



3DAROC16: 3C-based data analysis and 3D reconstruction of chromatin folding

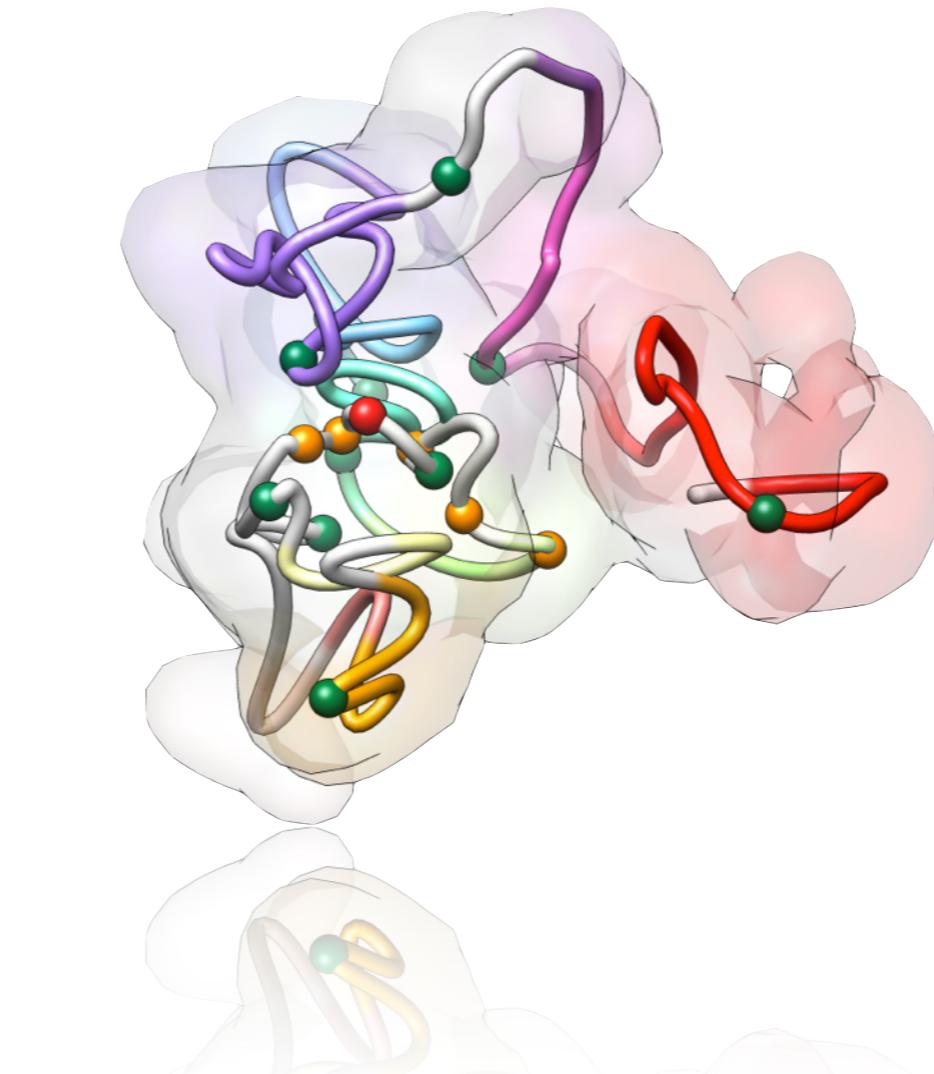
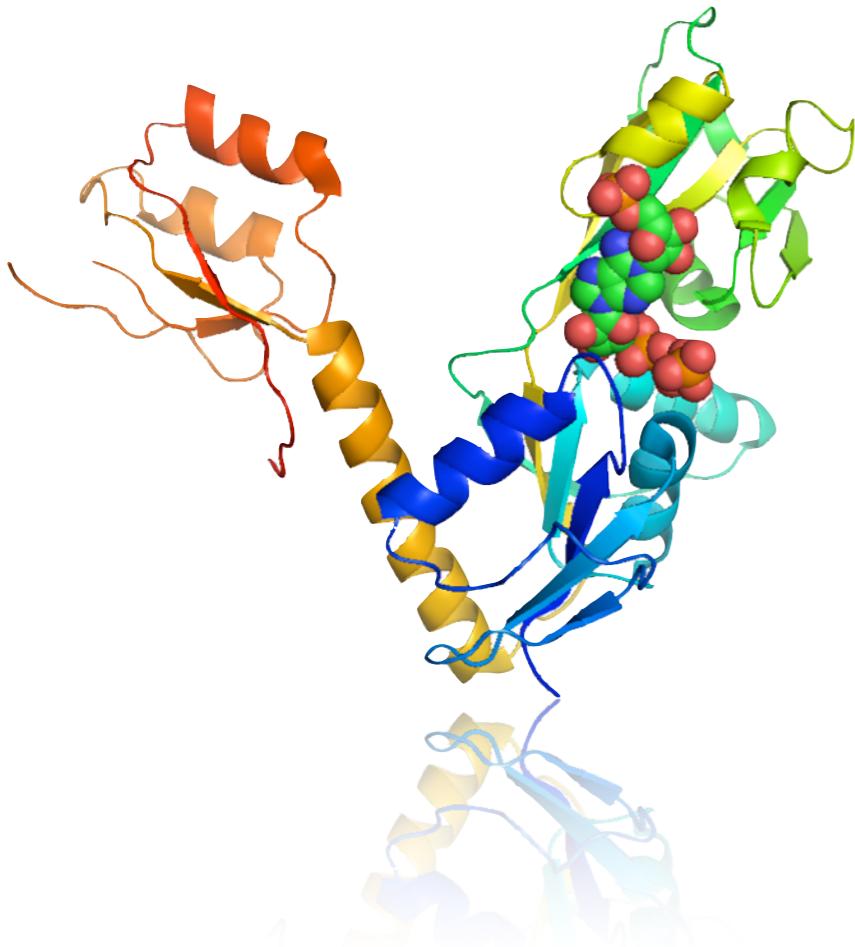
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Structural Genomics Group

