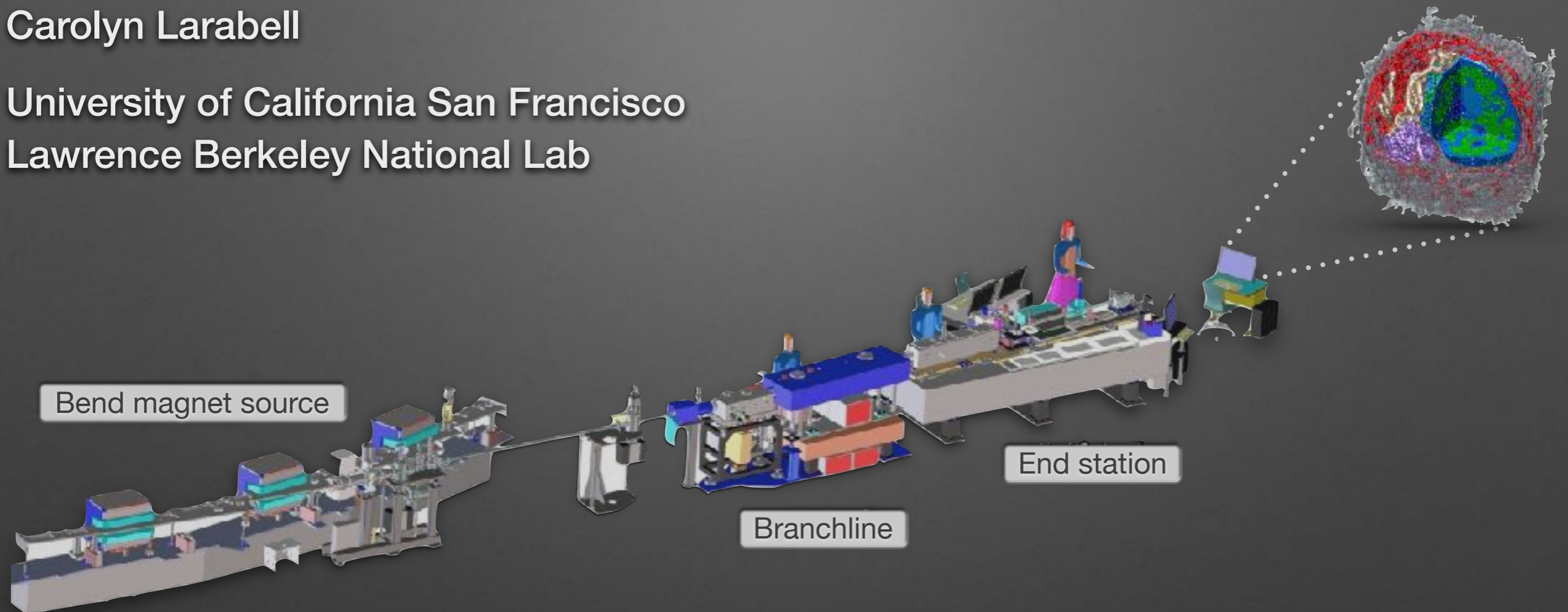


# Soft X-ray Tomography (SXT)

Carolyn Larabell

University of California San Francisco  
Lawrence Berkeley National Lab



National Center for X-ray Tomography

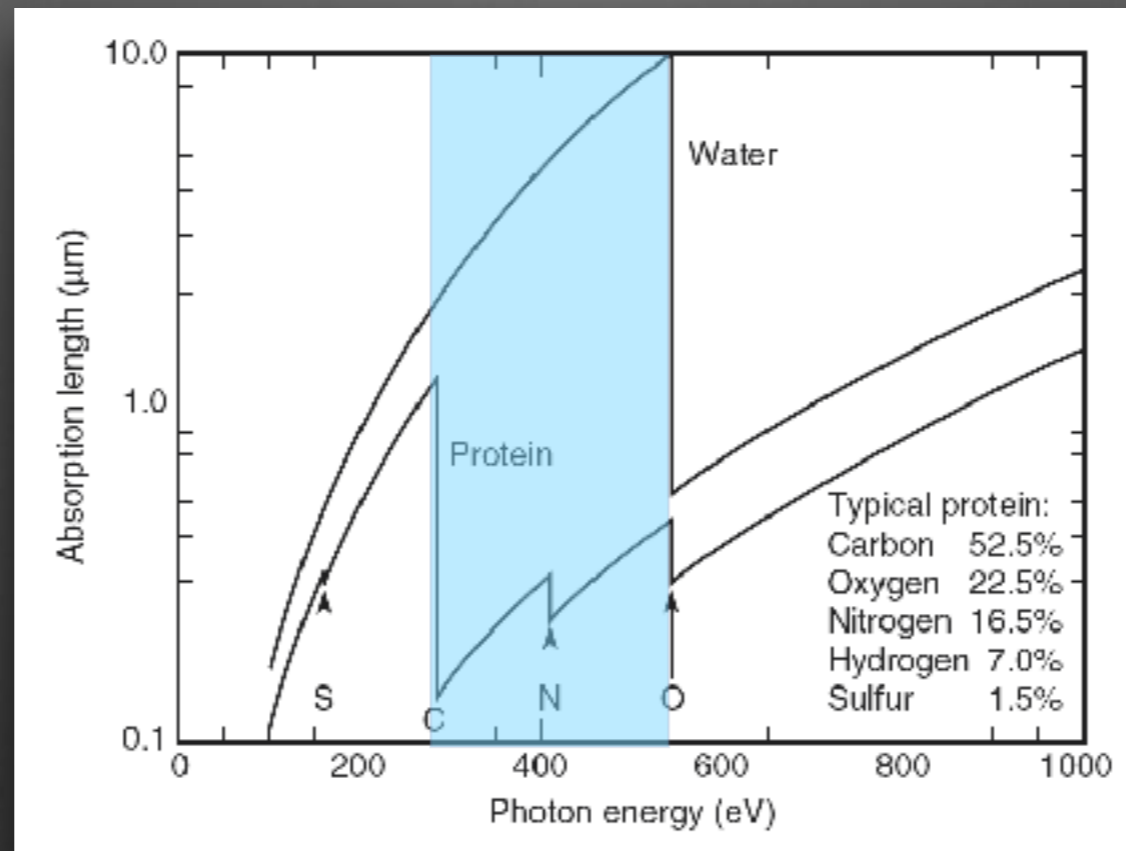
Supported by NIH-NIGMS and DOE-BER

# Soft X-ray Tomography (SXT)

- Imaging whole, hydrated cells in the native state
- No fixatives, no stains
- Cryo-immobilized
- 50 nm isotropic resolution (not limit; source is 2.4 nm)
- See molecules using correlated fluorescence and x-ray tomography

# Contrast: Imaging in the 'water window'

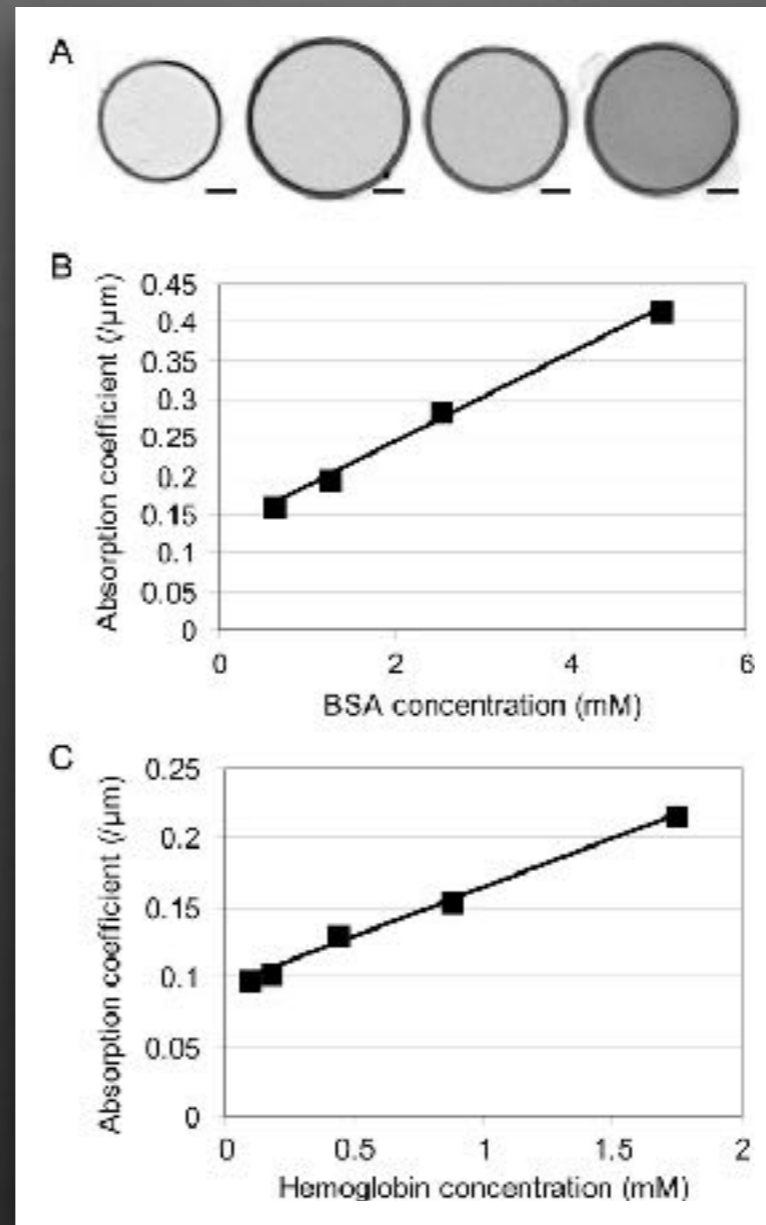
Between K shell absorption edges of C (284 eV) & O<sub>2</sub> (543 eV)



$$\lambda = 2.4 \text{ nm}$$

# Contrast: Imaging in the 'water window'

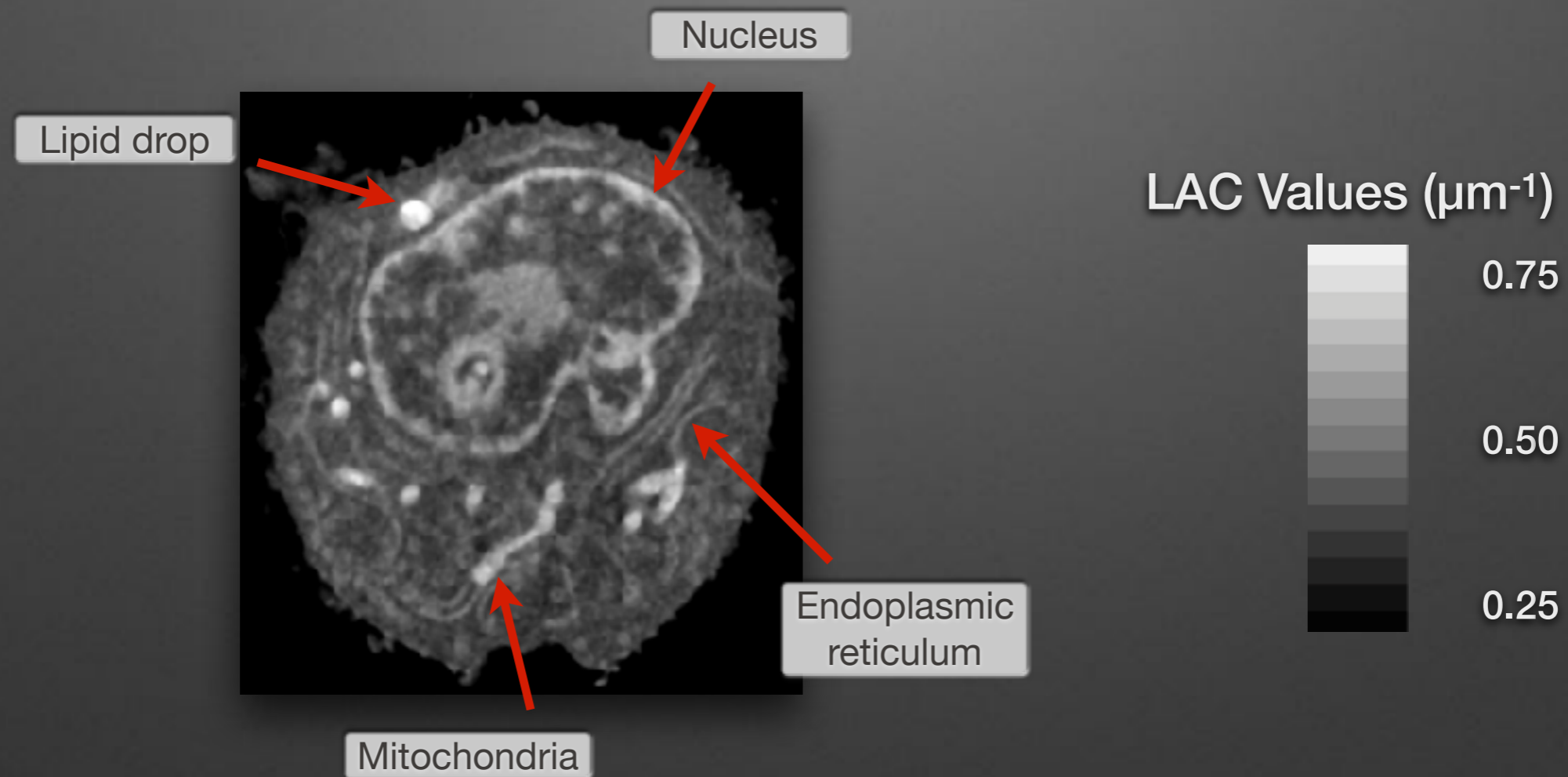
Absorption is linear with thickness & concentration



Hanssen et al (2012). *J. Struct. Biol.*  
177, 224-232

# Contrast: Imaging in the 'water window'

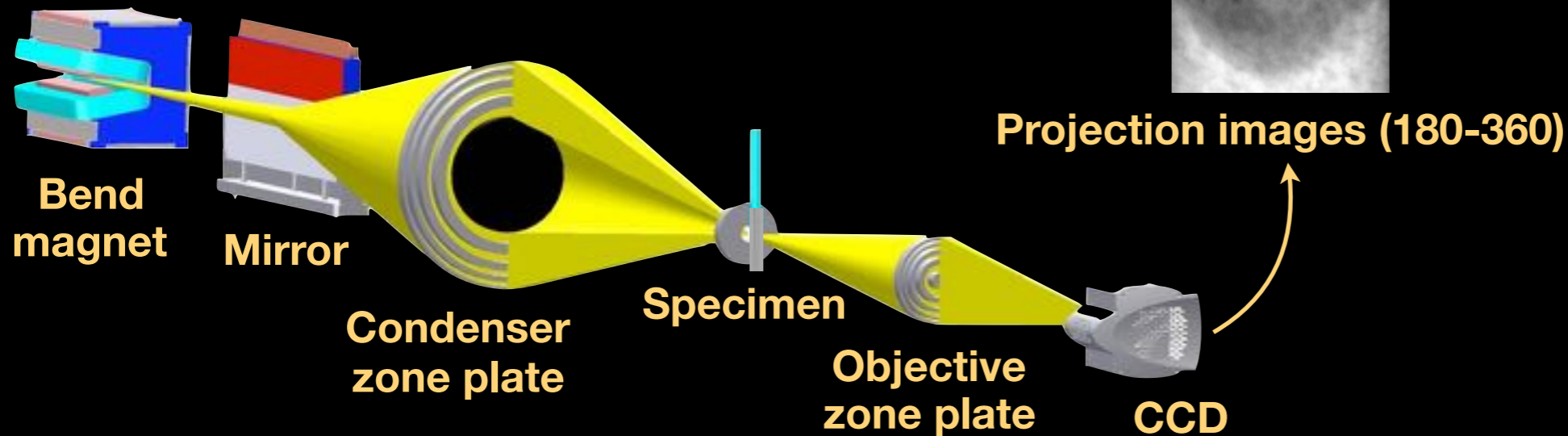
Absorption is linear with thickness & concentration



# Soft X-ray Tomography

2 minutes to reconstruct data

5 minutes to collect data



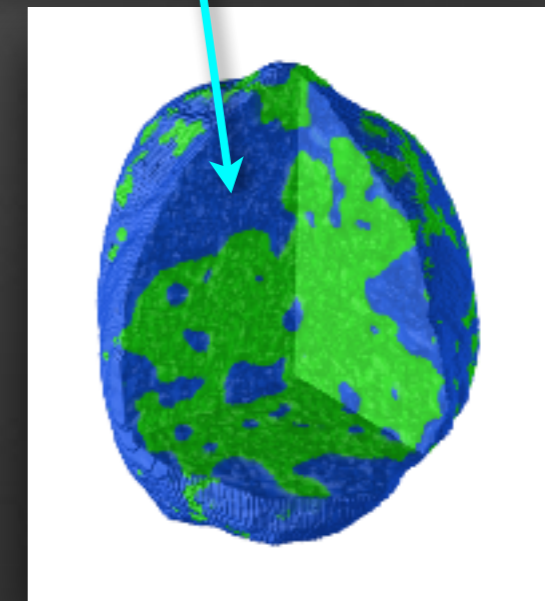
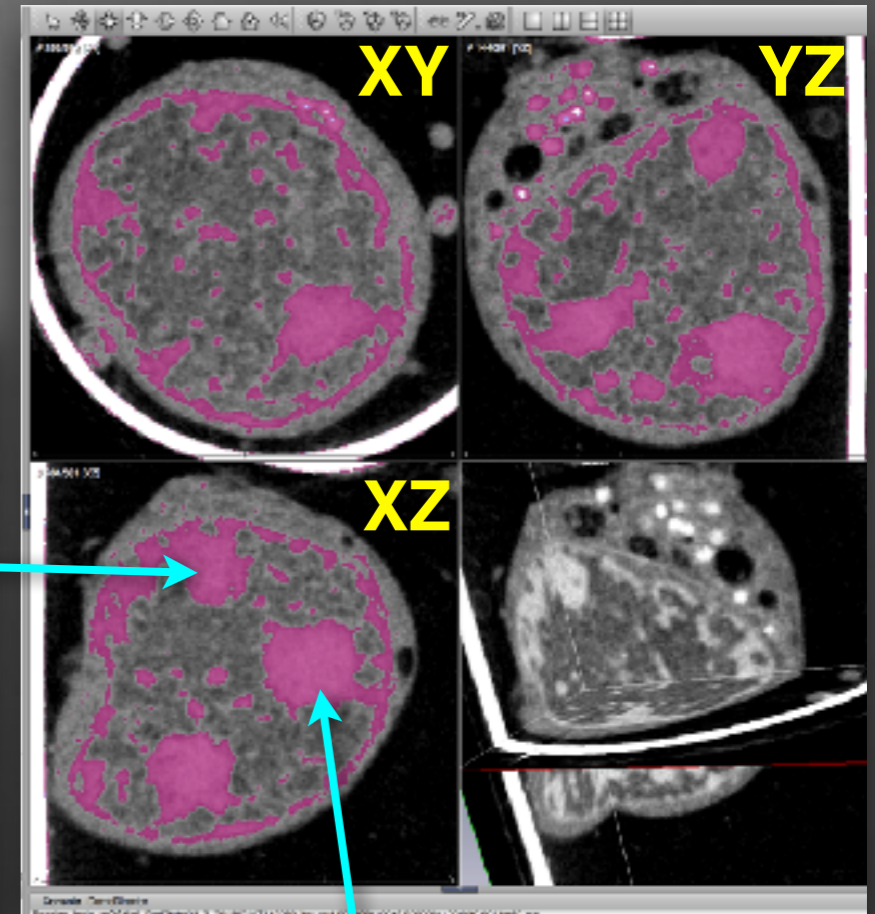
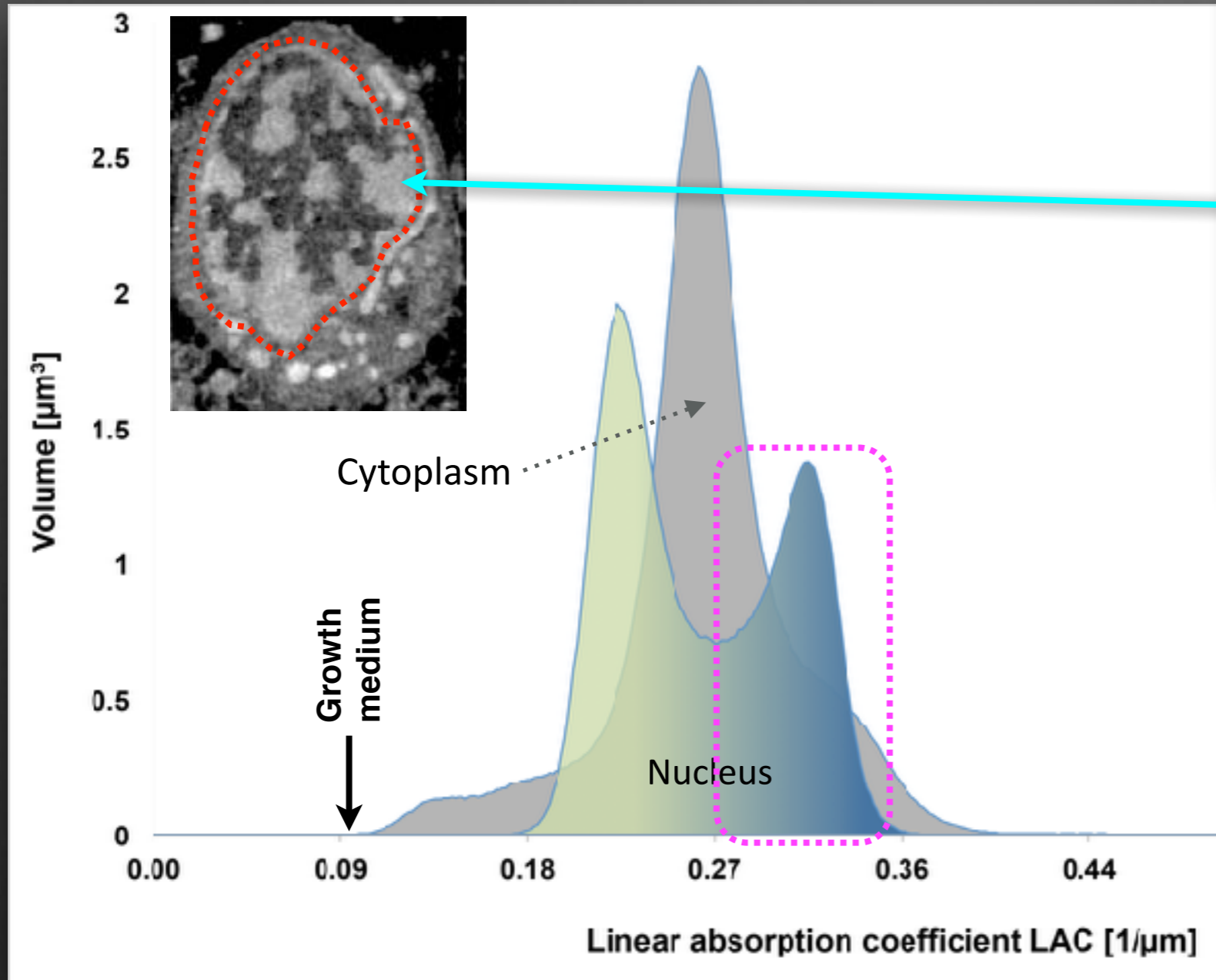
Reconstruct data

