Combining electron counting and beam-induced motion correction to achieve near atomic resolution single particle cryoEM

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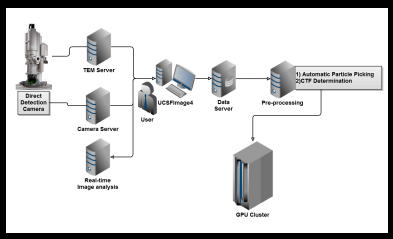
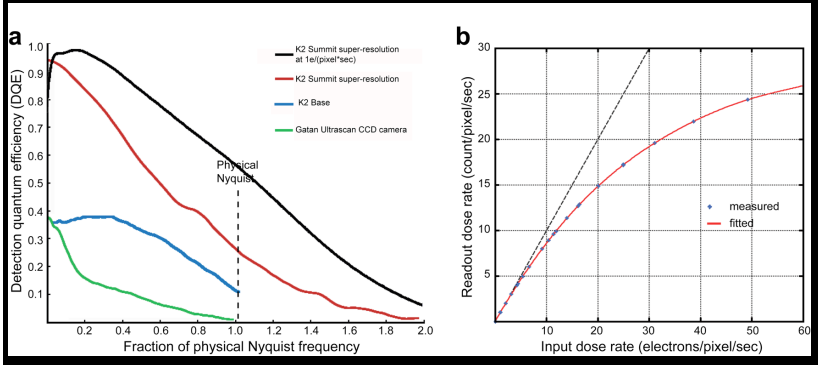
K2 camera with the Tecnai Polara



* K2 is fully embedded into our data acquisition procedures, both with UCSFTomo and UCSFImage4.
* Motion correction is implemented both on-the-fly with data acquisition and during image processing.
* Identified optimal dose rate for data collection.

Xueming Li, Shawn Zheng,
Paul Mooney, Chris Booth

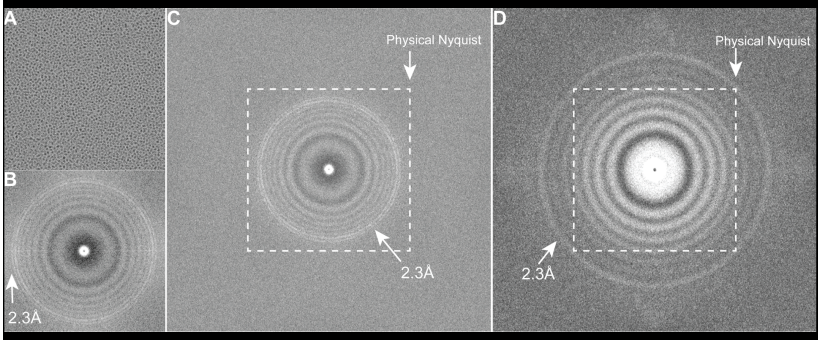
DQE and dose rate



* K2 is fully embedded into our data acquisition procedures, both with UCSFTomo and UCSFImage4.
* Motion correction is implemented both on-the-fly with data acquisition and during image processing.
* Identified optimal dose rate for data collection.
* DQE at 1 e-/(pixel*sec) dose rate is close to an ideal camera.

Xueming Li, Paul Mooney

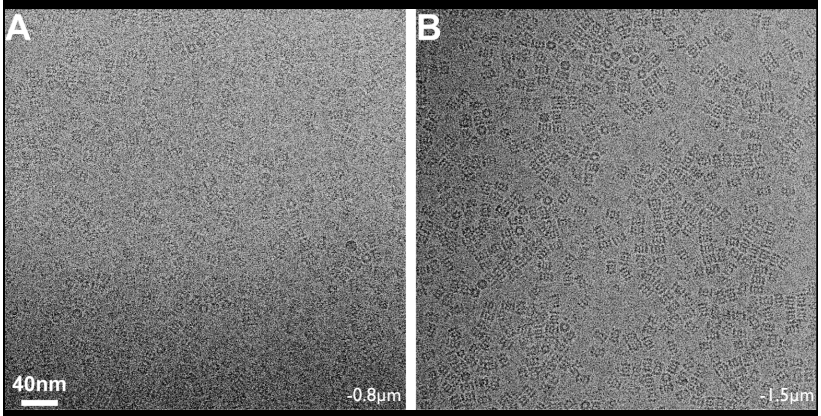
K2 is suitable for high-resolution low-dose imaging



* thin Pt/Ir film recorded at a magnification of 39kX, ~1Å/pixel;
* ~17e^-/Å^2 on specimen and ~17e^-/pixel on camera;
* D: super resolution image, 23kX, ~1.8Å/pixel, dose rate ~31 e/pixel*sec, ~28e^-/Å^2 on specimen and ~93 e^-/pixel on camera;

Chris Booth

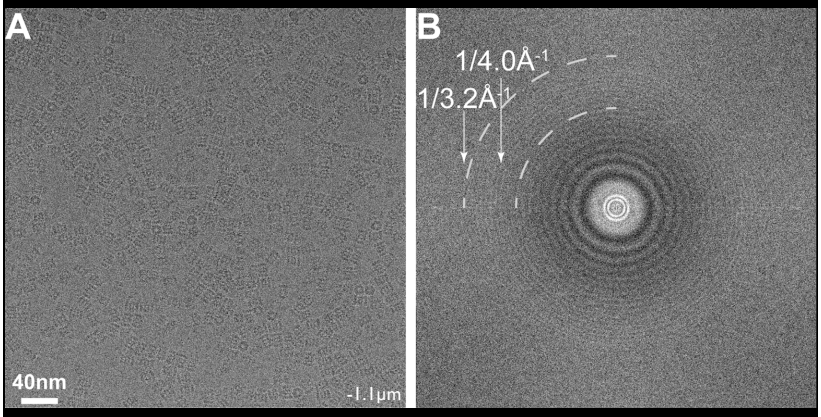
K2 image of frozen hydrated protein samples, T20S



