Heterogeneity in Single Particles

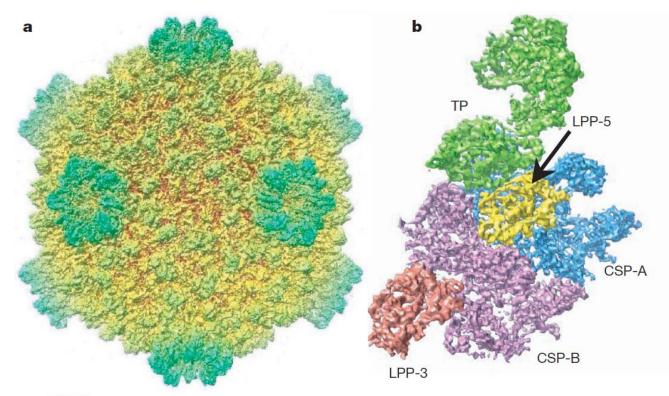
- Degrees of right and wrong
- Ways to increase reliability
- Detecting problems
- Different types of heterogeneity
- Overview of classification methods (Sigworth)
 - Classification as a problem of clustering in factor space
 - Brief intro to supervised classification
 - ML and the EM algorithm
 - ML with a prior probability (MAP estimation)

Heterogeneity in Single Particles...

- ML classification (Sigworth)
- ML-like restraints & classification
- Continuous deformation models (Sigworth)
 - Continuous vs. discrete models
 - Reconstructing continuous models using morphings--2D results.

