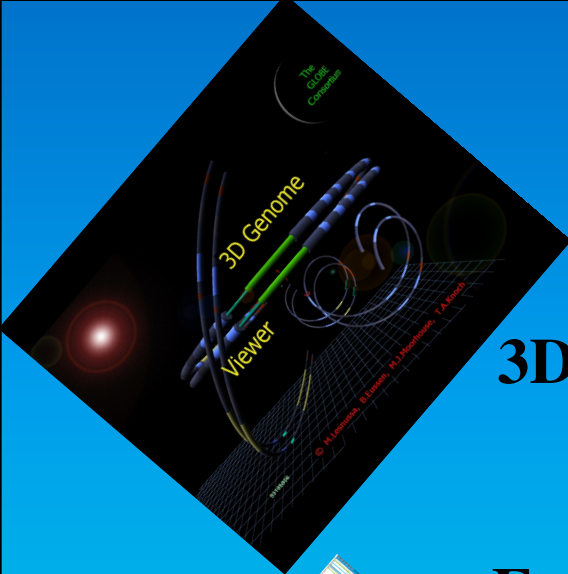
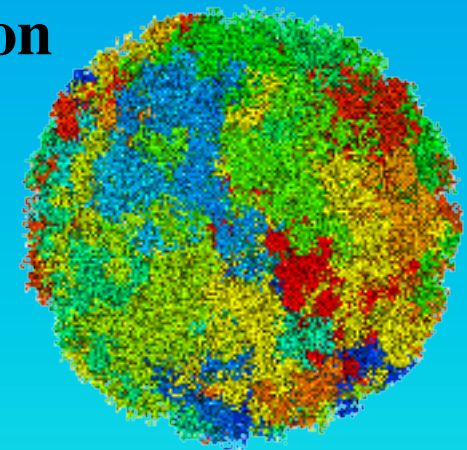
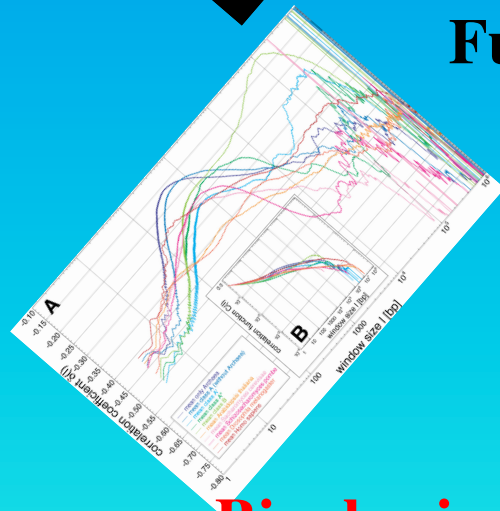




The Detailed 3D Multi-Loop Aggregate/Rosette Chromatin Architecture and Functional Dynamic Organization of the Human and Mouse Genomes

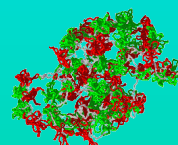
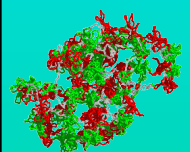


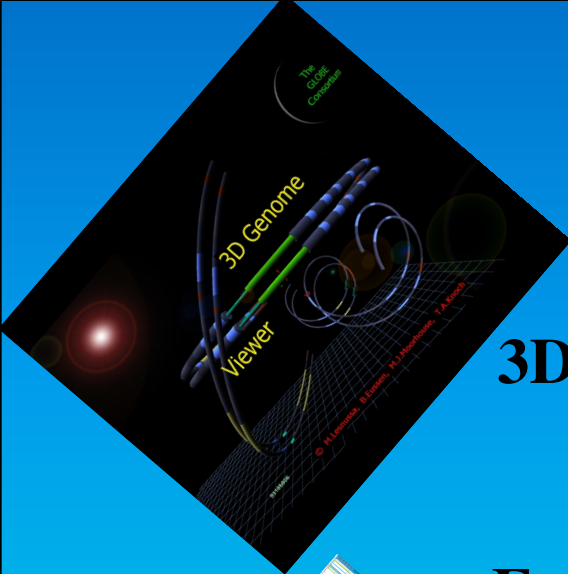
Tobias A. Knoch

Biophysical Genomics & Erasmus Computing Grid

Erasmus Medical Center

TA.Knoch@taknoch.org





The Detailed 3D Multi-Loop Aggregate Chromatin Architecture

Functional Domains

Heterochromatin and Euchromatin

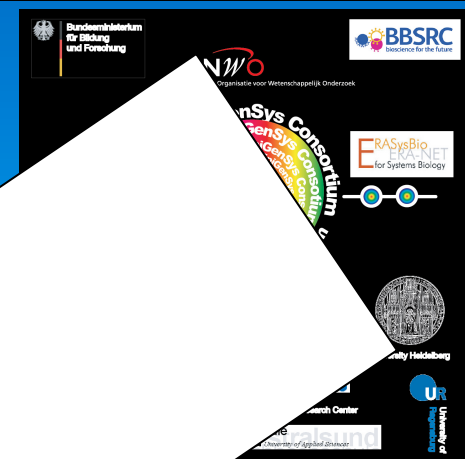
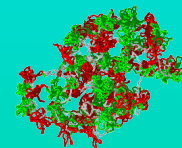
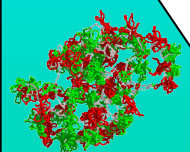
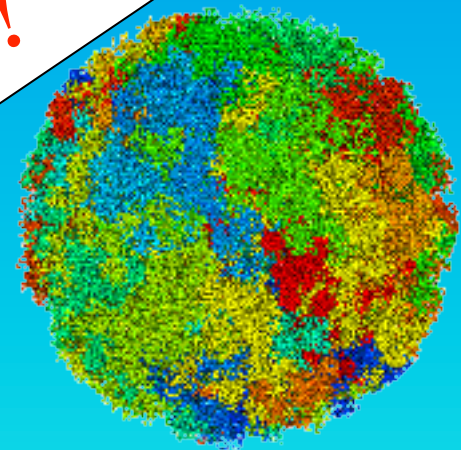
**Results and Perspectives
of a
Finally Solved Challenge!**

A. Knoch

Genomics & Erasmus Computing Grid

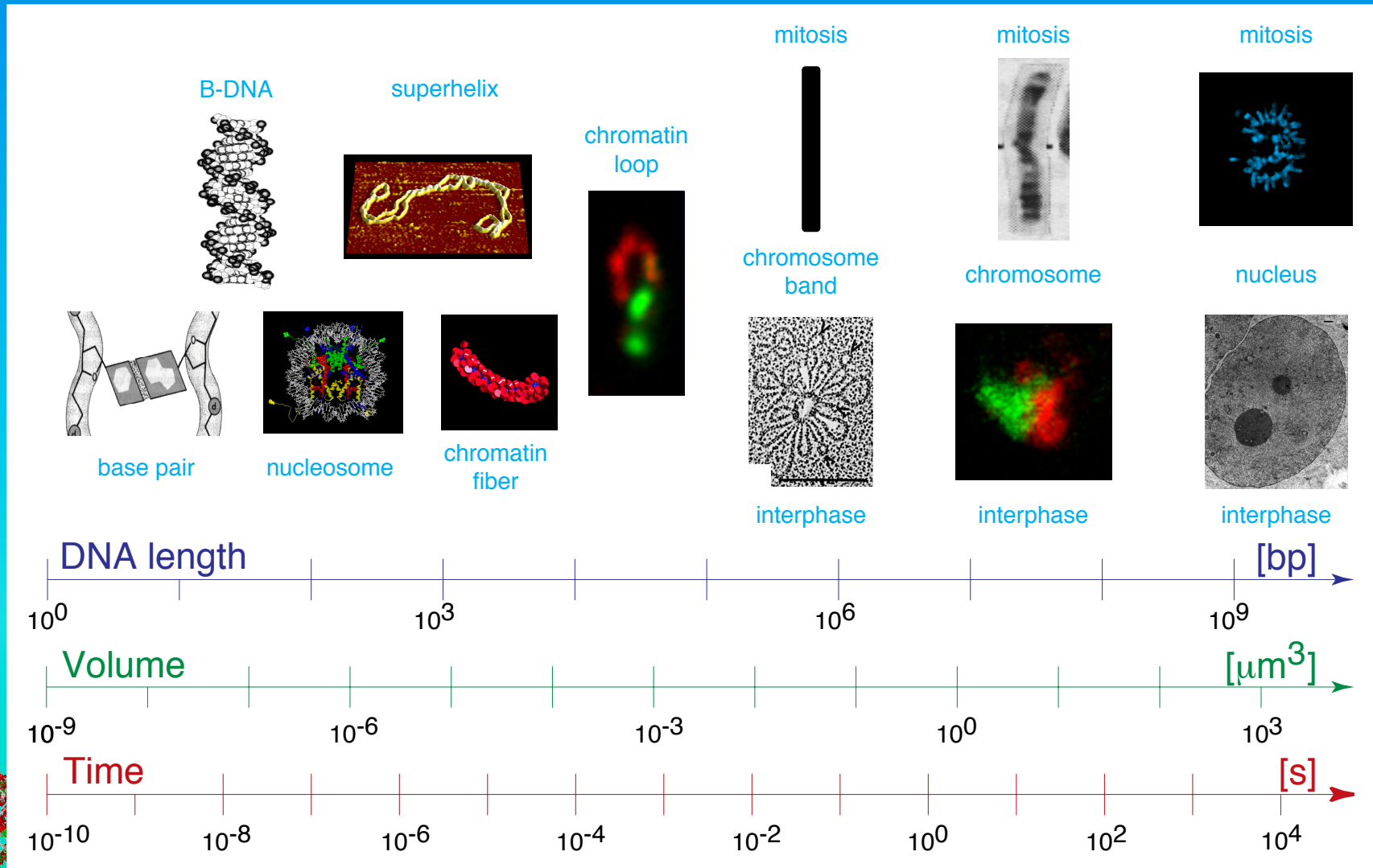
Erasmus Medical Center

TA.Knoch@taknoch.org



Dynamic and Hierarchical Genome Organization

The different organization levels of genomes bridge several orders of magnitude concerning space and time. How all of these organization levels connect to processes like gene regulation, replication, embryogeneses, or cancer development is still unclear?

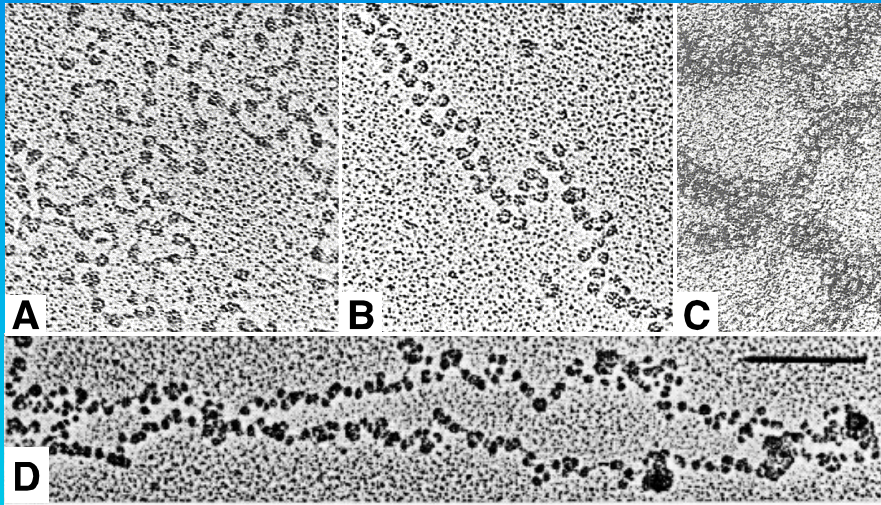


Chromatin Conformation and Higher-Order Topologies

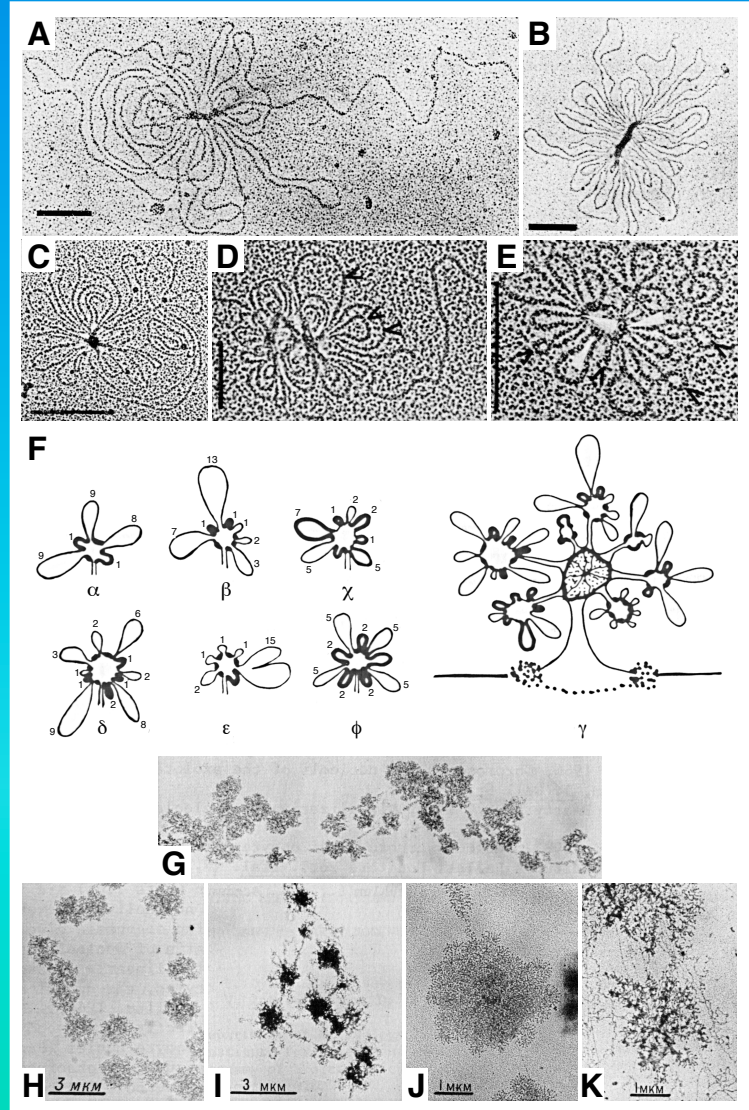
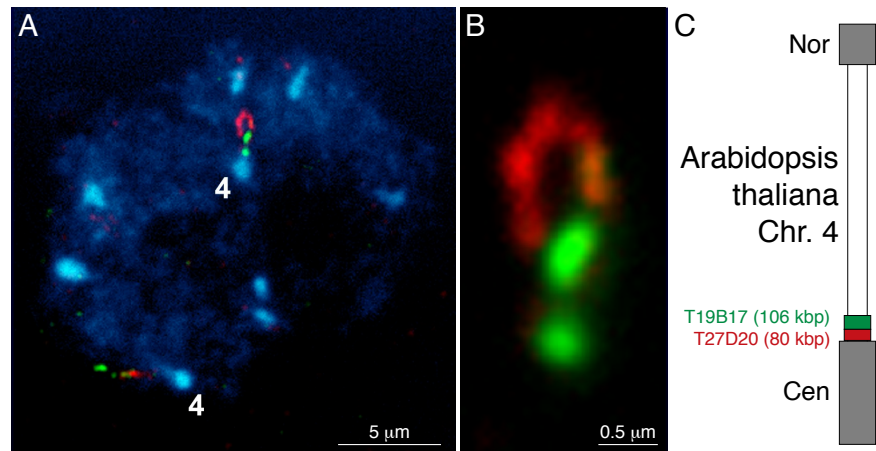
It becomes increasingly clearer, that the chromatin conformation is a random organization of nucleosomes, which depending on external or modification conditions has different condensation degrees, with a prevalence for the 30nm fiber with ~6nucleosomes per 11nm. This seems to make loops which further cluster to form aggregates more or less rosette-like which then constitute the chromosome.



A-C: Voet & Voet; D: Reznik *et al.*



Courtesy P. Fransz, Amsterdam



A: B. Aramova *et al.*; C: Salganik *et al.*; D-G: Frznik *et al.*; G-K: Tsvetkov & Pavlov.

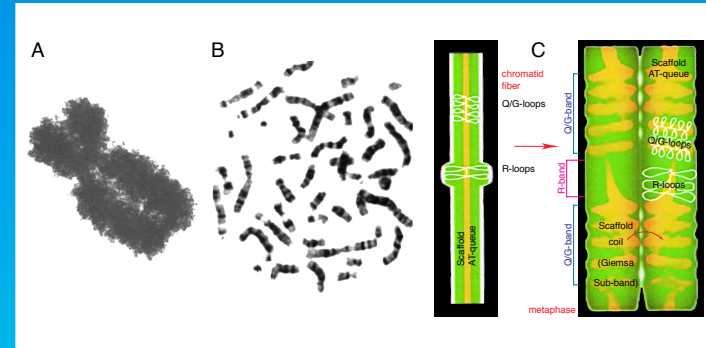
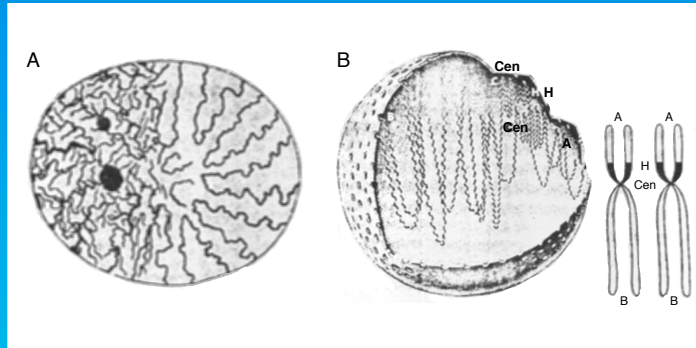


Integral Models of Cell Nuclear Organization I

Already Rabl and Boveri were aware of the obvious fact that the organization of genomes has to be consistent from the sequence level to the morphology of the whole cell nucleus. Although they might be different in detail their common seem is recursive folding and clustering thereof with variation/ modification and dynamics accounting for different nuclear states and function.

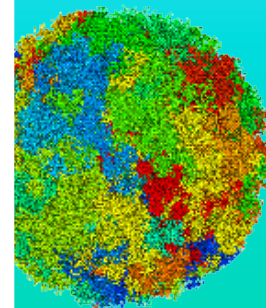
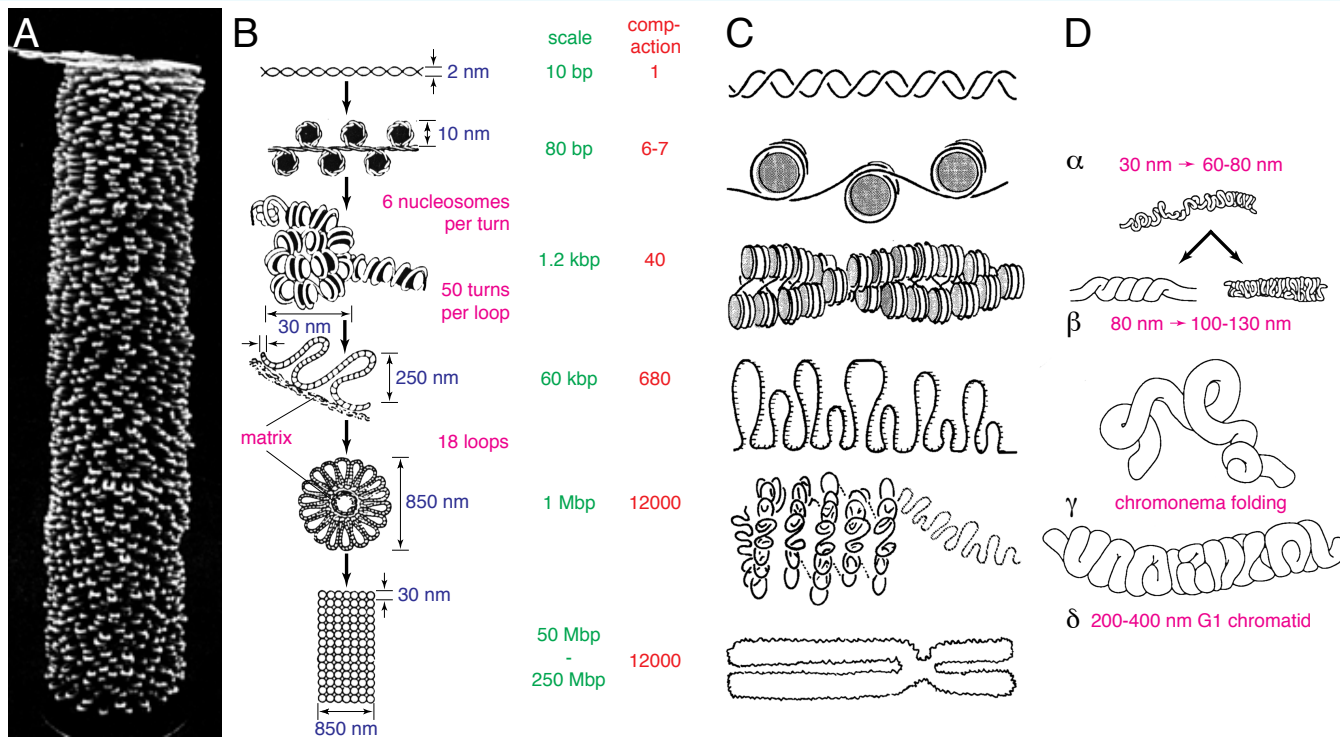


Rabl & Boveri



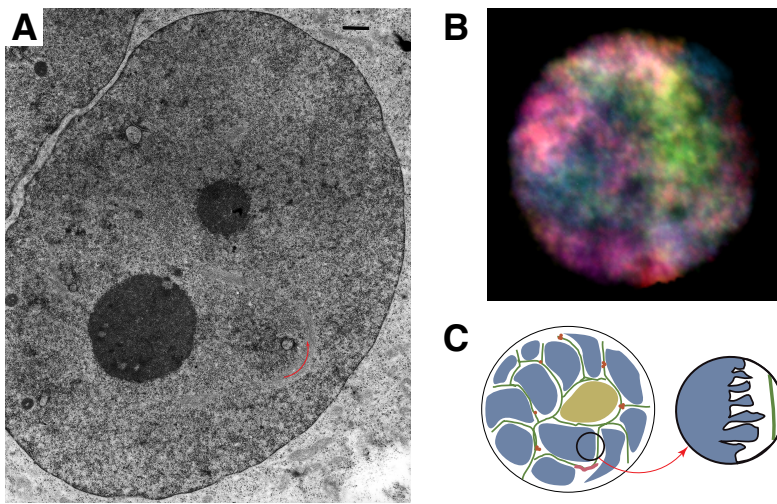
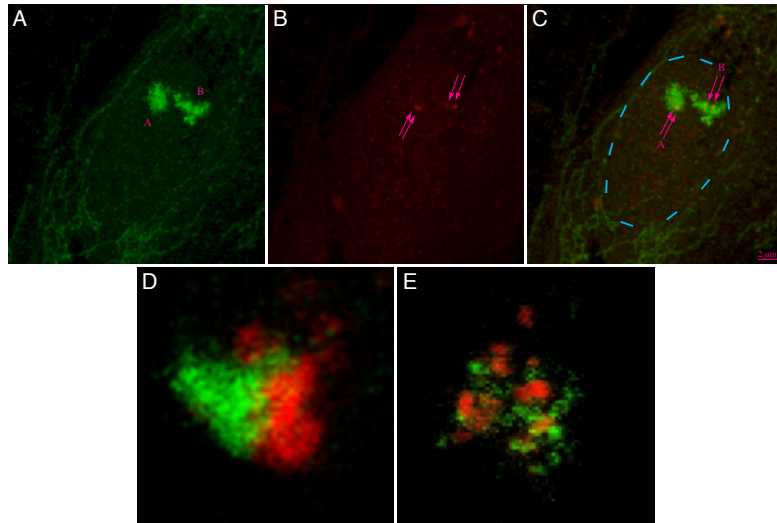
A: Bloom & Fawcett
B: Alberts *et al.*
C: Paulson & Laemmli

A, B: Pienta & Coffey; C: Alberts *et al.*; D: Belmont & Bruce

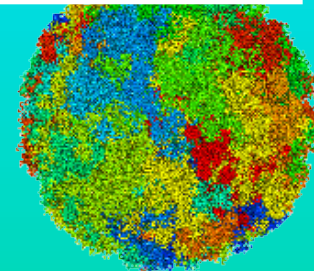
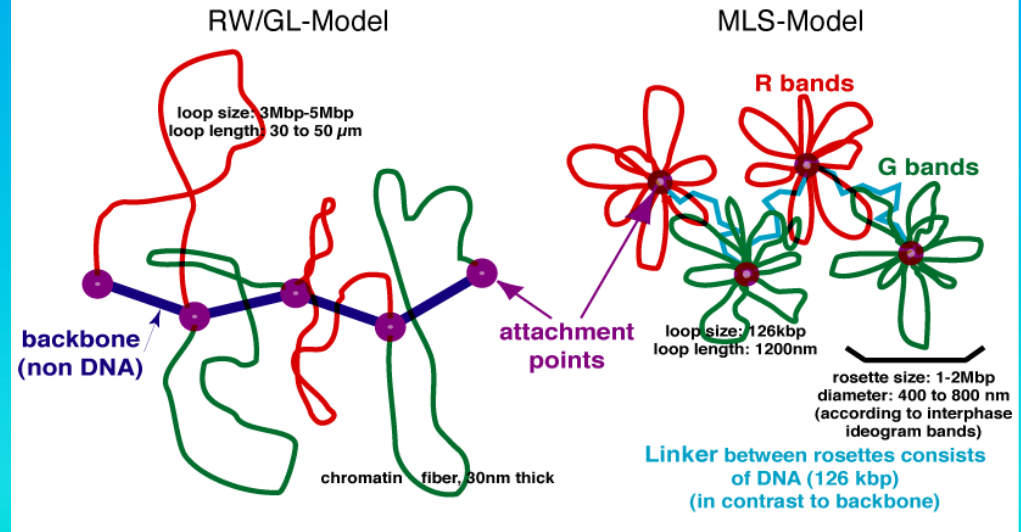


Integral Models of Cell Nuclear Organization

The biggest advantage of integral models is the again obvious and simple fact, that they allow the validation from the consistency of different levels of organization from the other levels. Thus, e.g. the so called Interchromosomal Domain Model can be ruled out by simple voluminous thought...



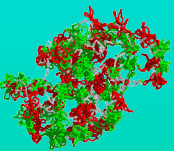
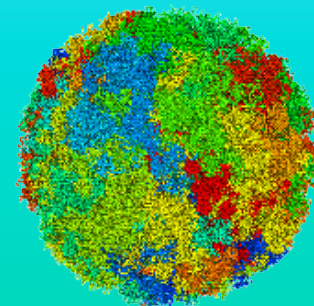
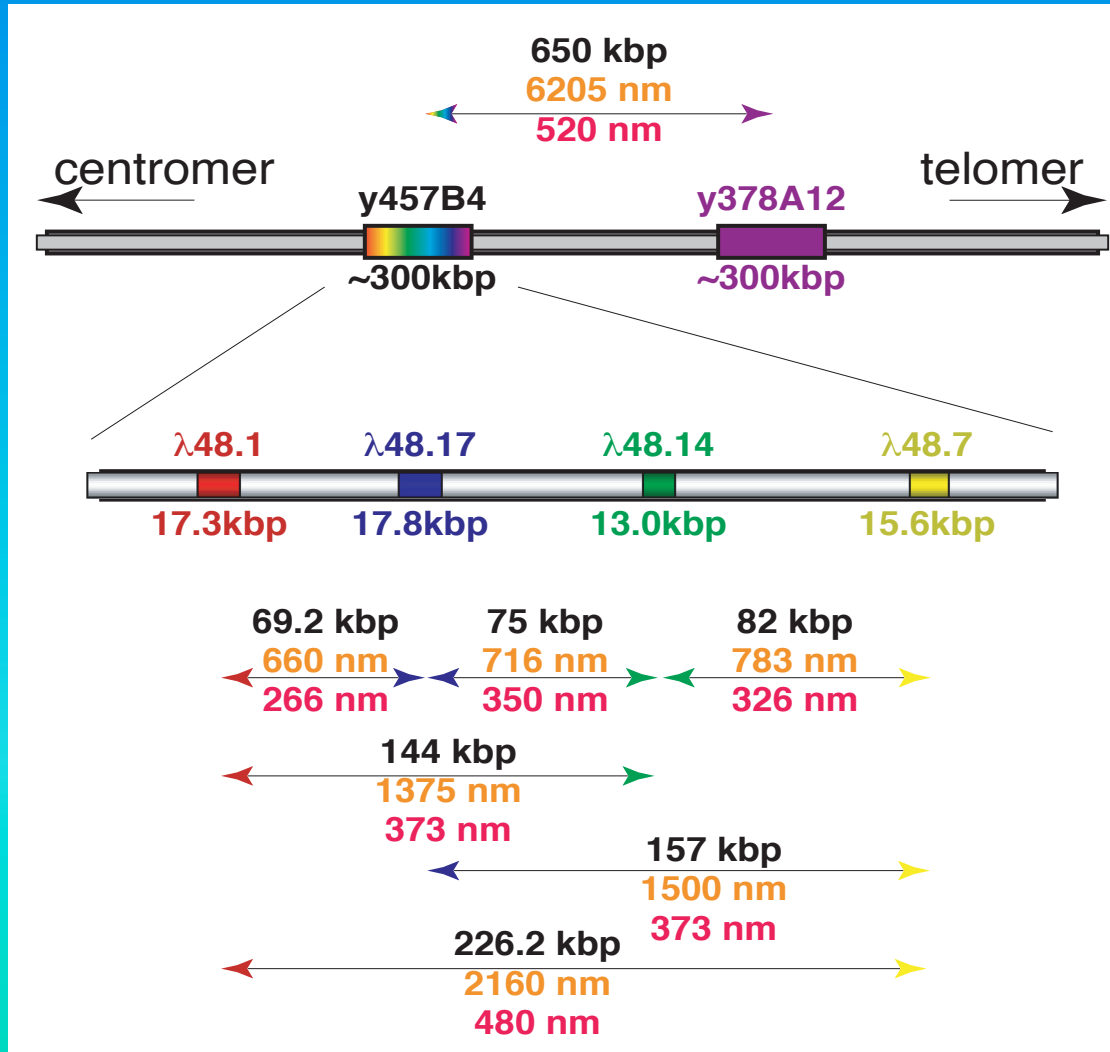
Random-Walk/Giant-Loop Multi-Loop-Subcompartment Model



A: courtesy K. Richter; B: courtesy K. Greulich-Bode

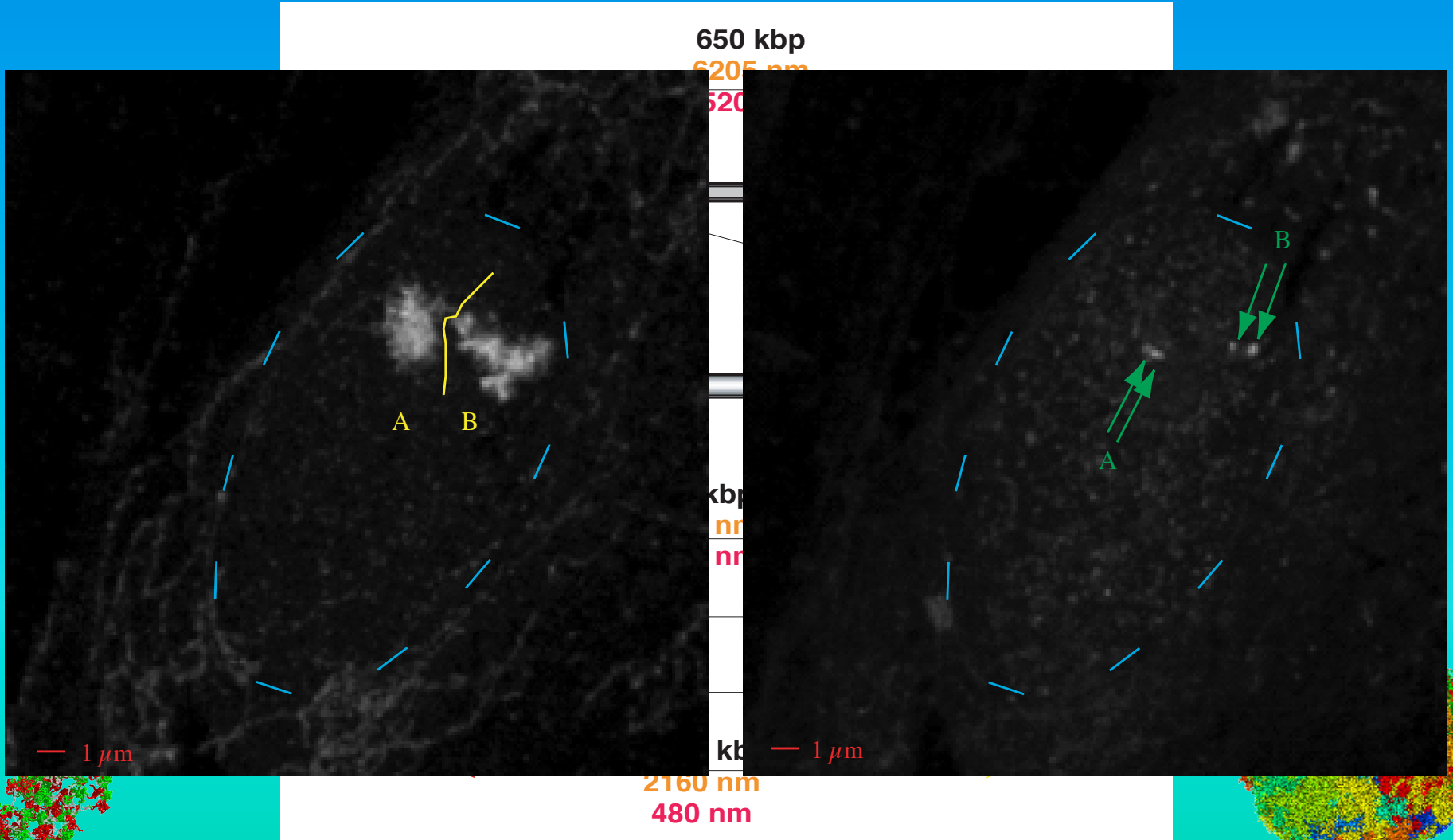
3D Architecture of the Prader-Willi Region

Fluorescence *in situ* hybridization with various protocols of small probes within the Prader-Willi region combined with spectral precision distance confocal laser scanning microscopy and comparison with large-scale computer simulations shows a Multi-Loop Subcompartment organization of the Prader-Willi region.