Segmentation

- Whole, hydrated cells in near-native state (cryo-immobilized)
- Natural, quantitative contrast; absorption of x-rays linear

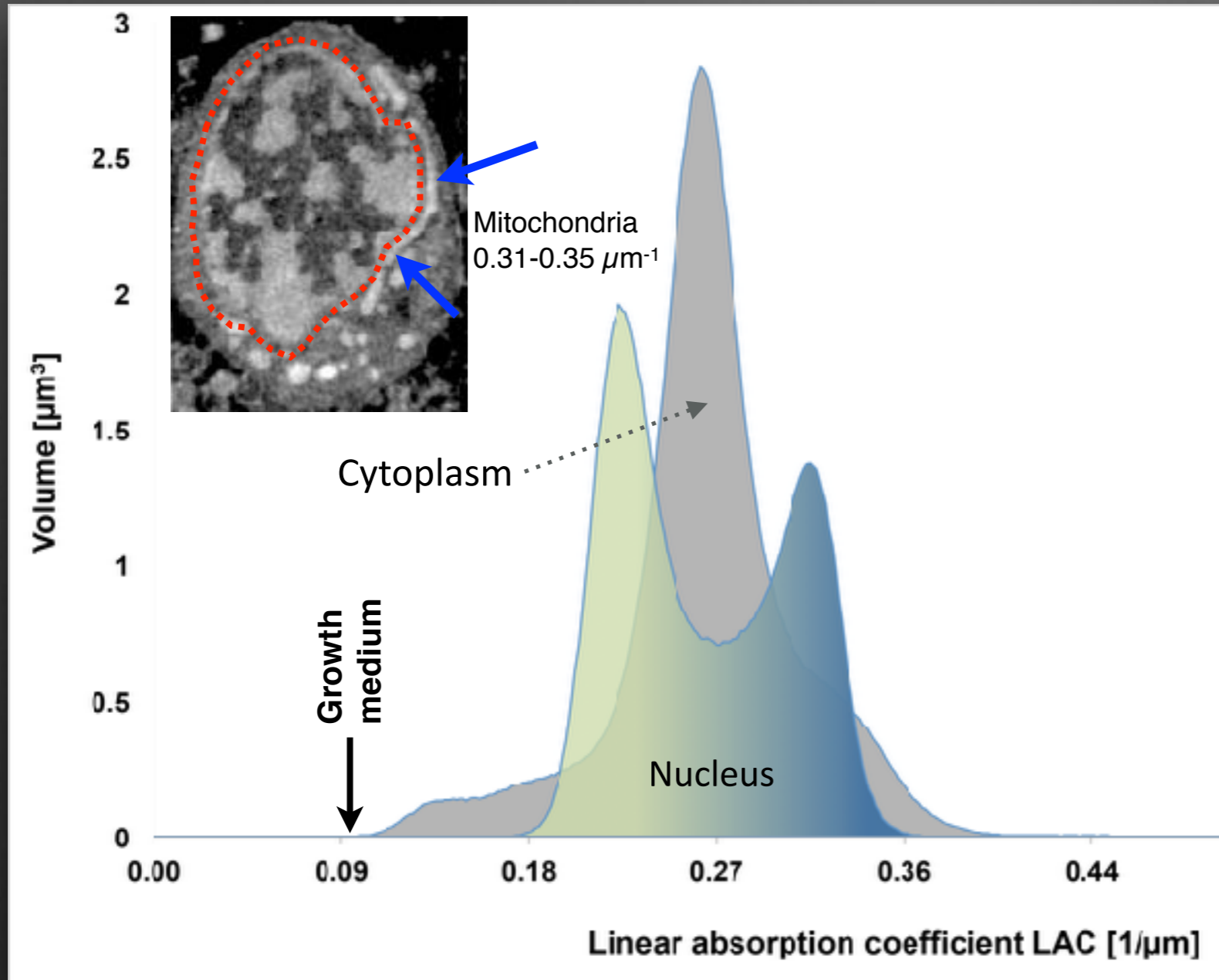
# Segmenting structures

Plot histogram of all voxels



# Segmenting structures

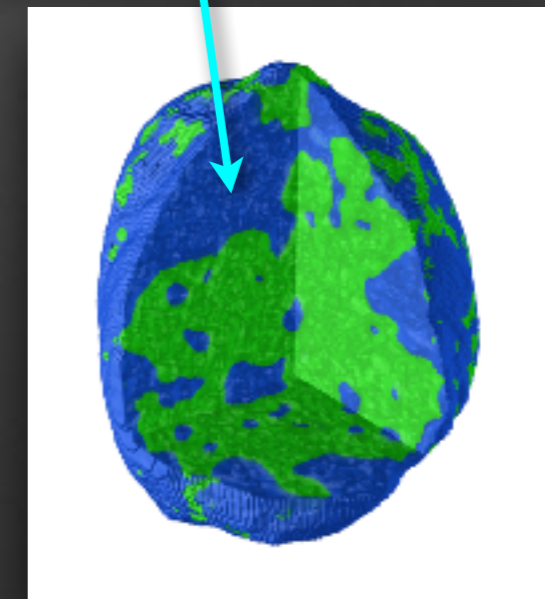
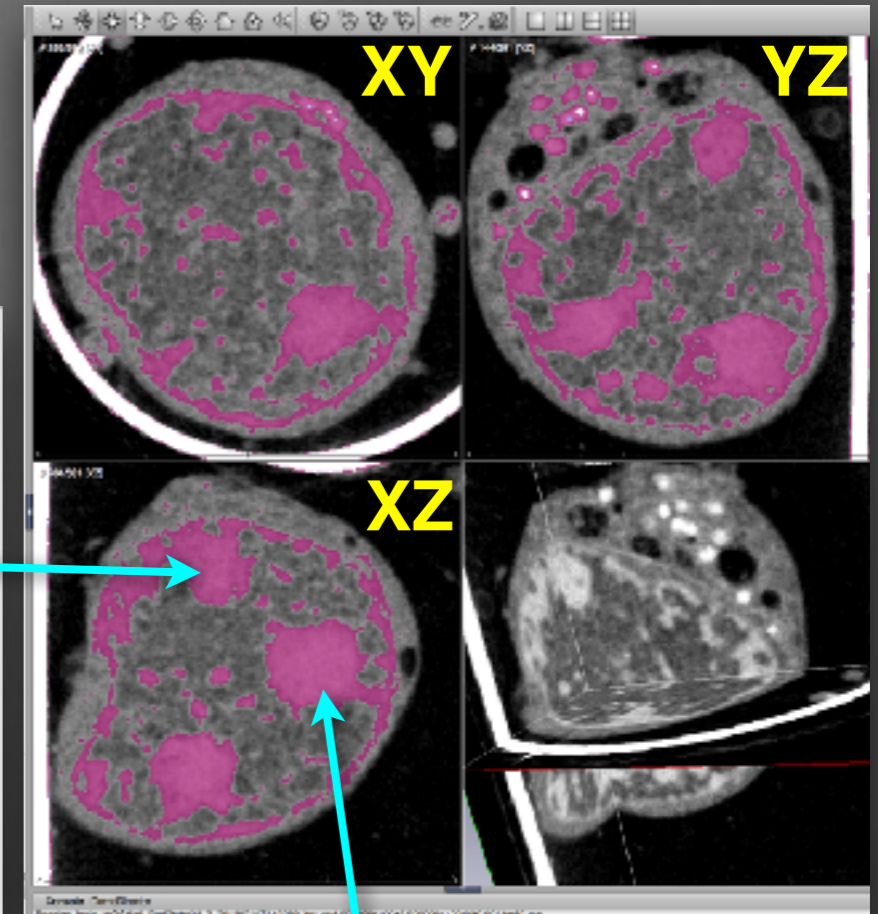
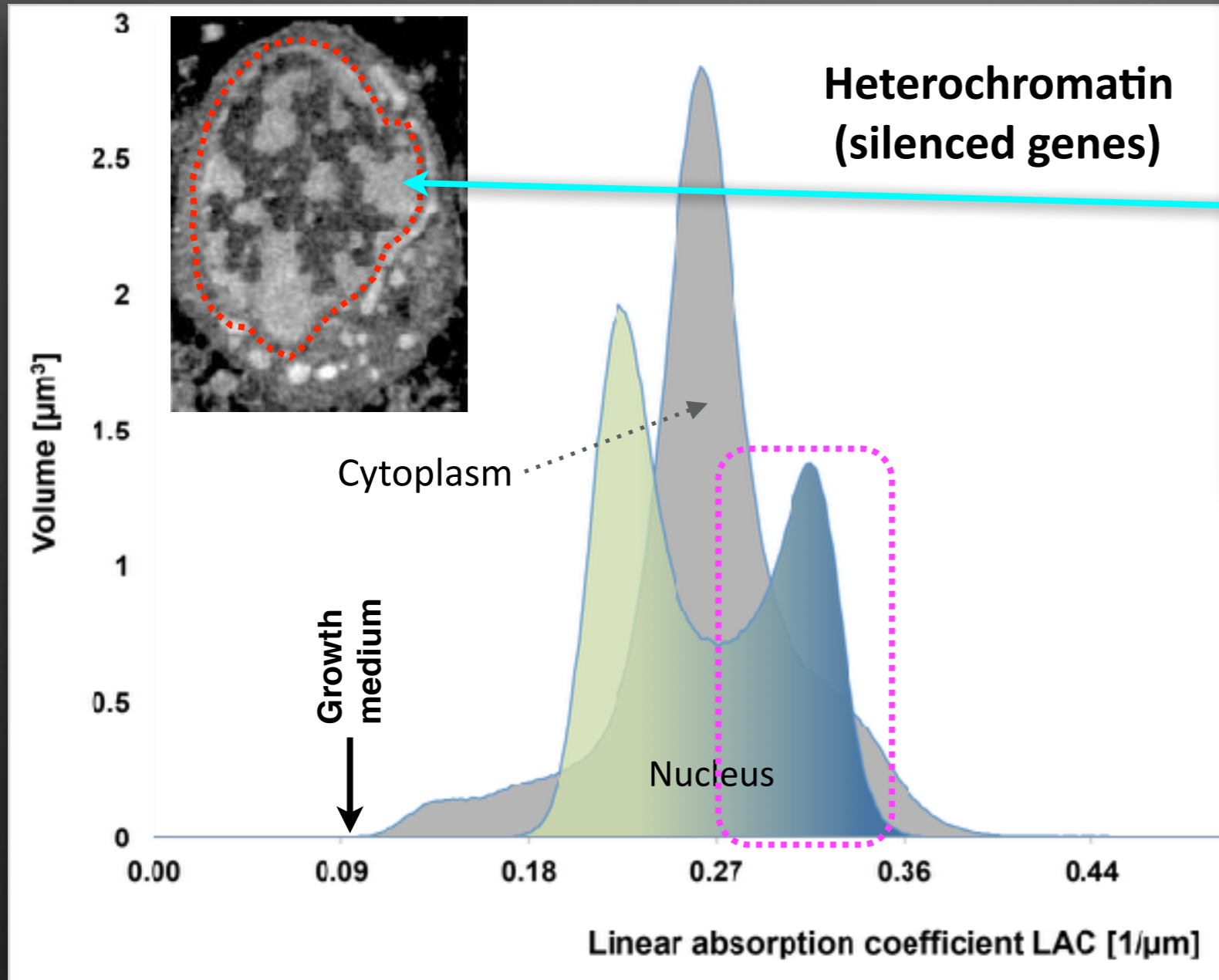
Plot histogram of all voxels





# Segmenting structures

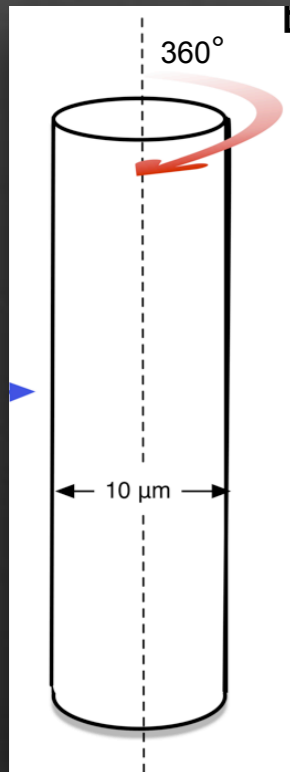
Plot histogram of all voxels



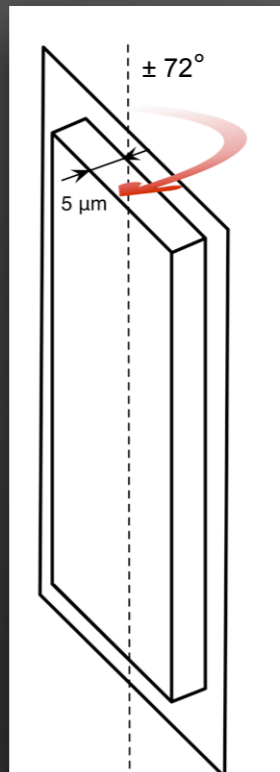
# Isotropic resolution

# Full rotation vs. limited tilt

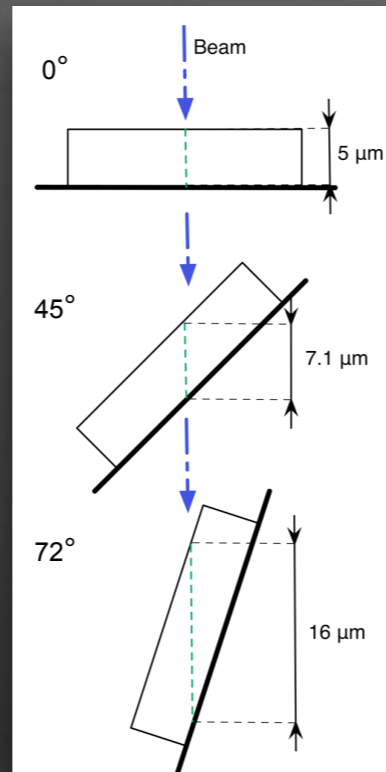
$\pm 90^\circ$



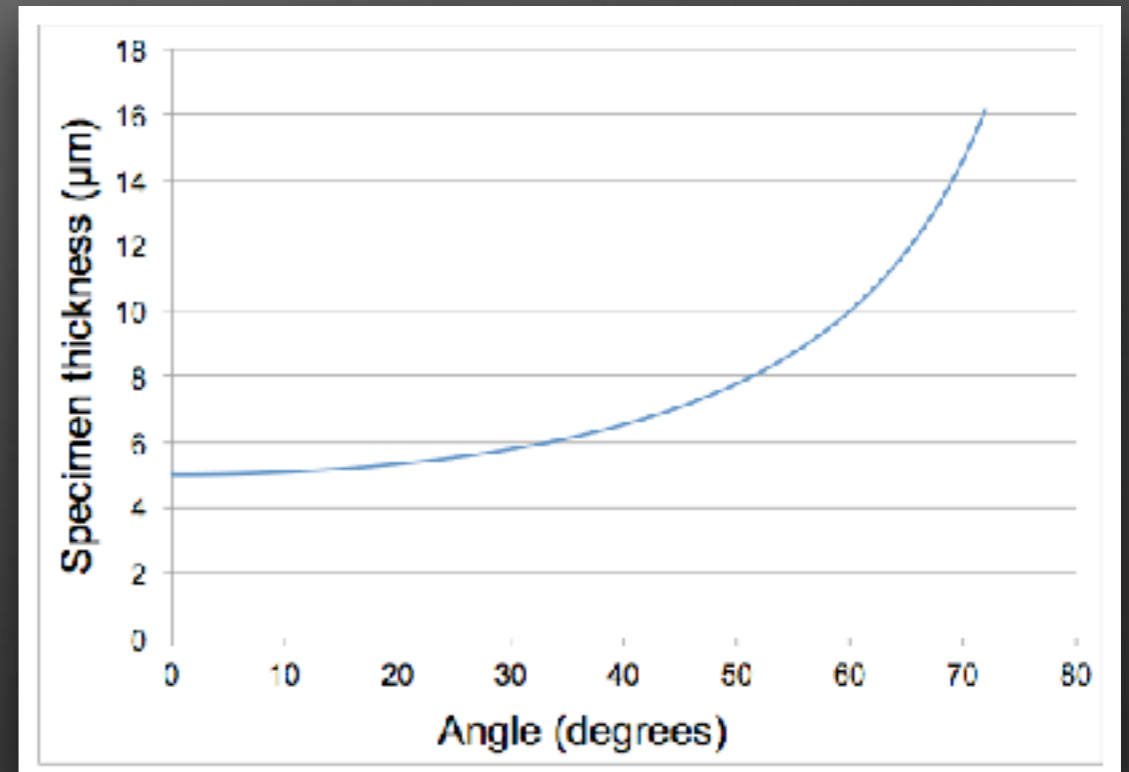
$\pm 75^\circ$



$16\ \mu\text{m}$  thick  
at  $\pm 75^\circ$



Specimen thickness  
increases with tilt



# Full rotation vs. limited tilt

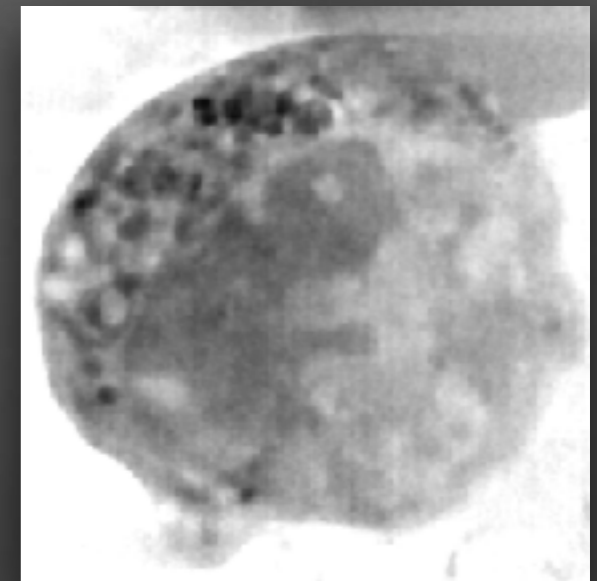
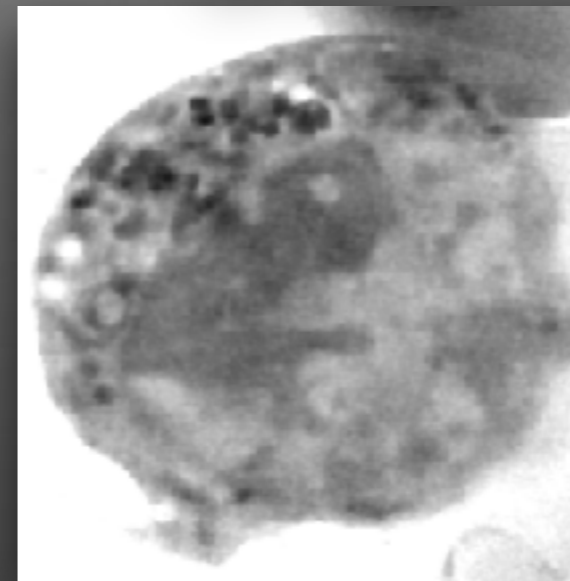
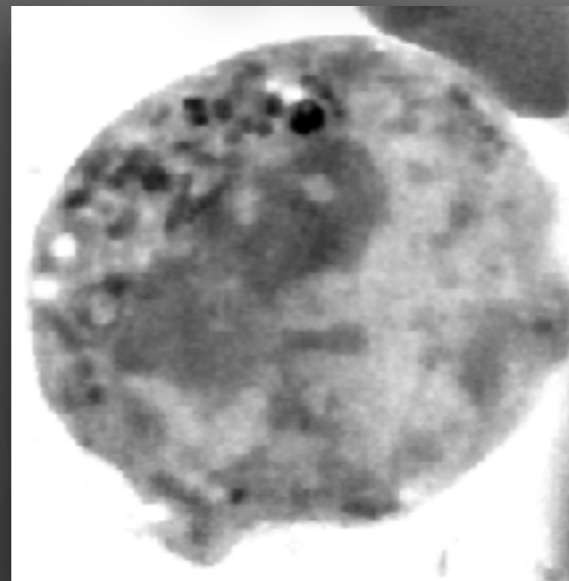
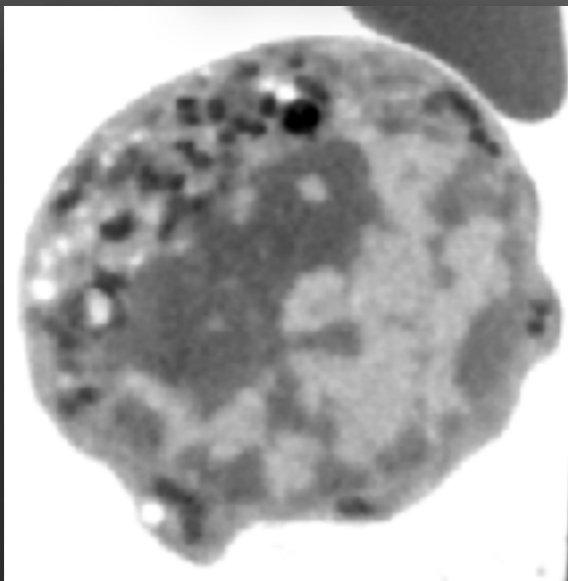
180° rotation  
(± 90°)