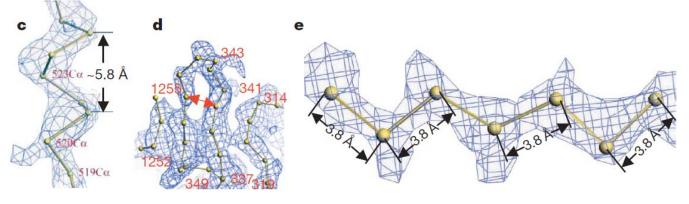


Cytoplasmic Polyhedrosis Virus



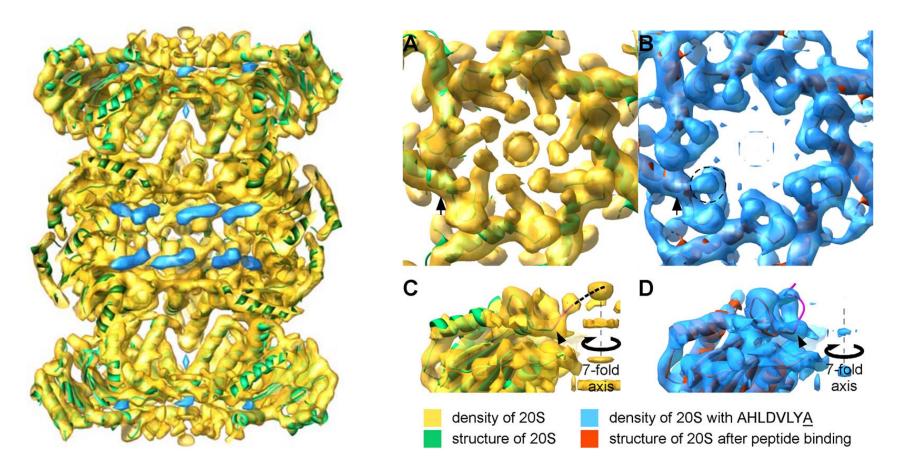
3.88 Å resolution

Atomic structure visible



Yu et al. 2008

20S Proteasome

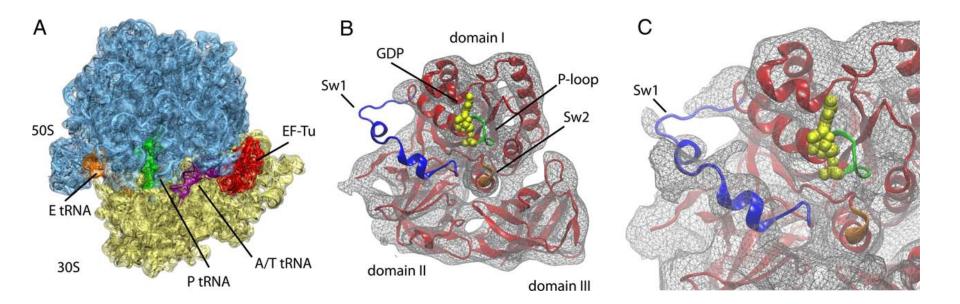


Resolution between 6 and 8 Å

Secondary structure visible Correlation with existing atomic models

Rabl et al. 2008

80S Ribosome

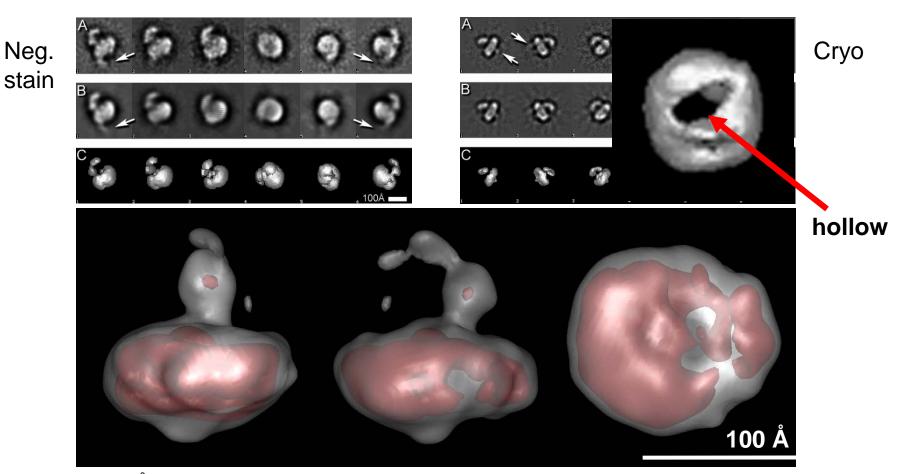


6.7 Å Resolution

Secondary structure visible Correlation with existing atomic models

Villa et al. 2009

L-Type Ca²⁺ Channel

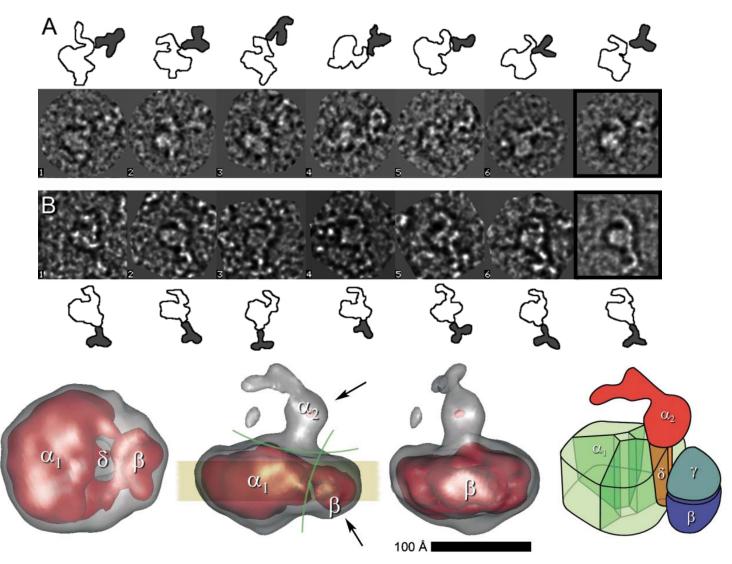


23 Å Resolution

Secondary structure NOT visible No existing atomic models available

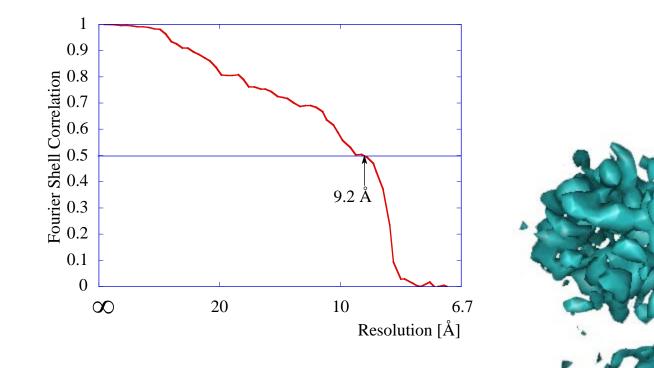
Wolf et al. 2003

Interpretation



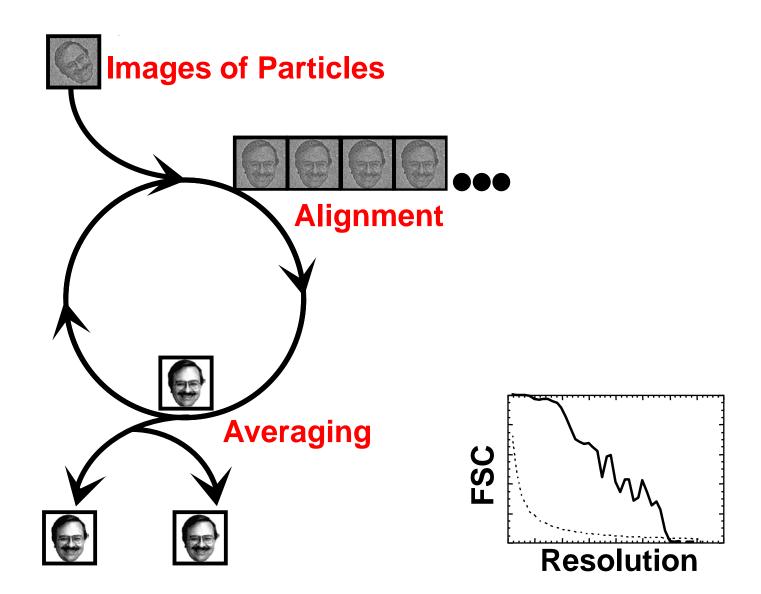
Wolf et al. 2003

