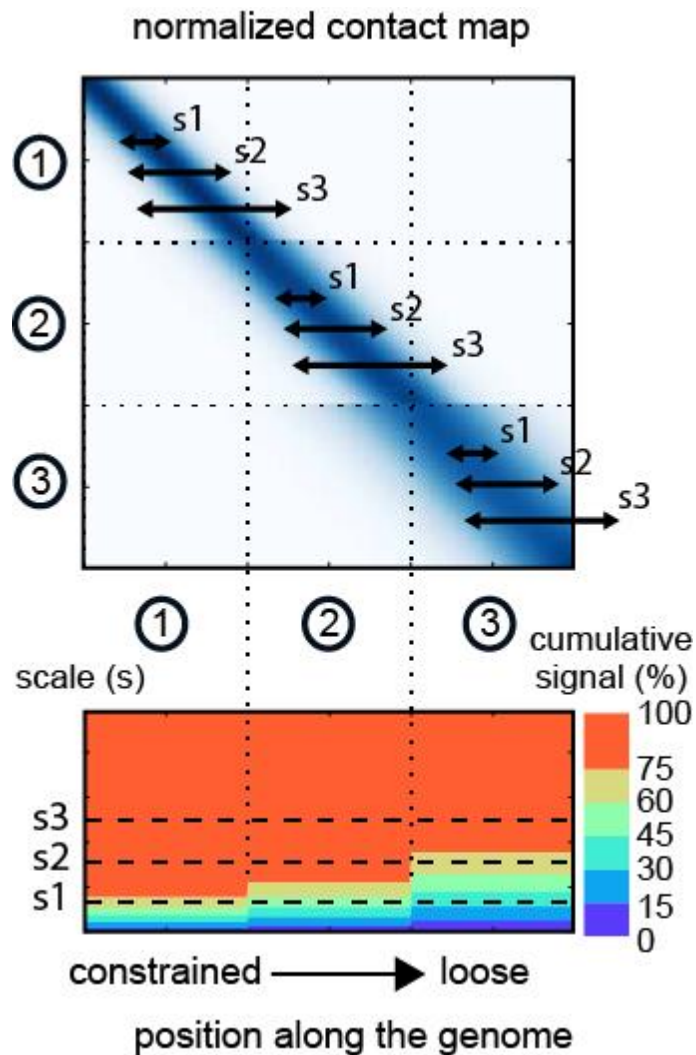
(22/31)

SRP genes
p-value < 0.001



(9/31)

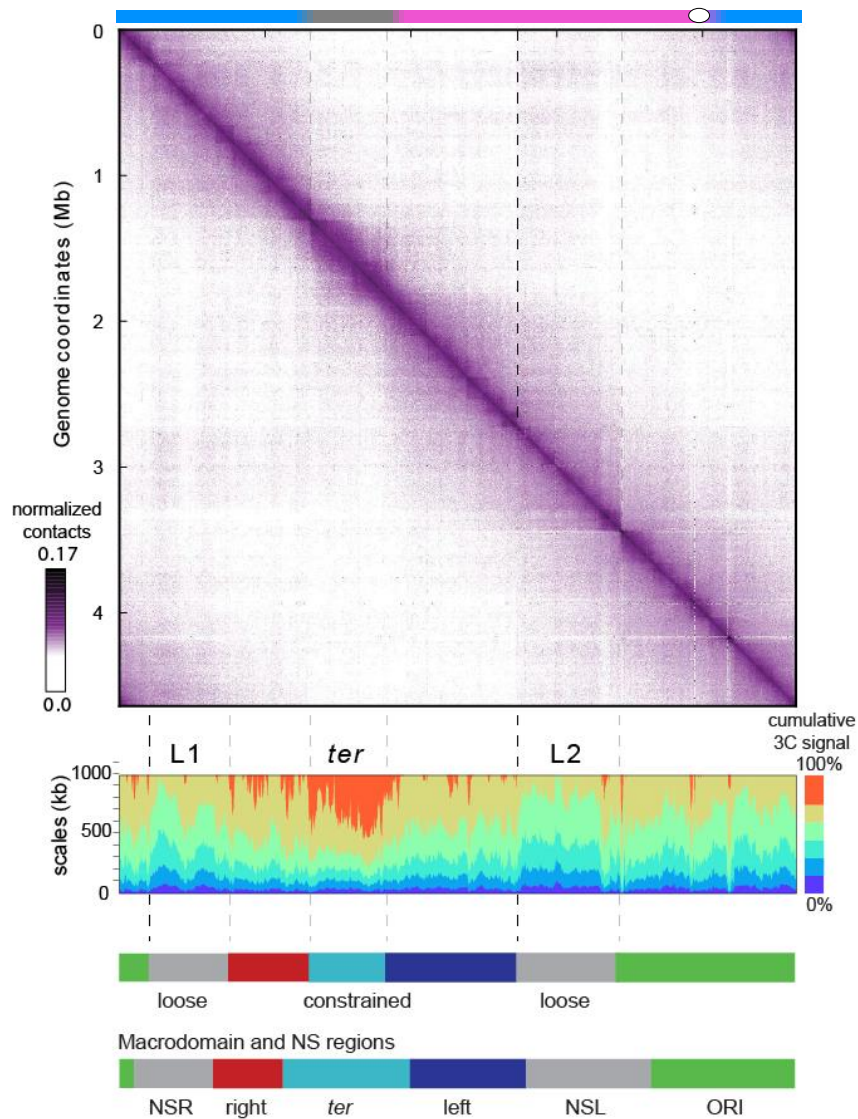
Scalogram: a new tool to analyze 3C contact frequencies



