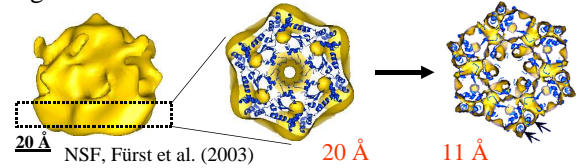


# Refinement Strategies for Single Particle Structure Determination

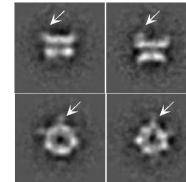
N. Grigorieff

## Goals

- Higher resolution



- Sorting of structural heterogeneity

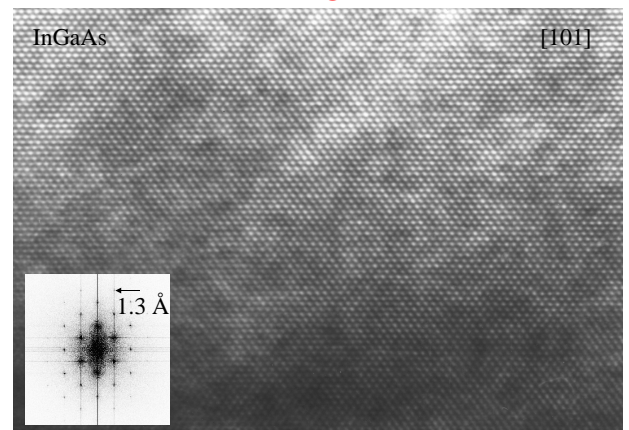


## The Prophecy

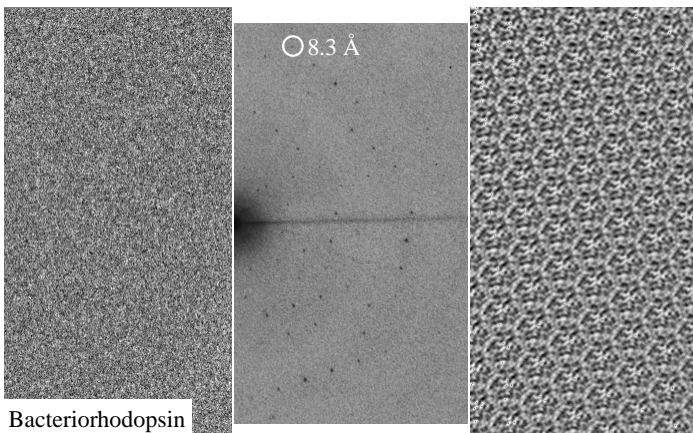
King Richard hath decreed... (QRB, 1995)

- Use 5 e<sup>-</sup> per Å<sup>2</sup>
- Demand a signal-to-noise ratio of 9 or better
- Aim for 3 Å resolution
- ②Thou shall need to image 13,000 molecules
- ②For 6 Å, thou shall need only 7,000 images

