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## Rapid Tilt-Series Acquisition for Electron Cryotomography

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## 11 **Abstract**

12 Using a new Titan Krios stage equipped with a single-axis holder, we developed two methods to  
13 accelerate the collection of tilt-series. We demonstrate a continuous-tilting method that can record  
14 a tilt-series in seconds (about 100x faster than current methods), but with loss of details finer than  
15 ~4 nm. We also demonstrate a fast-incremental method that can record a tilt-series about 10x  
16 faster than current methods and with similar resolution. We characterize the utility of both methods  
17 in real biological electron cryotomography workflows. We identify opportunities for further  
18 improvements in hardware and software and speculate on the impact such advances could have  
19 on structural biology.

20

## 21 **Introduction**

22 Electron cryotomography (ECT) allows the 3D visualization of intact cells and other biological  
23 samples *in situ* using a transmission electron microscope (TEM). In traditional ECT, a frozen-  
24 hydrated biological sample is placed on a goniometric stage inside the TEM and progressively  
25 tilted to different angles relative to the imaging electron beam, typically in 1°, 2°, or 3° increments,  
26 throughout a tilt range of approximately -60° to +60°. Two-dimensional projection images are  
27 recorded by a camera at each tilt angle, producing a tilt-series. These images are then aligned  
28 and computationally merged into a 3D reconstruction of the sample, or tomogram. Because high-  
29 energy imaging electrons damage biological materials, the total electron dose is limited and  
30 tomograms have poor signal-to-noise ratio (SNR). Where more than one copy of a structure is  
31 present, their reconstructions can be averaged (subtomogram averaging) to improve SNR and  
32 reveal high-resolution detail (Murphy et al., 2006, Briggs, 2013;). ECT workflows that involve  
33 subtomogram averaging often require users to collect hundreds or even thousands of tomograms  
34 over days or weeks on the cryo-EM, making them very expensive (Chang et al., 2016; Hu et al.,

35 2015). One major bottleneck in traditional ECT is the time taken to collect a tilt-series, typically  
36 ranging from 20-60 min. This inefficiency is due in large part to the mechanical movements of the  
37 TEM goniometer and cryoholder, which are generally not stable beyond the micrometer range.  
38 Many tomography software packages, including *SerialEM* (Mastronarde, 2005), *TOM* (Nickell et  
39 al., 2005), Tomography (Thermo Fisher), USCF Tomography (Zheng et al., 2010), Leginon  
40 (Suloway et al., 2009)), and *EM-Tomo* (TVIPS GmbH) compensate for these movements by  
41 including automated tracking and focusing steps for each tilt during data collection that  
42 electronically correct for stage shifts in x, y, and z. While these solutions help keep the target  
43 centered in the field of view, they make the process slow.

44 Using a new, more eucentric single-axis holder (Figure 1), here we developed two methods that  
45 accelerate tilt-series acquisition by eliminating tracking. The continuous-tilting method records  
46 movie frames while the stage is continuously tilted, resulting in a tilt-series containing thousands  
47 of extremely low SNR images. The fast-incremental method records movie frames while the stage  
48 is tilted incrementally, stopping briefly at discrete tilt angles to unblank the beam and record an  
49 image. We show that the fast-incremental method can achieve similar results as previous  
50 methods, but in a fraction of the time.

51

## 52 **Results & Discussion**

53

### 54 *Continuous-tilting method - speed*

55 In our continuous-tilting method, the camera is directed to record a long movie while the target is  
56 exposed to the electron beam and the stage is tilted continuously. Individual images were saved  
57 at a camera framerate of 20-40 fps and at various stage tilting speeds, resulting in tilt-series  
58 containing hundreds or thousands of images (Table 1). We first assessed the speed of the

59 continuous-tilting method by collecting tilt-series of *Bdellovibrio bacteriovorus* at several  
60 conventional pixel sizes, ranging from 4.32 Å/pixel to 1.09 Å/pixel (Table 1). In this method, the  
61 stage tilting speed is limited by the K2 camera's optimal counting rate of 10 e<sup>-</sup>/pix/s. For a given  
62 target total dose (in e<sup>-</sup>/Å<sup>2</sup>) to be delivered during the tilt-series, the higher the magnification, the  
63 greater the number of camera pixels are involved, allowing a faster tilting speed. In our tilt-series  
64 of *B. bacteriovorus*, for instance, a total dose of 100 e<sup>-</sup>/Å<sup>2</sup> was distributed in only 12 s of  
65 continuous-tilting and exposure at 1.09 Å/pixel, but 126 s were required at 4.32 Å/pixel (Table 1).  
66 Unfortunately, after the tilting and recording ended, the *SerialEM* interface remained disabled  
67 while the large movie file was transferred from the camera to the computer, preventing us from  
68 issuing any additional commands to the microscope. Therefore, instead of completing in seconds,  
69 tilt-series collected at 1.09 Å/pixel and containing 480 total images took 5.5 min to complete, and  
70 tilt-series collected at 4.32 Å/pixel and containing 1250 images took 9.7 min to complete (Table  
71 1). As discussed below, next-generation cameras should eliminate this delay.