* 300kV, 31kX mag, ~10e^-/pixel/sec; ~1.2Å/pixel, 25e^-/Å^2, 3.5sec exposure;

Xueming Li, Kiyoshi Egami

K2 image of frozen hydrated protein samples, T20S



* 300kV, 31kX mag, ~10e^-/pixel/sec; ~1.2Å/pixel, 25e^-/Å^2, 3.5sec exposure;

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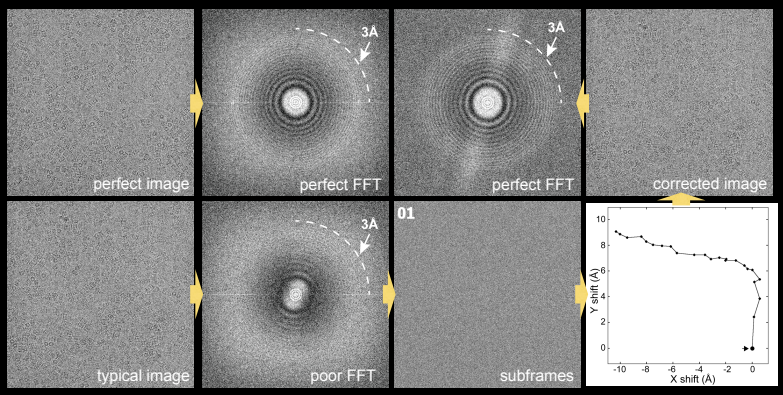
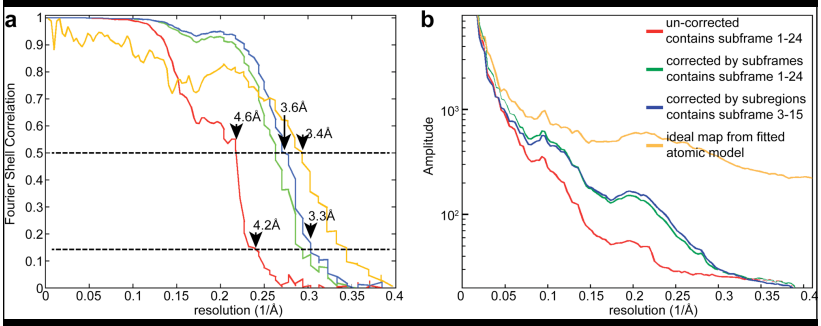
Charge induced image blurring can now be corrected



* Instead of recording one image at a time, we fractionate a single exposure into 24 subframes. By re-aligning all subframes, we can correct motion induced image blur.
* We can restore most of images to near perfect quality suitable for atomic resolution single particle cryoEM, ground breaking leap in high-resolution image acquisition.

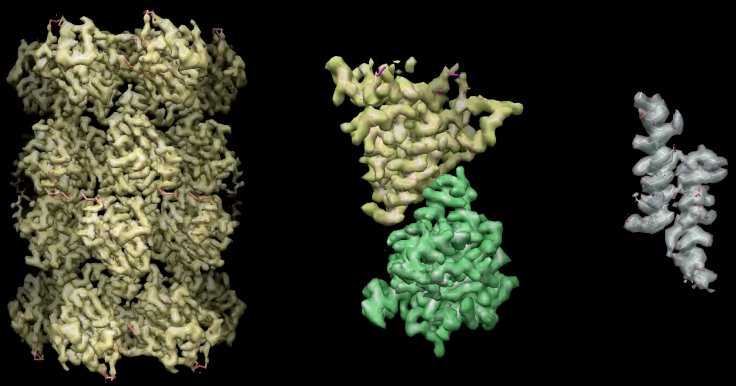
Xueming Li

Beam induced motion



Xueming Li

We achieved resolution comparable with X-ray crystallography



* We determined a 3D reconstruction of archaeal 20S proteasome to the resolution of ~3.3 Å, comparable to the resolution of X-ray crystal structure, 3.4Å.

Xueming Li

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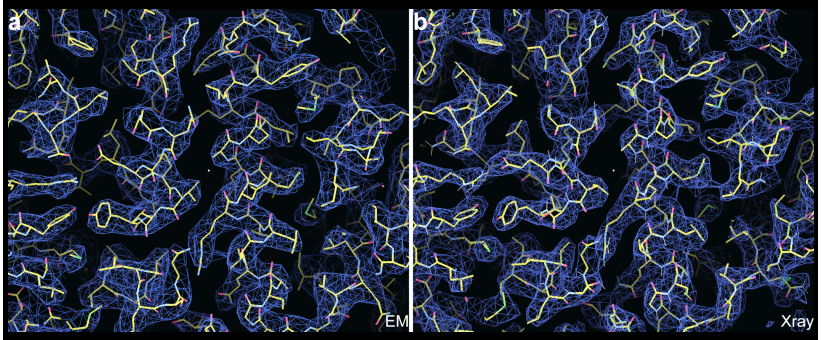

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