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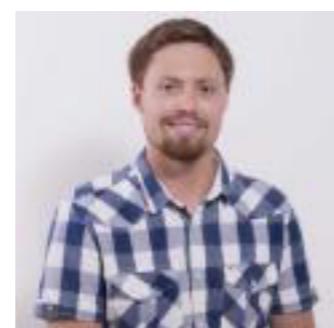
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FlexServ
FlexServ: Protein Flexibility Server
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Last most-relevant publications

- Prediction and validation of protein intermediate states from structurally rich ensembles and coarse-grained simulations *Nat Commun*
- Long-timescale dynamics of the Drew-Dickerson dodecamer. *Nucleic Acids Res*
- BIGNASim: a NoSQL database structure and analysis portal for nucleic acids simulation data. *Nucleic Acids Res*



Course outline

Theory · Examples · Practice

Day 1

- Overview to structure determination (Marc)
- 3D modeling of the genomes and genomic domains (Marc)
- Introduction to linux & python (François & Marco)
- NGS and data handling (François & Marco)
- Hi-C data (François & Marco)

Day 2

- Summary Day 1 (Marco)
- Chromatin structure and Hi-C data (Marc)
- Integrative modeling applied to chromatin (Marc)
- Biological applications (I) (Marc)
- Hi-C contact matrices (François & Marco)

Day 3

- Summary Day 2 (Marco)
- Biological applications (II) (Marc)
- Compartment detection and analysis (François & Marco)
- Topologically Associated Domains (François & Marco)
- Comparison between experiments (François & Marco)

Day 4

- Summary Day 3 (Marco)
- Biological applications (III) (Marc)
- 3D modeling of real Hi-C data (François & Marco)
- Analysis of the results (François & Marco)

Day 5

- Summary Day 4 (Marco)
- Multiscale Genomics: from genomes to structures (Marc)
- Coarse-Grained DNA and Chromatin Dynamics (Jürgen)
- Nucleosome positioning & Dynamics (Ricard)
- Final wrap-up session (Marc & François & Marco & Jürgen & Ricard)

MuG: Multiscale Complex Genomics

<http://www.multiscalegenomics.eu/MuGVRE/mug-community/>

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Multiscale Complex Genomics



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