

# An Epigenetic Switch: Prion Based Protein Regulation

**Directed Evolution of Substrate-Optimized GroEL**

Jue Wang  
 Kim Tipton  
 Christophe Herman  
 Carol Gross

**The Central Dogma of Molecular Biology**

Replication: DNA duplicates  
 Transcription: RNA synthesis  
 Translation: Protein synthesis

Replication Error Rate  $\sim 10^{-8}$   
 Transcription Error Rate  $\sim 10^{-5}$   
 Translation Error Rate  $\sim 10^{-3}-10^{-4}$

**A Protein's Function is Determined by its Fold**

**Potassium Ion Channel**

**Myosin Motor Protein**

**Protein Folding is the Most Challenging Step in the Reading of Genetic Information**

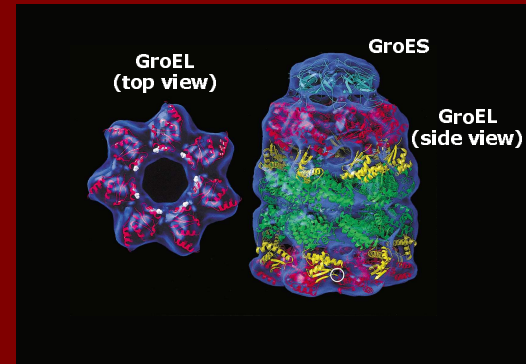
- Folding is an intrinsically complex problem: there is no way of subdividing it into simple steps
- Folding can be very slow: a protein synthesized in minutes may take hours to fold
- Folding is highly error prone: ~33% (up to 95% for some hard cases) of newly made proteins are rapidly degraded
- Many diseases (inherited, spontaneous and even infectious ones) are caused by protein misfolding

## An Epigenetic Switch: Prion Based Protein Regulation

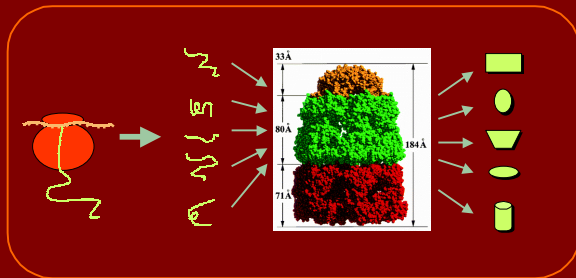
### Protein Folding in the Depends on Helper Proteins Termed Molecular Chaperones

- There are several completely unrelated classes of chaperones
- Chaperones consume energy to assist folding
- The “cocktail” of chaperones determine what proteins can be produced in a given cell type
- Different chaperones systems predominate in different organism (e.g. eukaryotes vs. prokaryotes)

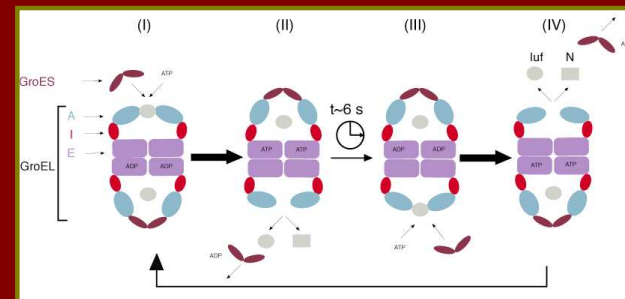
### GroEL/ES: A Conserved and Essential Chaperone Pair Uses ATP Hydrolysis to Enhance Folding



### GroEL Assists Folding of Many Different Proteins

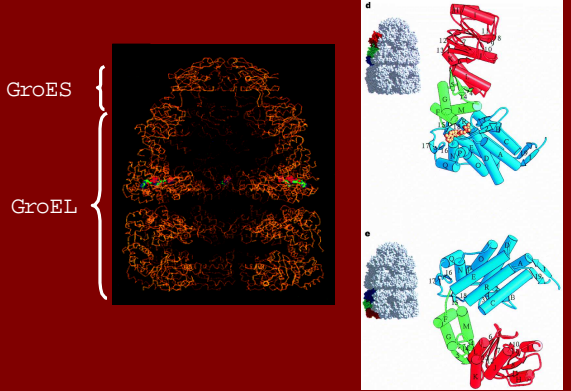


### GroEL Reaction Cycle



# An Epigenetic Switch: Prion Based Protein Regulation

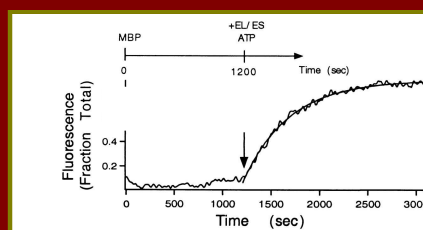
### GroEL-GroES Forms a Protected Folding Cavity



The diagram illustrates the GroEL-GroES complex as a large, orange, barrel-shaped structure. On the left, a bracket labels the top half as GroES and the bottom half as GroEL. To the right, two panels (d and e) show a protein chain (red and blue) folding within the GroEL cavity. Panel d shows the protein in a partially folded state, while panel e shows it in a more compact, folded state.

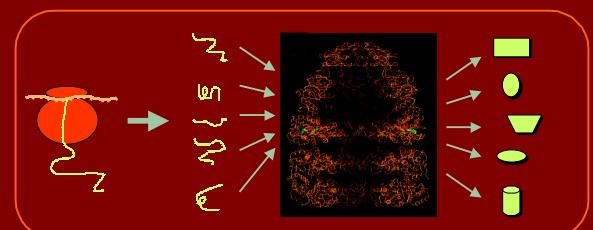
### Beyond the Passive Box: GroEL Catalyzes the Folding of Some Substrates

Substrate: MBP



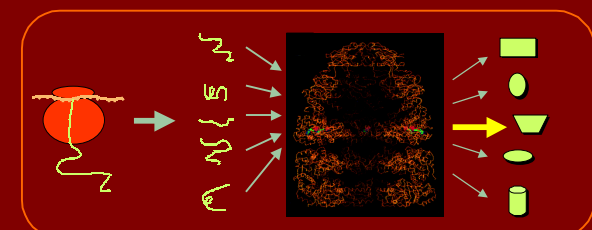
The graph plots Fluorescence (Fraction Total) on the y-axis (0 to 0.4) against Time (sec) on the x-axis (0 to 3000). The curve shows a baseline at 0 until approximately 1000 seconds, where an arrow labeled '+EU/ES' and 'ATP' indicates the start of the experiment. Following this, the fluorescence increases sharply, reaching a plateau of approximately 0.4 by 2500 seconds.

### What are the Limits to GroEL as a Universal Folding Machine?



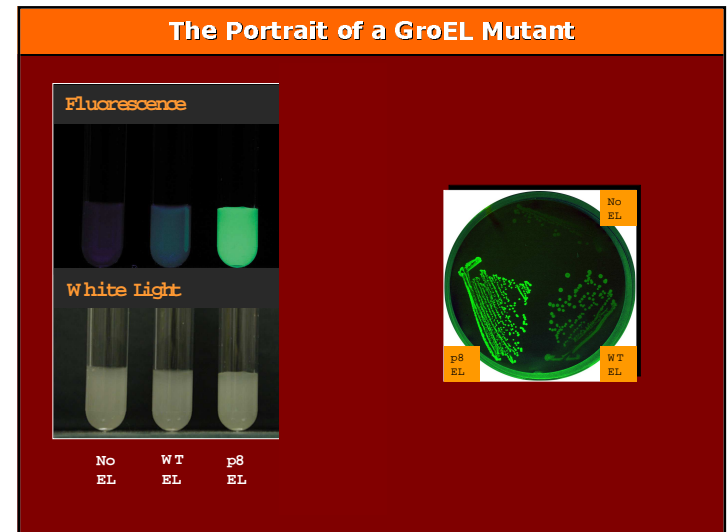
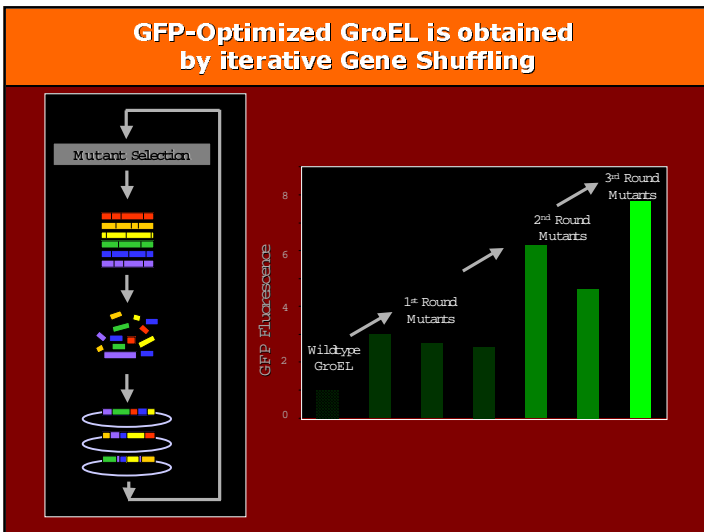
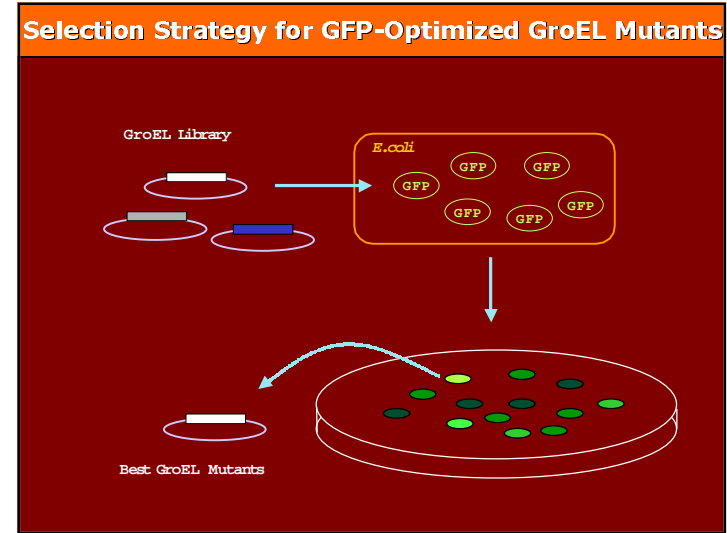
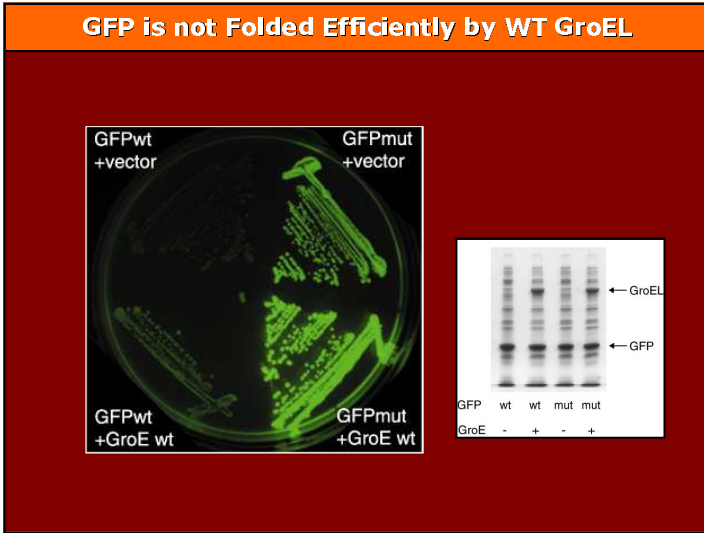
The diagram shows a red protein chain entering a GroEL cavity (orange barrel). Multiple arrows point from the protein into the cavity. On the right, several arrows point out from the cavity to various protein shapes, including a green square, a green oval, a green cylinder, and a green triangle, representing different possible protein conformations.

### What are the Limits to GroEL as a Universal Folding Machine?

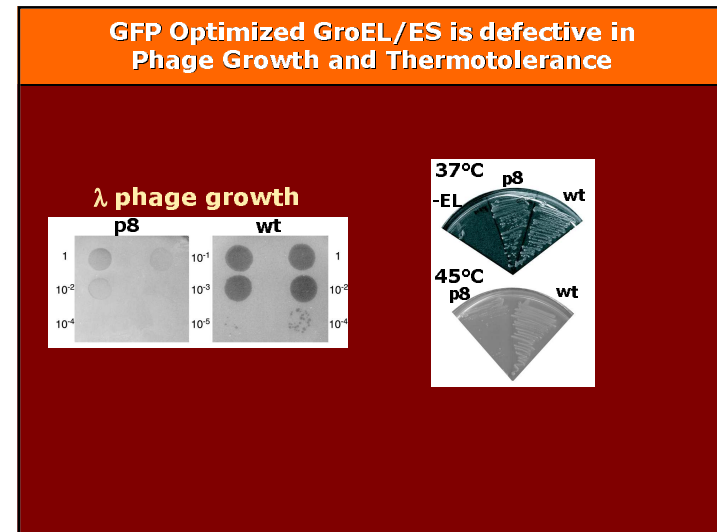
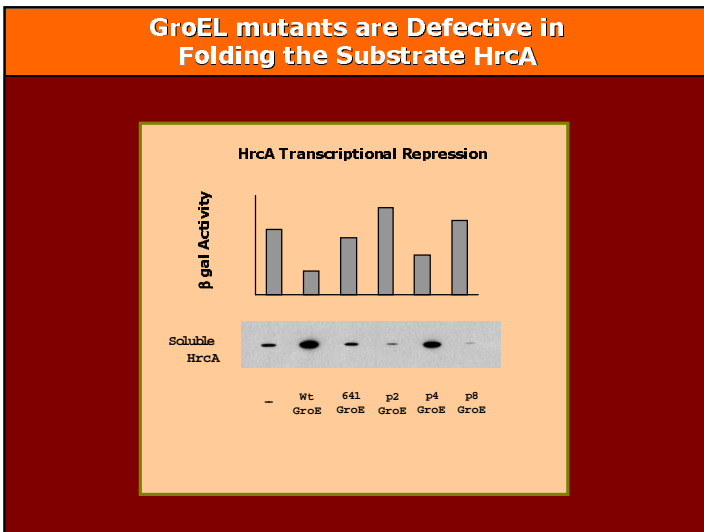
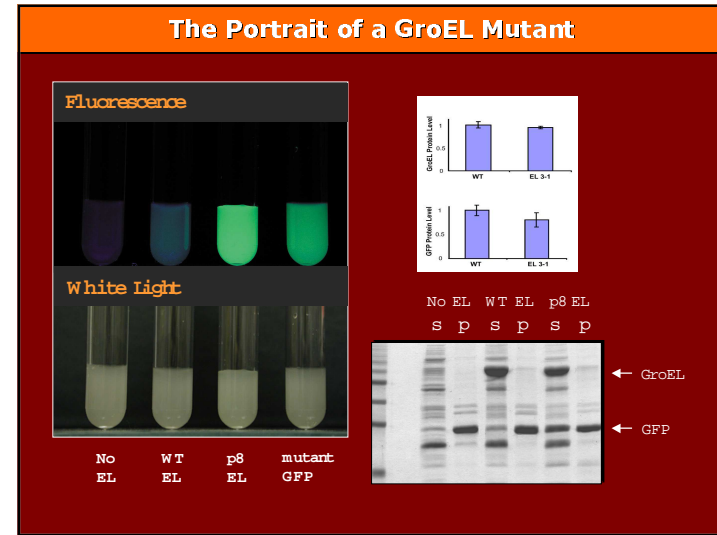
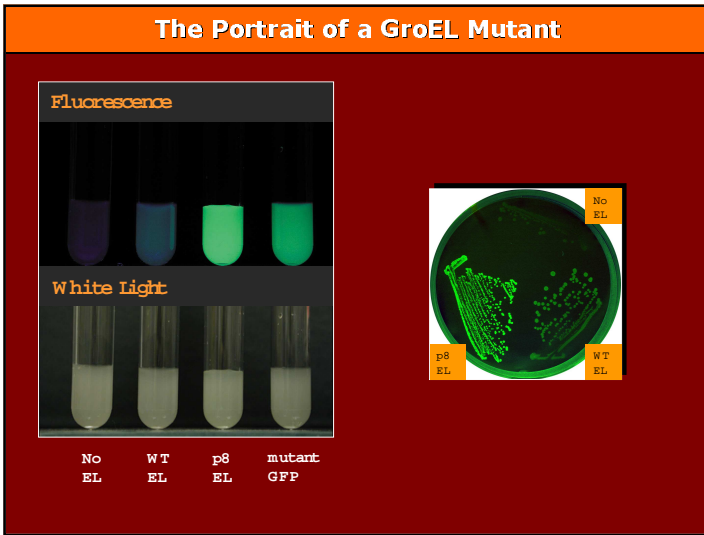


This diagram is identical to the previous one, but with a yellow arrow pointing from the GroEL cavity to a specific protein shape (a green triangle), highlighting a particular folding pathway or product.

