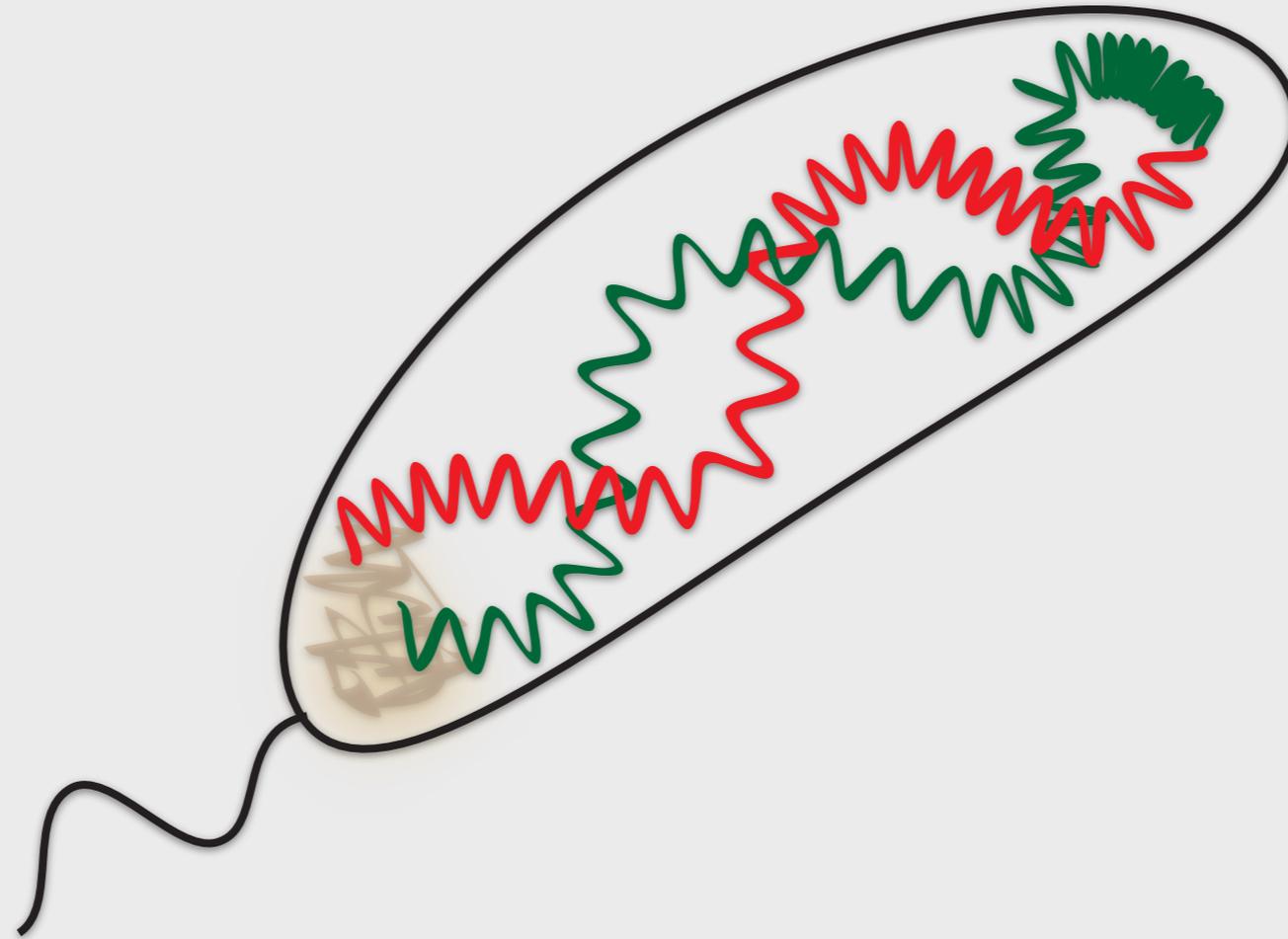


The 3D architecture of a bacterial genome



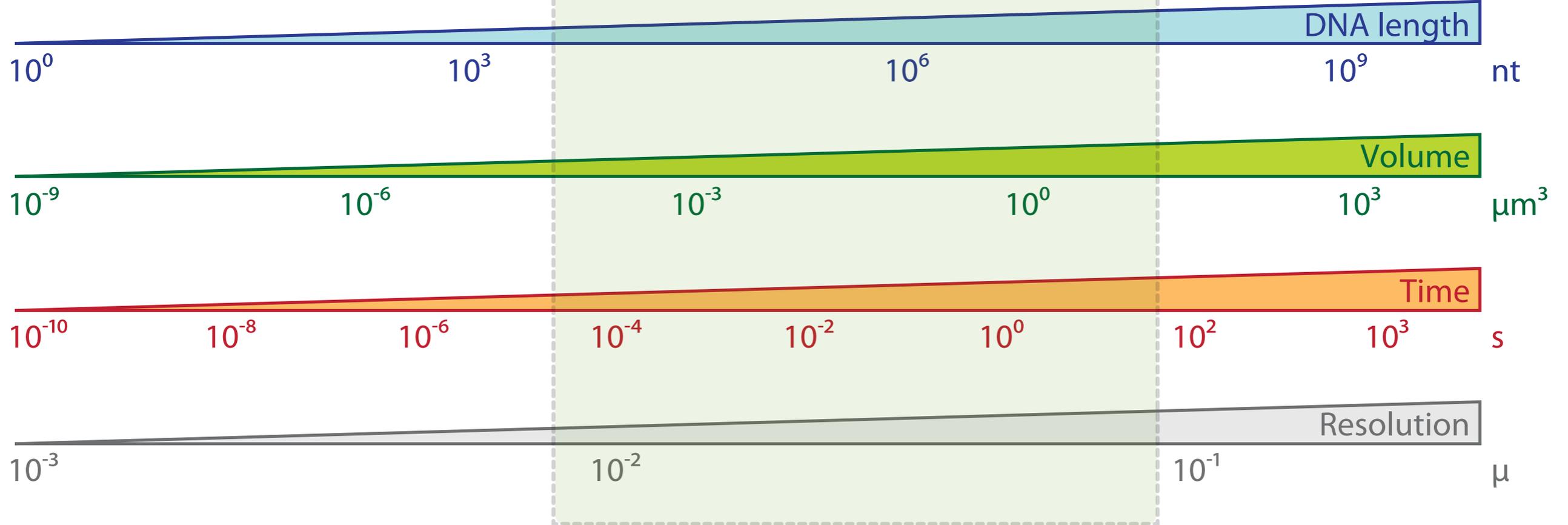
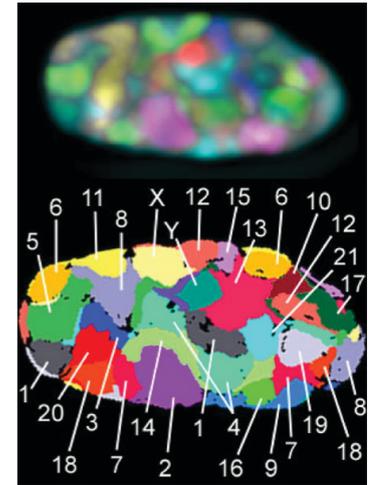
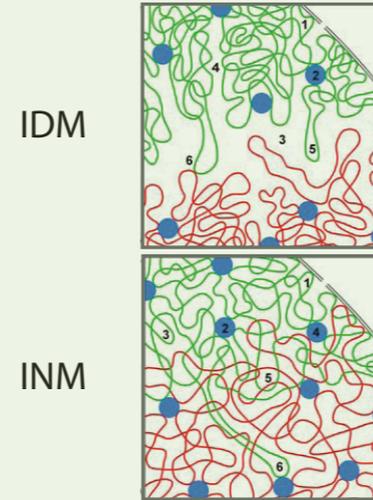
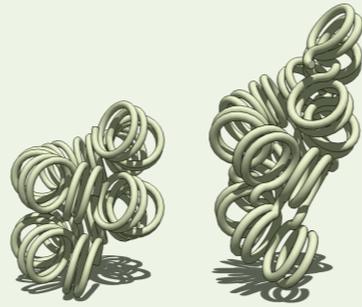
Structural Genomics Laboratory
Bioinformatics & Genomics Department
Prince Felipe Research Center (CIPF), Valencia, Spain

