The Three-Dimensional Architecture of a Bacterial Genome and Its Alteration by Genetic Perturbation

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The Three-Dimensional Architecture of a Bacterial Genome and Its Alteration by Genetic Perturbation

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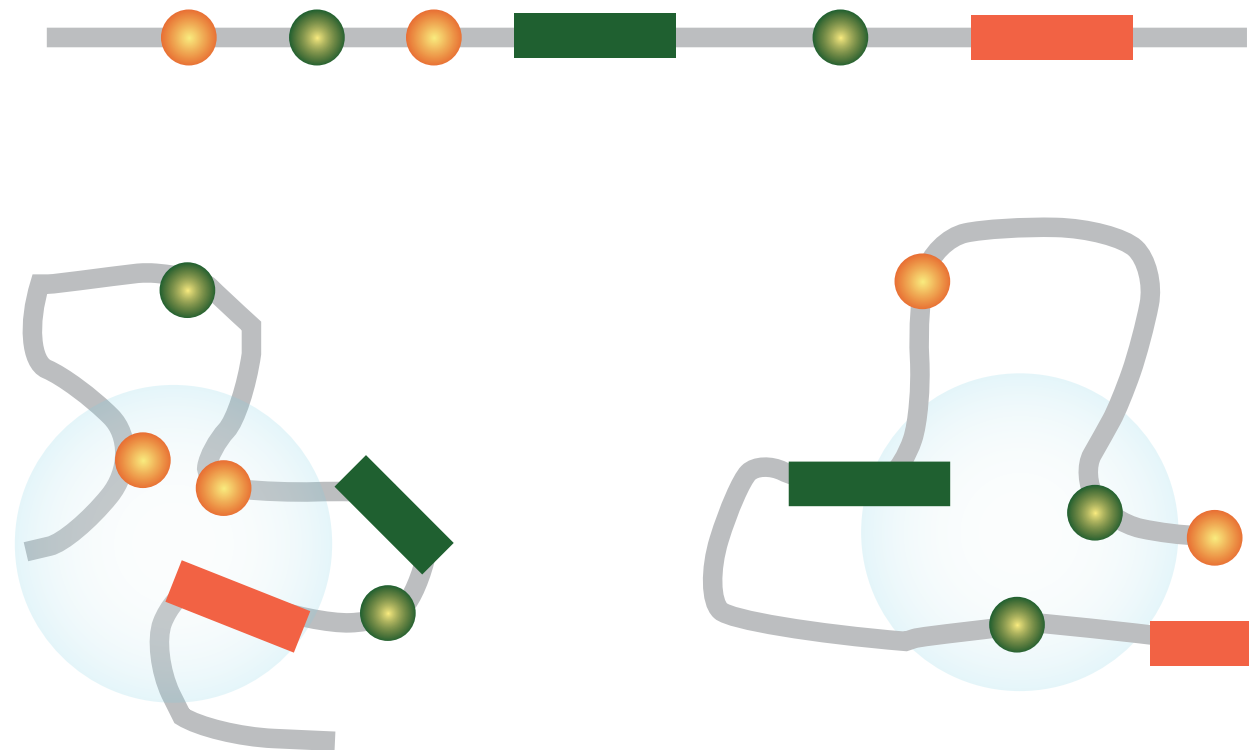[6]Department of Biochemistry and Molecular Pharmacology
[7]Program in Systems Biology
University of Massachusetts Medical School, Worcester, MA 01605, USA
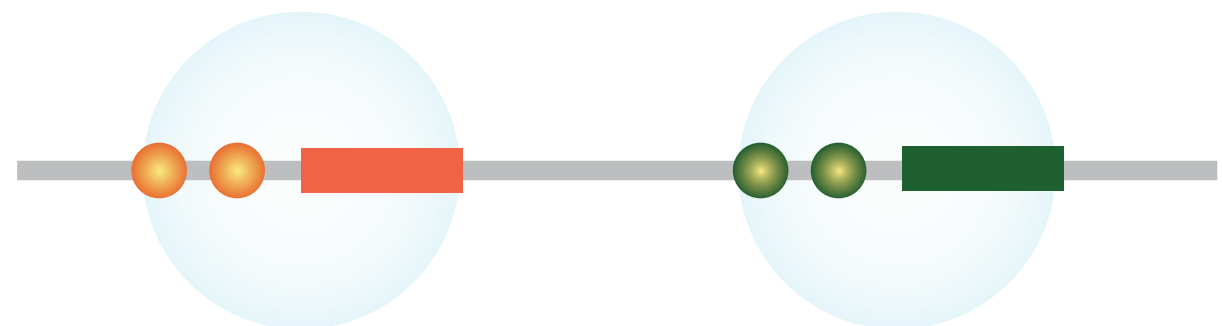[8]These authors contributed equally to this work
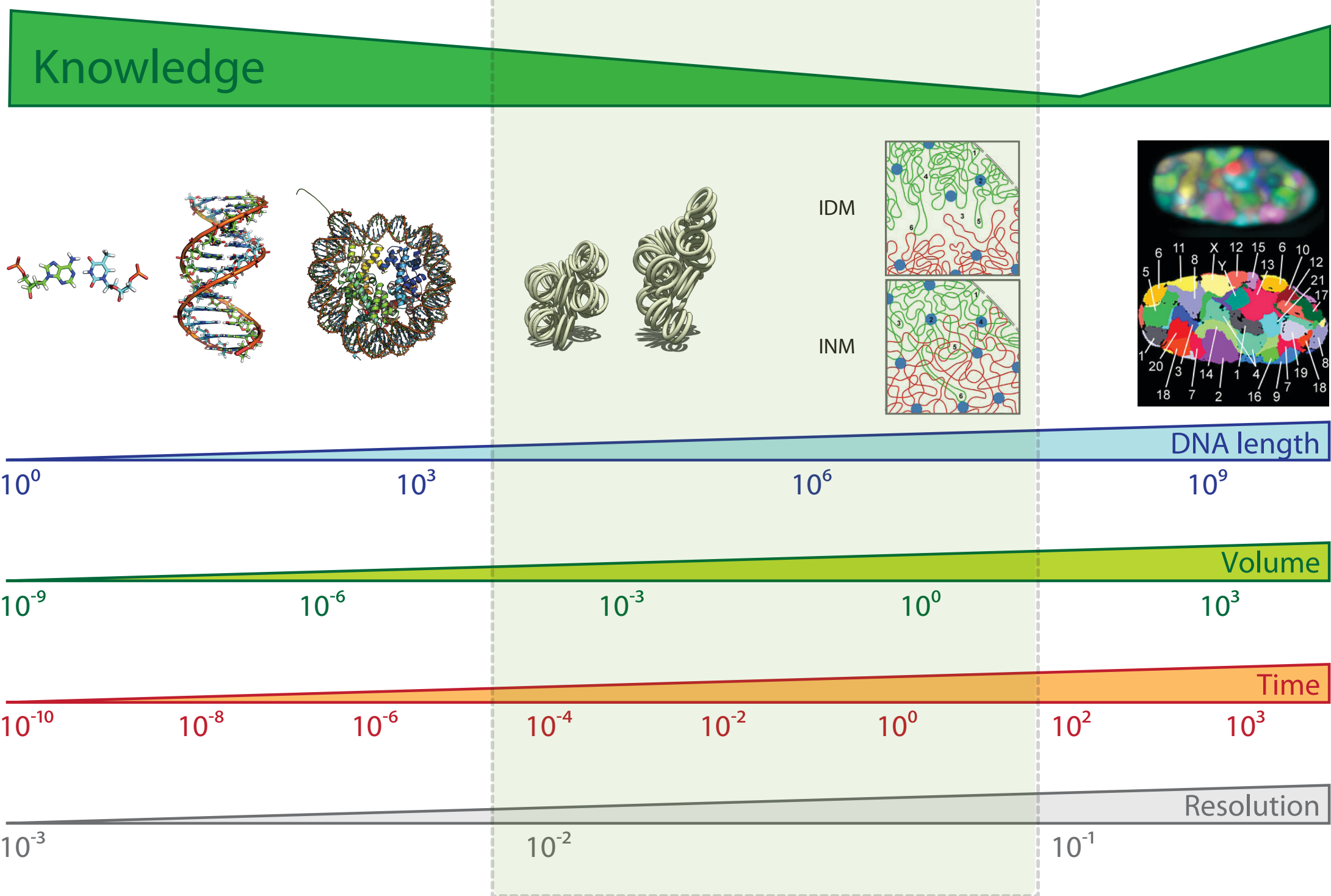*Correspondence: umbarger@post.harvard.edu (M.A.U.), mmarti@cipf.es (M.A.M.-R.), job.dekker@umassmed.edu (J.D.)
DOI 10.1016/j.molcel.2011.09.010