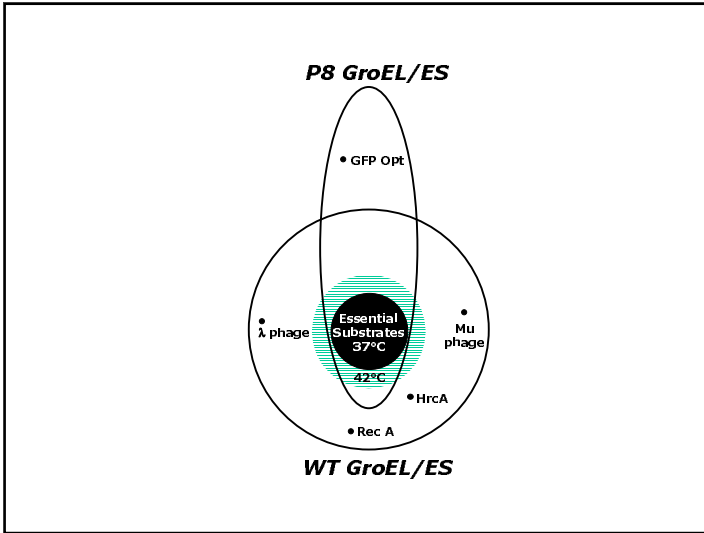
# An Epigenetic Switch: Prion Based Protein Regulation



# An Epigenetic Switch: Prion Based Protein Regulation



# An Epigenetic Switch: Prion Based Protein Regulation



### Conclusions

- There is a remarkable *plasticity* to GroEL which makes it possible to dramatically increase its ability to fold specific substrates
- There is an intrinsic *conflict* between the requirements of different substrates so that GroEL variants optimized for the folding of one protein lose the ability to fold others

Why haven't cells evolved many different GroEL Subtypes?

### The HSP70-HSP40(J) Chaperone system

**HSP70**

H<sub>2</sub>N- [ATPase 381] [Peptide binding 637] -EEVD-COOH

Peptide: NRLLLTG

GrpE ↑ DnaJ/Hsp40 ↓

low affinity fast exchange

high affinity slow exchange

ATP → ADP + Pi

Peptide binding → Peptide release

Detailed description: The diagram shows the HSP70 protein structure with ATPase and Peptide binding domains. A peptide (NRLLLTG) is bound to the Peptide binding domain. The cycle involves ATP binding to the ATPase domain, followed by peptide binding. GrpE and DnaJ/Hsp40 are involved in the cycle. The cycle then proceeds to ATP hydrolysis to ADP + Pi, leading to peptide release and ADP release.

**P8 GroEL/ES**

• GFP Opt

• λ phage

• Essential Substrates 37°C

• 42°C

• Mu phage

• HrcA

• Rec A

**WT GroEL/ES**

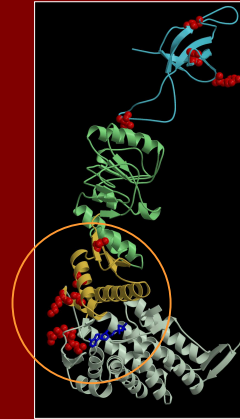
**Hypothesis:** as the proteome expanded, no single chaperone sufficed. The ring nature of GroEL made it relatively difficult to evolve new independent chaperones compared to Hsp70/40.

# An Epigenetic Switch: Prion Based Protein Regulation

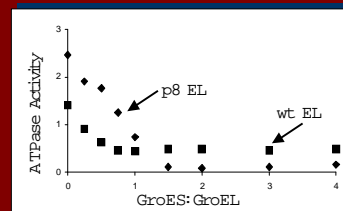
## Exceptions that "prove" the rule: the use of adaptors to expand the repertoire of a ring complex

- Nuclear Pores: Importin
- Proteasome: ubiquitin ligases

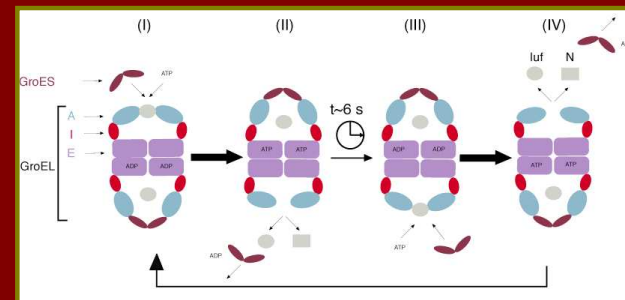
## Mutations of GroEL are Near ATP Binding Site



## Altered ATPase Activities in the GroEL Mutants




## GroEL Reaction Cycle



# An Epigenetic Switch: Prion Based Protein Regulation

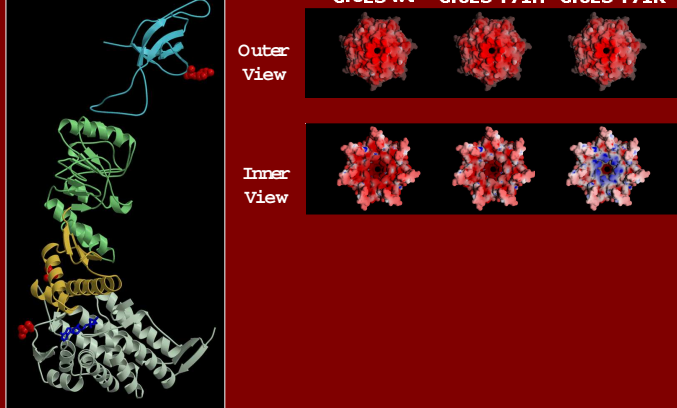
### GroES Residue Y71 is a Hotspot for Mutations



**Y71:**

- Extends into the Central Cavity
- Multiple mutations are selected from the screen: Y71H, Y71R, Y71C

### Altered Electrostatic Potential in the GroES Mutants




Outer View

Inner View

GroES wt   GroES Y71H   GroES Y71R

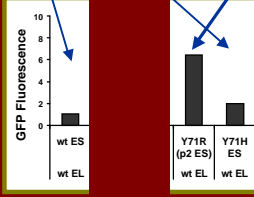
### Altered Central Cavity Might Improve GFP Folding



Outer View

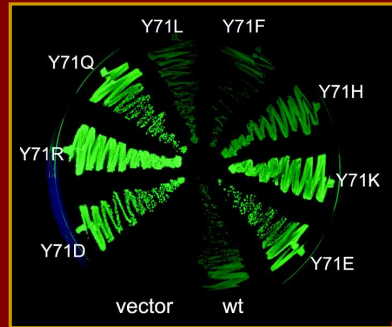
Inner View

GroES wt   GroES Y71H   GroES Y71R



Condition	GFP Fluorescence (approx.)
wt ES	1.0
wt EL	0.1
Y71R (p2 ES)	6.5
Y71H ES	2.0
wt EL	0.1
wt EL	0.1

### Hydrophilic Cavity Improves GFP Folding



Y71L   Y71F

Y71Q   Y71H

Y71R   Y71K

Y71D   Y71E

vector   wt



# An Epigenetic Switch: Prion Based Protein Regulation

### Summary of in vitro Studies

- **The period of ATP-driven capture-release cycle is altered perhaps to fit GFP folding kinetics better**
- **The folding environment : increased polarity of the central cavity lid enhances GFP folding**
- **Mutations were not found in peptide binding domain despite targeted mutagenesis of these regions**

### Amyloids Are Ordered Protein Aggregates

- self-propagating
- fibrillar cross-beta fold
- extremely stable
- associated with numerous diseases

from Serpell and Blake, Adv. Prot. Chem., V.50

### Requirements of the Prion Hypothesis

- **INFECTION: self-propagating structure**
- **SPECIES BARRIER: sequence specificity**
- **STRAINS: structural diversity**

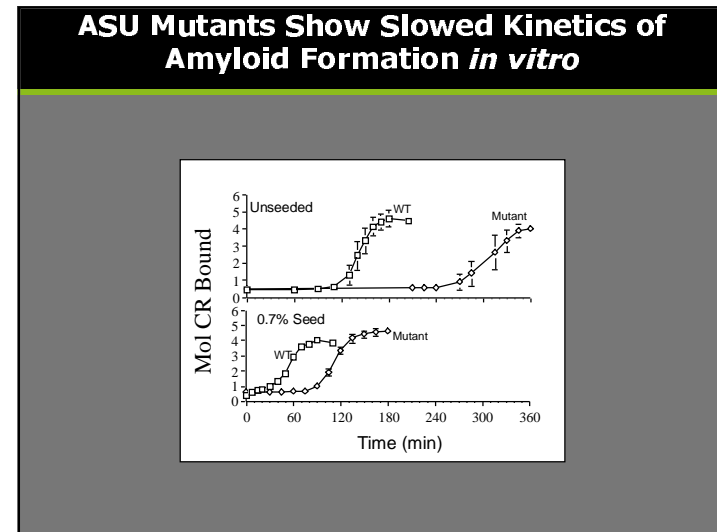
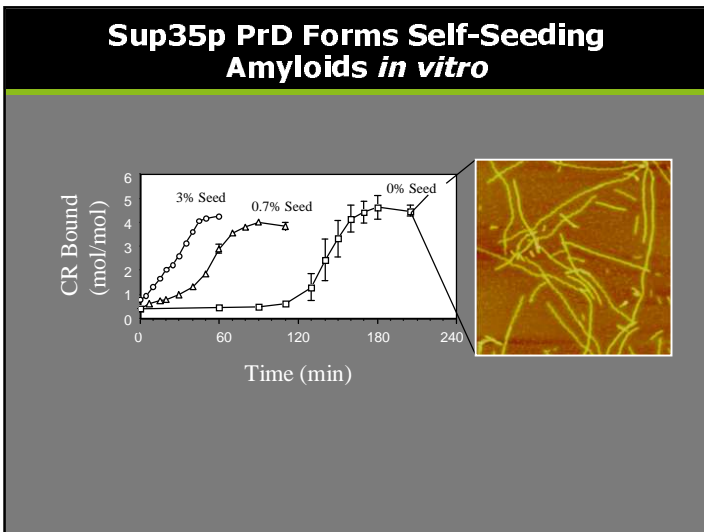
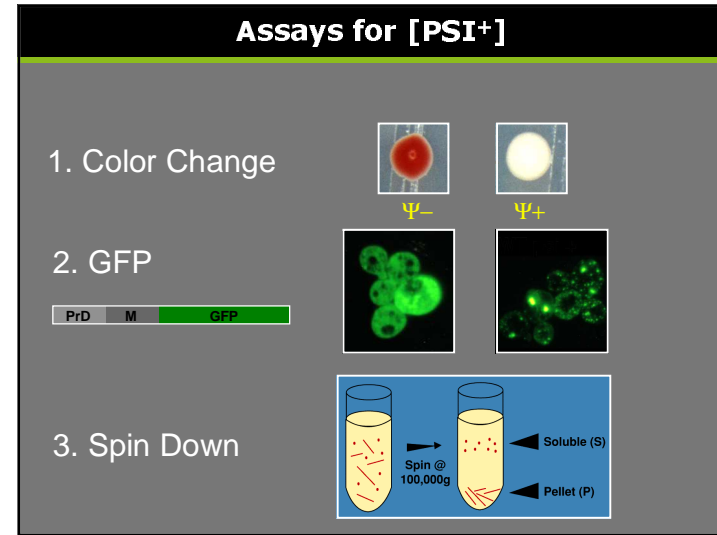
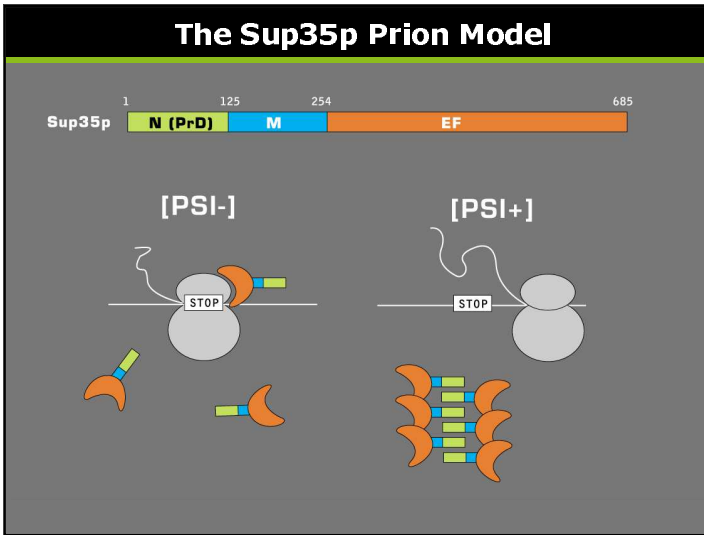
### [PSI+] Causes Suppression of Nonsense Mutations