Marc A. Marti-Renom

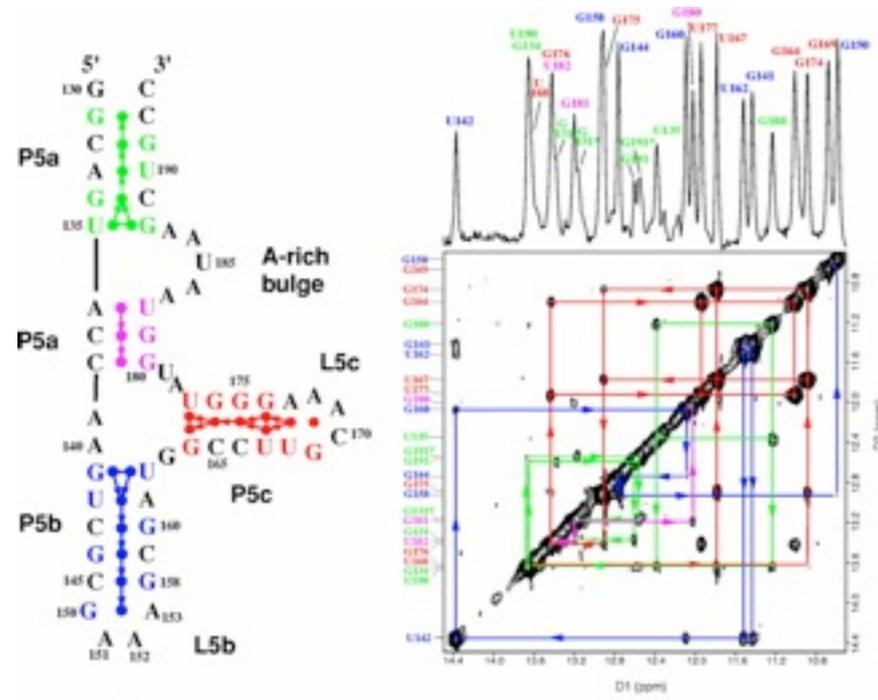


<http://sgu.bioinfo.cipf.es>

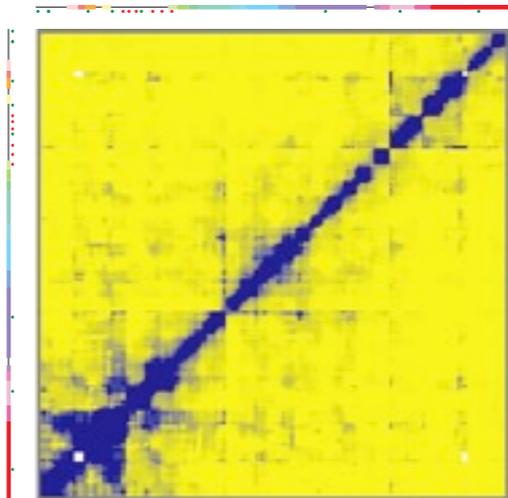
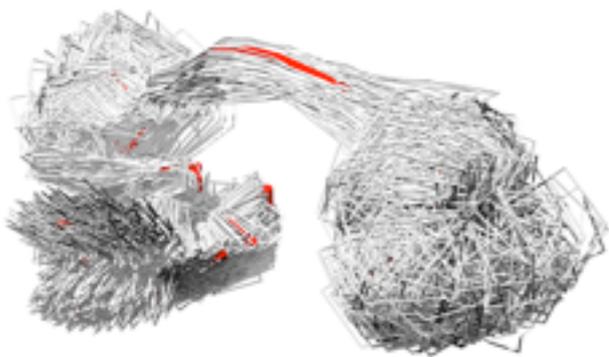
Knowledge



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



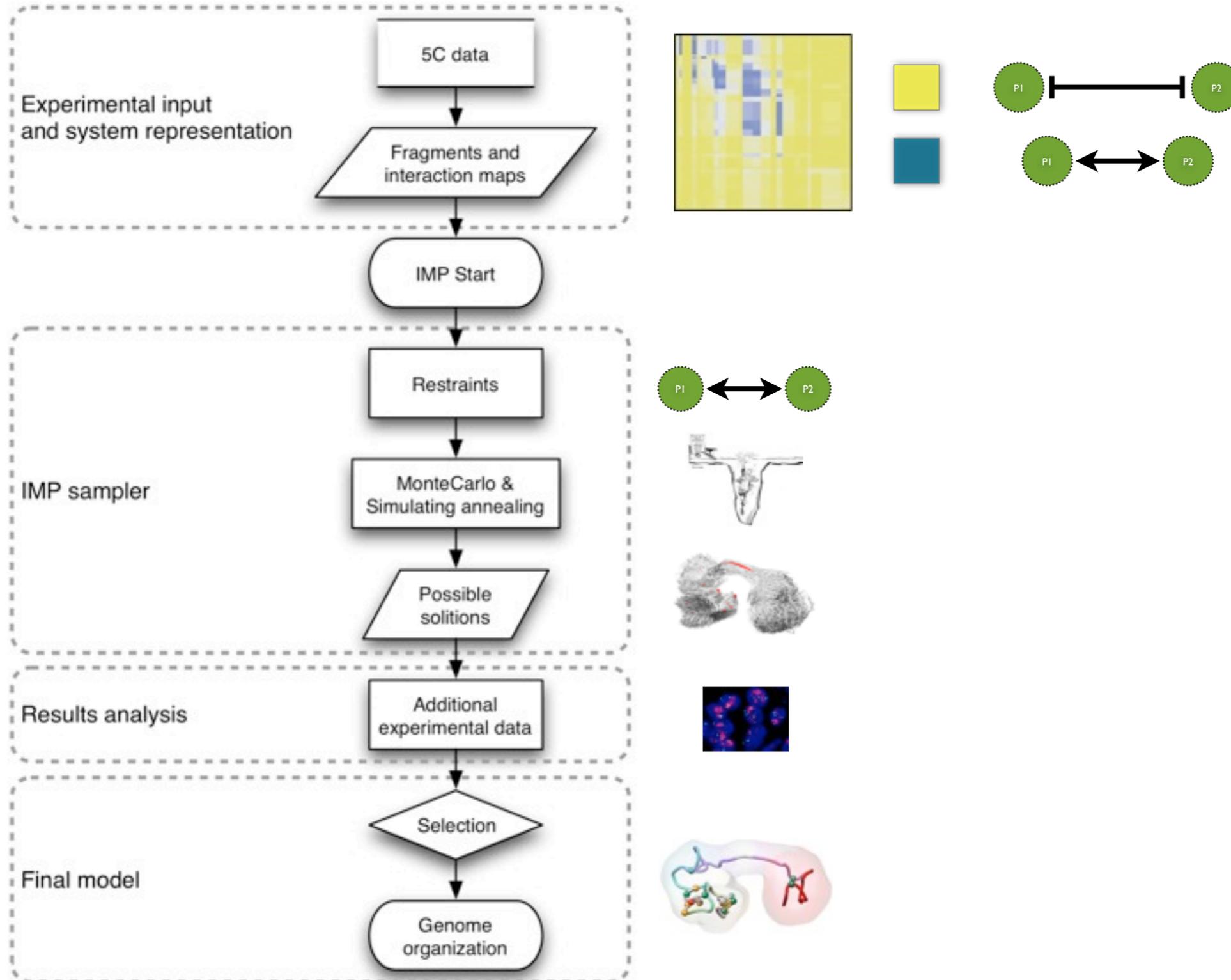
Biomolecular structure determination
2D-NOESY data



Chromosome structure determination
5C data

Integrative Modeling Platform

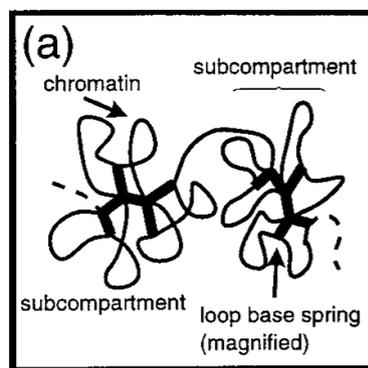
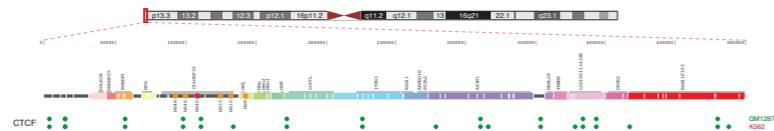
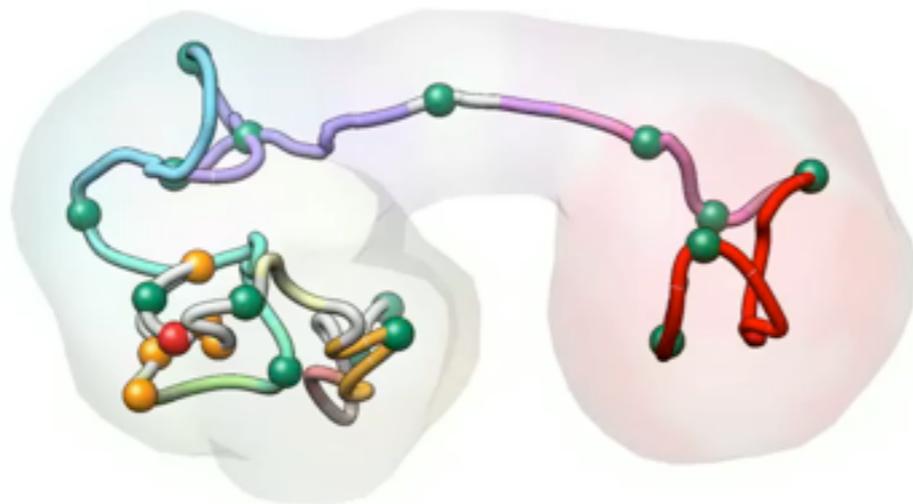
<http://www.integrativemodeling.org>



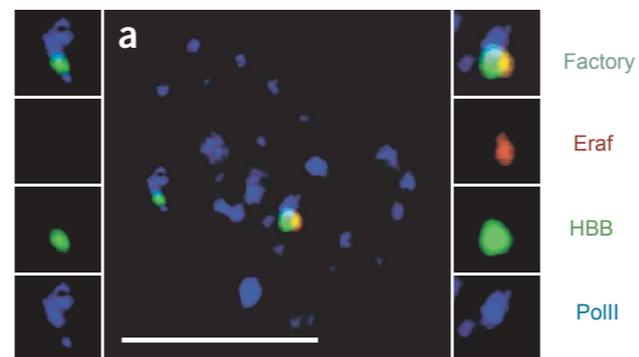
Alber et al. Nature (2007) vol. 450 (7170) pp. 683-94