## Resolving Power

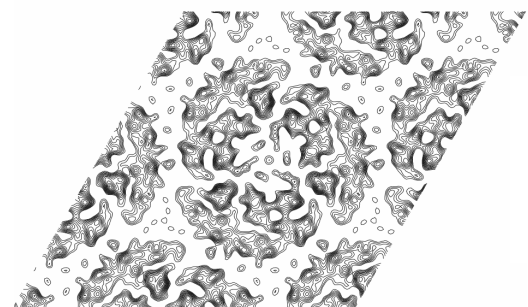


## Protein Crystals

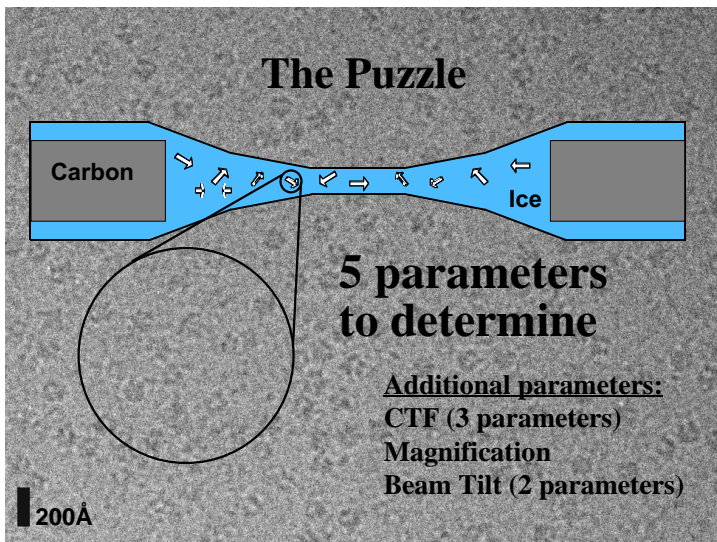


Bacteriorhodopsin

## Purple Membrane



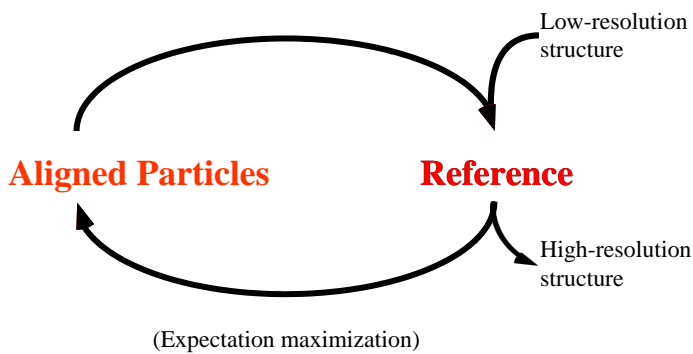
2.6 Å resolution



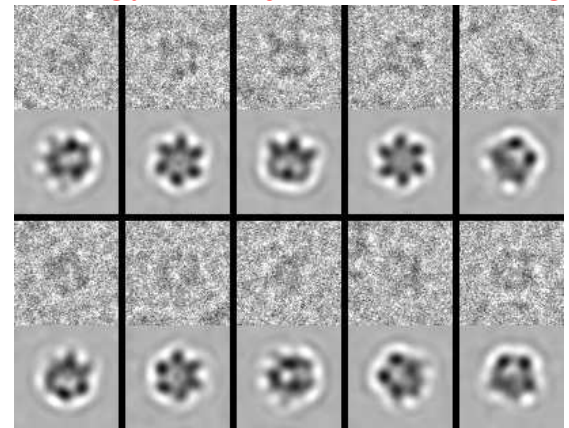
## A Crazy Idea

- Assume reliable resolution measure
- Search entire parameter space for highest resolution
- Given enough images, atomic resolution is reached
- Example:  
 3 angles, 1 deg step; two coordinates, 1 pixel step:  
 $360 \times 360 \times 360 \times 100 \times 100 = 5 \times 10^{11}$   
 13000 particles:  $(5 \times 10^{11})^{13000}$  structures to search
- This is a big number!

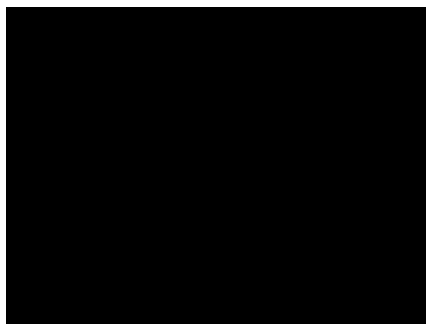
## Refinement



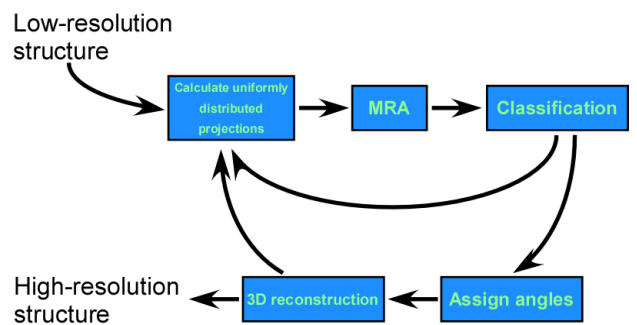
## Strategy 1: Projection Matching



## Strategy 2: Alignment in Reciprocal Space



## Strategy 3: MRA and Classification



## Strategy 4: Maximum Likelihood

Structure for  $n+1$  iteration

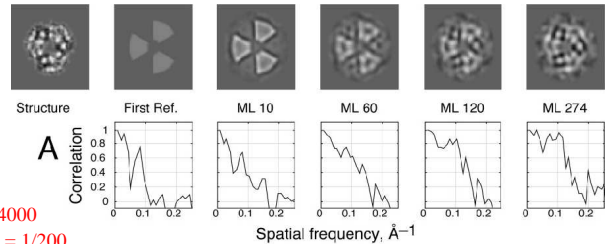
$$A^{(n+1)} = \frac{1}{N} \sum_{i=1}^N \frac{\int X_i(\phi) p_i(\phi, \Theta^{(n)}) d\phi}{\int p_i(\phi, \Theta^{(n)}) d\phi}$$