Over-Refinement

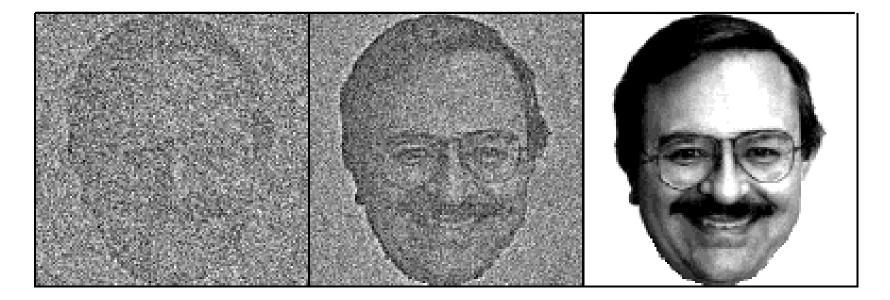


Wolf et al. 2002, unpublished

Resolution Measurement



Seeing is NOT Always Believing



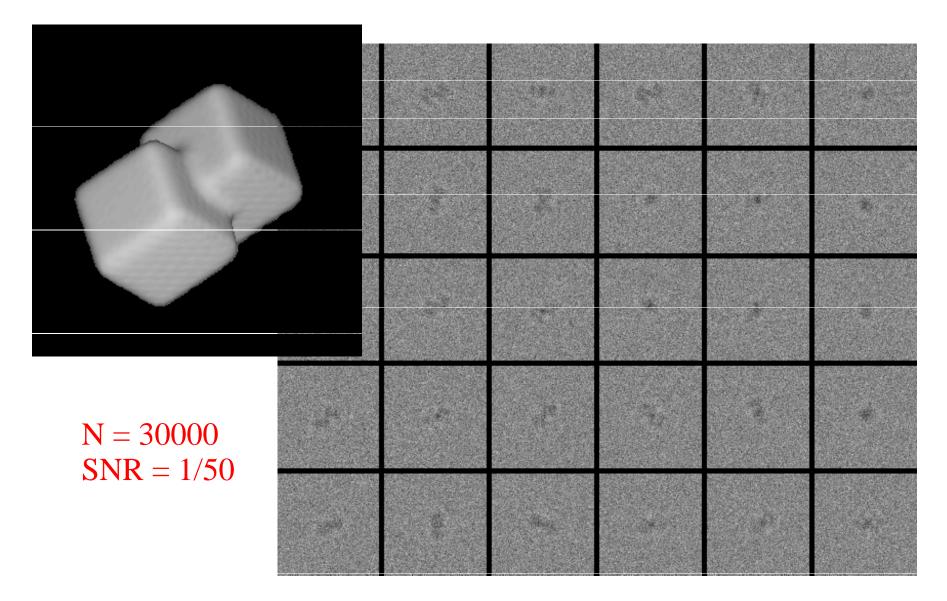
100 Images

1000 Images

Reference



Computer Simulation



Different Refinement Targets

0

0

0.1

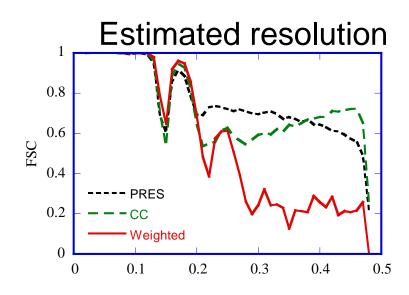
0.2

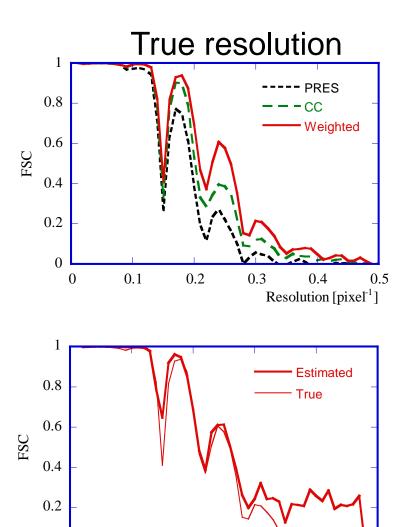
0.3

0.4

Resolution [pixel⁻¹]

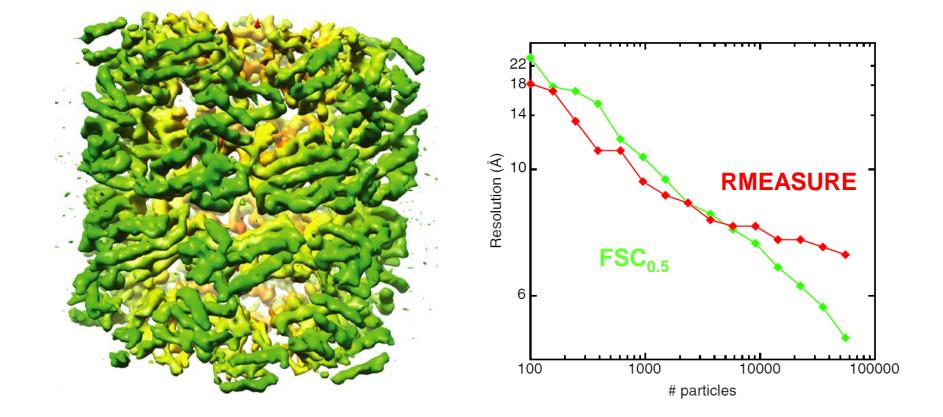
0.5





<u>Target functions:</u> Phase residual Linear correlation coefficient Weighted correlation coefficient (signal-to-noise weighting)

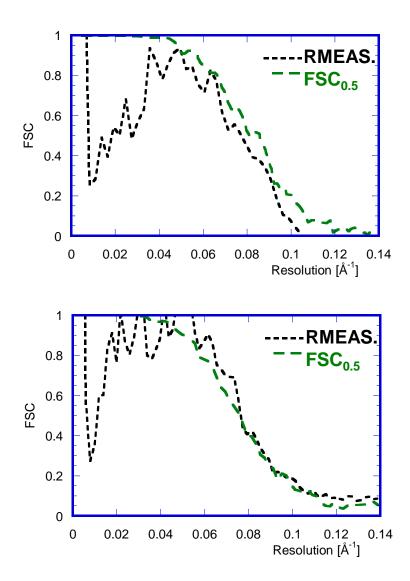
Resolution Measurement

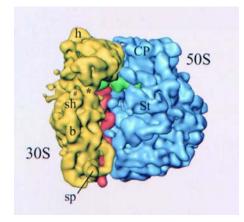


"The resolution reported by **RMEASURE** [...] was more consistent with the details observed in the reconstructions."