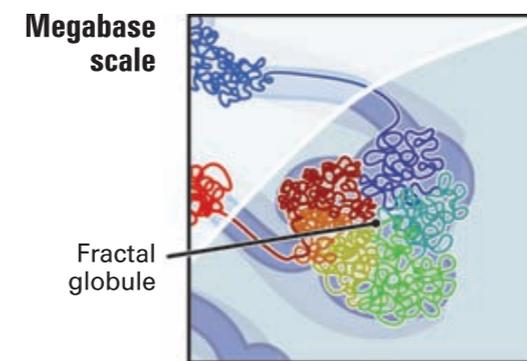
The “Chromatin Globule” model



Münkel et al. JMB (1999)



Osborne et al. Nat Genet (2004)

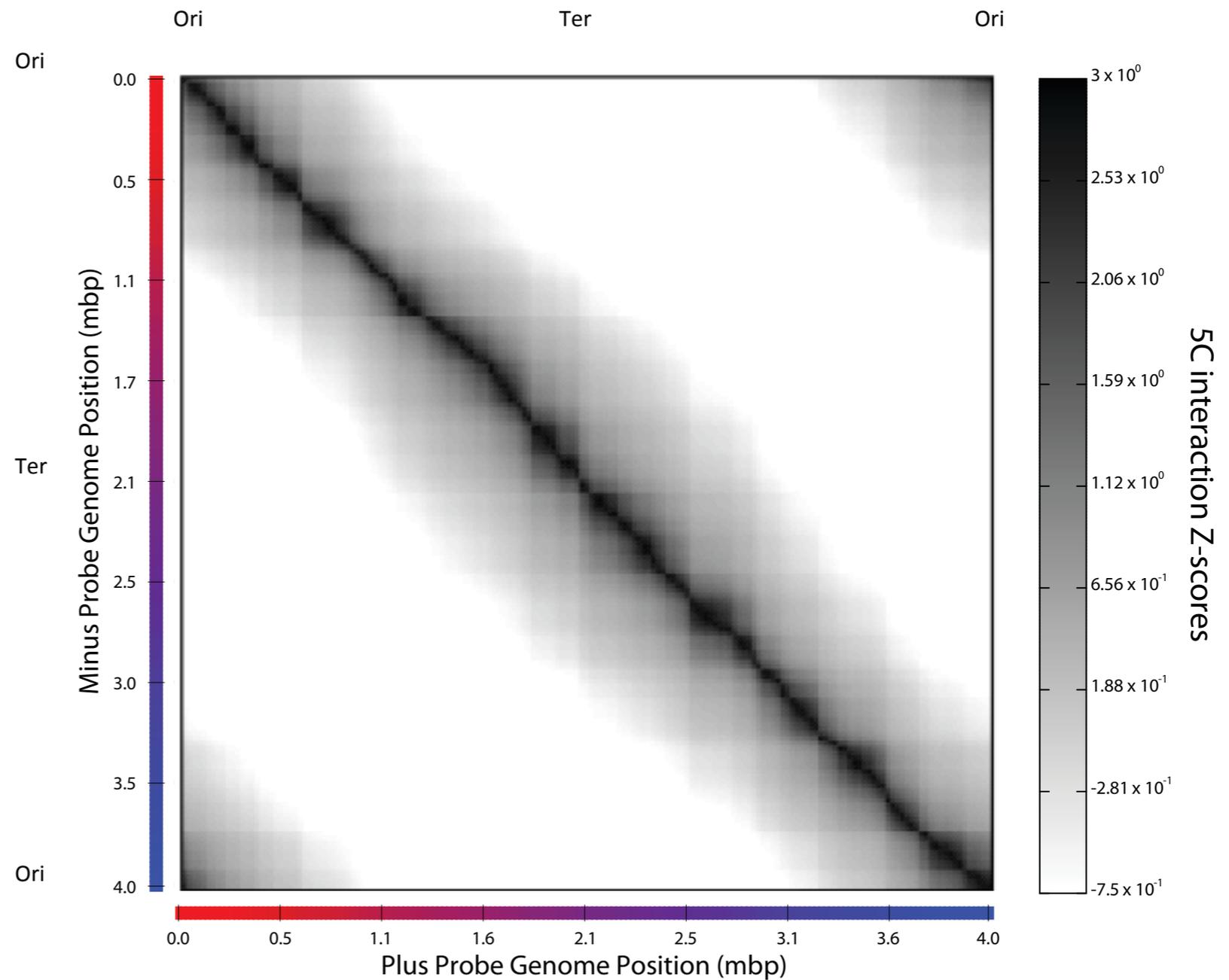
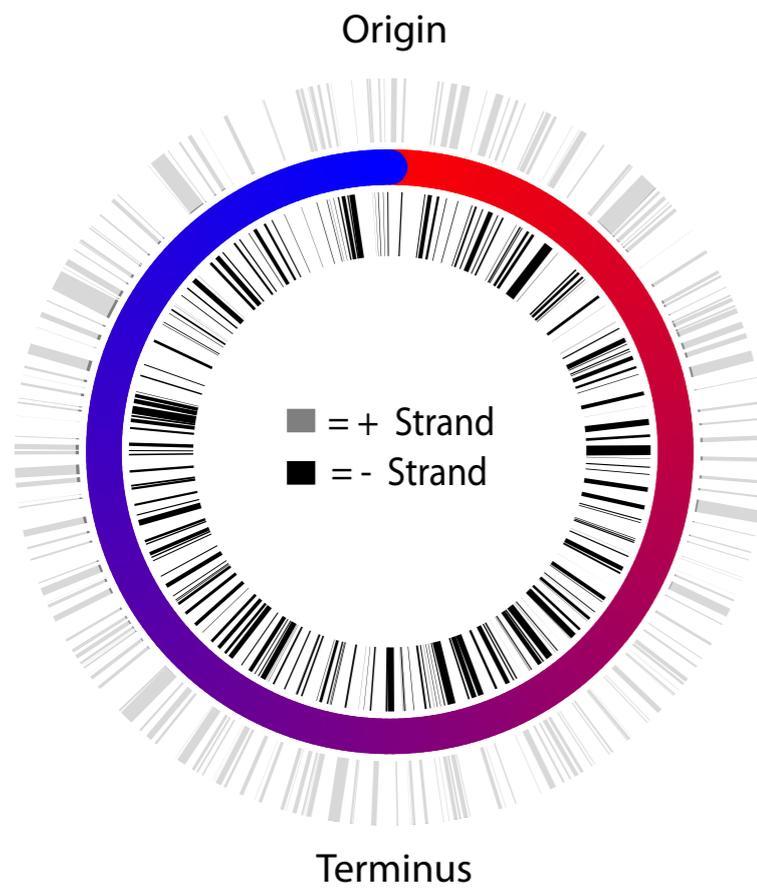


Lieberman-Aiden et al. Science (2009)

Baù et al. The three-dimensional folding of the α -globin gene domain reveals formation of chromatin globules. *Nat Struct Mol Biol* (2011) vol. **18** (1) pp. 107-14
 Baù, D., and Marti-Renom, M.A. (2011). Structure determination of genomic domains by satisfaction of spatial restraints. *Chromosome Res* 19, 25-35.
 Sanyal, A., et al. (2011). Chromatin globules: a common motif of higher-order chromosome structure? *Current Opinion in Cell Biology* in press.