Color Change

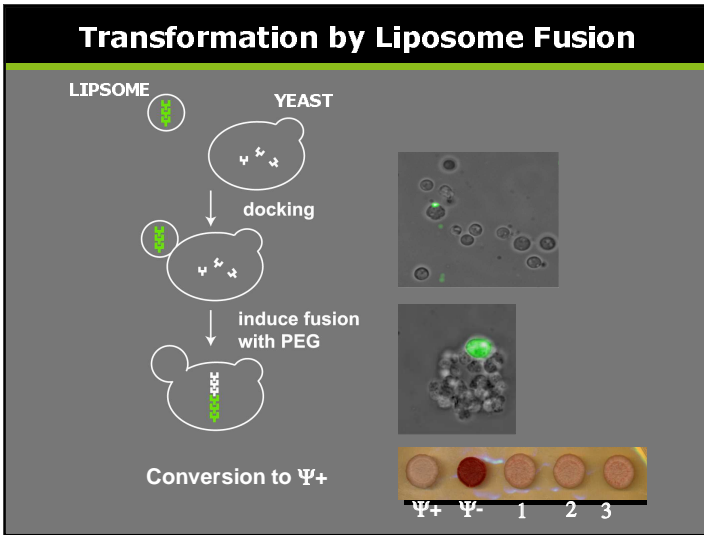
Growth on minus ADE1

**NO**      **YES**

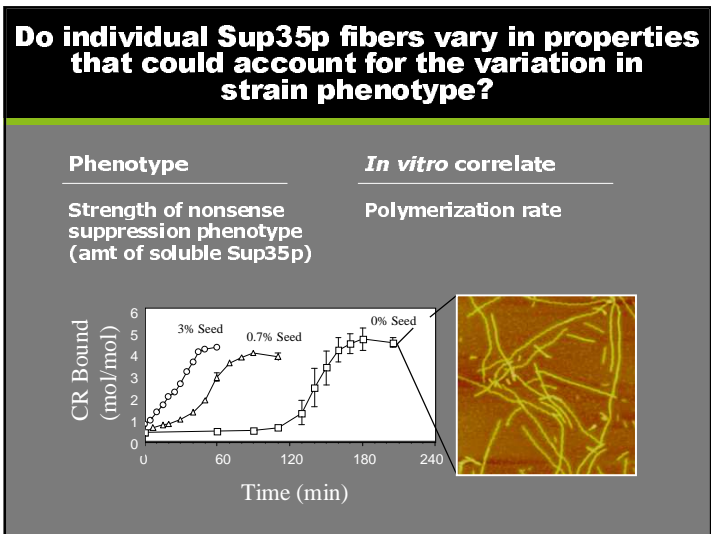
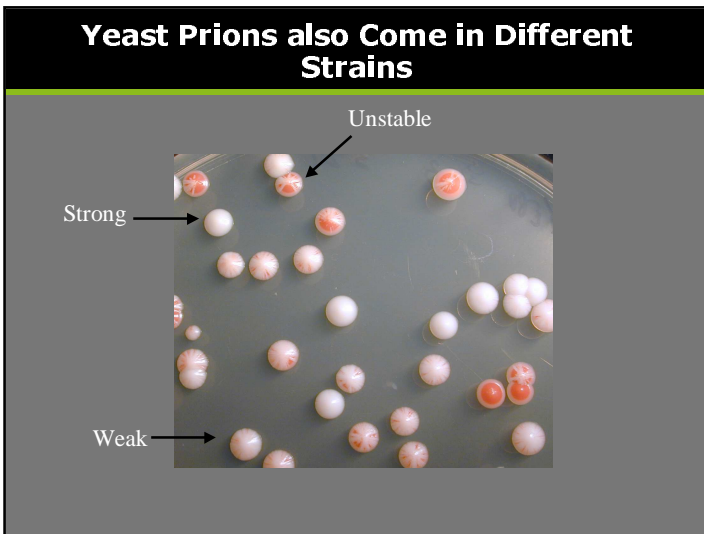
# An Epigenetic Switch: Prion Based Protein Regulation



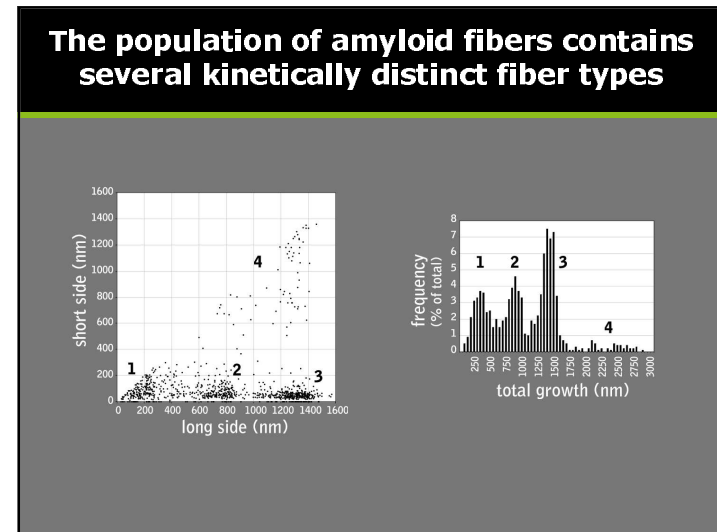
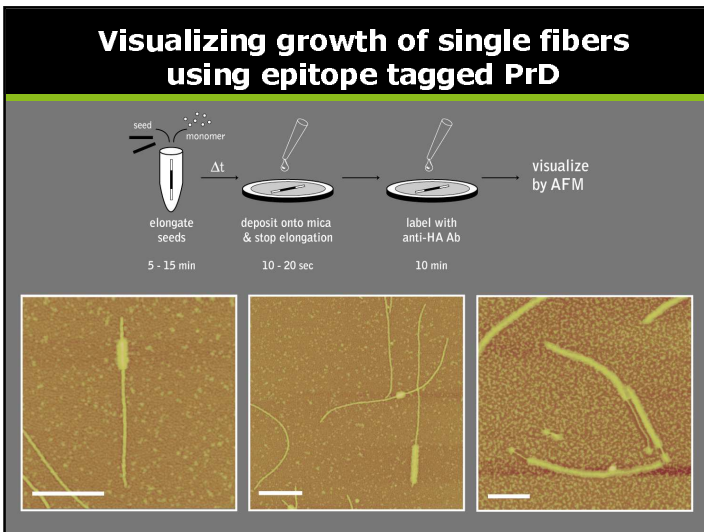
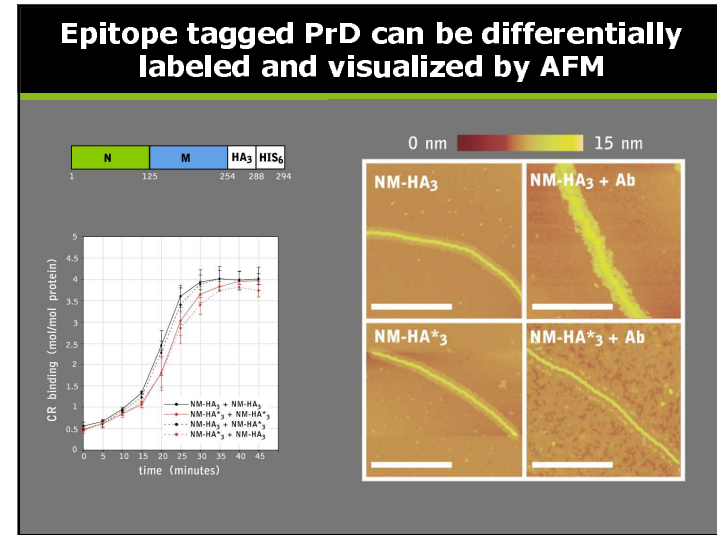
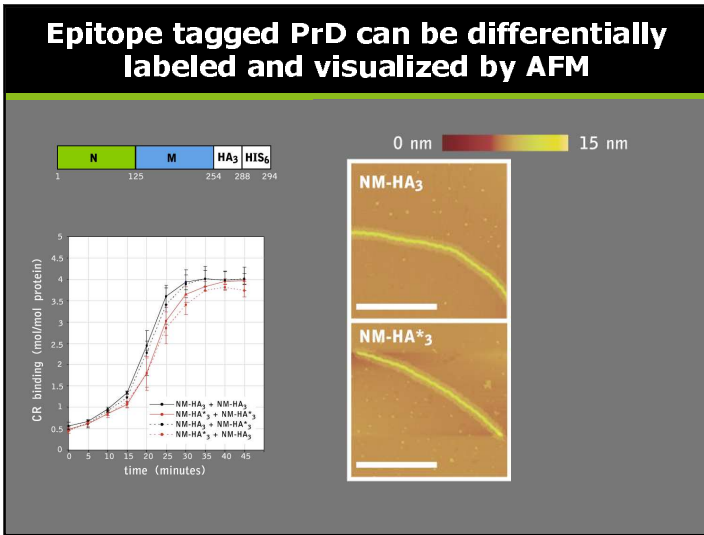
# An Epigenetic Switch: Prion Based Protein Regulation



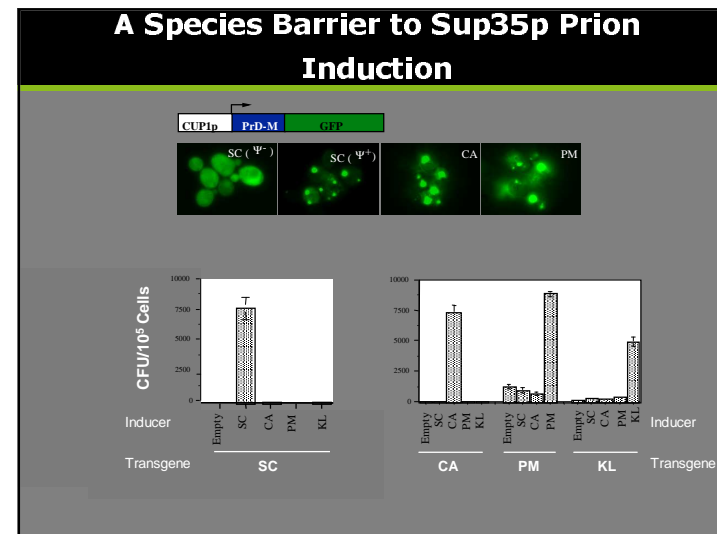
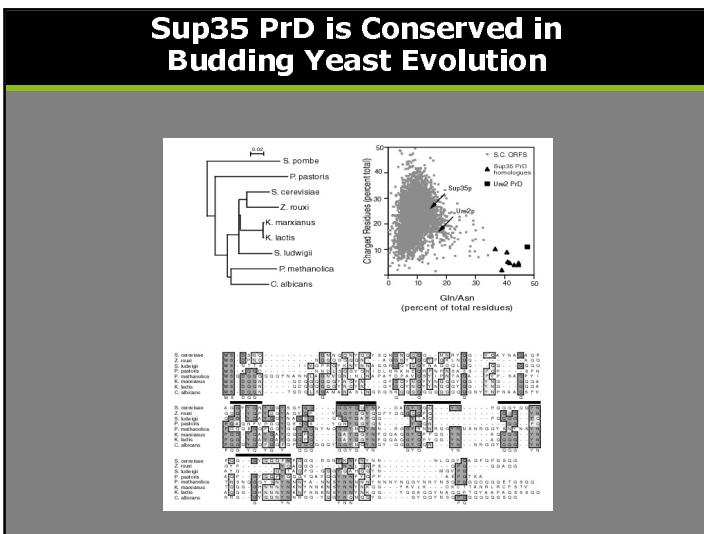
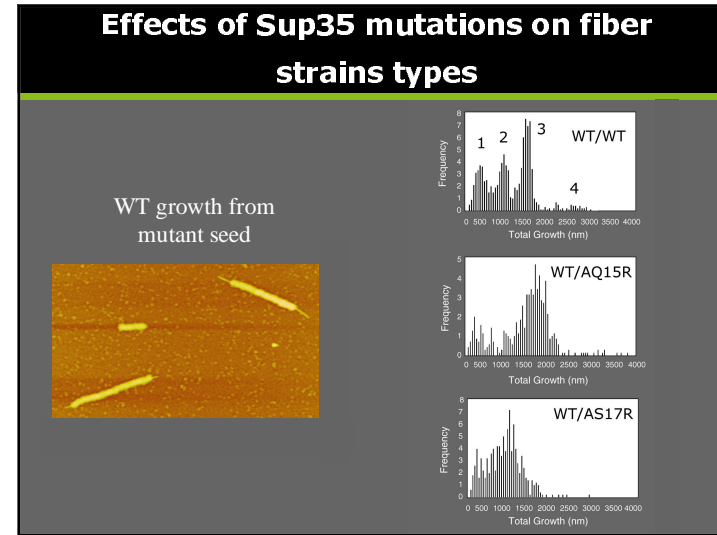
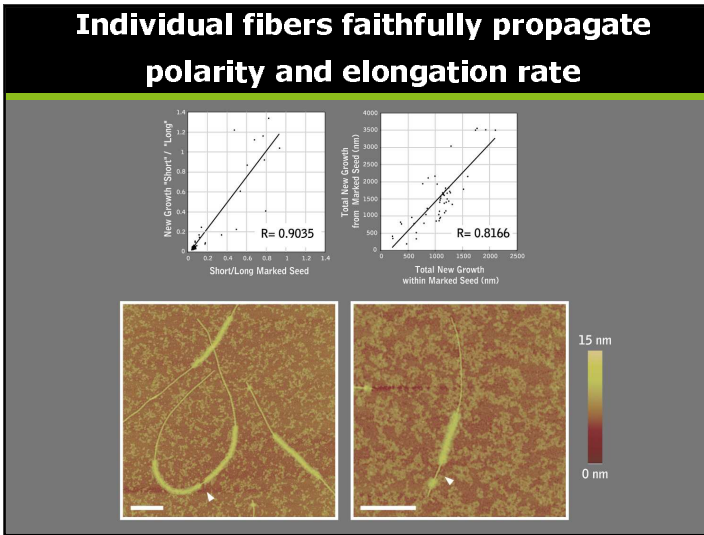
Prion strains: One protein can cause multiple different diseases.