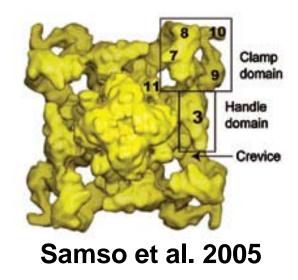
Stagg et al. 2008

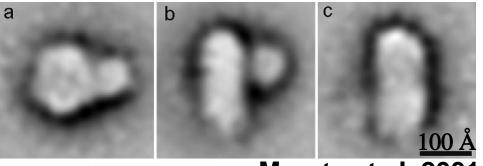
More RMEASURE Tests



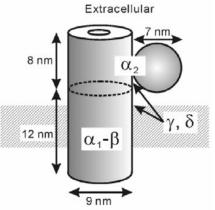


Gabashvili et al. 2000

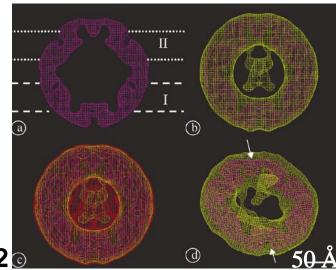




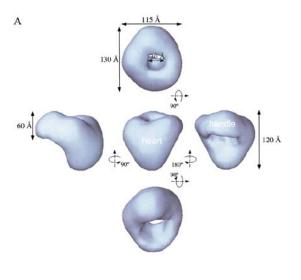
Murata et al. 2001



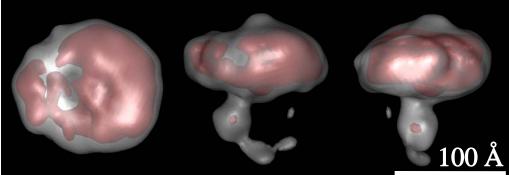
Cytoplasm



Serysheva et al. 2002

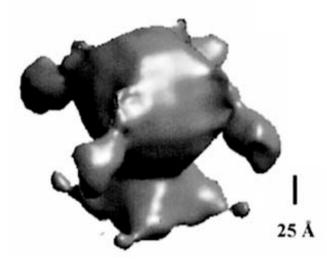


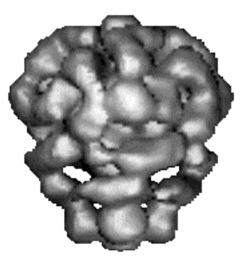
Wang et al. 2002



The Many Faces of a Channel

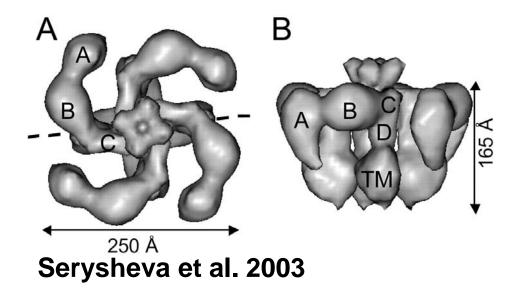
Wolf et al. 2003





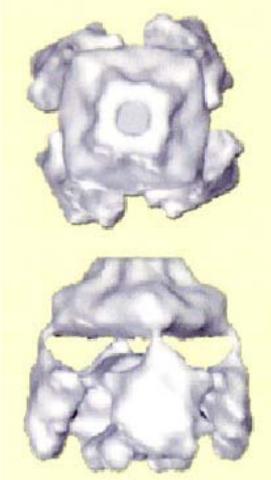
Jiang et al. 2002

Sato et al. 2004

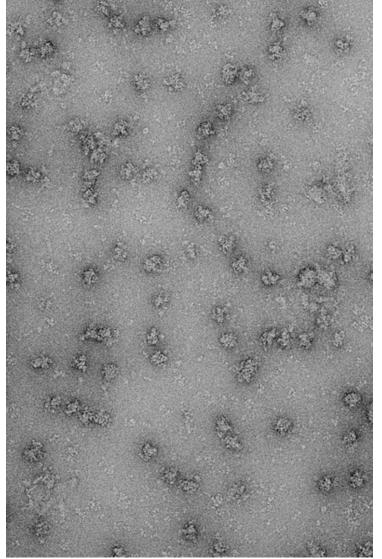


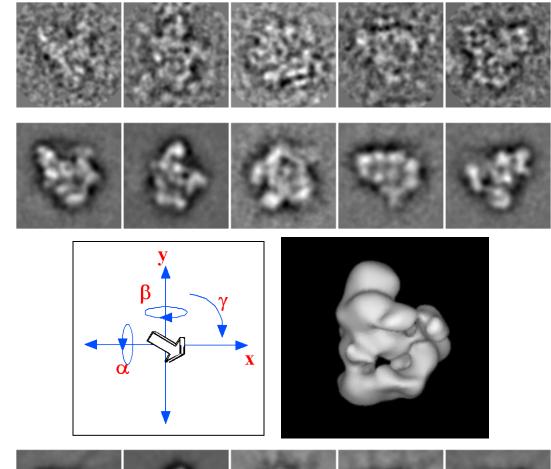
IP₃ Receptor

da Fonseca et al. 2003



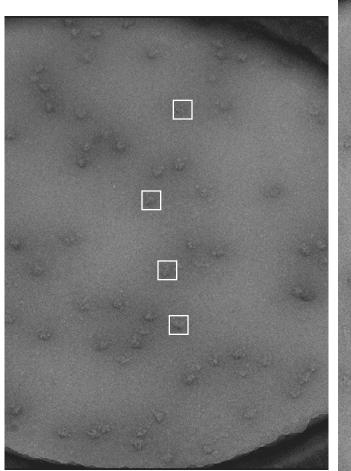
Spliceosome



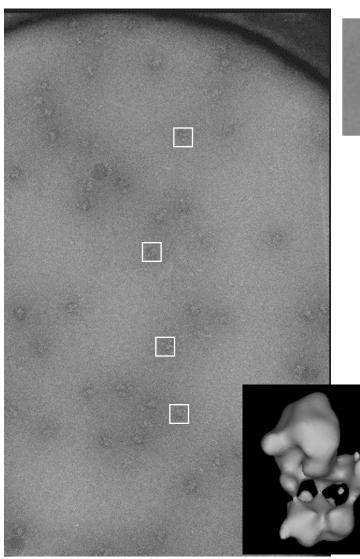


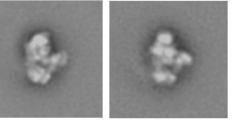
Jurica et al. 2002, unpublished

Random Conical Tilt

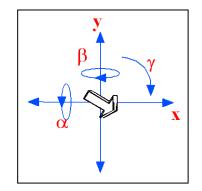


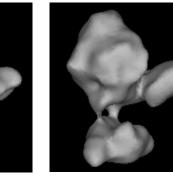
40° tilt Jurica et al. 2003





Class Averages

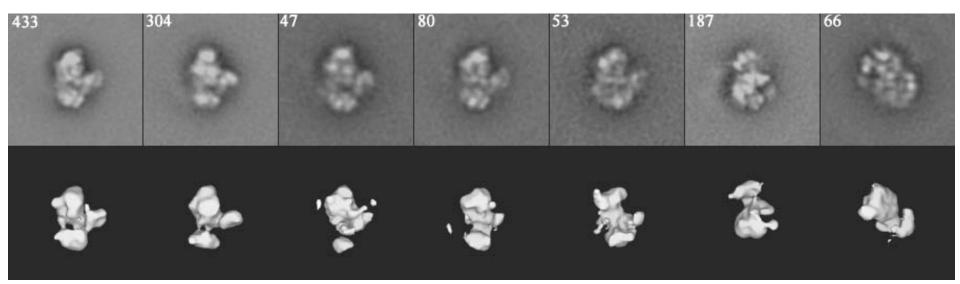




Untilted

Structures

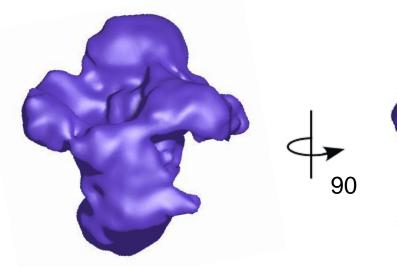
Classification

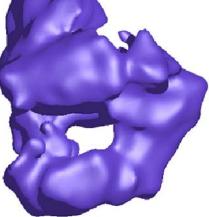


Jurica et al. 2003

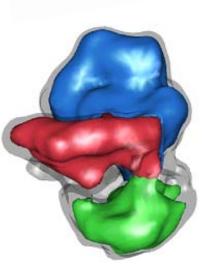
Two Methods - Two Structures

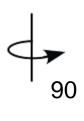
Angular reconstitution (no tilts)