The 3D architecture of *Caulobacter Crescentus*

4,016,942 bp & 3,767 genes

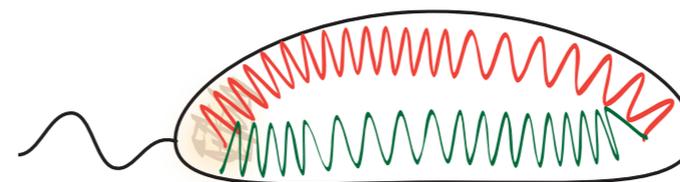
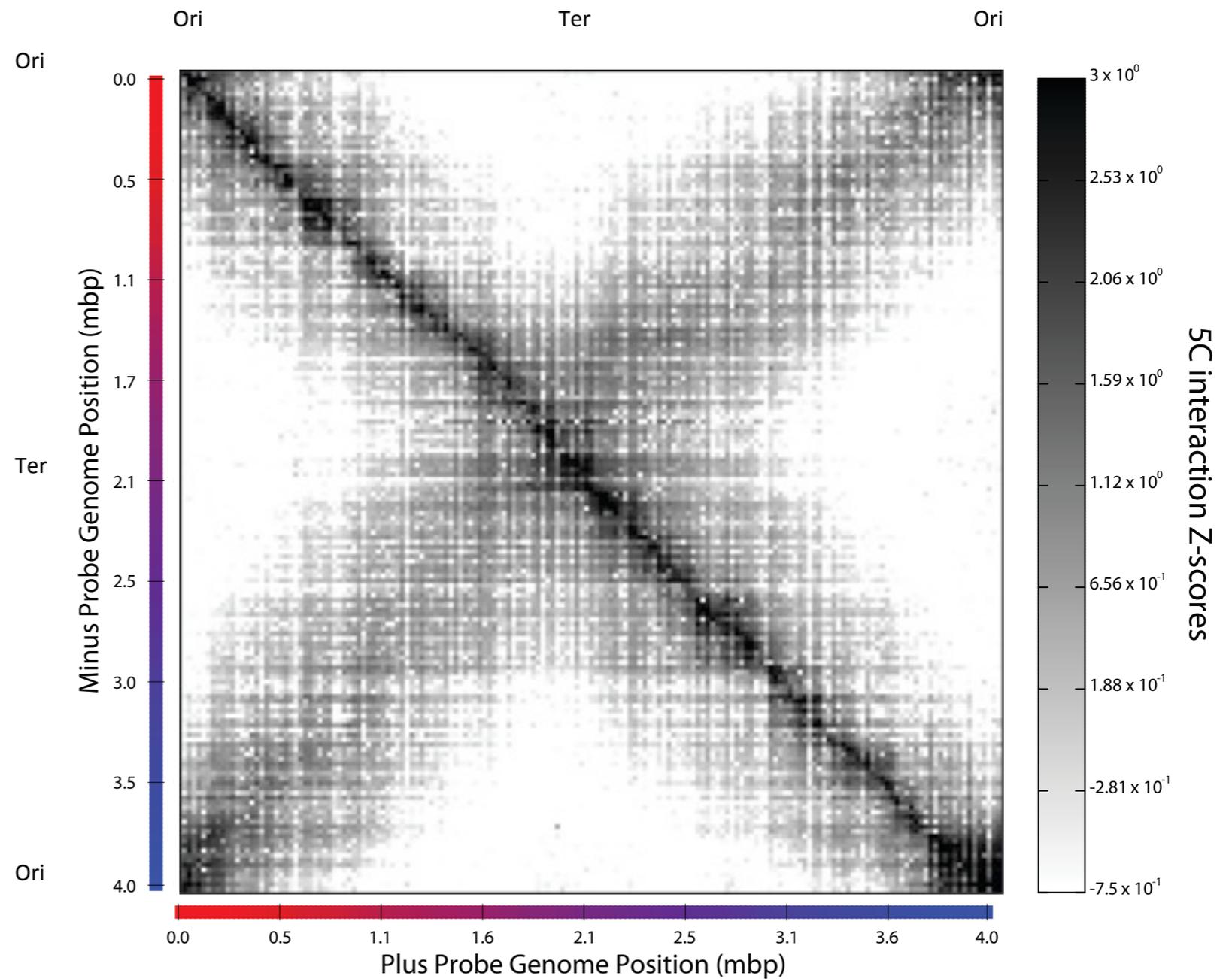
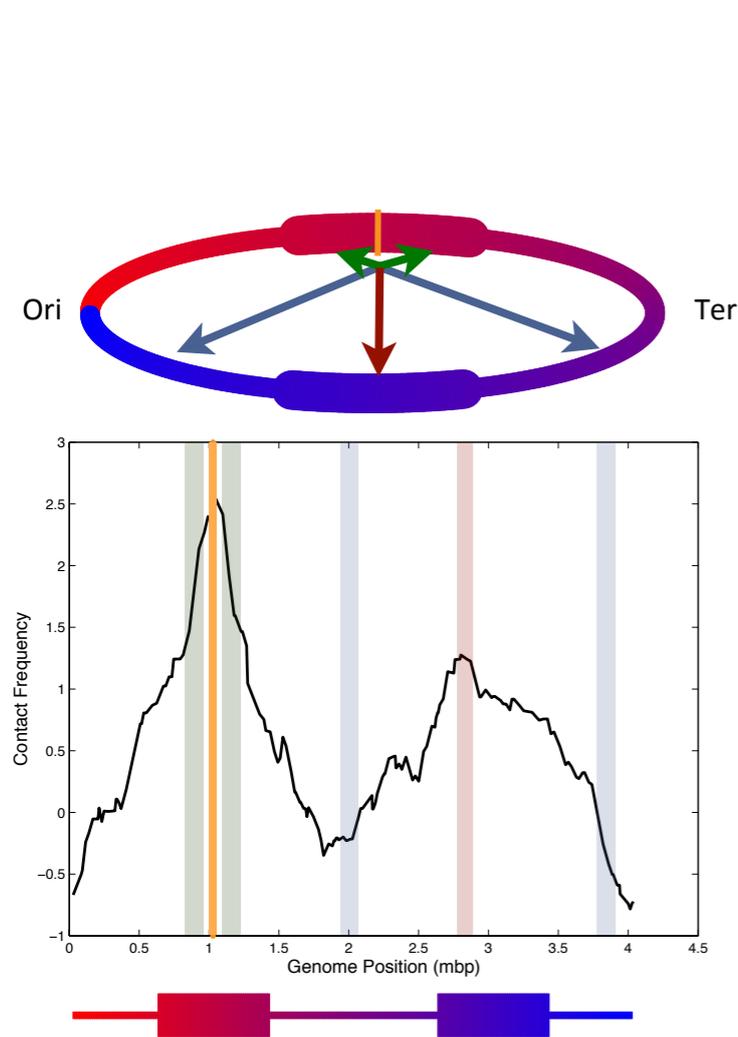


169 5C primers on + strand
170 5C primers on - strand
28,730 chromatin interactions

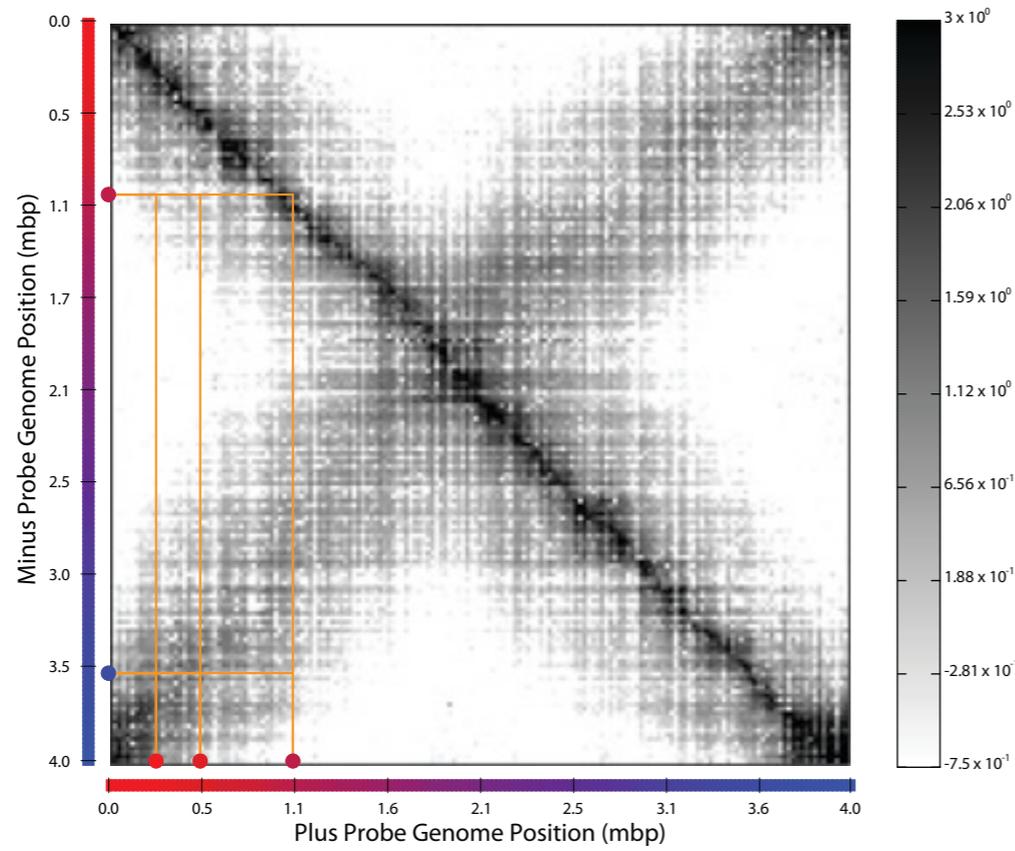
~13Kb

5C interaction matrix

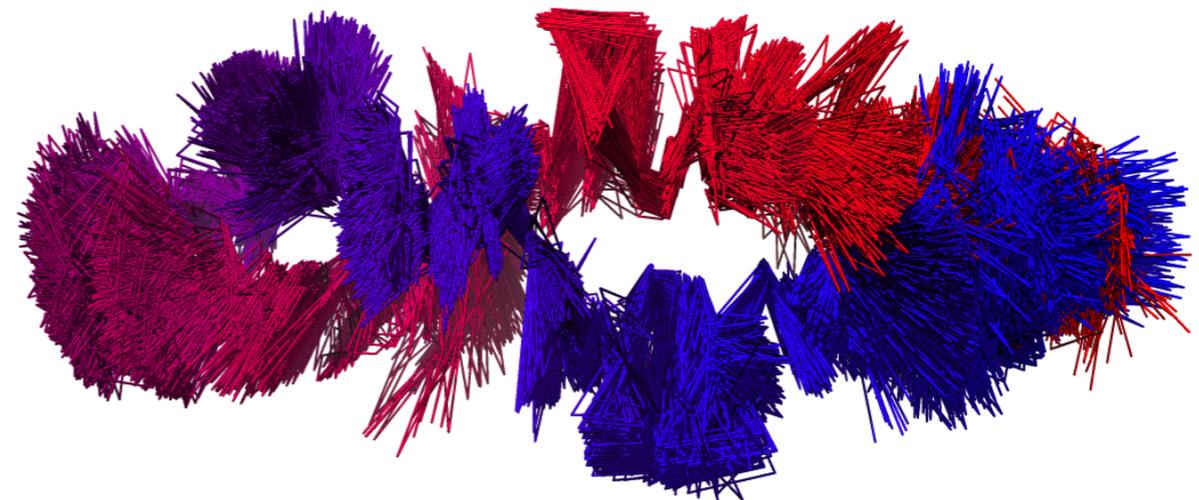
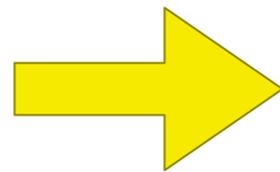
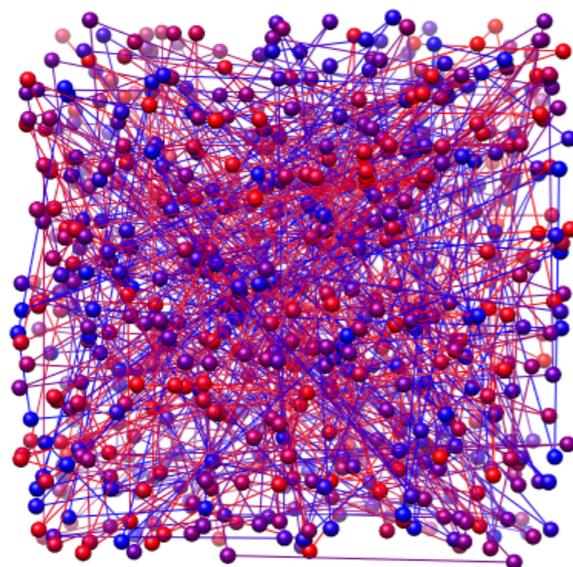
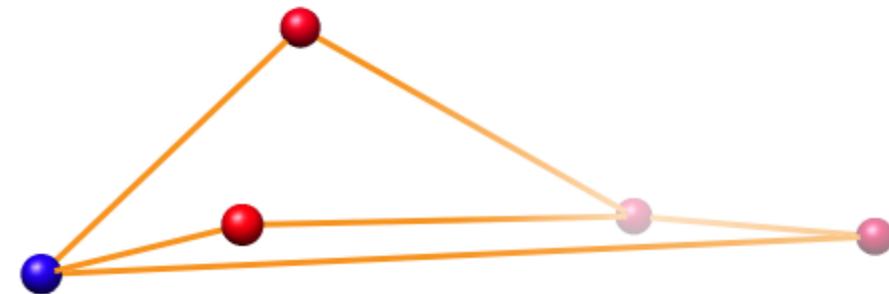
ELLIPSOID for *Caulobacter crescentus*