150° rotation  
(± 75°)

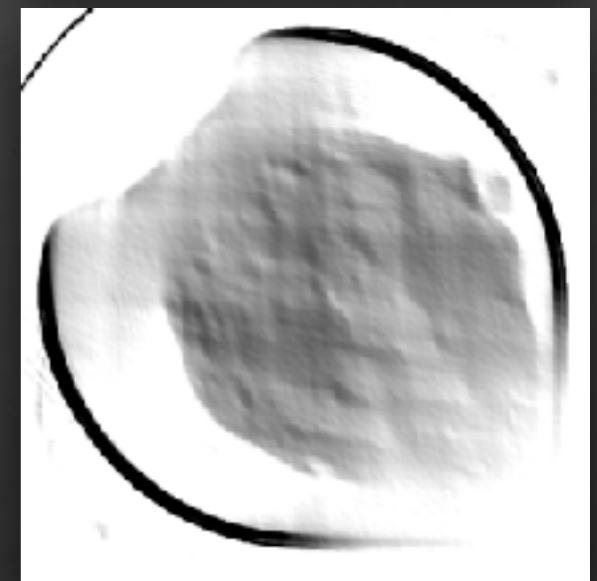
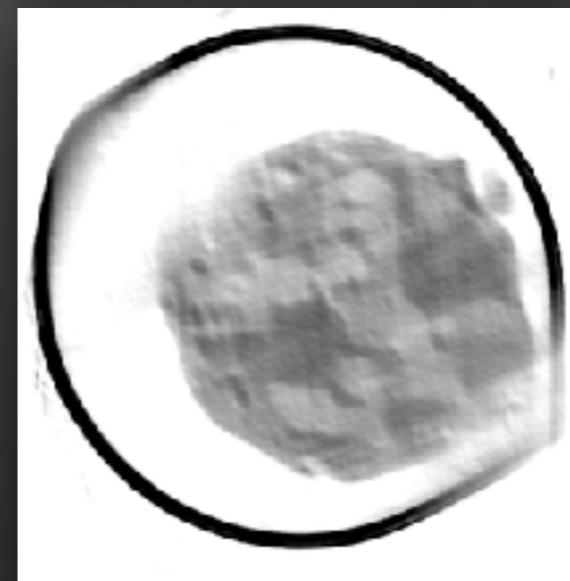
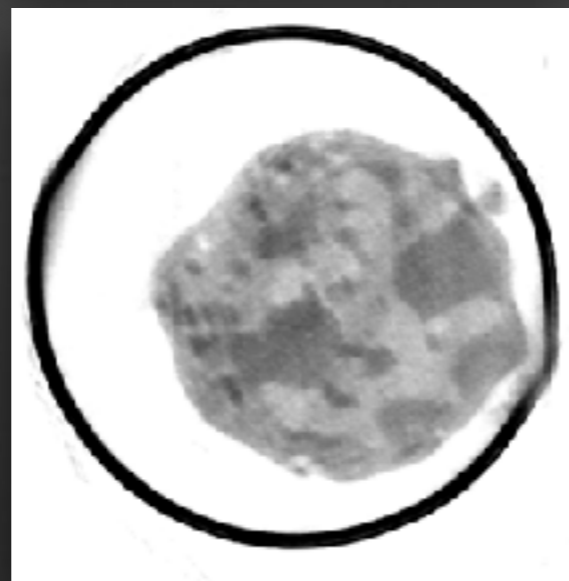
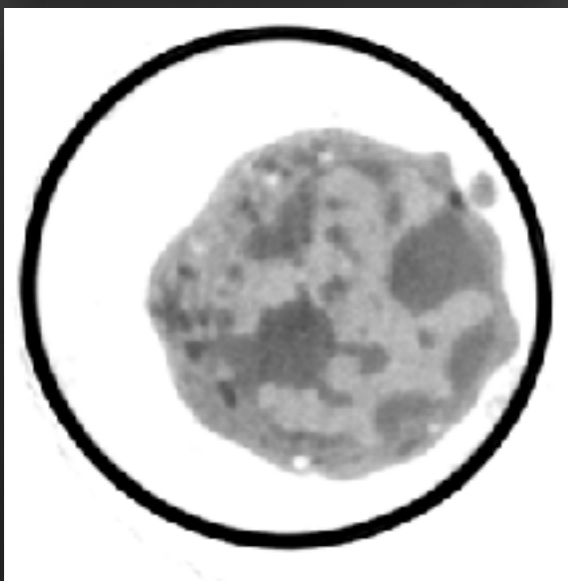
120° rotation  
(± 60°)

90° rotation  
(± 40°)

X-Y

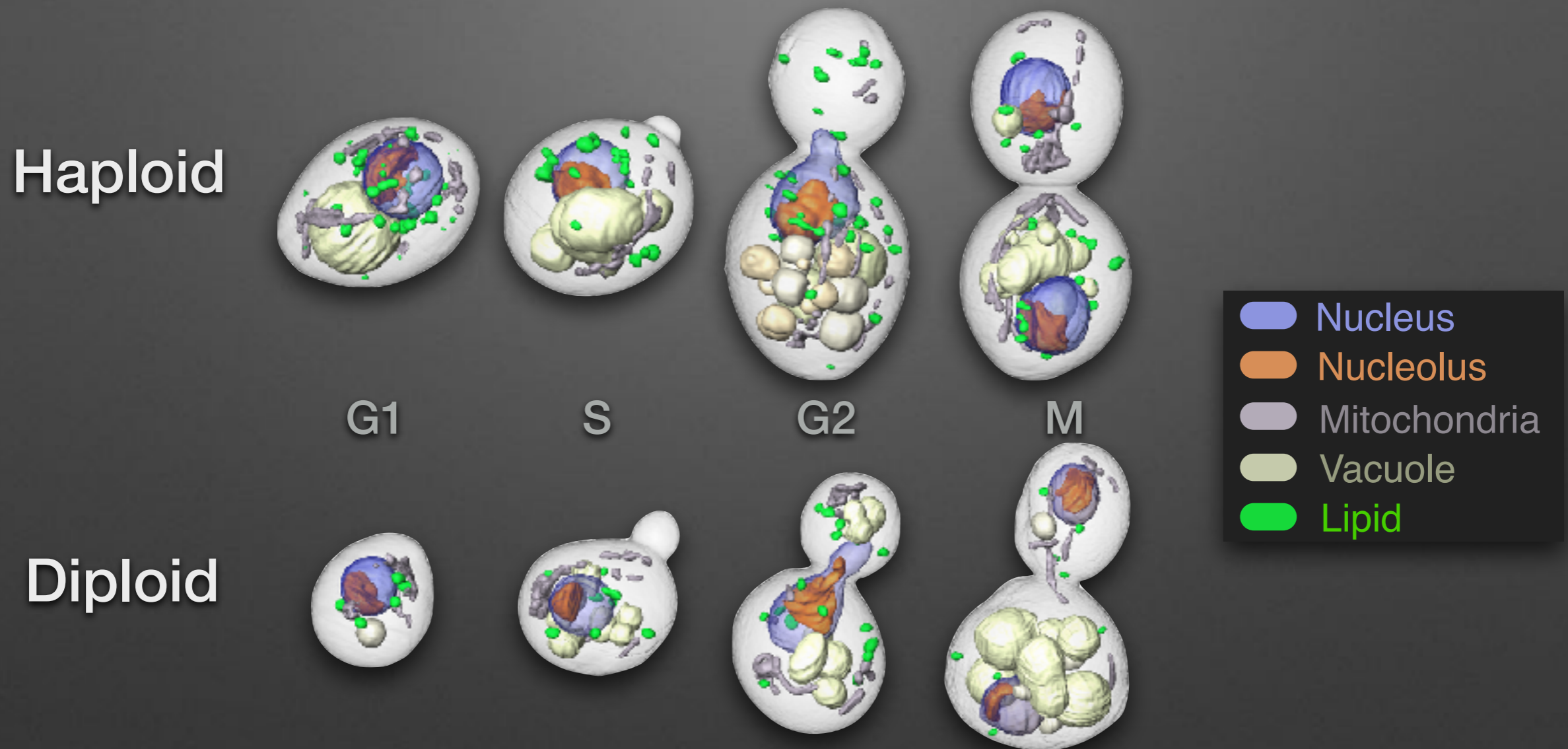


X-Z



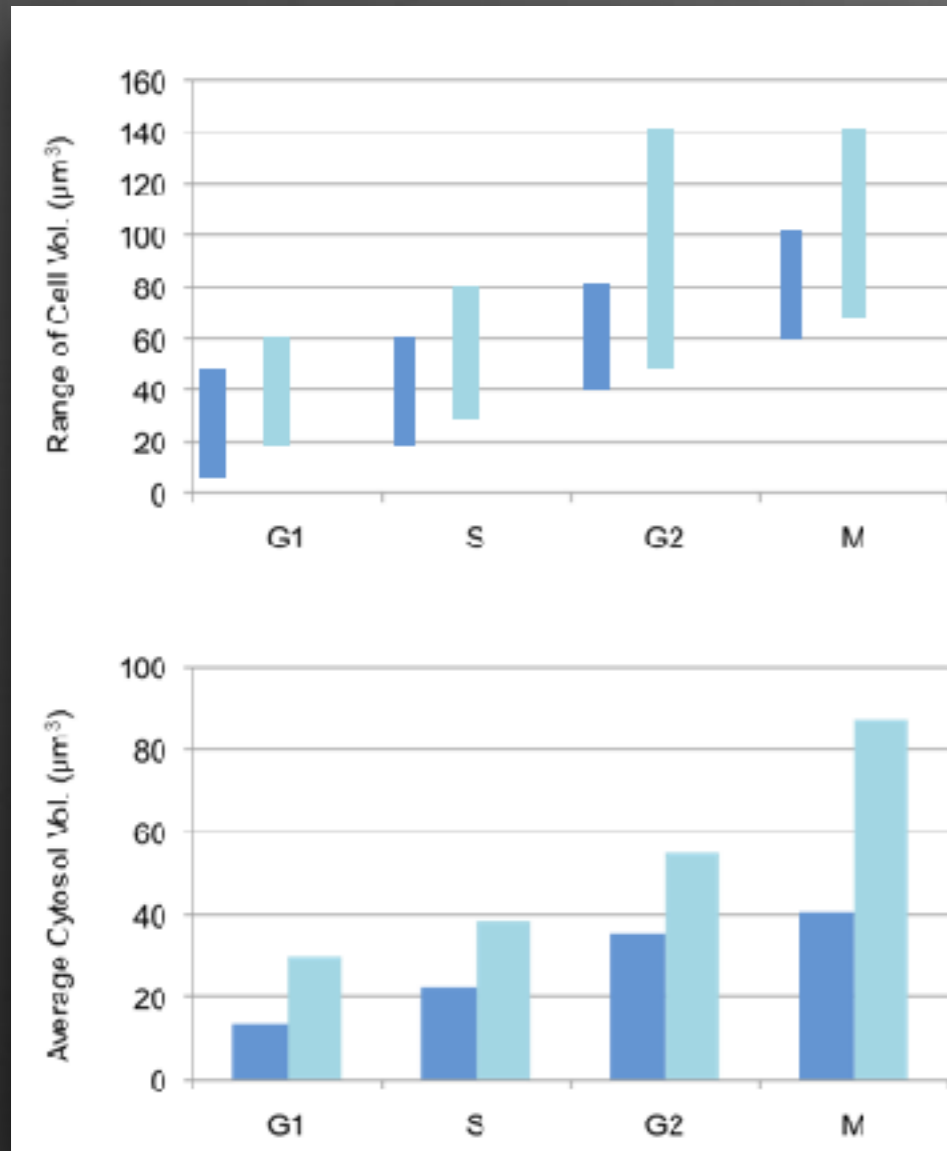
# **Phenotypic consequences of knocking out a gene**