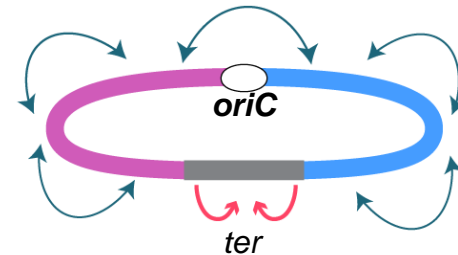
- Using windows of various sizes, the normalized contacts are sum
- This sum represents the fraction of total contacts made by a bin within a window size

➔ Reveals to which extent a genomic region can “see” their flanking sequences

A high resolution contact map of the *E. coli* chromosome



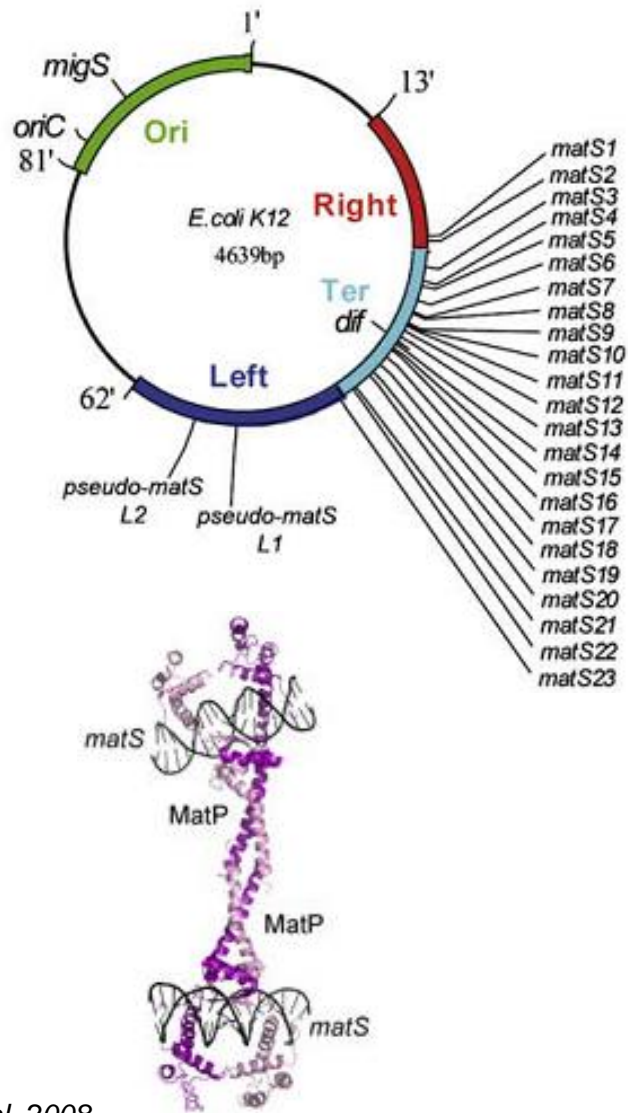
- ✓ *Scalogram* reveals 2 modes of DNA contacts:
 - in the Mb range outside *ter* / constrained contacts around *ter*



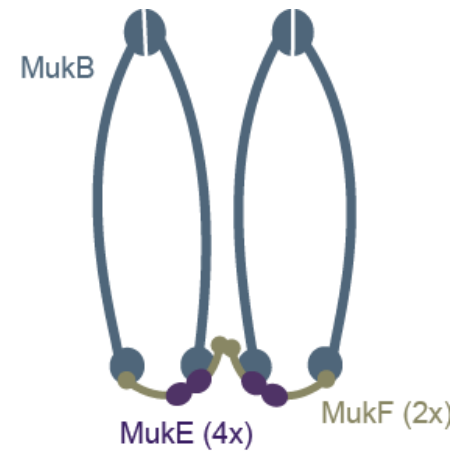
- ✓ Good correlation with MD and NSR regions