"Complex" genomes

"Simple" genomes

Knowledge

IDM

INM

DNA length
10^0 10^3 10^6 10^9 nt

Volume
10^{-9} 10^{-6} 10^{-3} 10^0 10^3 µm³

Time
10^{-10} 10^{-8} 10^{-6} 10^{-4} 10^{-2} 10^0 10^2 10^3 s
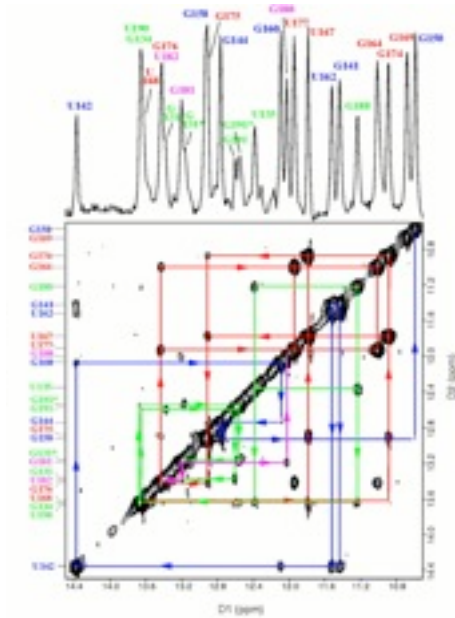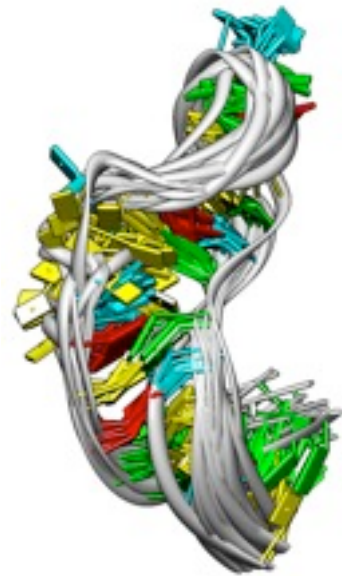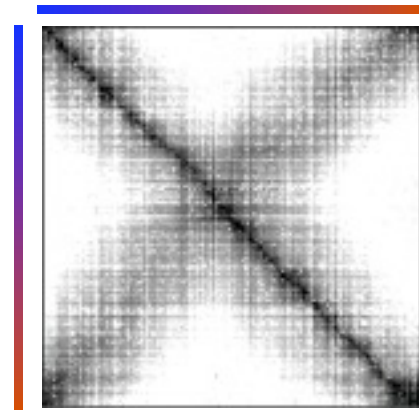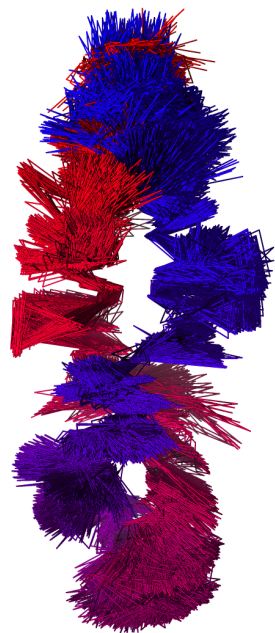
Resolution
10^{-3} 10^{-2} 10^{-1} µ

Adapted from:
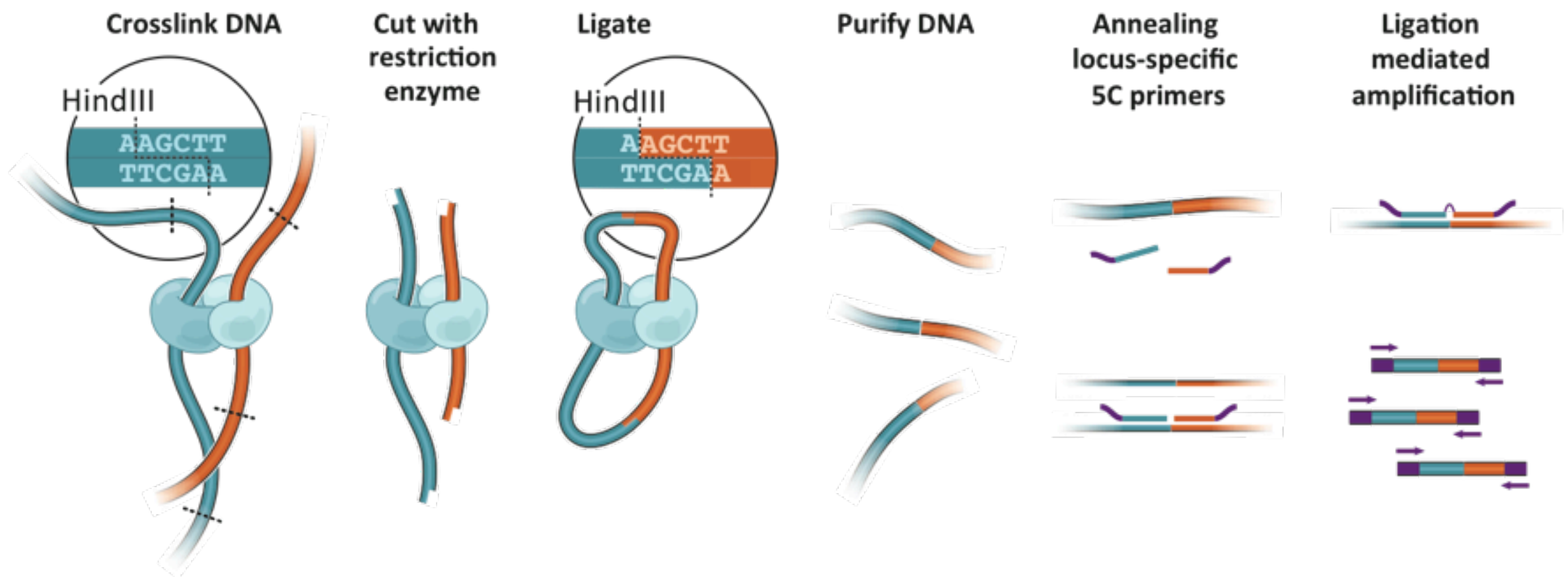*Langowski and Heermann. Semin Cell Dev Biol (2007) vol. 18 (5) pp. 659-67*