Probability function

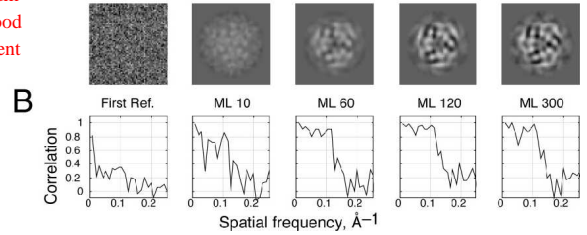
$$p_i(\phi, \Theta) = \left( \frac{1}{\sqrt{2\pi}\sigma} \right)^M \exp \left[ -\frac{|X_i(\phi) - A|^2}{2\sigma^2} \right] f(\phi | \Theta)$$

$X_i$ :  $i$ th image       $N$ : # of images       $\phi$ : alignment parameters  
 $\Theta$ : model parameters       $\sigma$ : noise in images       $f$ : positional probab.

Sigworth (1998), J. Struct. Biol. 122, 328-339

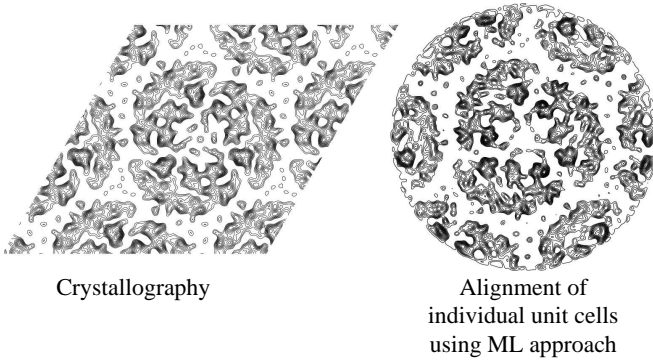


$N = 4000$   
 $SNR = 1/200$   
 Maximum likelihood alignment



Sigworth (1998), J. Struct. Biol. 122, 328-339

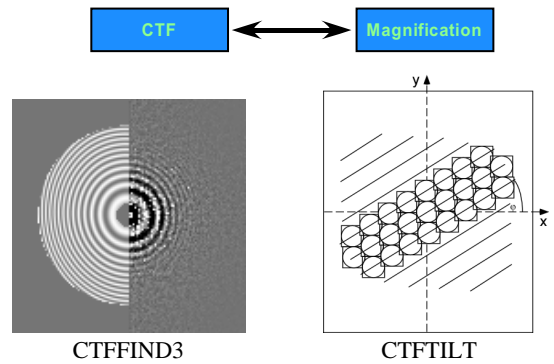
## ML processing of 2D crystals



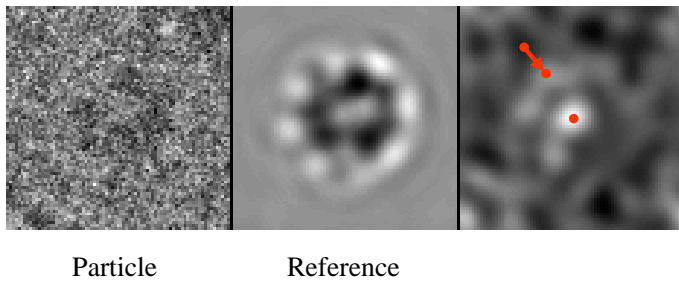
Crystallography

Alignment of individual unit cells using ML approach

## Defocus/Astigmatism and Magnification



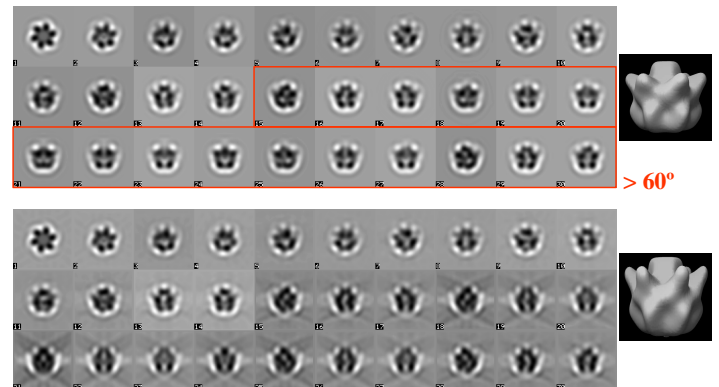
## Problem 1: Local Optima



Particle

Reference