72

### 73 *Continuous-tilting method - processing thousands of very-low-dose images*

74 Because one of the resolution limitations in a continuous-tilting method is the arc of tilt-angles  
75 superimposed in each movie frame, we recorded images at the highest frame-rate possible with  
76 our K2 camera (40 frames/second). Further, because the sensitivity of biological samples to  
77 radiation prevented us from increasing the total dose used, each image had a very low SNR,  
78 making fiducial tracking and tilt-series alignment impossible using a conventional ECT workflow.  
79 To overcome this obstacle, we wrote a script called *Neighbor-enhance* (Figure 2) that stretches,  
80 aligns, and averages blocks of neighboring frames in a tilt-series to enhance the contrast of the  
81 fiducial markers. This allowed the gold fiducials to be automatically detected and tracked. For  
82 more details on *Neighbor-enhance*, see the Methods section.

83

84 *Continuous-tilting method - stage eucentricity*

85 We characterized the eucentricity of the stage during continuous-tilting by determining the  
86 translations in X and Y required to align the projection images. We plotted these shifts in X and Y  
87 at different stage tilting speeds, from 1 °/s to 10 °/s, with the X-axis parallel to the tilt axis (Figure  
88 3). The overall stage behavior during continuous-tilting followed a similar trend at all tilting speeds,  
89 with the majority of the movement (about 250 nm total) occurring perpendicular to the tilt axis,  
90 and very little movement along the tilt axis (about 30-75 nm total). The stage movements were  
91 more consistent at higher tilt speeds (Figure 3C and 3D). Given a shift of 150 nm in any direction,  
92 the corresponding losses of field of view on our 4k x 4k camera were less than 10% at 4.32 Å/pixel  
93 (Figure 3A), and up to about 35% at 1.09 Å/pixel (Figure 3D), suggesting that the stage is  
94 eucentric enough that tracking can be omitted at most common pixel sizes. Because even small  
95 errors in stage height increase movements, our data actually underestimate stage performance.

96

97 *Continuous-tilting method - quality of reconstructions*

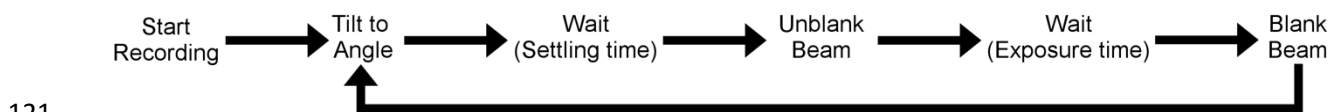
98 Tomograms obtained using the continuous-tilting method appeared by eye to be of similar quality  
99 as those obtained with conventional, slower methods (Figure 4). The two leaflets of the outer  
100 membrane lipid bilayer, which are typically 3-4 nm apart (Lewis and Engelman, 1983), were  
101 clearly visible (Figure 4A), suggesting a resolution of at least 4 nm. Other features, such as  
102 secretin pores (Figure 4B) (Chang et al., 2017), as well as side and top views of methyl-accepting  
103 chemotaxis protein (MCP) arrays (Figure 4C and 4D) (Briegel et al., 2009) also suggested ~4 nm  
104 resolution. Unfortunately, the power spectra of individual images in the tilt-series exhibited no  
105 Thon rings, preventing CTF correction. We initially attributed the absence of information in the  
106 power spectrum to the low contrast of individual frames, but every attempt at motion-correction

107 and averaging also failed to produce Thon rings (data not shown). To investigate why, we  
108 collected high-dose continuous tilt-series of cross gratings. Power spectra of the aligned images  
109 revealed partial Thon rings along the tilt axis, but rapid loss of information perpendicular to the tilt  
110 axis (Figure 5A). Varying the tilting speed produced the same effect. Averaging frames at different  
111 tilt angles and varying the number of frames included in averaged power spectra, down to 1°  
112 overall tilted angle, also produced power spectra with the same pattern. These observations  
113 suggest a vibration orthogonal to the tilt axis, most likely caused by the operation of the  $\alpha$  tilt motor  
114 of the stage. This pattern suggests a vibration orthogonal to the tilt axis, most likely caused by the  
115 operation of the  $\alpha$  tilt motor of the stage. Given these findings, the continuous-tilting method is  
116 only suitable for projects requiring low (~4 nm) resolution.