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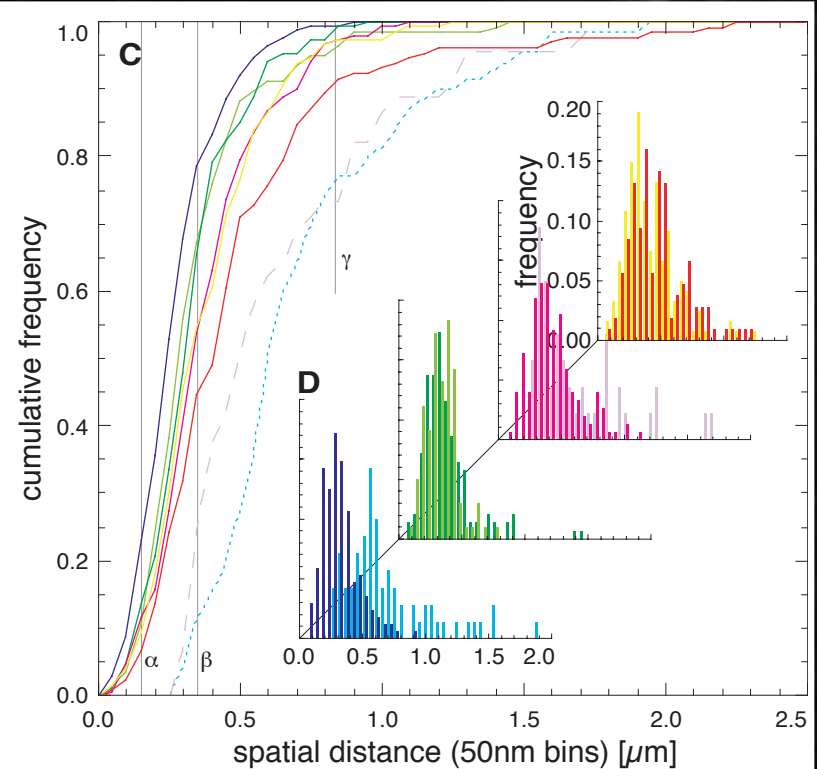
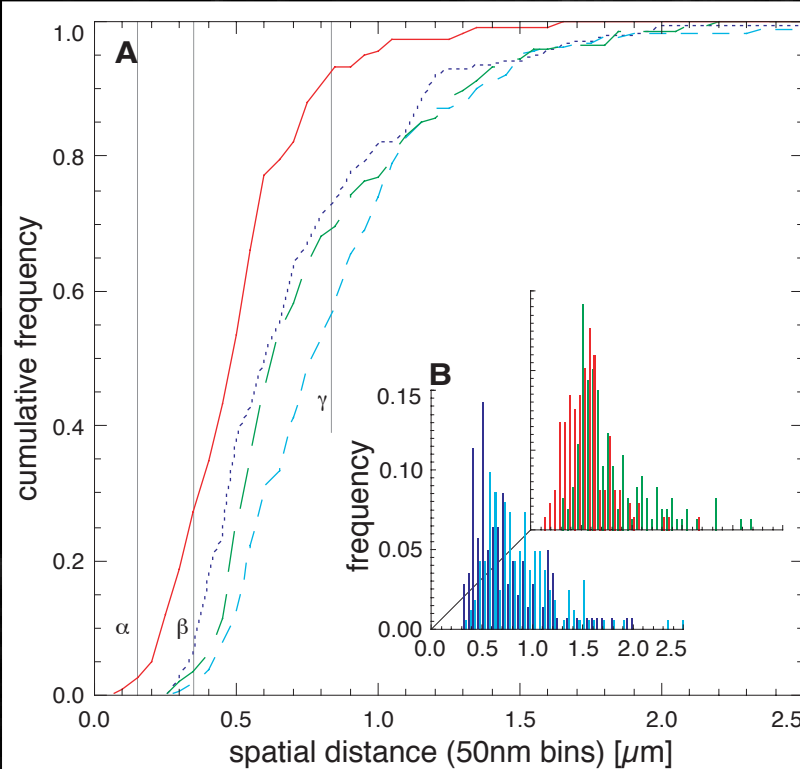
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650 kbp

6205 nm
520



2160 nm
480 nm

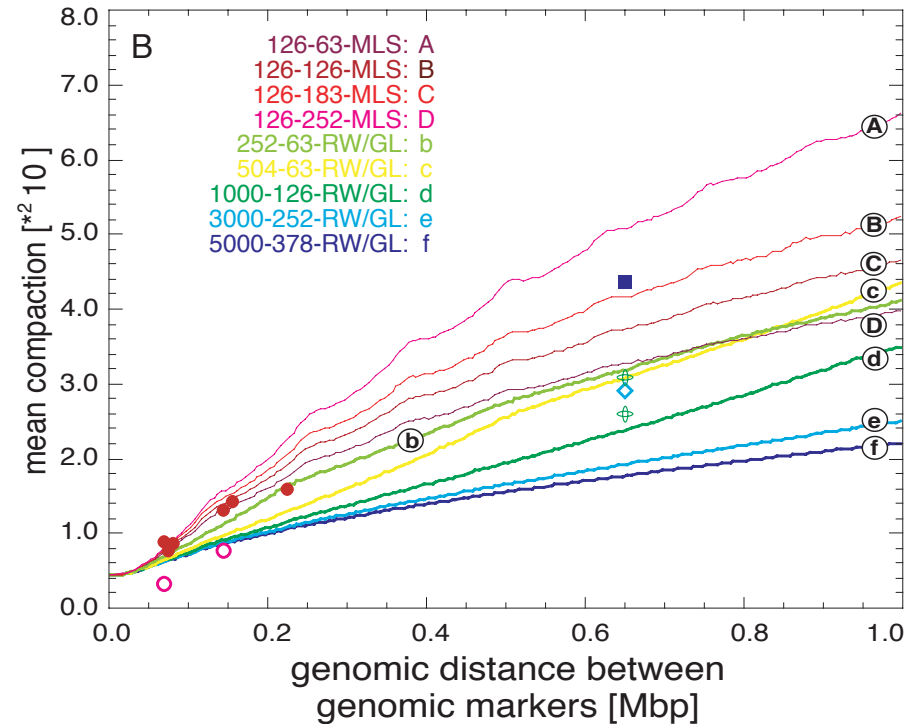
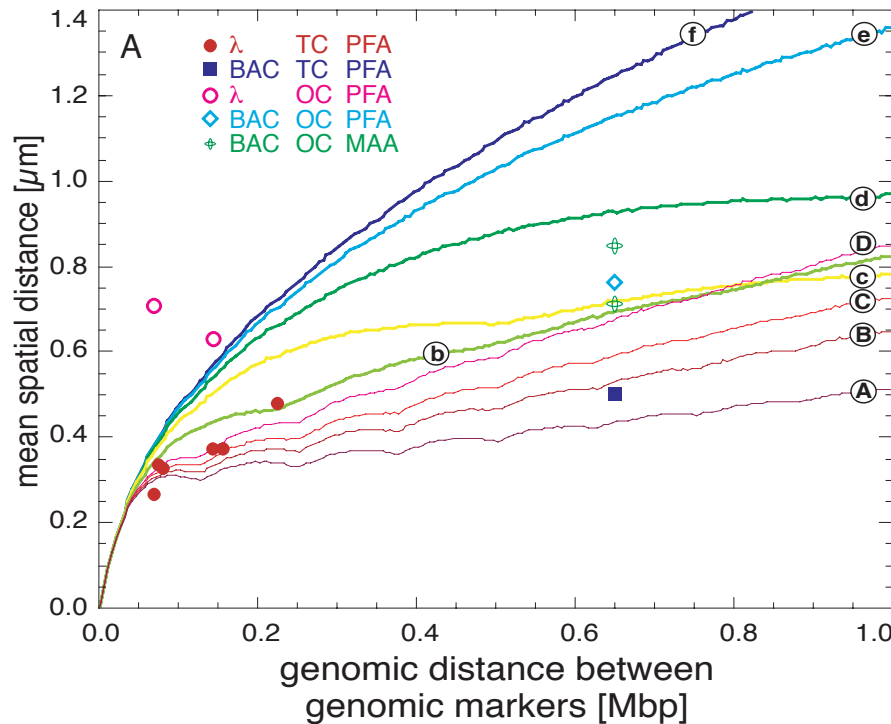
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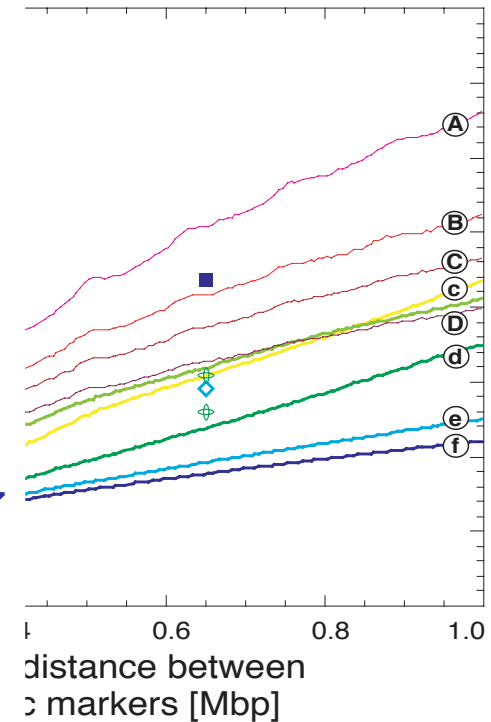
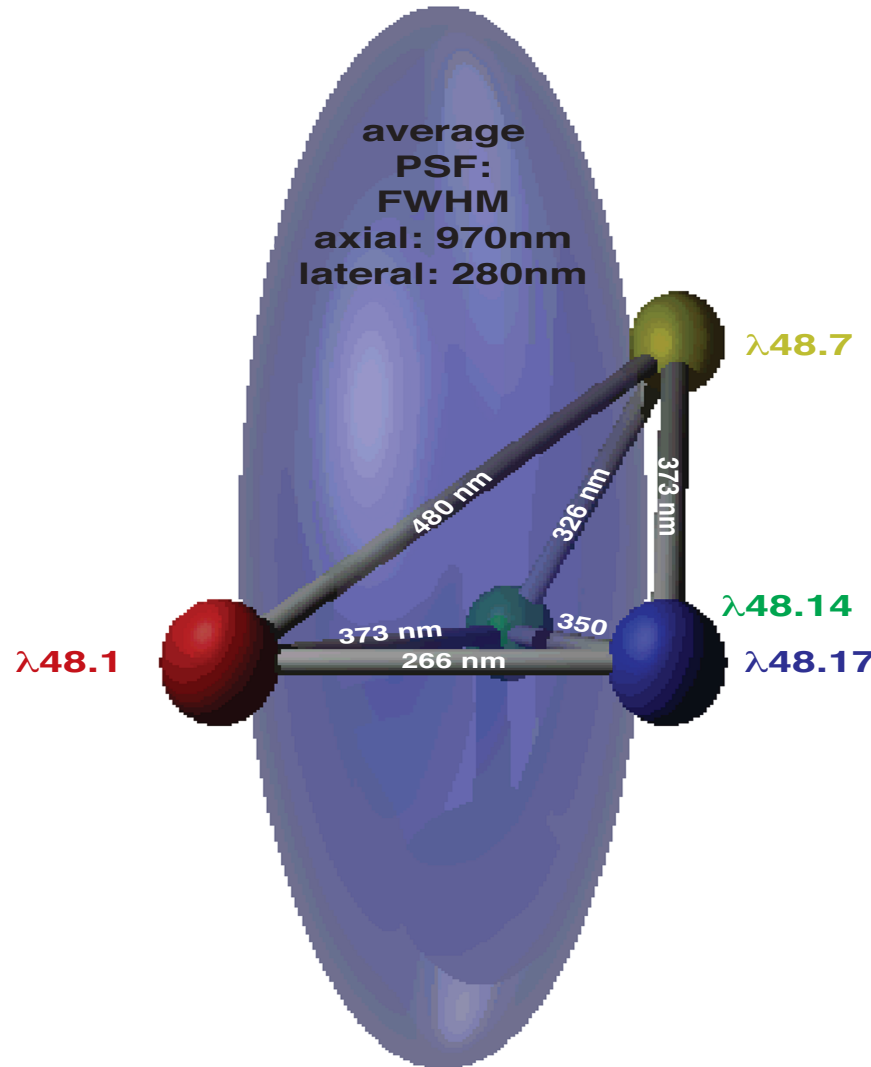
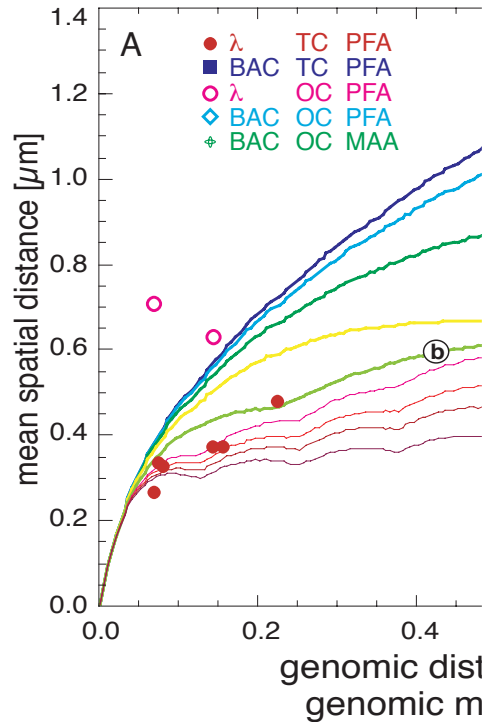


2160 nm

480 nm

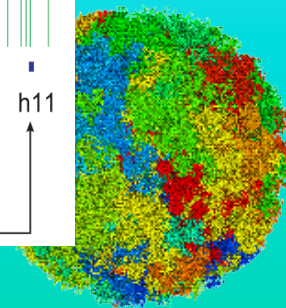
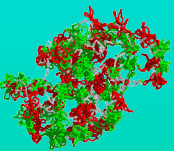
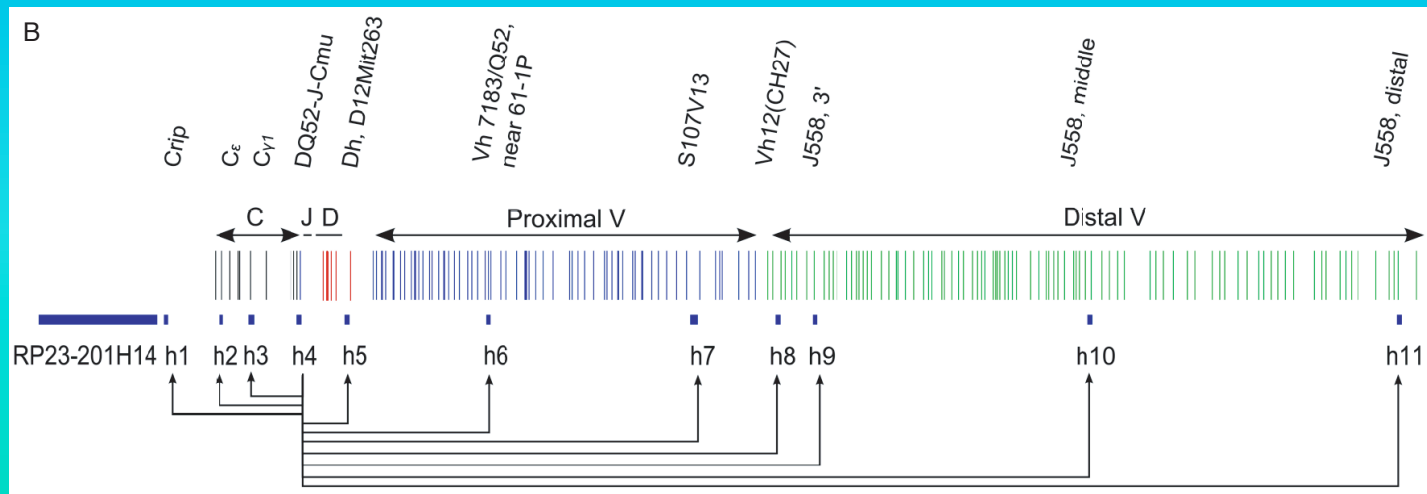
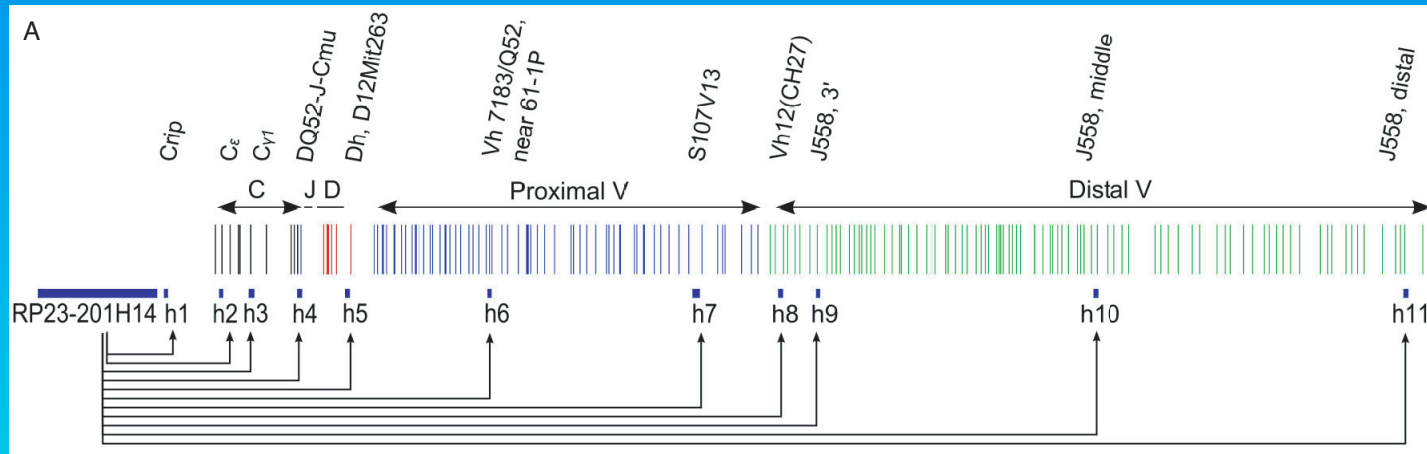
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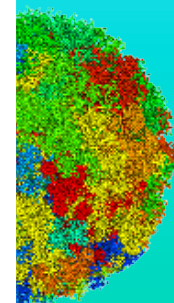
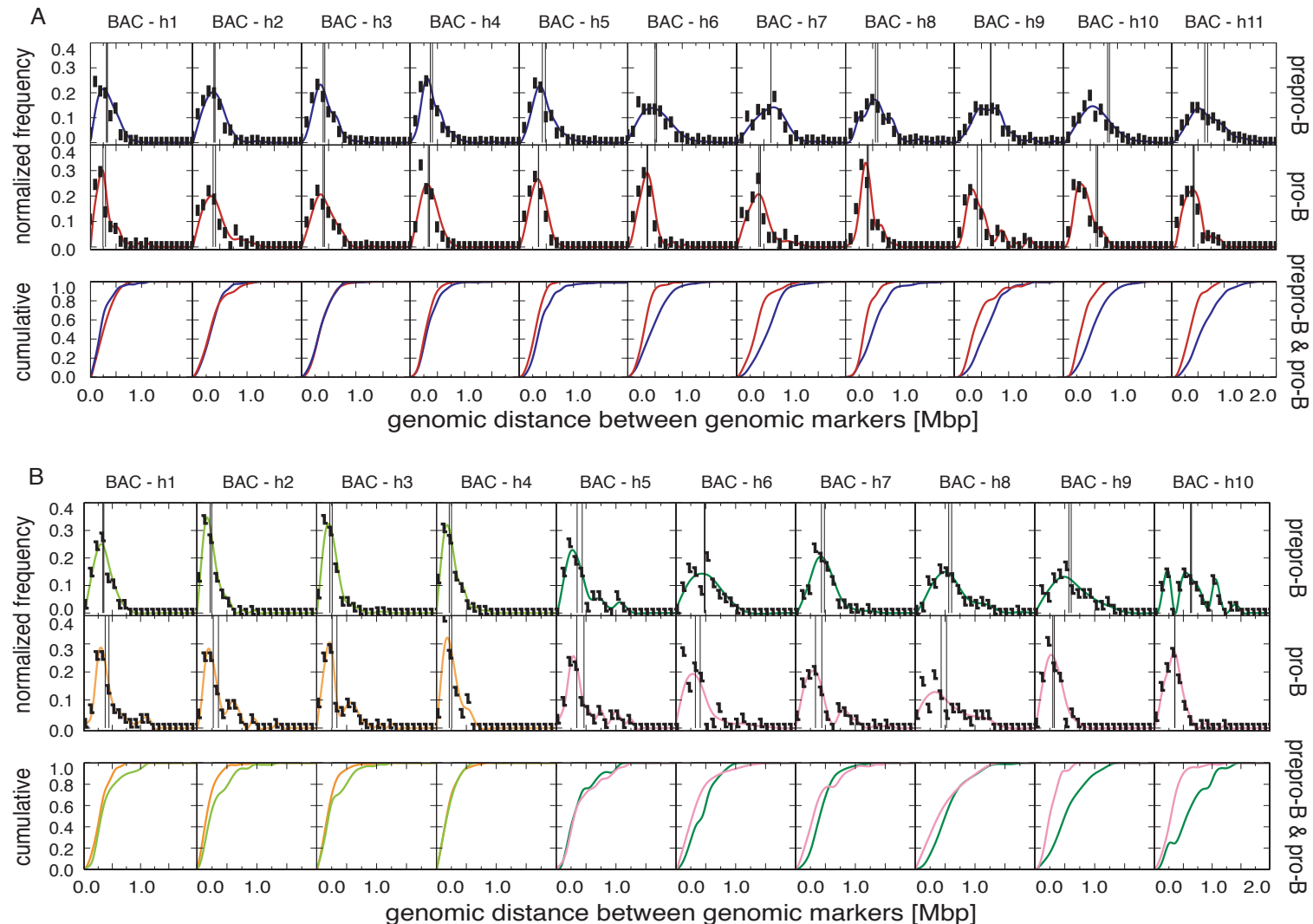
3D Architecture & Function of the IgH Locus

Fluorescence *in situ* hybridization of the IgH locus combined with spectral precision distance epifluorescence microscopy, analytical trilateration and comparison with computer simulations shows again a Multi-Loop Subcompartment organization of the IgH locus with functional relevant distances.



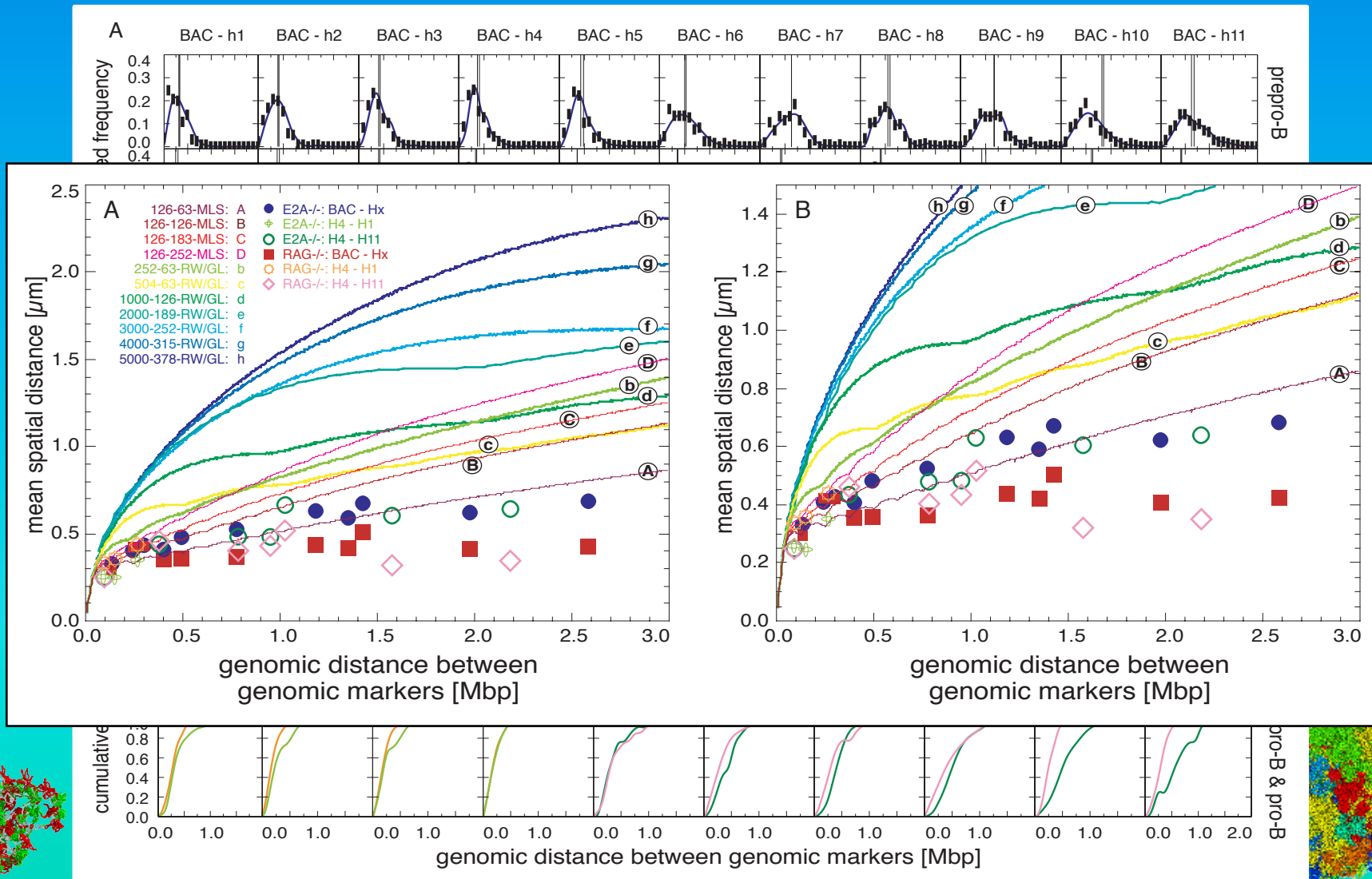
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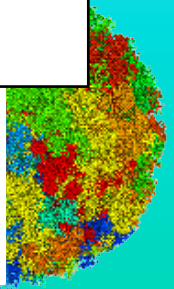
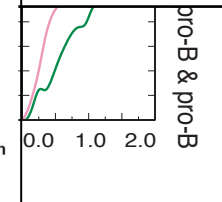
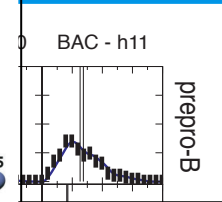
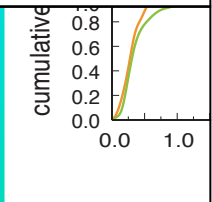
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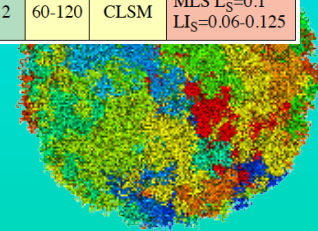
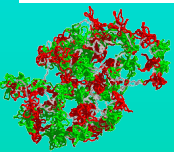
“Synoptic” 3D Architecture of Various Loci

A history “synoptic” comparison of the spatial distance mapping from their original background and aim, FISH methodological protocols, via microscopic imaging and restoration analysis procedures, to their interpretation, reveals that with time Multi-Loop Subcompartment models are favoured.