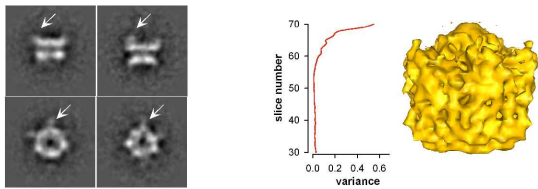
## Problem 2: Missing Views



> 60°



### Problem 3: Heterogeneity



- Misalignment of particles
- Lower resolution in disordered regions
- Loss of features

### Classification Using ML

Structure for  $n+1$  iteration

$$A_k^{(n+1)} = \frac{1}{\sum_i q_i^k(\Theta)} \sum_{i=1}^N \frac{\int X_i(\phi) p_i^k(\phi, \Theta^{(n)}) d\phi}{\sum_k \int p_i^k(\phi, \Theta^{(n)}) d\phi}$$

Probability function

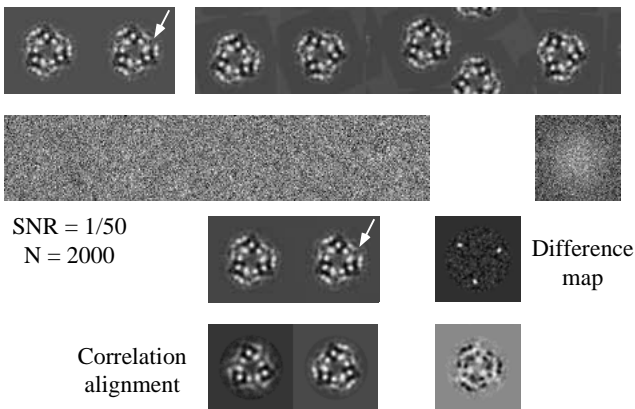
$$p_i^k(\phi, \Theta) = \left( \frac{1}{\sqrt{2\pi\sigma}} \right)^M \exp \left[ -\frac{|X_i(\phi) - A_k|^2}{2\sigma^2} \right] f(\phi | \Theta)$$

Probability for class  $k$

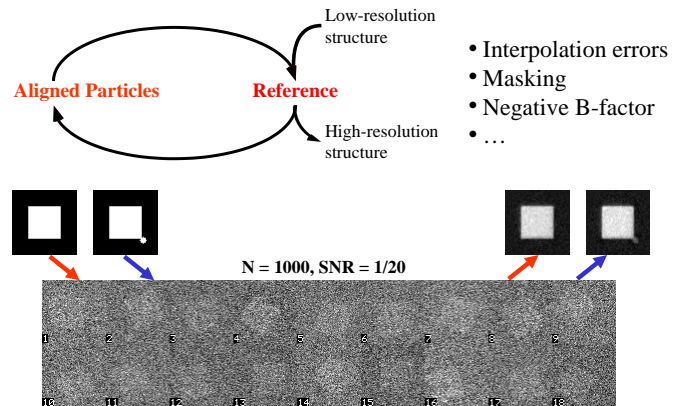
$$q_i^k(\Theta) = \int p_i^k(\phi, \Theta) d\phi$$

$X_i$ :  $i$ th image       $N$ : # of images       $\phi$ : alignment parameters  
 $\Theta$ : model parameters       $\sigma$ : noise in images       $f$ : positional probab.

