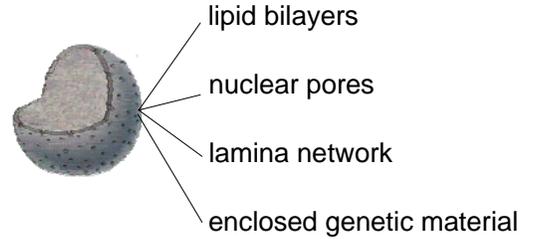


# The Nucleus

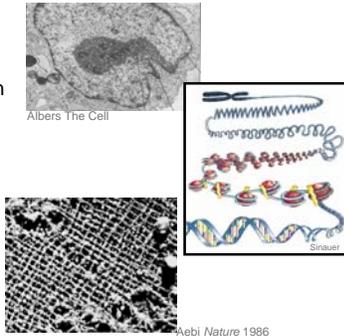
## Structure and Engineering

# Structures of the Nucleus



# The Biological Nucleus

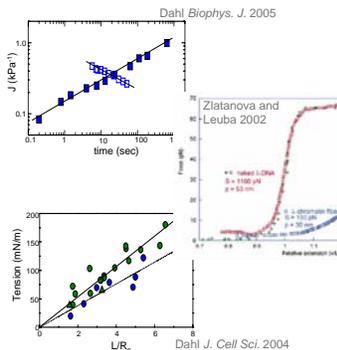
- The Whole Nucleus: nuclear domains and epigenetic modifications regulate gene expression
- DNA: DNA and higher order chromatin structures contain and regulate genetic information
- Lamina: the nuclear lamina organizes genes and regulates nuclear function



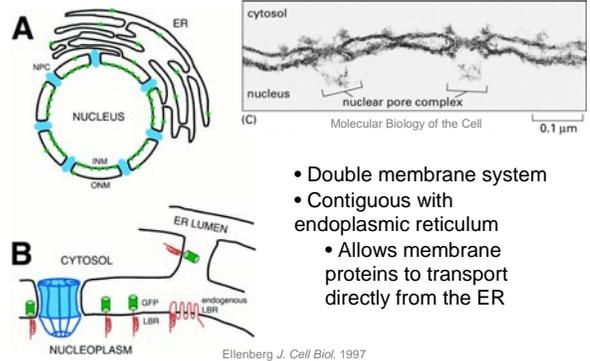
# The lipid membranes

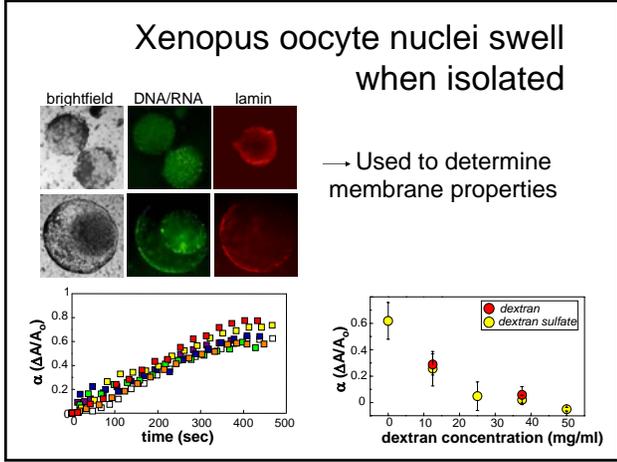
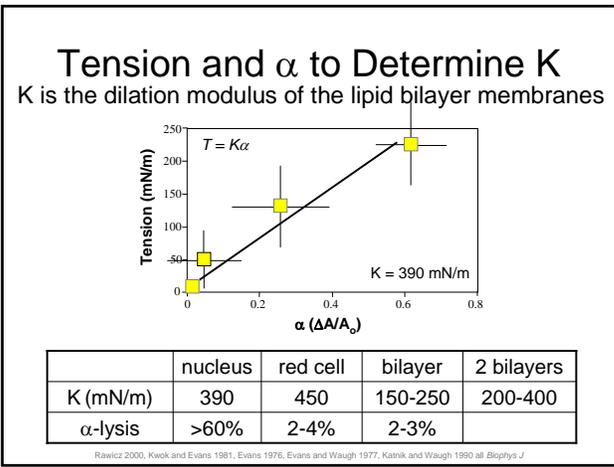
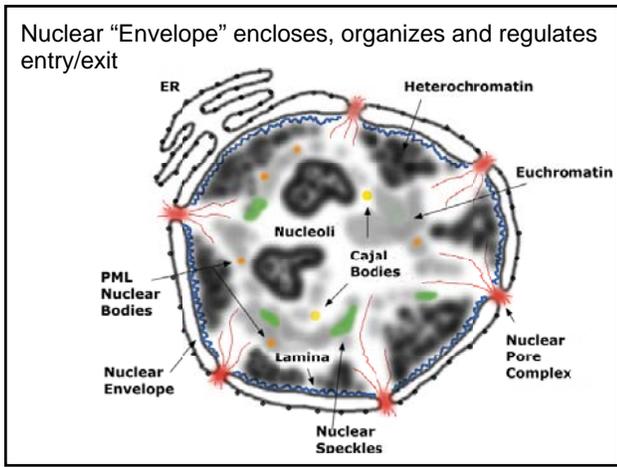
# The Biophysical Nucleus