Biomolecular structure determination
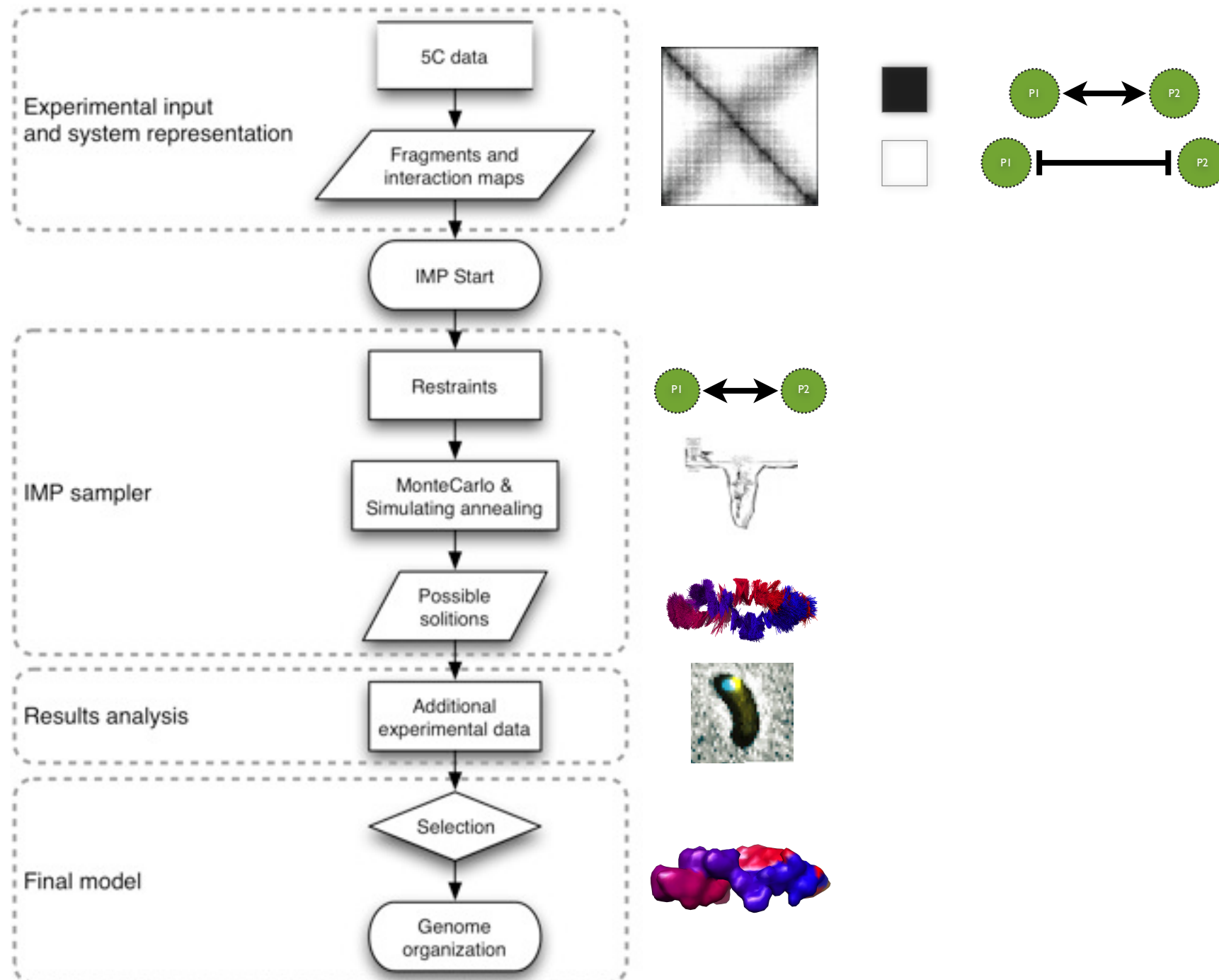2D-NOESY data

Chromosome structure determination
5C data

5C technology

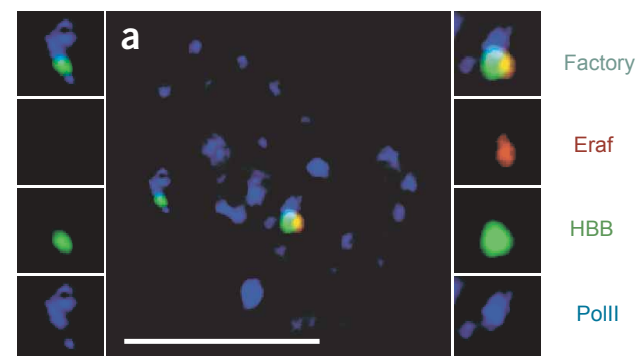*Dostie et al. Genome Res (2006) vol. 16 (10) pp. 1299-309*

Integrative Modeling

http://www.integrativemodeling.org

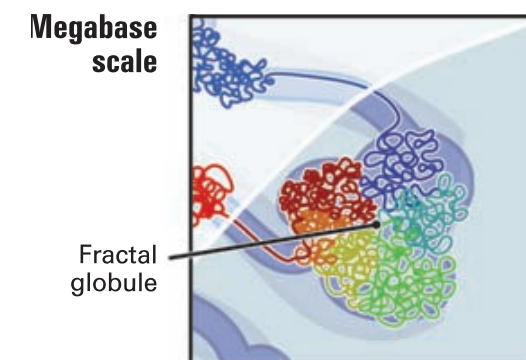# The "Chromatin Globule" model

D. Baù et al. Nat Struct Mol Biol (2011) 18:107-14
A. Sanyal et al. Current Opinion in Cell Biology (2011) 23:325–33.
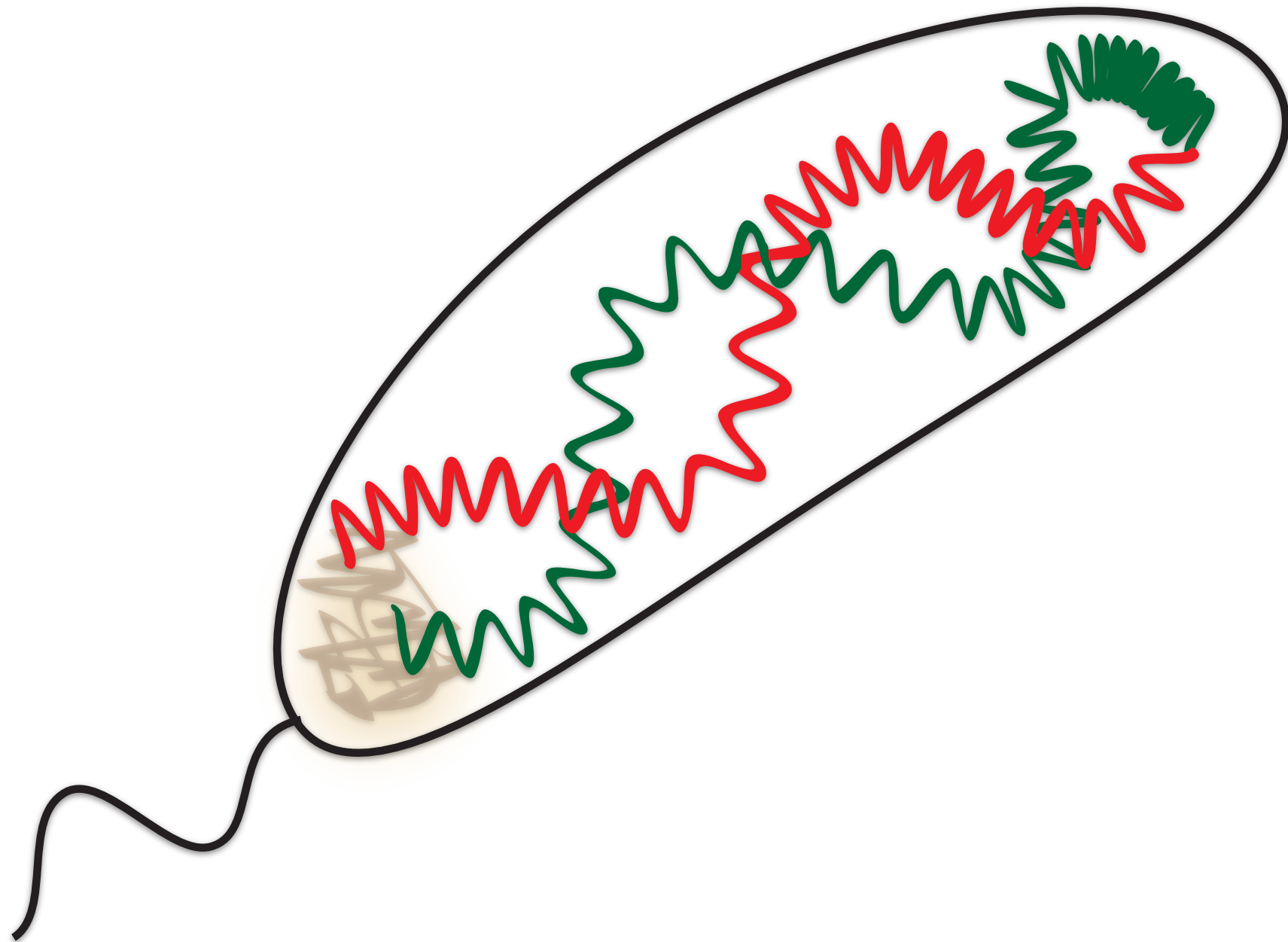