Study	Location	Preparation of Cells			FISH			Microscopy		Fit to model
		Cell cycle	KCl [nM]	Fixative	Melting	Label	Colours	# of nuclei	Image acquisition	
Fig. 3B, Trask '89	DHFR	UA41 G1-cf	75 dropped	MAA 3:1	FM 50 %	Biotin	1	20-37	photo, wall	RWGL 0.08-J RWGL 1.0
Fig. 3B, Lawrence '90	Dystrophin	WI38F G1	75 dropped	MAA 3:1	FM 50 %	Biotin	1	20-60	photo, wall	RWGL 0.5-1
Fig. 3A, Trask '91	Xq28	F G1-cf	75 dropped	MAA 3:1	FM 50 %	Biotin	1	30-60	photo, wall	RWGL 0.7 J RWGL 2.0- >5.0
Fig. 3B, Trask '91	Xq28	F G1-cf	75 dropped	MAA 3:1	FM 50 %	Biotin Dig	2	30-60	photo, wall	RWGL 1.0-3.0
Fig. 3, v.d. Engh '92 or Fig. 5A, Trask '93	4p16.3	F G1-cf	75 dropped	MAA 3:1	FM 50 %	Biotin Dig	2	?	photo, d-board	$L_S \leq 0.1$ for $GS < 0.5 < RWGL > 5.0$
Fig. 5B, Trask '93	6p21	F G1-cf	75	MAA 3:1	FM 50-70 %	Biotin Dig	2	?	photo, d-board	$L_S \leq 0.1$ for $GS < 1.0 < RWGL 1.0-5.0$
Fig. 5, Senger '93	MHC 6p21.31	HFF G1-cf	?	?	FM 50 %	Biotin	1	> 30	photo, wall	MLS L_S & $LI_S = 0.12-0.25$ RWGL 0.1-0.5
Fig. 5, Senger '93	MHC 6p21.31	HFF G1-cf	?	?	FM 50 %	Biotin Dig	2	> 30	photo, wall	MLS $L_S = 0.1$ $LI_S = 0.18$ RWGL 0.1-0.5
Fig. 1, Warrington '94	4p16.3	F G1-cf	75	MAA 3:1	FM 50 %	Biotin Dig	2	?	?	RWGL > 5.0
Tab. 1, Warrington '94	5q31-33	L	?	?	?	?	?	?	CLSM BioRad	RWGL > 5.0
Fig. 2B, Yokota '95	4p16.3	F G1-cf	40 dropped	MAA 3:1	FM 70 %	Biotin Dig	2	40-360	photo, d-board	RWGL 2.0-4.0
Fig. 3B, Yokota '95	4p16.3	F G1-cf	-	PFA 4 %	FM 70 %	Biotin Dig	2	40-350	photo, d-board	MLS L_S & $LI_S = 0.1-0.125$

Study	Location	Preparation of Cells			FISH			Microscopy		Fit to model
		Cell cycle	KCl [nM]	Fixative	Melting	Label	Colours	# of nuclei	Image acquisition	
Fig. 2A, Yokota '97	4p16.3 R-band	F G1-cf	40 dropped	MAA 3:1	FM 70 %	Biotin Dig	2	37-178	photo, d-board	RWGL 2.0-3.0
Fig. 2B, Yokota '97	6p21.3 R-band	F G1-o	40 dropped	MAA 3:1	FM 70 %	Biotin Dig	2	37-178	photo, d-board	RWGL 4.0-5.0
Fig. 2C, Yokota '97	21q22.2 G-band	F G1-o	40 dropped	MAA 3:1	FM 70 %	Biotin Dig	2	37-178	photo, d-board	RWGL 1.0-2.0
Fig. 2D, Yokota '97	Xp21.3 G-band	F G1-o	40 dropped	MAA 3:1	FM 70 %	Biotin Dig	2	37-178	photo, d-board	RWGL 0.5-0.9
Fig. 2D, Yokota '97	Xq28 R-band	F G1-of	40 dropped	MAA 3:1	FM 70 %	Biotin Dig	2	37-178	photo, d-board	RWGL 1.0-5.0j
Fig. 2A, Yokota '97	Xp21.3 G-band	F	-	PFA 4 %	FM 70 %	Biotin Dig	2	37-178	photo, d-board	RWGL 0.25 MLS $L_S = 0.126$ $LI_S = 0.200$
Fig. 2A, Yokota '97	Xq28 R-band	F	-	PFA 4 %	FM 70 %	Biotin Dig	2	37-178	photo, d-board	RWGL 1.0
Fig. 4B, Yokota '97	Xp21.3 G-band	HeLa	40 dropped	MAA 3:1	FM 70 %	Biotin Dig	2	37-178	photo, d-board	RWGL 0.25 MLS $L_S = 0.126$ $LI_S = 0.200$
Fig. 4B, Yokota '97	Xq28 R-band	HeLa	40 dropped	MAA 3:1	FM 70 %	Biotin Dig	2	37-178	photo, d-board	RWGL 1.0
Monier '97	11q13	F	-	PFA 4 %	FM 70 %	Biotin Dig	1	22-69	CLSM	MLS $L_S = 0.126$ $LI_S = 180$
Monier '97	11q13	L	-	PFA 4 %	FM 70 %	Biotin Dig	1	22-69	CLSM	MLS $L_S = 0.1$ $LI_S = 0.18-0.24$
Knoch '98/ Rauch '99	15q11-21	F	-	PFA 4 %	FM 70 %	Biotin Dig	1 & 2	60-120	CLSM	MLS $L_S = 0.1$ $LI_S = 0.06-0.125$

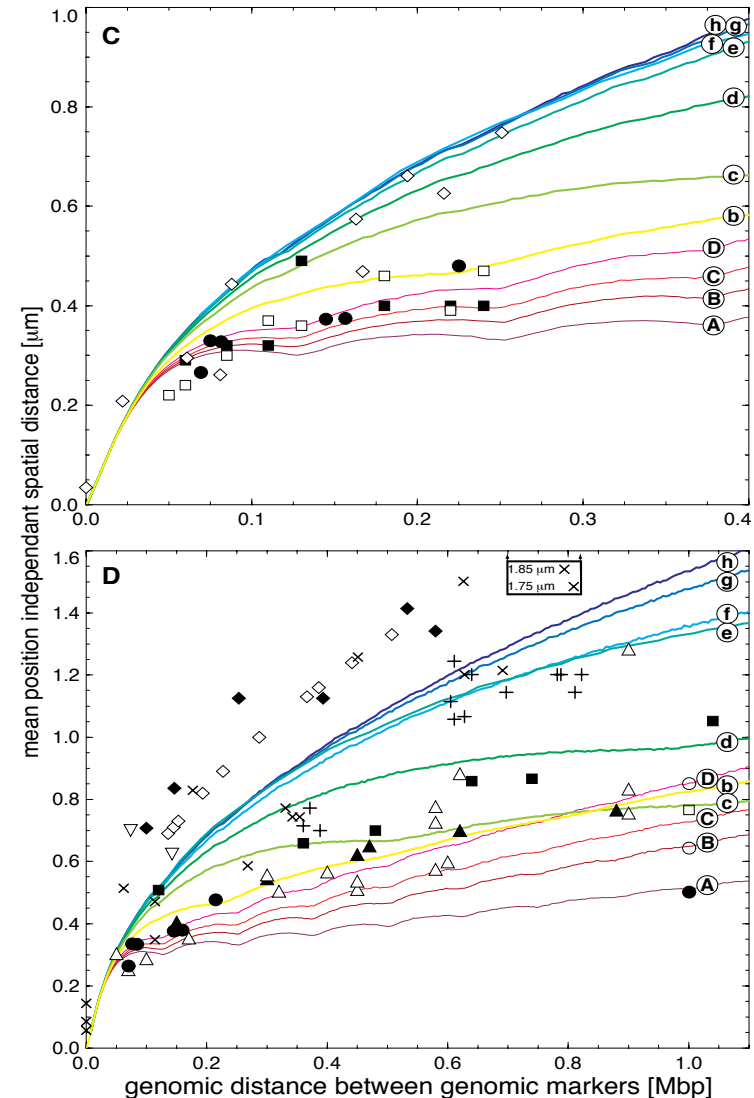
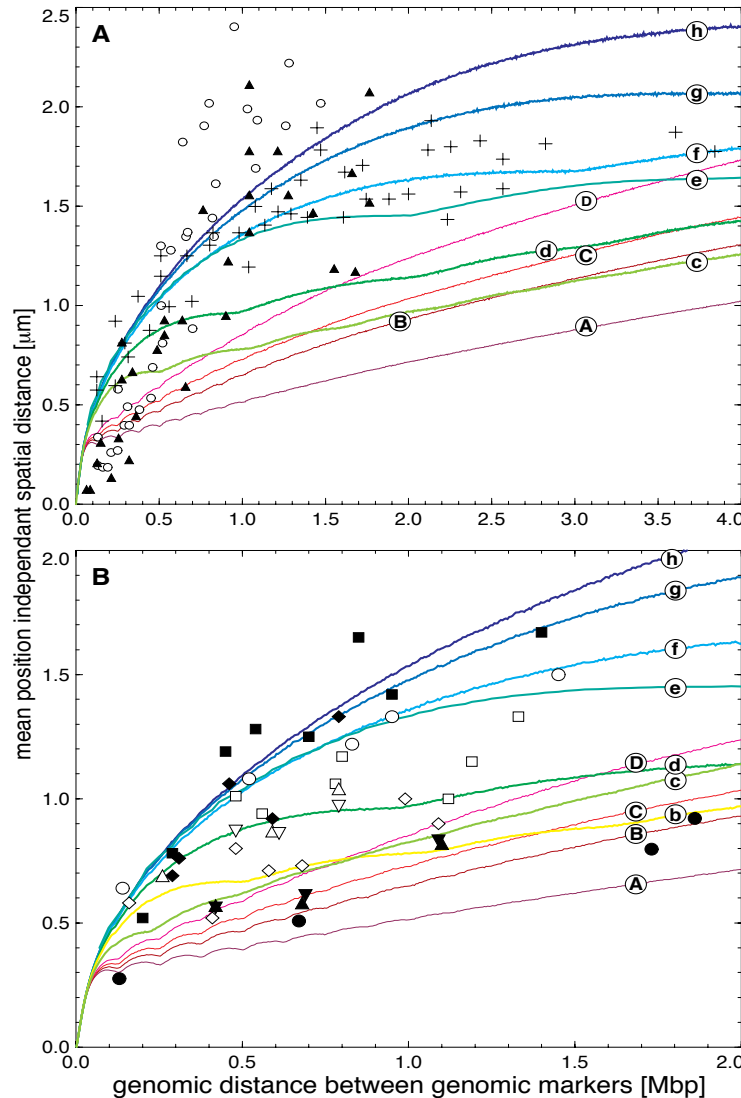


“Synoptic” 3D Architecture of Various Loci

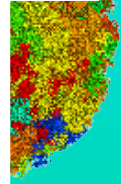
A history “synoptic” comparison of the spatial distance mapping from their original background and aim, FISH methodological protocols, via microscopic imaging and restoration analysis procedures, to their interpretation, reveals that with time Multi-Loop Subcompartment models are favoured.



Study
Fig. 3B, Tr '89
Fig. 3B, Lawrence '91
Fig. 3A, Tr '91
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Fig. 3, v.d. '92 or Fig. Trask '93
Fig. 5B, Tr '93
Fig. 5, Senger '93
Fig. 5, Senger '93
Fig. 1, Warrington
Tab. 1, Warrington
Fig. 2B, Ye '95
Fig. 3B, Ye '95

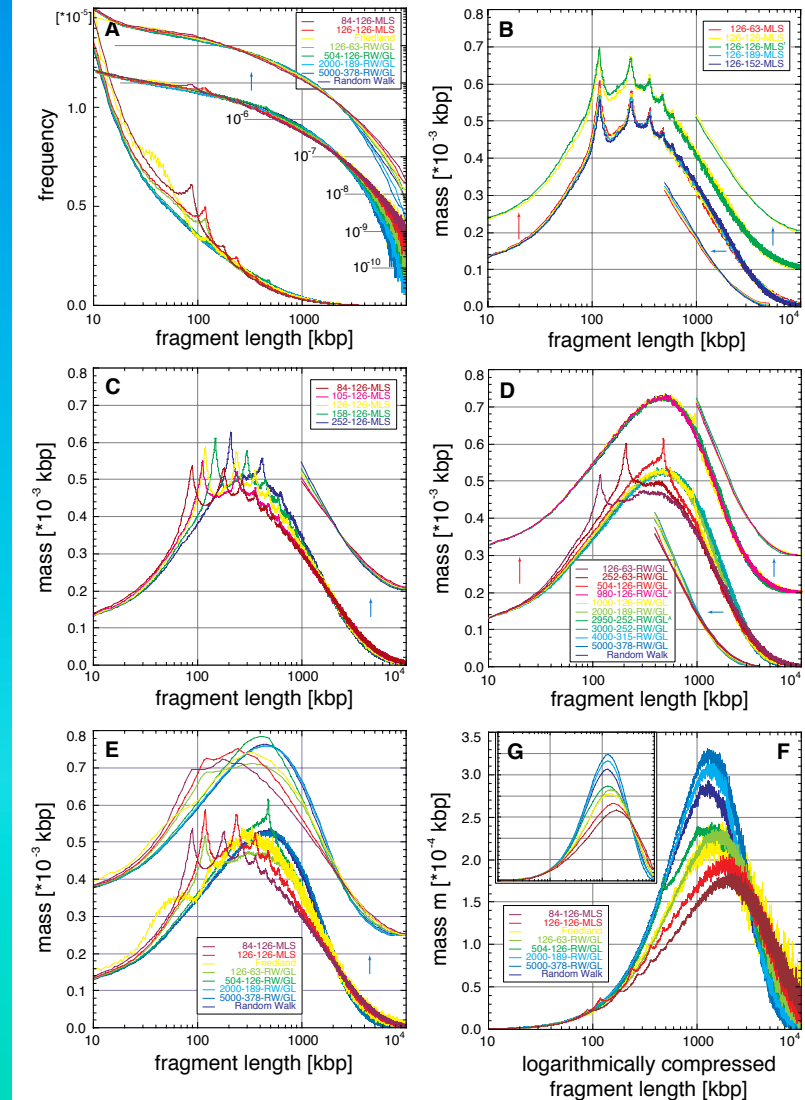
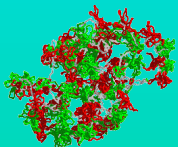
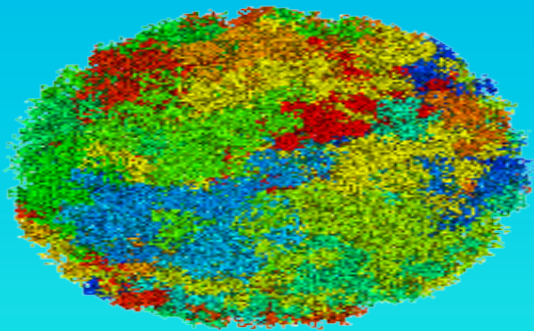


to model
L 2.0-3.0
L 4.0-5.0
L 1.0-2.0
L 0.5-0.9
L 1.0-5.0j
L 0.25 L _S =0.126 0.200
L 1.0
L 0.25 L _S =0.126 0.200
L 1.0
L _S =0.126 180
L _S =0.1 0.18-0.24
L _S =0.1 0.06-0.125



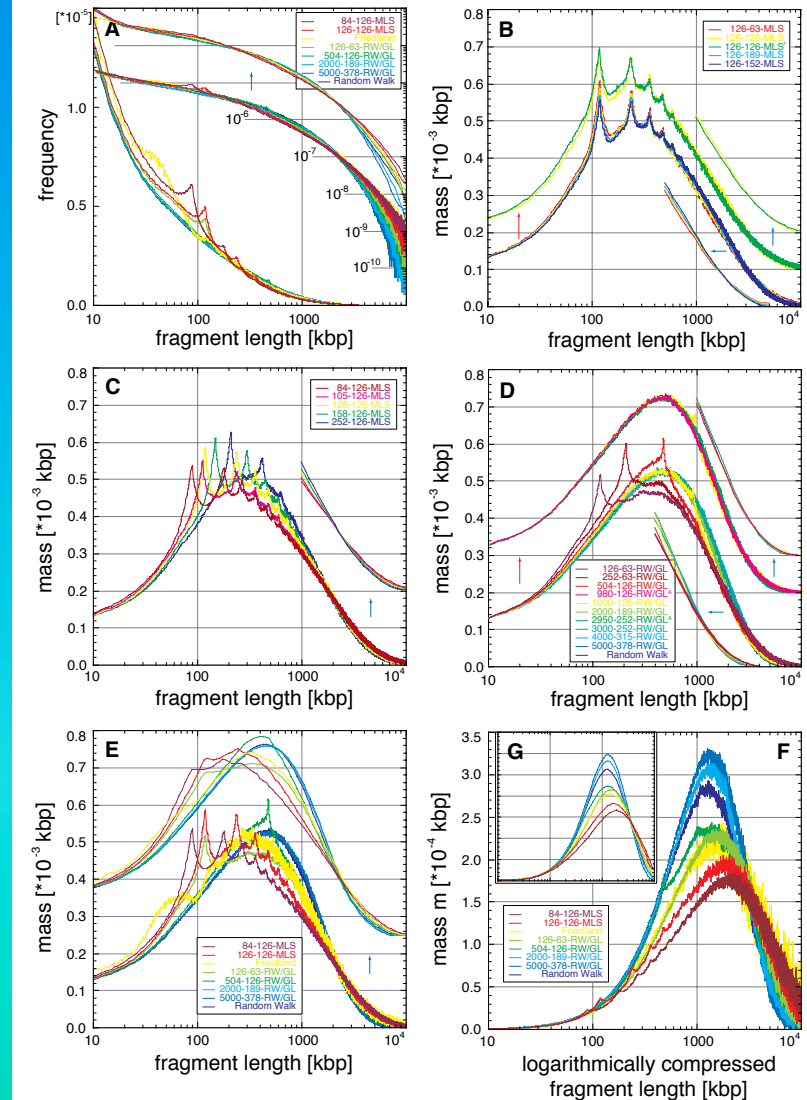
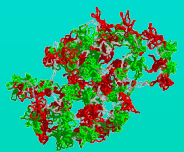
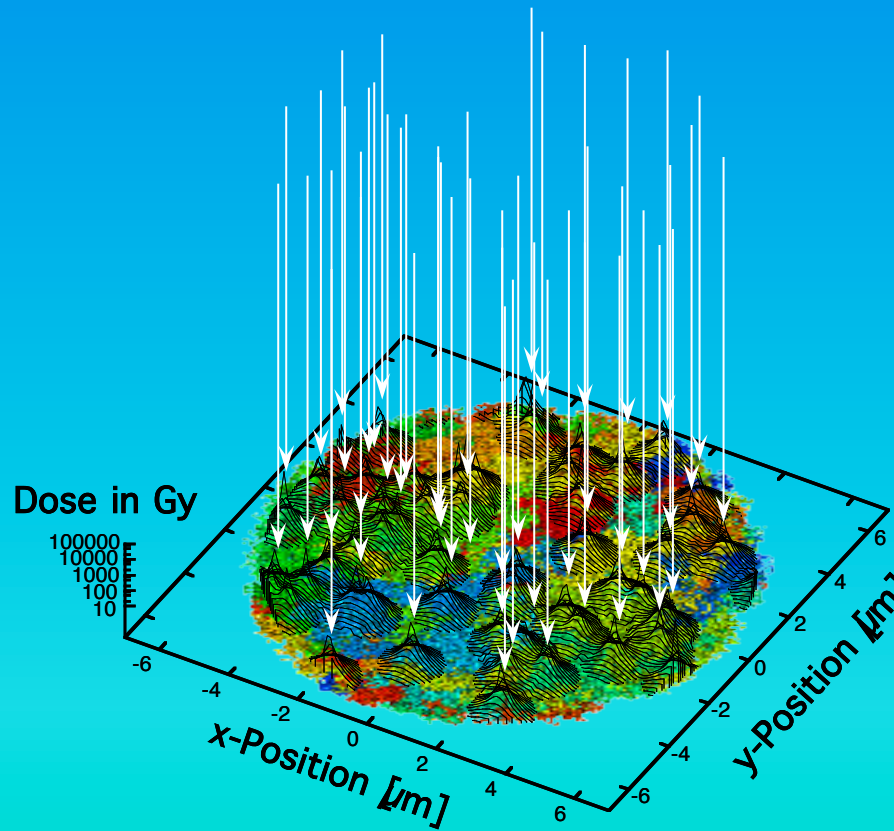
DNA Fragment Distribution after Ione-Irradiation

The length distribution of DNA fragments after irradiation with e. g. C or Ca with an inhomogeneous spatial double strand breakage probability depends on the detailed folding topology of the chromatin fiber and the RW/GL and MLS models differ largely.



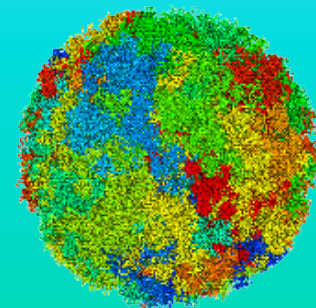
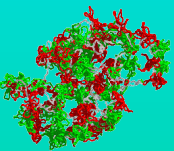
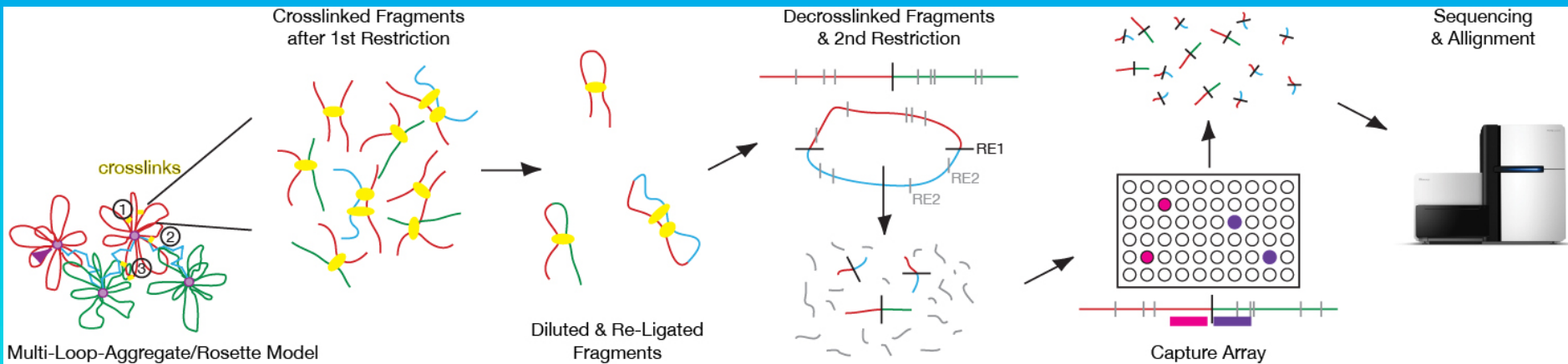
DNA Fragment Distribution after Ione-Irradiation

The length distribution of DNA fragments after irradiation with e. g. C or Ca with an inhomogeneous spatial double strand breakage probability depends on the detailed folding topology of the chromatin fiber and the RW/GL and MLS models differ largely.



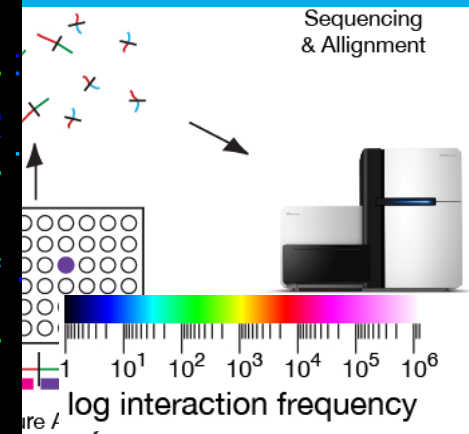
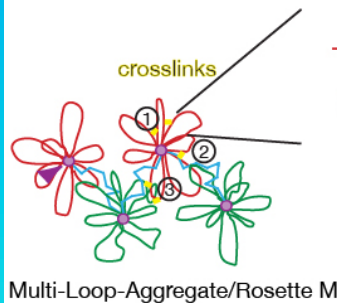
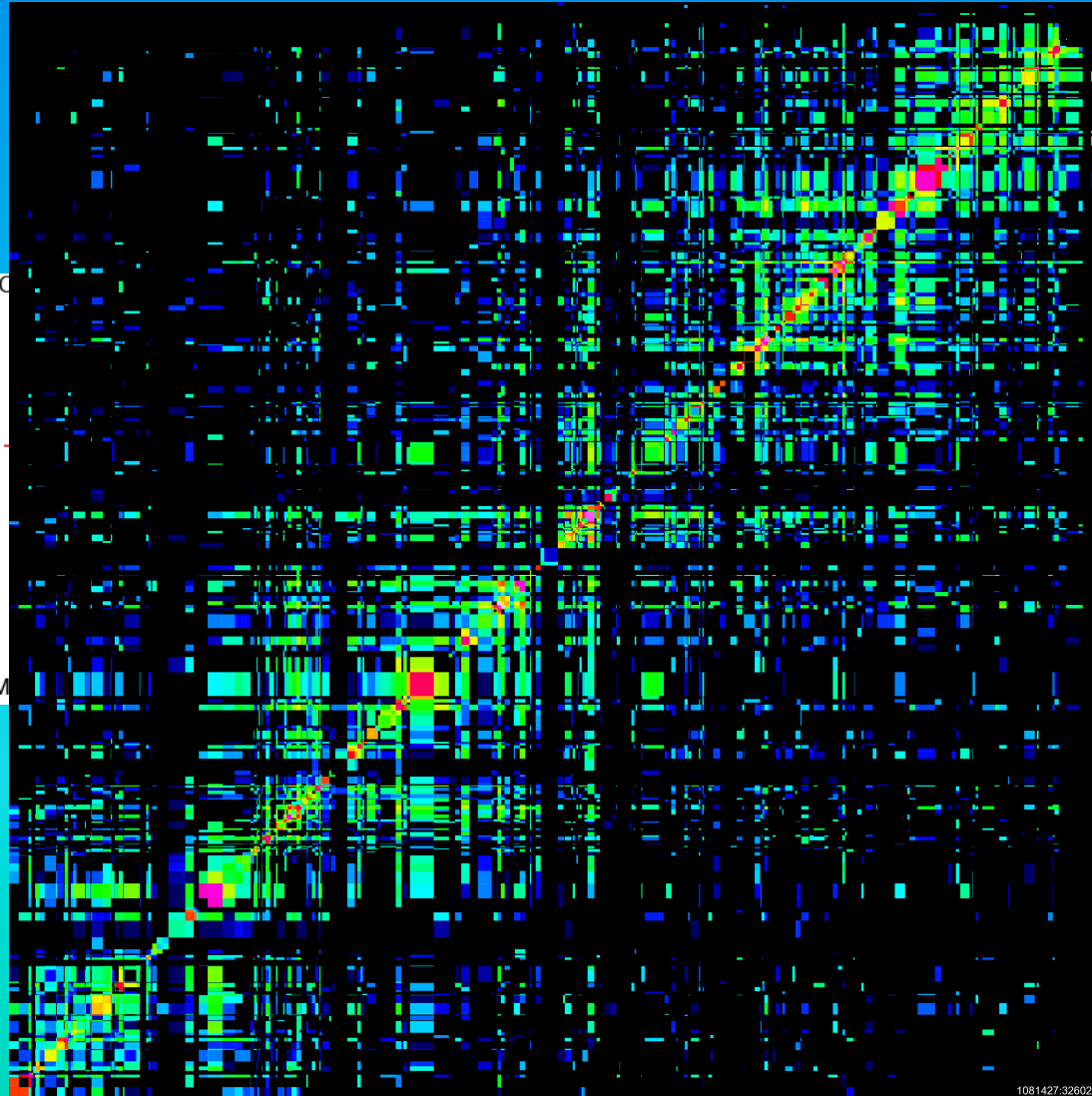
Selective Chromosome Interaction Capture (T2C)

T2C is a novel selective high-resolution high-throughput chromosome interaction capture, in which the relation between, region size, resolution, interaction frequency range, and sequencing depth can be designed towards the goal of the experiment. T2C reaches the limit of the “genomic” uncertainty principle and statistical mechanics.