# Structural organization of *S. cerevisiae*

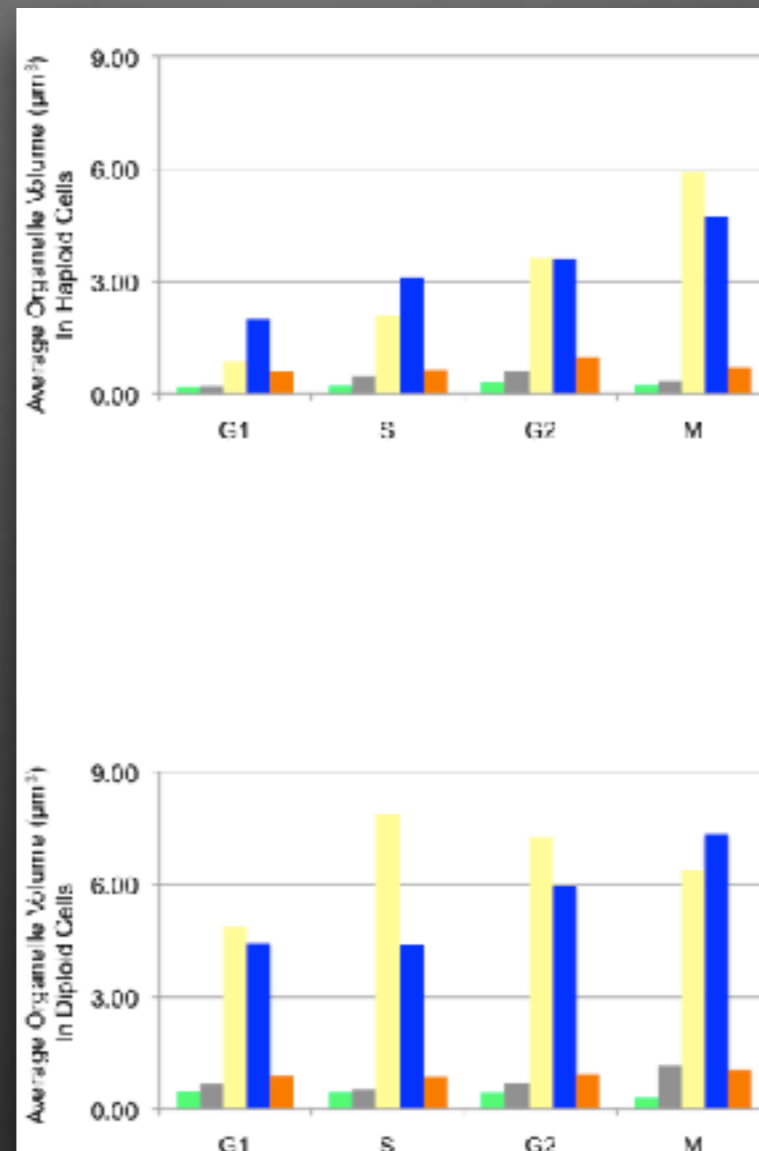


# Quantitative analysis of *S. cerevisiae*

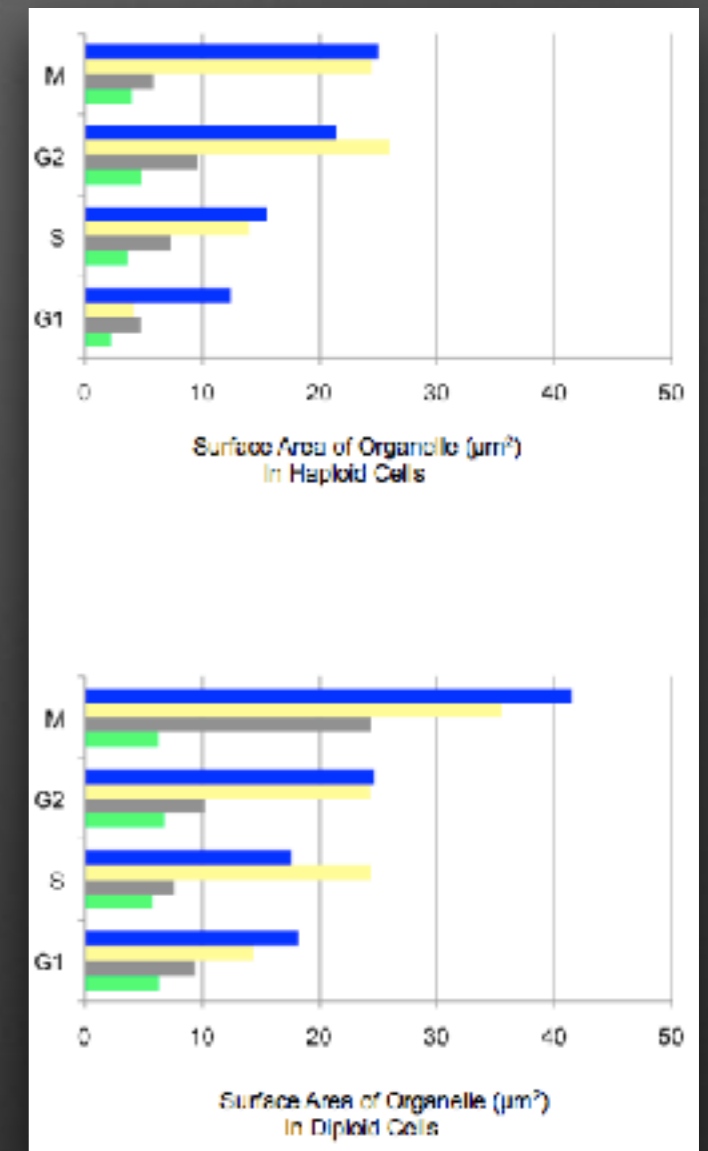
## Cell volume



## Organelle volume

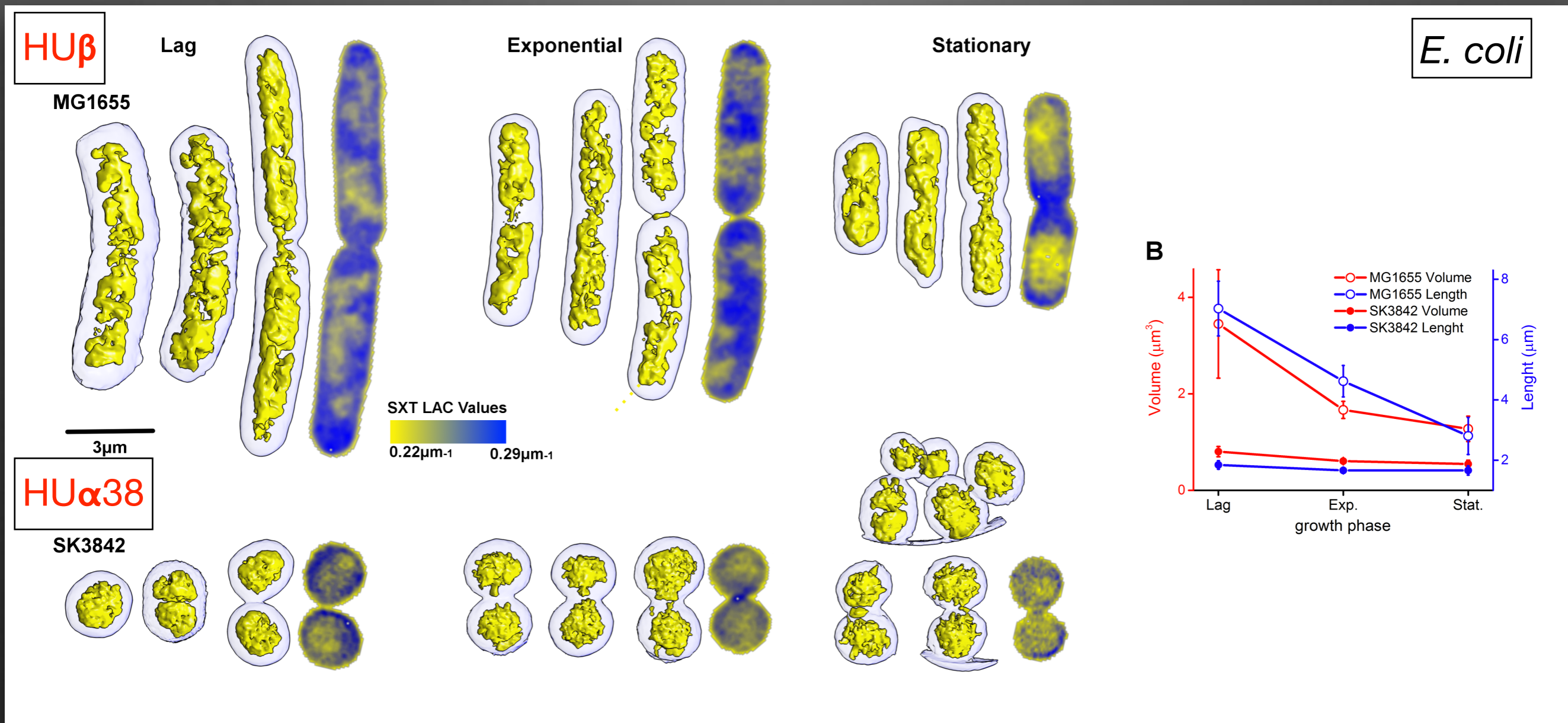


## Organelle surface area



# HU multimerization shift controls nucleoid compaction

HU - histone like protein





# Testing drugs for sickle cell disease

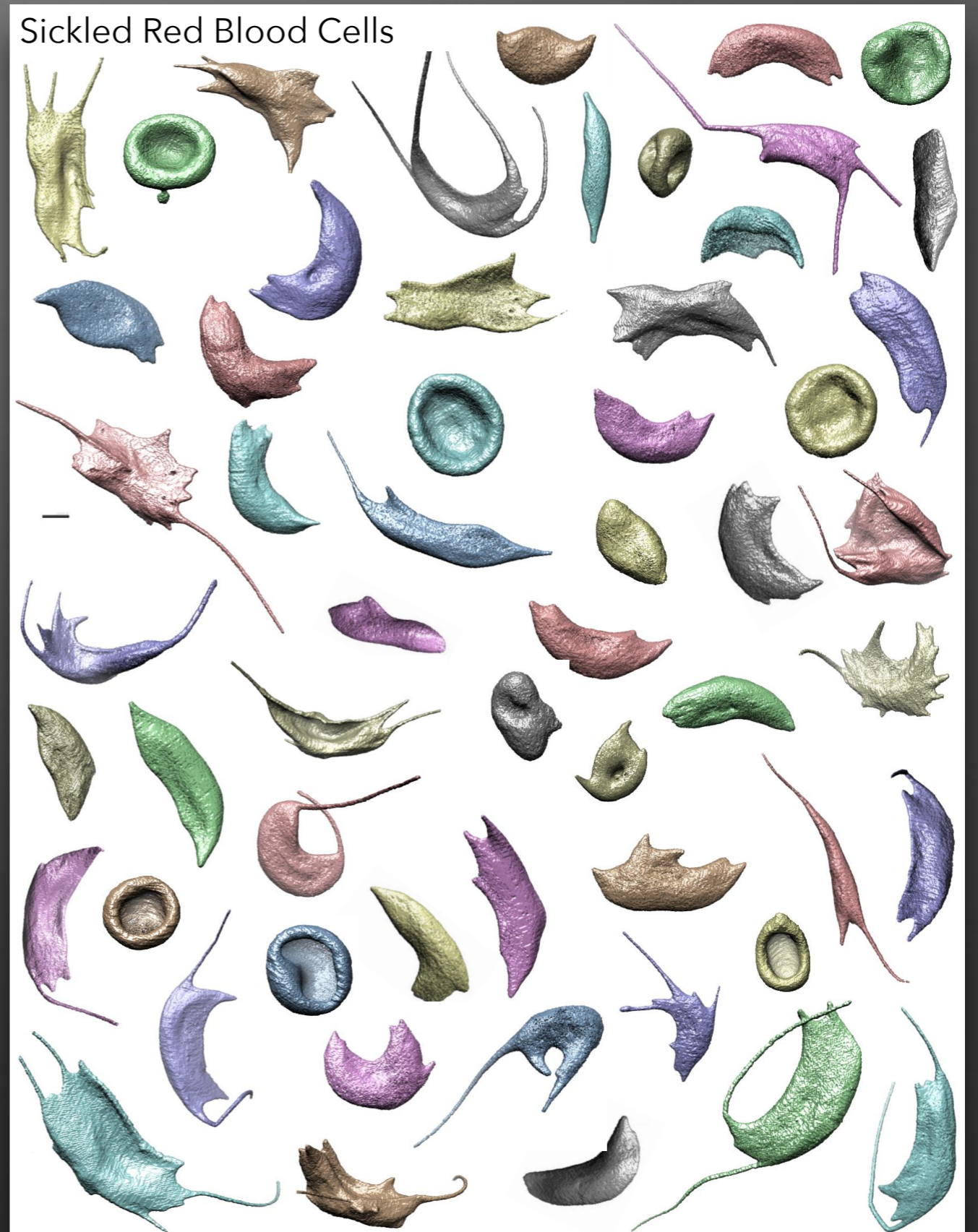
Wah Chiu

Michele Darrow

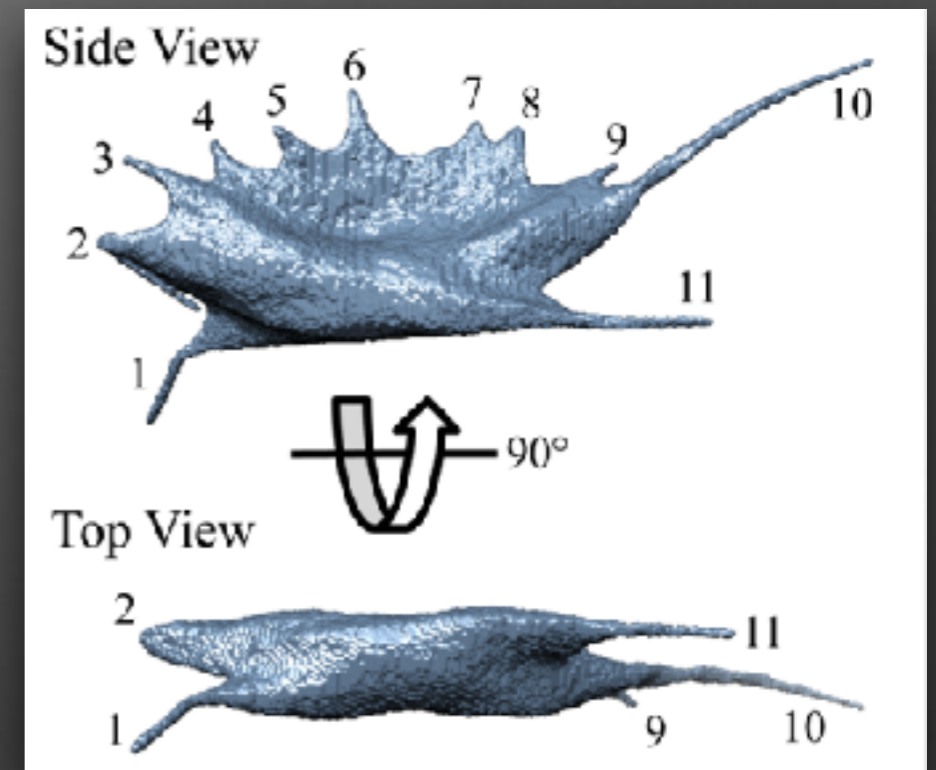
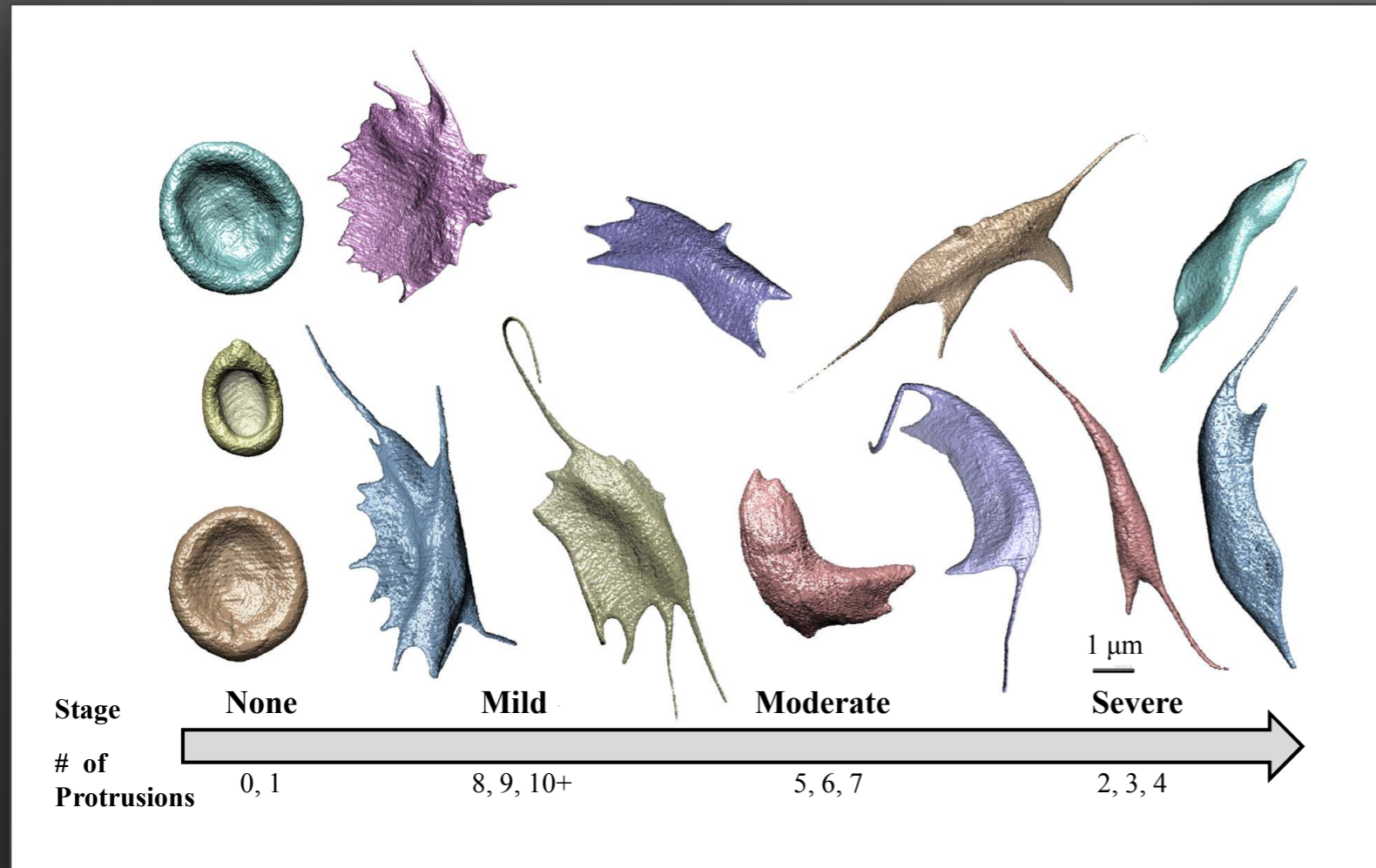
Baylor College of Medicine

Yang Xia

University of Texas Health  
Science Center



# Testing efficacy of drugs to reverse sickling



# Malaria-infected red blood cells

Leann Tilley  
Eric Hanssen

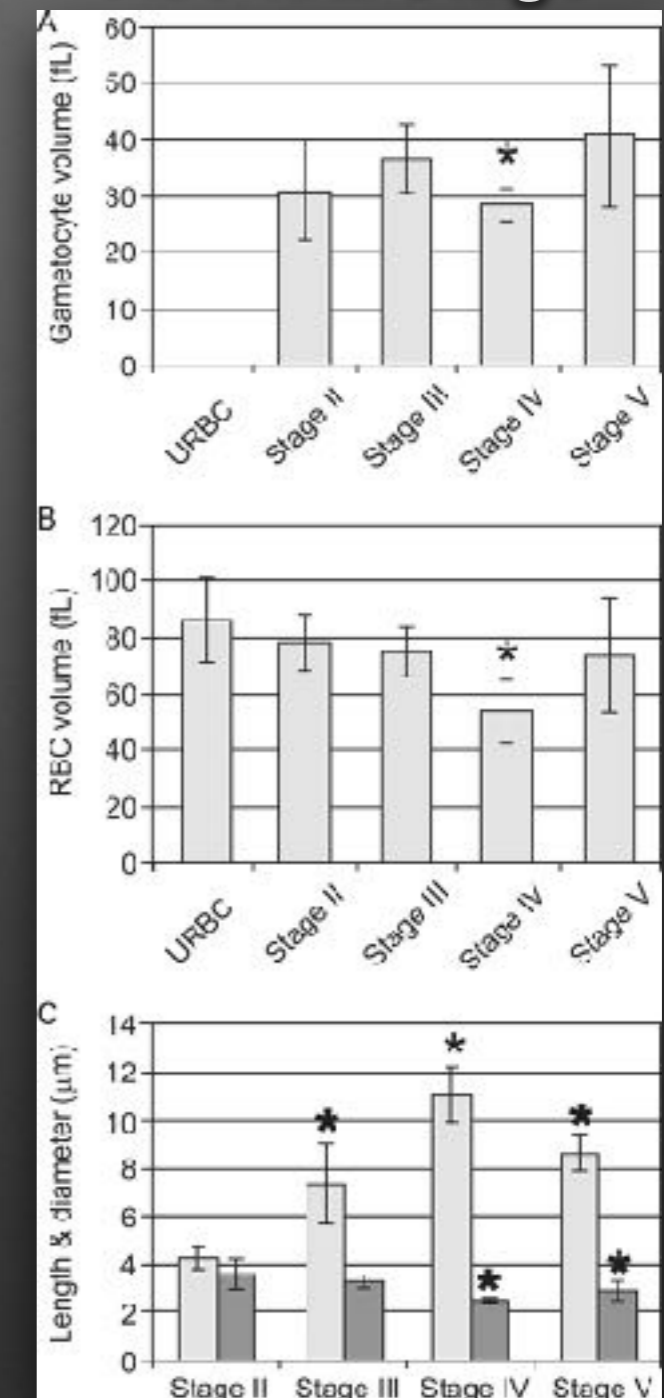
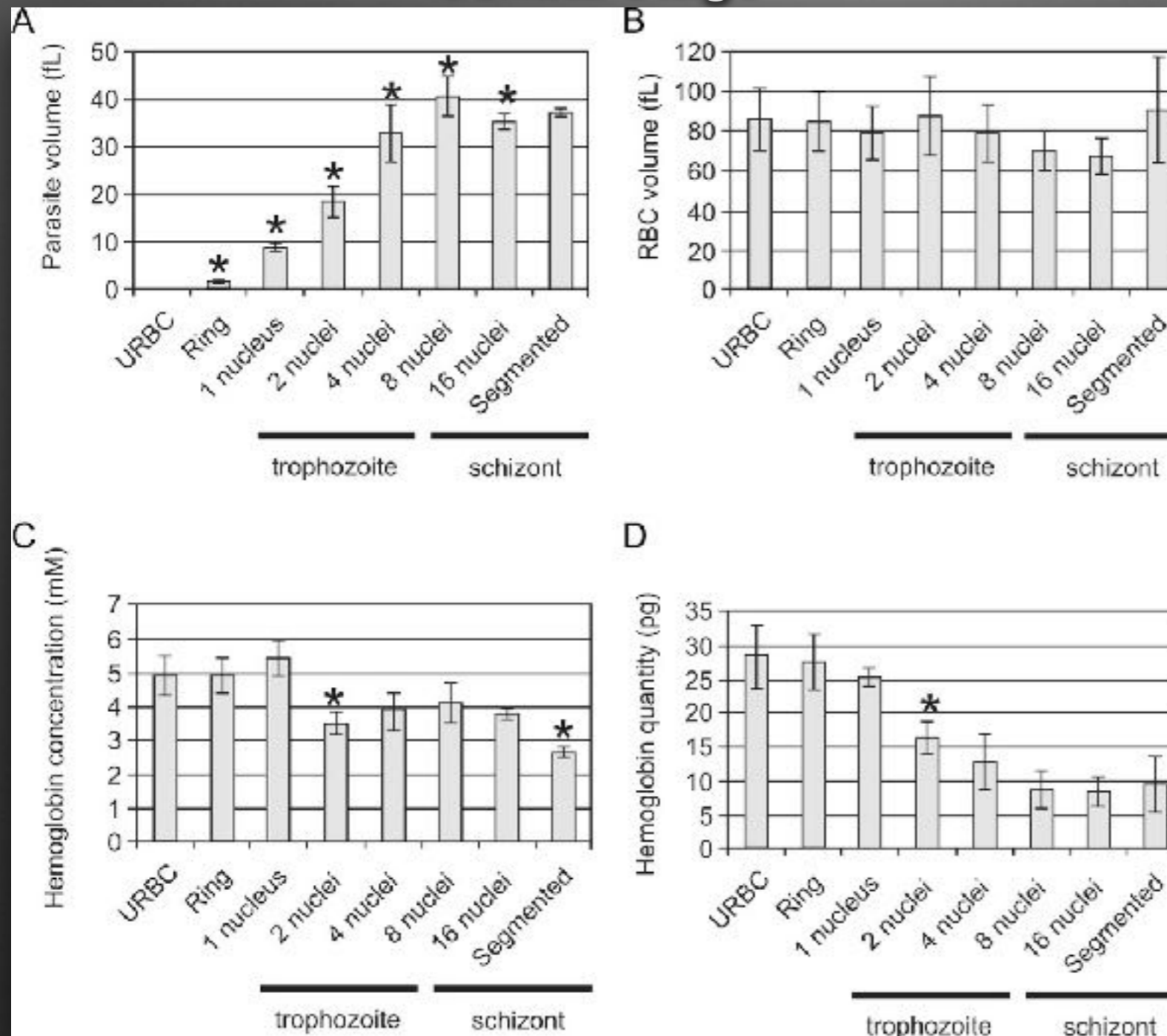
University of Melbourne  
Australia



# Malaria-infected RBC

Sexual stage

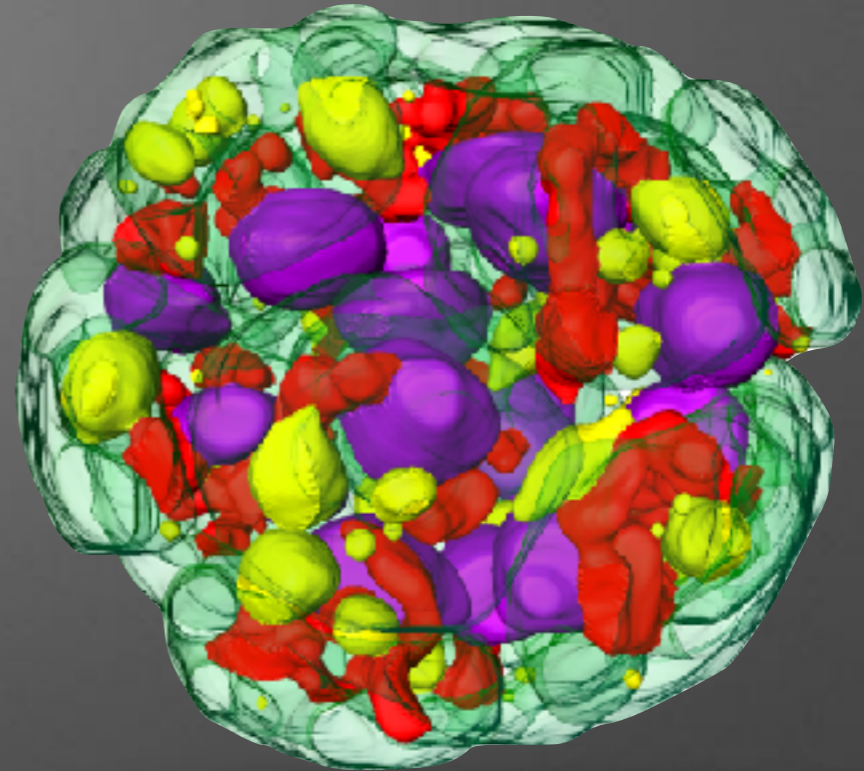
Asexual stage



# Photosynthesis, Bioenergy

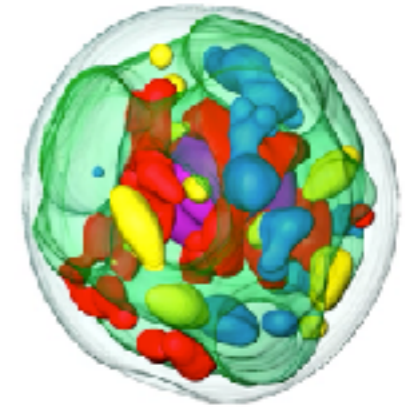
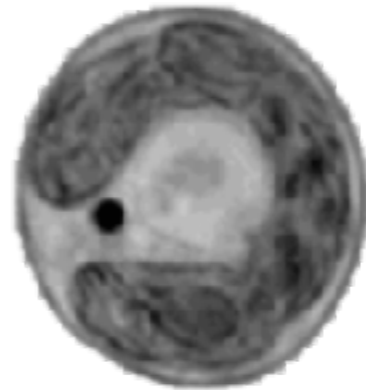
Krishna Niyogi