Factors involved in chromosome organization in *E. coli*

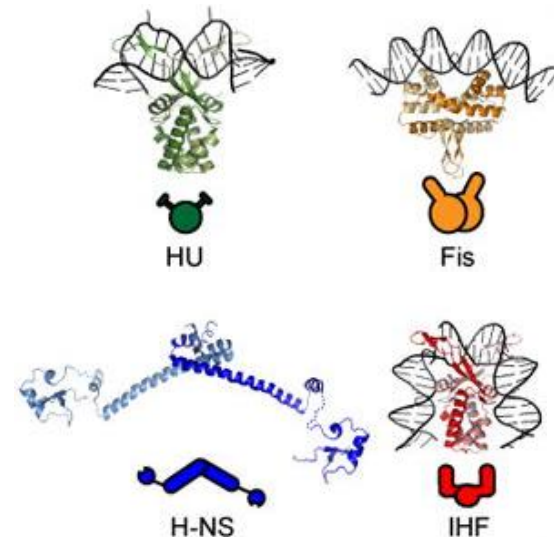
- Specific organizers (**MatP/matS**) / Ter MD



- SMC complex: **MukBEF**

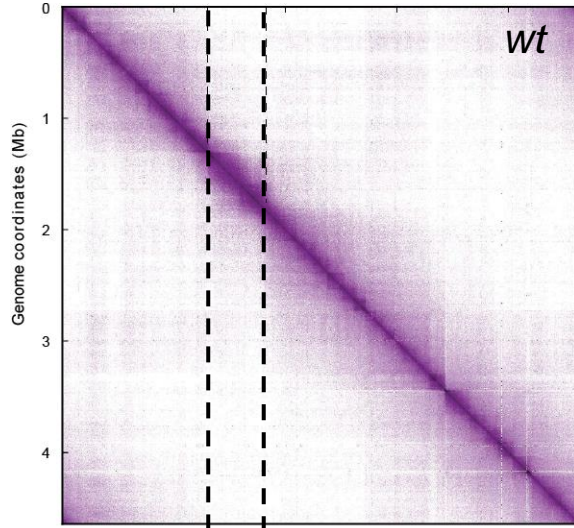


- Nucleoid associated proteins (NAPs)