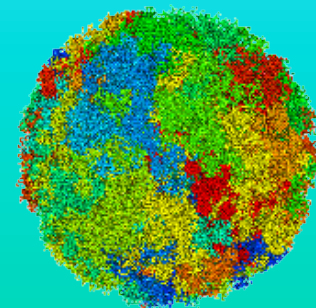
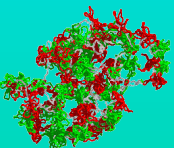


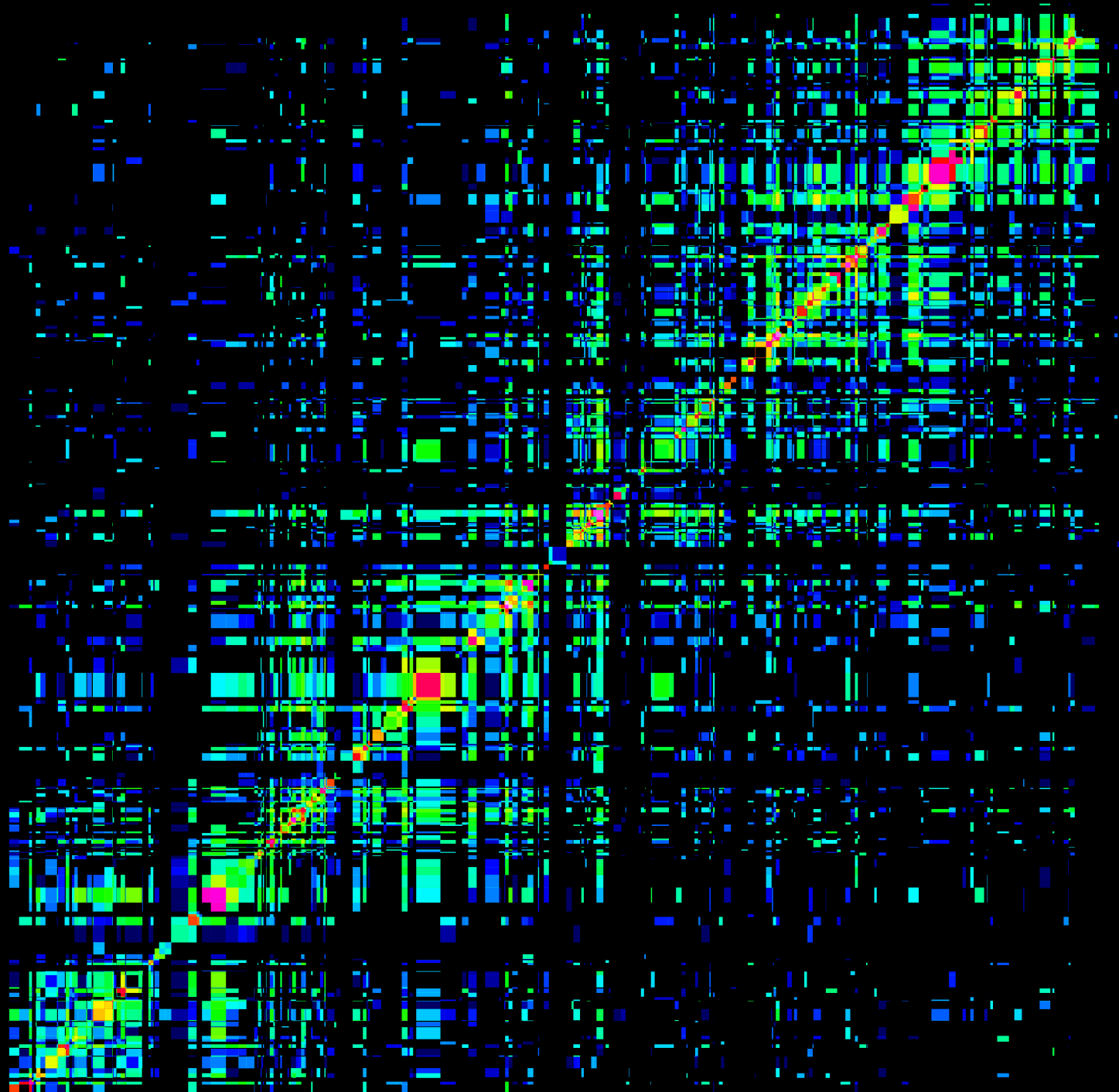
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HS IGF locus
~2.1 Mbp



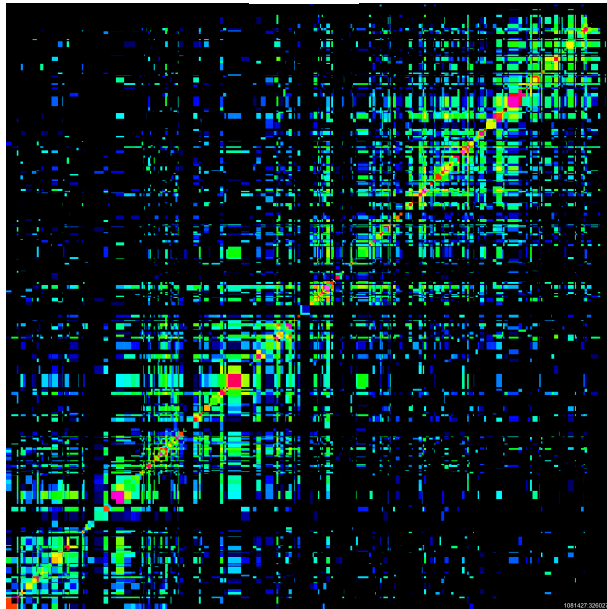


Stable Consensus Architecture of Genomes

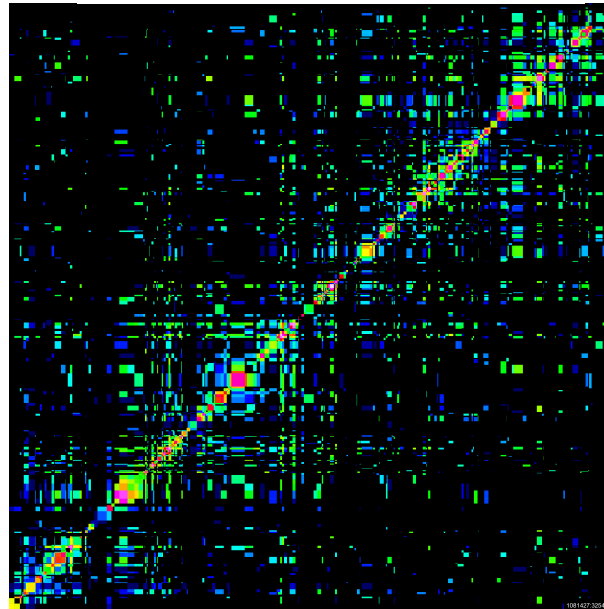
Due to the high signal-to-noise ratio of T2C reaching 5-6 orders of magnitude interaction maps reveal definitely an extremely high degree of similarity between different species, cell types, or functional states, thus functional differences are variation of a stable theme persisting through the cell cycle



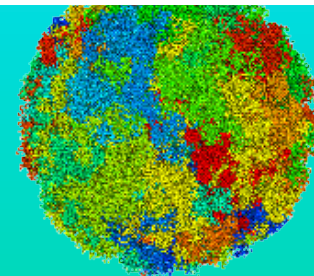
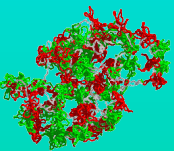
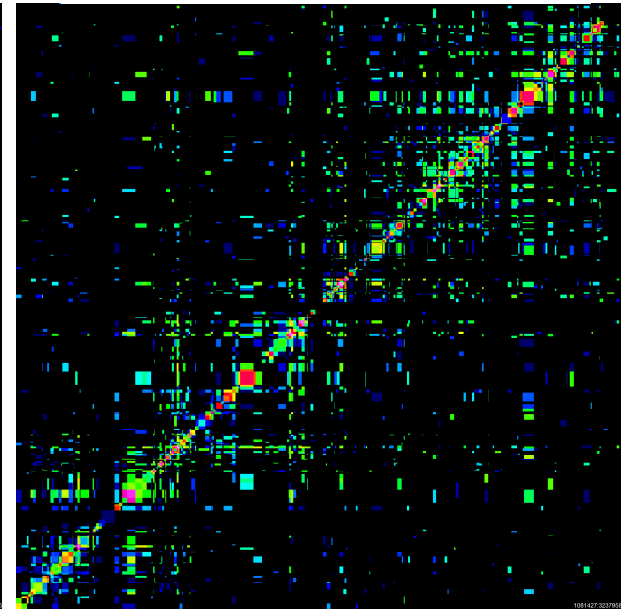
HB2



TEV-HEK293T cohesin intact



HRV-HEK293T cohesin cleaved

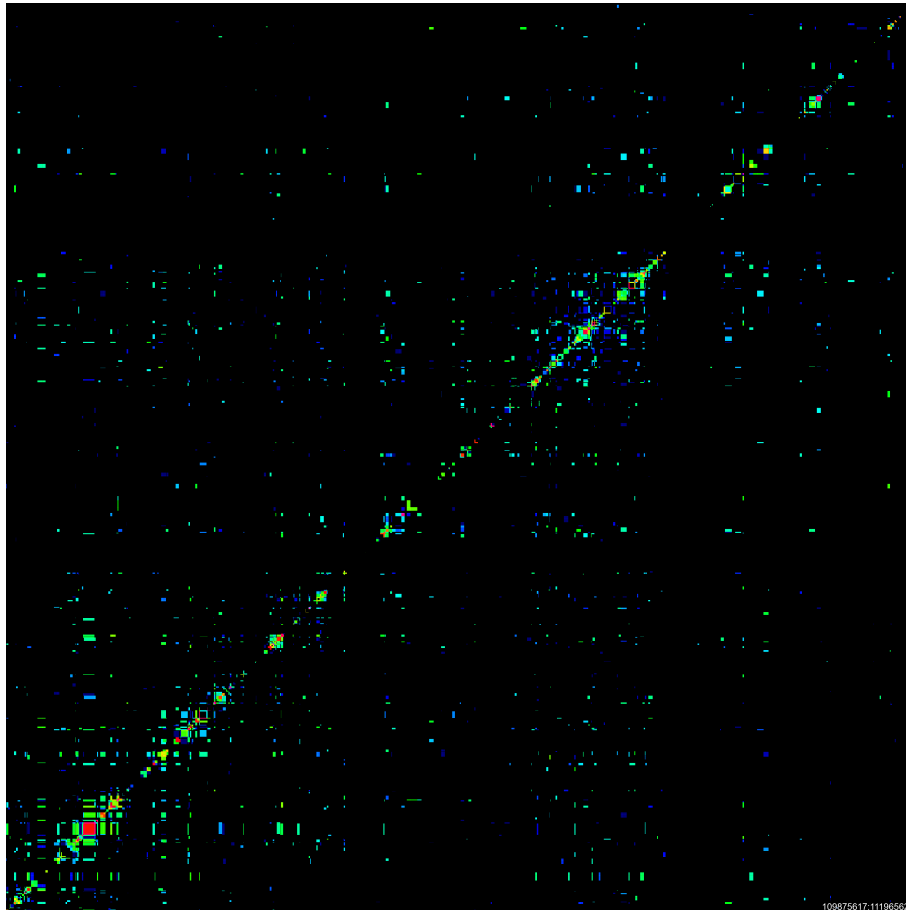


Stable Consensus Architecture of Genomes

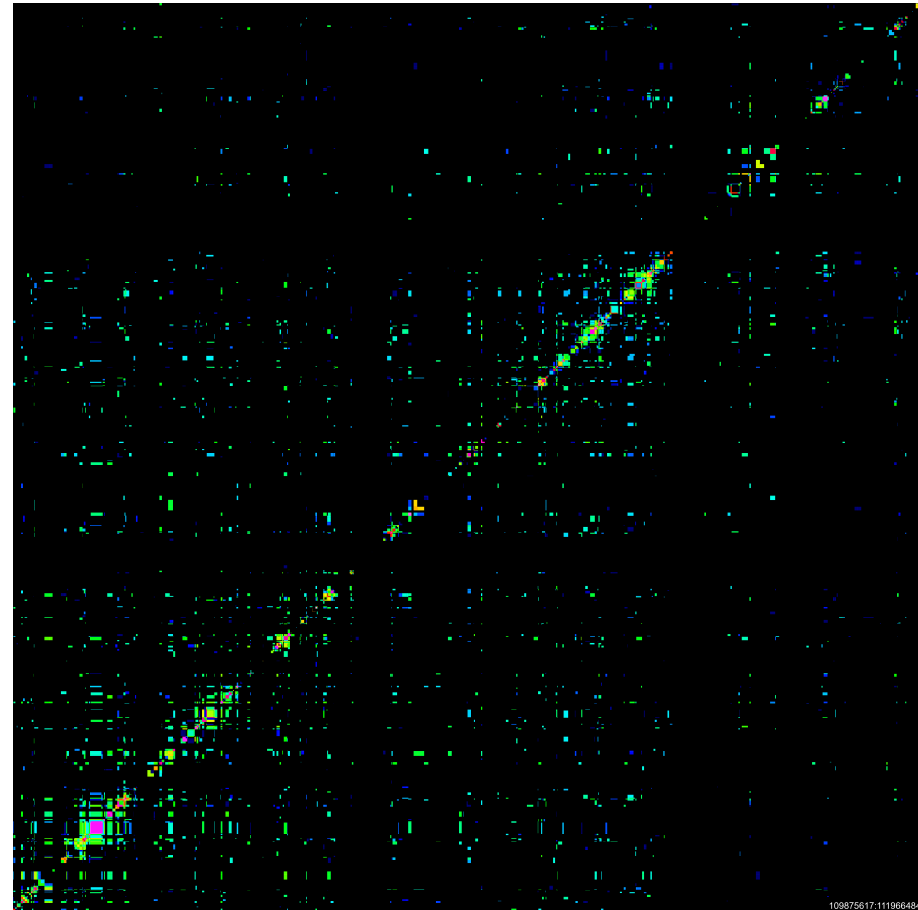
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Fetal Brain (inactive β -Globin)



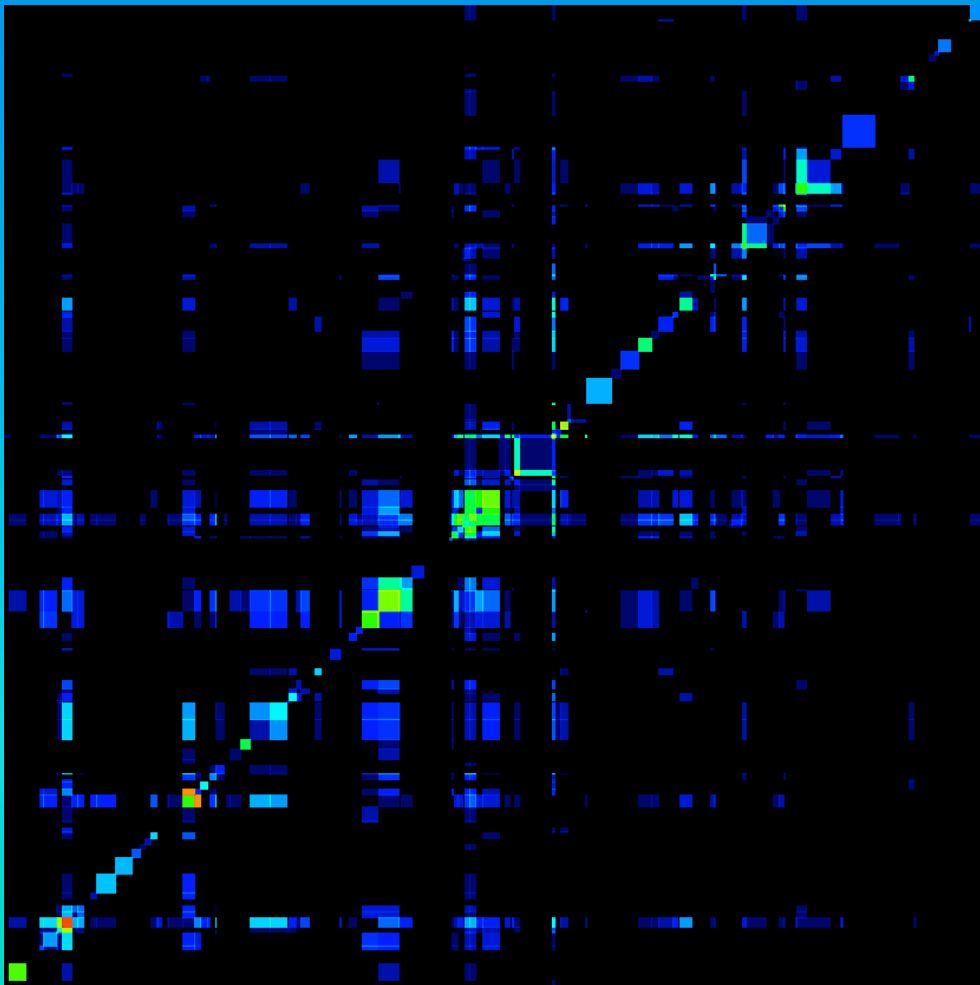
Fetal Liver (active β -Globin)



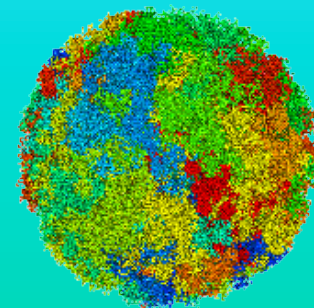
MM β -Globin 2.1 Mbp

Fine Structure of Loop Aggregates/Rosettes

Depending on the resolution, the loops within a domain and their arrangement in loop aggregates/rosettes can be shown as well as the details of how the loops are organized at their base as well as their aggregated rosette core: parallel loop fibres exist at the loop base with ~6kbp and these form the core.

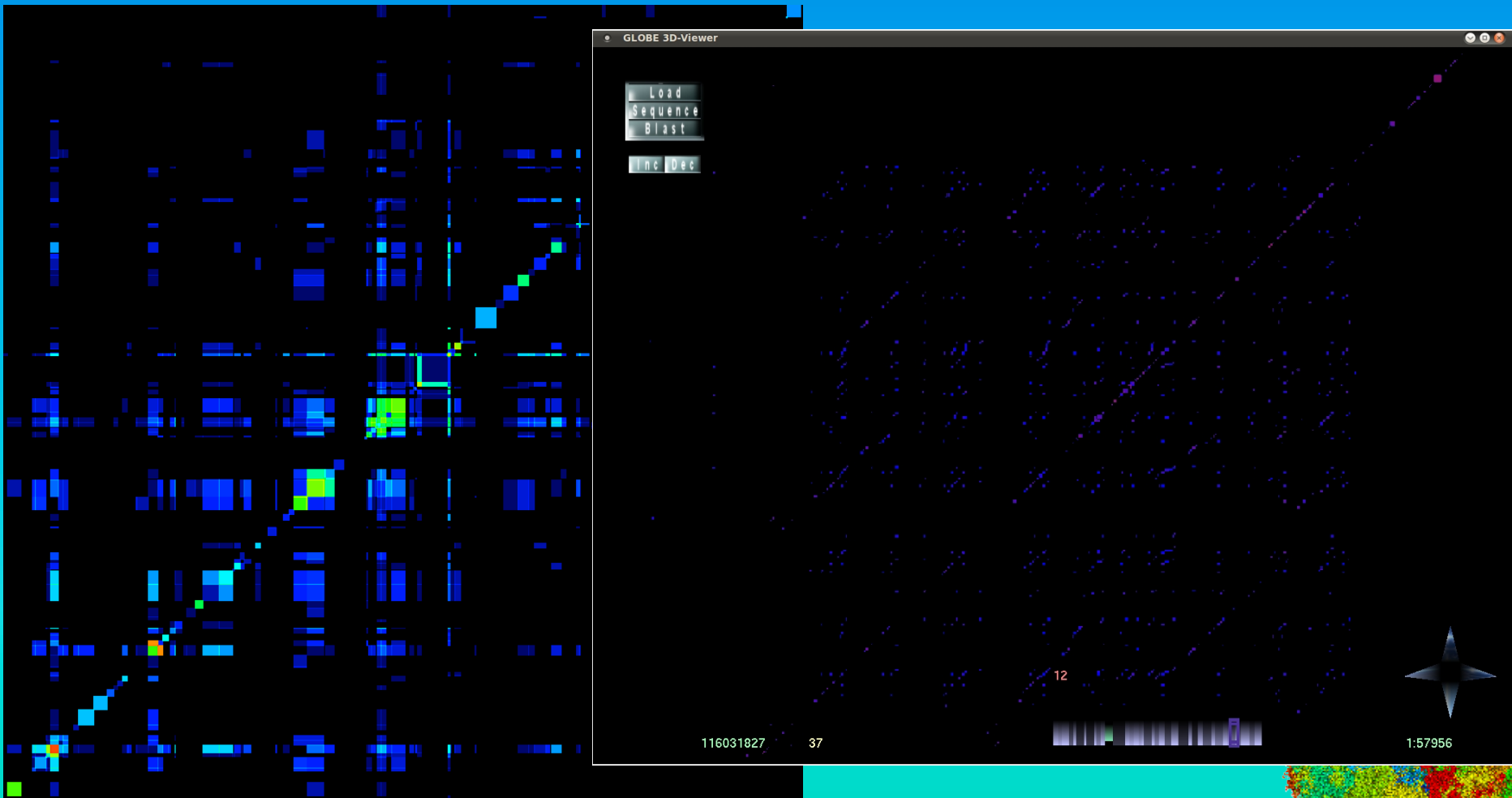


~ 400 kbp

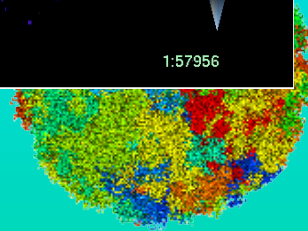


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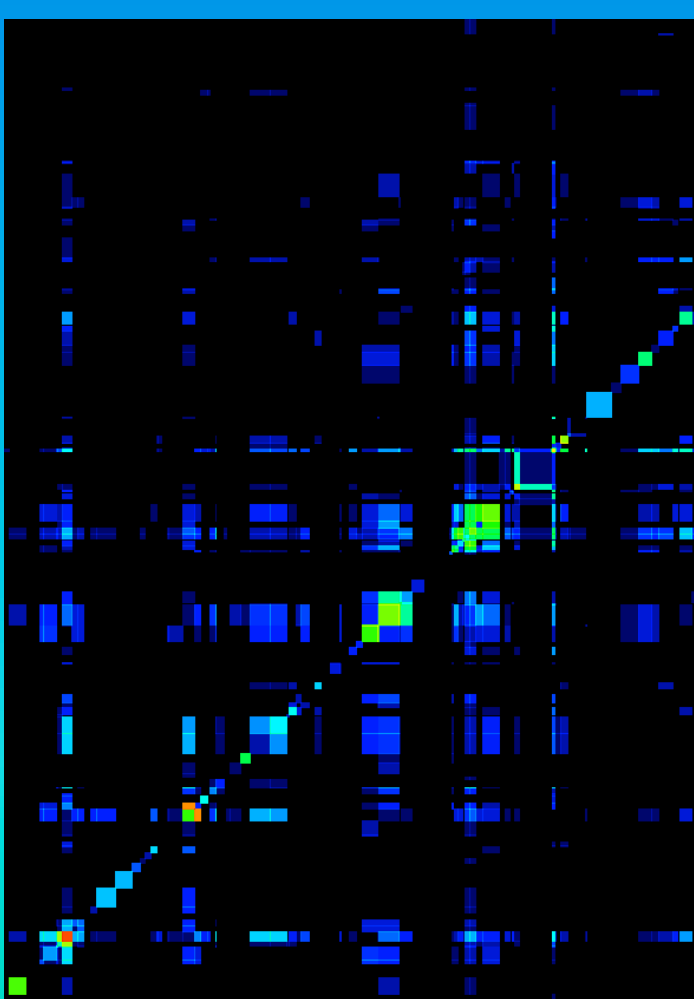


~ 400 kbp

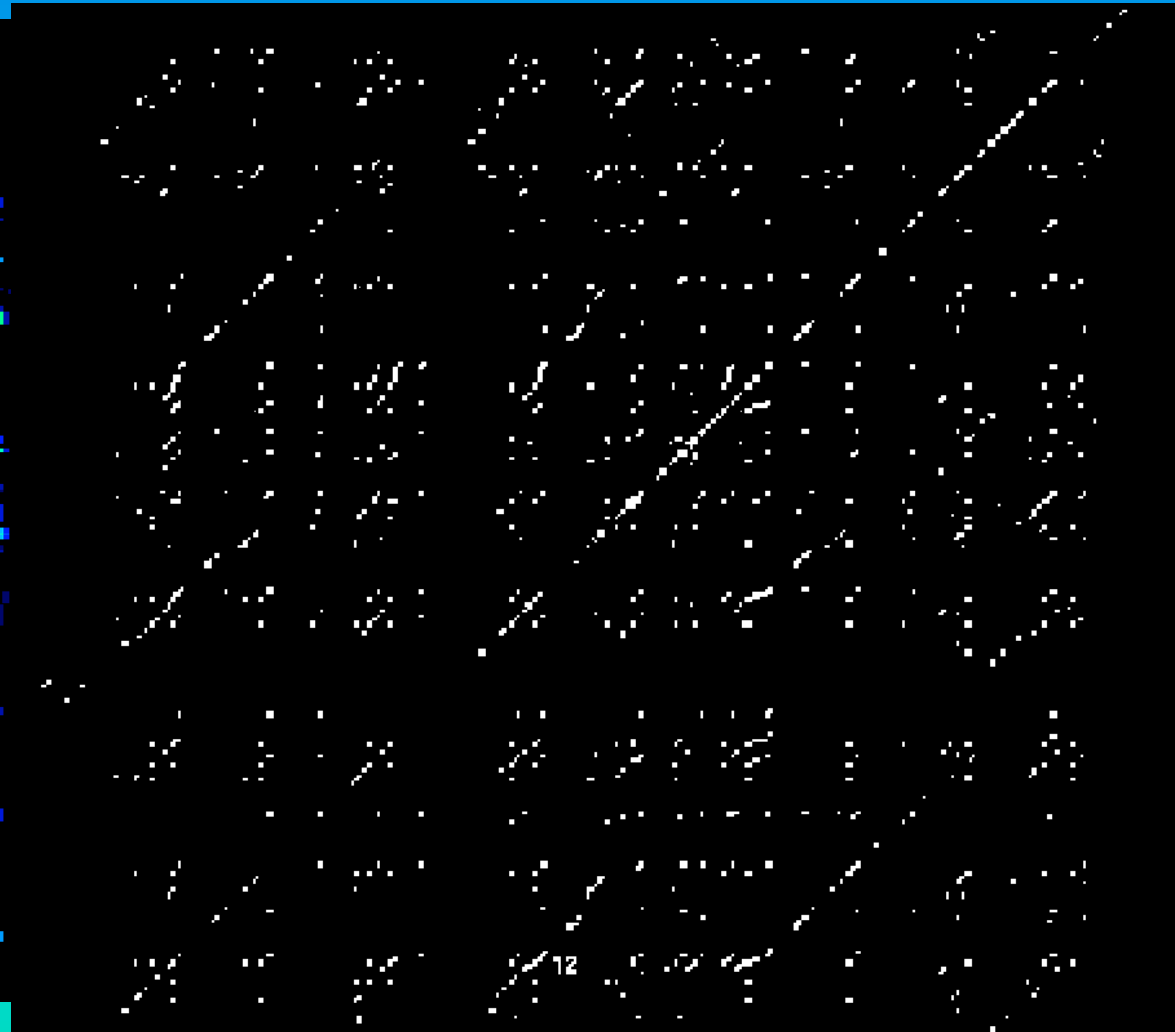


Fine Structure of Loop Aggregates/Rosettes

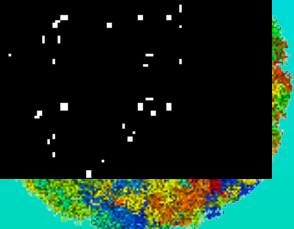
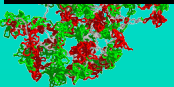
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~ 400 kbp

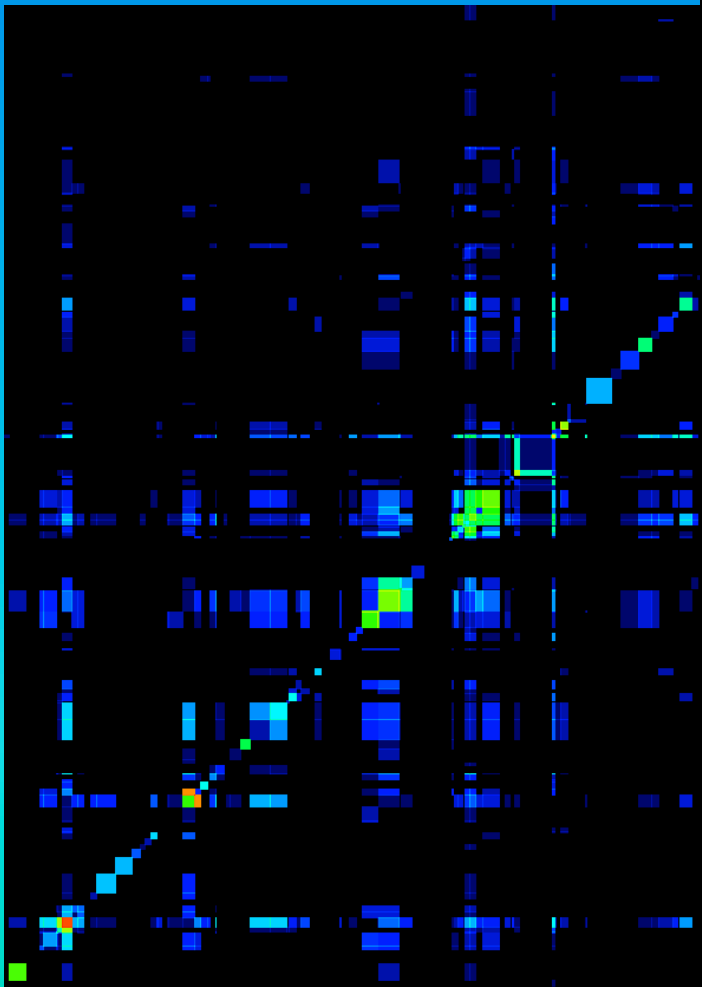


~ 380 kbp

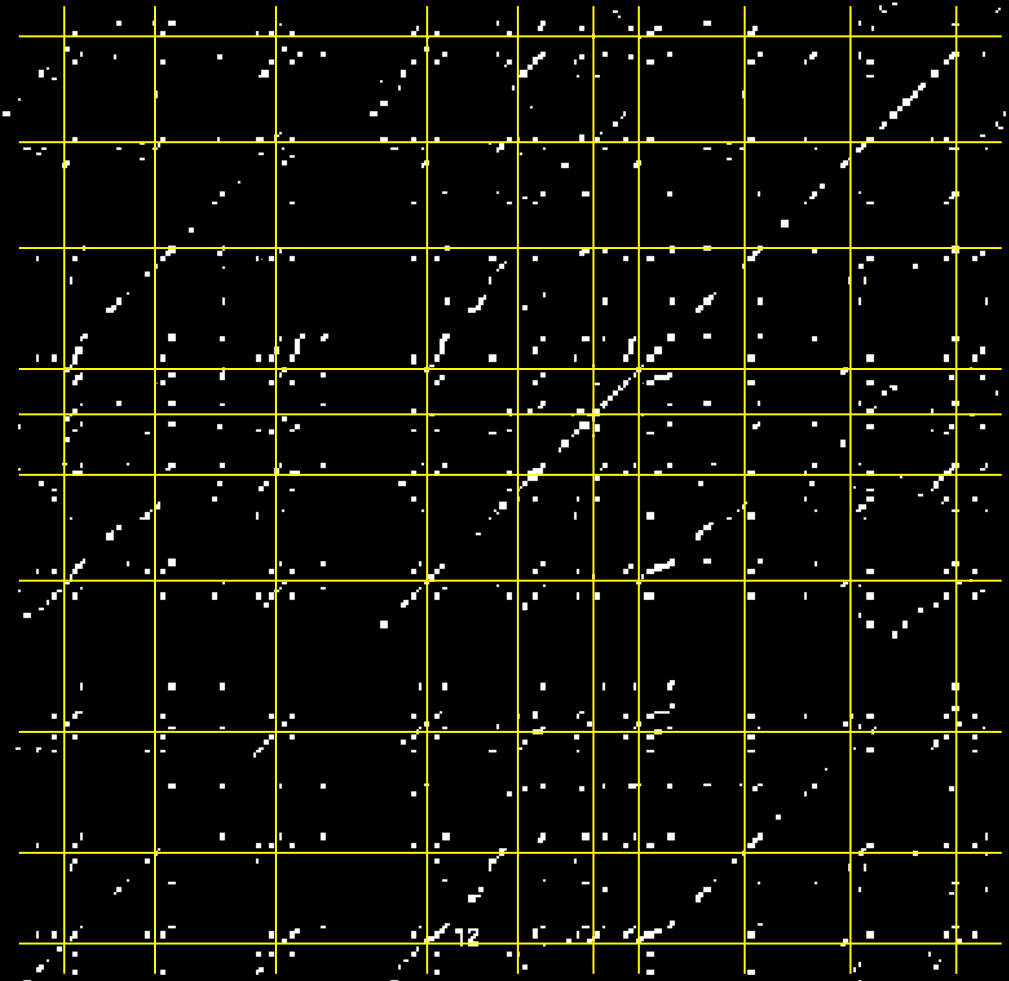


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~ 400 kbp



~ 380 kbp

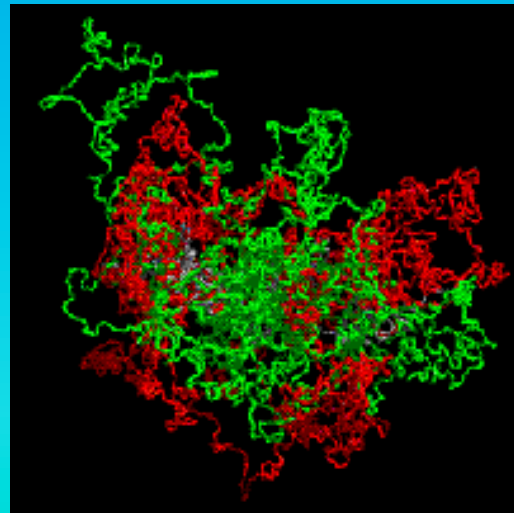
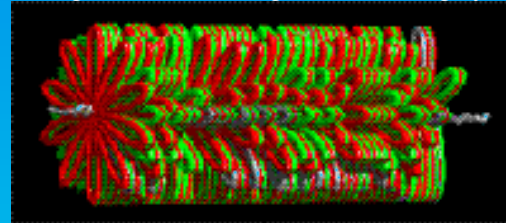
Simulation of Single Chromosomes

The 30 nm chromatin fiber is modeled as a polymer chain with stretching, bending, and excluded volume interactions. Monte Carlo and Brownian Dynamic methods lead to thermodynamical equilibrium configurations.