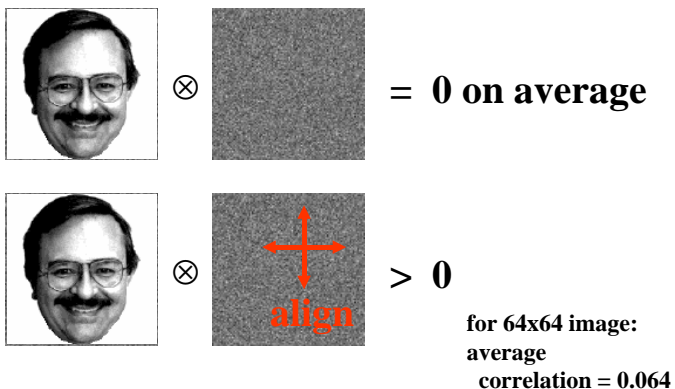
### Classification Using ML



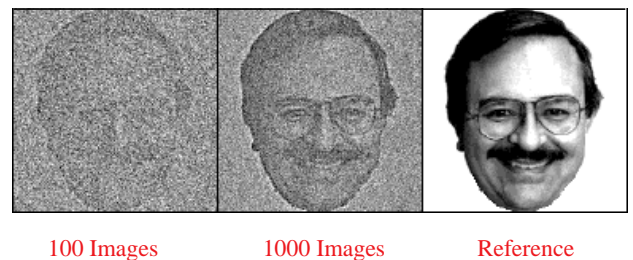
### Problem 4: Processing Artifacts



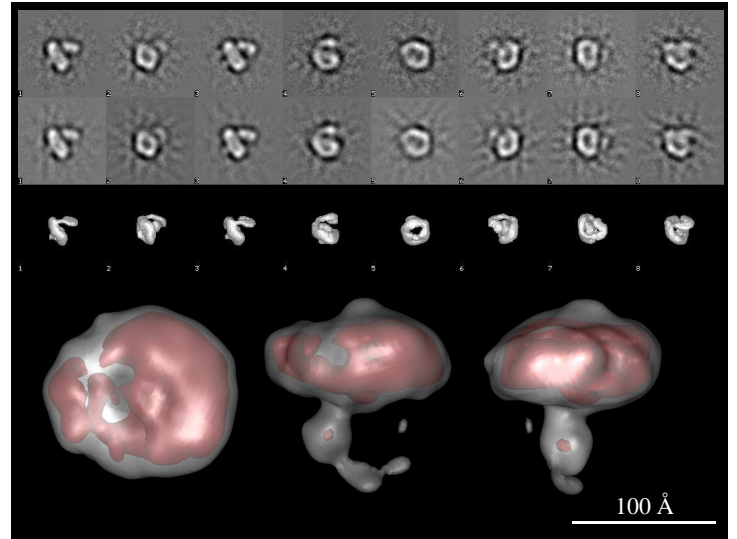
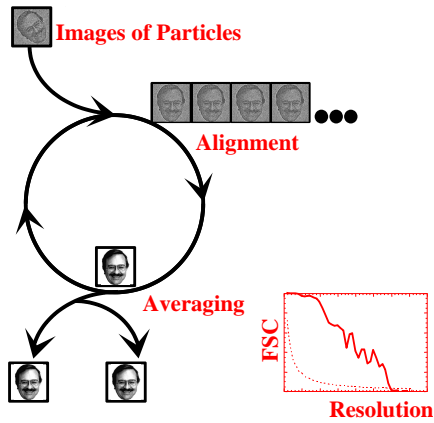
### Problem 5: Noise Bias



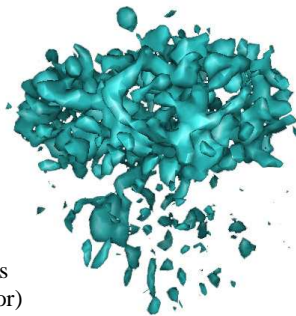
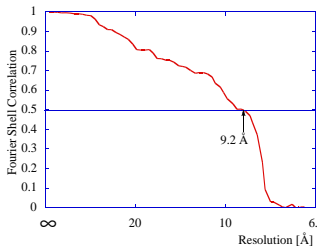
### Seeing is NOT Always Believing