117

#### 118 *Fast-incremental method - speed*

119 We next developed a fast-incremental method, which solves the stage motor vibration problem  
120 by stopping the stage at discrete tilt angles. This method is depicted in the following scheme:



121

122 With a blanked electron beam, the camera is set to begin recording a long movie. The stage is  
123 then tilted to the first tilt angle in the tilt-scheme. After a specific settling time, defined as a delay  
124 time to allow the stage to settle after tilting, the beam is unblanked and the sample exposed for a  
125 preset exposure time. The beam is then blanked and the stage tilted to the next angle. This loop  
126 is repeated for each tilt angle in the tilt-scheme. We first characterized the settling time: how long  
127 does the stage need to settle after tilting to minimize vibration? We tested this by tilting the stage  
128 from -3° to 0°, varying the settling time from 0 ms to up to 5000 ms, and unblanking. After  
129 examining each resulting power spectrum for signs of vibration, we found that even with a settling

130 time of 0 ms, the power spectrum displayed full Thon rings and no evidence of vibration (Figure  
131 5B), suggesting that stage vibration we observed in continuous-tilting is associated with stage  
132 motion. We therefore proceeded with no settling time for all subsequent fast-incremental tilt-series  
133 collected. (Note that drift remains, but it can be compensated for by motion-correcting all the  
134 frames collected at each tilt angle.)

135 We then tested the speed of tilt-series acquisition using the fast-incremental method by recording  
136 tilt-series using three common tilt-series collection schemes: unidirectional, bi-directional and  
137 dose symmetric (Table 2). The total record time refers to the total time spent performing the tilt-  
138 schemes, while the total time per tilt-series refers to the total time required to re-gain microscope  
139 control. As expected, collection schemes which involved more tilting or a greater number of  
140 exposures resulted in a larger number of total frames and correspondingly longer times. We were  
141 surprised to find that the lock-out time for fast-incremental schemes is much shorter than those  
142 of the continuous-tilting method, even with tilt-series containing more frames. This is most likely  
143 due to the fact that most of the frames are blank, reducing the total amount of data needing to be  
144 stored.

145

146 *Fast-incremental method- How eucentric is the stage?*

147 We next characterized the eucentricity of the stage by plotting the XY translations required to  
148 align all the images of a tilt-series. Since we were able to see Thon rings in the power spectrum  
149 of individual images, we also measured the defocus for each image as an indicator of Z change  
150 throughout the tilt series. We characterized stage eucentricity for all 3 collection schemes:  
151 unidirectional, bidirectional, and dose symmetric (Figure 6A, 6C, and 6E). For all three collection  
152 schemes, most of the movement occurred perpendicular to the tilt axis and was remarkably  
153 consistent. Both unidirectional and bidirectional schemes exhibited larger shifts at tilt angles

154 beyond +/- 40° (Figure 6A and 6C). Larger shifts were seen in Z, as the defocus changed by  
155 about 2-3 μm throughout the tilt series (Figure 6B, 6D, and 6F). This behavior could be partly due  
156 to a lateral offset between the optical axis and the tilt axis. The dose symmetric scheme exhibited  
157 the smallest overall shifts in both Y and Z (Figure 6E and 6F), which suggests that tilting back and  
158 forth may compensate for additive backlashes present in the other tilt-schemes. While overall the  
159 stage movements in the fast-incremental method were greater than those in the continuous-tilting  
160 method, the patterns were more predictable. This predictability should allow pre-calibration of the  
161 image movement prior to data collection (Ziese et al., 2002). The calibrated shifts could then be  
162 applied during data collection to compensate for sample movement in x, y, and z and greatly  
163 reduce field of view loss and defocus variation with the fast-incremental method.

164

165 *Fast-incremental tilting method - How does the quality of reconstructions compare to conventional*  
166 *ECT?*

167 To assess the quality of the tomograms produced by the fast-incremental method, we collected  
168 tilt-series of *Bdellovibrio bacteriovorus*. We observed small (7-8 nm width) barrel-shaped proteins  
169 in the cytoplasm (Figure 7A) which could be GroEL, a 65 kDa chaperone found in many bacterial  
170 species (Kohda et al., 2000; Zeilstra-Ryalls et al., 1991). The double leaflets of both outer and  
171 inner membrane lipid bilayer were also clearly visible, as were side (Figure 7B) and top views  
172 (Figure 7C) of MCP arrays. A subtomogram average of 300 particles of an MCP array clearly  
173 revealed individual MCP dimers (Figure 7D), suggesting a resolution of at least 2.5 nm. These  
174 results are comparable to our previous work (Briegel et al., 2012), and suggest that the fast-  
175 incremental method is able to deliver similar resolutions as conventional ECT methods.