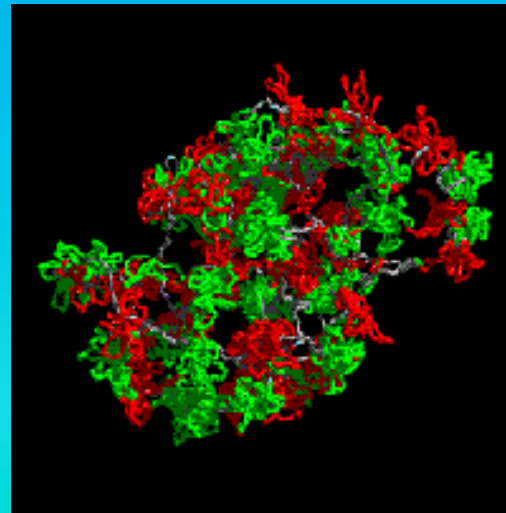
All models form chromosome territories with big voids and different chromatin morphologies. Experimental territory and subcompartment diameters agree best with an MLS model with 80 to 120 kbp loops and linkers.



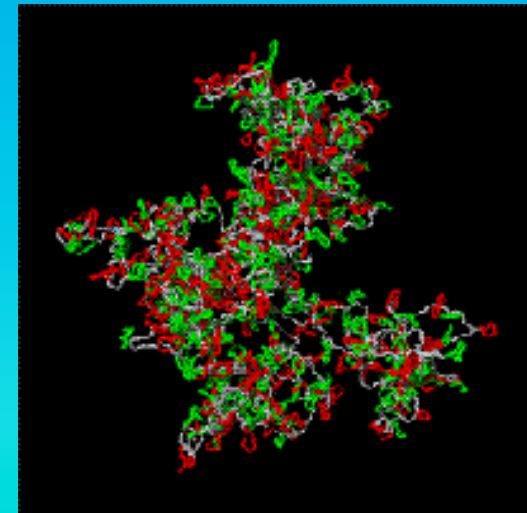
Metaphase starting configuration with ideogram bands in red/green, linker in grey.



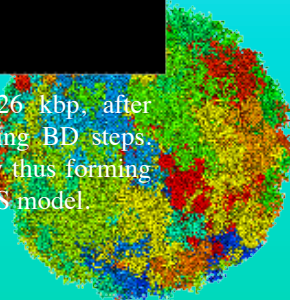
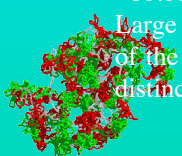
RW/GL model, loop size 5 Mbp, after ~80.000 MC and 1000 relaxing BD steps. Large loops intermingle freely and reach out of the chromosome territory, thus forming no distinct features like in MLS model.



MLS model, loop size 126kbp, linker size 126 kbp, after ~50.000 MC and 1000 relaxing BD steps. Here rosettes form subcompartments as separated organizational and dynamic entities.



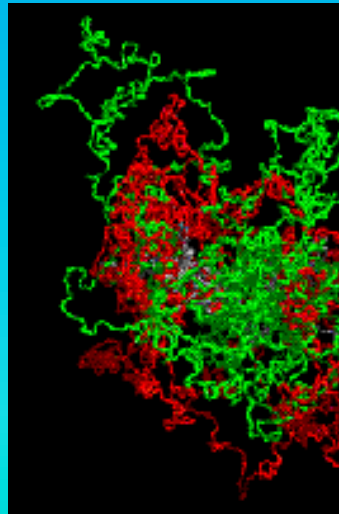
RW/GL model, loop size 126 kbp, after ~80.000 MC and 1000 relaxing BD steps. Large loops intermingle freely thus forming no distinct features like in MLS model.



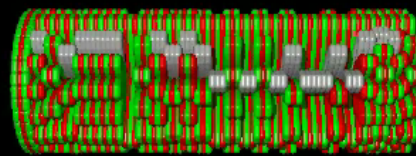
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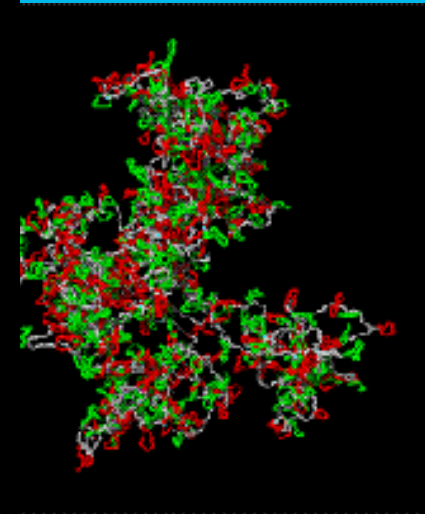
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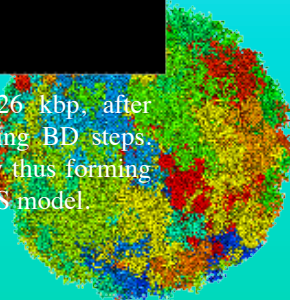
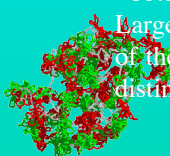
RW/GL model, loop size ~80.000 MC and 1000 relaxing BD steps. Large loops intermingle freely and reach out of the chromosome territory, thus forming no distinct features like in MLS model.



120 kbp, after ~50.000 MC and 1000 relaxing BD steps. Here rosettes form subcompartments as separated organizational and dynamic entities.



model, loop size 126 kbp, after ~80.000 MC and 1000 relaxing BD steps. Large loops intermingle freely thus forming no distinct features like in MLS model.



Bundesministerium für Bildung und Forschung

BBSRC

European Commission

Erasmus MC

BioGrid

University of Oxford

dtkfz

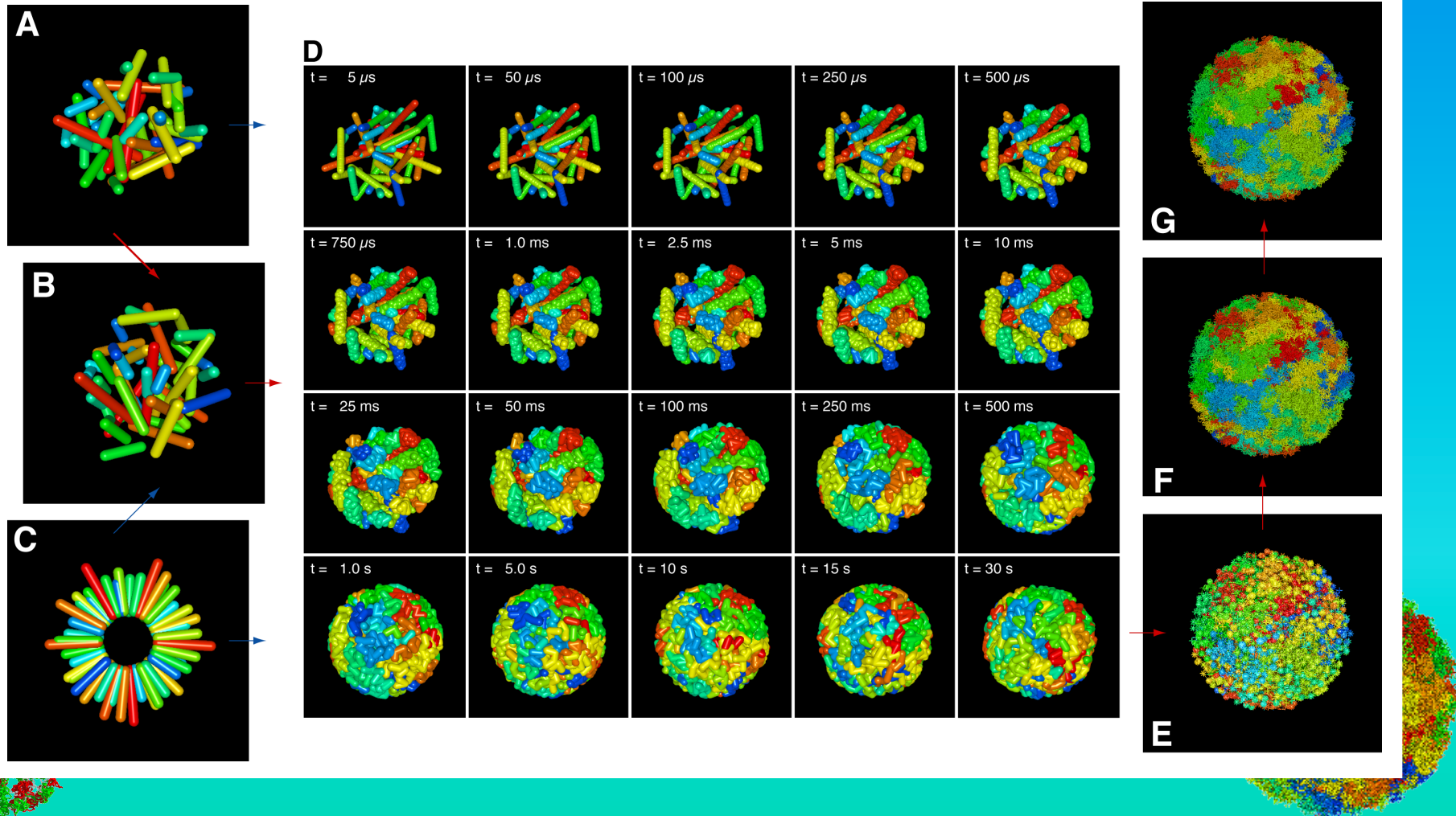
German Research Center for Environmental Health

Leibnizstrahlungsquelle

University of Hamburg

UFR

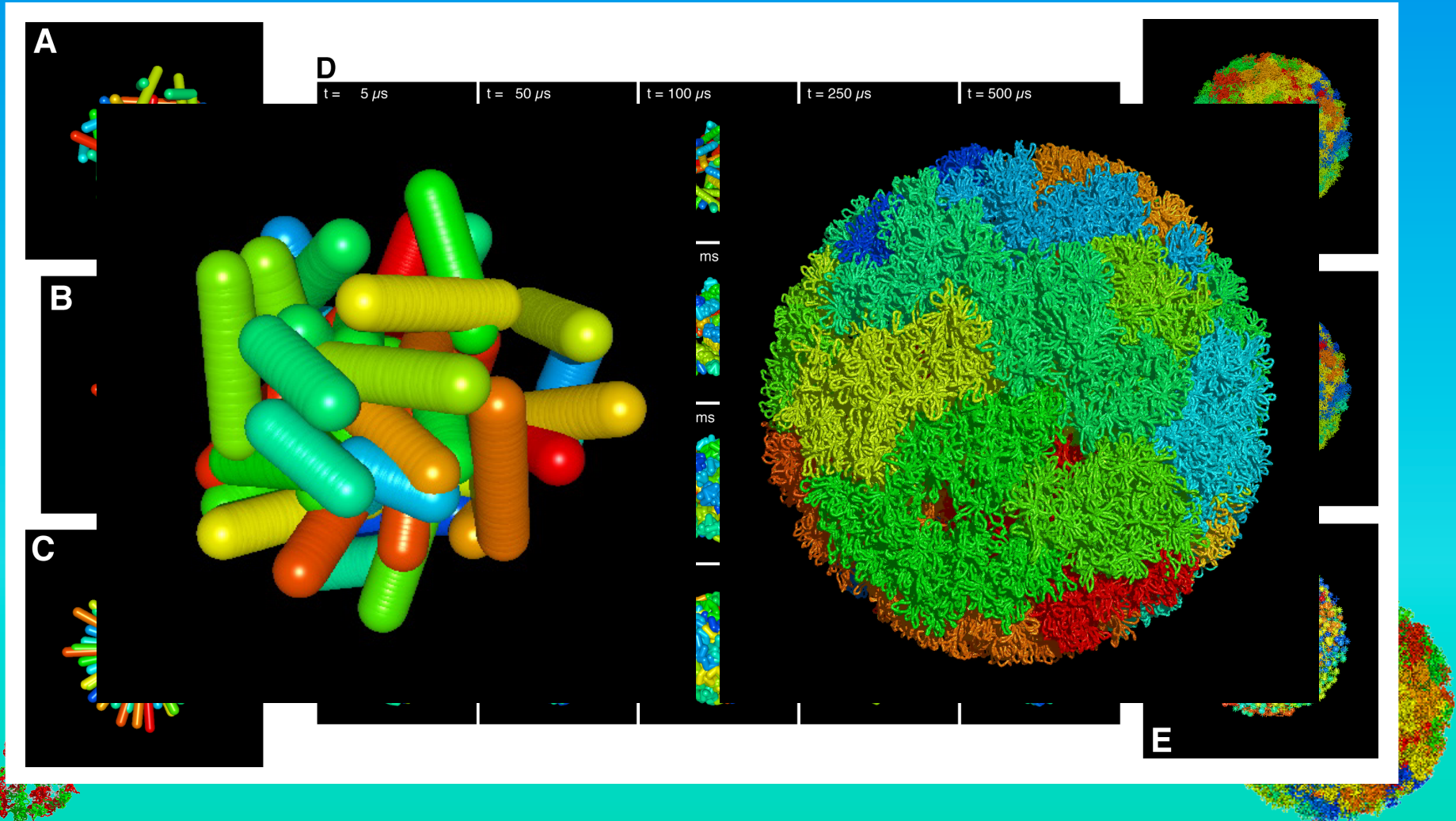
The chromosome territory position depends on their metaphase position and is reasonably stable.



Simulation of Whole Nuclei with all 46 Chromosomes

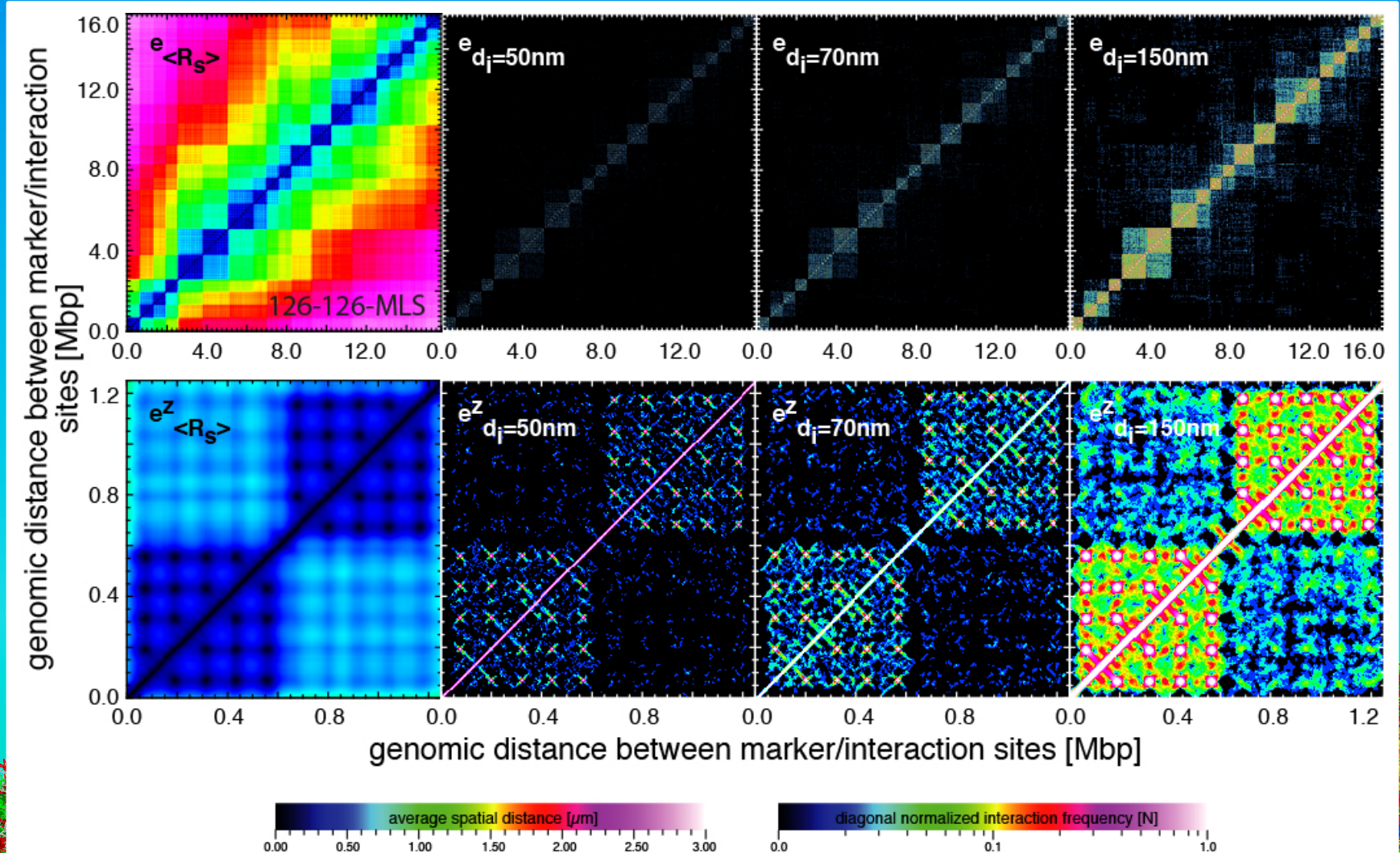
Starting with some metaphase arrangement of cylindrical chromosomes, interphase nuclei with a 30 nm fiber resolution and at thermodynamical equilibrium are created in 4 steps using simulated annealing and Brownian Dynamics methods with stretching, bending, excluded volume and a spherical boundary interactions.

The chromosome territory position depends on their metaphase position and is reasonably stable.



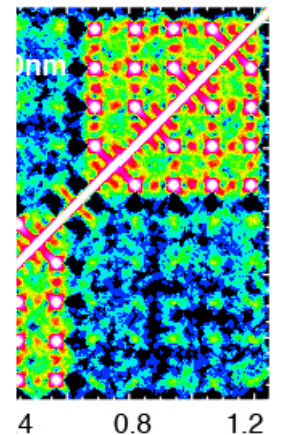
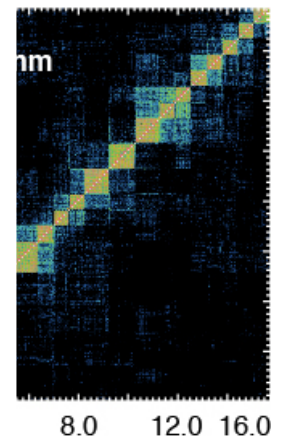
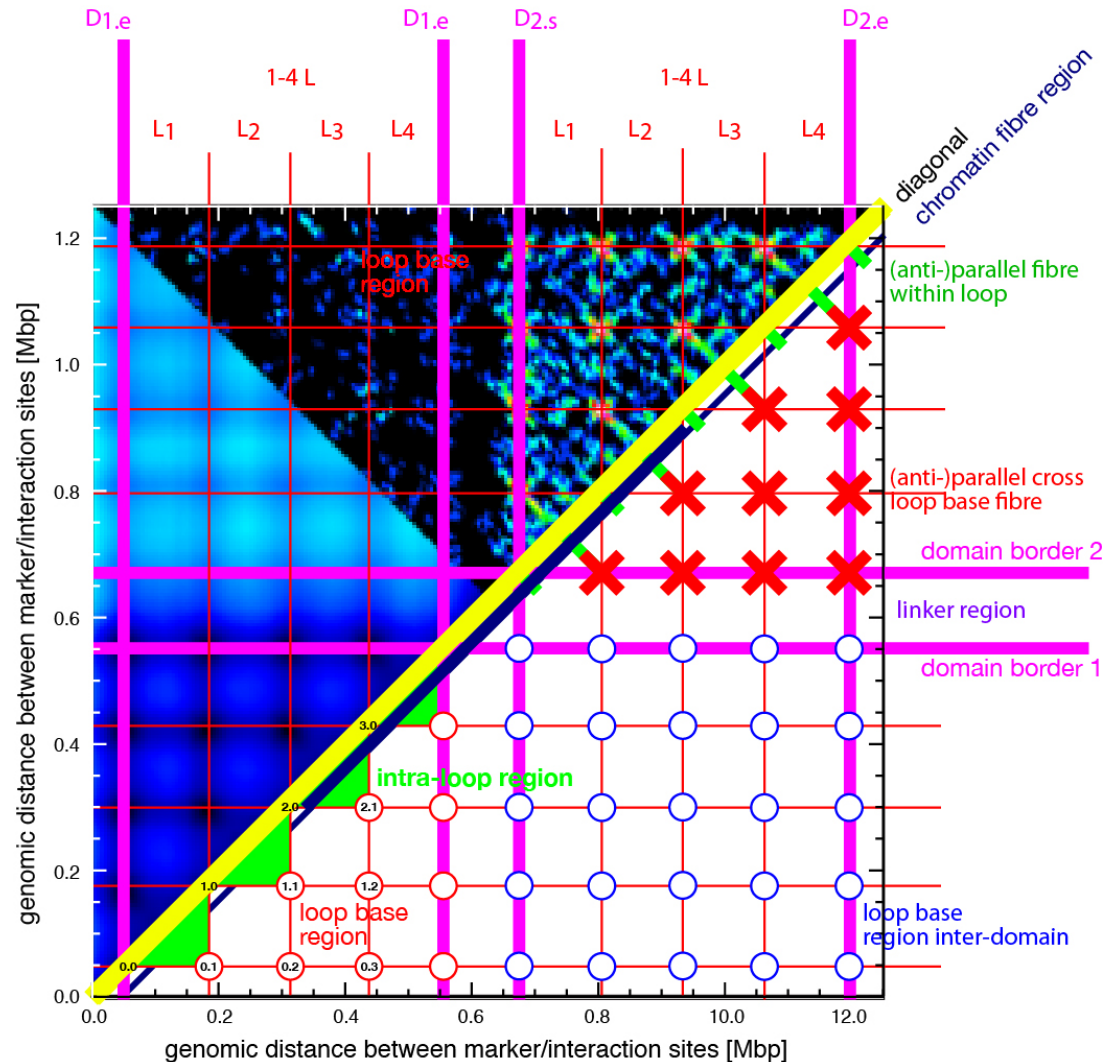
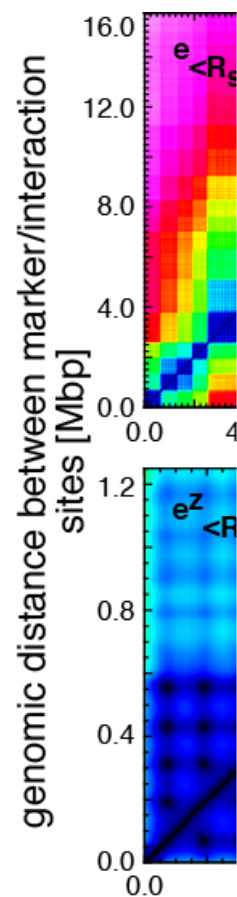
Simulated Interaction Maps

Simulated spatial distance maps as well as simulated interaction maps result in the representation of every parameter variation, and also exhibit the fine-structure describing the loop base as well as rosette core. Thus from the quasi-fibre to the entire chromosome the architecture can be understood in detail.



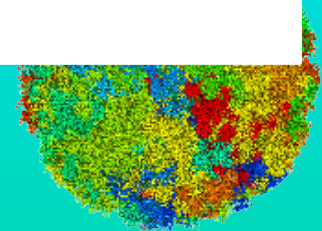
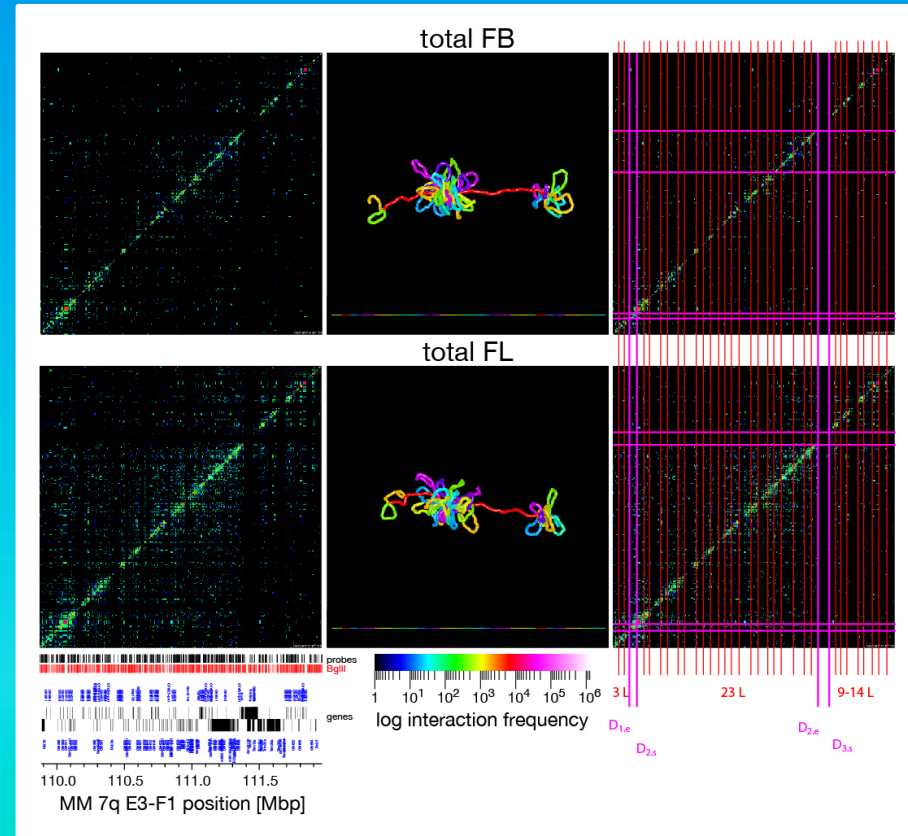
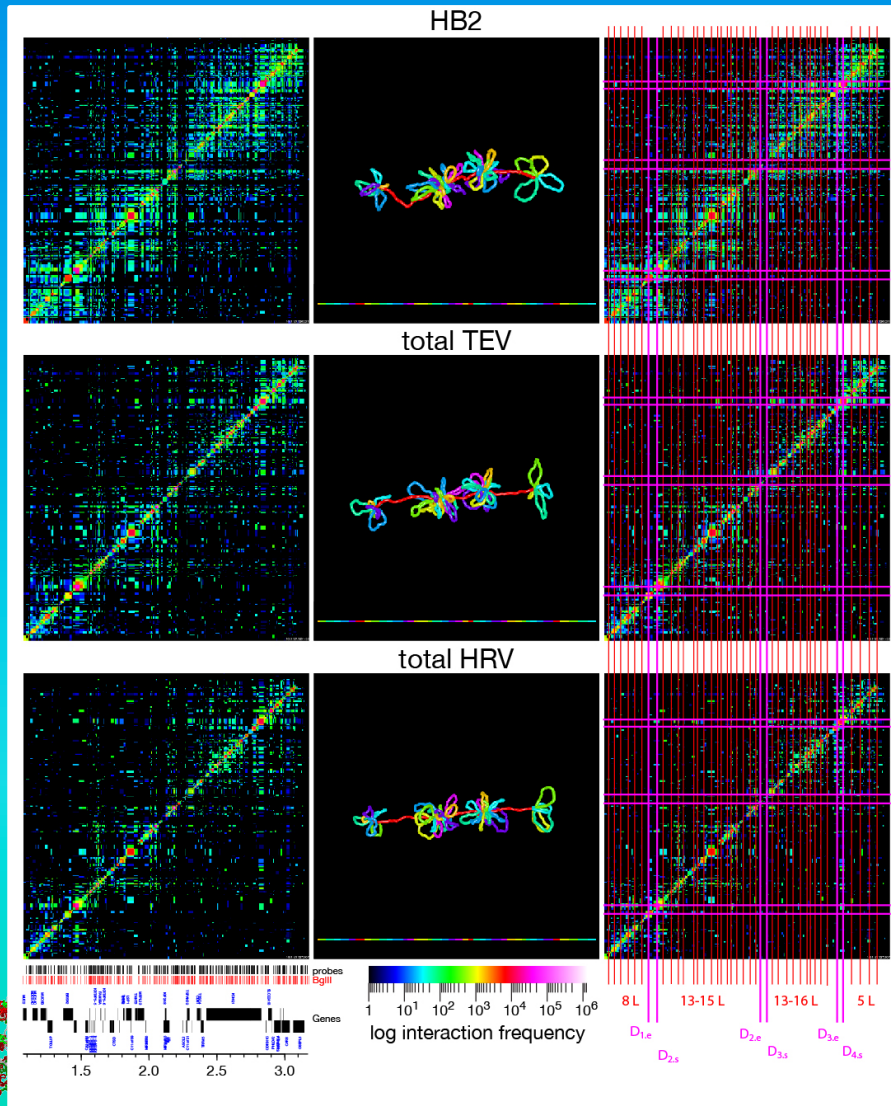
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Variation of a Consensus Architecture Scheme

The difference between different cell types, functional states or even species is minor despite depending on the region. From this, the chromatin fibre conformation, loop position, and their association into loop aggregates/rosettes can be derived, simulated by polymer models and finally visualized.