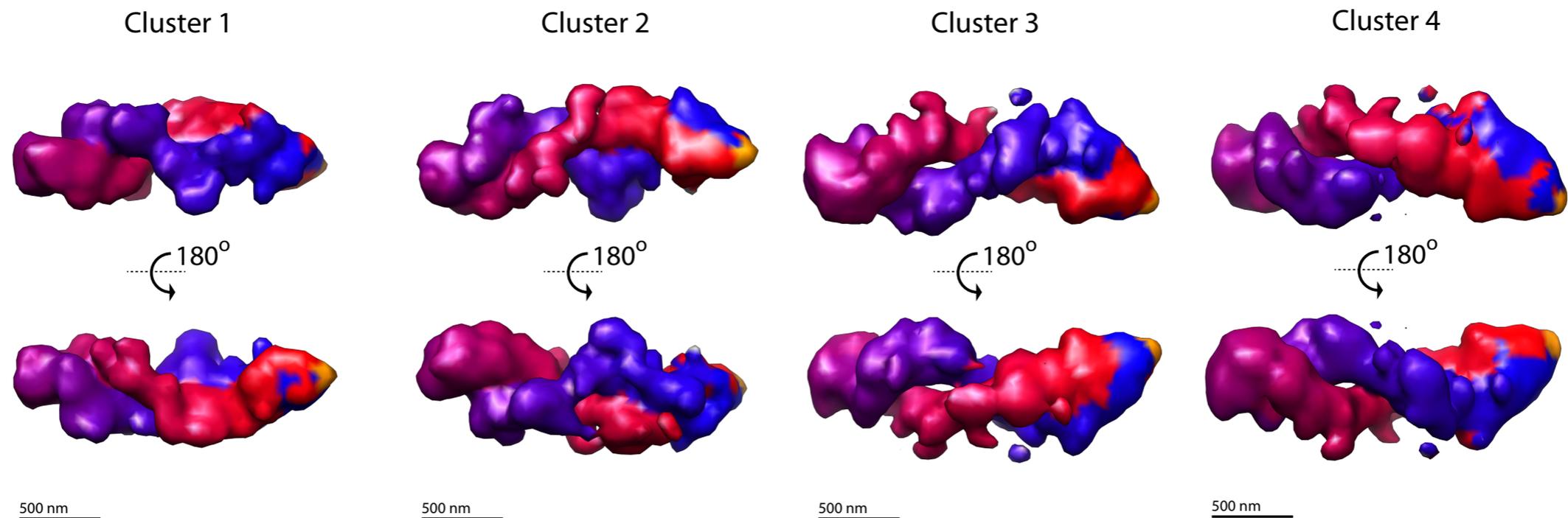
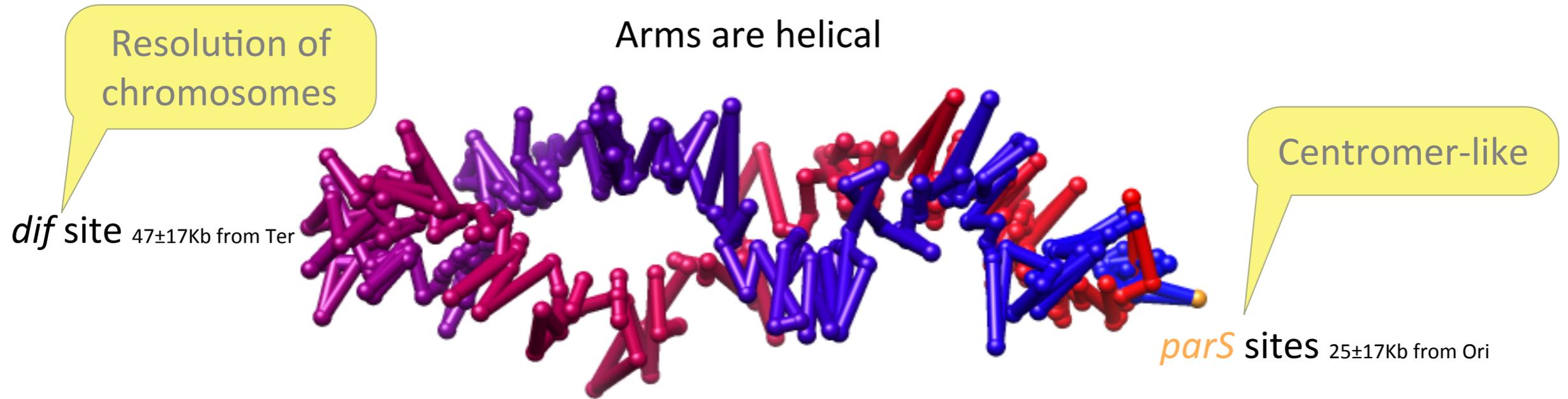
3D model building with the 5C + IMP approach



339 mers



Genome organization in *Caulobacter crescentus*

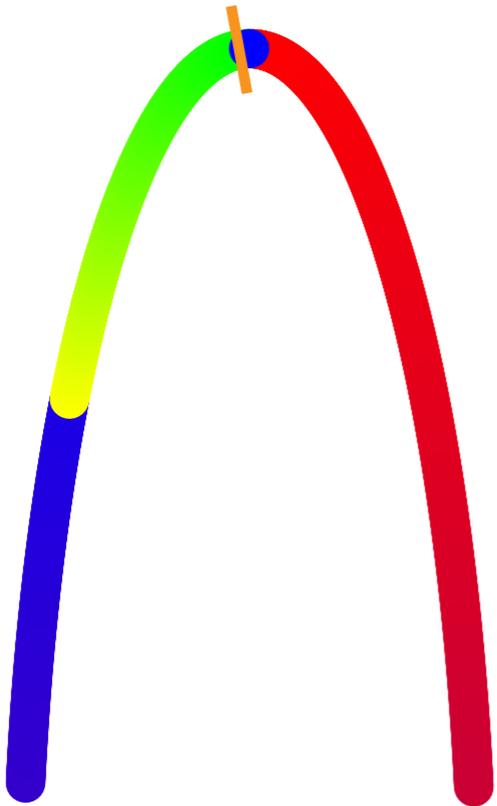


MIRRORS!