Münkel et al. JMB (1999)
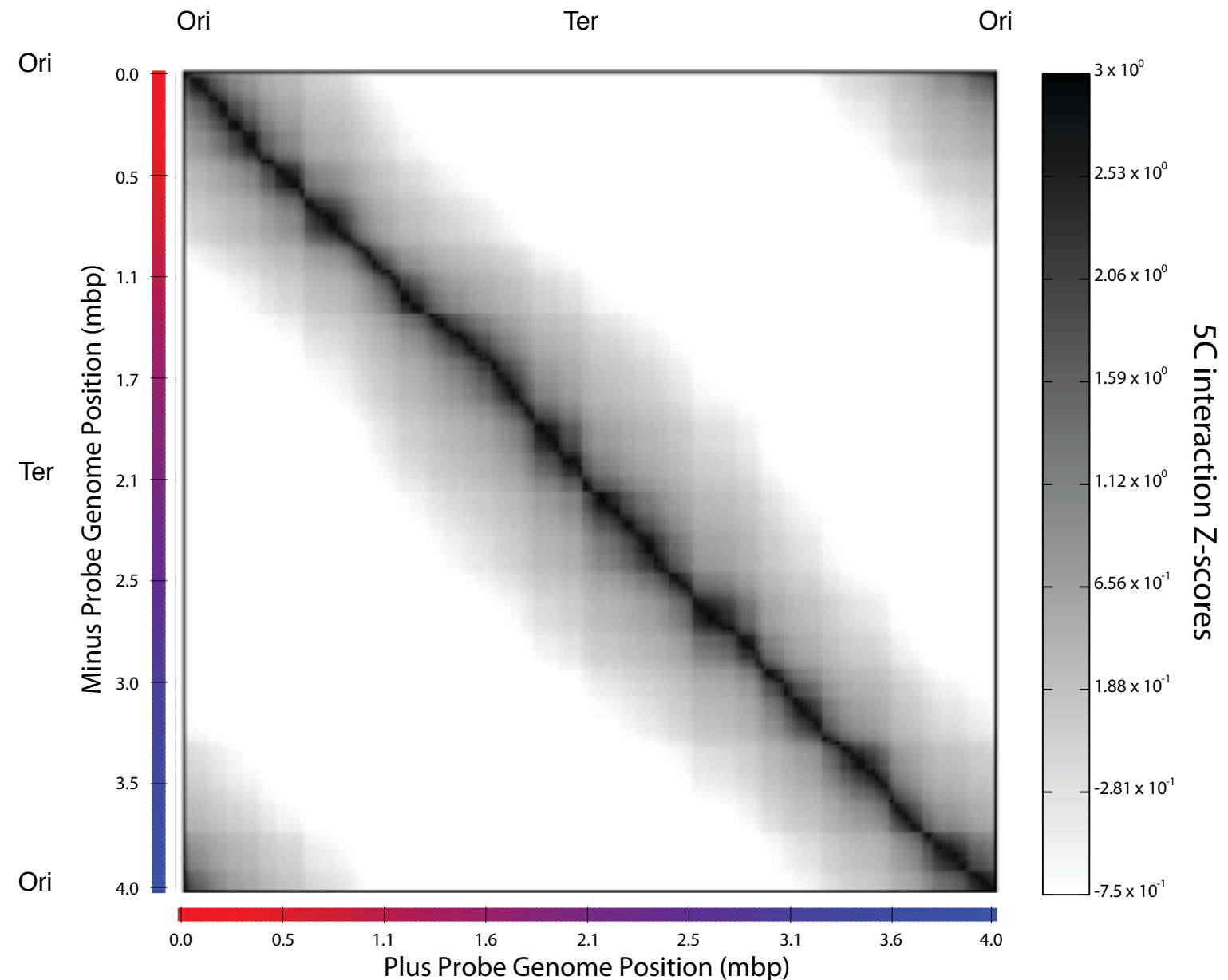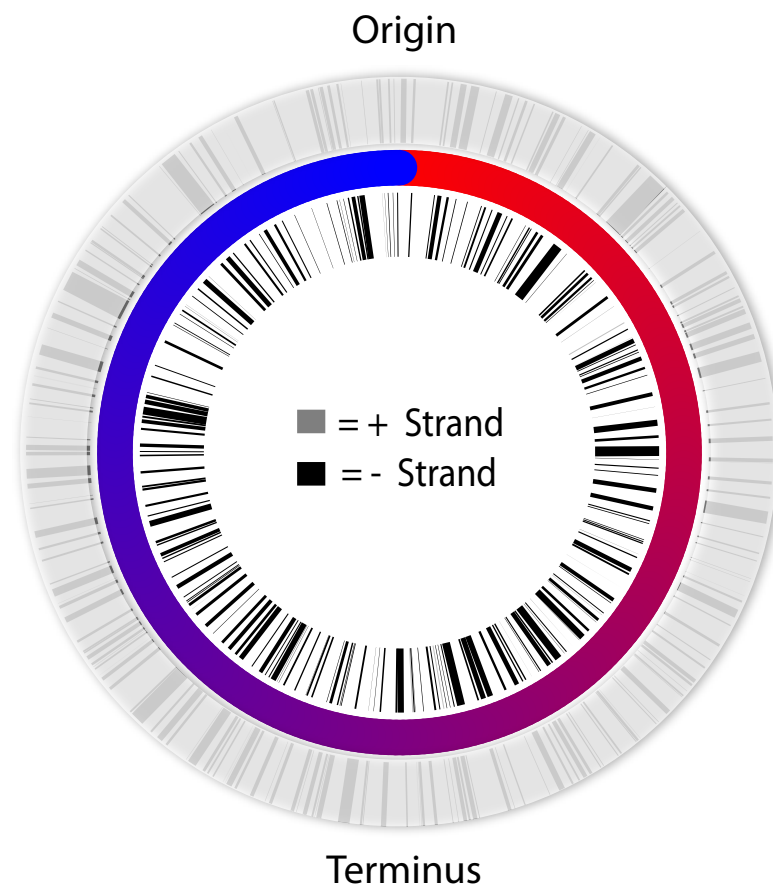
Osborne et al. Nat Genet (2004)

al. Science (2009)