- The Whole Nucleus: complex viscoelasticity suggests shear thinning under stress
- DNA: chromatin is more deformable than DNA which exhibits a 3-state deformation
- Lamina: the lamina appears to be purely elastic, highly extendible and reversible to protect interior chromatin from shear damage



# Nuclear membranes





- ### Unique stretch properties
- Similar membrane dilation modulus
  - Very high rupture modulus (>60% versus 3%)
    - Rupture is therefore not determined by lipid-lipid contacts
- 
- Pore stretching?
- Thinning of interstitia?

### Osmotic Swelling to Determine T

**Assumptions:**

- Continuous membrane
- Covered with rigid pores
- Pores modeled as cylinders
  - n pores
  - radius a
  - length l
- Poiseuille flow through pores

filtration coefficient  $\Phi = \frac{n \pi a^4}{8 \eta l}$   
from data on pores

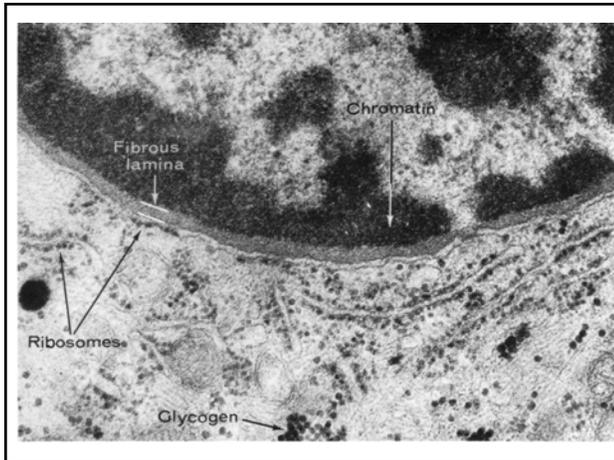
membrane pressure  $\Delta P = \frac{dV/dt_{initial}}{A \Phi}$   
from swelling data

membrane tension  $T = \frac{1}{2} \Delta P r$   
from Law of Laplace

a = radius of pore  
 A = nucleus surface area  
 l = length of pore  
 n = pore density  
 P = pressure  
 r = radius of nucleus  
 T = tension  
 V = volume of nucleus  
 h = viscosity  
 $\alpha$  = surface area expansion  
 F = filtration coefficient

### Nuclear Pore Complexes (NPCs) and Nucleo-cytoplasmic transport

(How stuff gets in and out of the nucleus)



~3,000 NPCs per mammalian nucleus

Mediate ALL traffic into/out of nucleus

Allow passive diffusion of ions and small proteins (<40 kD)

Nuclear Pore Complexes (NPCs) occupy 'pores' formed by the inner and outer membranes.

Each NPC = 8-32 copies (each) of 30 different proteins called *nucleoporins* ('Nups')

Translocation through the Nuclear Pore Complex

size of proteins that enter nucleus by free diffusion

size of proteins that enter nucleus by active transport

50 nm

Hydrophobic interior

FG-Repeat Containing Nucleoporins Form Intermolecular Meshwork

Receptor/Cargo Compete for Interactions and Partition into NPC

Nuclear Pore Complexes viewed by transmission electron microscopy (TEM)

(C) 0.1 μm

(D) 0.1 μm

NPCs are HUGE: 150 x 80 nm  
~100,000 kDa

8-fold radial symmetry

Disassemble and reassemble with each mitosis

Figure 12-10 part 2 of 2, Molecular Biology of the Cell, 4th Edition

Molecules over ~40 kD require a peptide **signal** to cross the NPC\*

**Import:** Nuclear Localization Signal ('NLS')

**Export:** Nuclear Export Signal ('NES')

\*The nuclear envelope is a 'border zone', with 'walls', import and export regulations, and smuggling activity (eg, viruses)

Anything, including gold nanoparticle up to ~25 nm diameter, bearing an NLS (or NES) peptide can be imported (exported) through NPCs; Ribosome subunits (10-20 nm) are continually exported from the nucleus

Import:

- NLSs include PKKKRKV, KR[PAATKKAGQA]KKKK, etc.
- NLS is recognized by receptors called importins
- Complex then binds NPC and enters the nucleus
- In the nucleus, Ran-GTP dissociates the imported complex

Export:

- NES are hydrophobic
- NES is recognized by a receptors called exportins and require Ran-GTP
- Complex then binds NPC, translocates through and

A gradient of RanGTP drives nuclear transport, and determines DIRECTION of movement

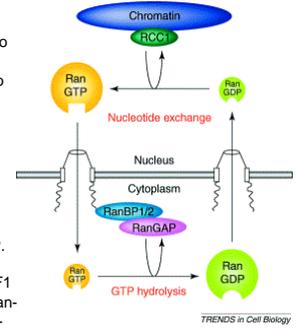
How do molecules know IN from OUT??