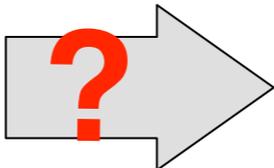
Moving the *parS* sites 400 Kb away from Ori

ParB PopZ

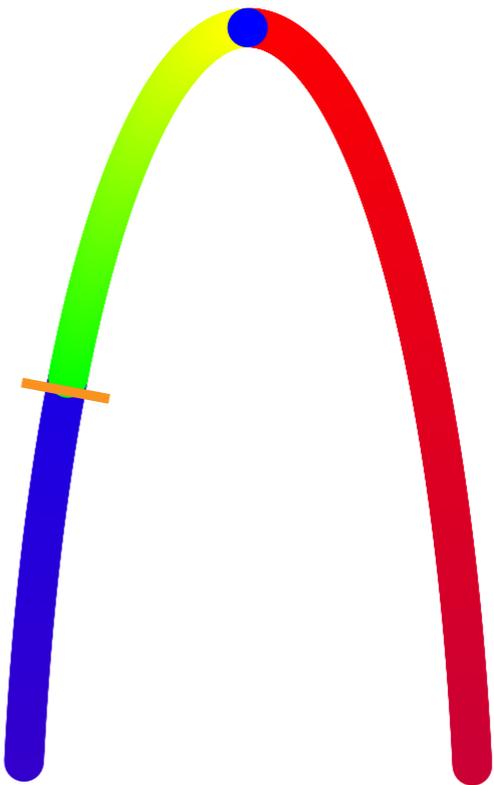
parS



Wild-type

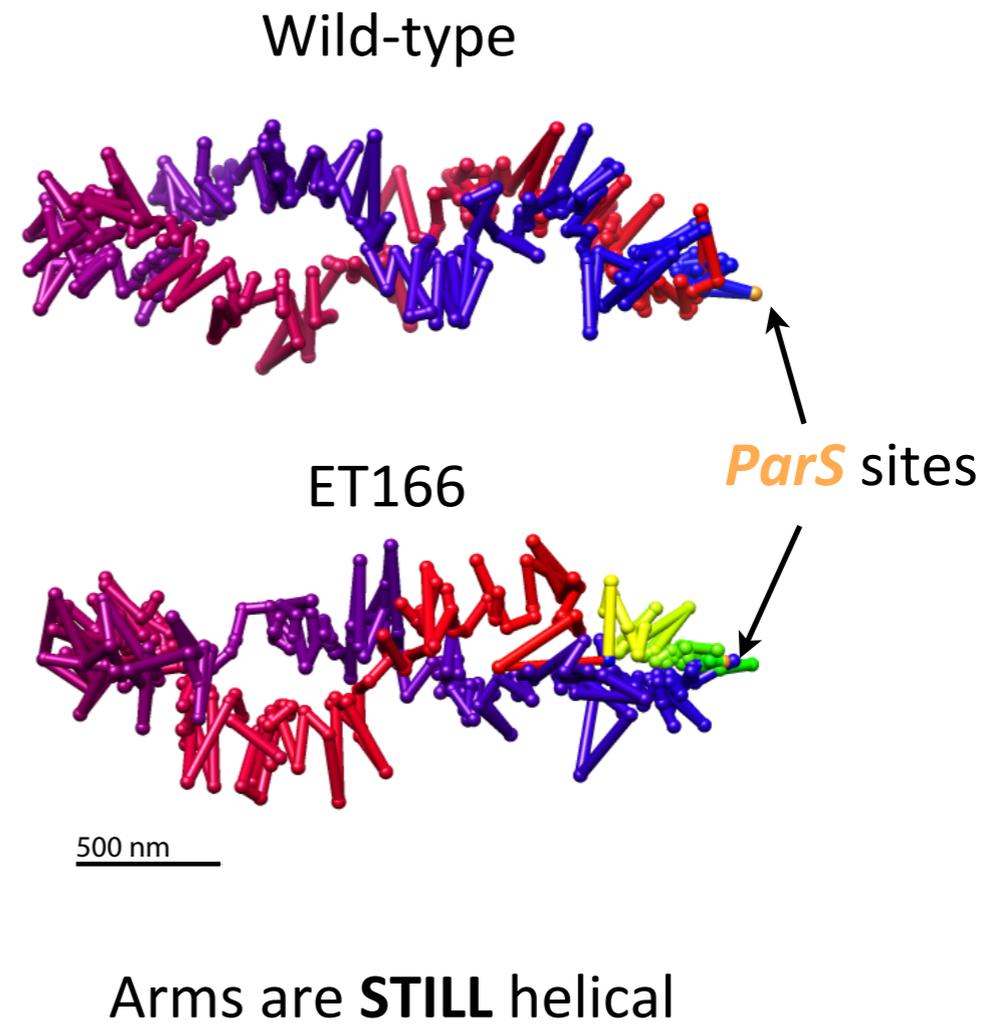
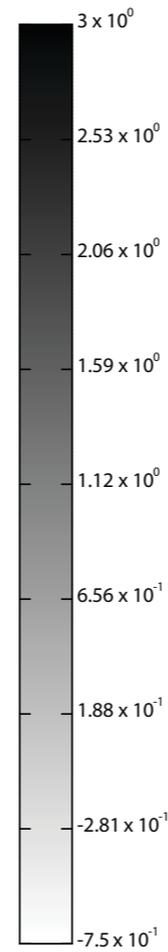
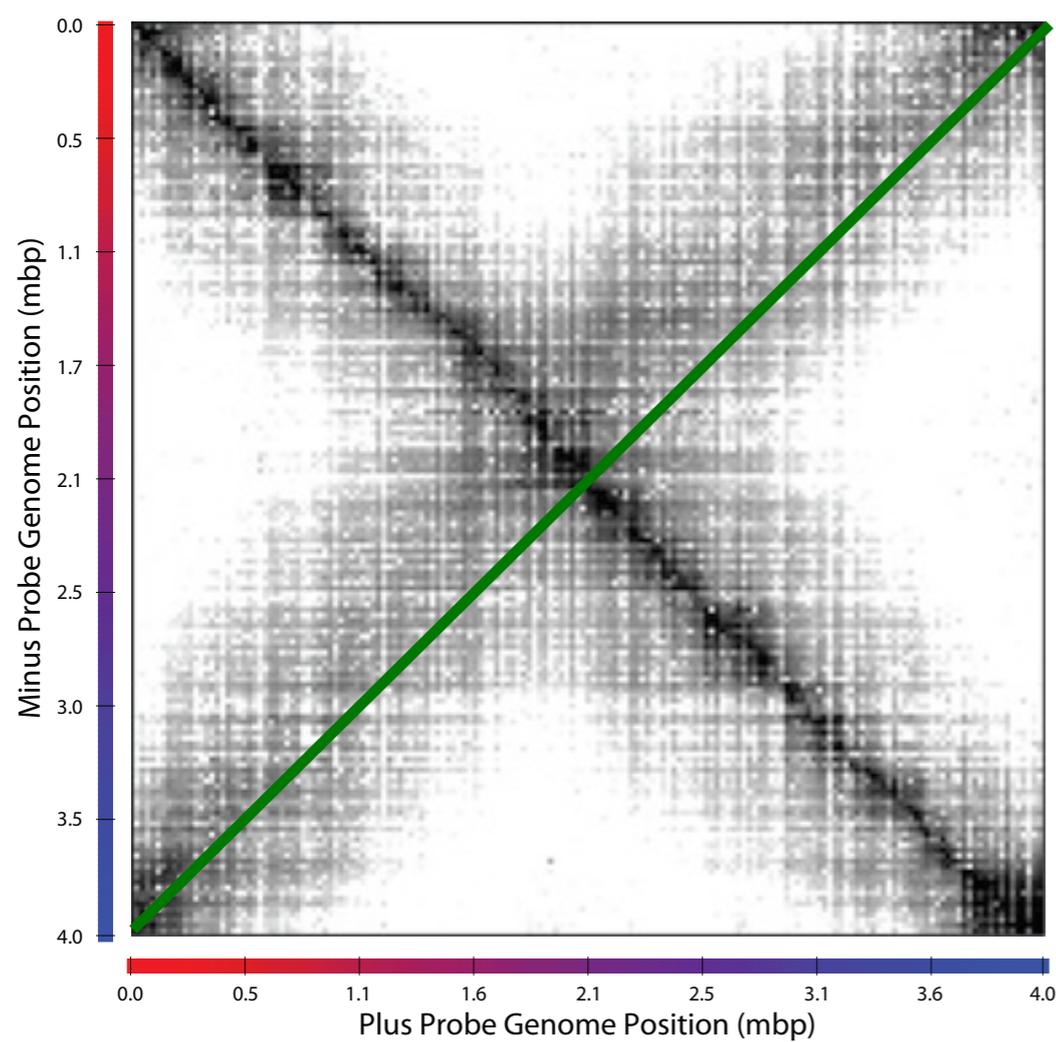