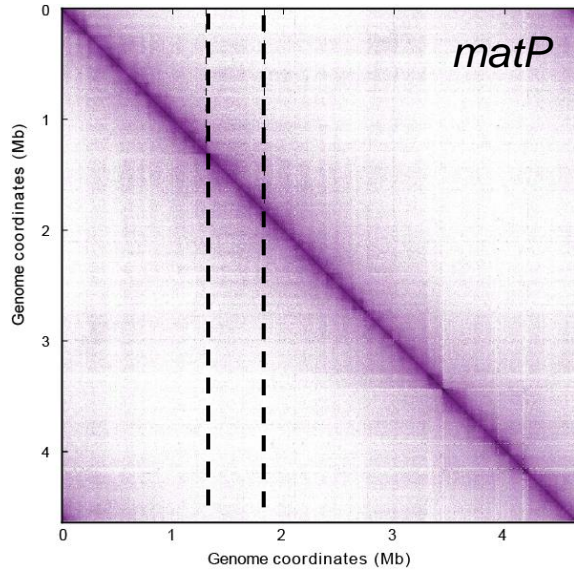


Organization of the *ter* region in the absence of MatP

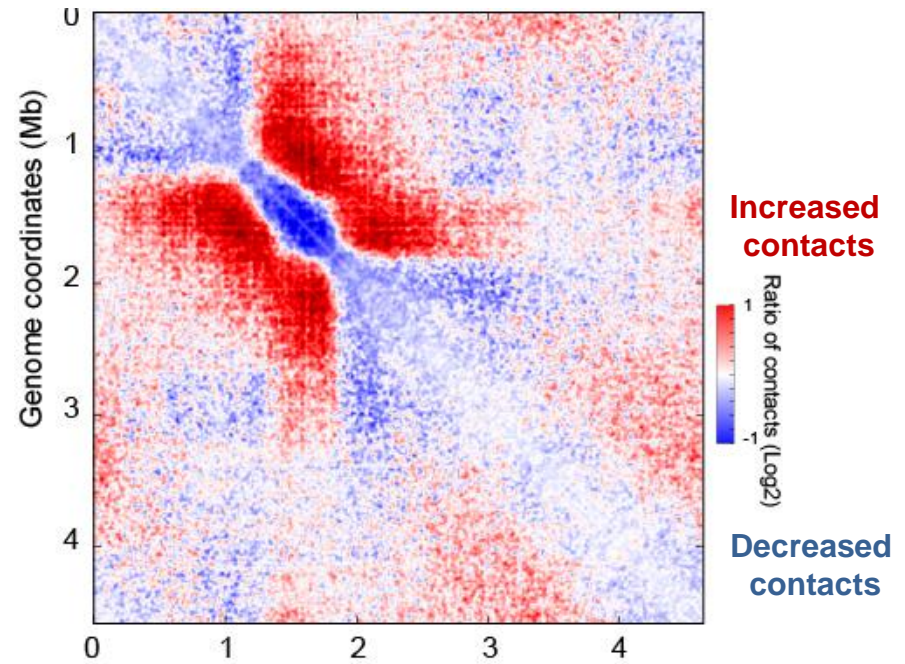
ter



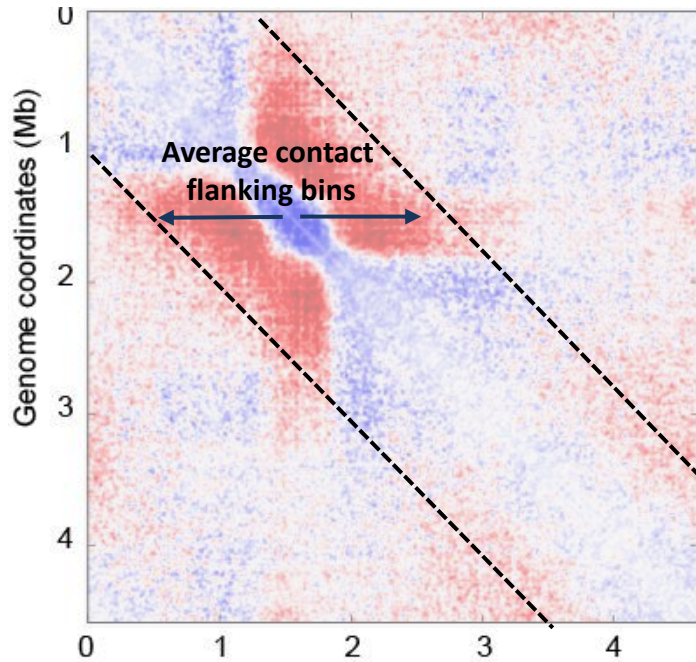
ter



matP/wt

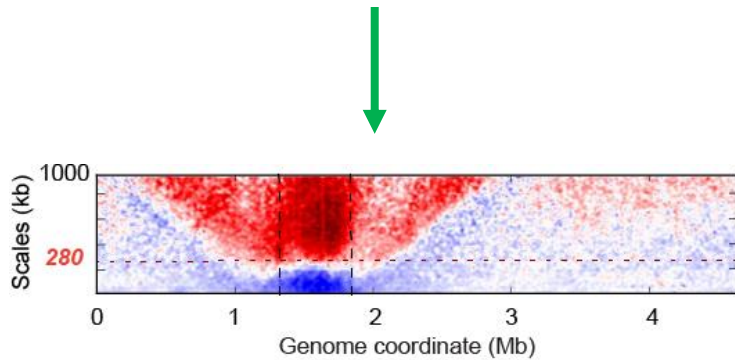


Ratio-plot: a new tool to compare contact maps



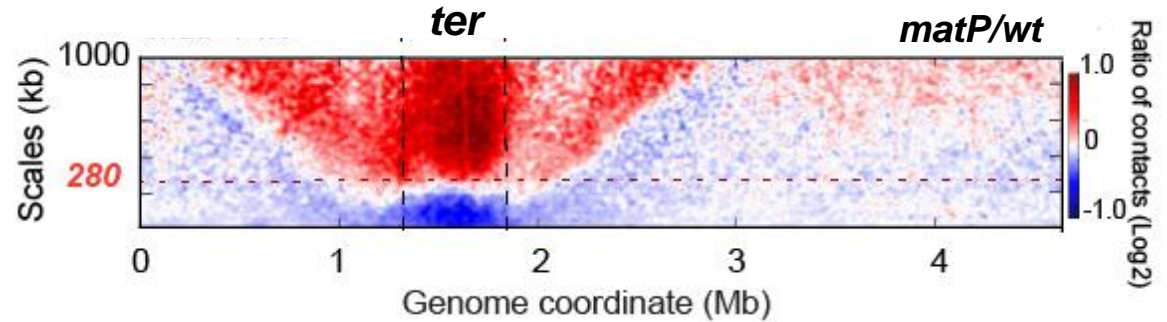
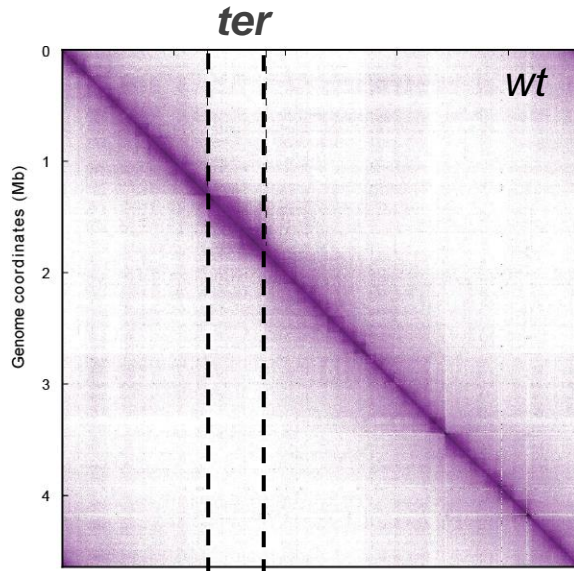
- Ratio-plots represent the **average contacts** made by a bin along the genome with its flanking bins at increasing distances (from 5kb to 1000kb)