# An Epigenetic Switch: Prion Based Protein Regulation

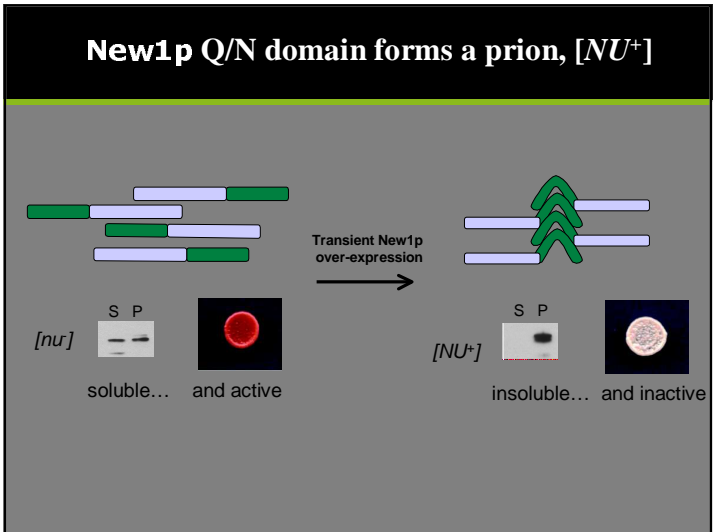
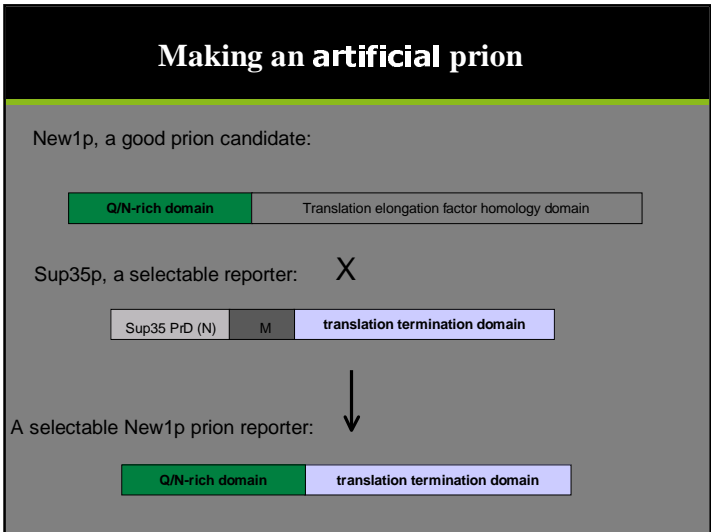
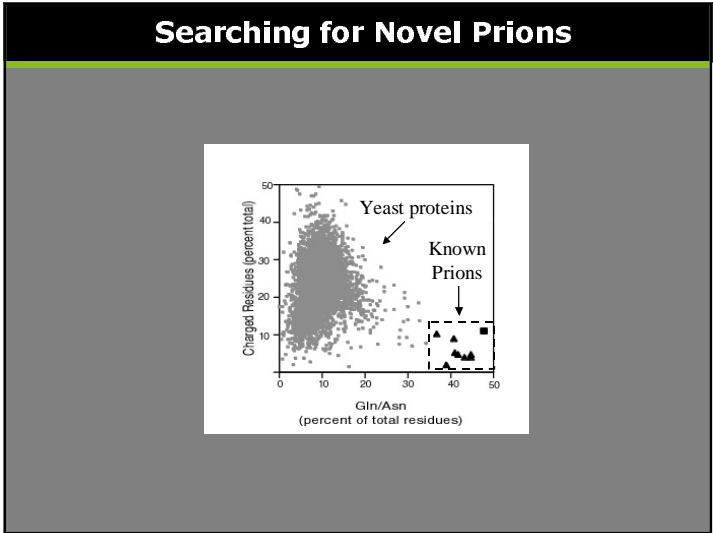


# An Epigenetic Switch: Prion Based Protein Regulation

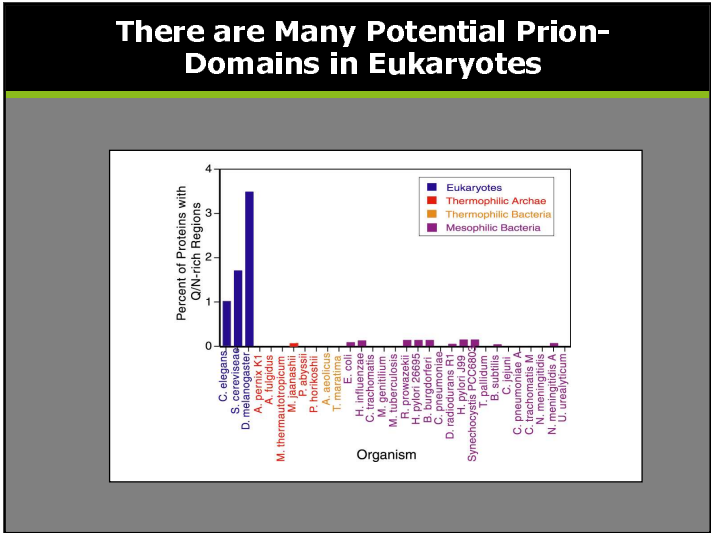


# An Epigenetic Switch: Prion Based Protein Regulation

## How Many Prions Are There?

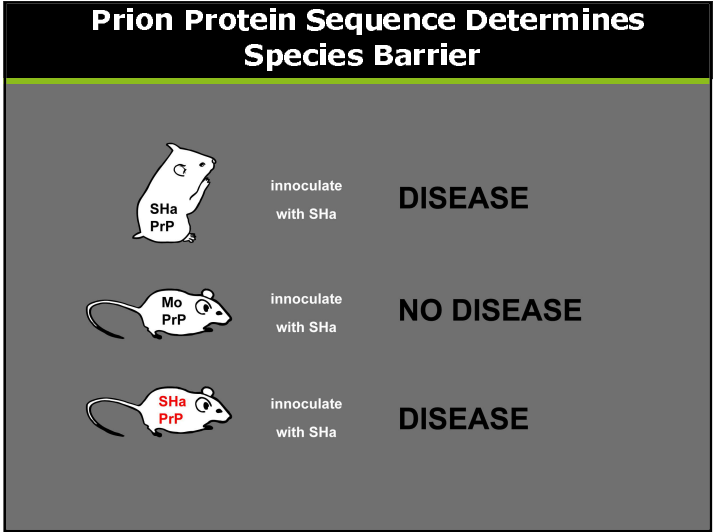
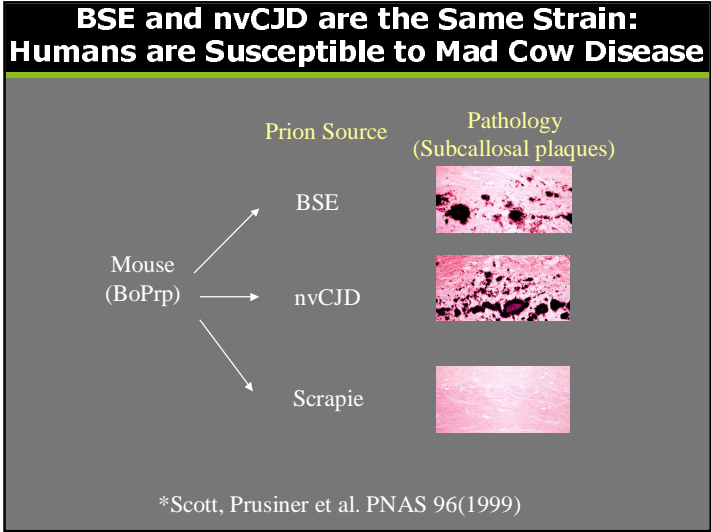


# An Epigenetic Switch: Prion Based Protein Regulation

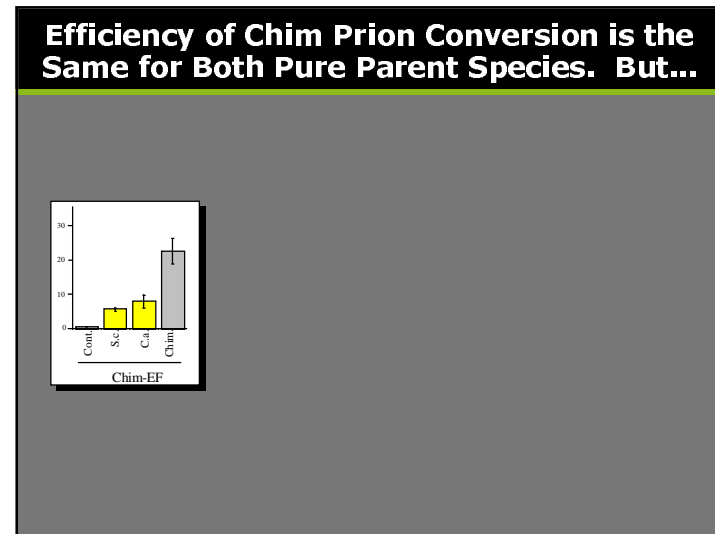
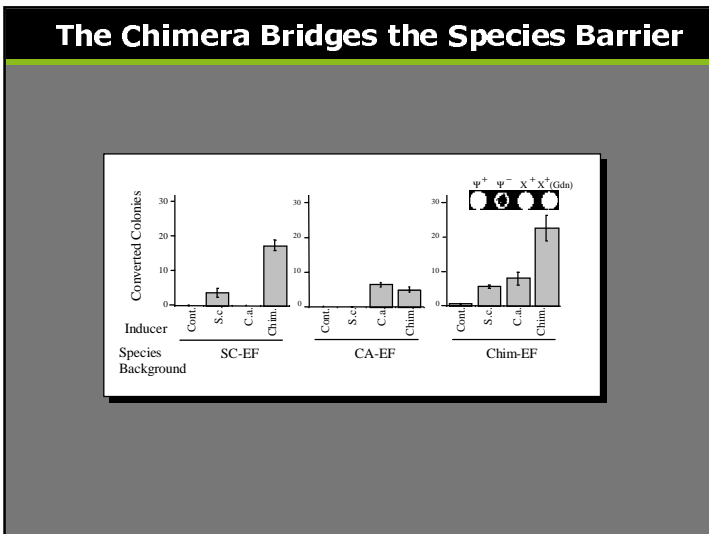
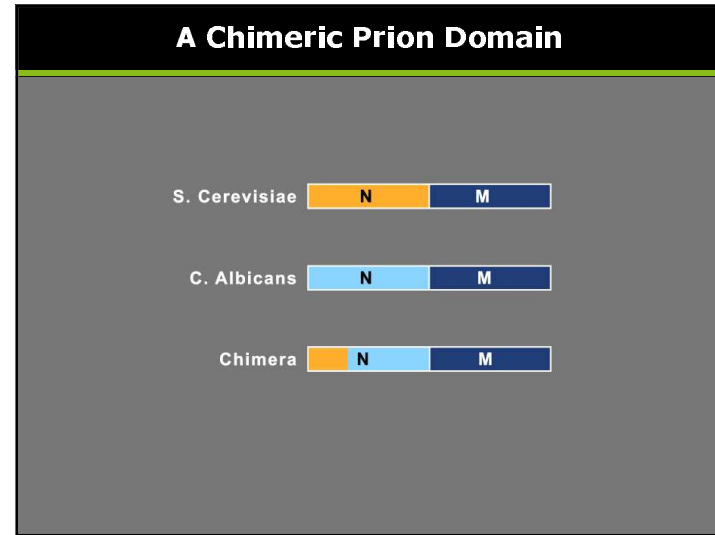
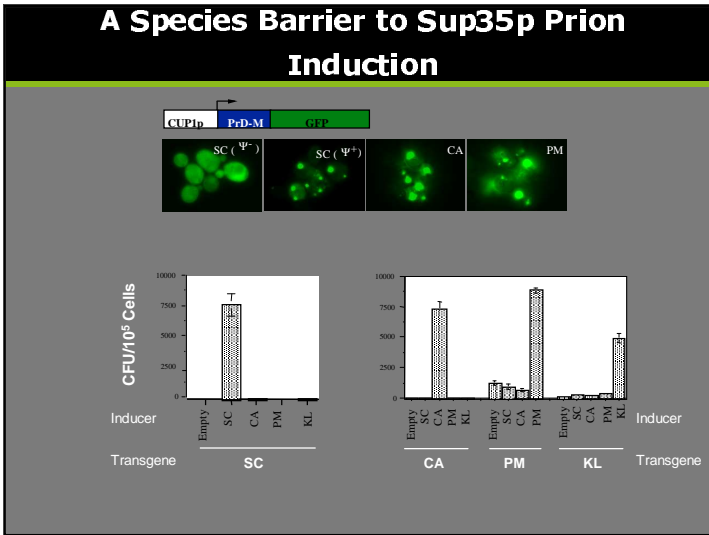


### Acknowledgments

- **Prion Strains:** Peter Chien
- **Prion Mutants Screen:** Angela DePace and Alex Santoso
- **Single Fiber Assay:** Angela DePace
- **Species Barrier:** Alex Santoso and Peter Chien
- **Protein Infection:** Helmut Sparrer
- **New Prions:** Lev Osherovich and Melissa Michelitsch