parS

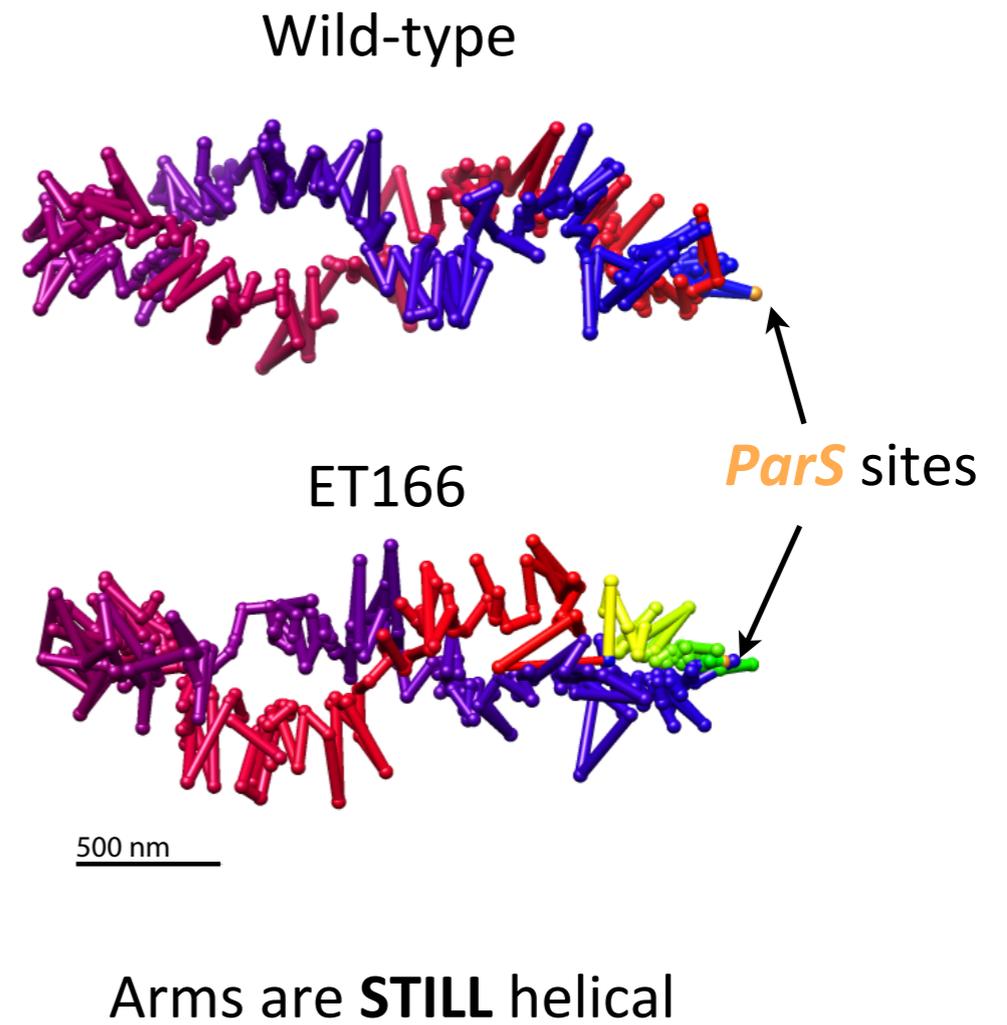
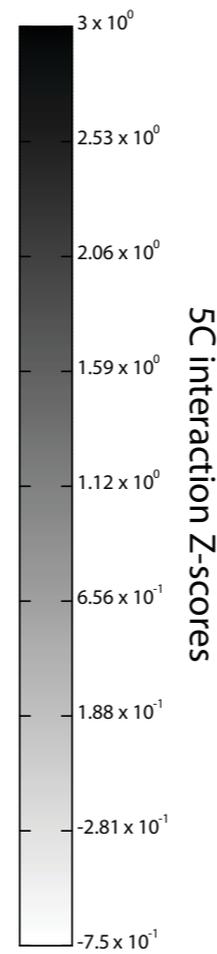
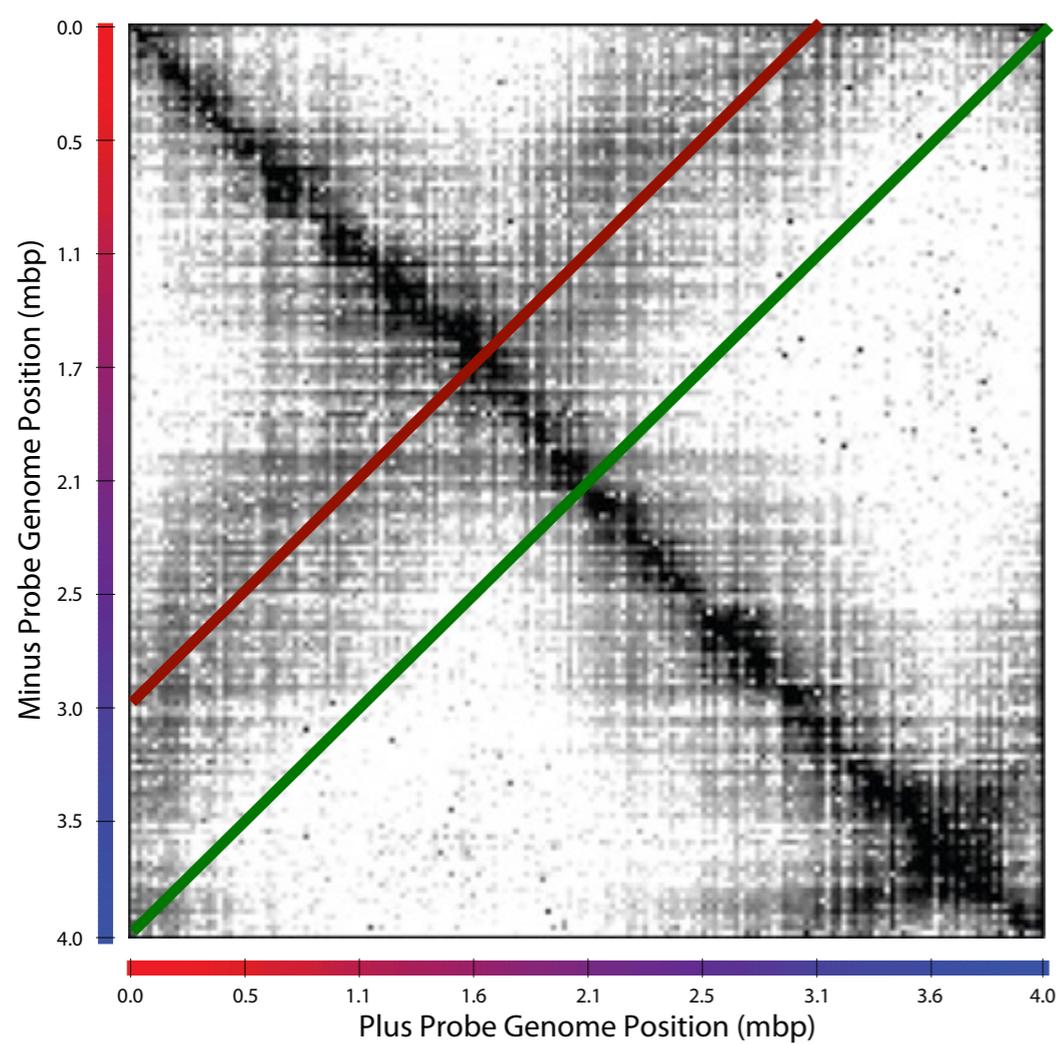


ET166

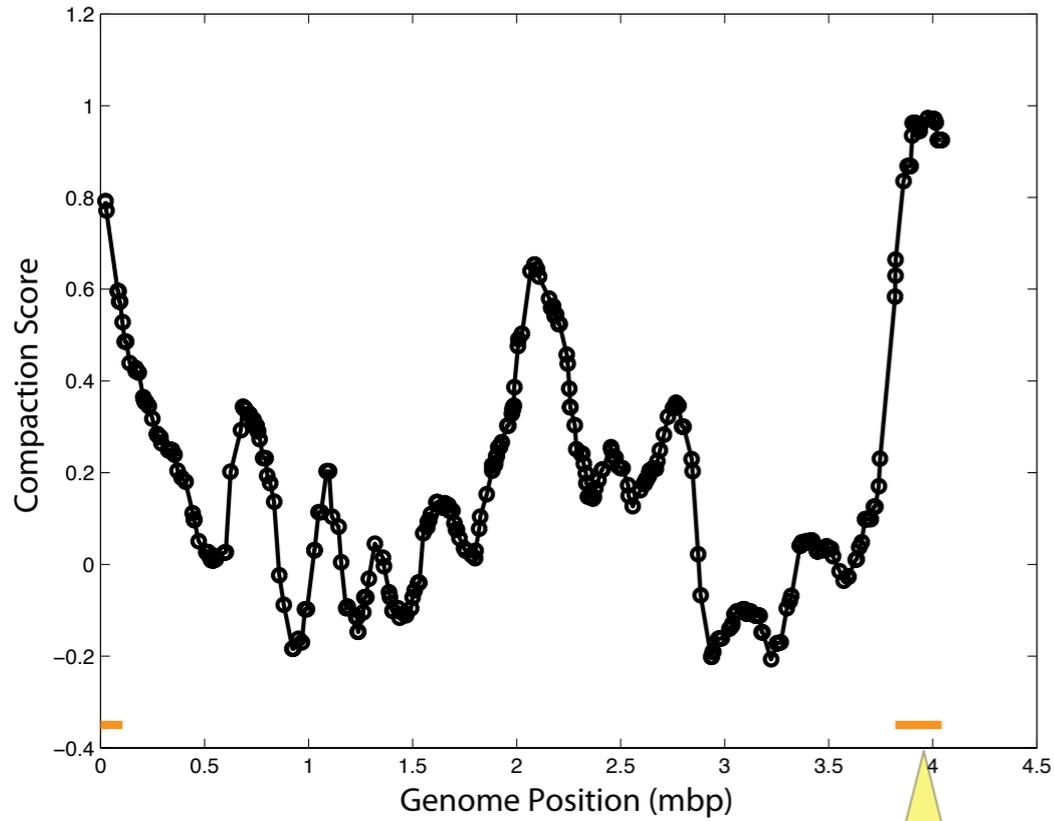
Moving the *parS* sites results in whole genome rotation!



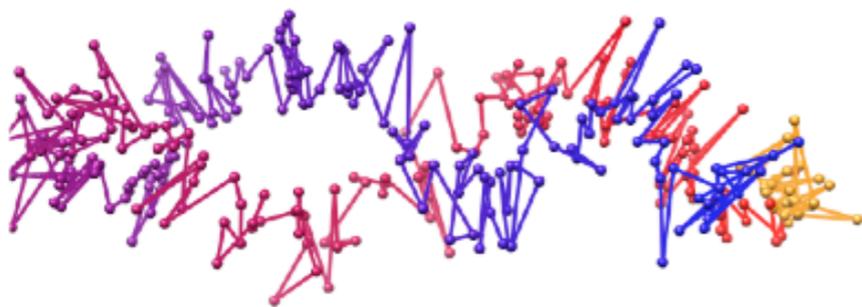
Moving the *parS* sites results in whole genome rotation!