Caulobacter crescentus 3D genome

M.A. Umbarger, et al. Molecular Cell (2011) 44:252–264

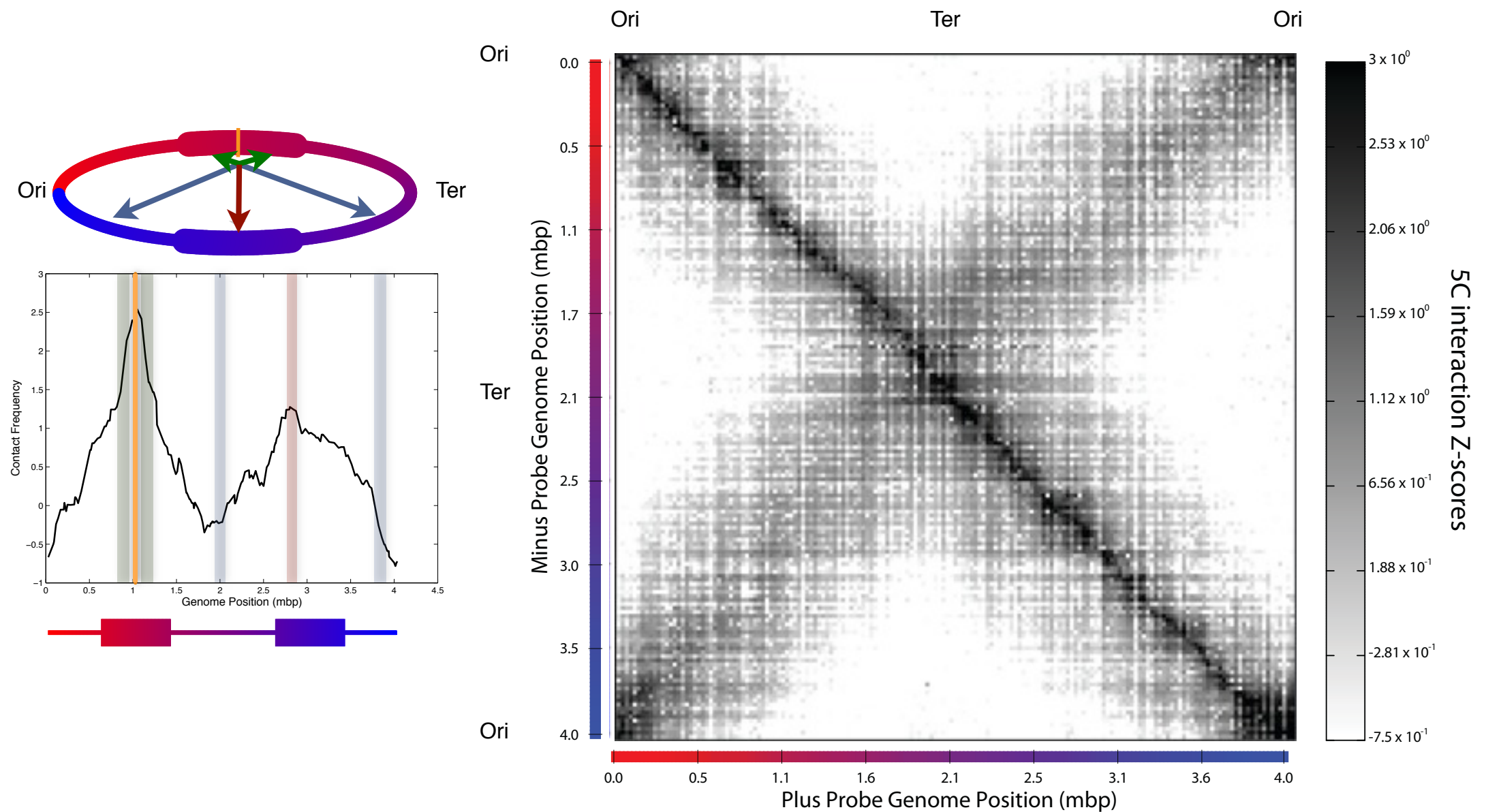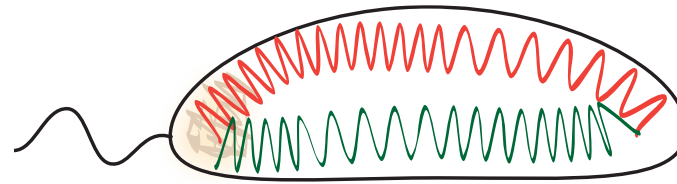# The 3D architecture of Caulobacter Crescentus

4,016,942 bp & 3,767 genes

169 5C primers on + strand

170 5C primers on − strand

28,730 chromatin interactions

~13Kb

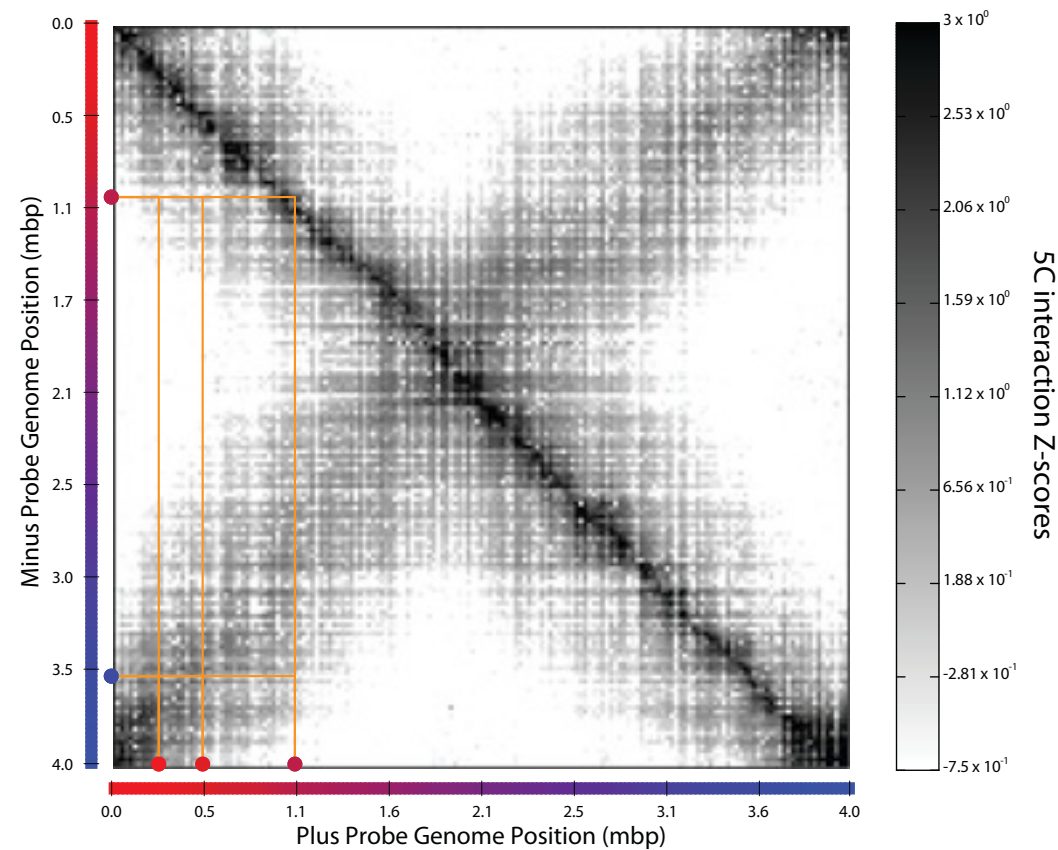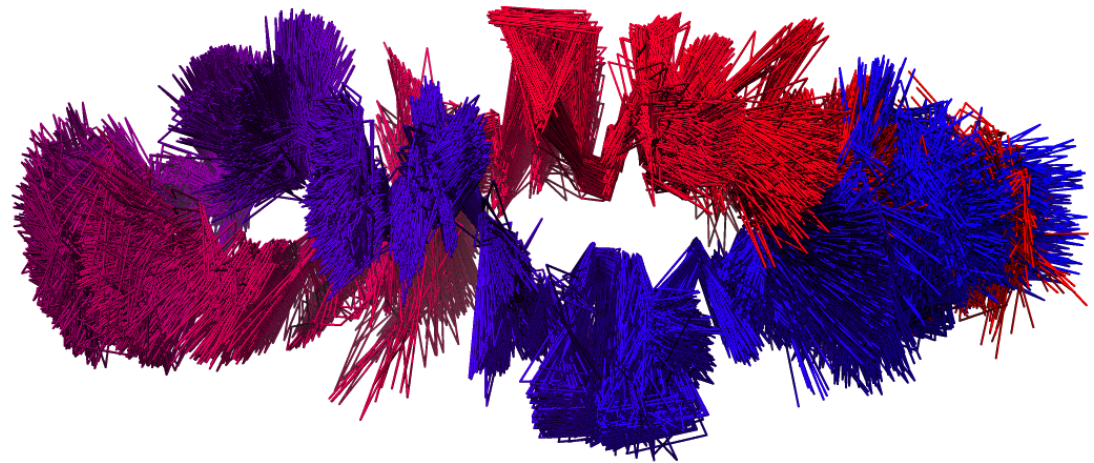# 5C interaction matrix