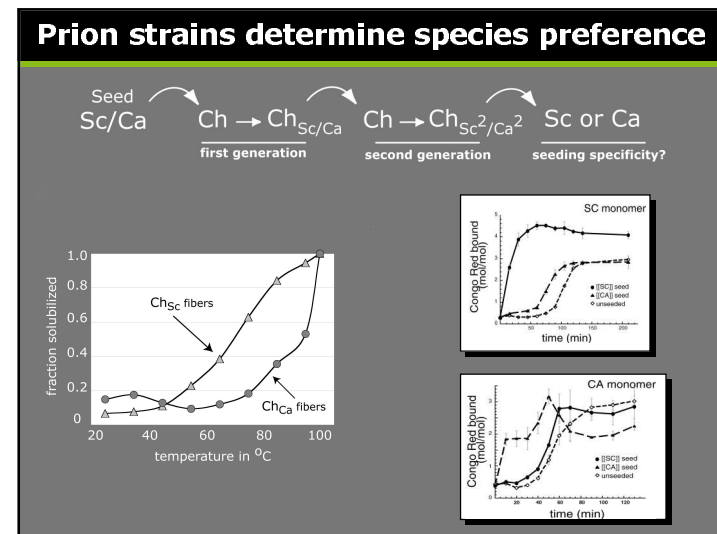
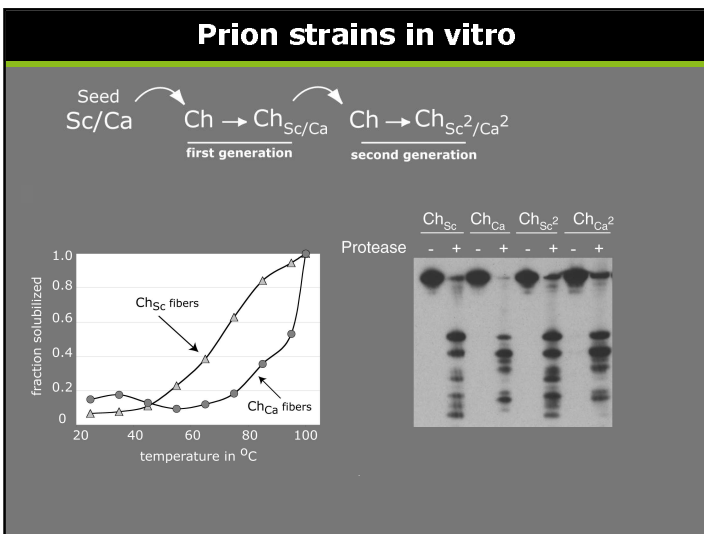
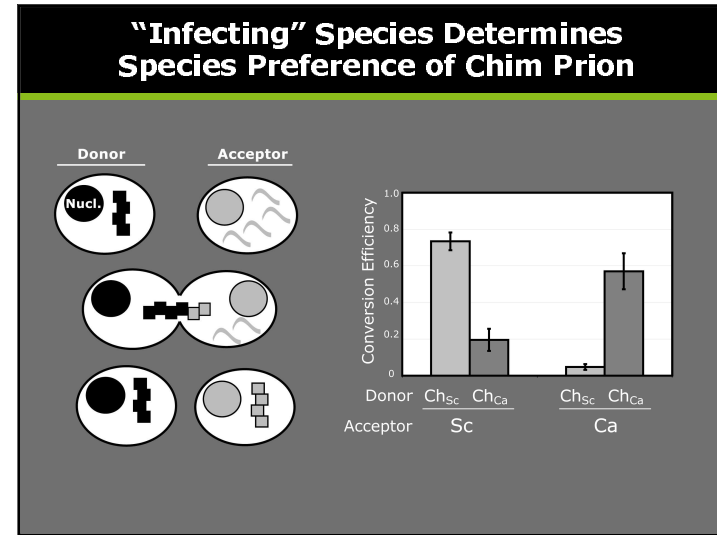
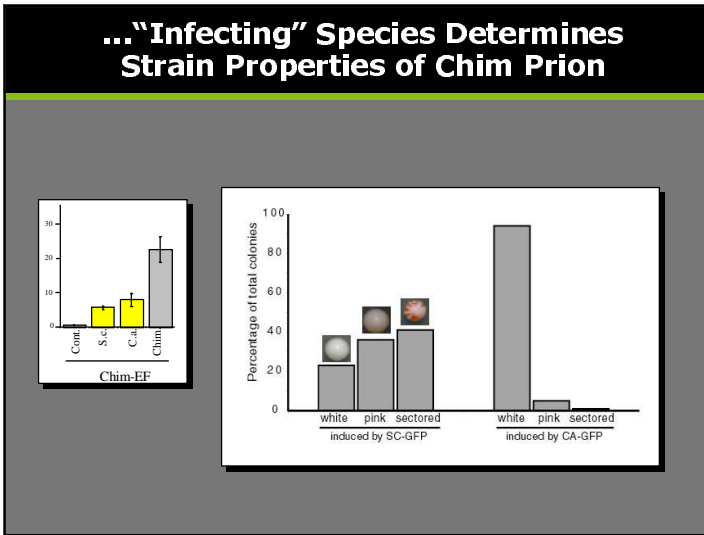


# An Epigenetic Switch: Prion Based Protein Regulation



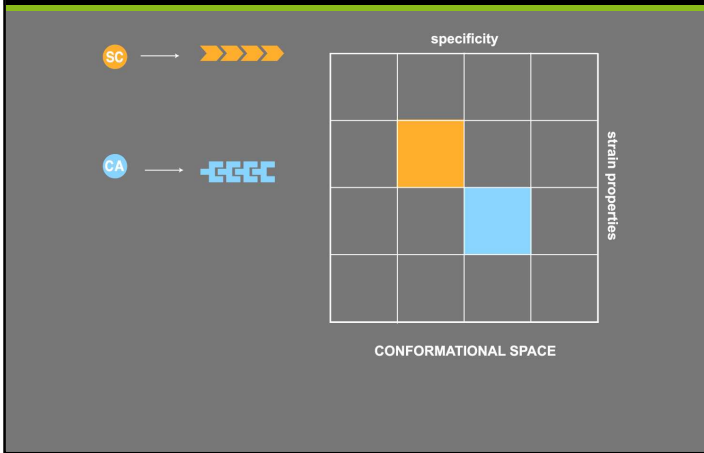


# An Epigenetic Switch: Prion Based Protein Regulation

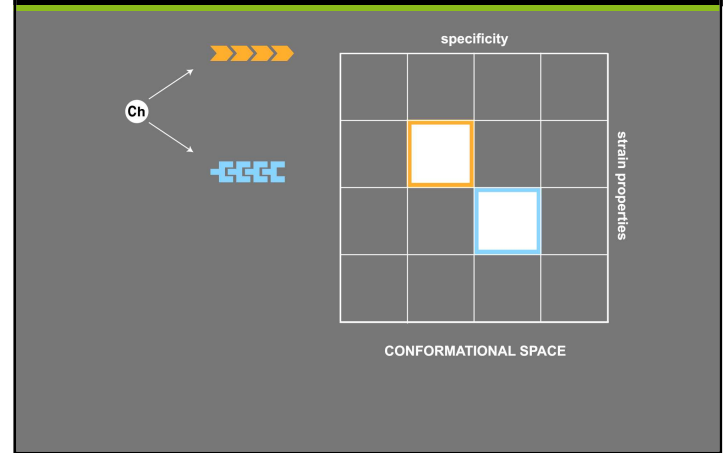


# An Epigenetic Switch: Prion Based Protein Regulation

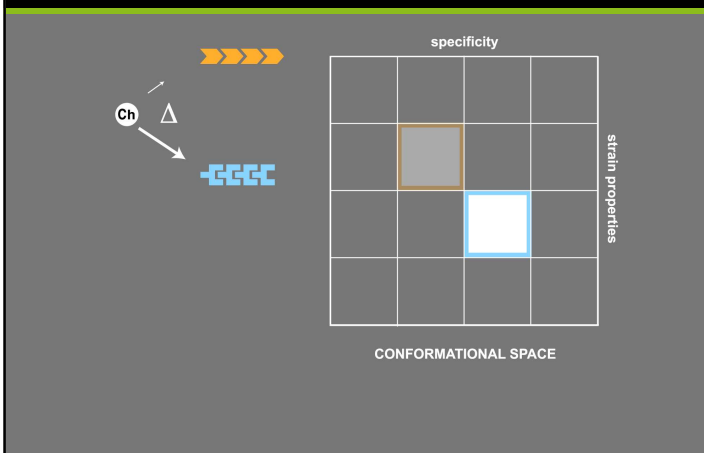
## Prion Strains and Species Barriers Results from Misfolding into Multiple Distinct Forms



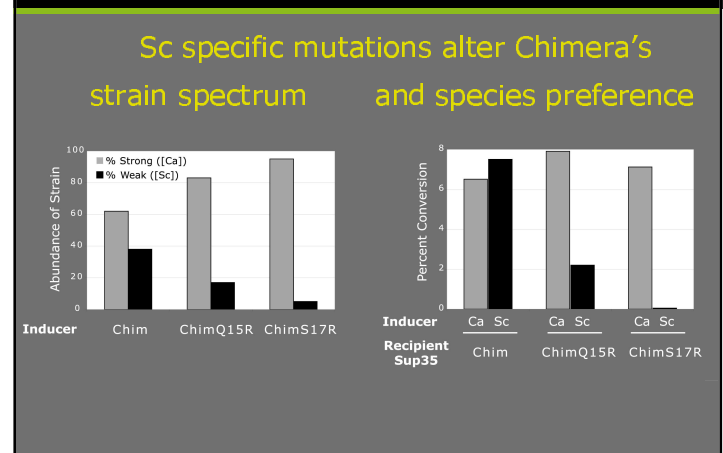
## Prion Strains and Species Barriers Results from Misfolding into Multiple Distinct Forms



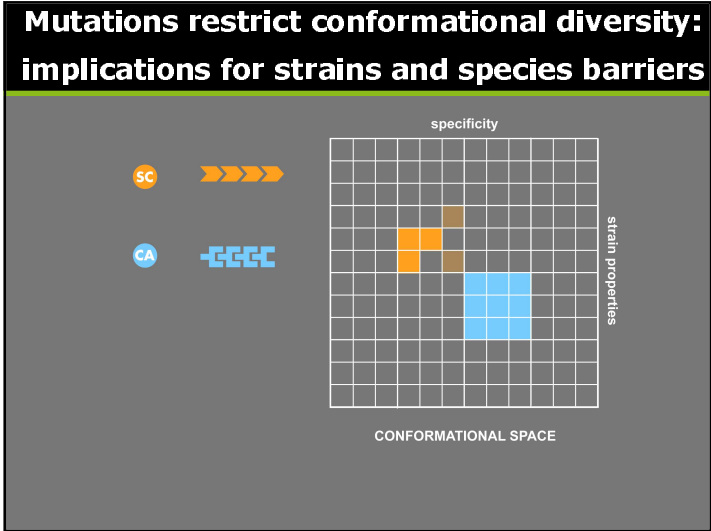
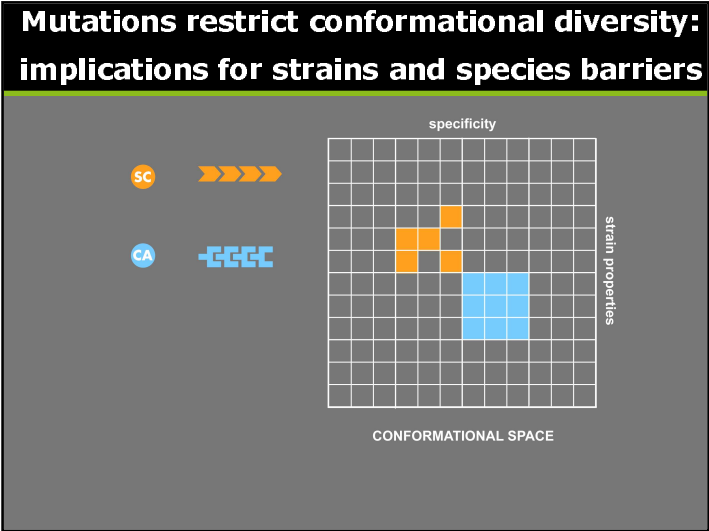
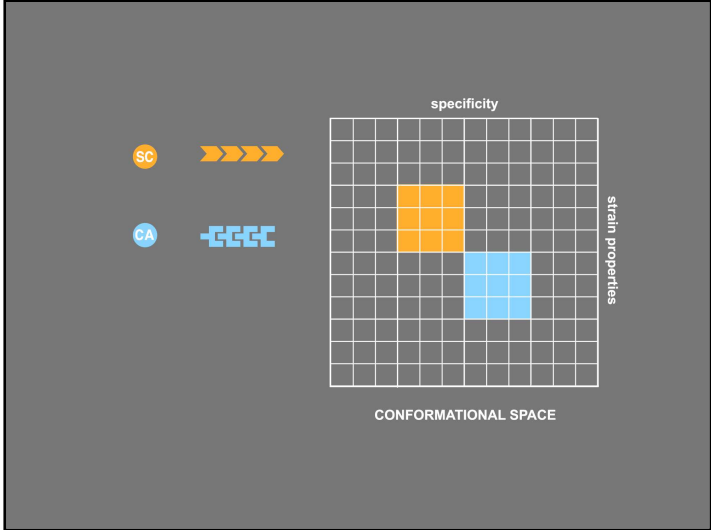
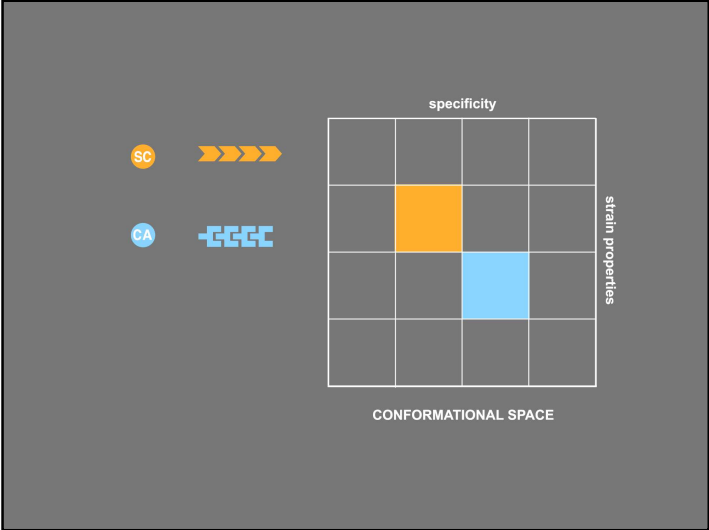
## Prion Strains and Species Barriers Results from Misfolding into Multiple Distinct Forms



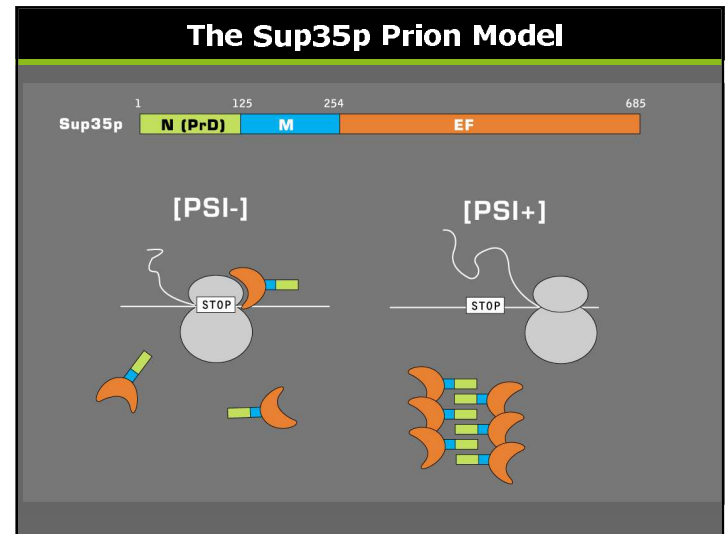
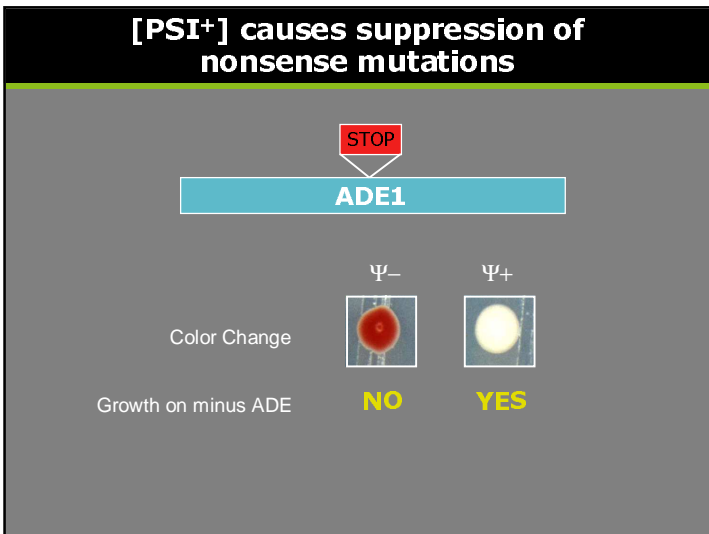
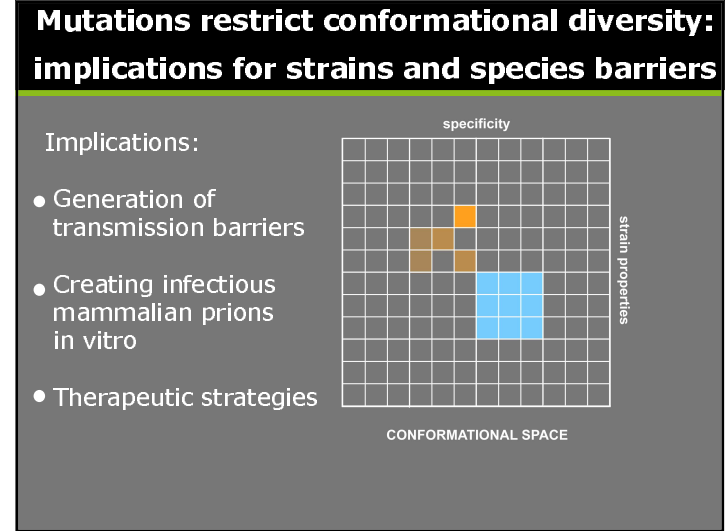
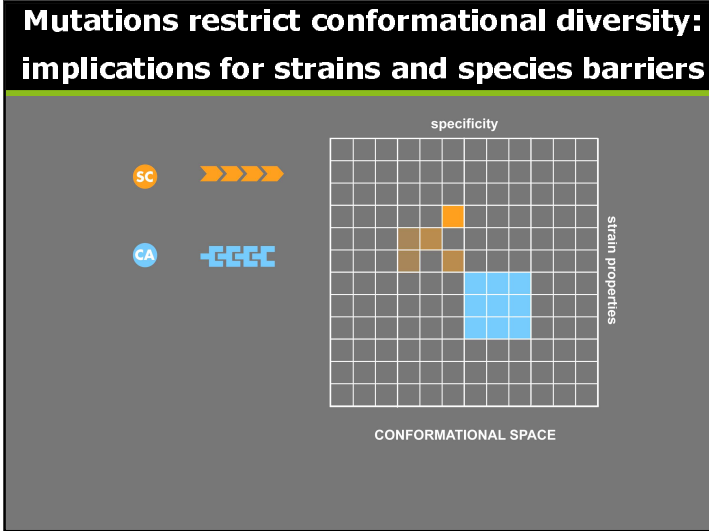
## Mutational Control of Prion Strains and Species