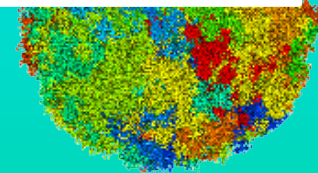
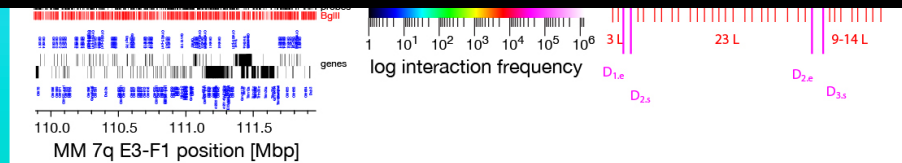
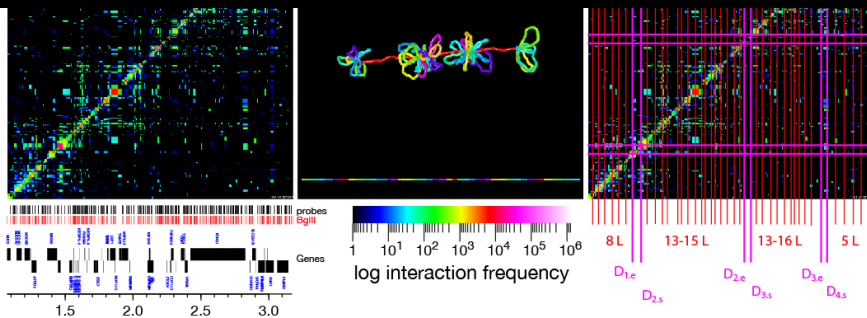


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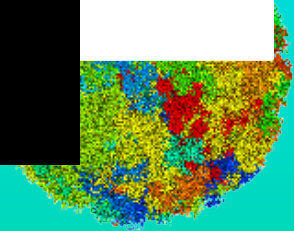
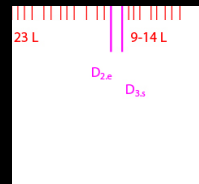
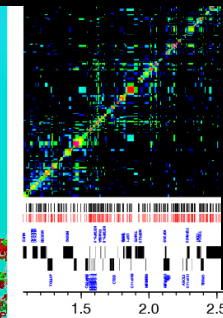


HB2

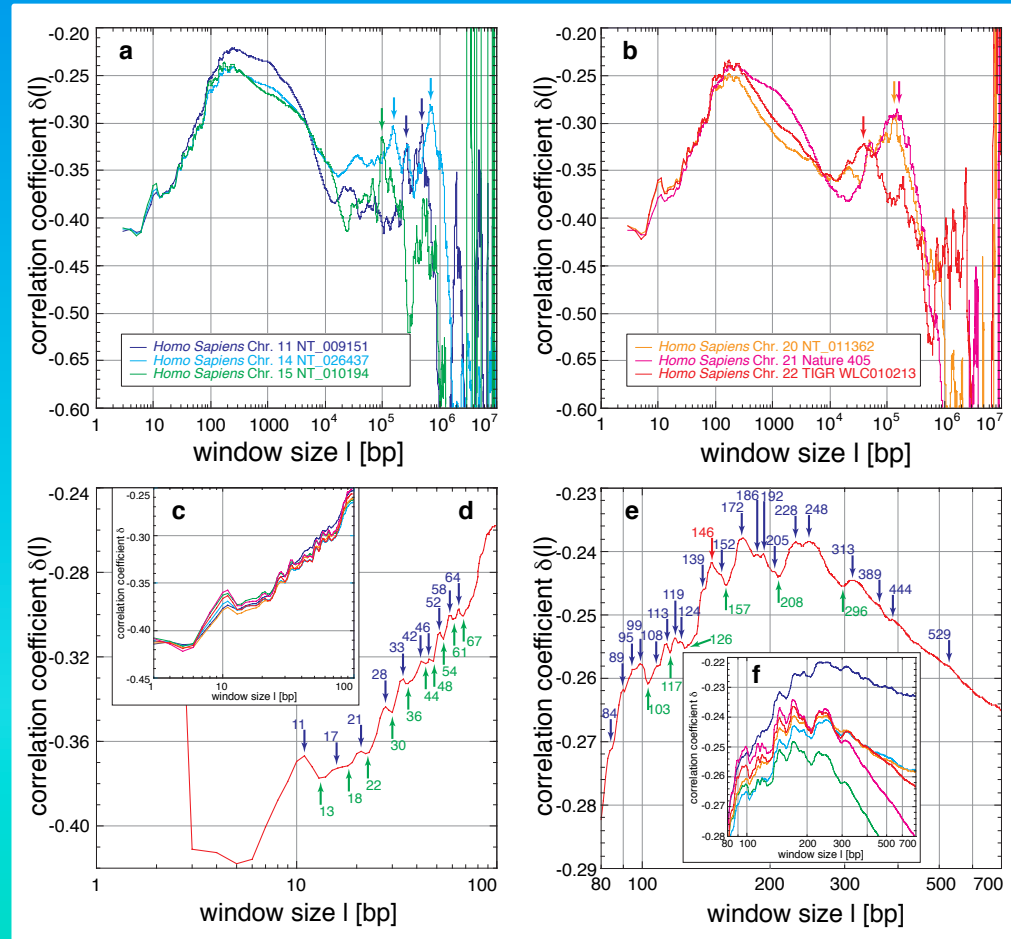
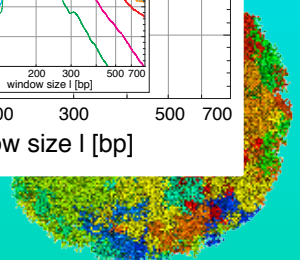


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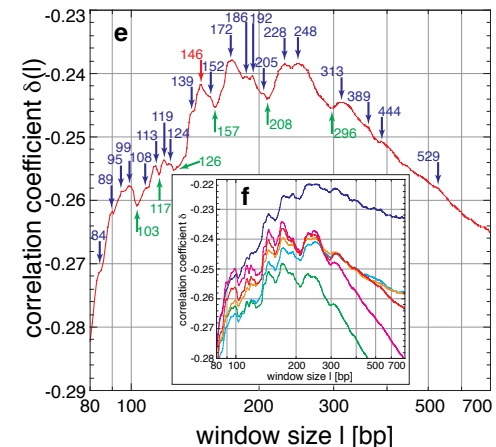
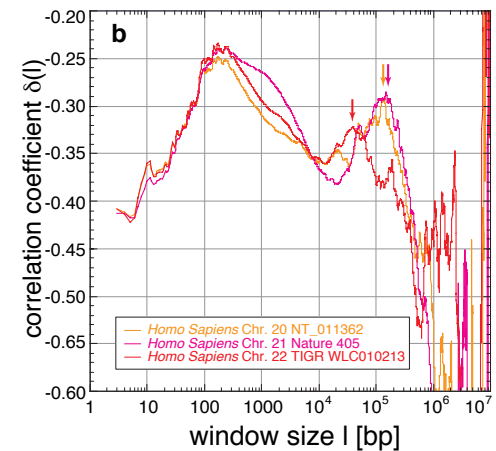
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The image displays a central circular diagram for the EpiGenSys Consortium, surrounded by logos of its member institutions. The central diagram is a circular flow chart with 'EpiGenSys Consortium' at the top and 'Structure - Function' at the bottom. The inner ring lists various sub-systems: Genes, Genomes, Proteins, Metabolites, Cells, Tissues, Organisms, and Environments. The outer ring lists various research areas: Genomics, Transcriptomics, Proteomics, Metabolomics, Cell Biology, Tissue Biology, Organismal Biology, and Environmental Biology. Surrounding the diagram are logos for the German Research Foundation (DFG), European Commission, BBSRC, NWO, Erasmus MC, EpiGenSys, Oxford, dktz, University of Würzburg, and others.



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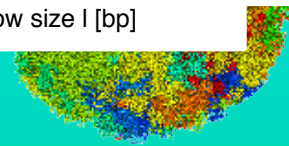
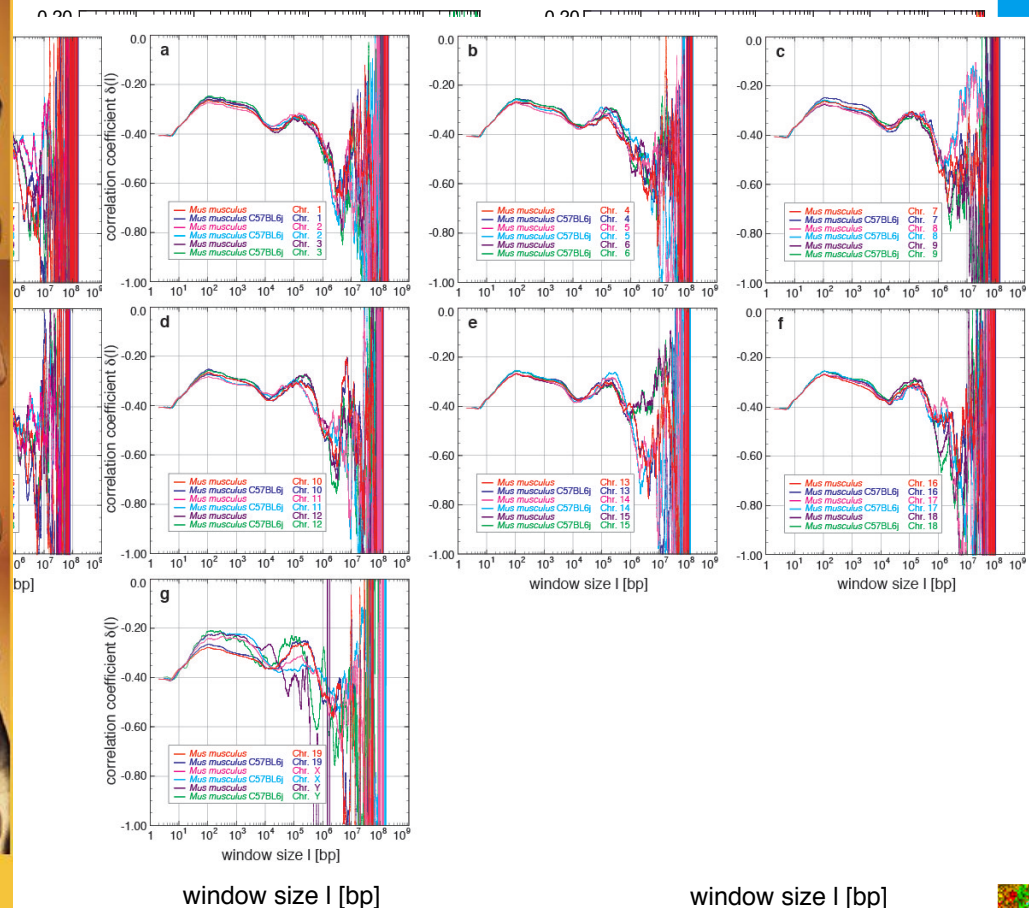


DNA Sequence Organization

Determination of the concentration fluctuation function $C(l)$ and its local slope the correlation coefficient $\delta(l)$ are an indication for the i) degree of long-rang scaling behaviour, ii) general multi-scaling, and iii) fine-structure features, which all are connected to all levels of genome organization and especially also the three-dimensional genome architecture.

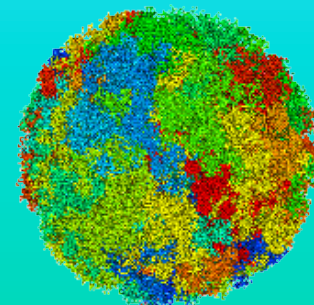
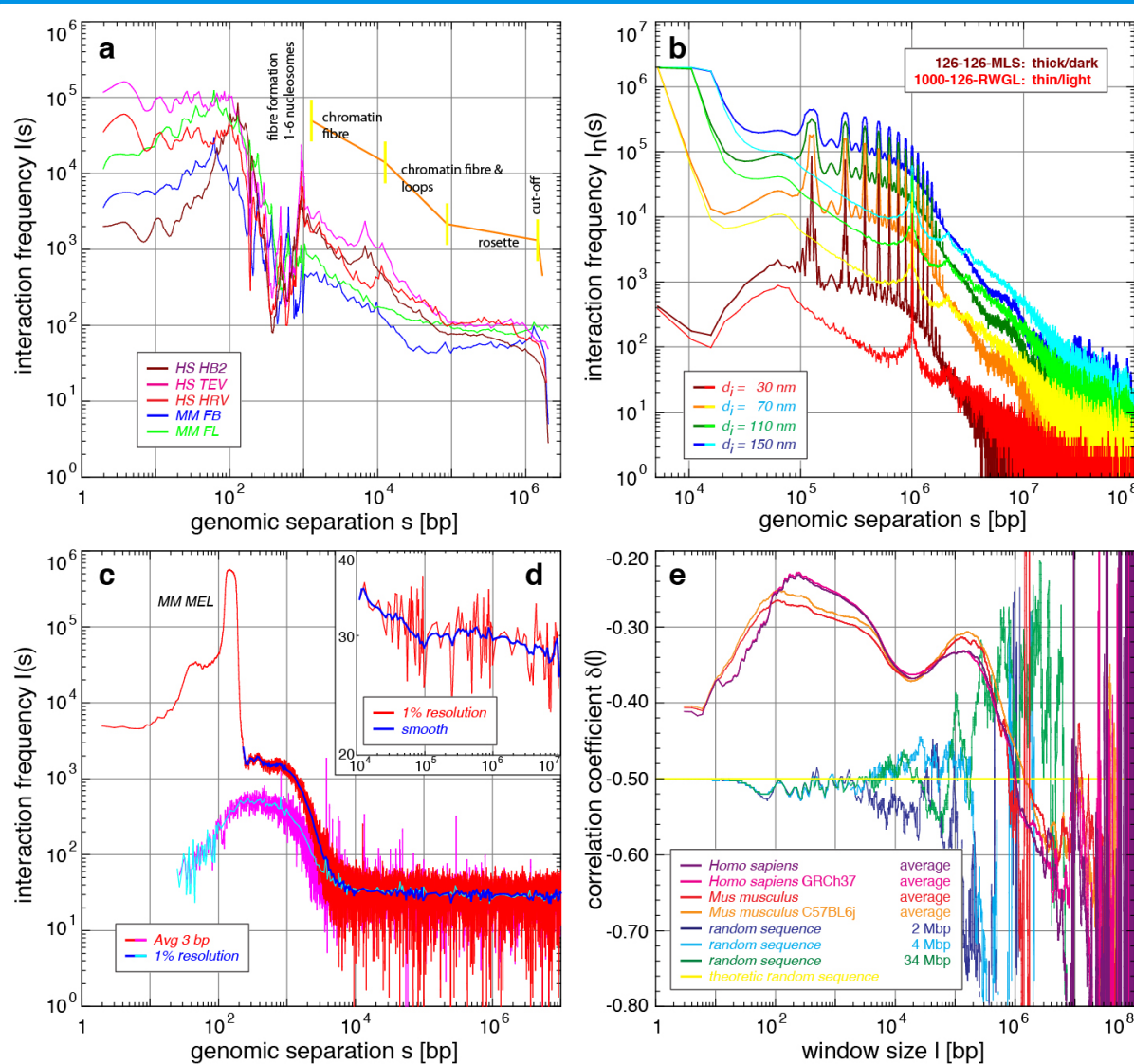


FunFire.de



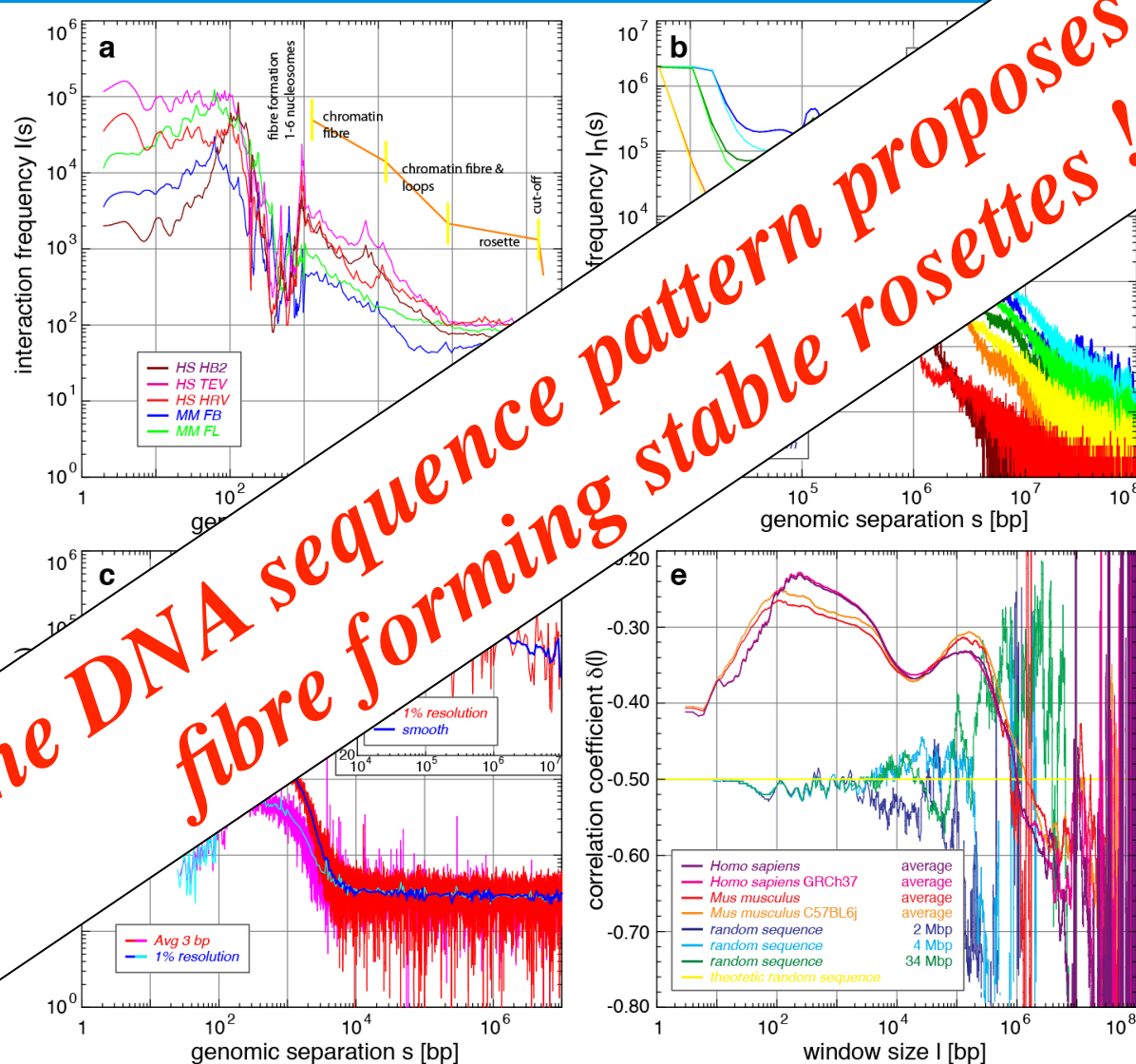
Scaling Analysis

Scaling analysis show again the entire bandwidth of architectural effects in an aggregated manner. Beyond, they show the scale bridging of the structures and the evolutionary holistic entanglement between the 3D architecture and the DNA sequence organization itself.

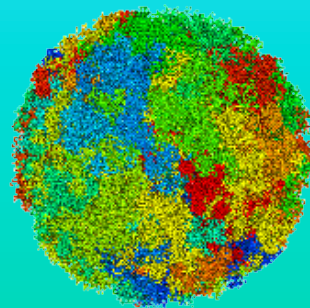


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Also the DNA sequence pattern proposes a quasi-fibre forming stable rosettes !

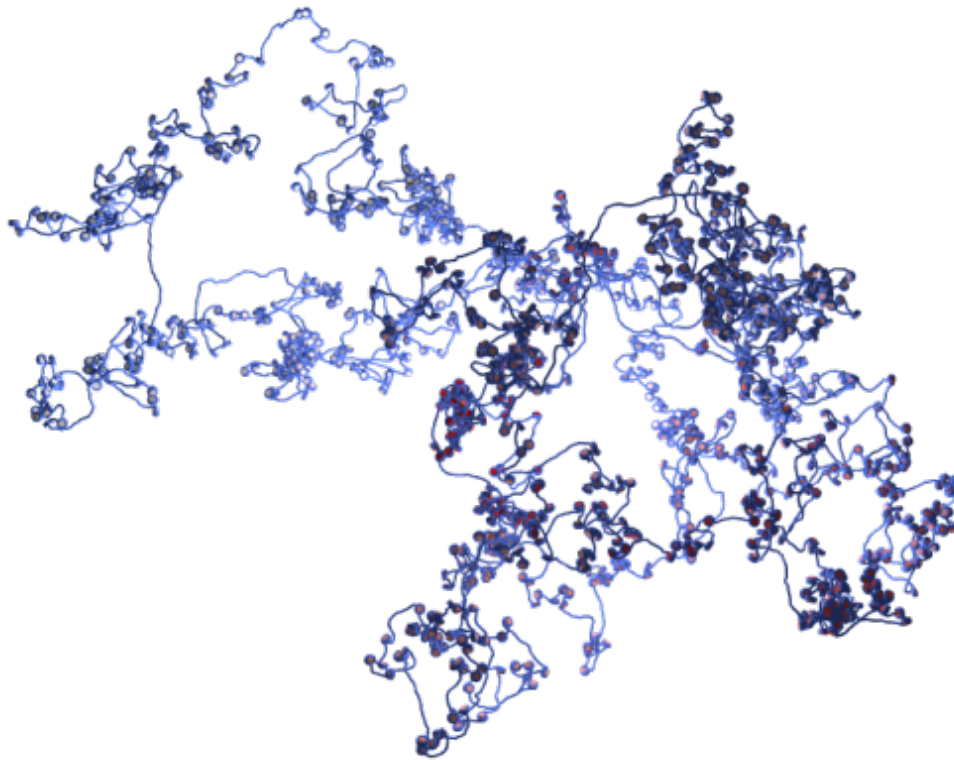


Simulation of Chromatin Quasi-Fibres

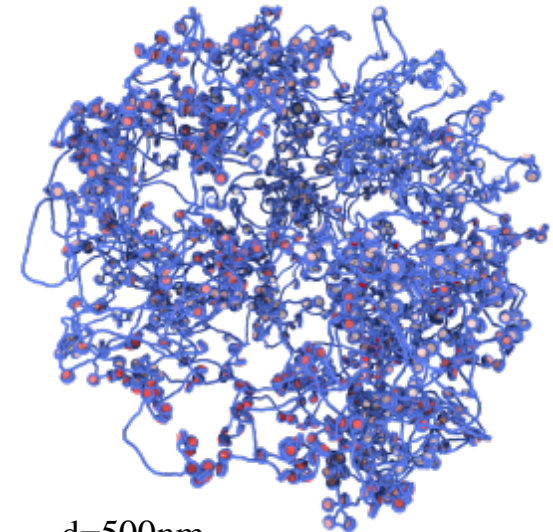
The position of nucleosomes influence greatly the structure of chromatin fibers done on super-computers. Here a dedicated workflow is applied, with which overlapping nucleosome populations can be analyzed and the best positioning of nucleosomes by Monte Carlo simulated annealing can be achieved. For an actual locus in a spherical confinement then a 3D independent nucleosome fiber conformation can be simulated.



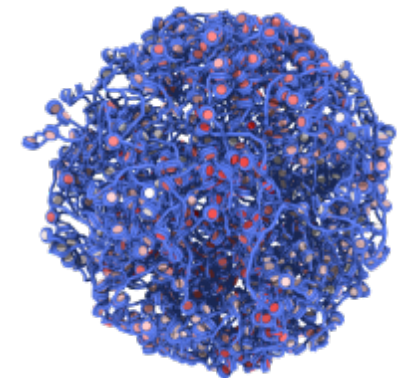
Monte Carlo Simulation of SAMD4A Mouse ES Cells



d=1000nm



d=500nm



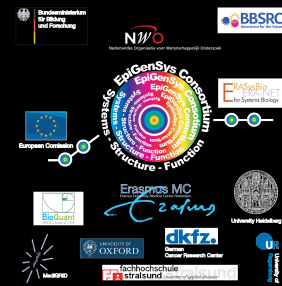
d=200nm



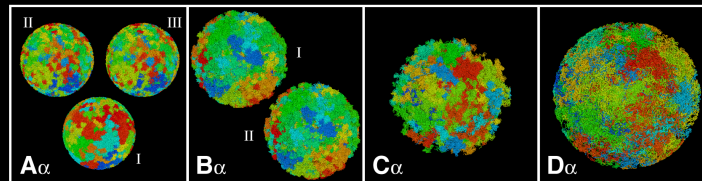
From Fiber Topology to Nuclear Morphology

Chromosome territories form in the RW/GL and the MLS model. However, only the MLS model leads distinct subcompartments and low chromosome and subcompartment overlap. Best agreement is reached for an MLS model with 80 to 120 kbp loops and linkers in nuclei with 8 to 10 μm diameter.

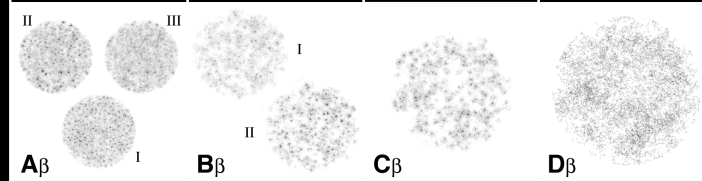
The simulated nuclear morphology reflects the chromosome fiber topology of different models in detail.



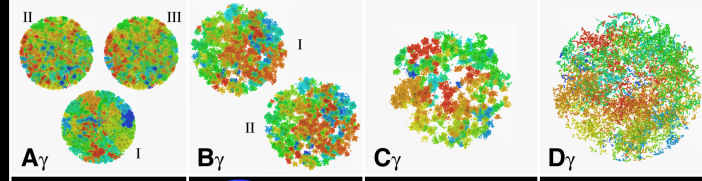
rendering



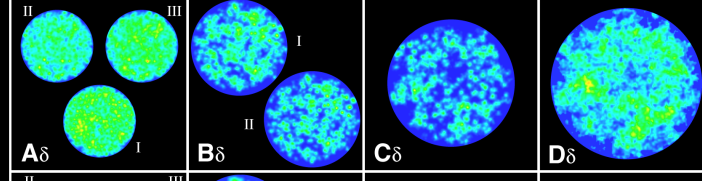
electron microscopy



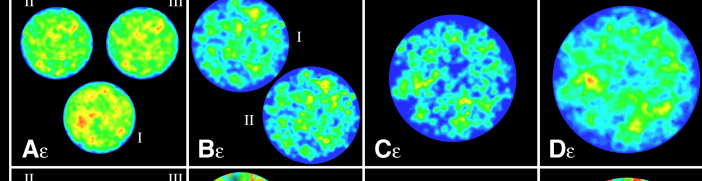
electron microscopy territory painting



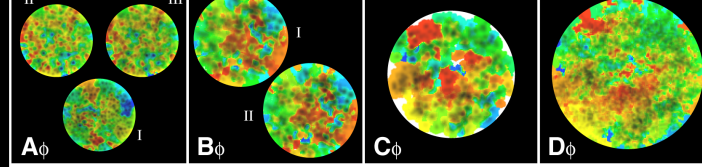
confocal microscopy
100x objective, theoretic resolution



confocal microscopy
63x objective, real resolution



confocal microscopy
territory painting

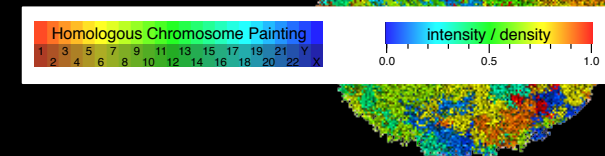
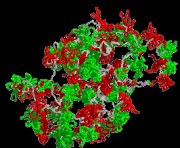


A: MLS in 6 μm nucleus
I: 63 kbp loops, 63 kbp linkers
II: 63 kbp loops, 252 kbp linkers
III: 126 kbp loops, 252 kbp linkers

B: MLS in 8 μm nucleus
I: 126 kbp loops, 126 kbp linkers
II: 84 kbp loops, 126 kbp linkers

C: MLS in 10 μm nucleus
126 kbp loops, 126 kbp linker,
not totally relaxed

D: RW/GL in 12 μm nucleus
5 Mbp loops
not totally relaxed



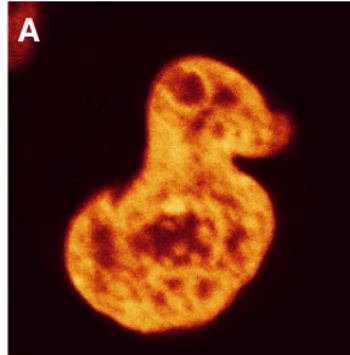
In vivo Morphology & Chromatin Distribution

The stable expression of fusions between histones and autofluorescent proteins and the integration into nucleosomes allows the minimal invasive investigation of the structure and dynamics of chromatin.

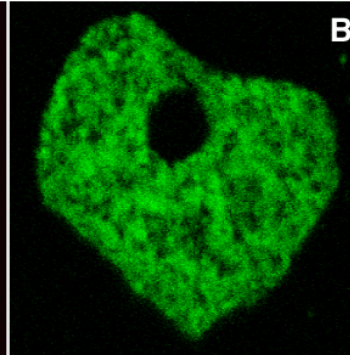
The clustered morphology in detail favour an MLS like chromatin topology.



