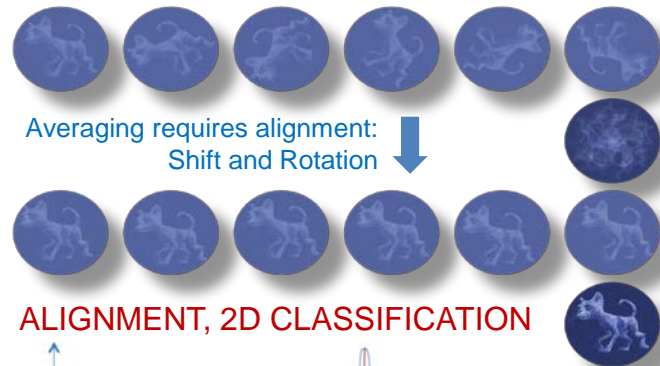


The Cryo-Electron Microscopy Revolution

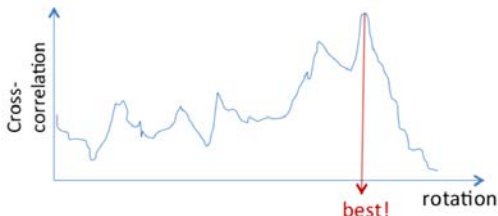
- better detectors: higher signal to noise ratio, super-resolution, recording movies rather than individual images.
- better software algorithms for image processing: e.g. maximum-likelihood, multivariate statistical analysis...

A cryo-EM data set comprises many images of individual particles (terabytes) embedded in vitreous ice representing different views of ideally the same particle – in practice there is heterogeneity in sample composition and conformation/mobility.

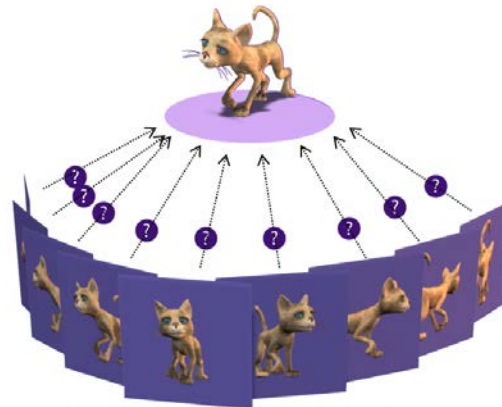
High (near-atomic) resolution can be achieved by **AVERAGING** over many identical particles:



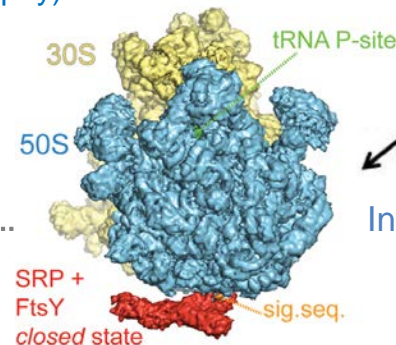
ALIGNMENT, 2D CLASSIFICATION



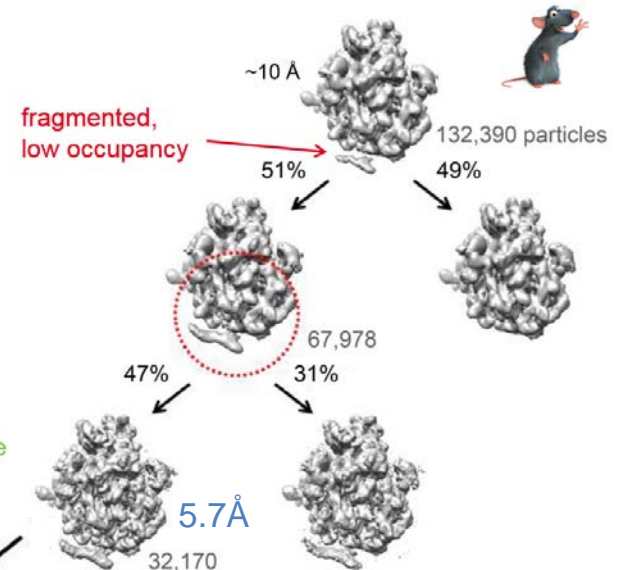
- Parallelization
- Many iterations required until convergence



3D RECONSTRUCTION
requiring a starting model (e.g. from tomography)



3D CLASSIFICATION
addressing heterogeneity in the sample



Interpretation of the 3D structure

bristol.ac.uk