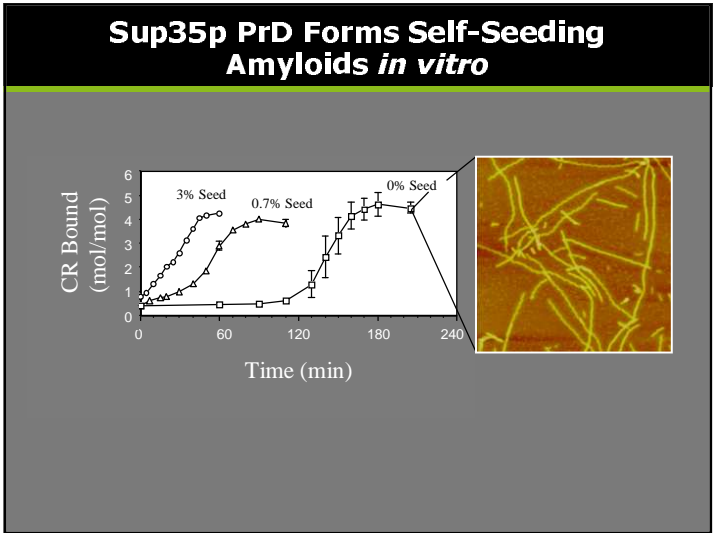
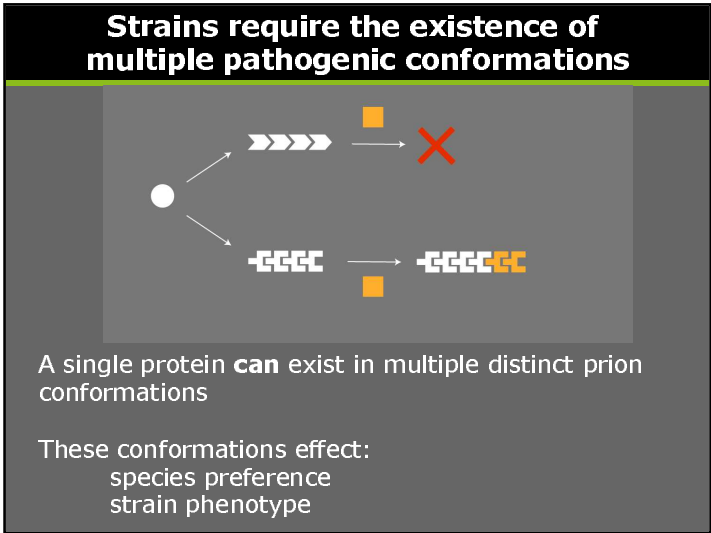
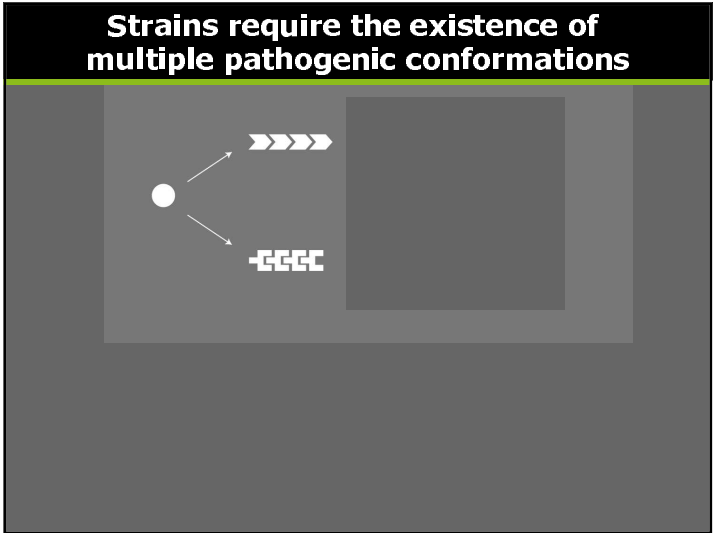
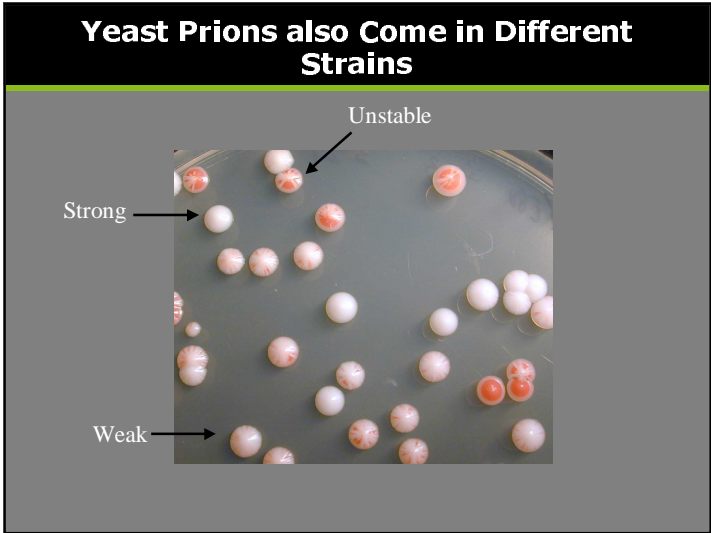
# An Epigenetic Switch: Prion Based Protein Regulation



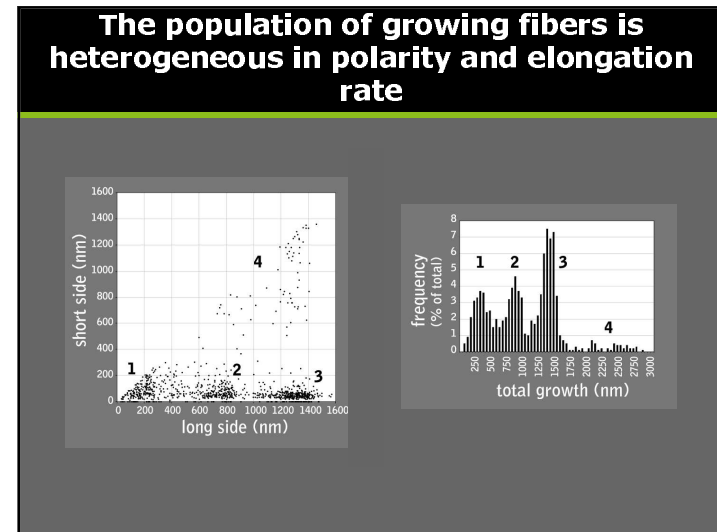
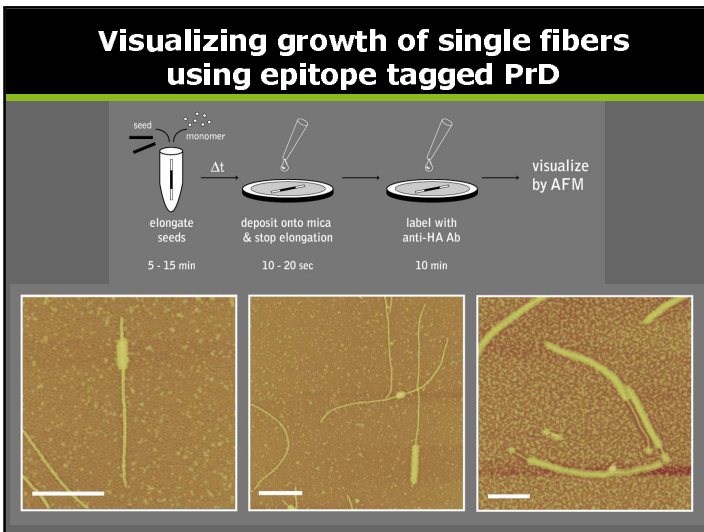
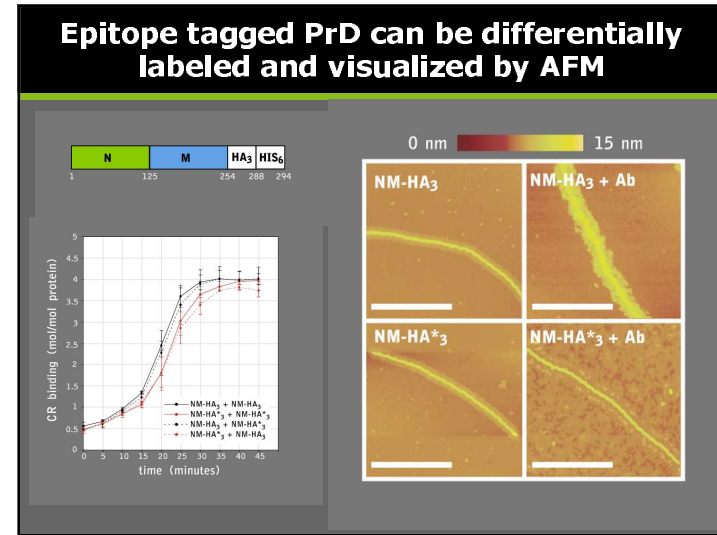
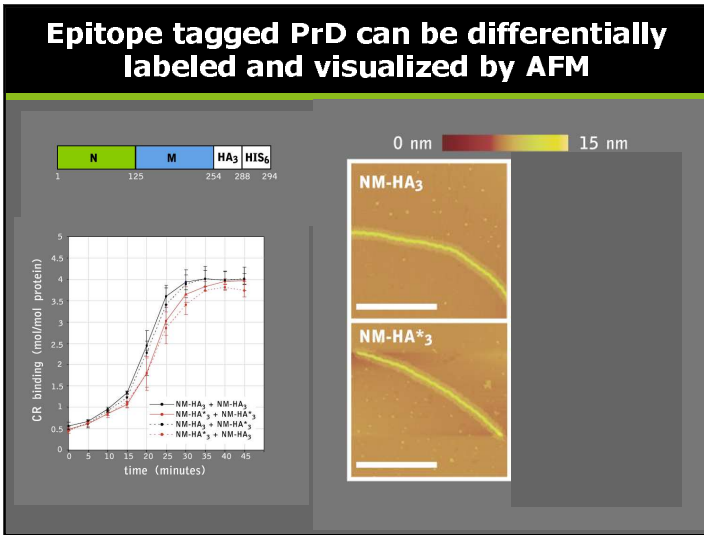
# An Epigenetic Switch: Prion Based Protein Regulation



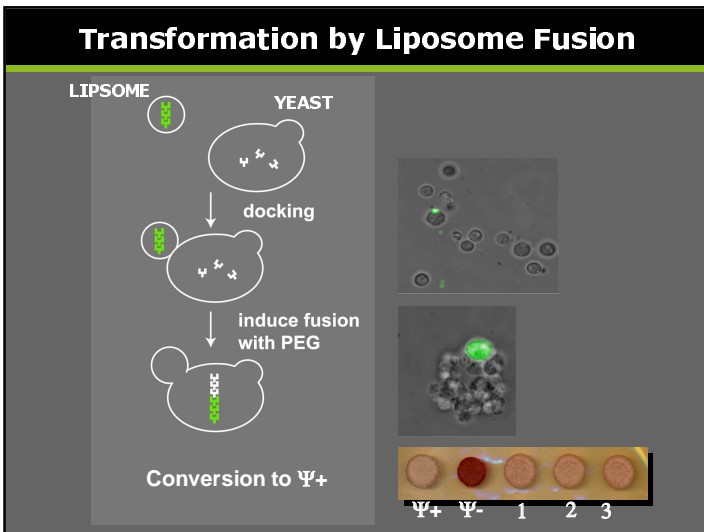
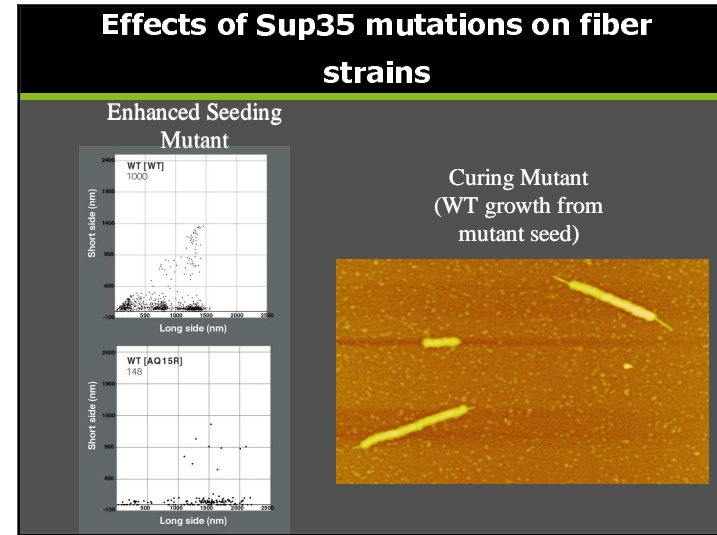
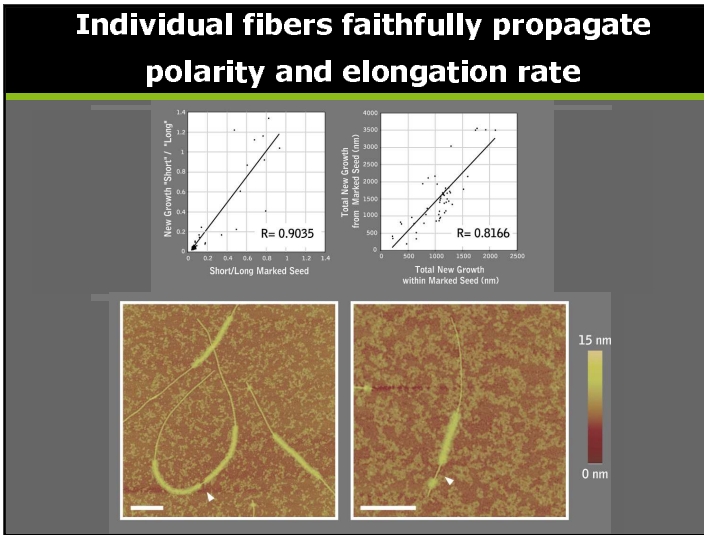
# An Epigenetic Switch: Prion Based Protein Regulation