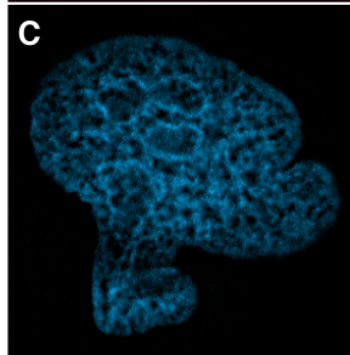
HeLa, H2A-YFP



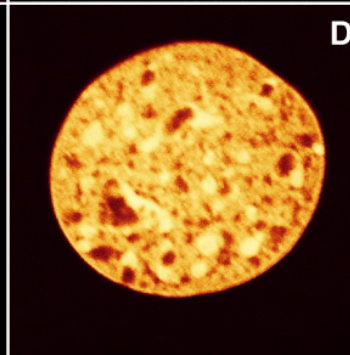
Cos7, H1.0-GFP



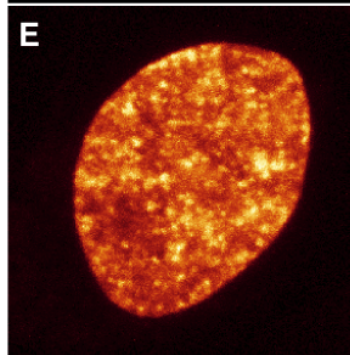
LCLC 103H, H2A-CFP



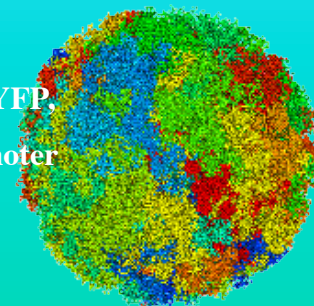
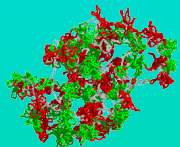
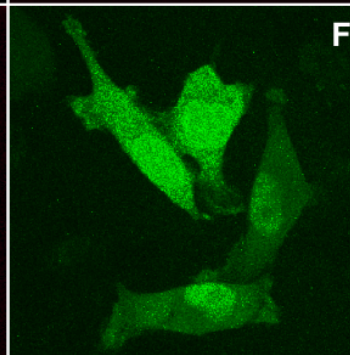
ID13, H2A-YFP



HeLa, mH2A1.2-YFP

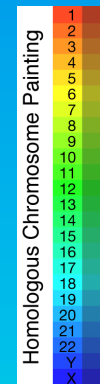
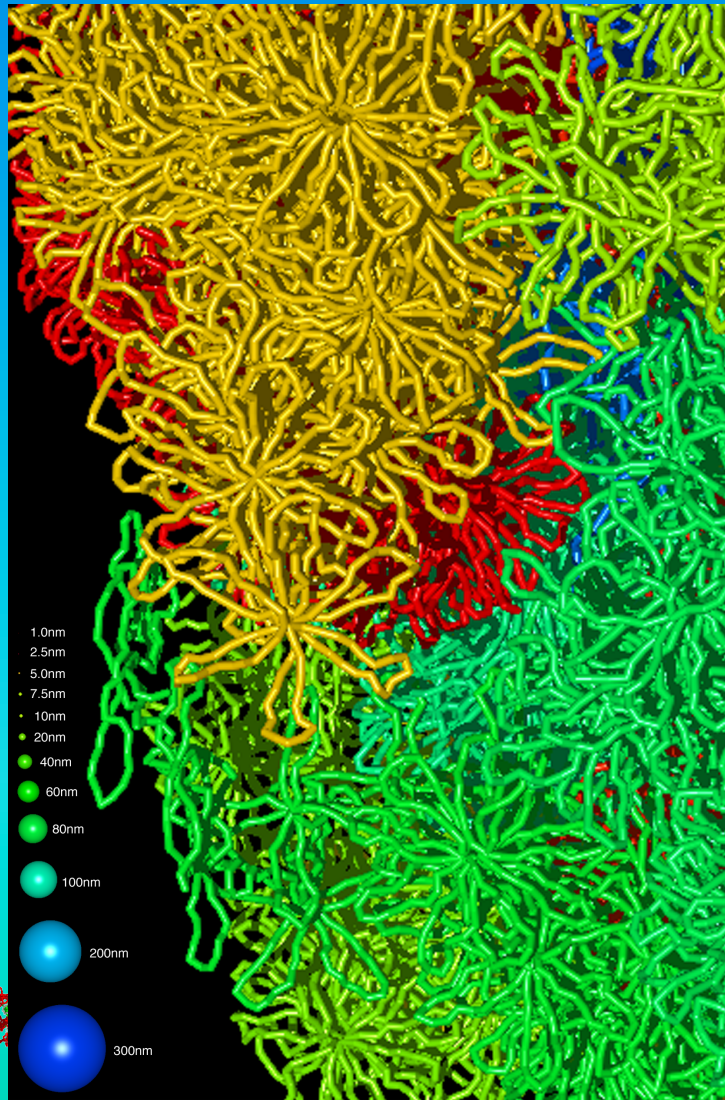


HeLa, H2A-YFP,
natural promoter

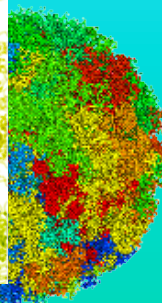
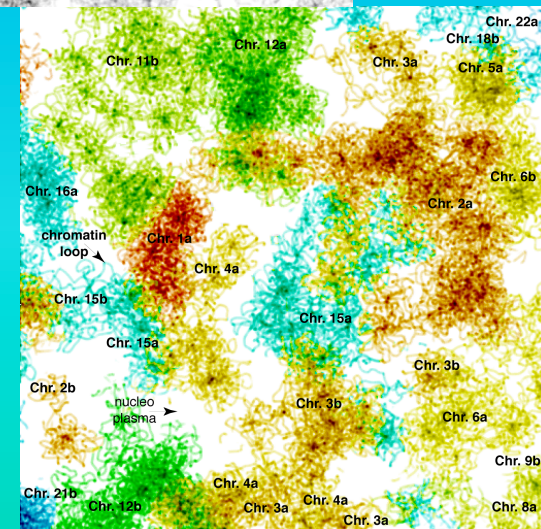


Fine Morphology of Nuclei

High resolution rendering and simulated electron microscopy including territory painting reveal not only again the model details but also that any location in the nucleus is accessible to biological molecules <15 nm in diameter and that even the Extended Interchromosomal Domain hypothesis is oversimplified.

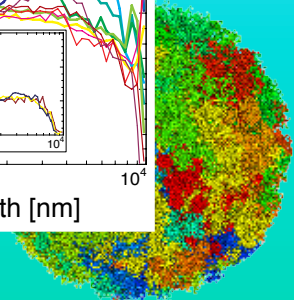
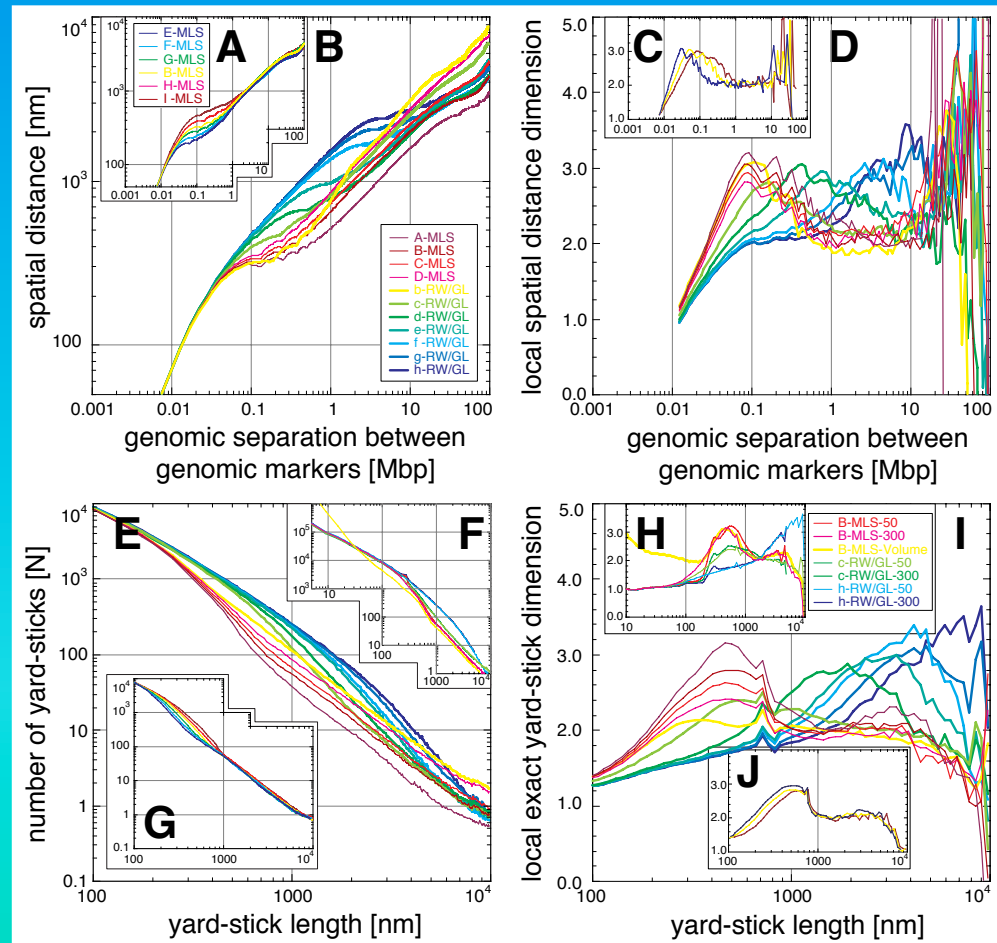
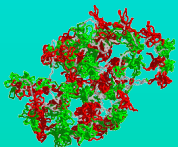
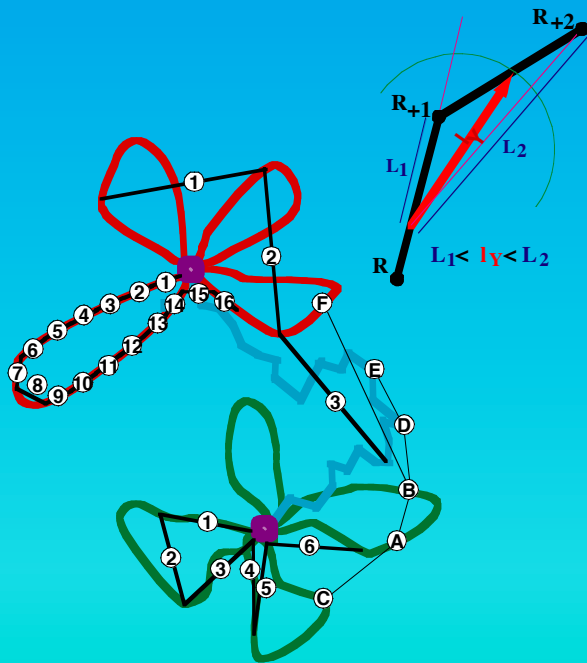


MLS models model with 126 kbp loops and linkers in a 10 μ m nucleus.



Scaling of the Chromatin Fiber Topology

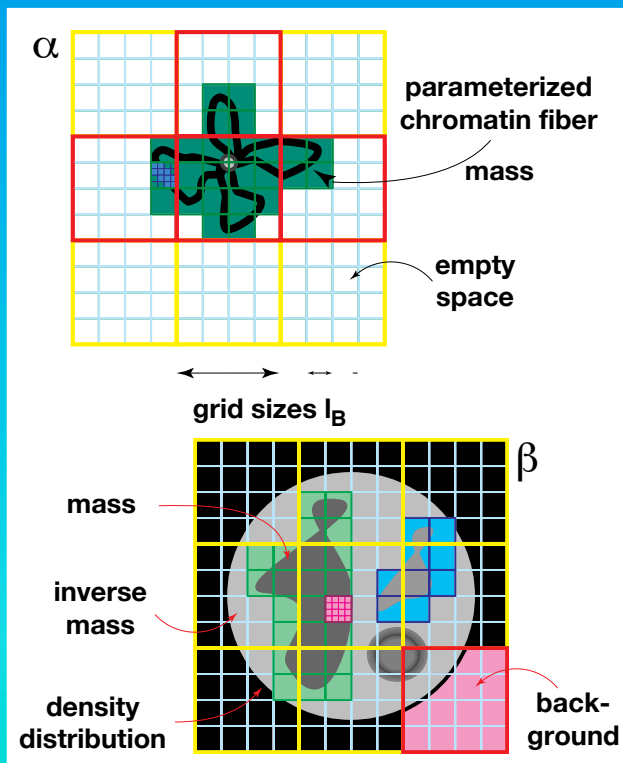
The spatial-distance and exact yard-stick dimension distinguish between the simulated models in detail. The MLS model shows a globular and fine-structured multi scaling behaviour due to the loops forming rosettes. This agrees with DNA fragmentation by Carbon ion irradiation and the appearance of fine-structured multi-scaling long-range correlations found in the sequential organization of genomes.



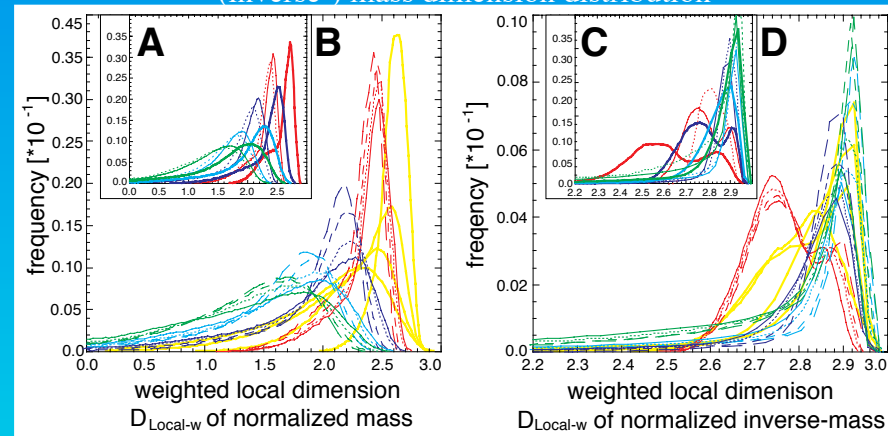
Scaling of the Chromatin Morphology & Distribution

The local (inverse-) mass dimension distribution distinguishes between the models in detail and show also a multi-scaling behaviour with globular feature for the MLS model like the scaling of the fiber topology. With the mass dimension as function of intensity separates very well between different nuclei *in vivo*.

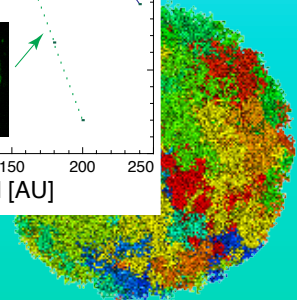
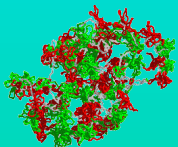
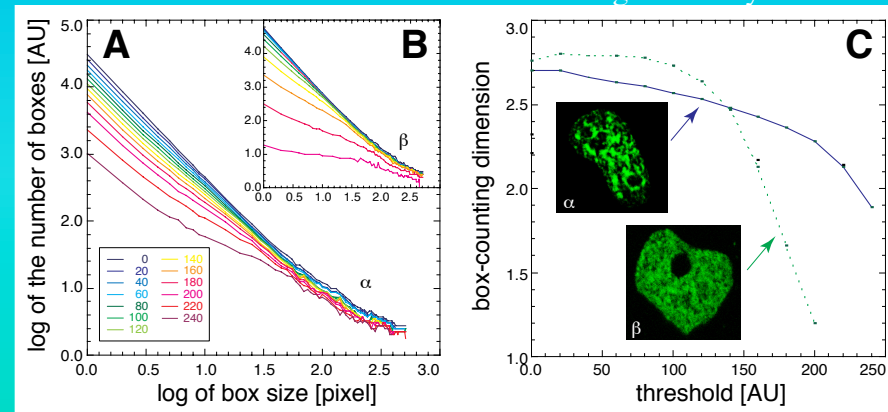
Consequently, the chromatin morphology is causally and quantitatively connected to the fiber topology.



(inverse-) mass dimension distribution

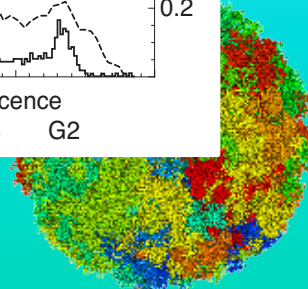
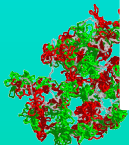
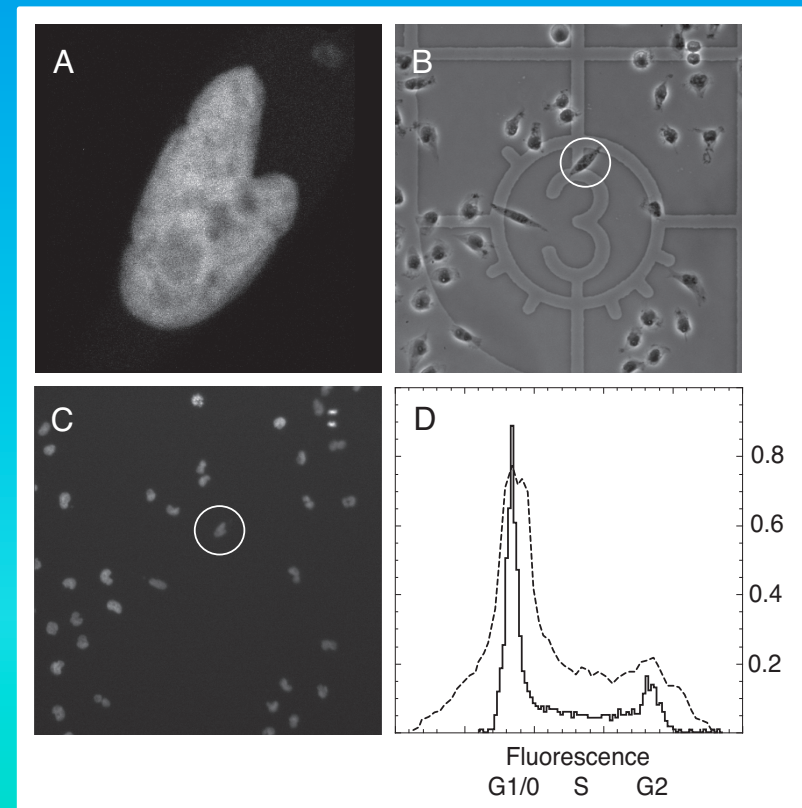
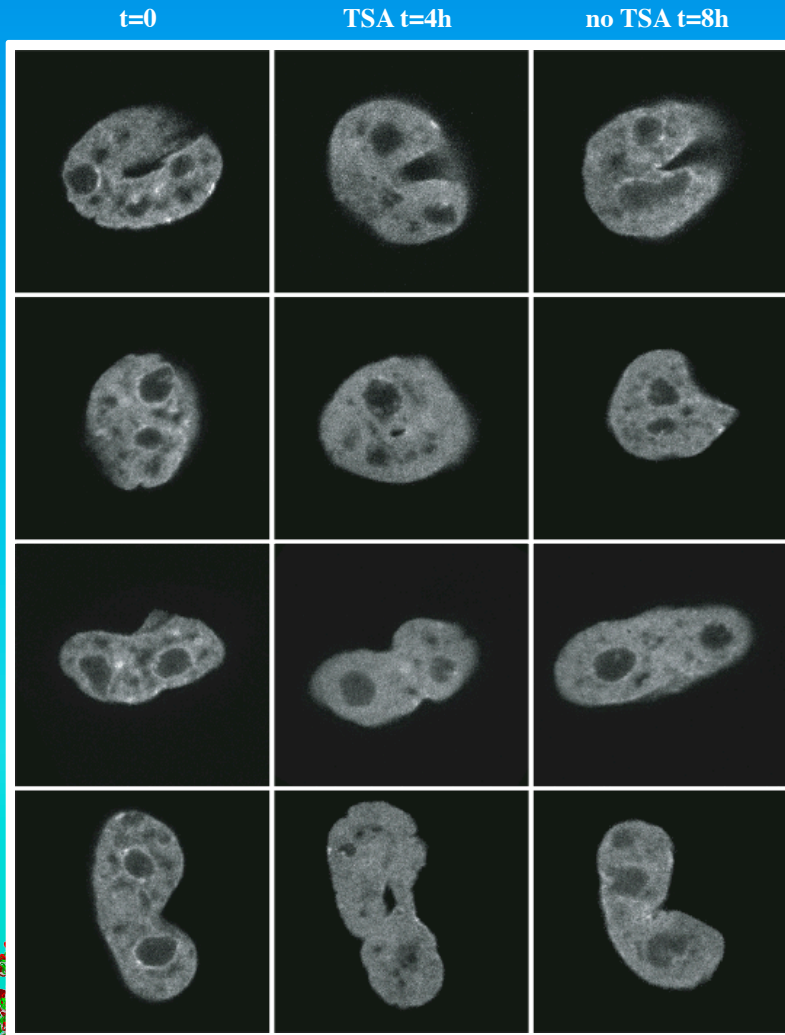


mass dimension as function of image intensity



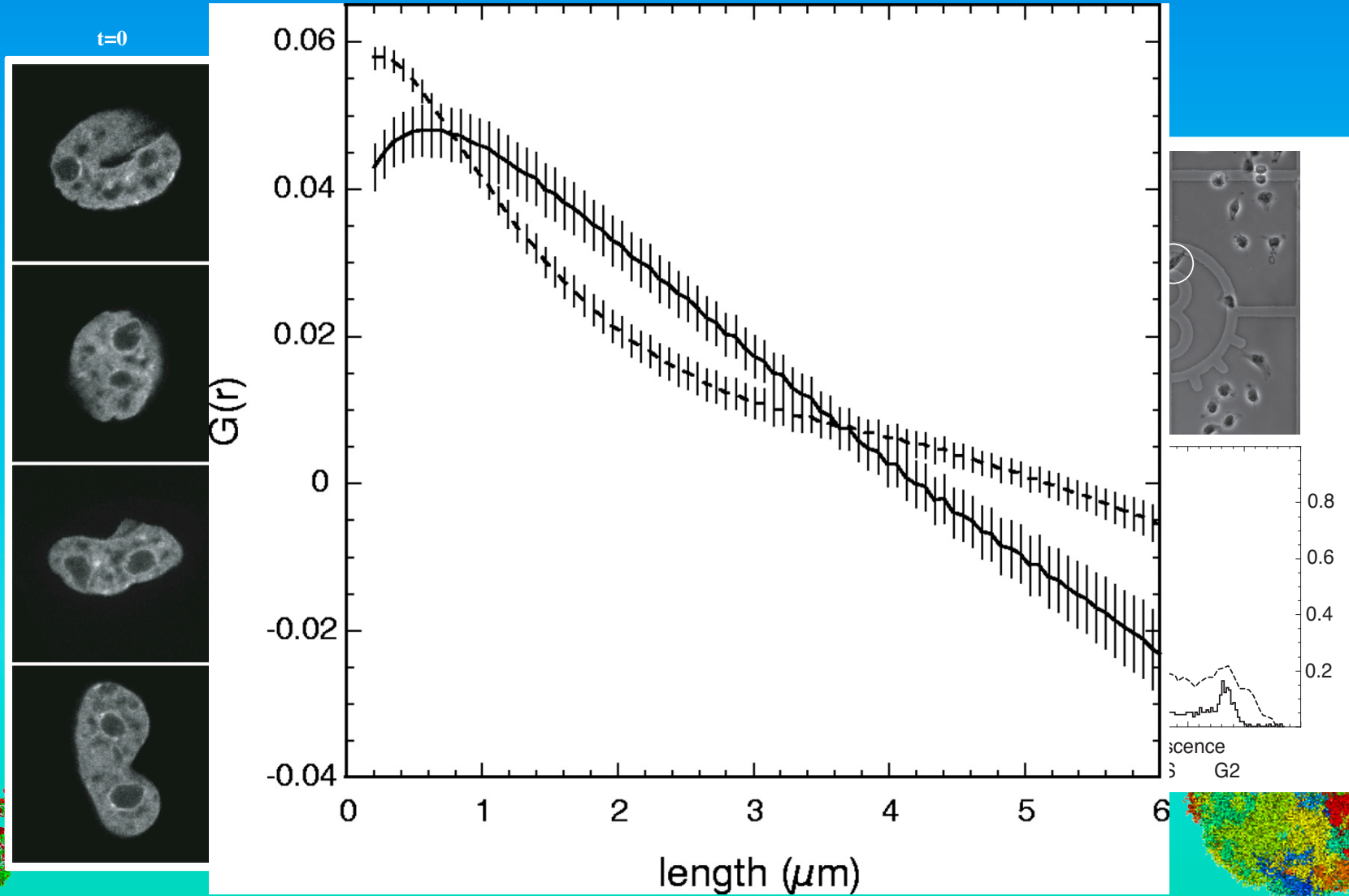
Quantified TSA induced Morphology Changes

Trichostatin A induced histone acetylation can be quantified by *in vivo* H2A-GFP confocal images and image correlation spectroscopy (iFCS), which is a scaling analysis, and reveals the opening of chromatin, and thus reorganization changes on scales from 0.2 to $\sim 1\mu\text{m}$, consistent with MLS models.



Quantified TSA induced Morphology Changes

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Diffusion of Particles in the Nucleus

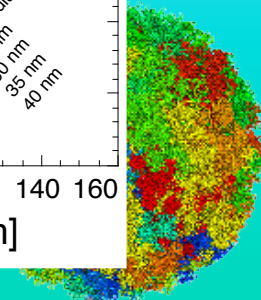
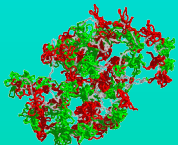
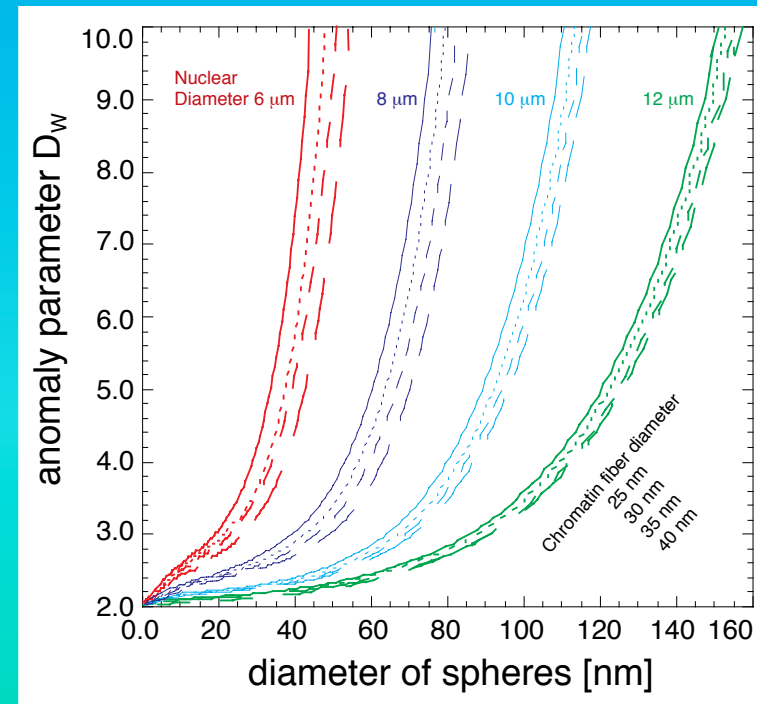
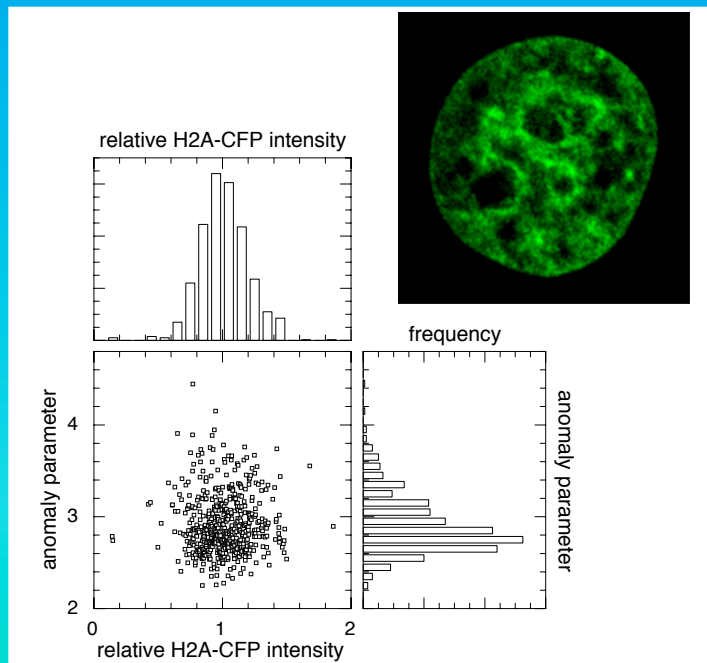
Due to the volume and spatial relationships in the nucleus typical particles reach almost any location in the nucleus by moderately obstructed diffusion: a 10 nm particle moves 1 to 2 μm within 10 ms.