2D → 1D



Shows the ability of a loci to interact with its flanking sequences along the entire genome

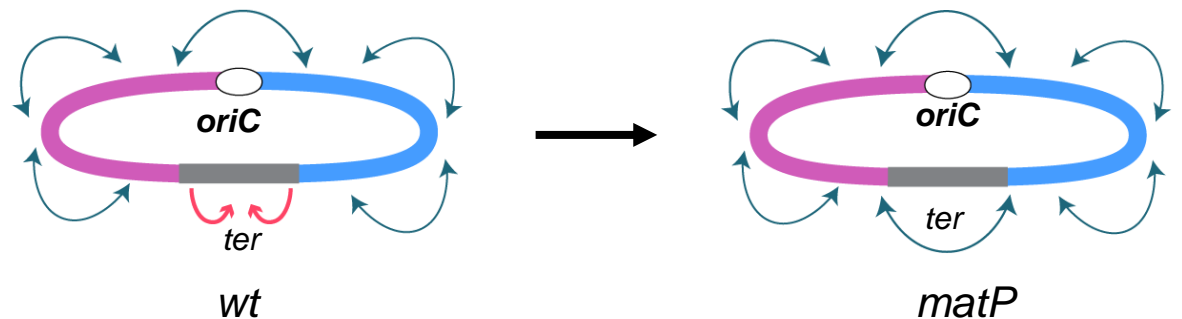
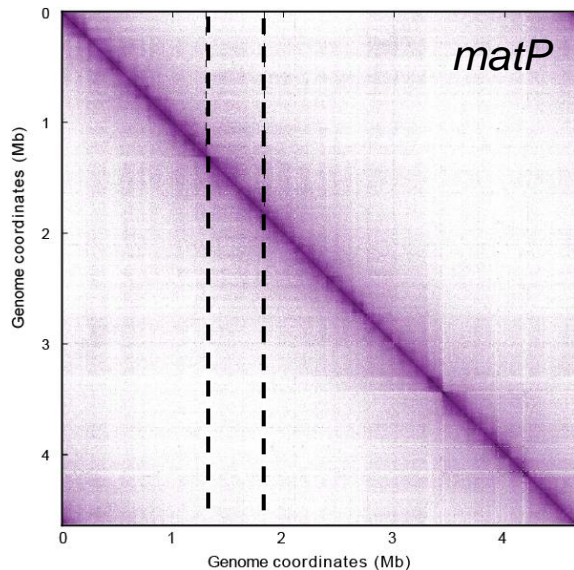
Organization of *ter* and a role for MatP in *ter* insulation



- ✓ enrichment of long-range contacts within *ter* and its flanking domains in the absence of MatP (>~280 kb).