Ran-GTP is abundant inside nucleus due to the action of RCC1, an abundant chromatin protein that removes GDP and puts GTP onto Ran.

Ran-GTP binds EXPORTINS, promotes exportin binding to NES-cargo, and exits with them.

Ran-GDP is abundant in cytoplasm due to cytoplasmic Ran-GAP (GTPase Activating Protein) that stimulates Ran to hydrolyze GTP.

Ran-GDP is shuttled by a protein named NTF1 back into nucleus, where it is recharged to Ran-GTP and promotes DISSOCIATION of newly-imported Importin/NLS-cargo complexes.



IMPORT requires a Nuclear Localization Signal (NLS)

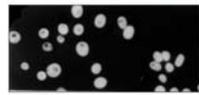
Positive charges, but no strict consensus. Signal must be **exposed on protein surface!!**

Classic NLS: **PKKKRKV**

'Two-part' NLS: **KRXXXXXXXXXXKxKK**

(A) LOCALIZATION OF T-ANTIGEN CONTAINING ITS NORMAL NUCLEAR IMPORT SIGNAL

Pro-Pro-Lys-Lys-Lys-Arg-Lys-Val-



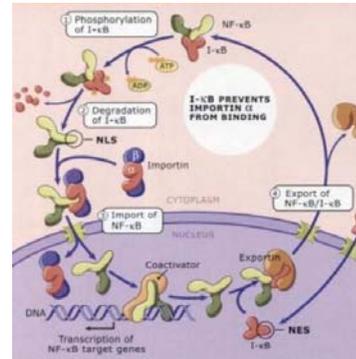
(B) LOCALIZATION OF T-ANTIGEN CONTAINING A MUTATED NUCLEAR IMPORT SIGNAL

Pro-Pro-Lys-Thr-Lys-Arg-Lys-Val-



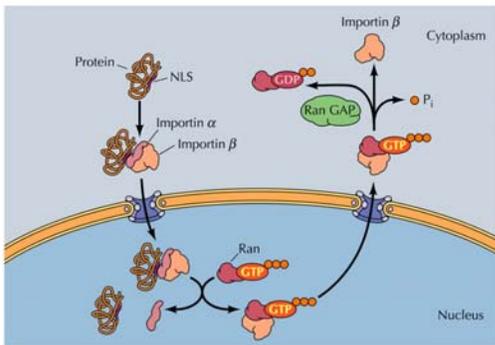
Figure 12-12. Molecular Biology of the Cell, 4th Edition.

Nuclear entry (or exit) can be regulated by hiding the NLS (or NES)



Cells by Lewin 2007

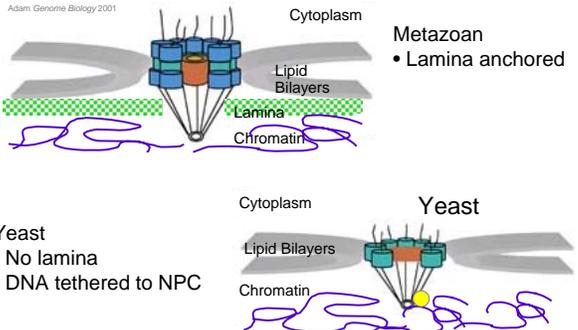
Cargo traverses NPC via importins. Cargo is released inside nucleus by Ran-GTP



© 2000 ASM Press and Garland Science, Inc.

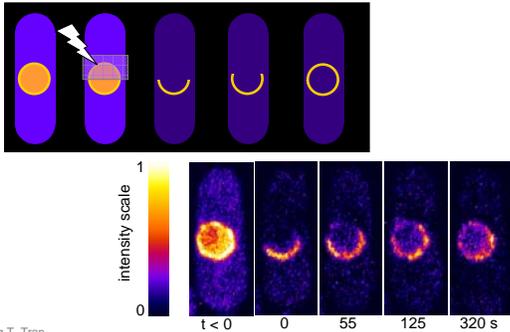
Nuclear Pore Complexes (NPC)

Adam Genome Biology 2001



- Yeast
- No lamina
  - DNA tethered to NPC

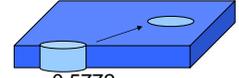
## FRAP of yNup85 in the Nuclear Envelope



Phong T. Tran

## Continuum Model of Pores Moving Through a Thick Membrane

$$D_{\text{trans}} = \frac{k_B T}{4\pi\eta h} \left( \ln\left(\frac{\eta h}{\eta_1 R}\right) - \gamma \right)$$

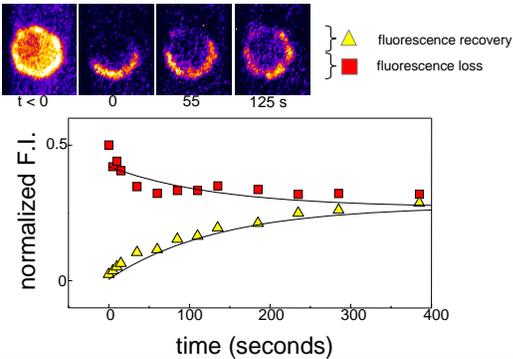


$\gamma$  = Euler's constant  
 $\eta$  = bilayer viscosity 5P  
 $\eta_1$  = cytoplasm viscosity 0.01P  
 $R$  = radius of the complex  $(960/2)\text{\AA}$   
 $h$  = bilayer height 300  $\text{\AA}$