The structural influence on the obstruction degree is random for Alexa 568 as function of the chromatin distribution visualized by H2A CFP in vivo and measured by fluorescence correlation spectroscopy (FCS)



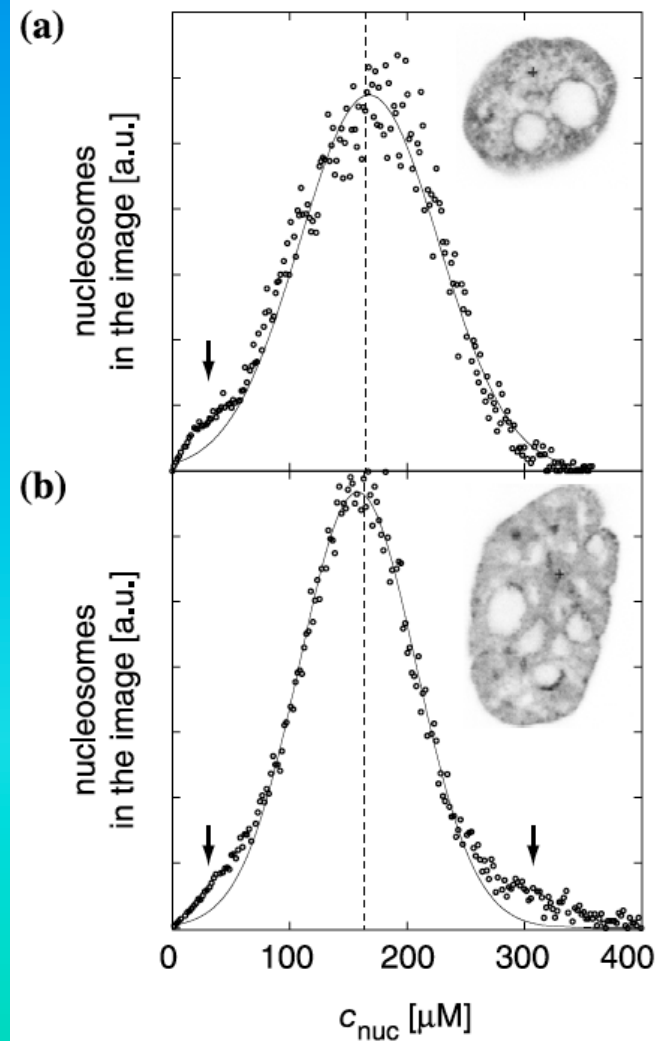
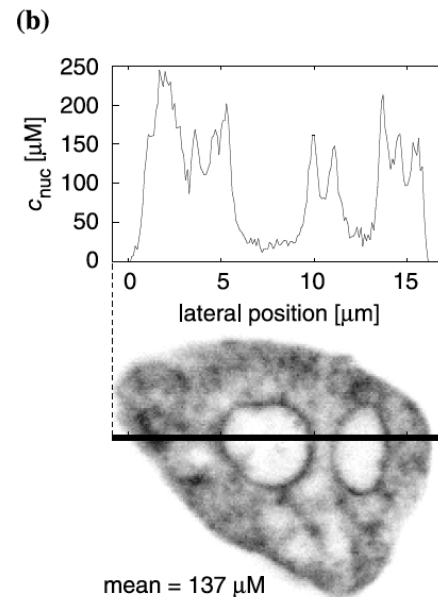
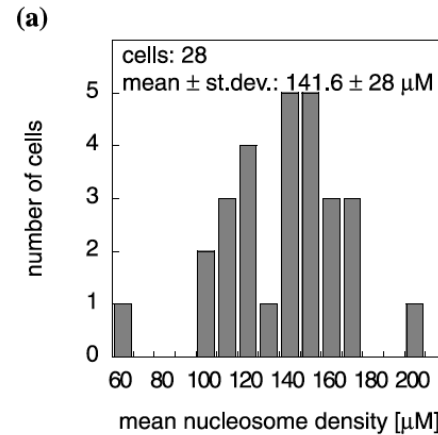
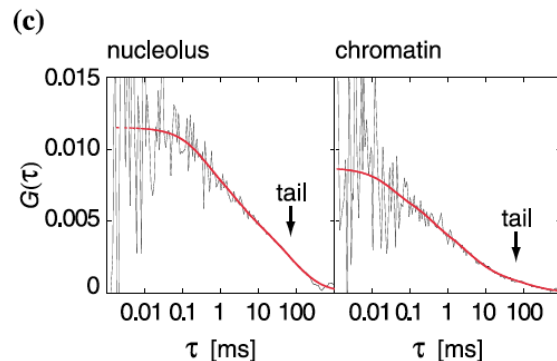
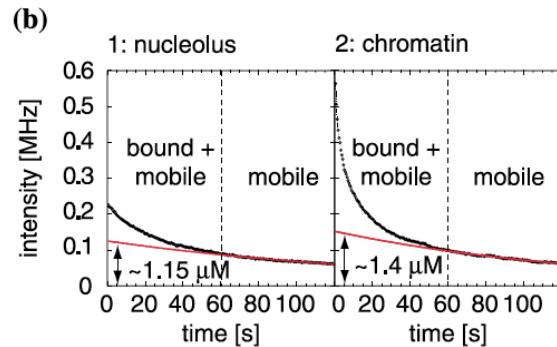
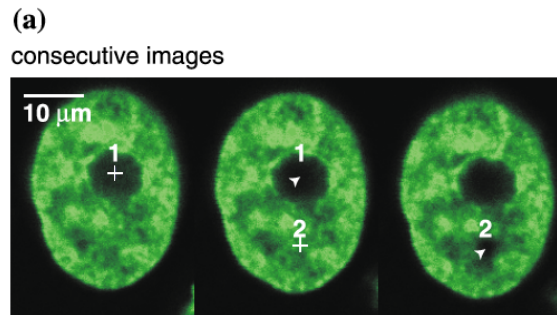
$$\langle r^2 \rangle \propto t^{2/D_w}$$

Nuclear diameter [μm]	Nuclear Volume [μm^3]	Mean Nucleosome Concentration [μM]	Chromatin Volume Fraction [%]	Mean Isotropic Mesh Spacing [nm]
6	115	251	20.1	41
8	268	107	8.6	64
10	523	55	4.4	90
12	904	32	2.6	117



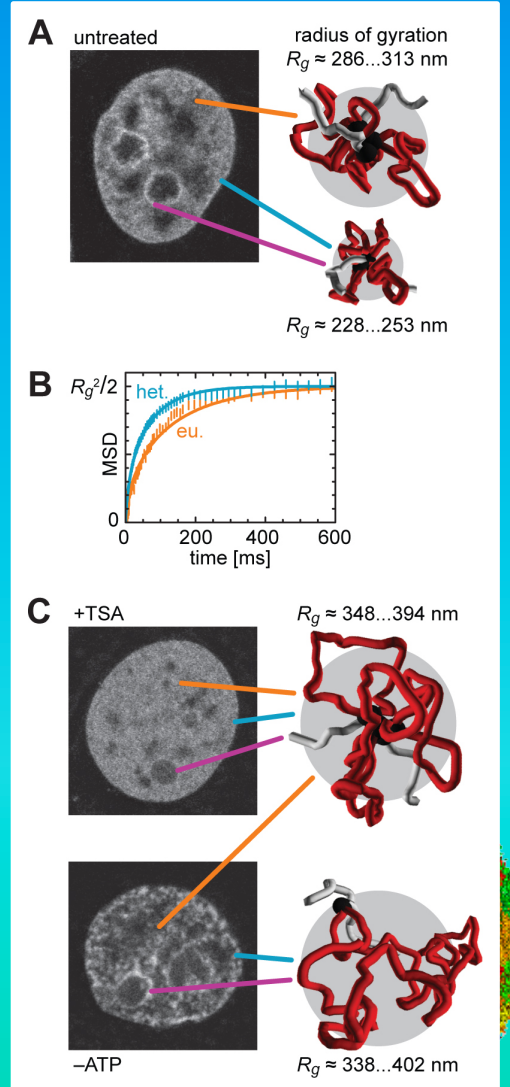
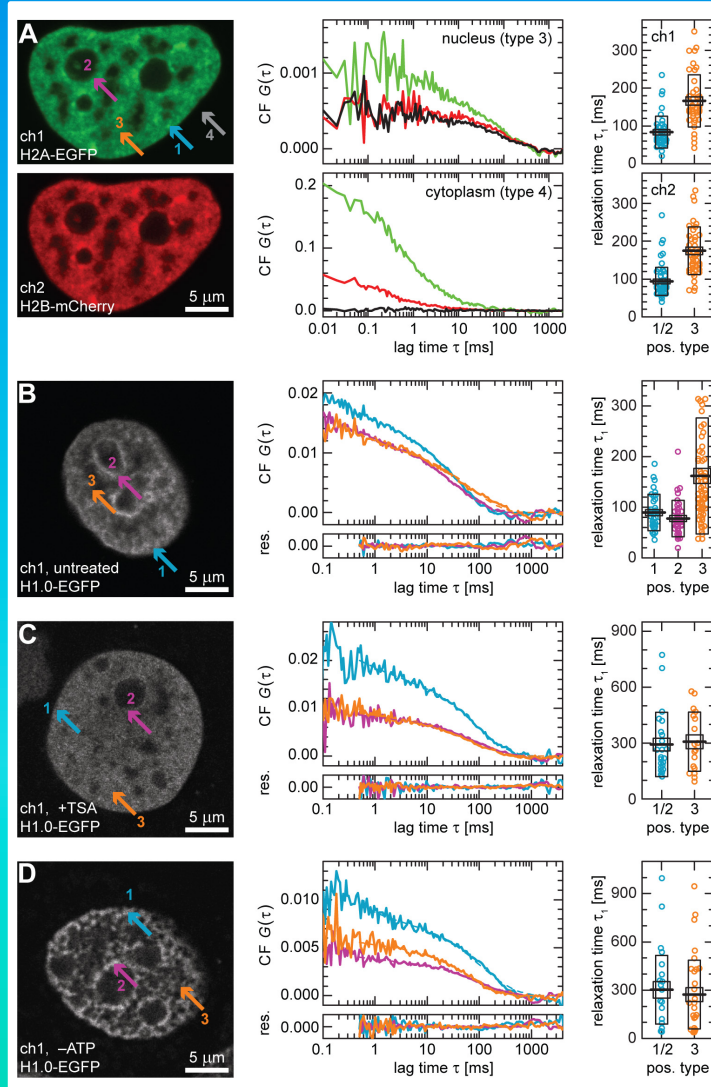
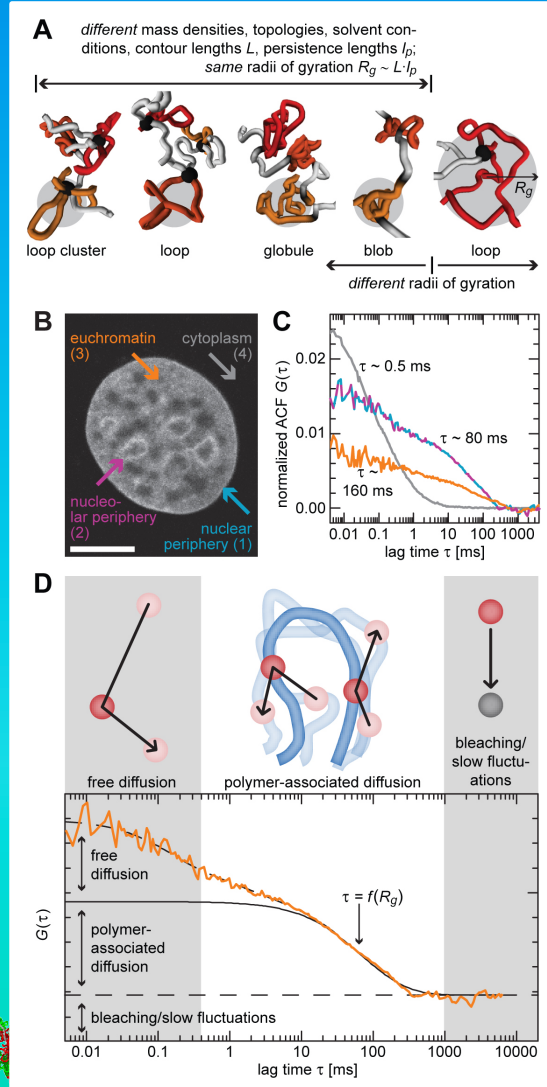
In Vivo Nucleosome Concentrations and 3D architecture

Counting nucleosomes in living cells with a combination of fluorescence correlation spectroscopy (FCS) and confocal laser scanning microscopy (CLSM) reveals the association of nucleosomes and their kinetics as well as again the typical expected distribution of a multi-loop aggregate/rosette.



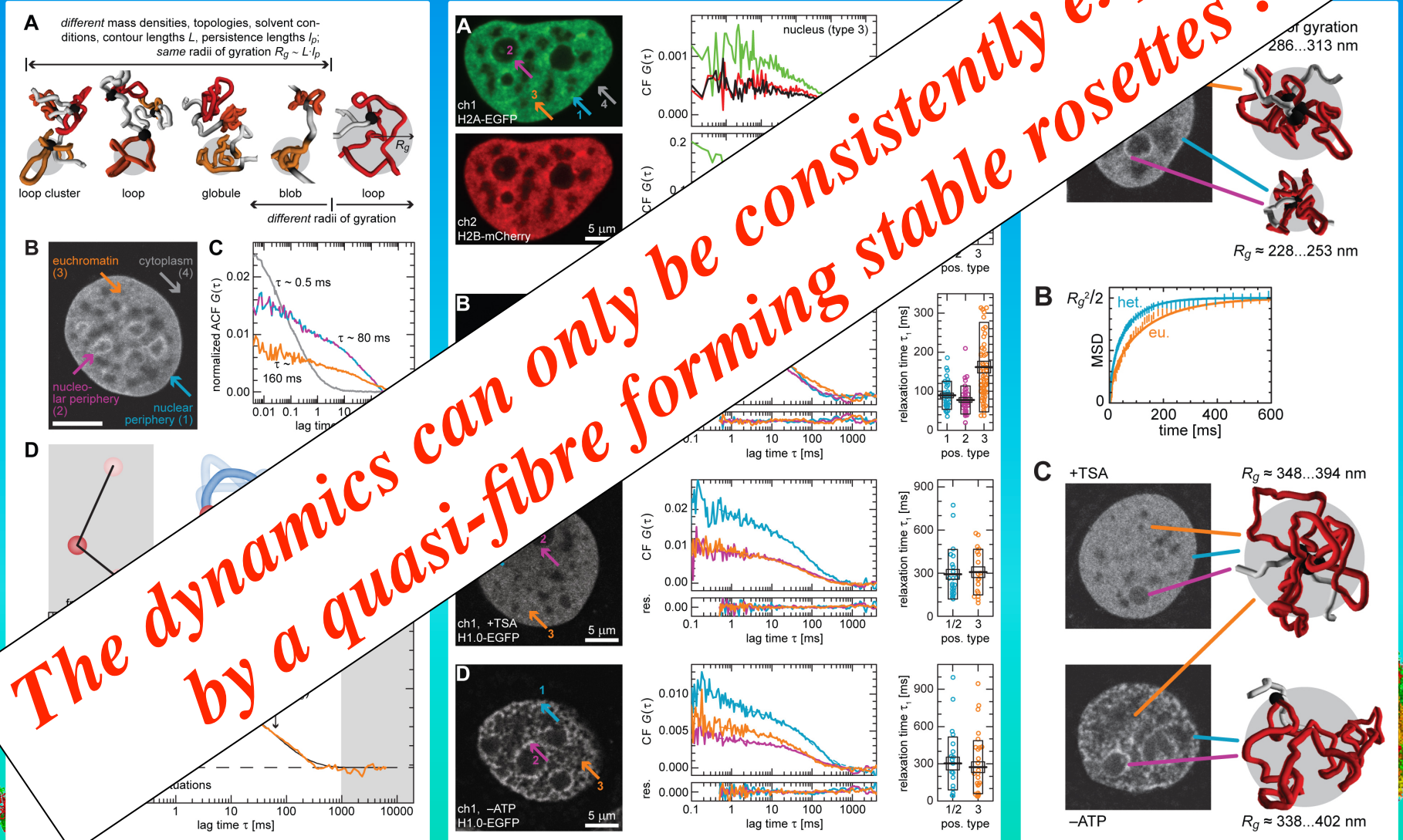
In Vivo Dynamics and 3D architecture

Fluorescence correlation spectroscopy (FCS) also reveals the dynamics of nucleosomes bound to DNA, i.e. FCS measures the movement of the chromatin quasi-fibre and its constraining architecture. This shows again a differentially compacted quasi-fibre folded into multi-loop aggregates/rosettes with functional differences as to e.g. hetero- and euchromatin or induced disturbances chromatin fiber (de-)condensation (+TSA, -ATP)



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Conclusion

The compacted chromatin quasi-fibre, folds into stable loop-aggregates connected by a linker !

Every structural level of nuclear organization including its dynamics is connected and represented in all the other levels in a holistic systems genomics manner.



Parameter/Observable			Simulation Single Chromosomes						Simulation Whole Nuclei							General Comparison	
Architectural Level	Observable Class	Spec. Feature	Applic. & Quality	Topological Parameter Dependence				Modell	Applic. & Quality	Topological Parameter Dependence					Modell	Experiment vs. Simulation	
				L _s /R _s	LI _s	C _{VOL}	EV			L _s /R _s	LI _s	NUC _{VOL}	EV	Chrom _s		Comp. Degree	Modell
Morphology: Chromatin Fibre to Nucleus	Morphology	Rendering	+++	+++	+++	+++	+++	MLS	+++	+++	+++	+++	+++	-	MLS	+	MLS
		EM	ND; but similar to the simulation of whole <u>nulcei</u> .						+	+	+	+++	+	-	~MLS	+	~ MLS +
		FISH-EM							++	++	++	+++	++	+++	~MLS	+	~ MLS +
		CLSM							+	+	++	+++	+	-	MLS	++	MLS ++
		FISH-CLSM							++	++	+++	+++	++	+++	MLS	+++	MLS +++
Nucleus	Radial Distribution Nuclei	Mass							+++	+	+	+++	++	+++	≈MLS	+	≈ MLS
		Density							+++	+	+	+++	++	+++	≈MLS	+	≈ MLS
	CLSM-Image Distribution	Intensity							+++	+	+	+++	++	-	MLS	+++	MLS +++
		Mass							+++	+	+	+++	++	-	MLS	+++	MLS +++
	Chromosome Position	Distance Mass Centre							+++	+	++	+++	++	+++	~MLS	+	~ MLS +
Chromosome	Radial Distribution Chromosomes	Mass	+++	++	+++	+++	++	MLS	+++	++	+++	++	+	+++	MLS	+	MLS +
		Density	+++	++	+++	+++	++	MLS	+++	++	+++	++	+	+++	MLS	+	MLS +
	Territory Shape	Roundness	ND; but similar to the simulation of whole <u>nulcei</u> .						++	+	+++	++	+	+++	MLS	++	MLS ++
	Territory Distance	Nearest							+++	+	++	+++	+	+++	MLS	++	MLS ++
		Arbitrary							+++	+	++	+++	+	+++	MLS	++	MLS ++
	Territory CLSM/Interaction	Volume CLSM							+++	+	++	+++	++	+++	MLS	+++	MLS +++
		Overlap CLSM							+++	+	++	+++	++	+++	MLS	+++	MLS +++
Subchromosomal Domain	SD Radial Distribution	Mass	+++	+++	+	+	+	MLS	+++	+++	+	+	~+	-	MLS	+++	MLS +++
		Density	+++	+++	+	+	+	MLS	+++	+++	+	+	~+	-	MLS	+++	MLS +++
	SD Distance	Genetically Adjacent	+++	++	+++	+	+	MLS	+++	++	+++	+	~+	-	MLS	+++	MLS +++
		Spatial Arbitrary	+++	+	+	++	++	MLS	+++	+	+	+++	~+	-	MLS	+++	MLS +++
		Spatial Nearest	+++	++/+	+++/+	++	++	MLS	+++	++/+	+++/+	++/+	~+	-	MLS	+++	MLS +++
	SD CLSM/Interaction	Volume CLSM	ND; but similar to the simulation of whole <u>nulcei</u> .						+++	+++	+	+	~+	-	MLS	+++	MLS +++
		Overlap CLSM							+++	+++	+	+++	~+	-	MLS	+++	MLS +++
Chromatin Loop/Fibre	Spatial Distance	Position Independent	+++	+++	+++	-/+	++	MLS	+++	+++	+++	-/+	+	-/+	MLS	+++	MLS +++
		Position Dependent	++++	+++	+++	-/+	++	MLS	++++	+++	+++	-/+	+	-/+	MLS	+++	MLS +++
		Marker Ensemble	++++	+++	+++	-/+	++	MLS	++++	+++	+++	-/+	+	-/+	MLS	+++	MLS +++

Evolutionary Architecture Perspective

Only a compacted chromatin quasi-fibre, folded into stable loop-aggregates connected by a linker allows to guaranty the functional informational requirements of genomes:

i) storage stability/flexibility, ii) readout, and iii) replication !



➤ Storage stability/flexibility:

The packaging ratio/scale into a quasi-fibre and stable loops forming rosettes is optimal for the physical stability of genomes, while it is flexible enough to allow functional differences as well as react to entropic and other damages.

➤ Readout:

The dynamics this architecture allows expression/regulation by self-organization into (in-)active units already in proximity, and guaranties at the same time accessibility to and from the information for factors as well transcripts.

➤ Replication:

The 2D knot-free topology as well as the packaging ratio/scale into a quasi-fibre and stable loops forming rosettes, allows concatenation free replication with low error/damage rate due to the easy block-wise proximity organization as well as the easy physical (de-)condensation during cell division.

Form follows function and function follows form!

Evolutionary Architecture Perspective

Only a compacted chromatin quasi-fibre, folded into stable loop-aggregates connected by a linker allows to guaranty the functional informational requirements of genomes:

i) storage stability/flexibility, ii) readout, and iii) replication !

➤ **Storage stability/flexibility:**

The packaging ratio/scale into a quasi-fibre and stable loops is optimal for the physical stability of genomes, while it is flexible to adapt to environmental differences as well as react to entropic and other damages.

➤ **Readout:**

The dynamics this architecture allows by self-organization into (in-)active units already in proximity, and the accessibility to and from the information for factors as well transcription.

➤ **Replication:**

The 2D structure of the packaging ratio/scale into a quasi-fibre and stable loops forms a template for error free replication with low error/damage rate due to the easy access to the information as well as the easy physical (de-)condensation during cell division.

Genomes are an Evolutionary Holistic Form-Function Entanglement !

Form follows function and function follows form!

[illegible]

EMBL

Malte Wachsmuth

EraSysBio+ Consortium Labs

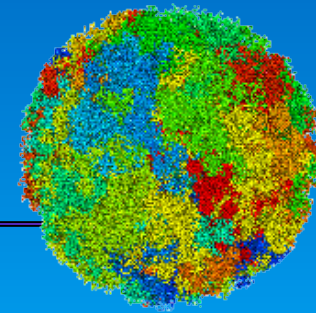
Peter R. Cook
Gernot Längst
Tobias A. Knoch
Karsten Rippe
Gero Wedemann

High-Performance Computing Center Stuttgart, University of Stuttgart; Supercomputing Center Karlsruhe, University of Karlsruhe; Computing Center, Deutsches Krebsforschungszentrum Heidelberg (DKFZ)

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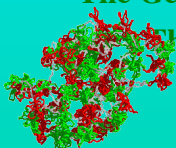


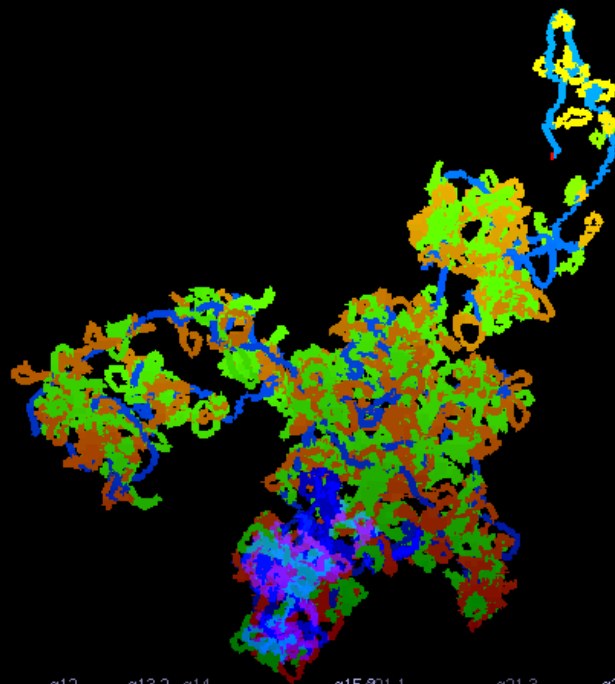
	Biophysical Genomics, Cell Biology, Erasmus MC	Biological Sciences, UCSD Suchit Jhunjunwala	The Cremer Labs Joachim Rauch	
Cell Biology & Biophysics EMBL Malte Wachsmuth	Petros Kolovos Anis Abuseiris Michael Lesnussa	Menno van Zelm Cornelis Murre	Irina Solovei Michael Hausmann Christoph Cremer Thomas Cremer	Biophysics of Macromolecules DKFZ Gabriele Müller Waldemar Waldeck Jörg Langowski
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Genome Org & Function BioQuant/DKFZ Karsten Rippe				

Erasmus Medical Center and BioQuant & German Cancer Research Center

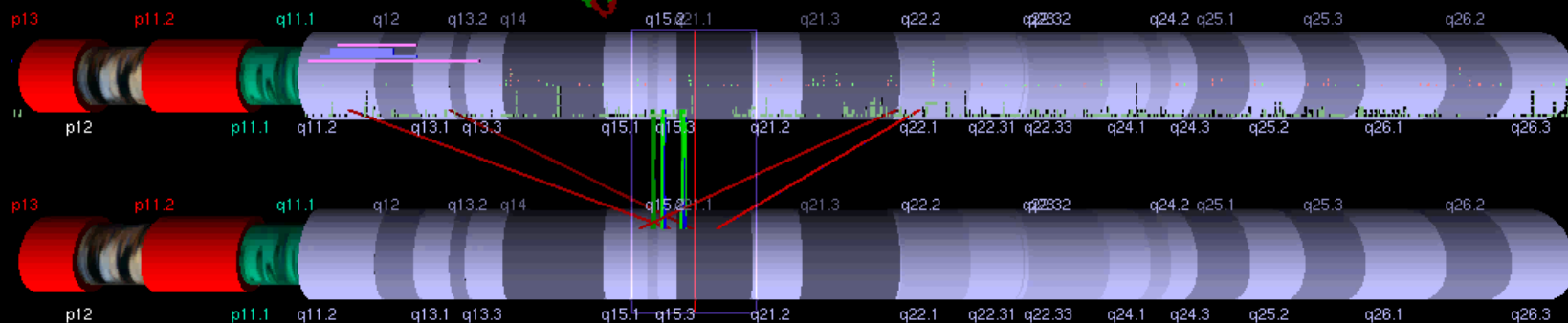
High-Performance Computing Center Stuttgart, University of Stuttgart; Supercomputing Center Karlsruhe, University of Karlsruhe; Computing Center, Deutsches Krebsforschungszentrum Heidelberg (DKFZ)

Erasmus Medical Center, Hogeschool Rotterdam, The Fraunhofer Society, The German MediGRID and Services@MediGRID, The German D-Grid Initiatives, The German Ministry for Science and Technology, The Dutch Science Organization (NOW), The European EGEE Initiative, The European EDGES Consortium, The German Society for Human Ecology, The International Society for Human Ecology, The European Commission





15
 Decipher
 Affy100KXba
 Refseqb36



43750000

15

1:500000

The
Detailed 3D Multi-Loop Aggregate/Rosette Chromatin Architecture
and
Functional Dynamic Organization
of the
Human and Mouse Genome
-
Results and Perspectives

Knoch, T. A.

*The 22nd Wilhelm Bernhard Workshop, Schloss Wilhelminenberg, Vienna, Austria,
17th – 22nd August, 2015.*

Abstract

The dynamic three-dimensional chromatin architecture of genomes and the obvious co-evolutionary connection to its function – the storage and expression of genetic information – is still debated after ~170 years. With a systems genomics approach combining a novel selective high-throughput chromosomal interaction capture (T2C) with quantitative polymer simulations and scaling analysis of architecture and DNA sequence, we determined and cross-proved the final architecture of genomes with unprecedented molecular resolution and dynamic range from single base pairs to entire chromosomes: for several genetic loci of different species, cell type, cell cycle, and functional states a chromatin quasi-fibre exists with 5 ± 1 nucleosome per 11 nm, which folds into stable(!) 40-100 kbp loops forming stable(!) aggregates/rosettes which are connected by a ~50 kbp chromatin linker. Polymer simulations using Monte Carlo and Brownian dynamics approaches confirm this and predict and explain additional experimental findings. Beyond, a novel fluorescence correlation spectroscopy (FCS) approach combined with analytical polymer models measures the architectural dynamics *in vivo*, and agrees with the before mentioned conclusion using completely independent means. Beyond, we find a fine-structured multi-scaling behaviour of both the architecture and the DNA sequence, showing for the first time directly the tight entanglement between architecture and sequence. This agrees with the outcome of a synopsis e.g. with previous spatial distance measurement studies, *in vivo* morphology of entire cell nuclei, or electron microscopy of chromosome spreading studies, as well as the heuristics of the field in the last 170 years. This architecture has fundamental consequences for the entire system of the storage and expression of genetic information as well as for its investigation: E.g. this architecture, its dynamics, and accessibility balance stability and flexibility ensuring genome integrity and variation enabling gene expression/regulation by self-organization of (in)active units already in proximity. Thus, both the T2C and FCS approaches open the door to “architectural and dynamic sequencing” of genomes at a resolution where a genome mechanics with corresponding uncertainty principles applies. Consequently, this will lead now to a detailed understanding of genomes with fundamental new insights and huge novel perspectives for diagnosis, treatment and genome engineering efforts in the future.

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Keywords:

Genome, genomics, genome organization, genome architecture, structural sequencing, architectural sequencing, systems genomics, coevolution, holistic genetics, genome mechanics, genome statistical mechanics, genomic uncertainty principle, multilism genotype-phenotype, genome function, genetics, gene regulation, replication, transcription, repair, homologous recombination, simultaneous co-transfection, cell division, mitosis, metaphase, interphase, cell nucleus, nuclear structure, nuclear organization, chromatin density distribution, nuclear morphology, chromosome territories, subchromosomal domains, chromatin loop aggregates, chromatin rosettes, chromatin loops, chromatin quasi fibre, chromatin density, persistence length, spatial distance measurement, histones, H1.0, H2A, H2B, H3, H4, mH2A1.2, DNA sequence, complete sequenced genomes, molecular transport, obstructed diffusion, anomalous diffusion, percolation, long-range correlations, fractal analysis, scaling analysis, exact yard-stick dimension, box-counting dimension, lacunarity dimension, local nuclear dimension, nuclear diffuseness, parallel super computing, grid computing, volunteer computing, polymer model, analytic mathematical model, Brownian Dynamics, Monte Carlo, fluorescence *in situ* hybridization (FISH), targeted chromatin capture (T2C) confocal laser scanning microscopy, fluorescence correlation spectroscopy, spatial precision distance microscopy, super-resolution microscopy, two dimensional fluorescence correlations spectroscopy (2D-FCS) auto-fluorescent proteins, CFP, GFP, YFP, DsRed, fusion protein, *in vivo* labelling, information browser, visual data base access, holistic viewing system, integrative data management, extreme visualization, three-dimensional virtual environment, virtual paper tool, human ecology, e-human grid ecology, society, social systems, e-social challenge, inverse tragedy of the commons, grid phenomenon, micro-sociality, macro-sociality, autopoietic tragedy of social sub-systems, micro subsystems, macro subsystems, micro operationality, macro operationality, grid psychology micro riskmanagement, macro riskmanagement.

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