University of California  
Berkeley & HHMI

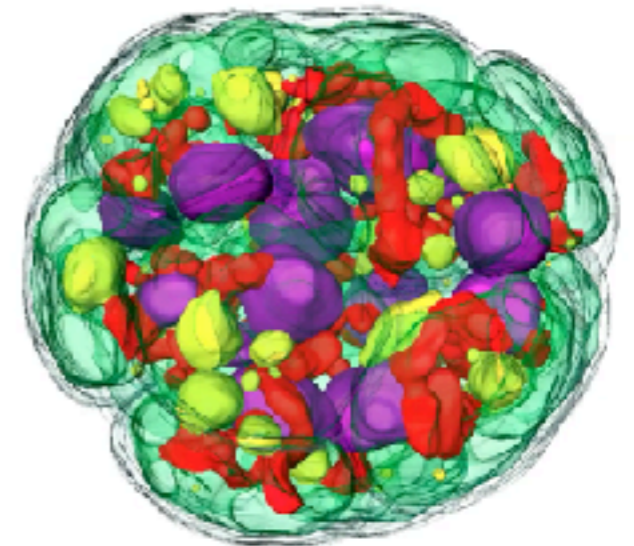
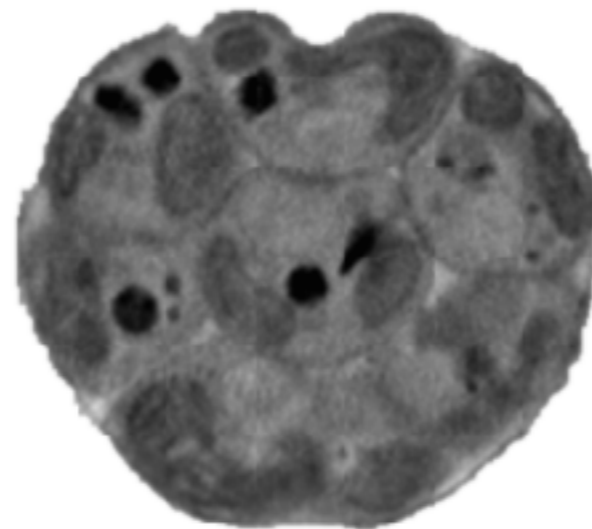


# *Chromochloris zofingiensis*

Single cell



16 cells



- Chloroplast
- Starch
- Mitochondria
- Nucleus
- Lipid bodies

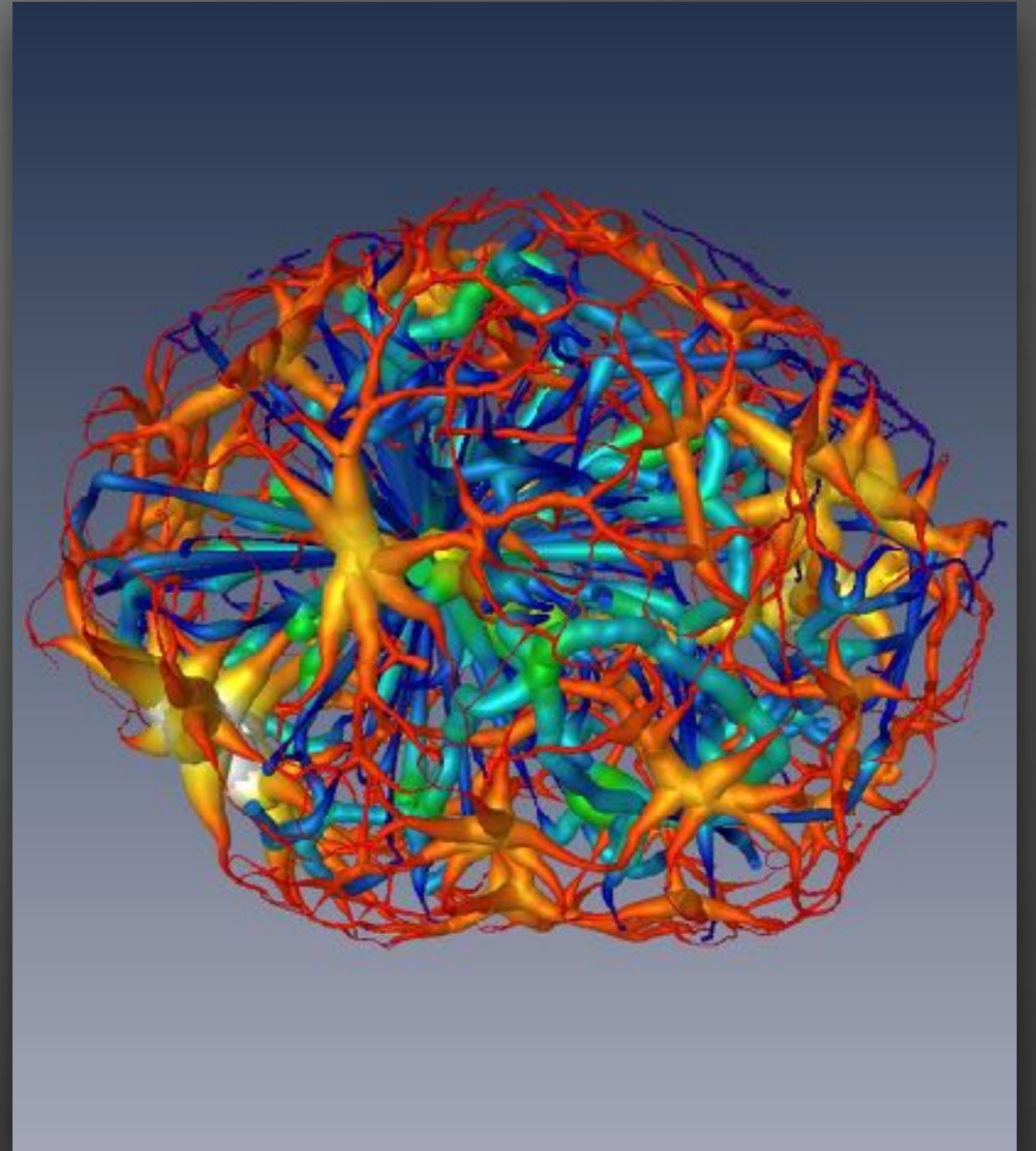
*Roth et al., PNAS, in revision.*

# **Role of nuclear organization in gene expression**

# Chromatin condensation during neurogenesis

Stavros Lomvardas  
Columbia University

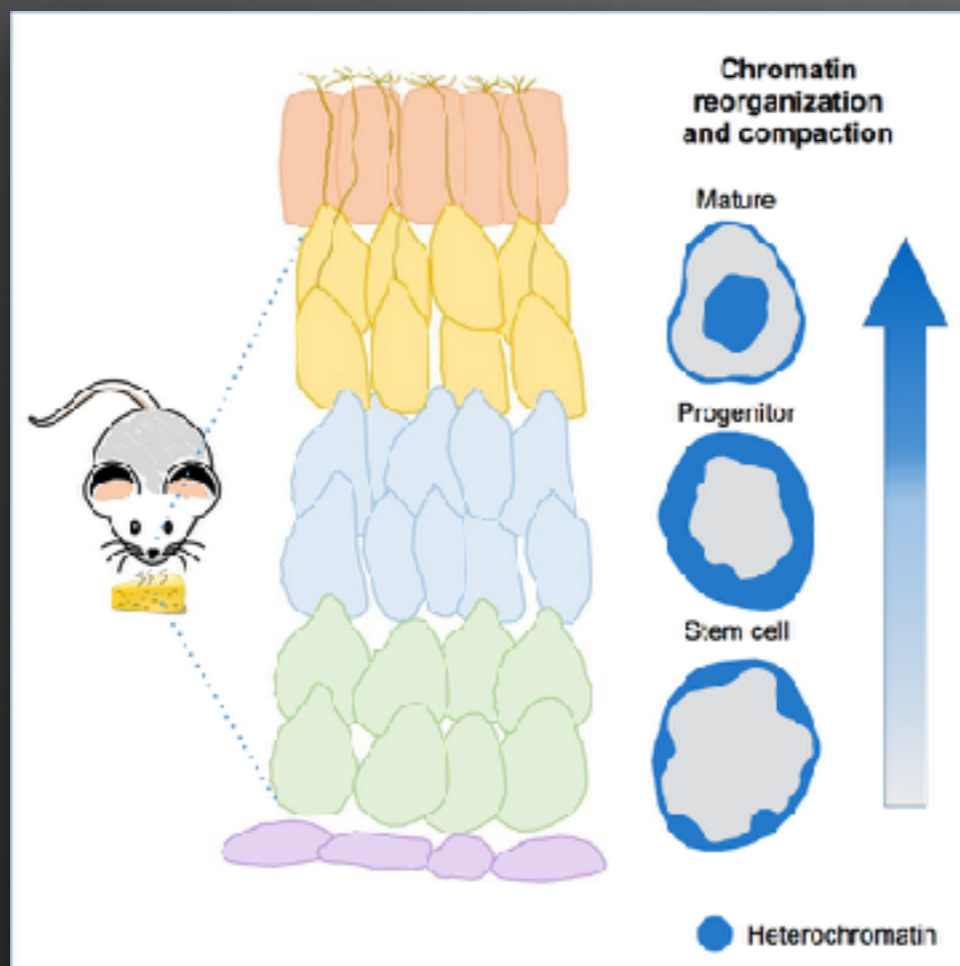
Mark Le Gros & Carolyn Larabell  
University of California  
San Francisco



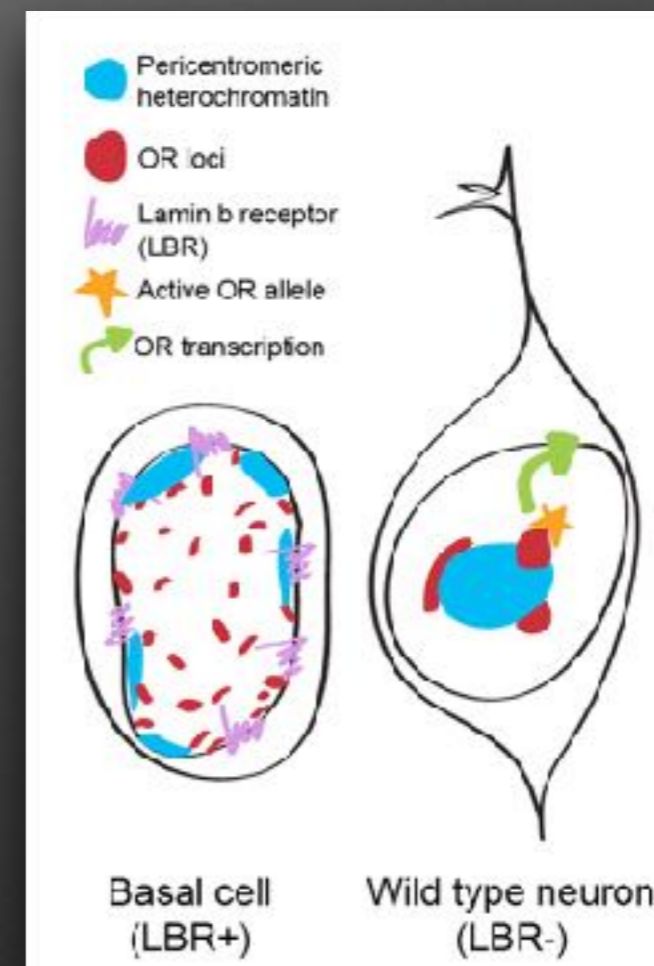


# Neurogenesis: from stem cell to neuron

- About 1200 Olfactory Receptor (OR) genes found in 18 mouse chromosomes
- Each neuron transcribes *one* out of ~2400 OR alleles
- Allele selection occurs during neurogenesis



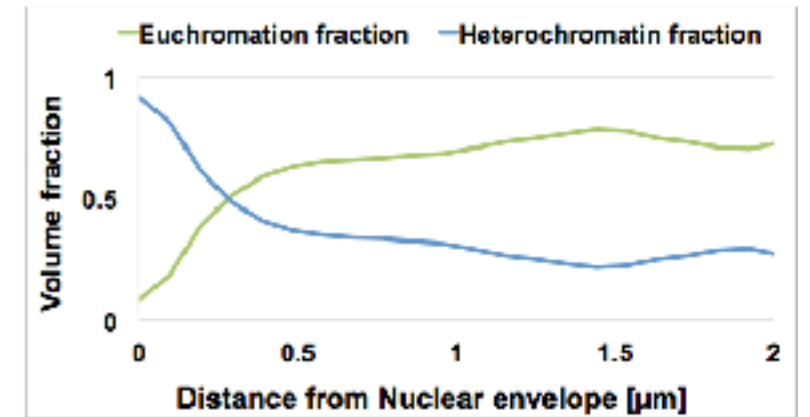
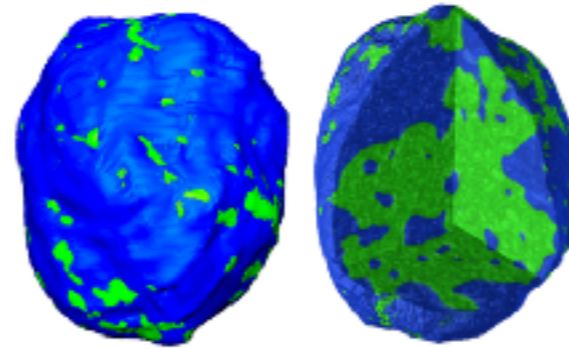
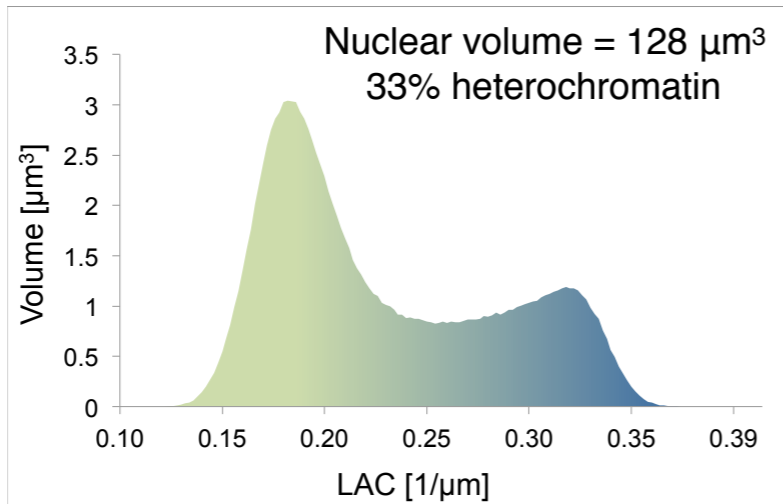
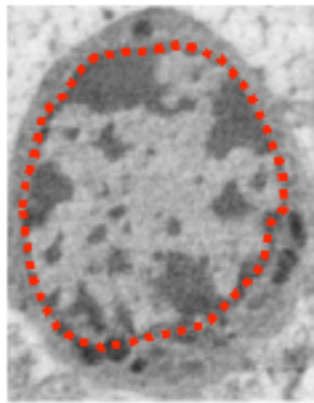
*Le Gros et al. (2016) Cell Reports. 17(8), 2125-2136*



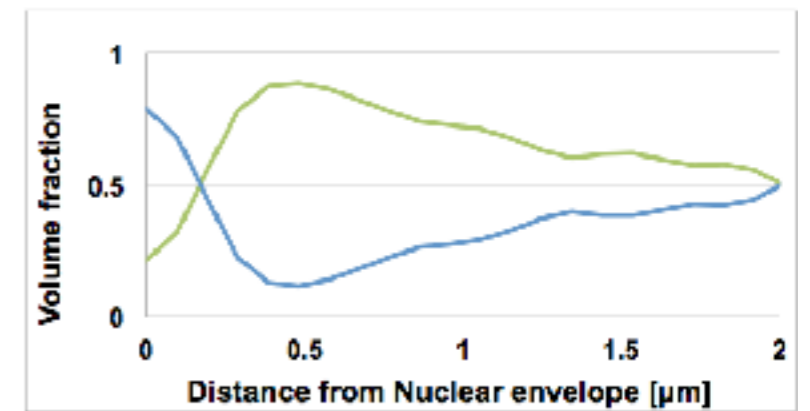
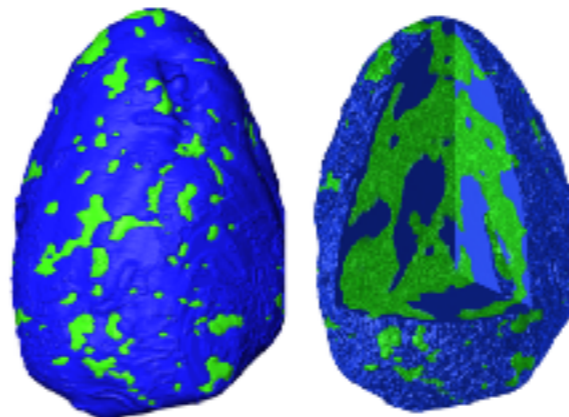
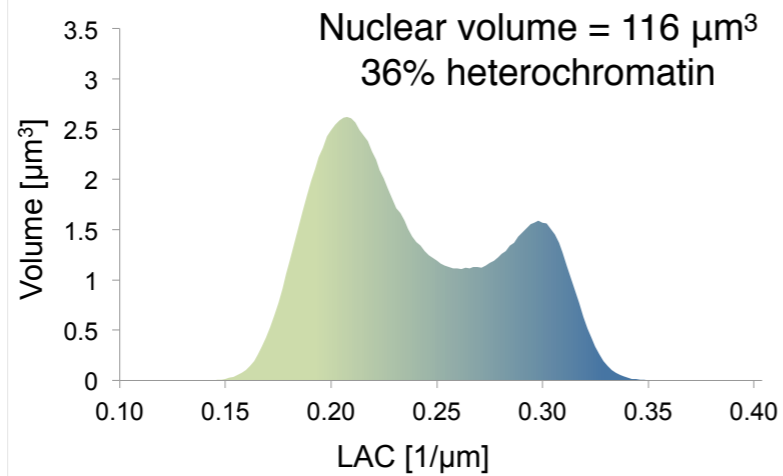
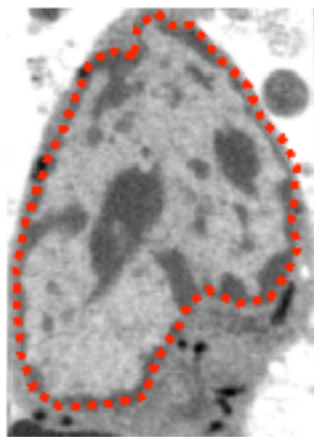
*Clowney et al. Cell. 151, 724-737*

# From stem cell to neuron

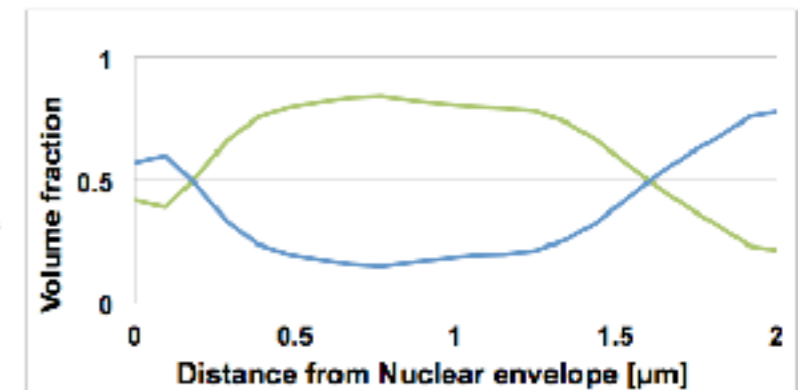
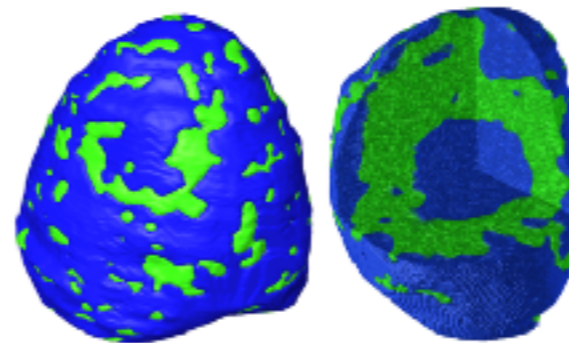
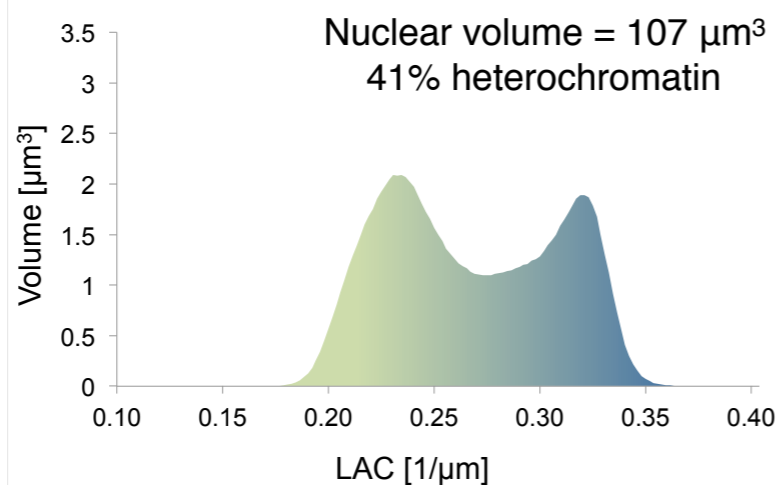
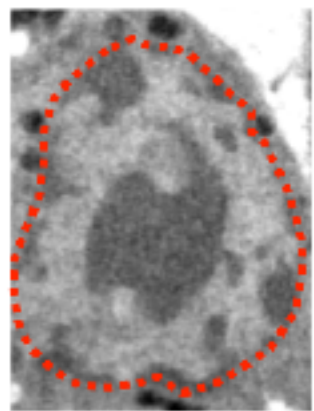
Stem cell