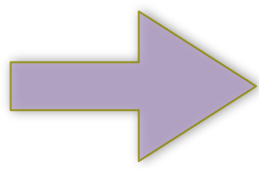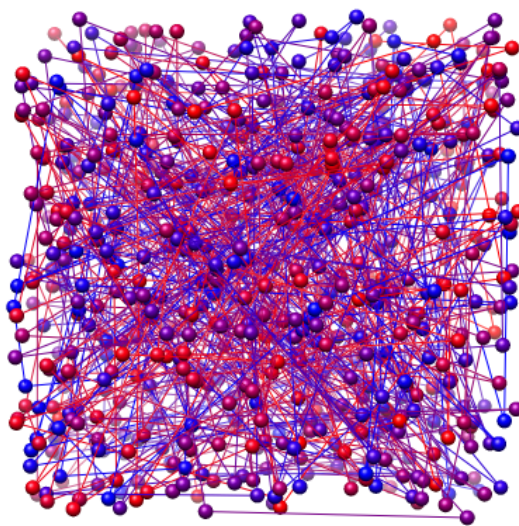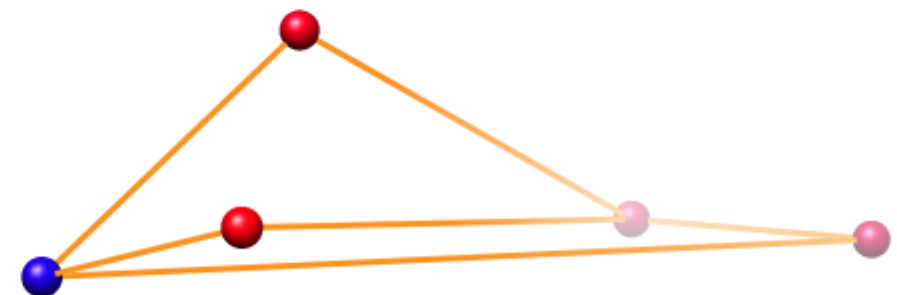## ELLIPSOID for Caulobacter cresentus