$D_{\text{trans}} = 0.11 \mu\text{m}^2/\text{s}$  freely diffusing body  
 $D_{\text{FRAP-calc}} = 0.04 \mu\text{m}^2/\text{s}$

Saffman and Delbruck PNAS 1975

## FRAP Quantification



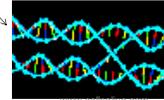
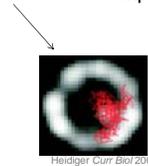
## Yeast NPC Mobility

Diffusion rate comparable to cellular transmembrane proteins with slight cytoplasmic steric hindrance

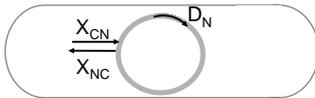
$D_{\text{nuc}} = 0.04 \mu\text{m}^2/\text{sec}$      $D_{\text{band 3}} = 0.004 - 0.20 \mu\text{m}^2/\text{sec}$

Poo and Cone Nature 1974, Golan and Veitch PNAS 1980

Allows chromatin more freedom at nuclear envelope, important for homologous recombination



## Half-times of yNup85 Movement

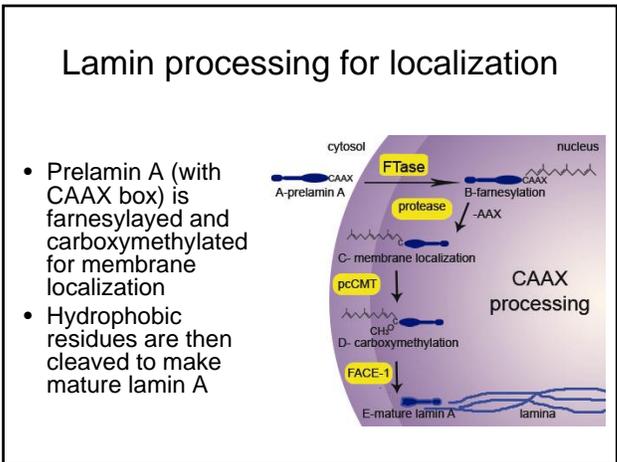
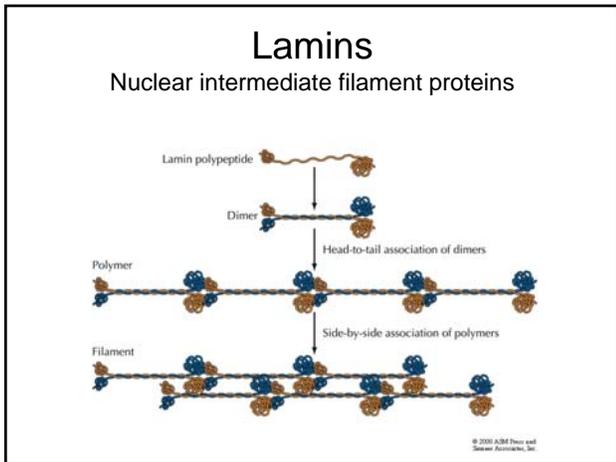
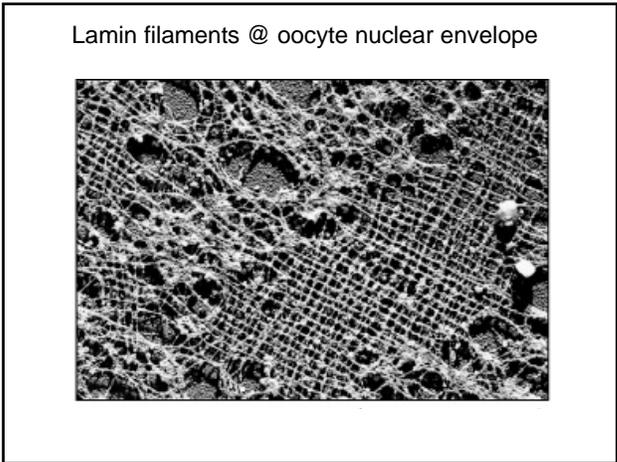
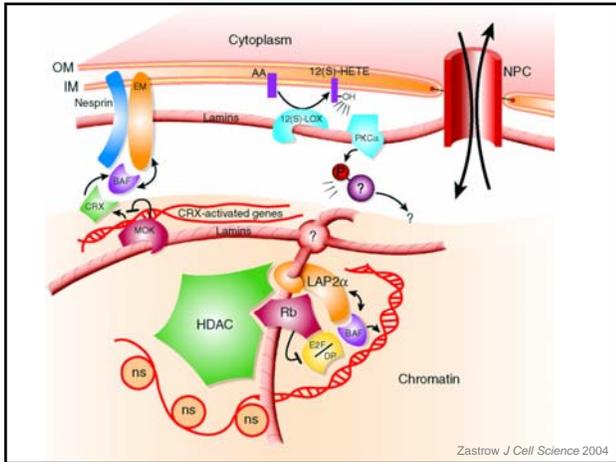
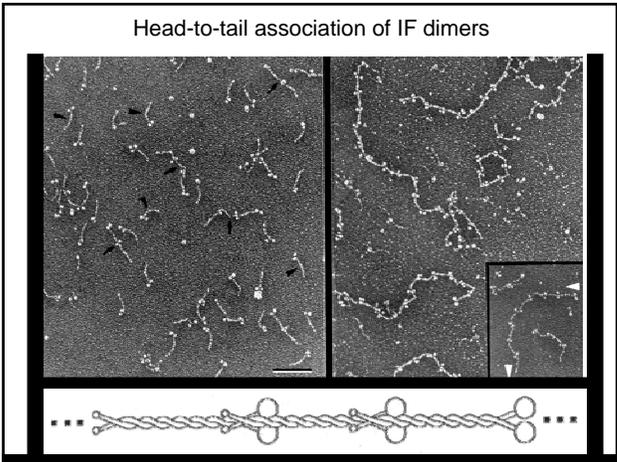
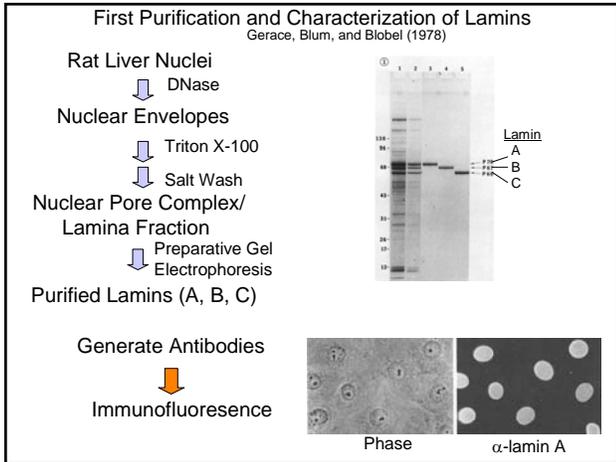