## Resolution Measurement

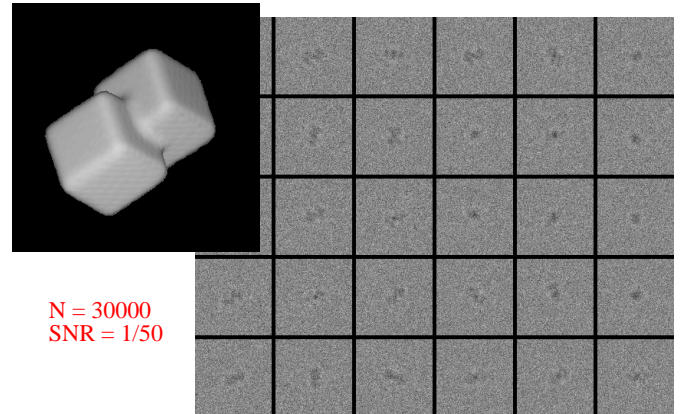


## Swiss Cheese

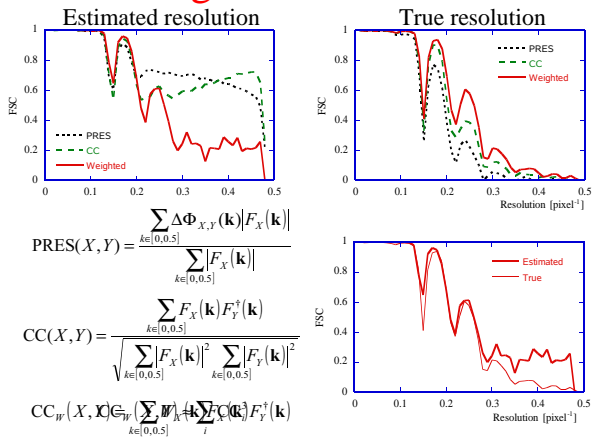


**Dangerous:**  
Boosting of high-resolution terms  
(application of a negative B-factor)

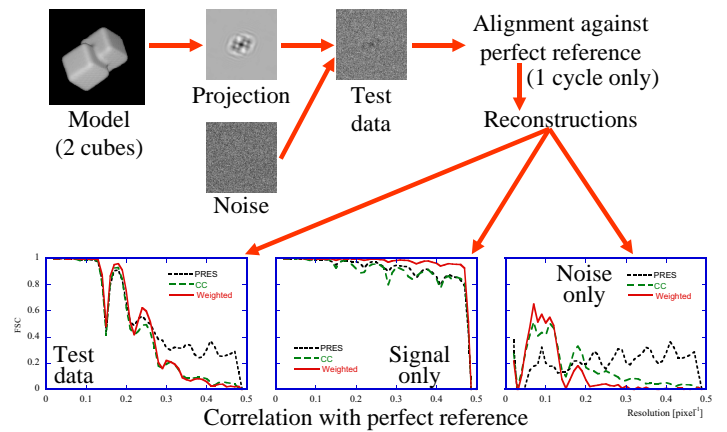
## Gedanken Experiments



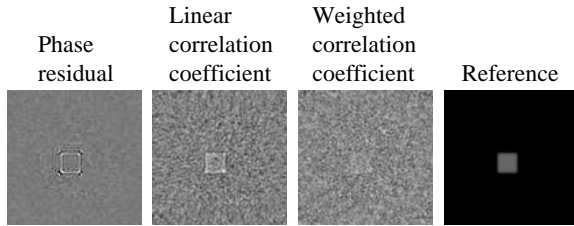
## Weighted Correlation



## Noise Bias

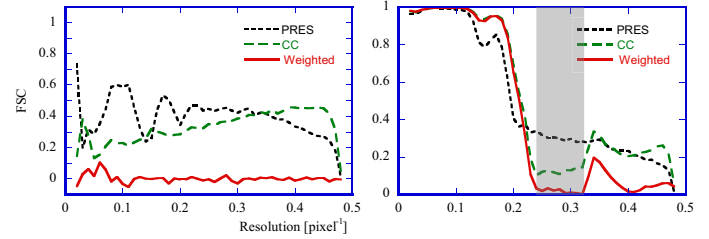


## Noise Reconstruction



## Coherence Constraint

$$CC_W(X, Y) = \sum_i |CC_i|^3$$



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- Ca Channel
- NSF/20S
- Noisy Face

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David DeRosier

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