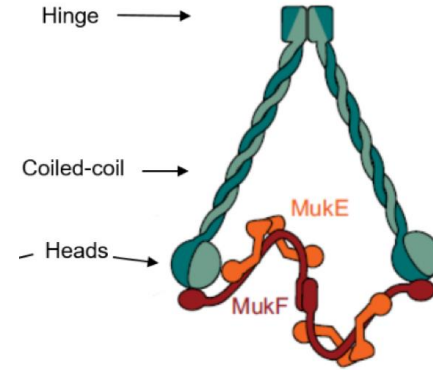
➤ Confirmed by Genetics

- ✓ *ter* now appears similar to the rest of the genome

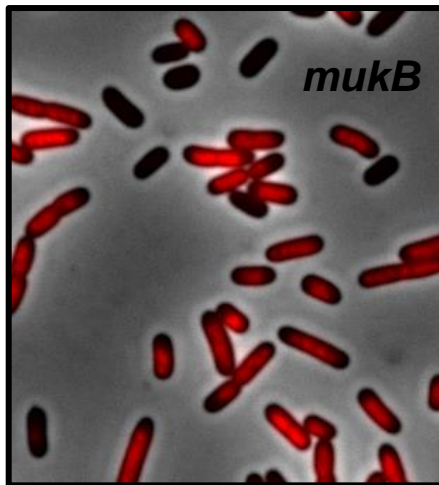


MukBEF complex

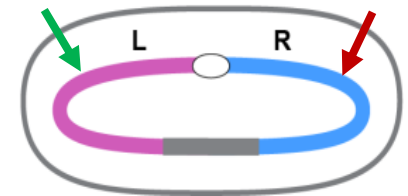
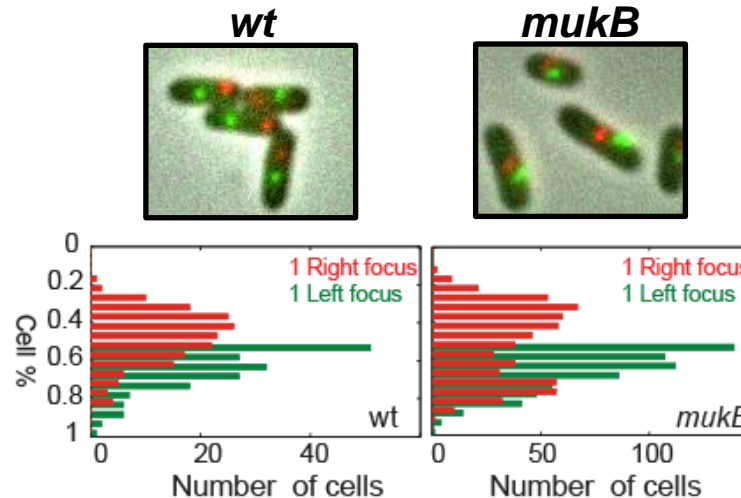
- **MukBEF :**
 - Distantly related in sequence to SMC-ScpAB
 - Role in chromosome segregation
 - Role in chromosome positioning
 - Interplay with TopoIV and **MatP**



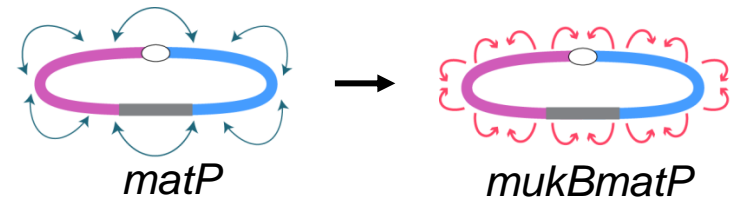
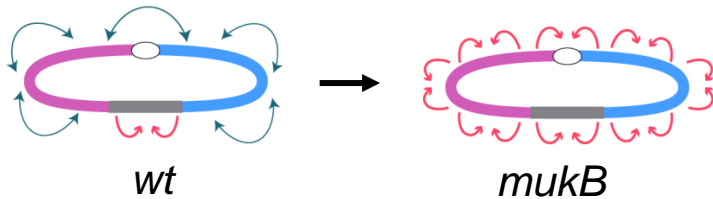
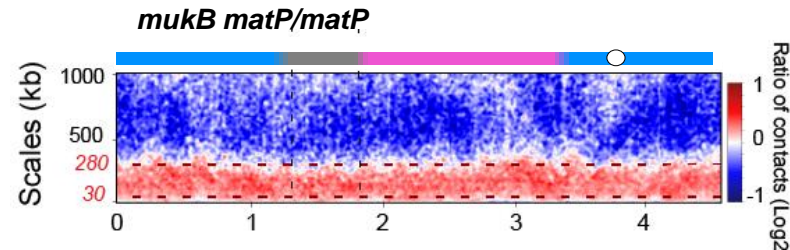
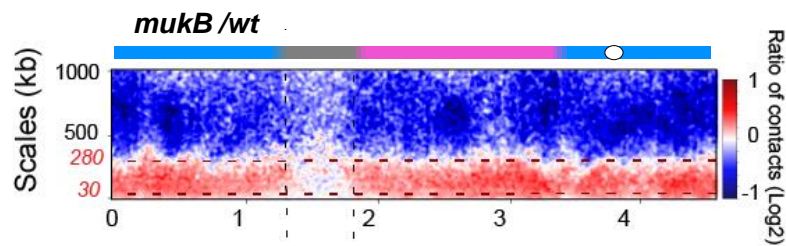
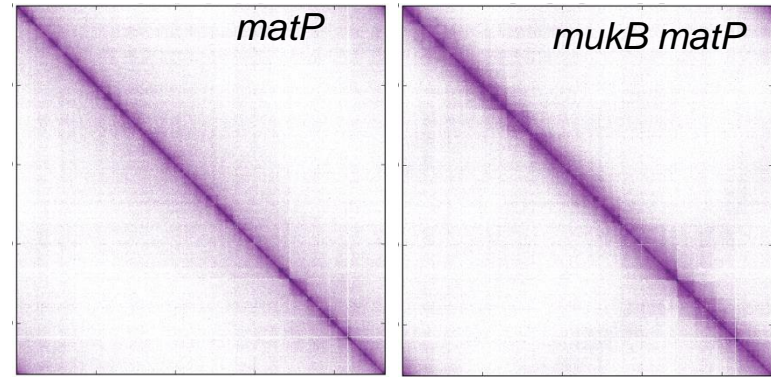
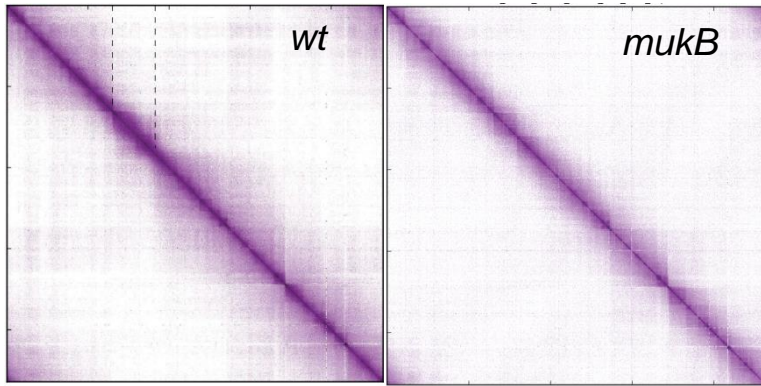
~20 % anucleated cells



