



# Unit Refresher

(orders of magnitude)

- 1 Angstrom ( $\text{\AA}$ ) = 0.1 nm  $\sim$  size of an atom (C-C bond  $\sim$ 1.4  $\text{\AA}$ )
- 10  $\text{\AA}$  = 1 nm  $\sim$  diameter of an alpha helix
- 100  $\text{\AA}$  = 10 nm  $\sim$  size of typical proteins
- 1000  $\text{\AA}$  = 100 nm  $\sim$  size of a typical virus particle
- 10,000  $\text{\AA}$  = 1  $\mu\text{m}$   $\sim$  size of prokaryotic cell
- 100,000  $\text{\AA}$  = 10  $\mu\text{m}$   $\sim$  size of a eukaryotic cell
- $<3 \text{\AA}$  resolution required in x-ray crystallography for a protein backbone trace

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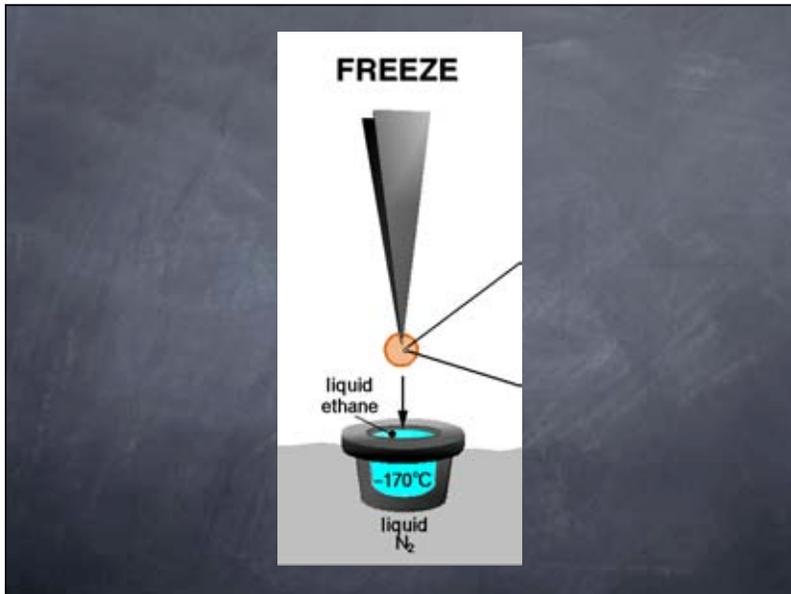
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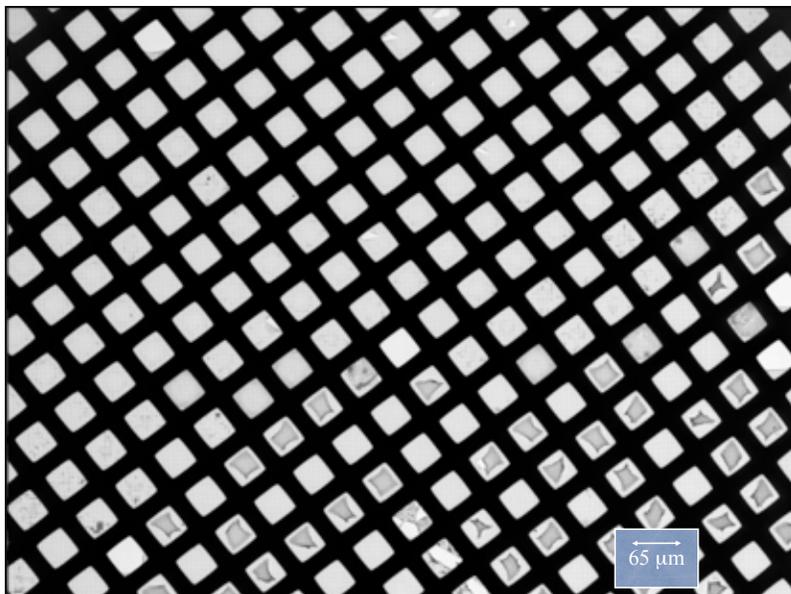
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# 3-D Reconstruction

- Iterative (automated) process
- Start with particles and an initial 'guess' at the 3-D structure
- The 'guess' need not be very good

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# GroEL

- ~800 kDA
- homo 14-mer
- Type 1 chaperonin (GroES co-chaperonin)
- Several crystal structures available

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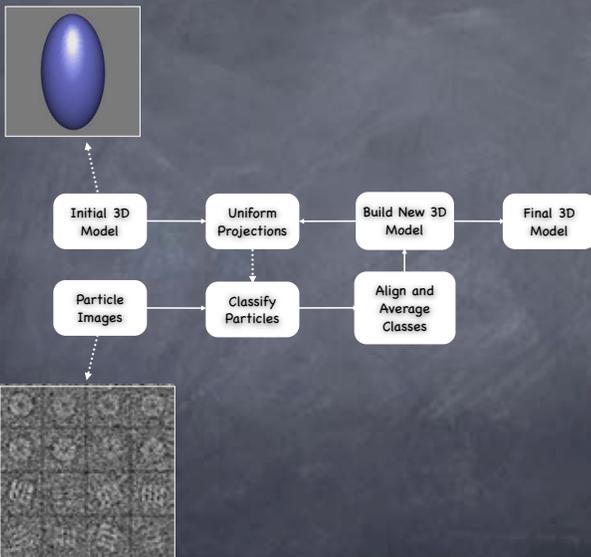
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