	$D_N$	$X_{CN}$	$X_{NC}$
	Nuclear Diffusion	Cytoplasm to Nucleus	Nucleus to Cytoplasm
$\tau_{1/2}$ (s)	58 +/- 4	289 +/- 42	553 +/- 94
n	15	10	10

compared with metazoan NPC  
 $\tau_{1/2} = 20$  hours

Daigle J Cell Biol 2001

## Nuclear Lamins



### **B-type lamins** (~1-2 million copies / nuc)

Ancestral  
Expressed in all human cells  
Essential for LIFE in multicellular eukaryotes  
**Required for DNA replication, mRNA transcription**

### **A-type lamins** (~1 million copies / nuc)

Non-essential  
Absent from stem cells  
Expressed upon differentiation  
*Partners: Rb, actin, histones, NE proteins*

### **"Laminopathies"**

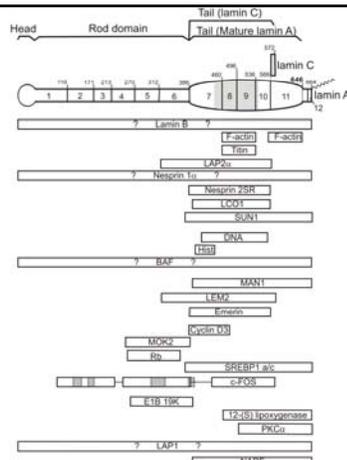
Diseases caused by mutations in *LMNA* or lamin-binding proteins

<b>Striated muscle+</b>	EDMD <i>EMERIN, NESPRIN-1, NESPRIN-2</i> Limb-girdle muscular dystrophy <i>EMERIN</i> Dilated cardiomyopathy <i>EMERIN, LAP2</i>
<b>Adipose tissue</b>	Lipodystrophy <i>Lamin B2</i>
<b>Neurons?</b>	Charcot-Marie-Tooth axonal neuropathy
<b>Bone+</b>	Mandibuloacral dysplasia Heart-Hand syndrome
<b>Human development</b>	Restrictive dermopathy (lethal at birth)
<b>Human aging</b>	Hutchinson-Gilford Progeria Syndrome atypical Werner Syndrome

**Profound disruption of lamina network, as seen in progeria patients, disturbs epigenetic regulation**

### **Lamin A polymers as 'scaffolds'**

Many nuclear proteins bind lamin A directly



Zastrow J Cell Sci 2004

### **Other pathologies suggest widespread and subtle roles for lamins and nuclear membrane proteins in human physiology**

#### **White blood cell development/function [LBR]**

**Neutrophil migration/oxidative burst defects:** Ichthyosis  
Pelger-Huet anomaly of neutrophils

#### **Bone disorders [LBR]**

Lethal HEM (Hydrops-Ectopic calcification-Moth-eaten) skeletal dysplasia  
Syndactyly  
Brachydactyly [short fingers/toes]

#### **STEM CELL dysfunction**

Epidermal stem cells [*LAP2, LMNA*]  
Erythroid stem cells [*LAP2, LMNA*]  
Ovarian germ cells in *Drosophila* [*Otefin*]