3D model building with the 5C + IMP approach

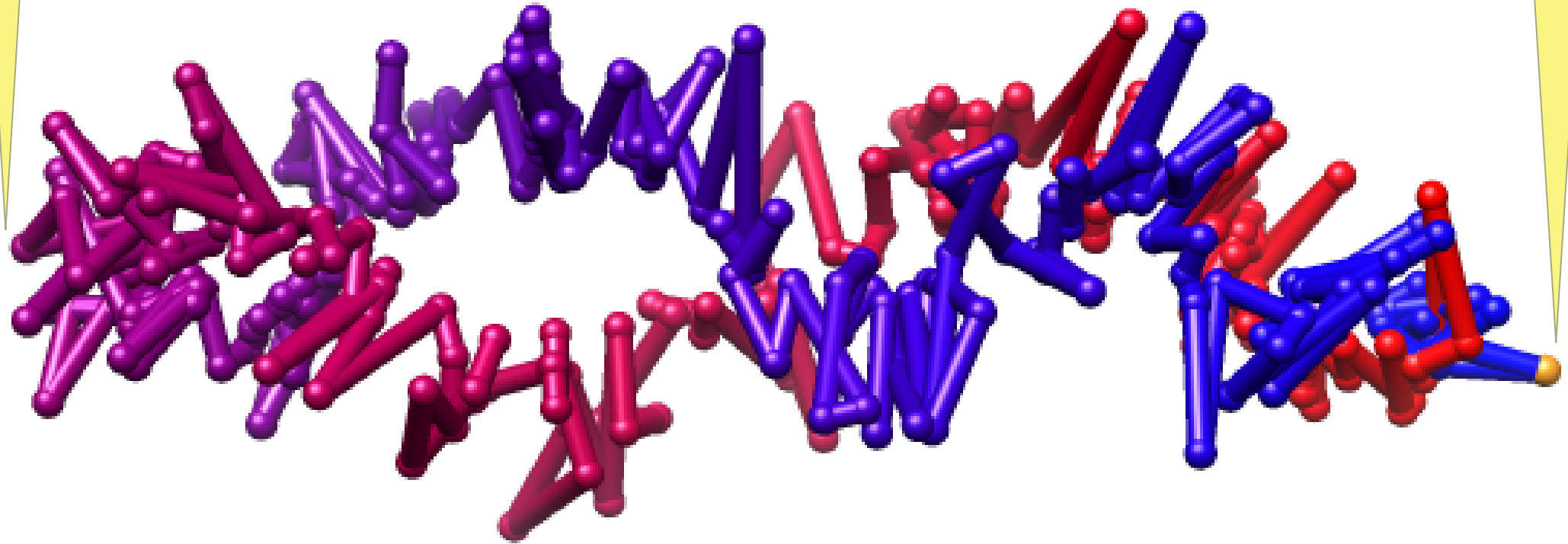

339 mers

Genome organization in Caulobacter crescentus

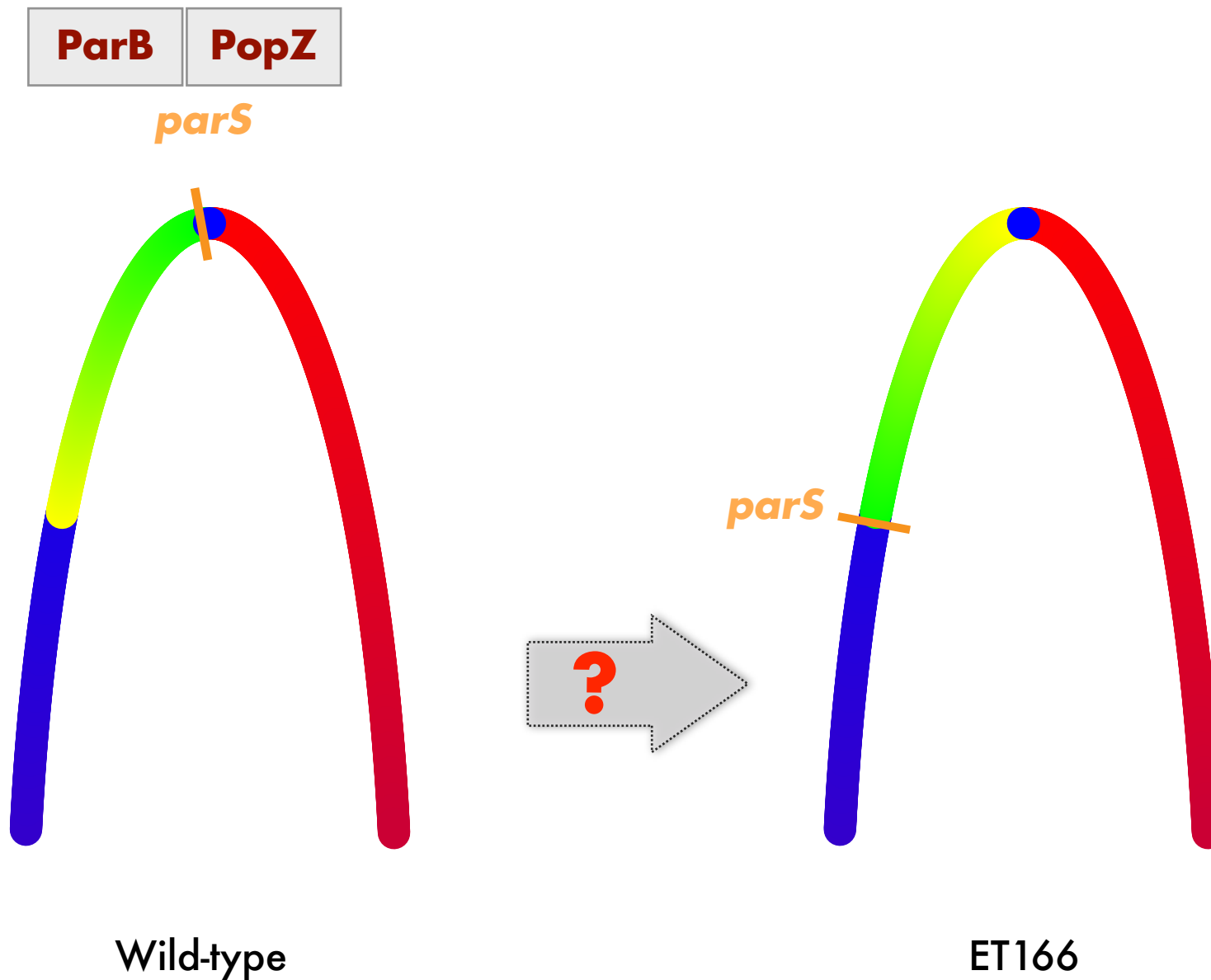## Arms are helical

dif site 47±17Kb from Ter

Resolution

parS sites 25±17Kb from Ori

Centromer-like

cnag CRG
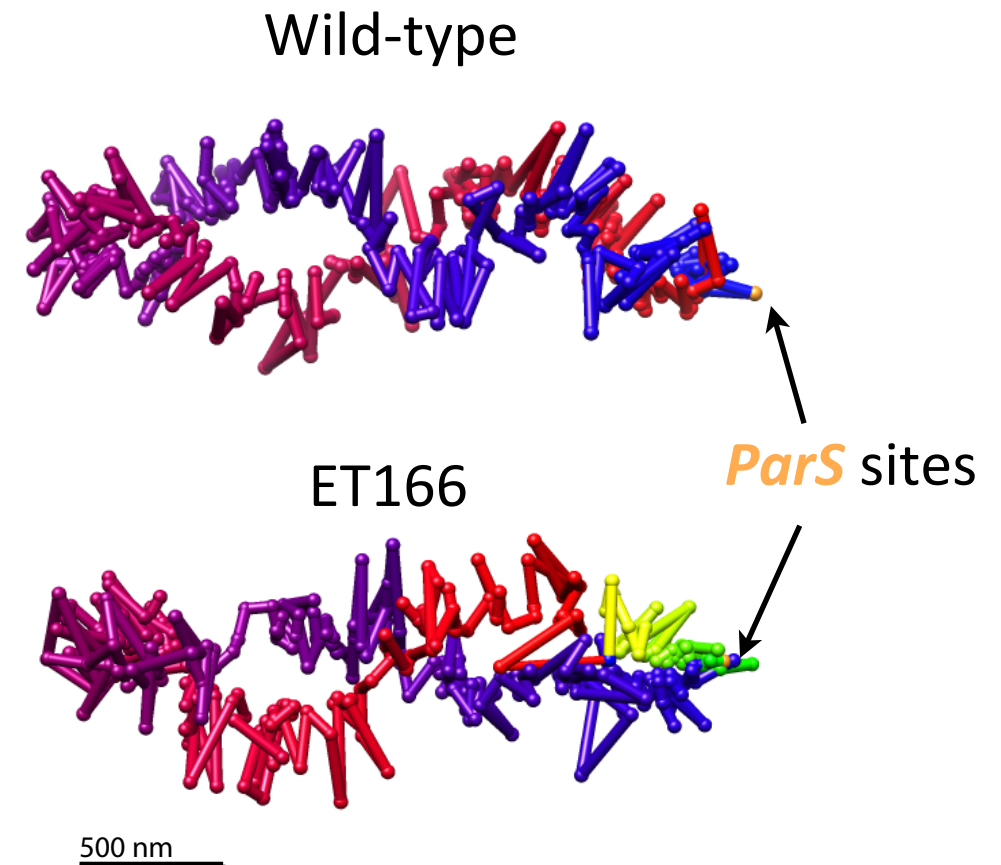
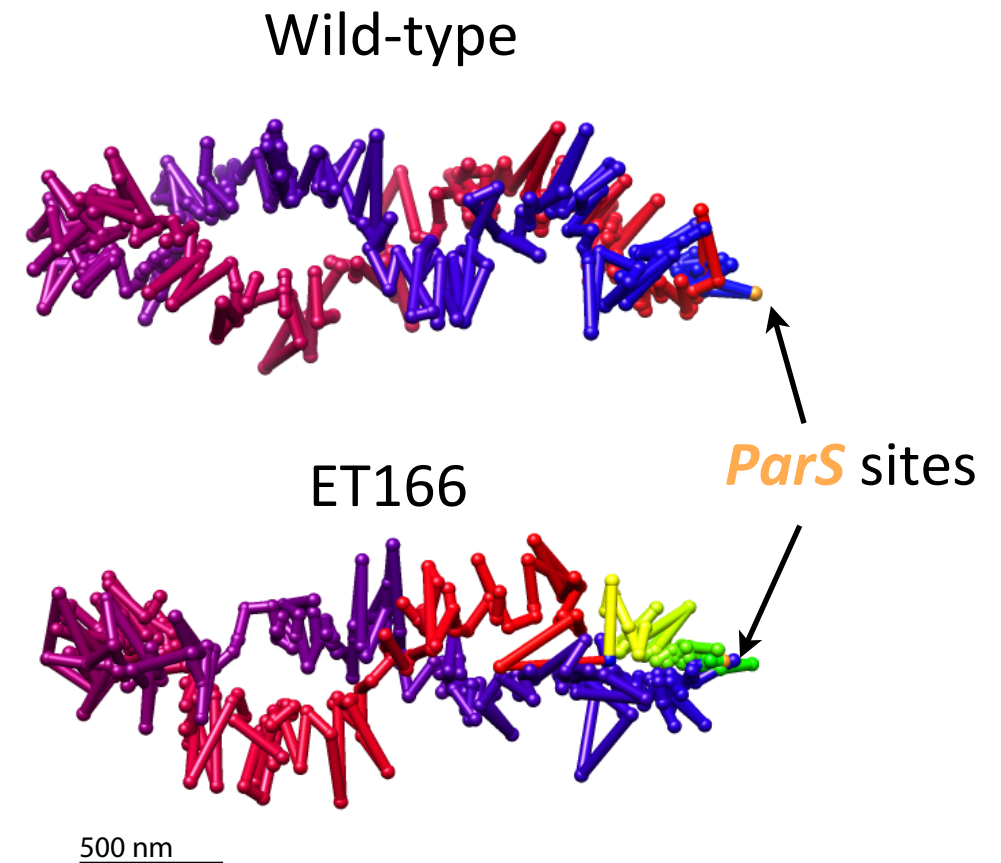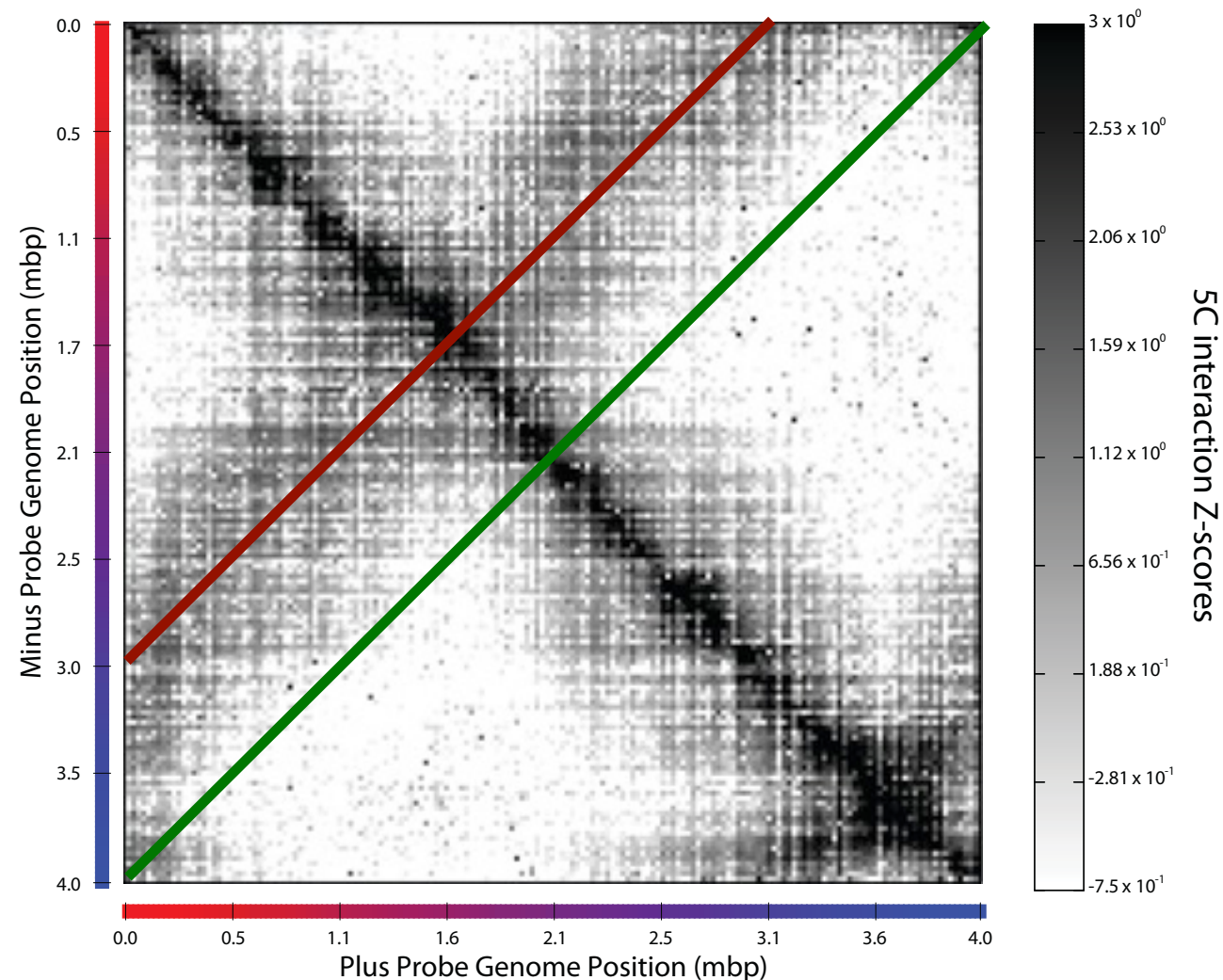# Moving the parS sites 400 Kb away from Ori