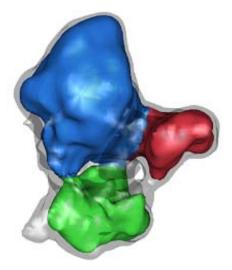




Random conical tilt

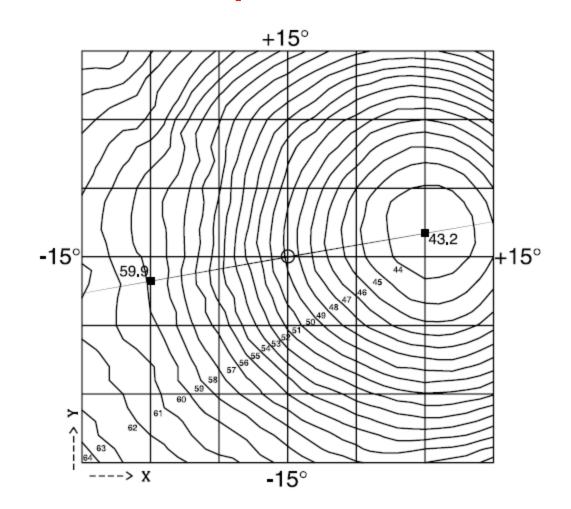






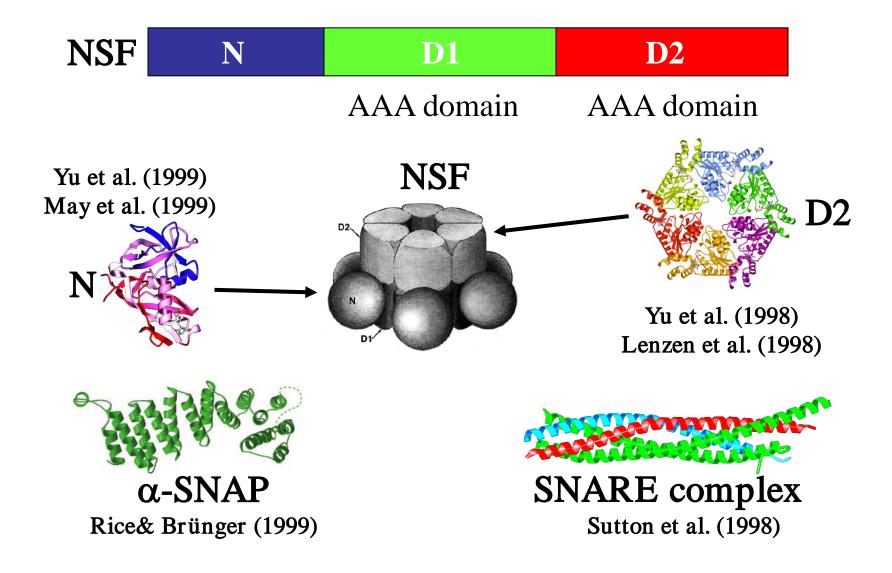
Jurica et al. 2003

Tilt Experiments

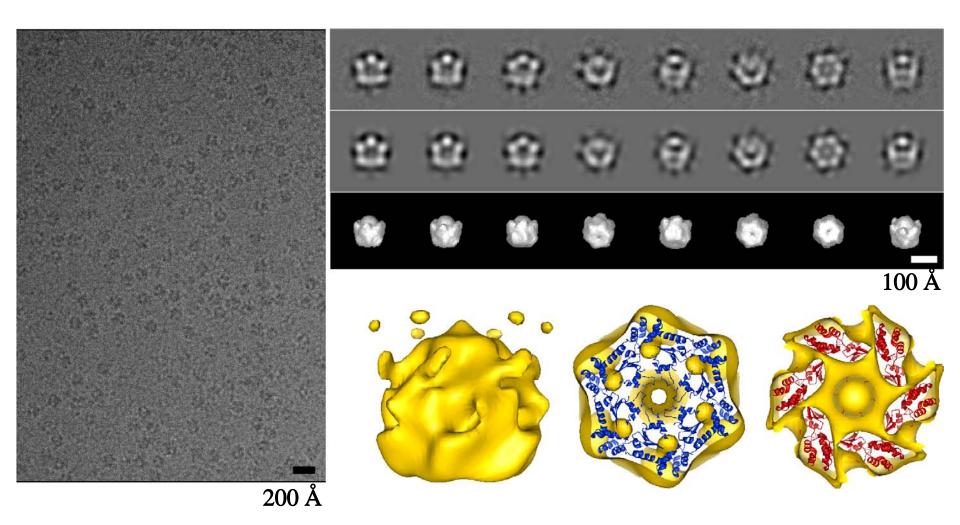


Rosenthal & Henderson 2003

N-ethylmaleimide Sensitive Factor

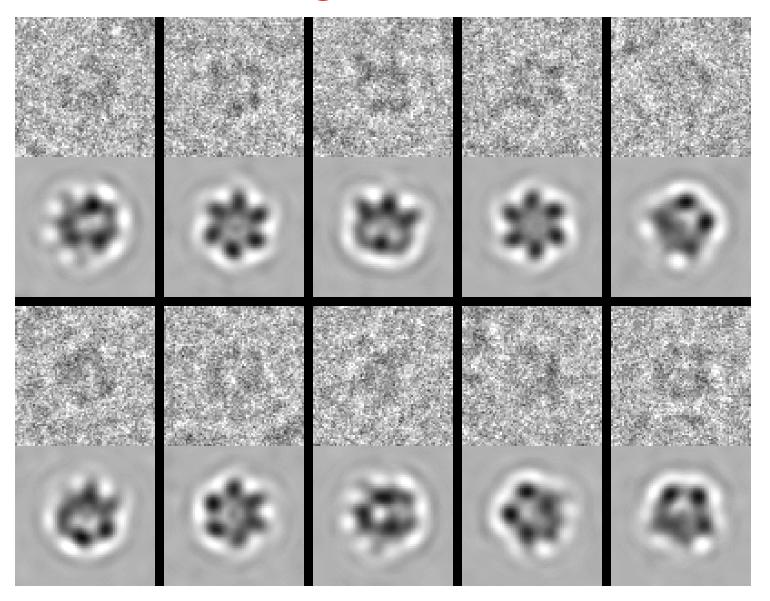


Reconstruction

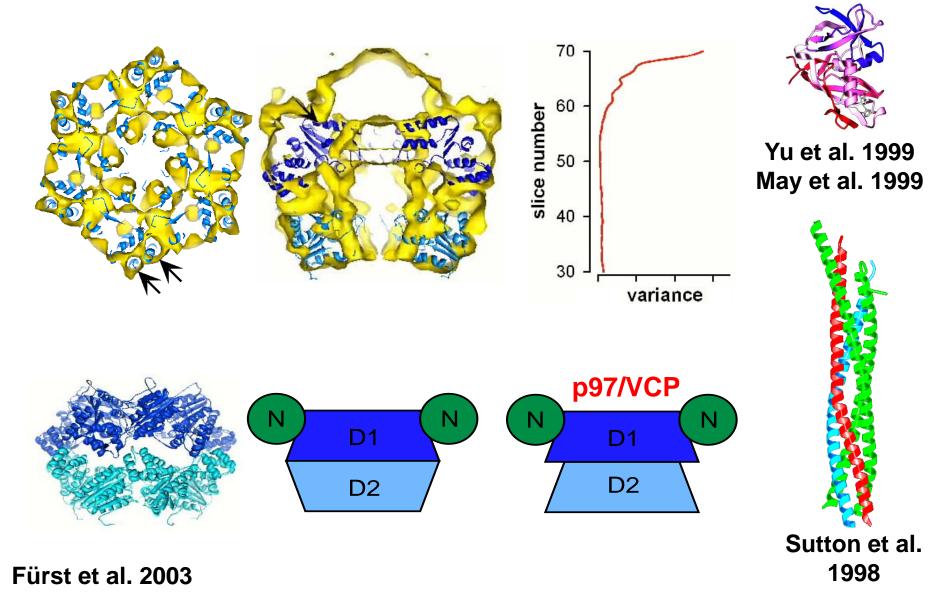


Fürst et al. 2003

Matching References



Interpretation?



Detecting Problems

- Often not straight forward!
- Does it look like a ball?
- Is it hollow?



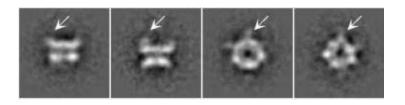
- Does the reference match the particles?