#### **CENTRAL NERVOUS SYSTEM**

**CNS demyelination** (adult-onset AD Leukodystrophy) [*LMNB1 duplic'n*]  
**Cerebellar hypoplasia**, cataracts, mental retardation [*Nesprin-1/SYNE-1*]  
**Lissencephaly** (AR cerebellar ataxia and atrophy) [*Nesprin-1/SYNE-1*]

### **"LAMINOPATHIES"**

>15 human diseases/conditions caused by mutations in lamins or lamin-binding proteins

E.g., *LMNA* mutations can disrupt specific tissues (muscle, heart, fat, skin, bone, neurons), or cause **accelerated aging** (Hutchinson Gilford Progeria; atypical Werner syndrome)

*Lamins are required for.*

Nuclear SHAPE

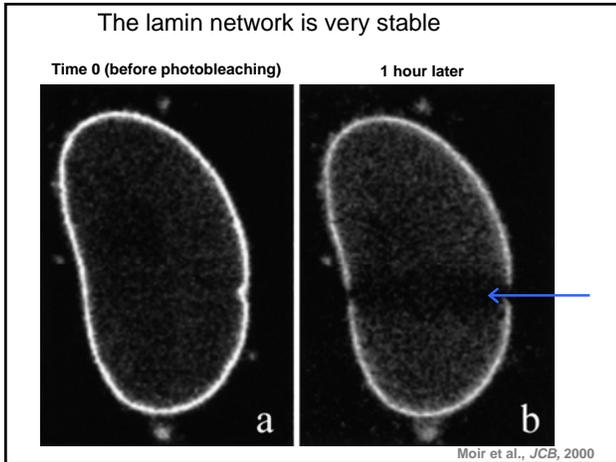
MECHANICAL strength (molecular 'shock absorber')

Chromatin attachment to NE

Nuclear Pore Complex anchorage/spacing

DNA replication (!!)

mRNA transcription (!!)



### Comparison of Red Cell and Nuclear Membrane Skeletons

	nucleus	red cell
E (mN/m)	25	0.01
filament	lamin	spectrin
lp (nm)	100-500	2.5-10

Mohandas and Evans Annu Rev Biophys Biomol Struct 1994; Hohenadl Biophys J 1999; Discher 1998 Biophys J 1999; Lenormand Biotechnology 2003

### Micropipette aspiration of lamina network in *Xenopus* oocyte nucleus

**Membrane Wrinkles**  
Suggests solid-like nature of the envelope

**Distance Between Spots**  
Show stretch of membrane during aspiration

**Hypothesis**  
Resistance to aspiration dominated by the lamin network

## Chromatin

### Tension and $L/R_p$ to Determine E

E is the extensional modulus of the membrane skeleton

swollen  
no DNA involved  
E=24±9 mN/m

unswollen  
DNA deformable  
E=28±8 mN/m

**E = 25 mN/m**  
measure of lamina  
not nucleoplasm interior  
not lipid bilayers

DNA double helix  
2 nm

DNA  
Core of eight histone molecules

Nucleosome: DNA winds around a histone

Histone H1  
30 nm

Chromatin: packed nucleosomes

300 nm

700 nm

1400 nm

Chromosome: bundled and interconnected chromatin

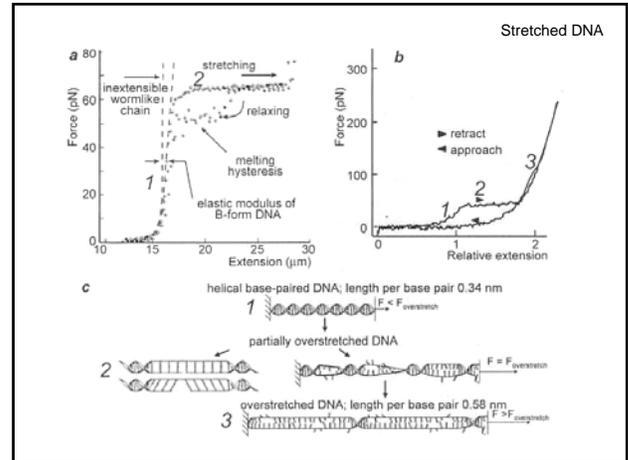
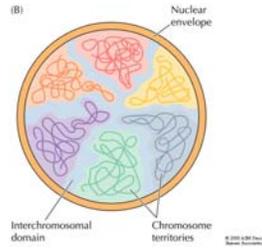
## Higher-order chromatin structure is regulated and dynamic

### Chromosome 'territories'

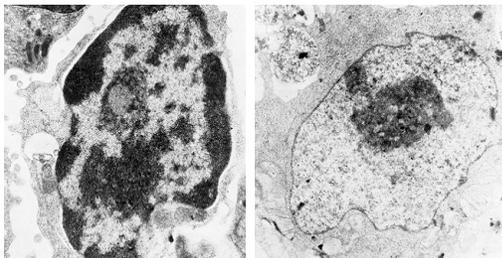
Can infiltrate neighbors.  
No 'fences'!!