ParB | PopZ

parS

Wild-type

parS

ET166

Moving the parS sites results in whole genome rotation!

Wild-type

ParS sites

ET166

500 nm

Arms are **STILL** helical

Structure & function PRESERVED!!!

Moving the parS sites results in whole genome rotation!

Wild-type

ET166

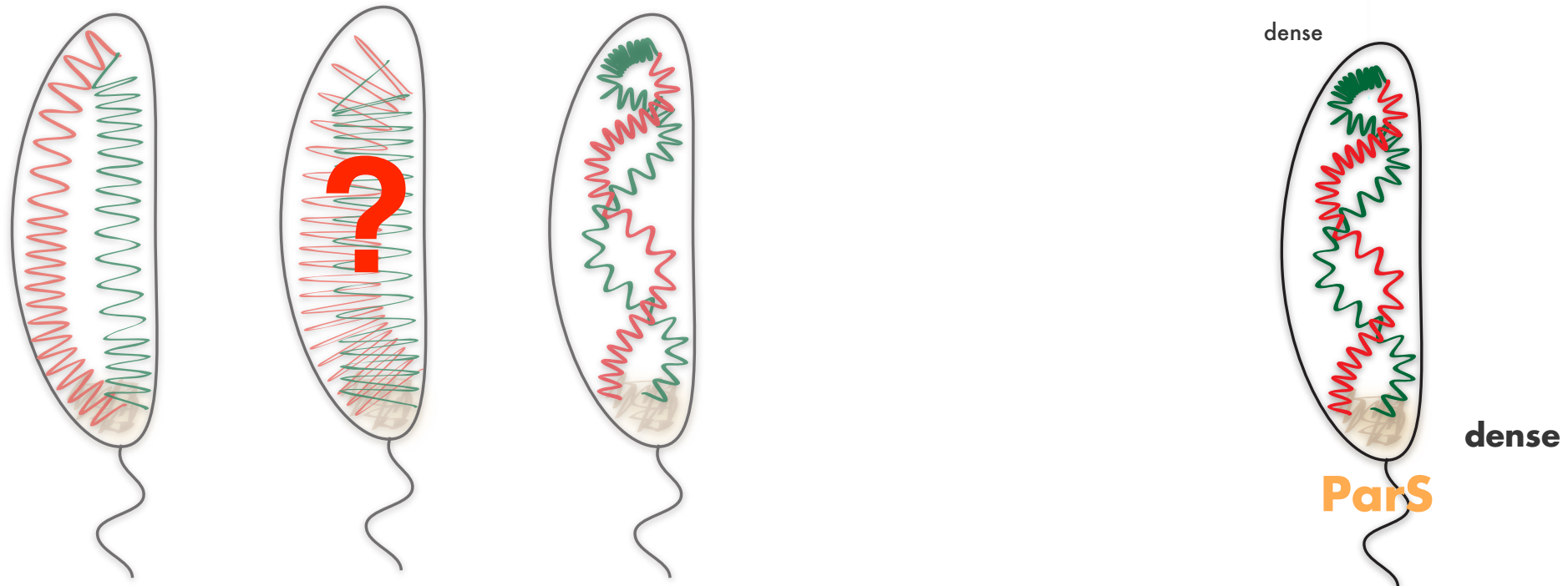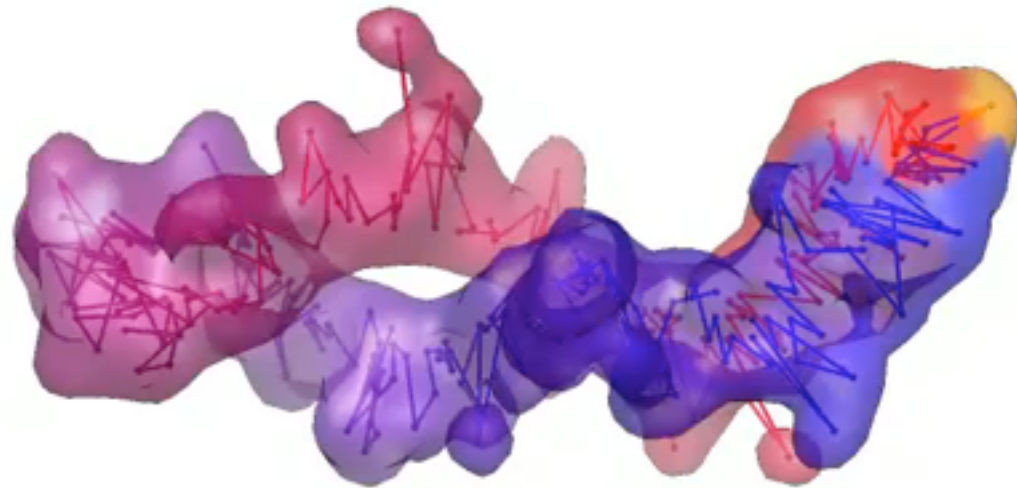*ParS* sites

500 nm

Arms are **STILL** helical

Structure & function PRESERVED!!!

Genome architecture in Caulobacter

From Sequence to Function

D. Baù and M.A. Marti-Renom Chromosome Res (2011) 19:25-35.

Function!

Funtion!

PLoS CB Outlook

Marti-Renom MA, Mirny LA (2011) PLoS Comput Biol 7(7): e1002125.

MURRE
Cell (2008) **133**:265-79

DOSTIE/BLANCHETTE
Genome Biol (2009) **10**: R37

DEKKER/LANDER/MIRNY
Science (2009) **326**:289-93

NOBLE
Nature (2010) **465**: 363-7

DEKKER/MARTI-RENOM
NSMB (2011) **18**:107-14

Acknowledgments

http://marciuslab.org
http://integrativemodeling.org
http://cnag.cat · http://crg.cat