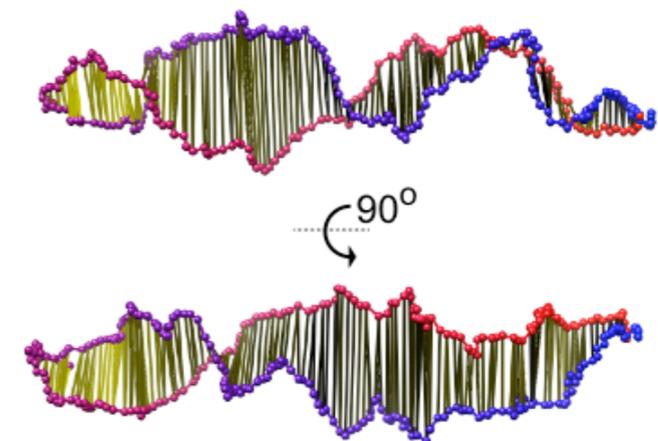
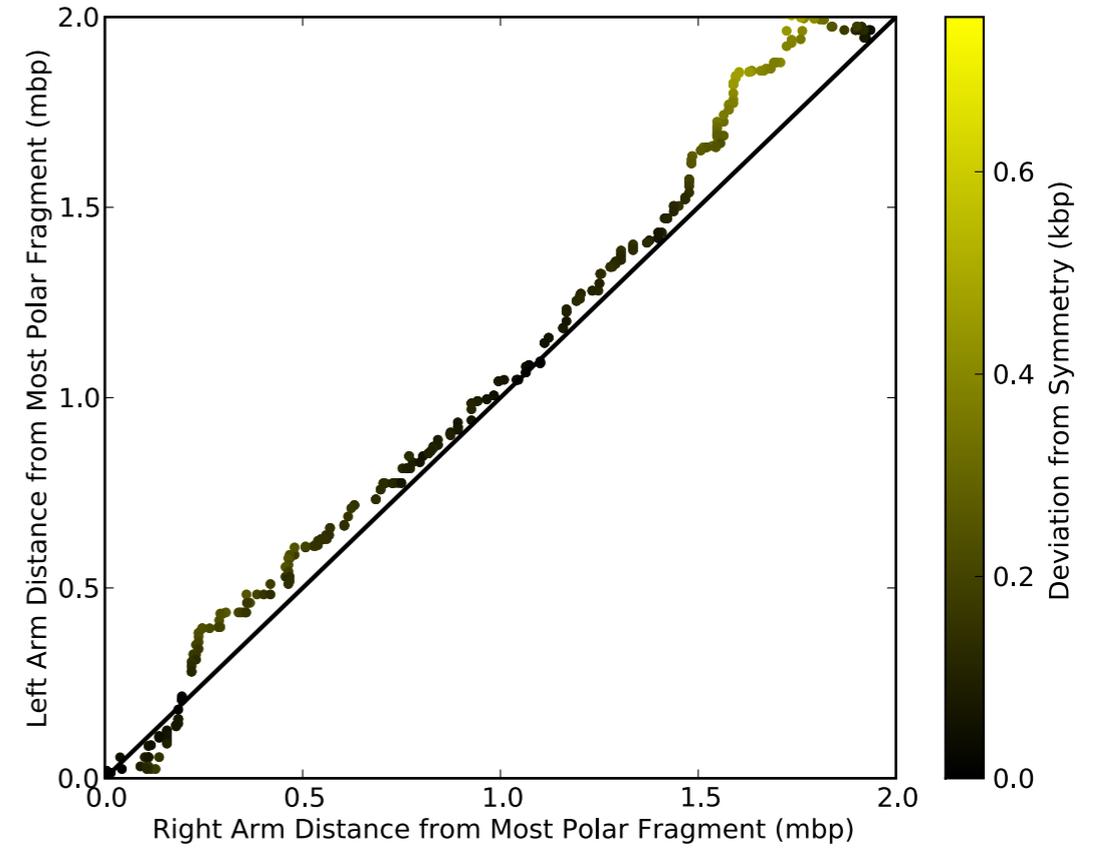
parS sites initiate compact chromatin domain



100-200Kb

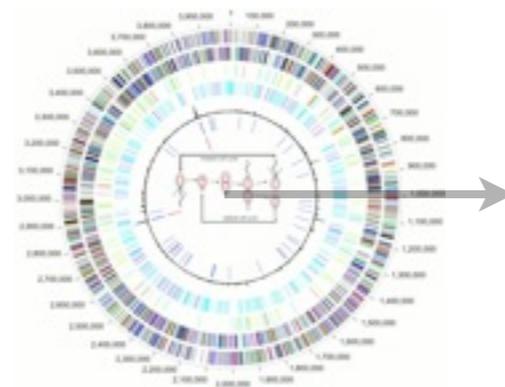
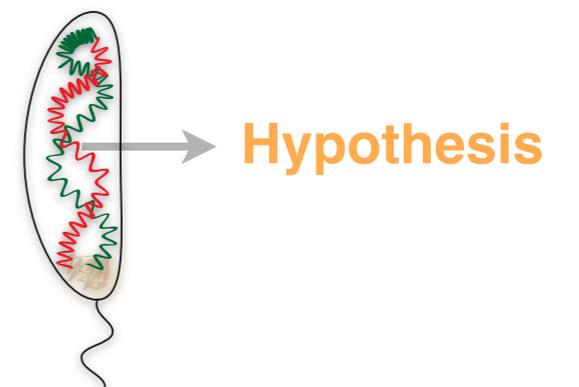
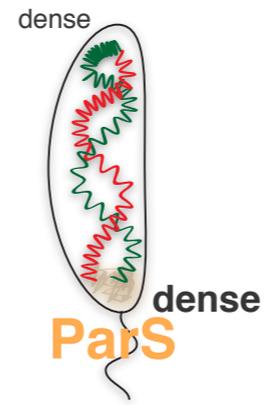
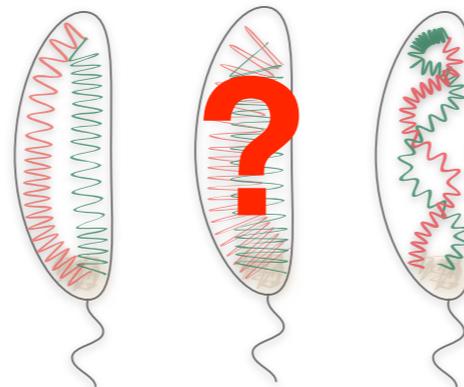
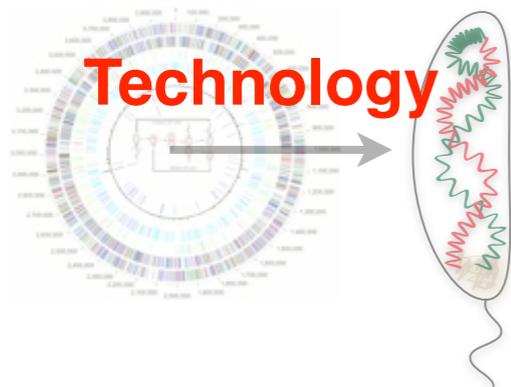
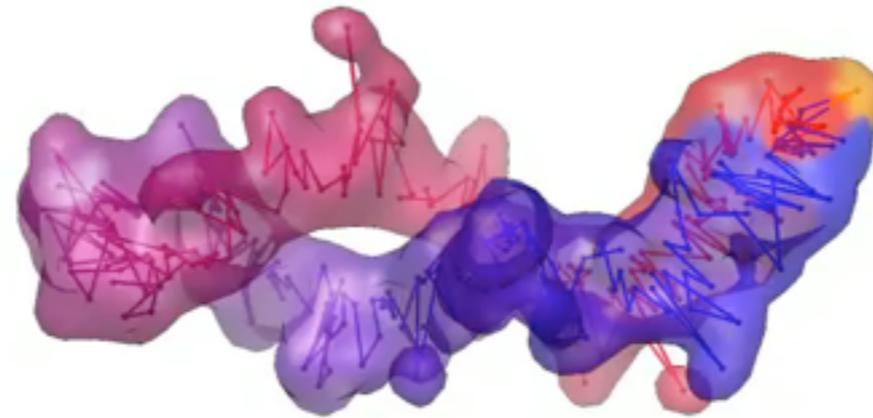


Chromosome arms are equidistant to the cell center



From Sequence to Function

Genome architecture in *Caulobacter*



Function!

OPEN STUDENT & POST-DOC POSITIONS IN THE LAB
Starting mid-late 2011

Acknowledgments



Job Dekker

Program in Gene Function and Expression
Department of Biochemistry and Molecular Pharmacology
University of Massachusetts Medical School
Worcester, MA, USA



Lucy Shapiro

Department of Developmental Biology,
Stanford University
School of Medicine,
Stanford, CA. USA



George M. Church

Department of Genetics,
Harvard Medical School,
Boston, MA. USA



PRINCIPE FELIPE
CENTRO DE INVESTIGACION

Marc A. Marti-Renom

Structural Genomics Unit
Bioinformatics and Genomics Department
Centro de Investigación Príncipe Felipe
Valencia, Spain

Jeanne Lawrence

Department of Cell Biology
University of Massachusetts Medical School
Worcester, MA, USA

D. Baù, A. Sanyal, B. Lajoie, E. Capriotti, **M. Byron**, J. Lawrence, J. Dekker*, and M.A. Marti-Renom*
Nature Structural & Molecular Biology (2011) 18(1):107-14

M.A. Umbarger*, **E. Toro**, M.A. Wright, G.J. Porreca, **D. Baù**, S-H Hong, M.J. Fero, M.A. Marti-Renom*,
H.H. McAdams, L. Shapiro, J. Dekker*, and G.M. Church
Molecular Cell (under revision)

<http://sgu.bioinfo.cipf.es>
<http://integrativemodeling.org>