Certain pairs of chromosomes are consistently found as 'near neighbors' in specific tissues.

When a gene activates, its chromatin UNFOLDS to occupy a huge volume as diffusible proteins arrive to transcribe, splice and process the mRNA.



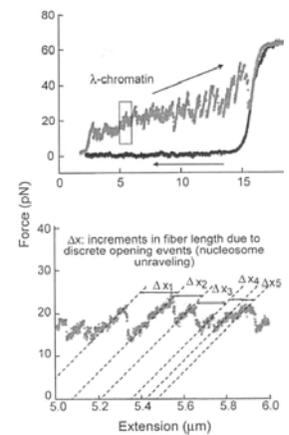
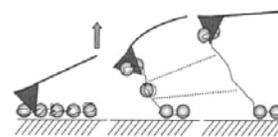
## Chromatin can re-organize rapidly!



Inactive Lymphocyte

Activated Lymphocyte

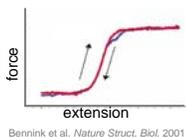
### Stretched and unfolded chromatin



## DNA, chromatin, chromosomes

### λ-DNA

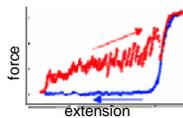
DNA: very little hysteresis



Bennink et al. *Nature Struct. Biol.* 2001

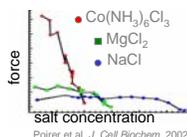
### chromatin

chromatin: hysteresis  
stepwise unfolding  
from histones



Bennink et al. *Nature Struct. Biol.* 2001

### chromosomes

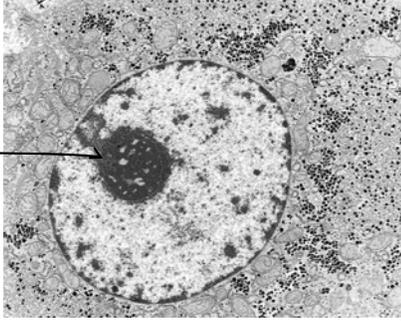
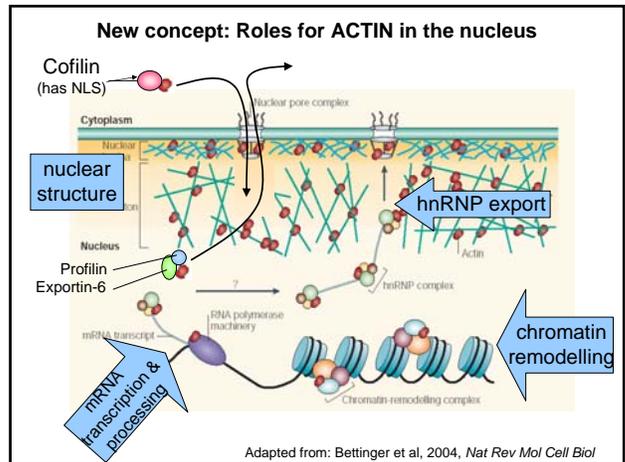


Poirer et al. *J. Cell Biochem.* 2002

## Other Nuclear Bodies

Subnuclear organelles have specific roles, e.g.:

**The nucleolus** (factory for making ribosomes)

**Inside the cell nucleus**



**Cajal Bodies:** ribosome biogenesis and transcription and are involved in small nuclear and nucleolar RNA metabolism, snRNP biogenesis

**Gems:** coincident or adjacent to Cajal bodies; assembly of snRNP and snRNP maturation

**Nucleolus:** ribosome synthesis and assembly

**Heterochromatin:** inactive chromatin

**PcG bodies:** contain polycomb group proteins (silencing proteins) such as RING1, BMI1 and hPc2

**Nuclear Speckles:** contains groups of pre-mRNA splicing factors

**IGC:** interchromatin granule clusters assembly, modification of pre-mRNA splicing factors

**Transcription Sites:** diffuse in nucleus and on periphery of IGC, several thousand foci

**OPT Domains:** (Oct1/PTF/transcription) appear in G1 but disappear in S phase; contain transcription factors but not RNA processing factors

**Cleavage Bodies:** cleavage and polyadenylation of pre-mRNA processing

**PNC (perinucleolar compartment) SAM68 nuclear body:** contain RNA and RNA binding proteins found mainly in cancer cells

**PML bodies:** transcriptional regulation affected by viral infection

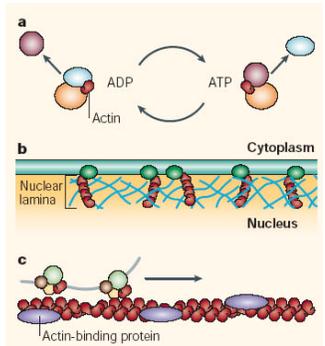
David Spector

**Possible Forms of Nuclear Actin**

**Monomeric G-actin**  
Conformation changes through ATPase activity might regulate the composition or function of multiprotein complexes