- Does is correlate with known structures?
- Can the high-resolution details be verified?
- Does it make sense (biology, molecular mass)?
- How does the structure refine?
- Is there heterogeneity (variance, classification)?

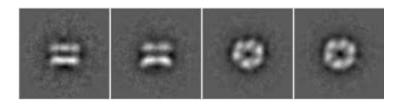


Different Types of Heterogeneity

Different Types of Heterogeneity

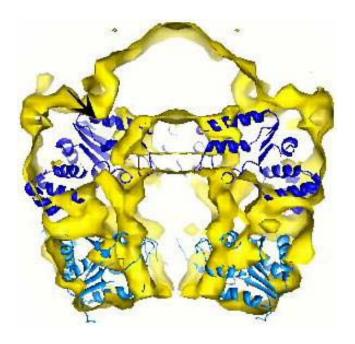
Conformational Heterogeneity

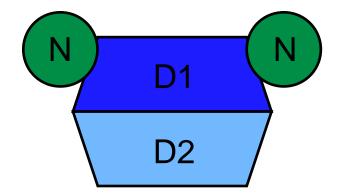




NSF

NSFΔN

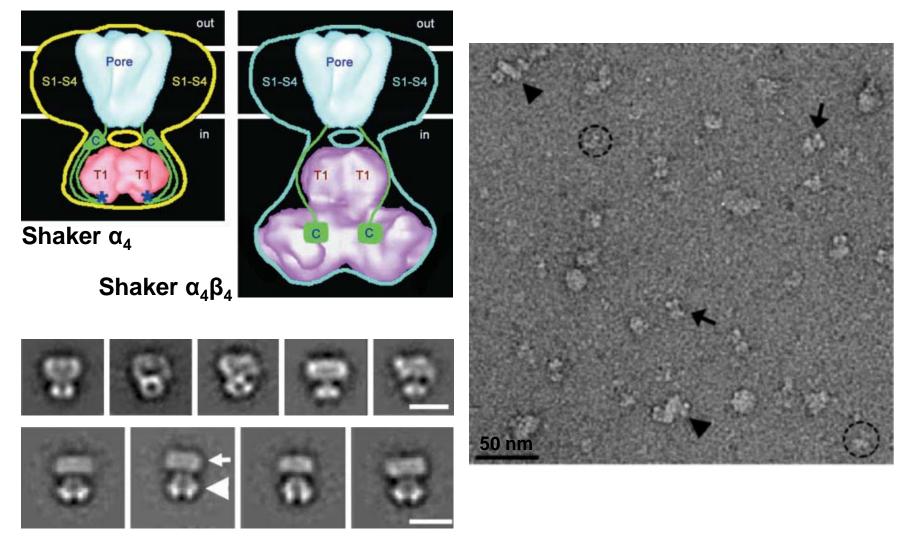




Fürst et al. 2003

Different Types of Heterogeneity

Compositional Heterogeneity



Sokolova et al. 2003

Classification Methods...