Increased Right locus mispositioning (11% vs 22 %)



MukBEF is essential to promote long range communications

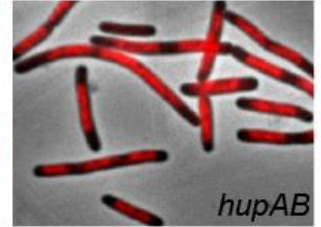
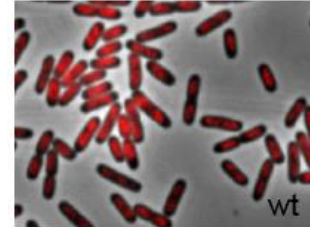


- ✓ **MukBEF** promotes **intra-arm** DNA contacts in the Mb range
- ✓ **MatP** restricts DNA contacts and prevents **MukBEF** activity in *ter*

3 major NAPs in *E. coli*

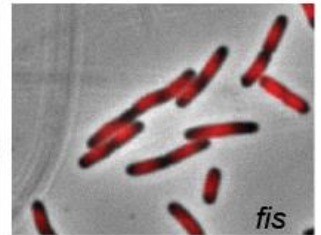
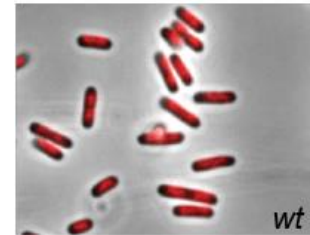
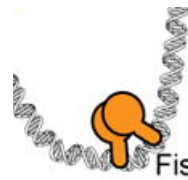
HU:

- DNA bending
- Transcriptional factor - low sequence specificity
- Hi-C *C. crescentus*: promote short-range contacts



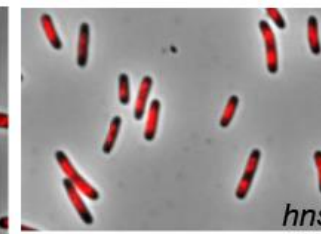
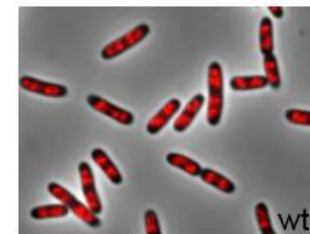
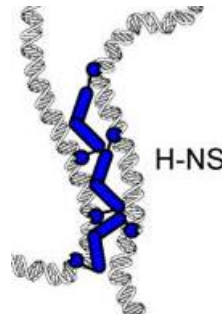
Fis:

- DNA bending
- The most abundant NAP in exponential phase
- Transcriptional factor: binds to AT rich regions



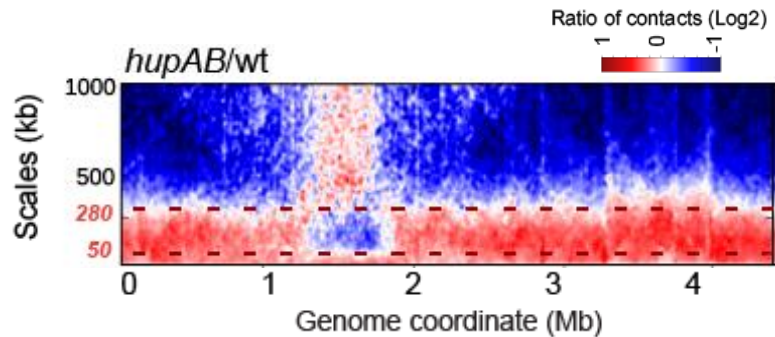
H-NS:

- DNA bridging.
- Oligomerizes along DNA
- Xenogeneic silencer (AT rich regions)