Progenitor

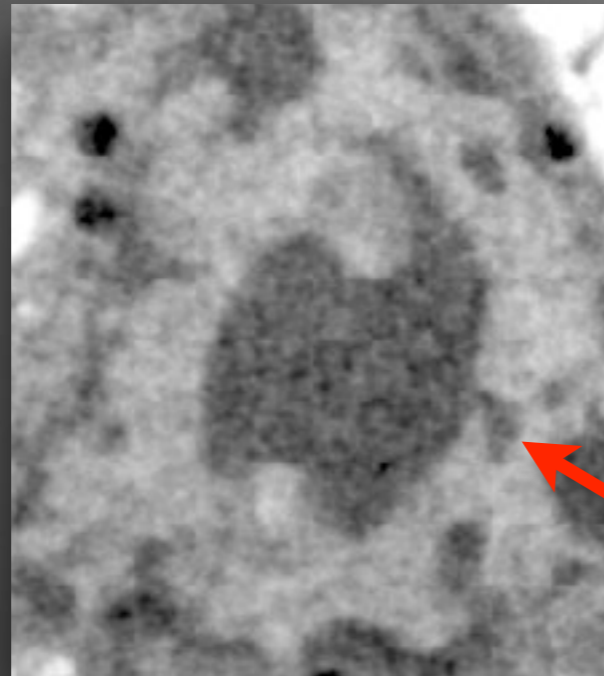


Mature

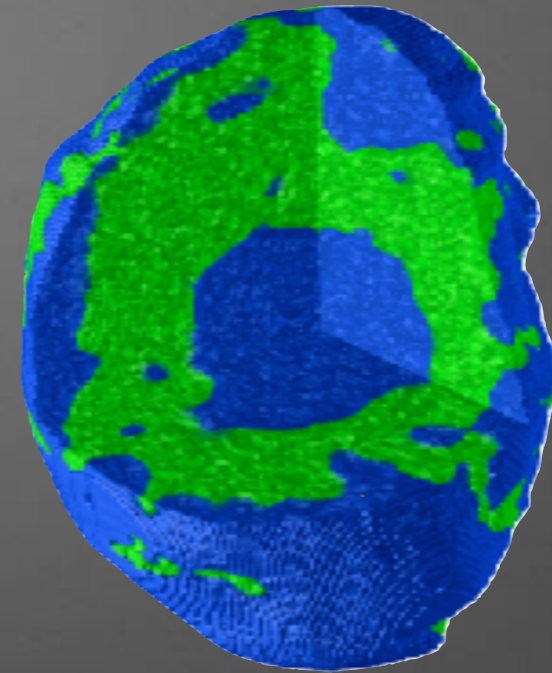


# Nuclear structure and gene selection

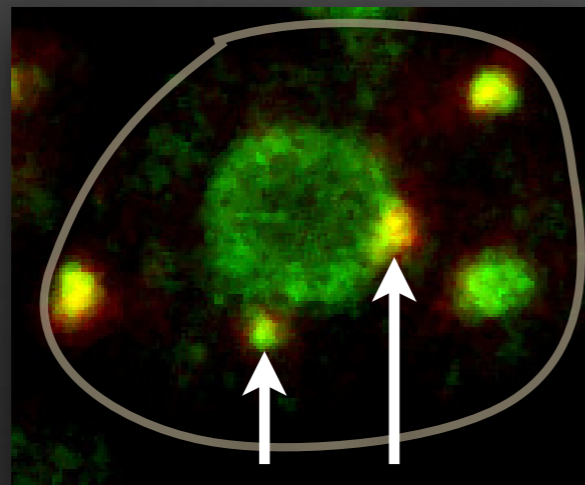
SXT



Silenced genes

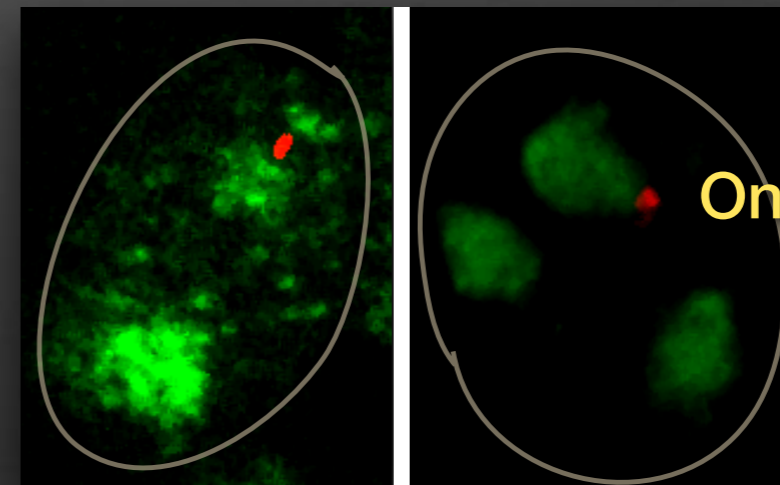


Pan OR



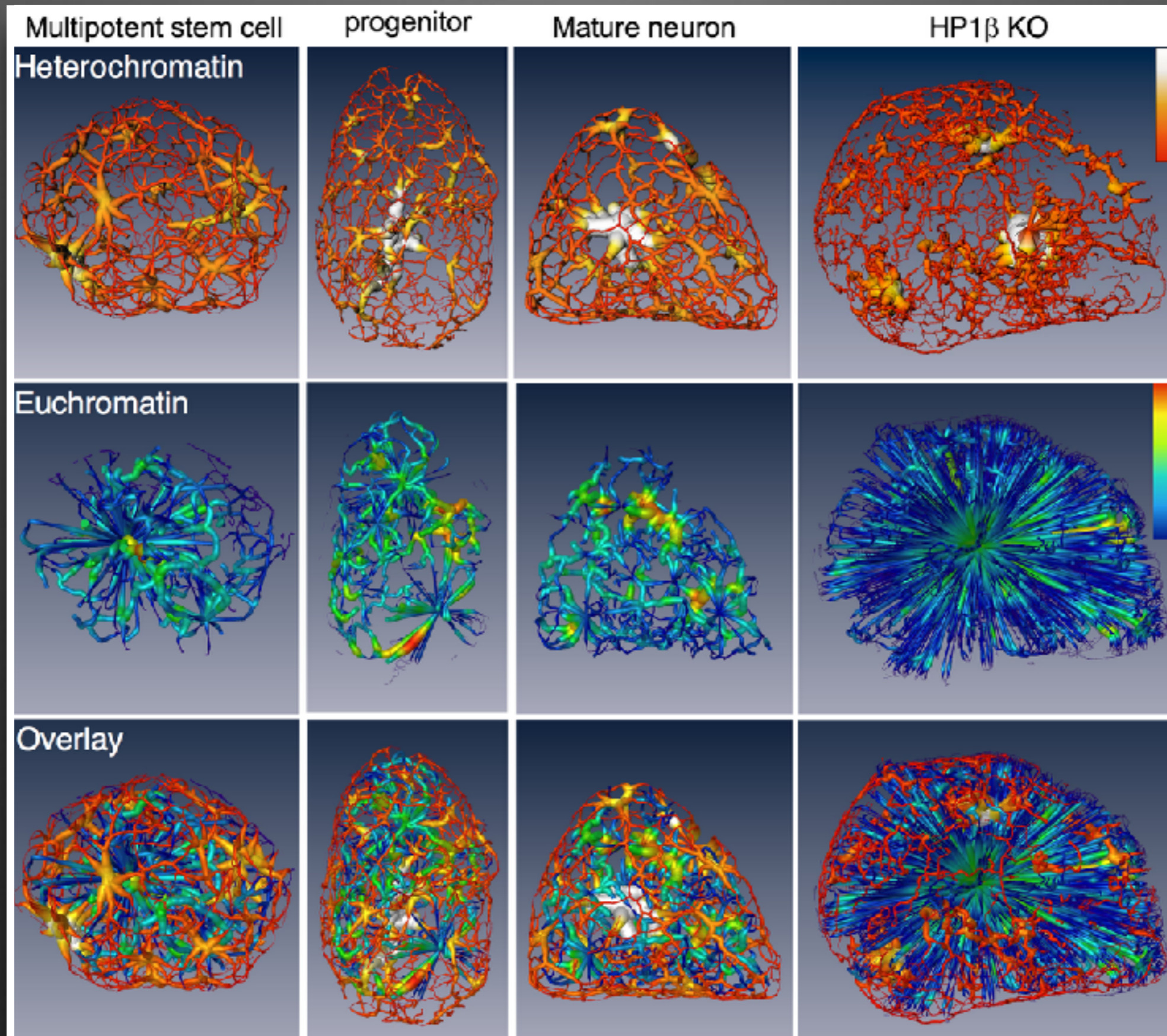
Silenced genes

Mor28



One active allele

# Chromatin networks

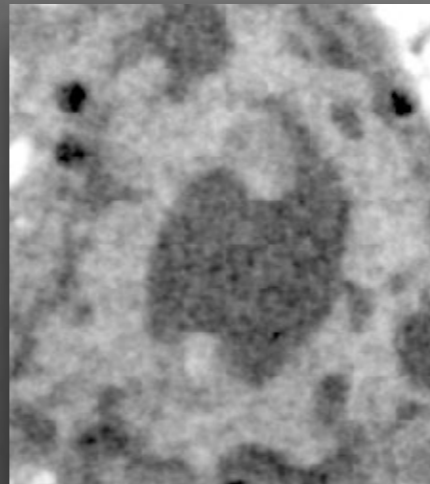


**3D organization of the nucleus**  
**critical for normal differentiation**

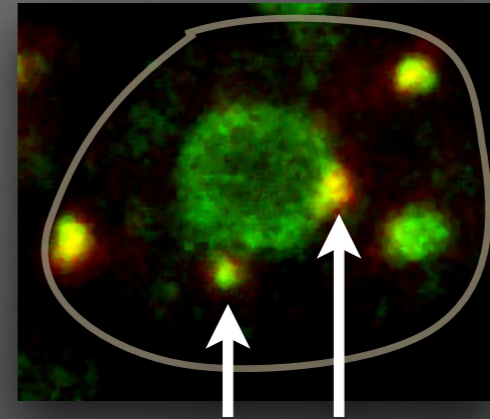
# Nuclear structure and gene selection

Wild type cell

SXT



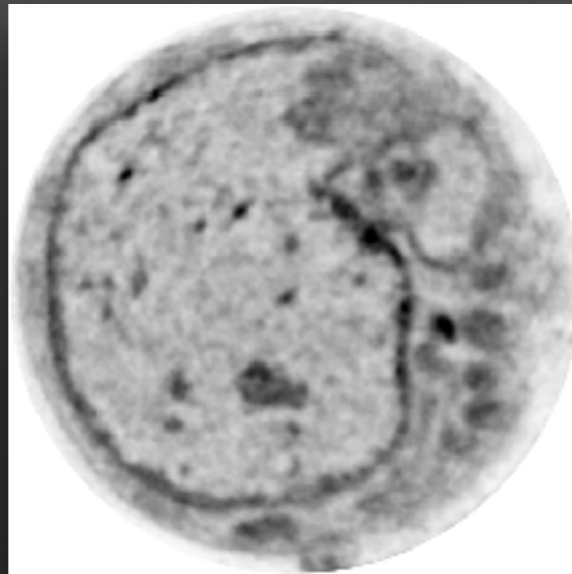
FISH



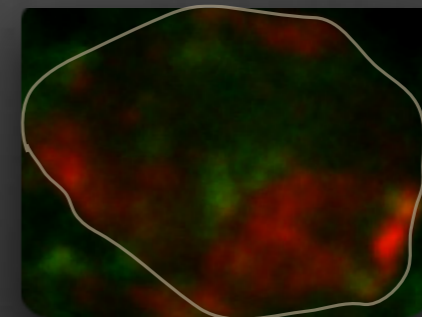
Silenced genes

LBR expressing cell

SXT



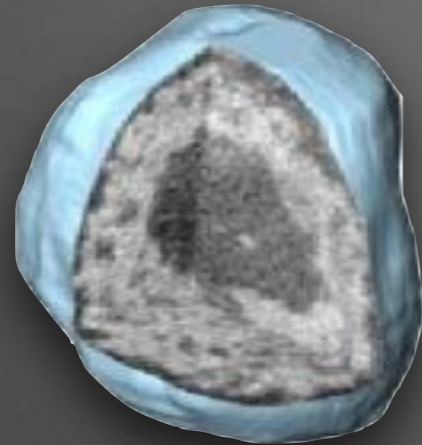
FISH



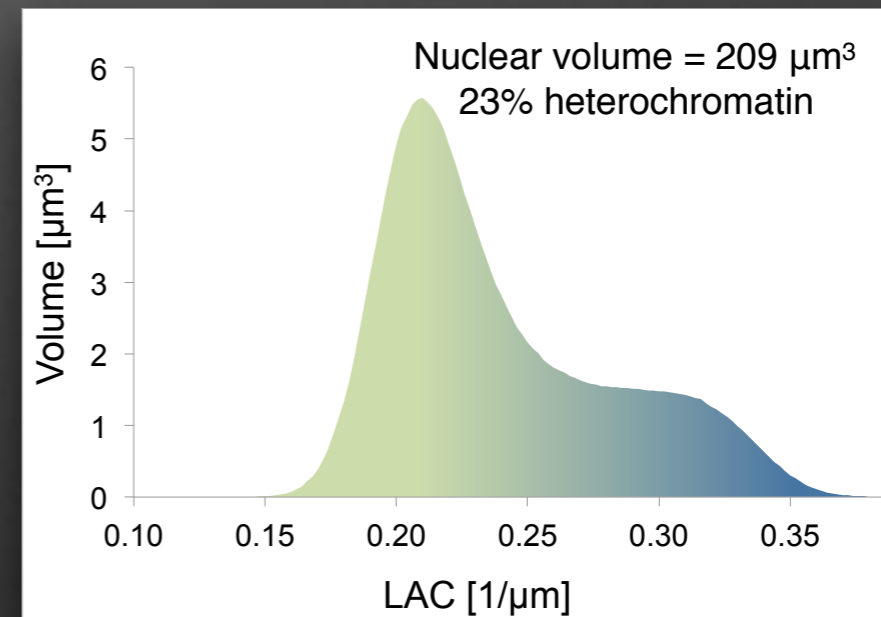
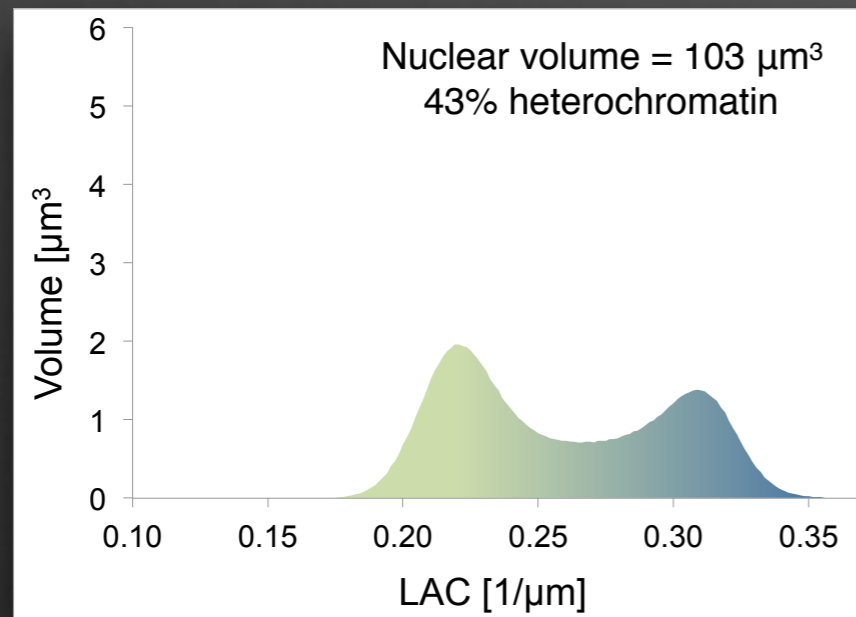
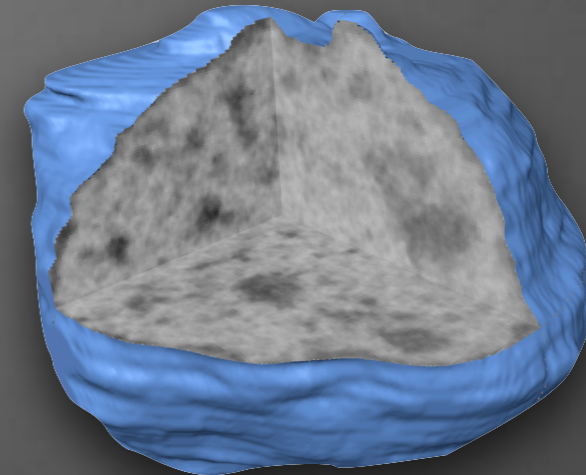
OR expression disrupted

# Nuclear structure and gene selection

Wild type



Hp1 $\beta$  KO



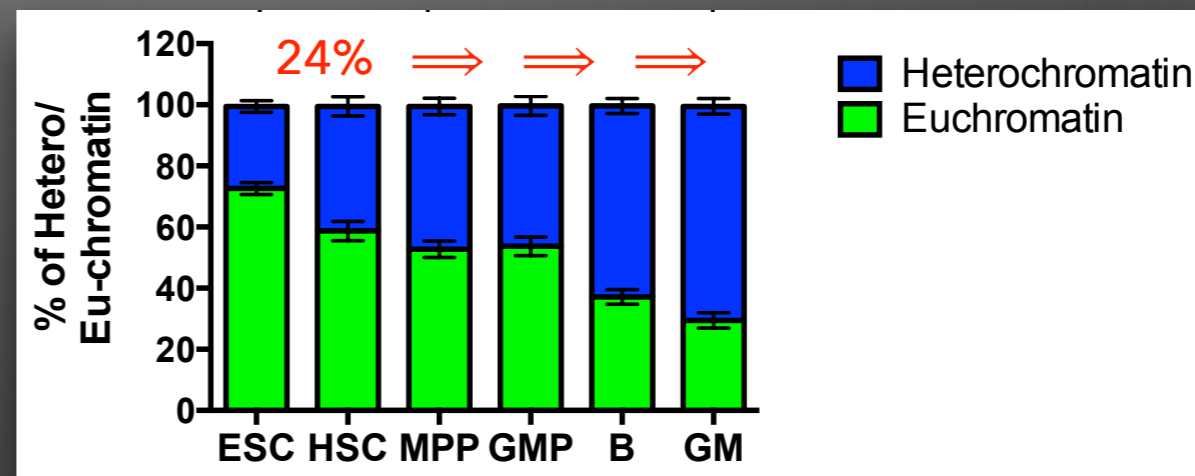
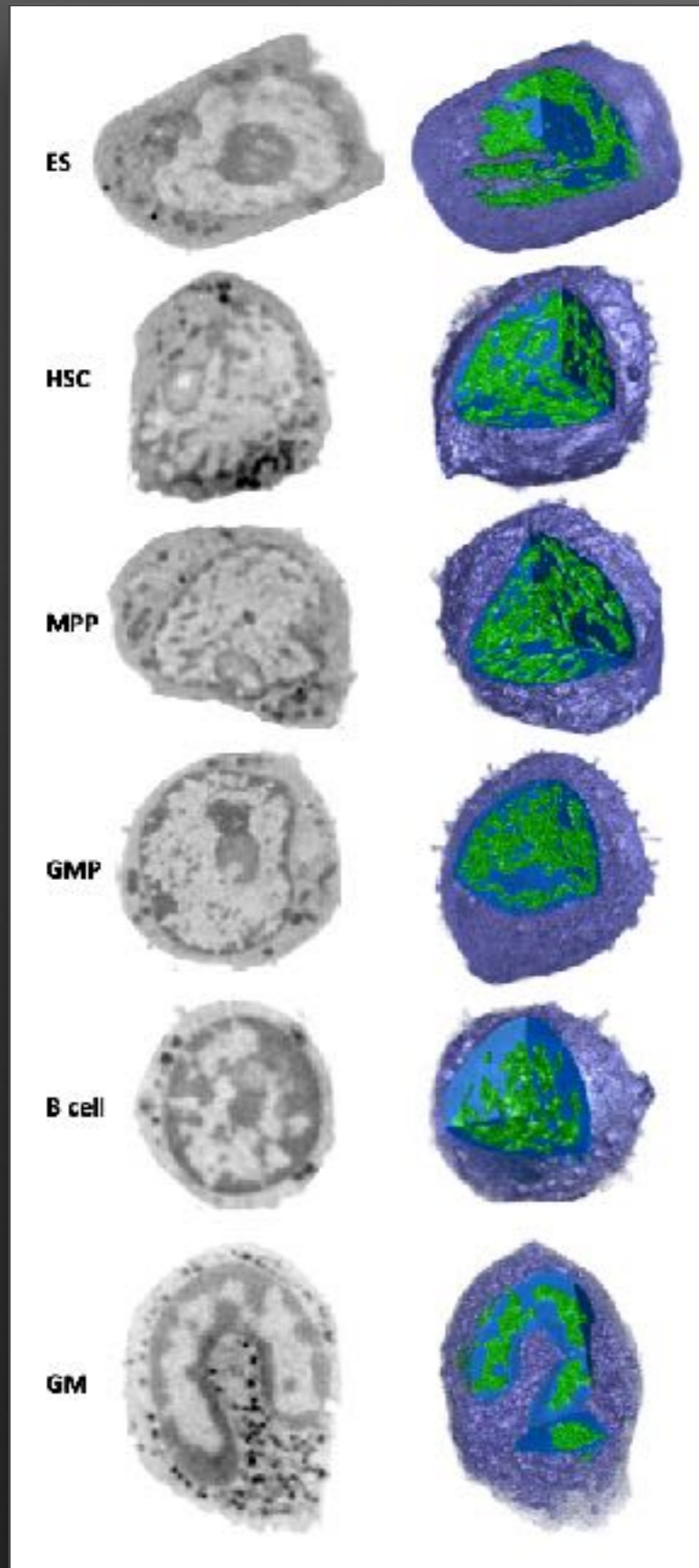
# **Nuclear organization**



# From stem cell to blood cell

During differentiation:

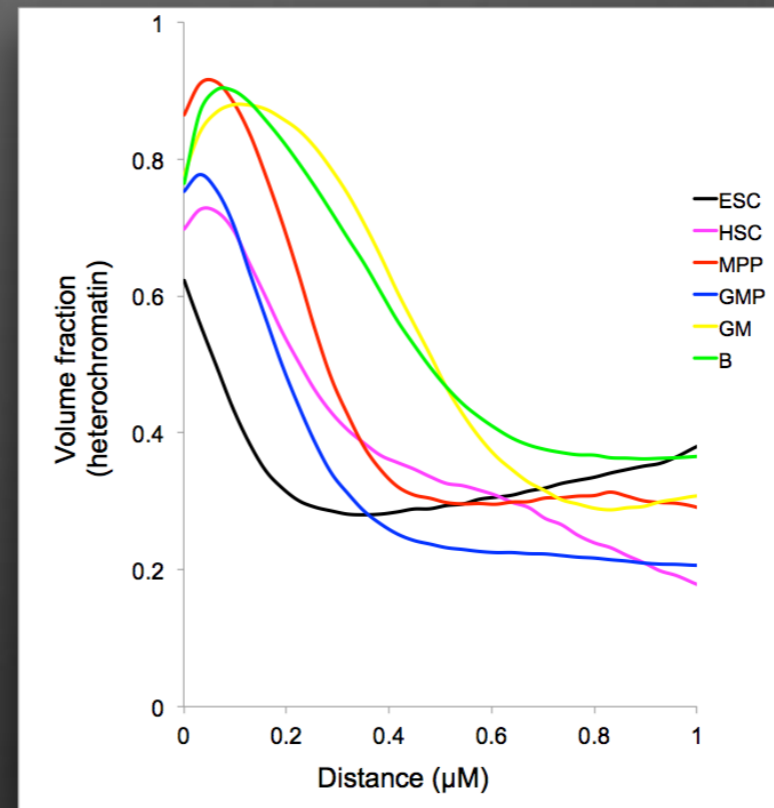
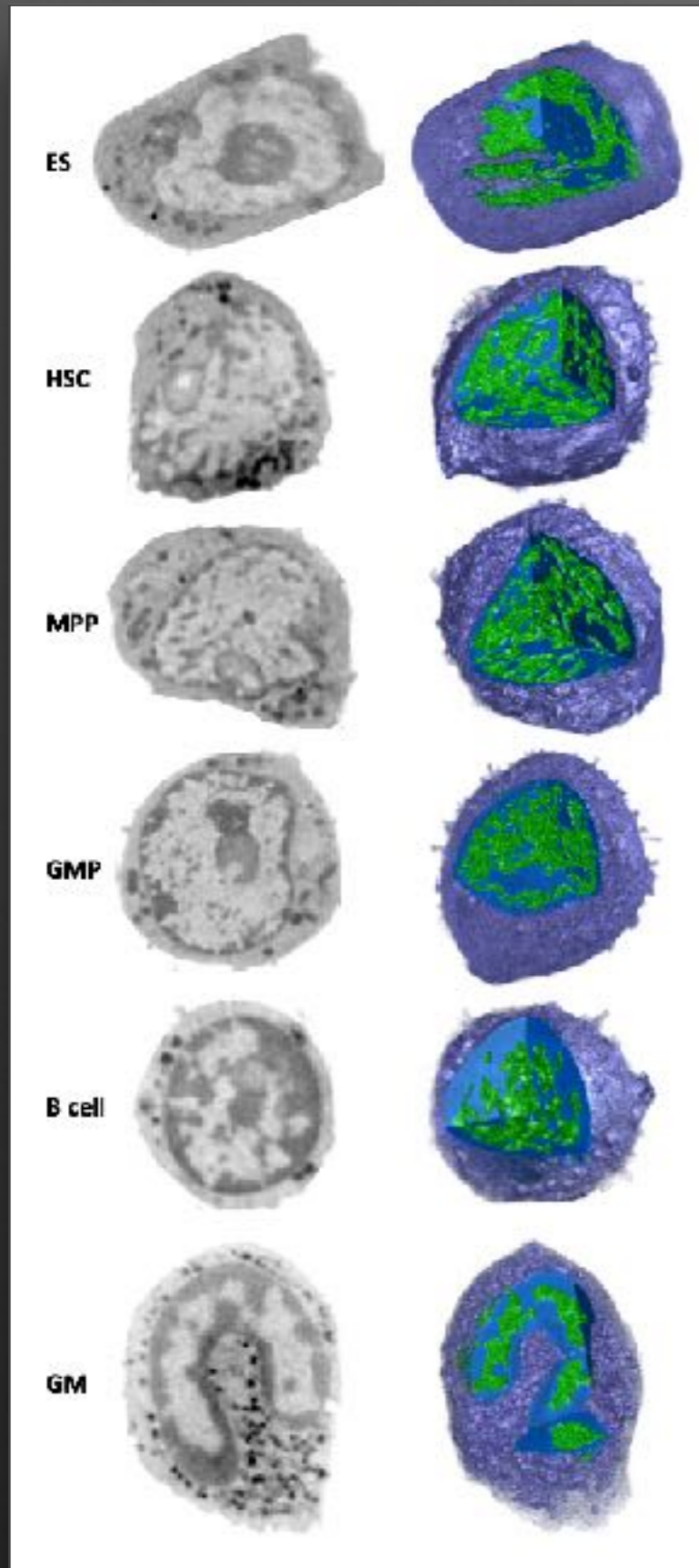
Percent heterochromatin increases



# From stem cell to blood cell

During differentiation:

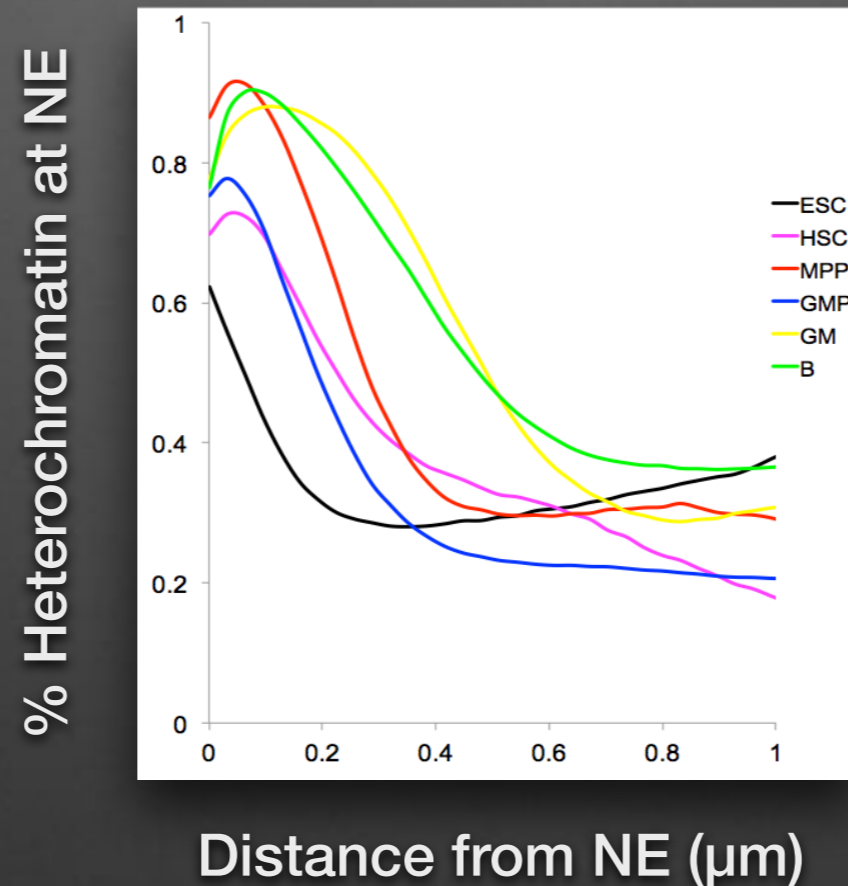
Nuclear volume decreases and peripheral heterochromatin thickens



# Peripheral heterochromatin

- Increases during differentiation
- Decreased in transformed and tumor cells

## Hematopoiesis

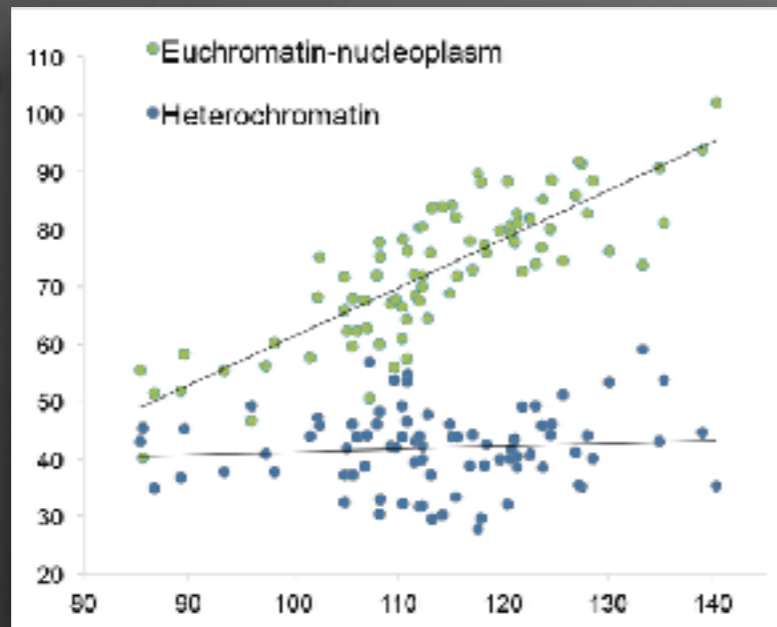


# Nuclear volume

Proportional to volume of euchromatin region

## Neurogenesis

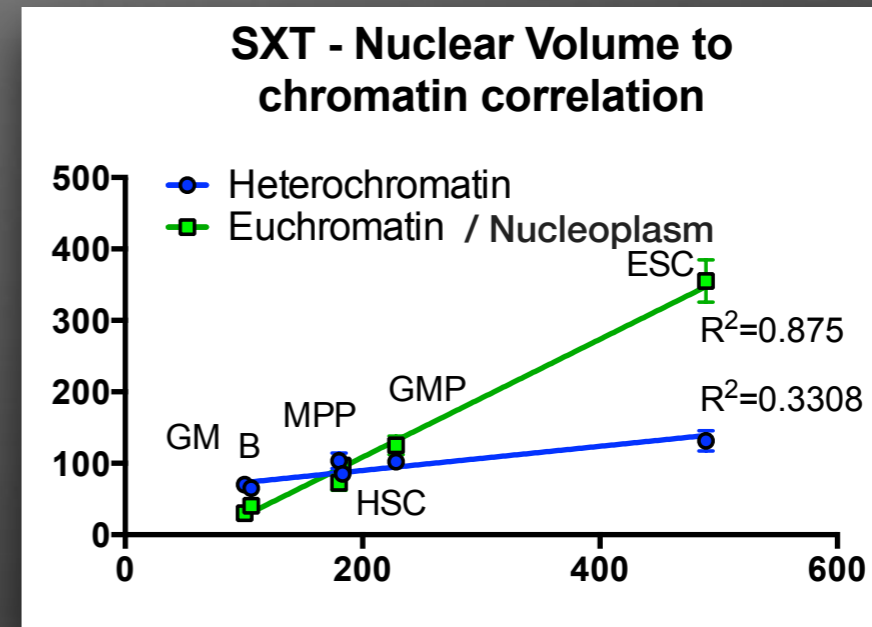
Chromatin volume ( $\mu\text{m}^3$ )



Nuclear volume ( $\mu\text{m}^3$ )

*Le Gros et al. (2016) Cell Reports. 17(8), 2125-2136*

## Hematopoiesis

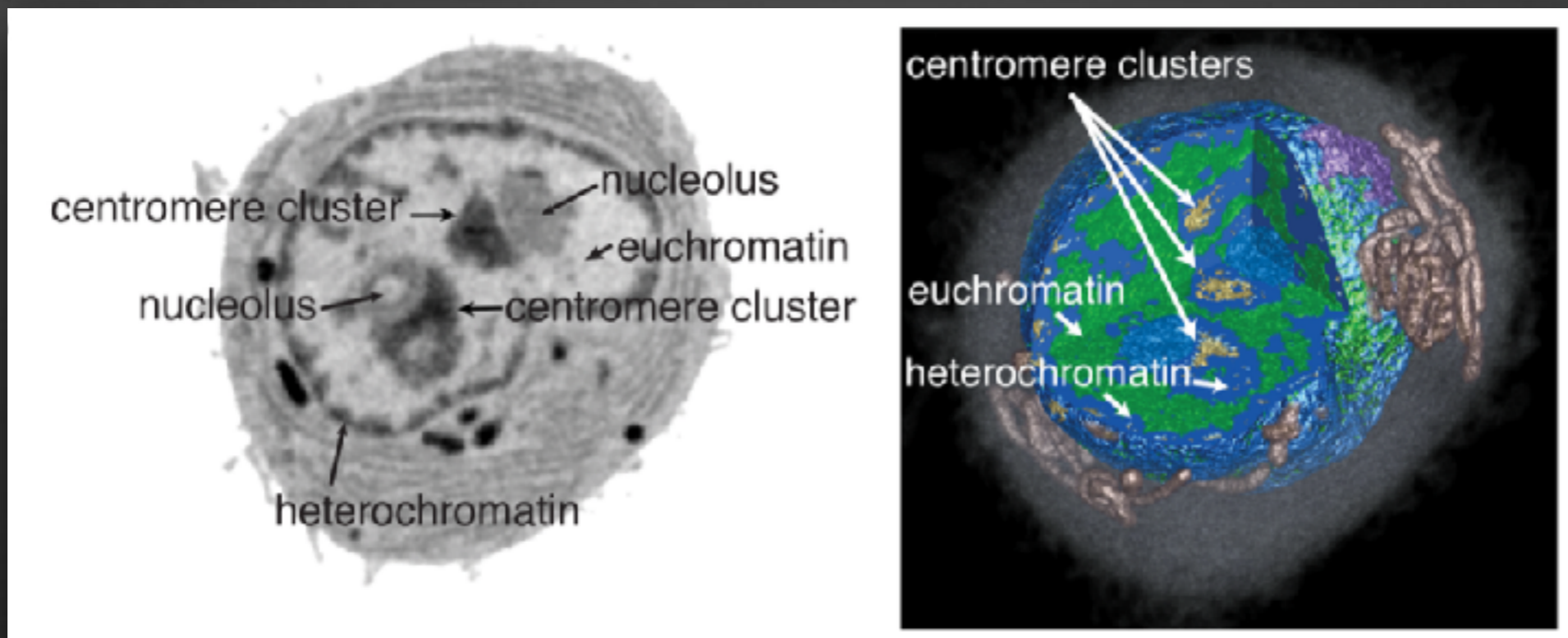
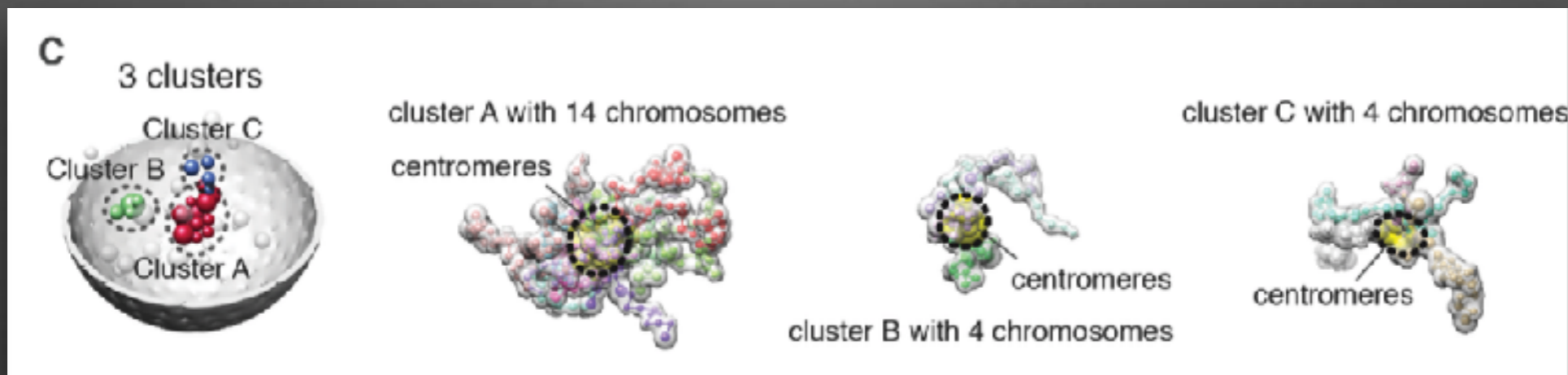


Nuclear volume ( $\mu\text{m}^3$ )

*Ugarte et al. (2015) Stem Cell Reports. 5(5), 728-470*

# Topology of the human genome

3D structural models of the human genome at 4Mb resolution



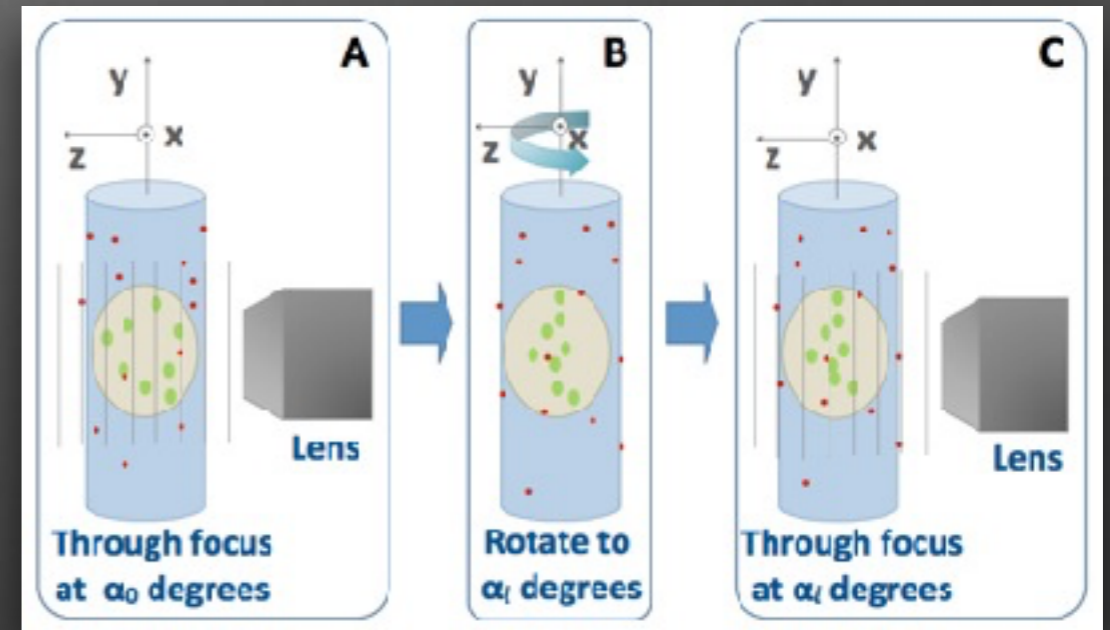
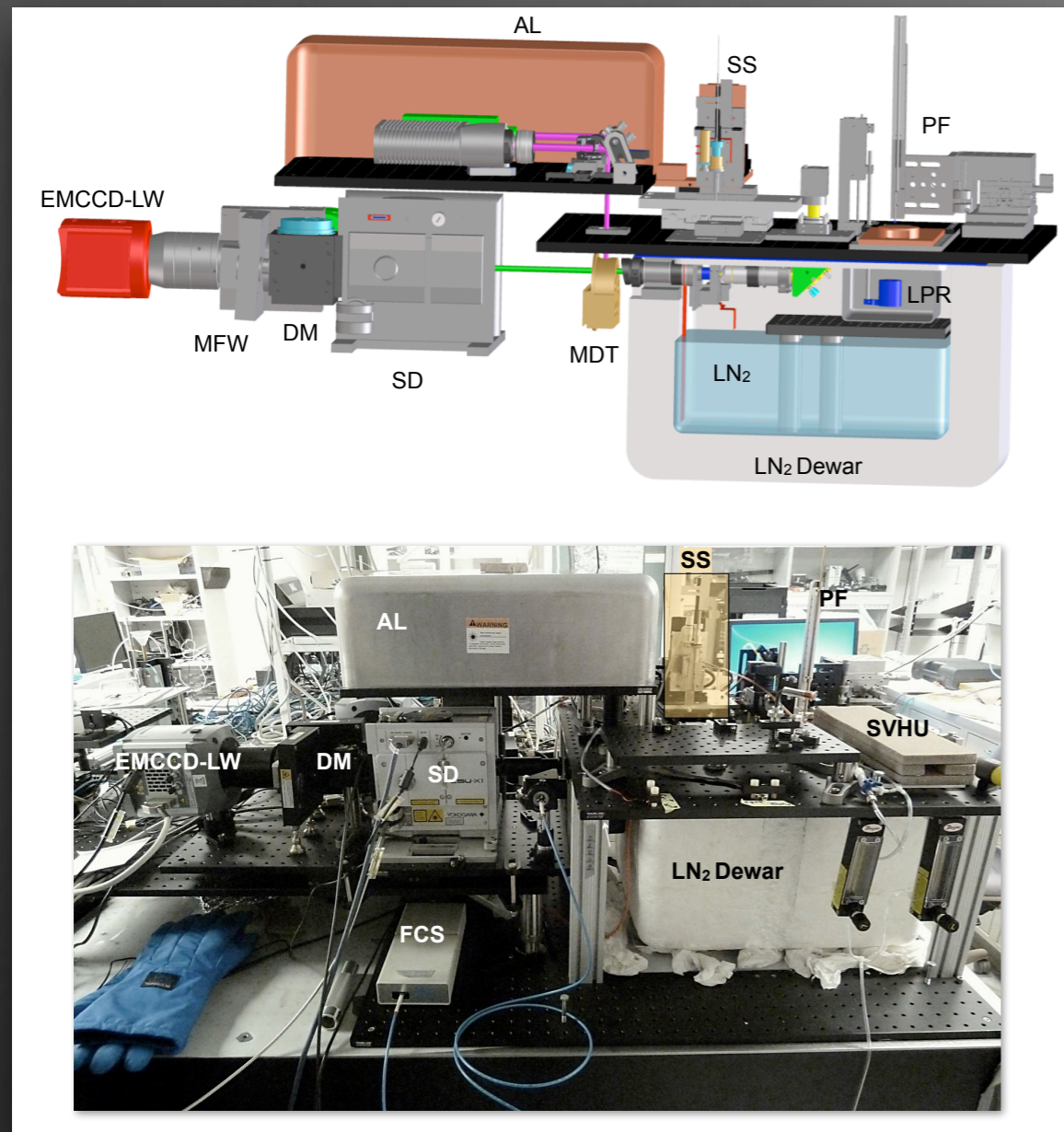
Future