# An Epigenetic Switch: Prion Based Protein Regulation

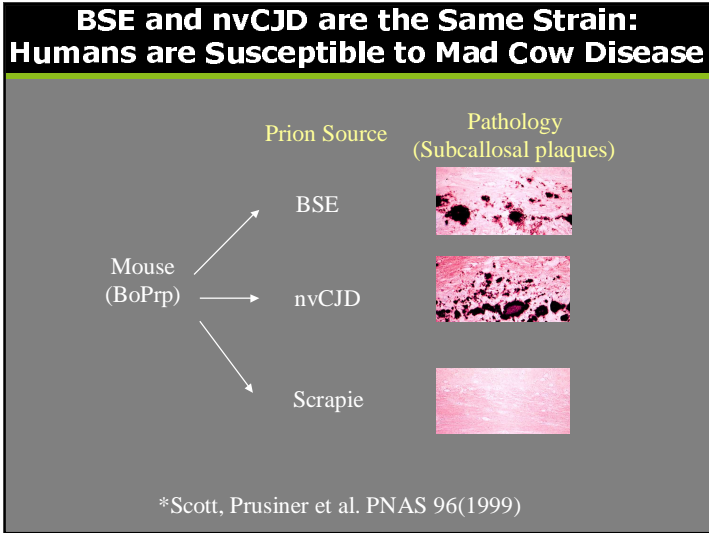


# An Epigenetic Switch: Prion Based Protein Regulation

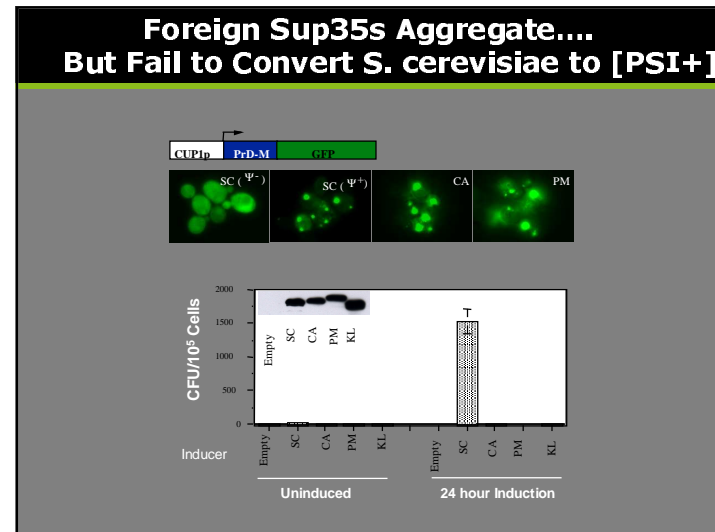
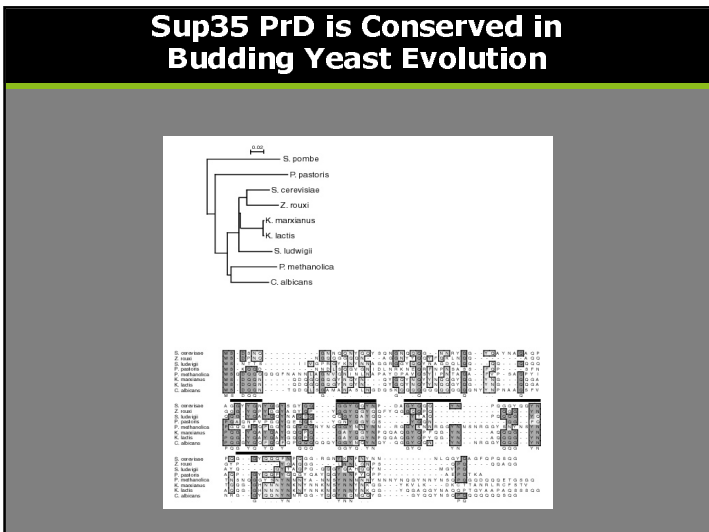


## Molecular Basis of Prion Strains

## An Epigenetic Switch: Prion Based Protein Regulation

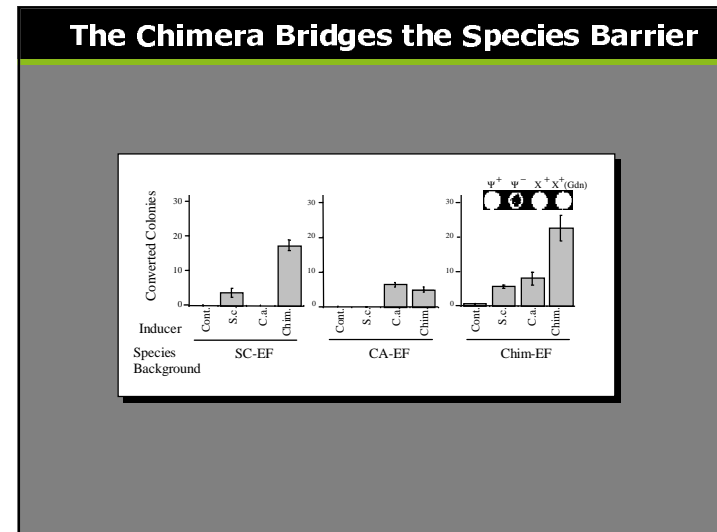
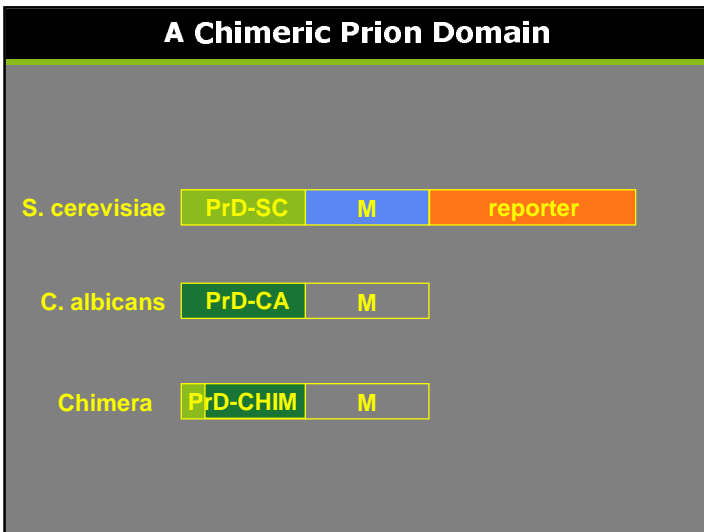
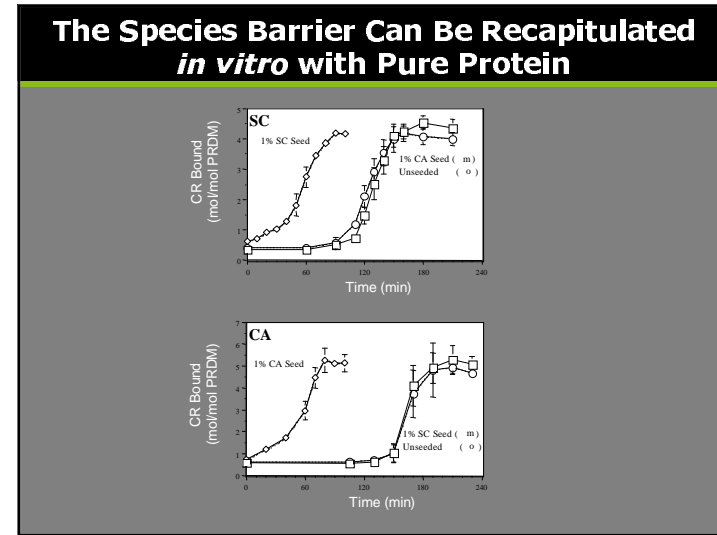
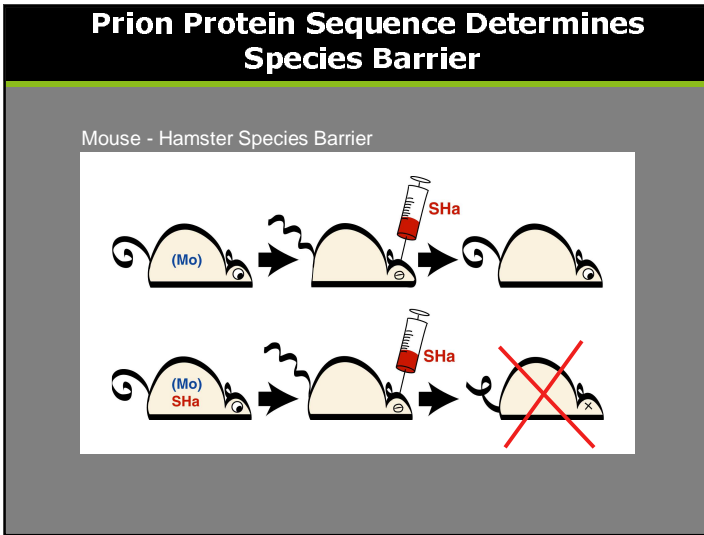


## Conservation and speciation in a yeast prion

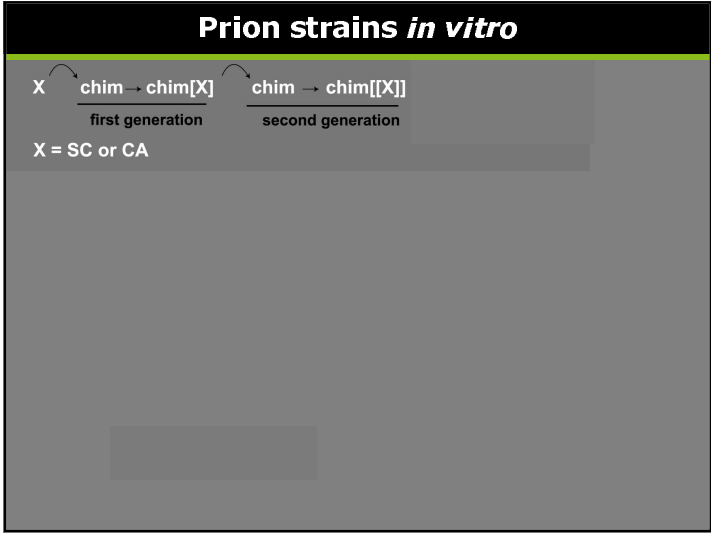
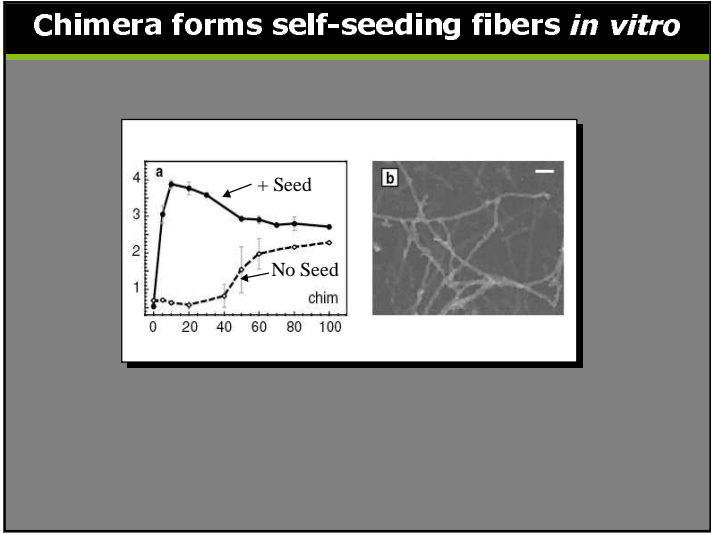
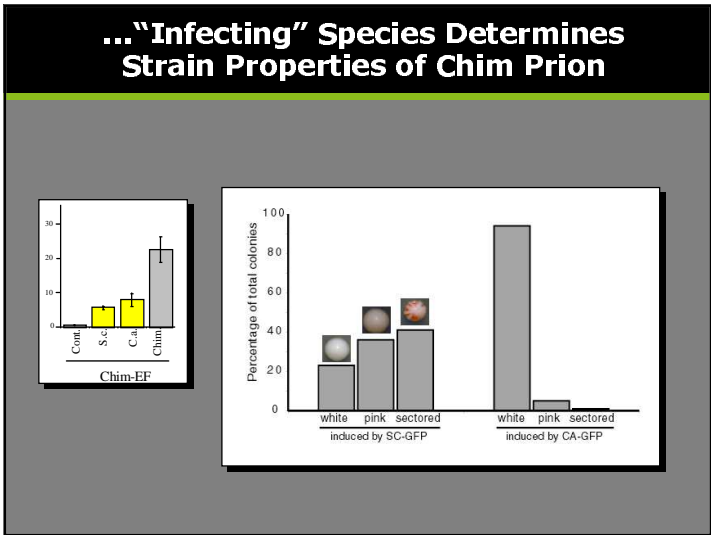
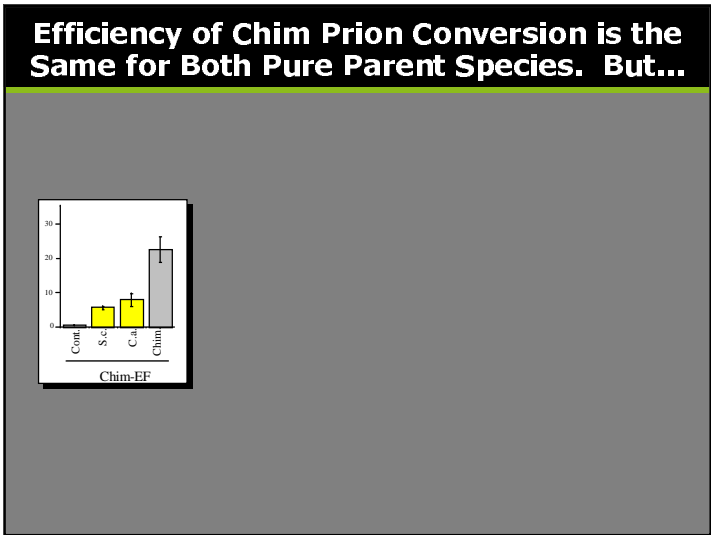