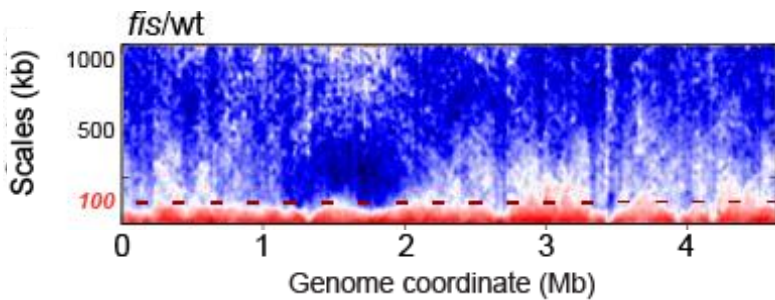


➔ **Exact role in chromosome organization is unknown**

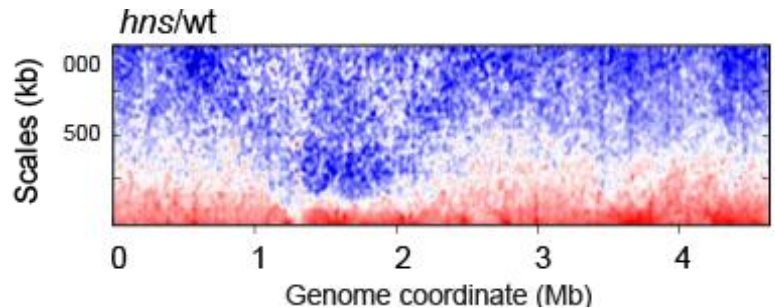
Different activities of 3 major NAPs



- ✓ **HU** promotes **intra-arm** DNA contacts in the Mb range (similar to **MukBEF**)
- ✓ **HU** promotes optimal DNA contacts in **ter** (~300 kb)



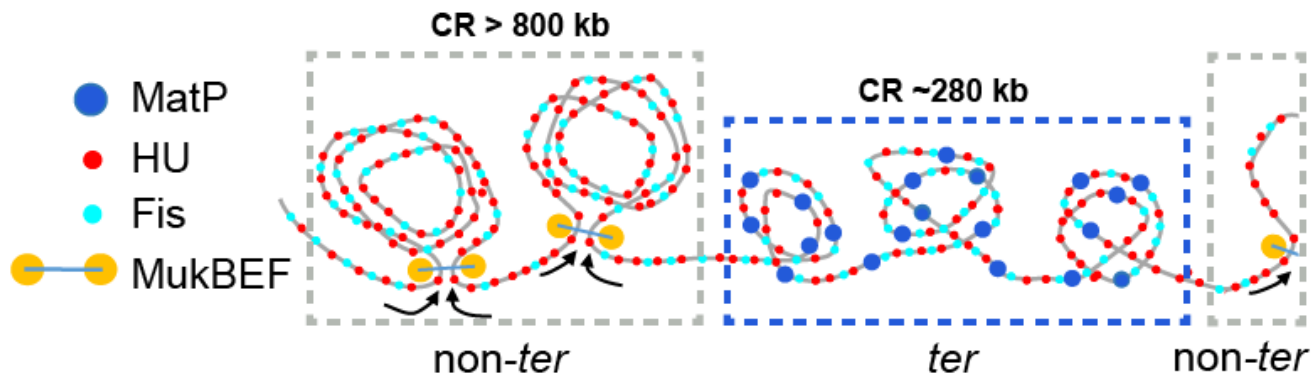
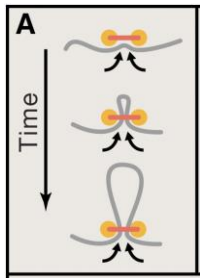
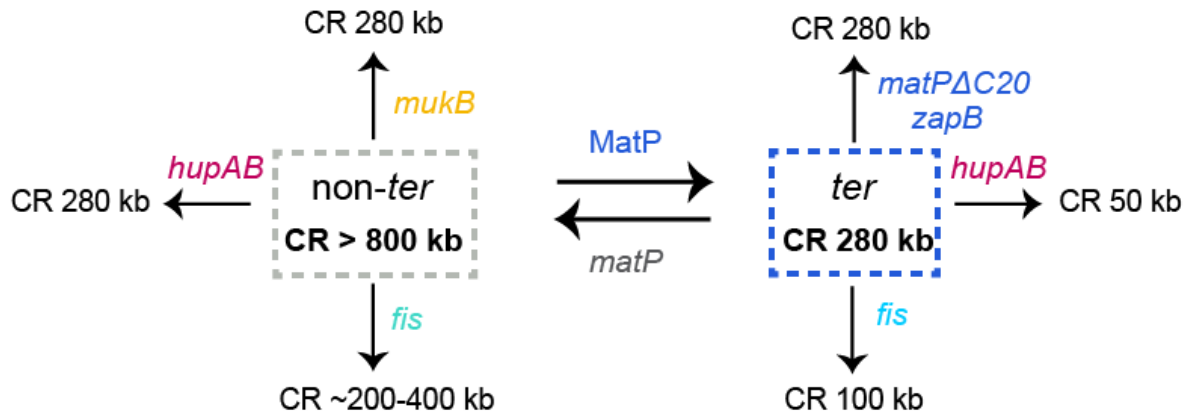
- ✓ **Fis** is required for long-range interactions
 - Confirmed by Genetics
- ✓ No correlation between DNA binding/increased DNA contacts
- ✓ Variable effect along the genome (ter and non ter)



- ✓ **H-NS** slightly effect on long-range contacts
- ✓ Increased short-range contacts in *hns* cells.
- ✓ Correlation with DNA binding sites (~70%)

➔ **HU** and **Fis**: Long range effect
H-NS : Restricts short range contacts (Gene repressor)

Multiscale organization of the chromosome



Acknowledgments



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- Olivier Espéli



- Julien Mozziconacci