# **Correlated fluorescence and x-ray tomography**

# Fluorescence, super-resolution, etc.



# Cryo confocal tomography

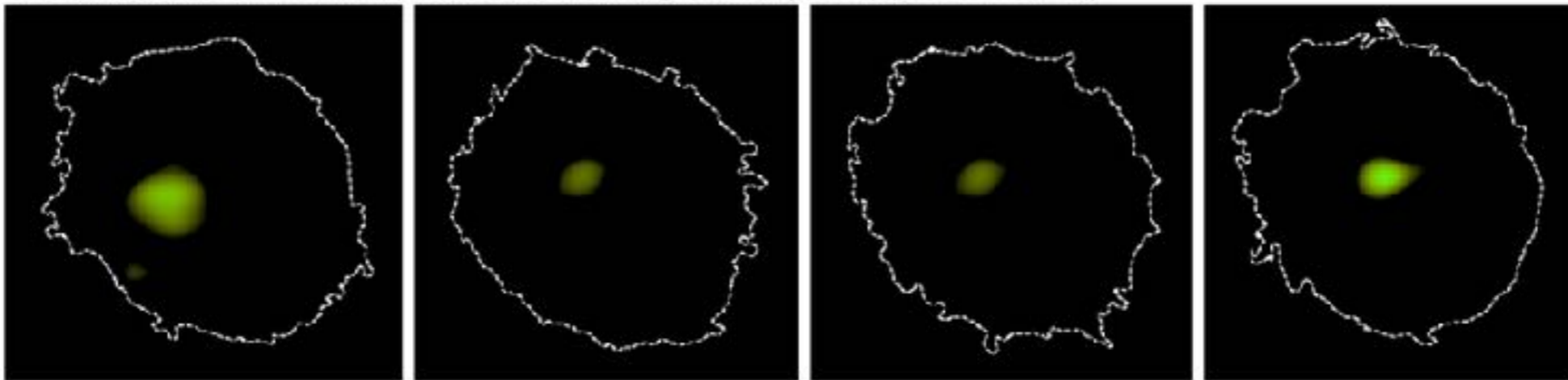


*Le Gros et al. (2009) J. Microscopy. 235(1), 1-8*

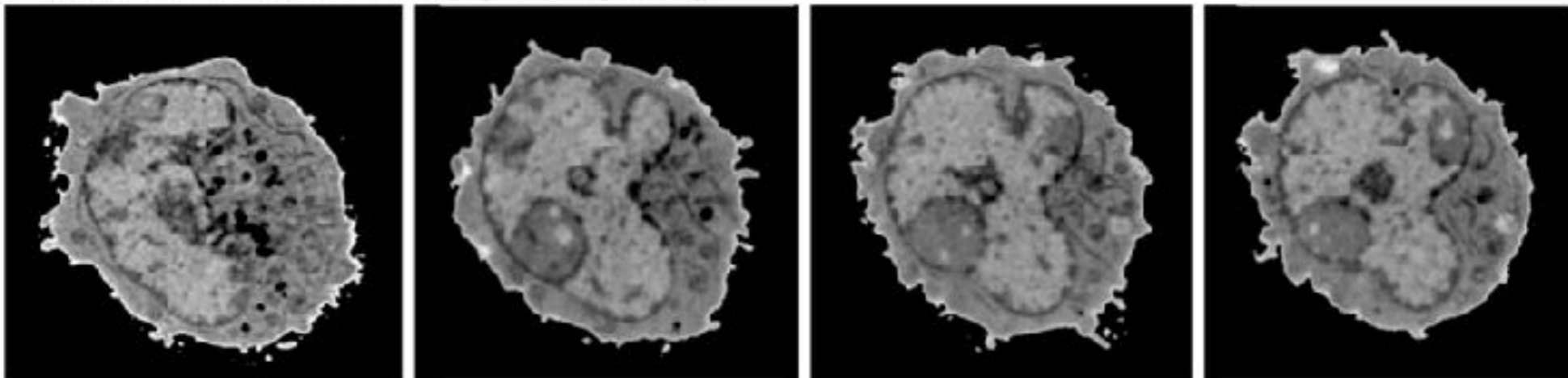


# Inactive X chromosome

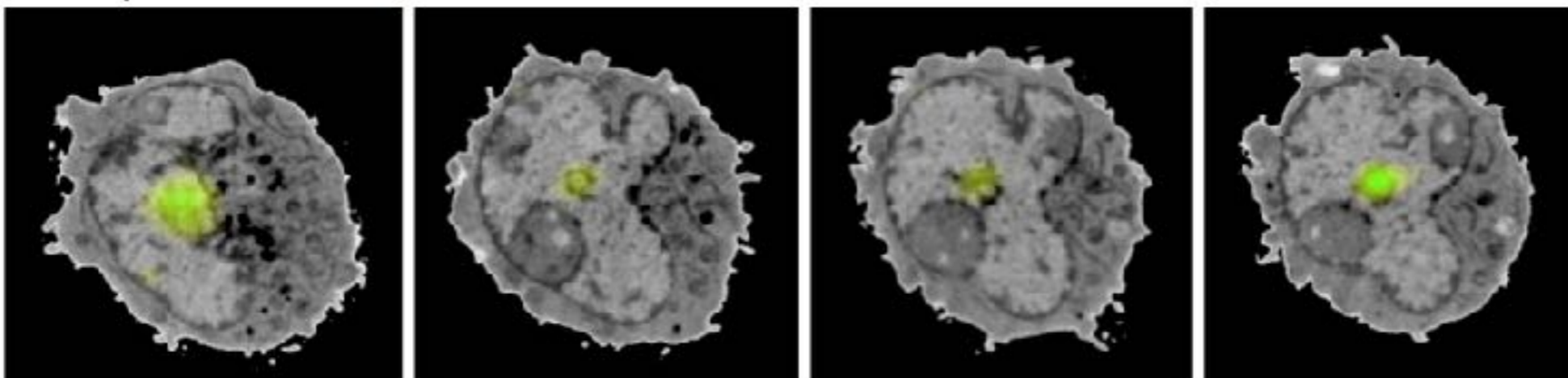
2D orthoslices from fluorescence tomography (MacroH2A-EGFP)



2D orthoslices from soft x-ray tomography



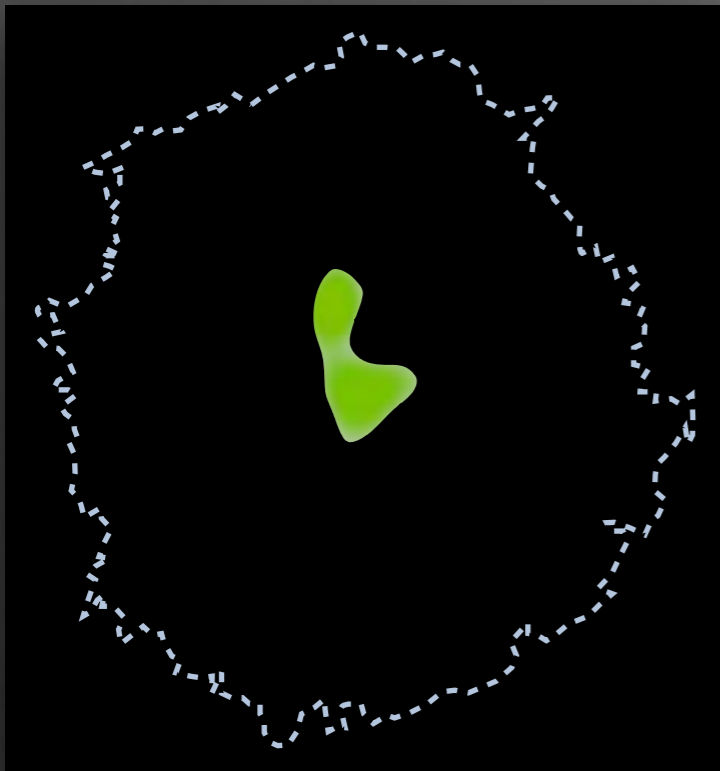
Overlay of above fluorescence on SXT orthoslices



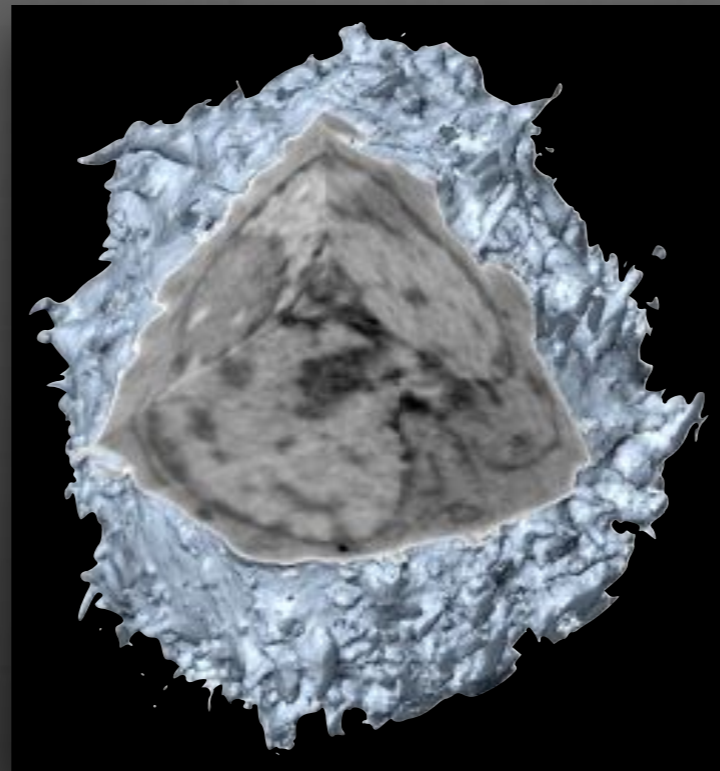
# Correlated fluorescence and x-ray tomography

## Inactive X chromosome

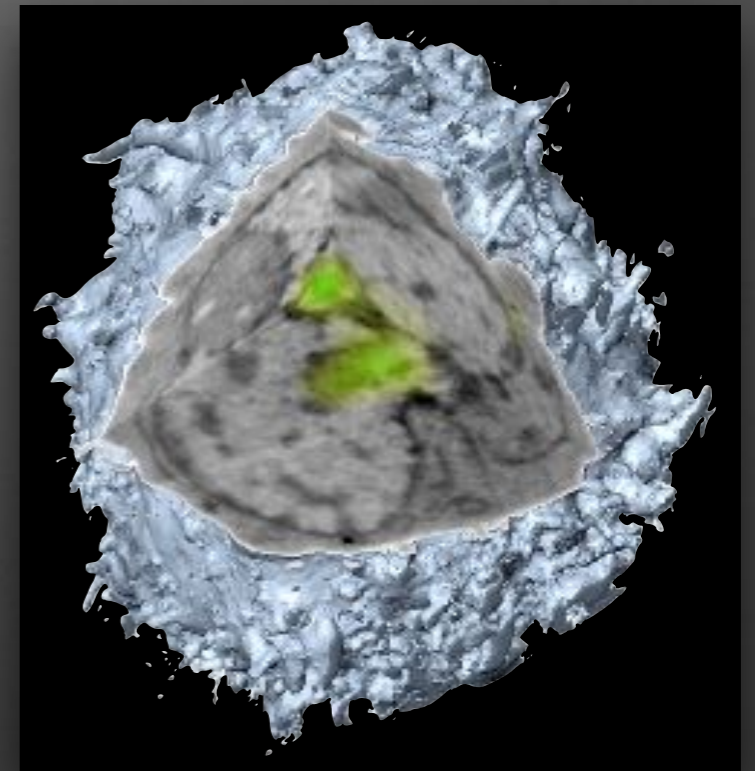
Fluorescence



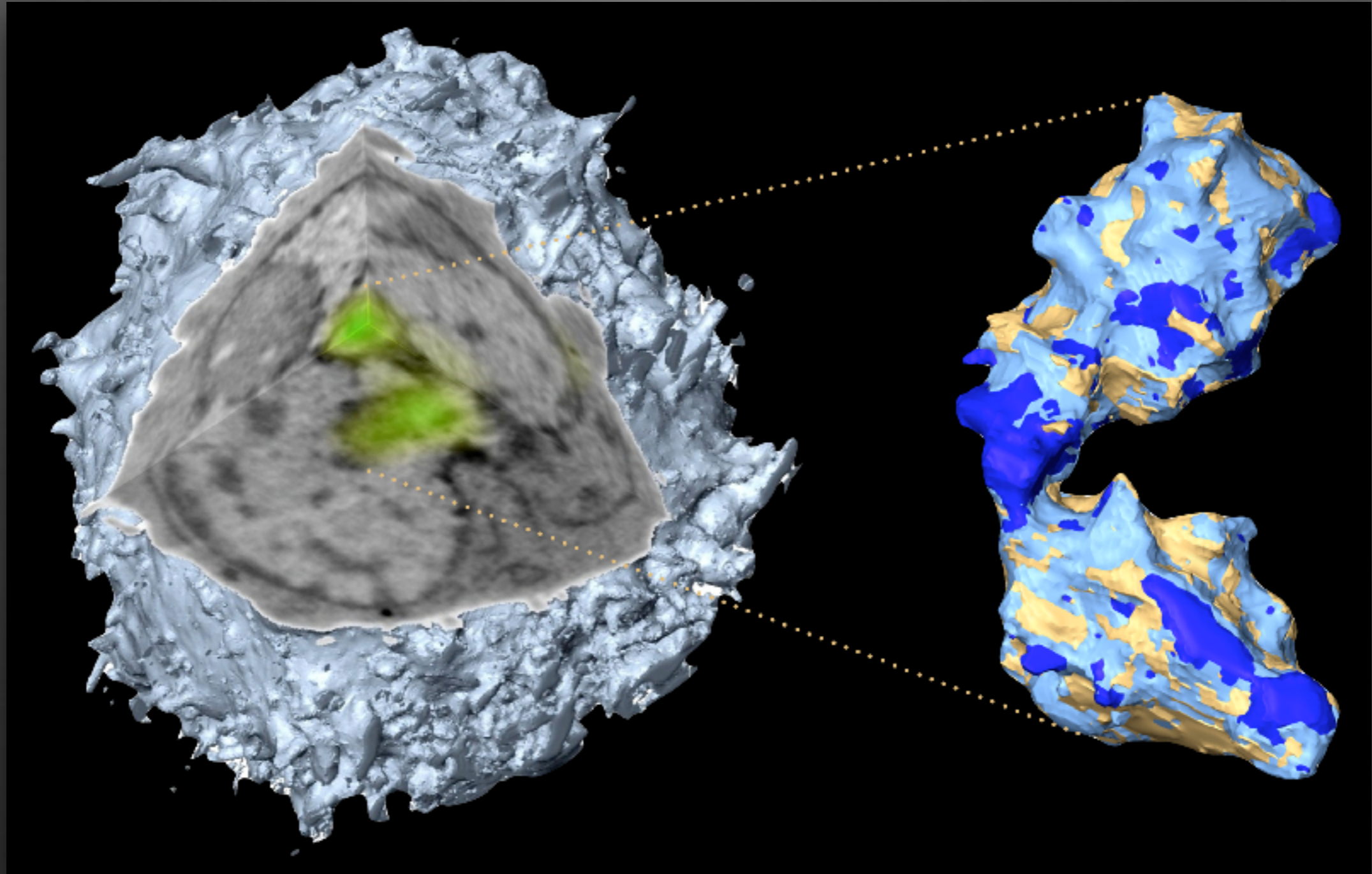
X-ray



Overlay



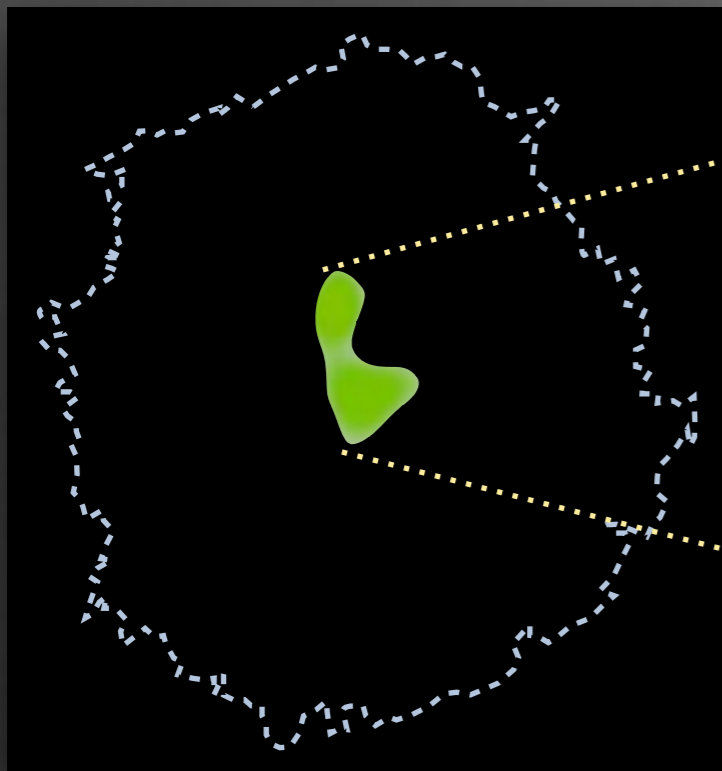
# Correlated cryo fluorescence & x-ray tomography



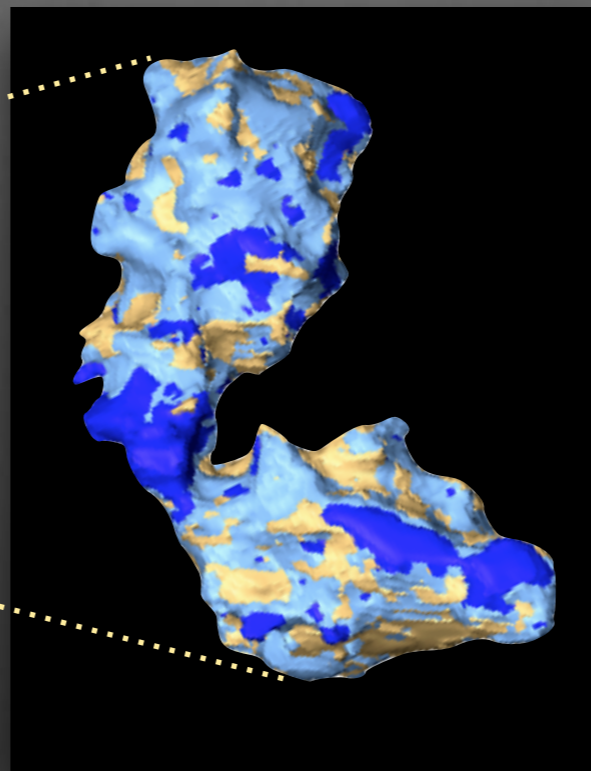
*Smith et al. (2014) Biophysical J. 107, 1988-96*

# Inactive X chromosome

Fluorescence



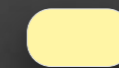
X-ray



**High LAC**  
0.34-0.36  $\mu\text{m}^{-1}$



**Medium LAC**  
0.32-0.34  $\mu\text{m}^{-1}$



**Low LAC**  
0.30-0.32  $\mu\text{m}^{-1}$

## National Center for X-ray Tomography

Mark Le Gros  
Gerry McDermott  
Jian-Hua Chen  
Axel Ekmann  
Venera Weinhardt  
Rosanne Boudreau  
Chao Yang  
Jeff Gamsby  
Tia Plautz  
Andreas Walter  
Elizabeth Smith

## Collaborators

Stavros Lomvardas & Josie Clowney, UCSF, Columbia  
Barbara Panning & Karen Leung, UCSF  
Camilla Forsberg & Fernando Ugarte, UCSC  
Frank Alber, Univ Southern California  
Markko Myllys, & Jussi Timonen, U. Jyväskylä  
Wah Chiu, Baylor College of Medicine  
Michal Hammel, LBNL  
John Tainer, MD Anderson Cancer Center  
Leann Tilley, Eric Hanssen, Univ Melbourne  
Krishna Niyogi, UC Berkeley

National Center for X-ray Tomography  
<http://ncxt.lbl.gov>

### Supported by:

NIH-NIGMS  
DOE-Biological & Environmental Research  
NIH Epigenomics Roadmap Grant  
NIH 4D Nucleome Project  
NIH-NIDA  
Gordon and Betty Moore Foundation