Fred Sigworth



Poor Man's Maximum Likelihood

$$L(\Theta) = \sum_{i=1}^{N} \ln \int p_i(\phi, X_i | \Theta) d\phi \qquad p_i = \text{joint probability} \\ \Theta = (A, \sigma, x_0, y_0, \sigma_{xy})$$

If SNR high, then p_i essentially zero everywhere except when particle aligned with reference (p_i similar to delta function):

$$\phi_{i} = \operatorname{argmax} \left[p_{i}(\phi, X_{i} | \Theta) \right] = \operatorname{argmax} \left[\ln p_{i}(\phi, X_{i} | \Theta) \right]$$
$$= \operatorname{argmax} \left[X_{i} \bullet A + \sigma^{2} \ln f(\phi | \Theta) \right]$$

 X_i : image I σ : standard deviation of noise in imageA : reference image ϕ : particle params

Sigworth 1998

Parameter Restraints

$$\phi_{i} = \operatorname{argmax} \left[X_{i} \bullet A + \sigma^{2} \ln f(\phi | \Theta) \right]$$

$$f(\phi, \Theta) = \frac{1}{4\pi^{2} \sigma_{xy}^{2}} \exp \left[-\frac{(x - x_{0})^{2} + (y - y_{0})^{2}}{2\sigma_{xy}^{2}} \right]$$

$$f(\phi, \Theta) = \frac{1}{4\pi^{2} \sigma_{xy}^{2}} \exp \left[-\frac{(x - x_{0})^{2} + (y - y_{0})^{2}}{2\sigma_{xy}^{2}} \right]$$

- X_i : image *i*
- A : reference image
- : particle params φ

 x_0, y_0 : average x, y coords in data set

- σ_{xy} : std. deviation of *x*, *y* coords
- σ : standard deviation of noise in image

Computer Simulation

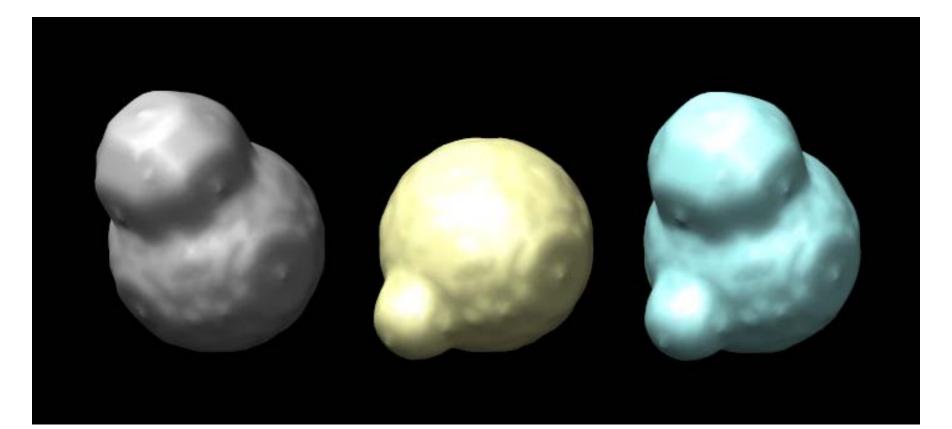


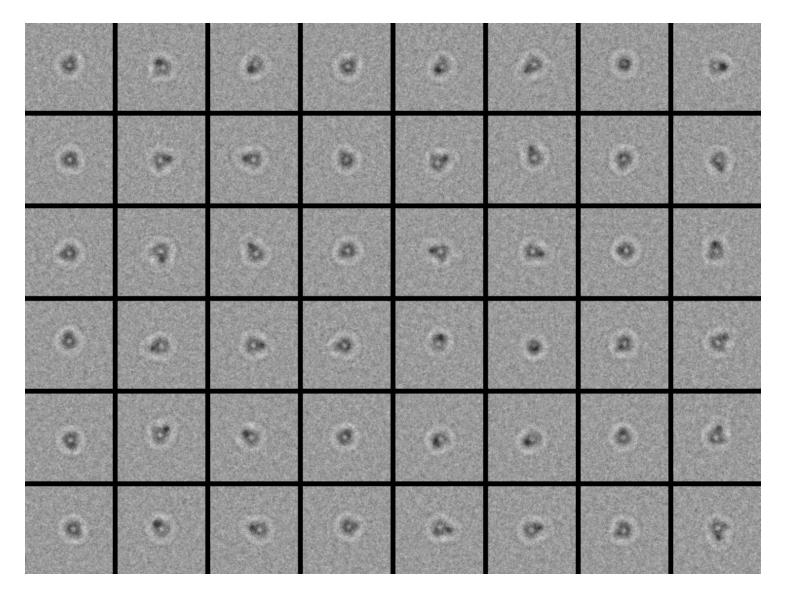
Poor Man's ML Classification

Assume *K* classes with class averages A_k :

$$A_{k}^{(n+1)} = \frac{\sum_{i=1}^{N} X_{i}(\phi_{i,k}) q_{i,k}^{(n+1)}}{\sum_{i} q_{i,k}^{(n+1)}}$$
$$q_{i,k}^{(n+1)} = p_{i,k}^{(n)}(\phi_{i,k}, X_{i} | \Theta_{k}^{(n)}) a_{k}^{(n)} / \sum_{k=1}^{K} p_{i,k}^{(n)}(\phi_{i,k}, X_{i} | \Theta_{k}^{(n)}) a_{k}^{(n)}$$