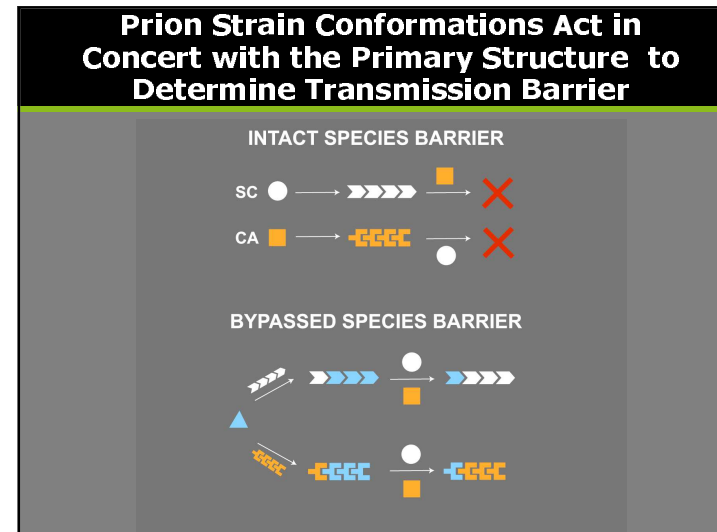
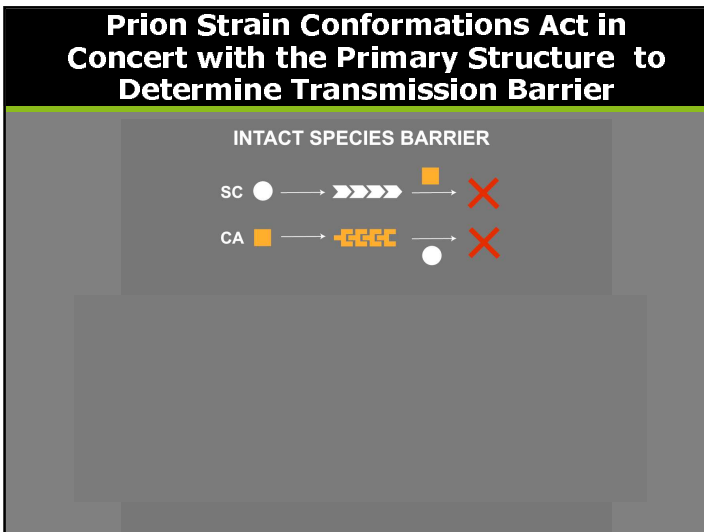
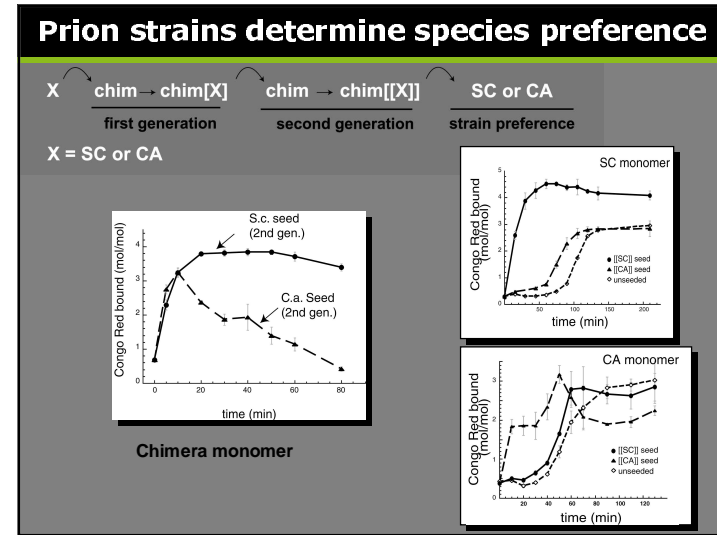
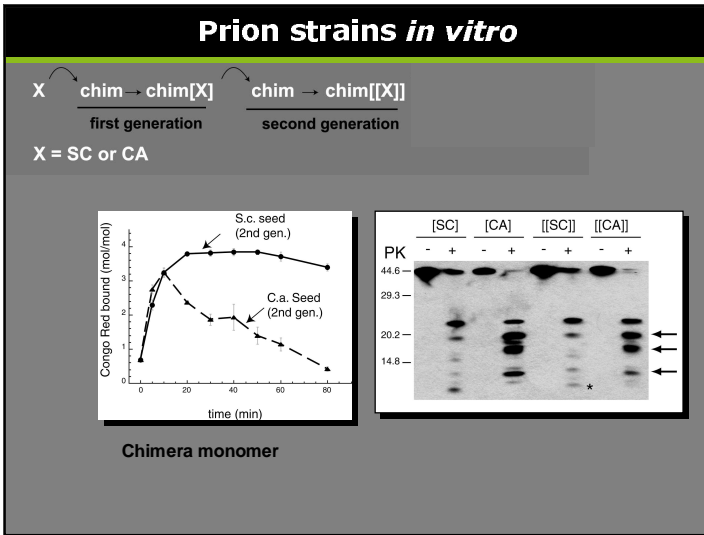
# An Epigenetic Switch: Prion Based Protein Regulation



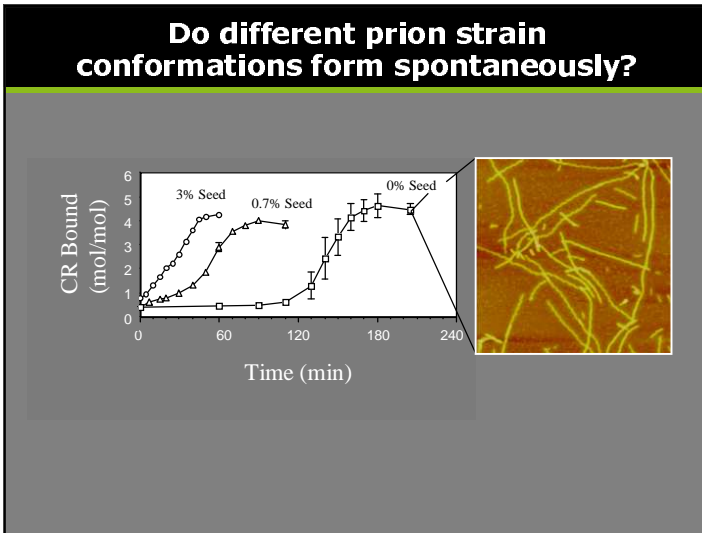
# An Epigenetic Switch: Prion Based Protein Regulation



# An Epigenetic Switch: Prion Based Protein Regulation



## An Epigenetic Switch: Prion Based Protein Regulation

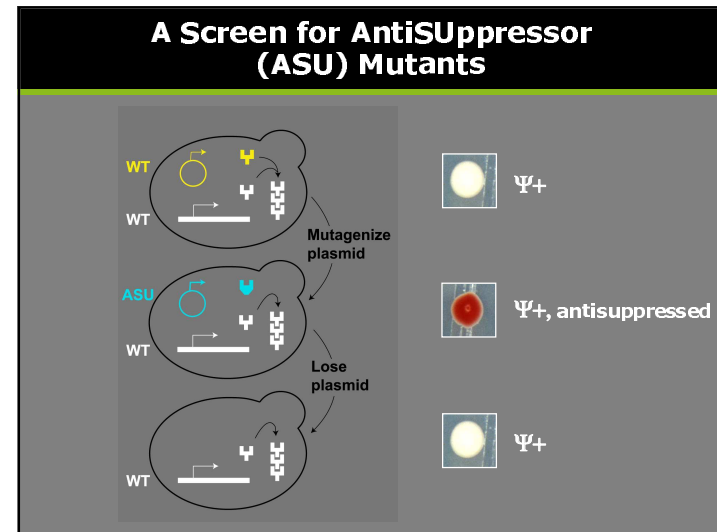
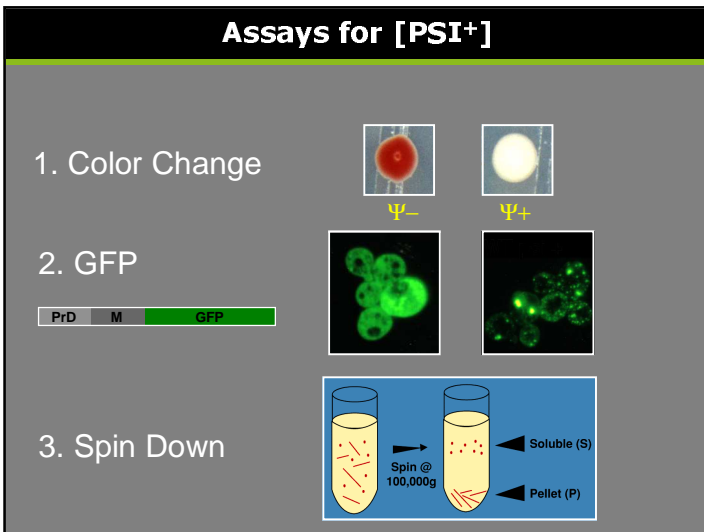
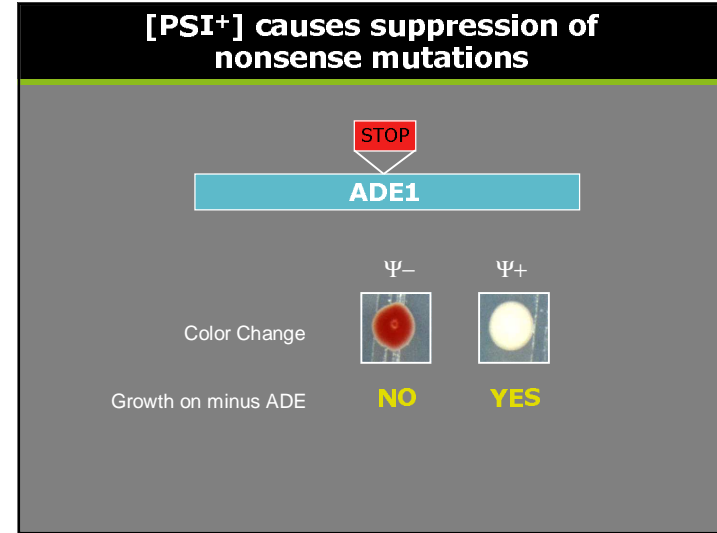
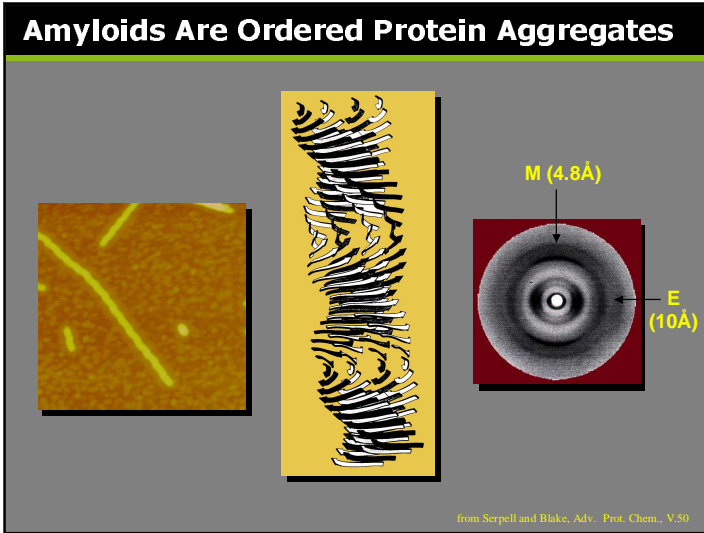


- ### Summary
- An epigenetic switch: Prions as a novel and conserved mechanism of regulating protein function
  - Molecular basis of a yeast prion species barrier
  - A prion's conformation (strain) plays a critical role in determining its ability to be transmitted across a species barrier
  - Identified a novel yeast prion [NU<sup>+</sup>] which acts as a general regulator of protein aggregation

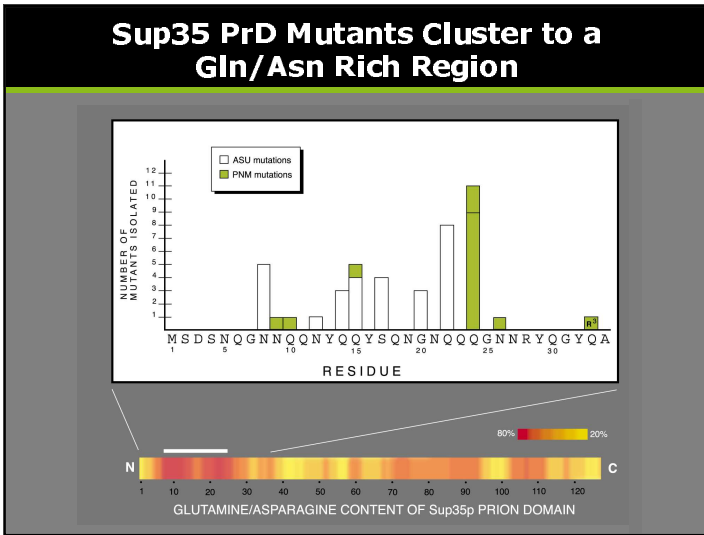


- ### Acknowledgments
- **Prion Strains:** Peter Chien
  - **Prion Mutants Screen:** Angela DePace and Alex Santoso
  - **Single Fiber Assay:** Angela DePace
  - **Species Barrier:** Alex Santoso and Peter Chien
  - **Protein Infection:** Helmut Sparrer
  - **New Prions:** Lev Osherovich and Melissa Michelitsch

# An Epigenetic Switch: Prion Based Protein Regulation



# An Epigenetic Switch: Prion Based Protein Regulation



### CAG repeats (polyGln) cause protein aggregation and neurodegeneration

- Nuclear aggregates are a common feature CAG-repeat diseases
- Expression of protein fragments containing Gln repeats leads to nuclear aggregates and Neurodegeneration in Mice Worms, and Drosophila
- Poly Gln-repeats form amyloids in vitro (as predicted by Perutz)
- Poly Gln aggregates in prion-like manner in yeast

\* Immuno-EM Showing Huntingtin Nuclear aggregates

\*Bates et al. Cell 90, pp537.