**Short filaments**  
Proposed structural roles at the nuclear envelope

**Novel oligomeric forms**  
Structural roles?



Jianmei Zhu, S-1

Bettinger BT et al, *Nat Rev Mol Cell Biol*, 2004

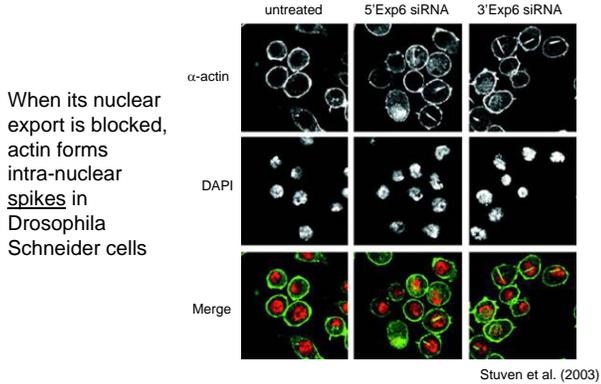
**Other Nuclear Structures**

Actin  
Titin  
Spectrin  
LINC  
INM proteins and signaling

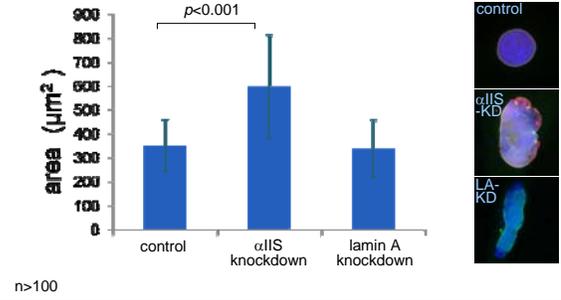
**Evidence for nuclear actin polymers**

- FRAP experiments suggest ~20% of nuclear actin is in a polymeric state (McDonald et al. 2006)
- Inhibition of N-WASP-dependent actin polymerization reduces RNA Polymerase II-dependent transcription (Wu et al. 2006)
- Polymerizable actin and Nuclear Myosin 1c (nMyo1c) are required for RNA Polymerase I-dependent transcription (Ye et al. 2007)
- Movement of active genes from heterochromatic to euchromatic regions requires polymerizable actin and nMyo1c (Chuang et al. 2006; Dundr et al. 2007)
- Emerin, an inner nuclear membrane protein, caps F-actin *in vitro* (Holaska et al. 2004)

### Too much actin in the nucleus is BAD

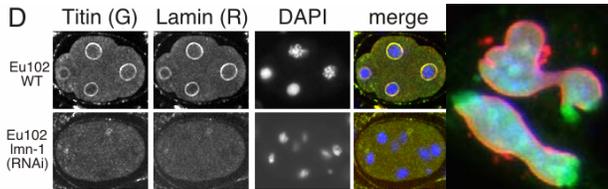
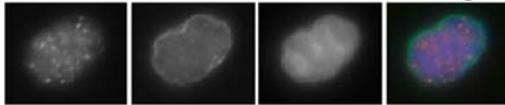


### Increase in Nuclear Area from $\alpha$ IISpectrin reduction

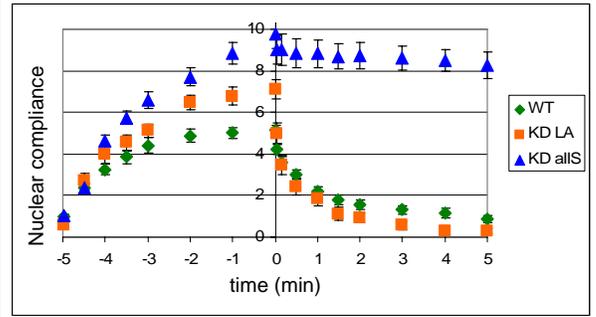


### Nuclear Titin

titin    lamin A    DNA    merge

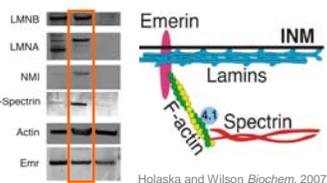
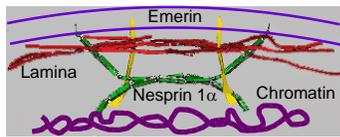


### $\alpha$ IIS Helps Nuclei Recover From Deformation

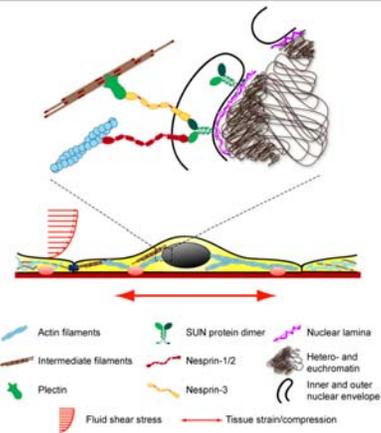


### Lamin-Associated Spectrin Proteins

- nesprin: spectrin-homolog nesprin-1 $\alpha$  binds lamin A and emerin
- spectrin: pull down assays show  $\alpha$ IISpectrin in emerin complex with lamins and actin



### LINC Complex



**New concept: NE proteins regulate signal transduction**  
(e.g., Man1, Smads and Bmps)