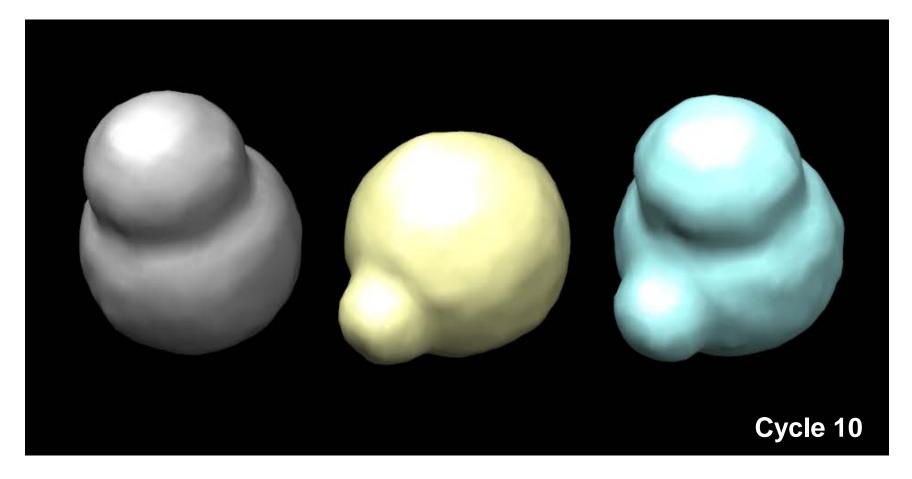
Test Structures





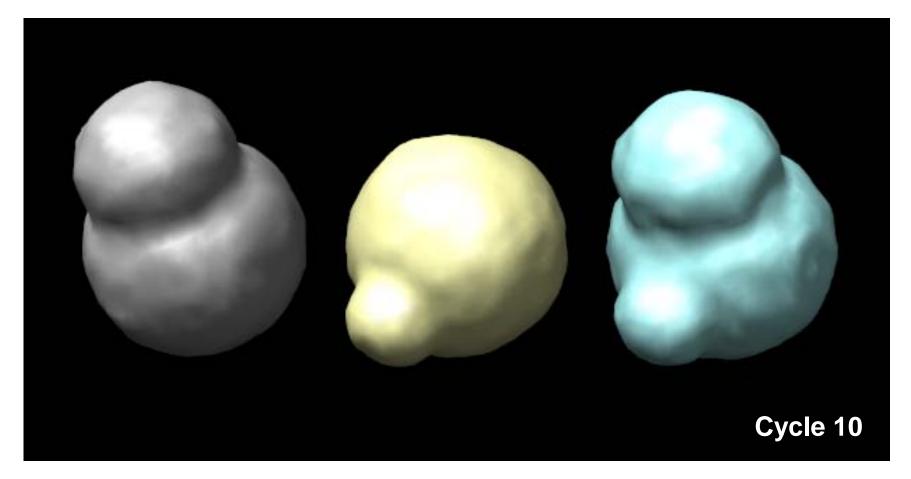
10000 images of each structure in random orientations SNR ~ 1

Correlation Classification

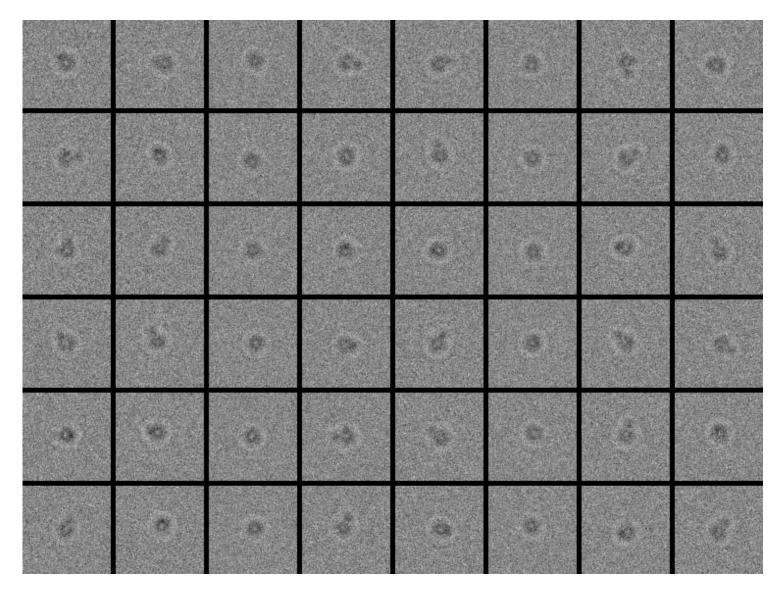


SNR ~ 1 Correct: 99.2%

ML-Like Classification

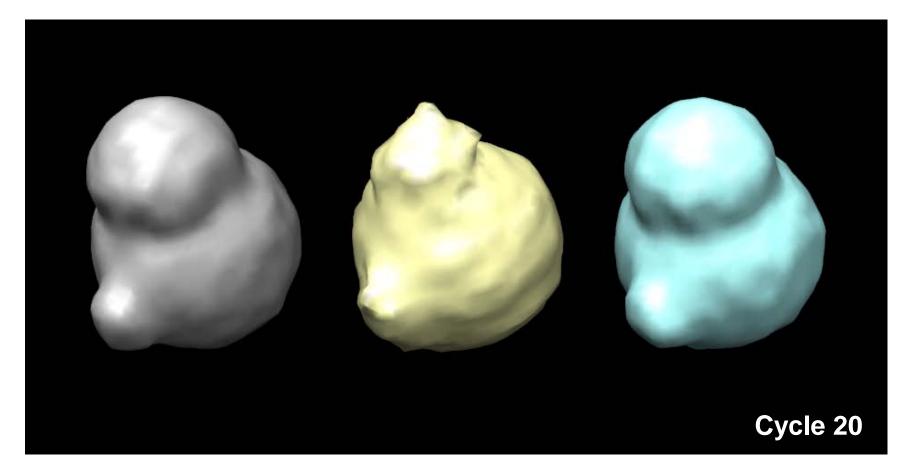


SNR ~ 1 Correct: 94.3%



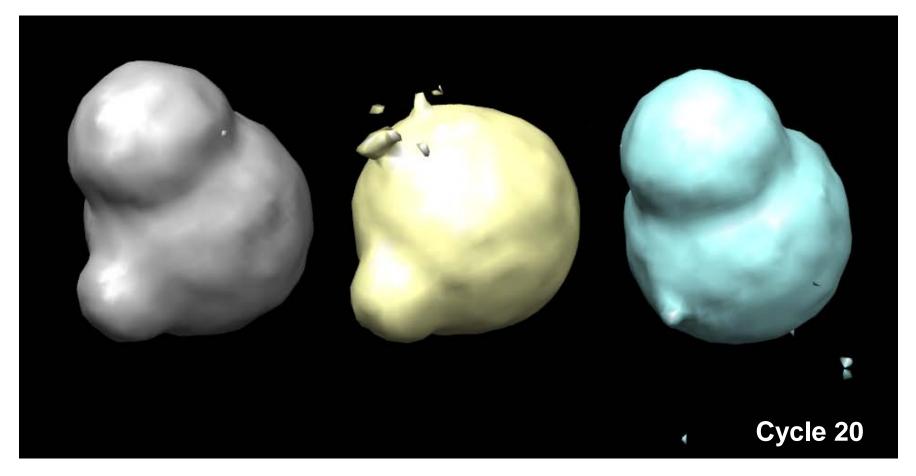
10000 images of each structure in random orientations SNR ~ 0.1

Correlation Classification



SNR ~ 0.1 Correct: 62.6%

ML-Like Classification



SNR ~ 0.1 Correct: 86.5%

Continuous Deformation Models...

Fred Sigworth