176

177 *Fast-incremental method - Potential to become the method of choice for ECT?*



178 To assess whether the fast-incremental method is a good candidate to replace traditional ECT,  
179 we asked how much microscope time could be saved if it were applied to a conventional project  
180 that involved subtomogram averaging. To test this, we recorded 50 tilt-series of *B. bacteriovorus*  
181 using the fast-incremental method. Using a bidirectional tilt-scheme and 1° tilt increment, 7.5 mins  
182 per tilt-series were required: approximately 40 s were taken to find each target, 45 s to tune  
183 eucentric height, 5 s to autofocus and 6 min to perform the bidirectional collection scheme and  
184 regain control of the microscope (Table 2). Our conventional methods require similar times to find  
185 targets and tune the eucentric height, but much longer collection times due to tracking and to  
186 saving individual images, resulting in about 35 mins per tilt series, nearly 5 times longer than what  
187 we can currently achieve with the fast-incremental method.

188 While this improvement is significant, the fast-incremental method should soon become even  
189 faster. Most importantly, next-generation direct detectors will have much faster write speeds,  
190 eliminating latency. Target picking and eucentric height tuning could be automated. Finally, the  
191 tilt speed between exposures could be increased. Together, we estimate that the fast-incremental  
192 method could become 10-12 times faster than conventional ECT methods, allowing the  
193 acquisition of up to 500 tilt-series per day. If future stages can be built that do not vibrate when  
194 tilting, and next-generation cameras with much higher electron-counting speeds (Gatan's K3  
195 camera records 1500 frames per second) are used, the continuous-tilting method could allow tilt-  
196 series acquisition in just seconds. Methods to more reliably fine-tune eucentric height would result  
197 in a more accurately centered target, smaller field of view loss and less defocus variation. Once  
198 hundreds of tilt-series per day are collected, more reliable fiducial tracking software for tilt-series  
199 alignment will be needed. Finally, software that can automatically identify and pick objects for  
200 subtomogram averaging will allow the entire ECT and subtomogram averaging workflow to  
201 become automated.

202 The development of methods to collect tilt-series in just tens of seconds will obviously accelerate  
203 what we think of today as tomography projects, making entirely new kinds of structural studies  
204 possible, but it may also profoundly alter other cryo-EM workflows as well. Because for a given  
205 dose, a tilt-series provides more information than a single projection (the dose fractionation  
206 theorem, Hegerl and Hoppe, 1976) we expect future single particle workflows, for instance, to  
207 begin with a medium-dose ( $\sim 30 \text{ e}^-/\text{\AA}^2$ ) projection image and end with a fast tilt-series. While only  
208 the initial, early-dose projections will likely be used in the final reconstruction, the tomograms  
209 could be used to identify potentially damaged particles at the air/water interface, improve per-  
210 particle defocus estimates, improve initial models, improve particle alignment, and disambiguate  
211 conformational changes from different orientations.

212

## 213 **Methods**

### 214 ***Bdellovibrio bacteriovorus* cell growth and preparation for ECT**

215 Host-dependent *B. bacteriovorus* cells were grown as previously described (Lambert and Sockett,  
216 2008). First, wild type *Escherichia coli* cells were inoculated into 2 mL of LB media and incubated  
217 for 8 h at 37 °C with agitation. 1% YPSC agar was poured onto a plate and allowed to solidify as  
218 a bottom layer. 100  $\mu\text{L}$  of *E. coli* starter culture was then mixed with a small volume of warm 0.6 %  
219 YPSC agar, poured onto the plate and allowed to solidify as a top layer. A small amount of  
220 previously prepared *B. bacteriovorus* glycerol stocks were pipetted at the very center of the plate  
221 and incubated upright at 29 °C until a lawn of *E. coli* growth appeared. The plate was then flipped  
222 upside-down and incubated for 4 additional days until a clear halo appeared at the center,  
223 indicating prey cells had been killed. The clear halo portion of agar was then transferred into 2  
224 mL HEPES buffer supplemented with 10 mM  $\text{CaCl}_2$  and 150  $\mu\text{L}$  of fresh *E. coli* culture, and  
225 incubated at 29 °C with agitation for 3 days. Suitable *B. bacteriovorus* cell growth and

226 concentration were confirmed by negative stain and imaging on a Tecnai T12 electron microscope  
227 (FEI Company). 3  $\mu$ l of cells mixed with 10nm gold beads were pipetted onto freshly glow-  
228 discharged Quantifoil copper R2/2 200 EM grid (Quantifoil Micro Tools GmbH) and plunge-frozen  
229 into a liquid ethane-propane mixture using an Vitrobot Mark-IV (Thermo Fisher Scientific).

### 230 ***Electron tomography data collection***

231 All tomographic tilt-series were collected in electron-counting mode using *SerialEM* software  
232 versions 3-7-0beta4 to 3-7-0beta10 (Mastronarde, 2003) on a Titan Krios (Thermo Fisher  
233 Scientific) equipped with a Gatan energy filter and a K2 Summit direct electron detector (Gatan).  
234 *B. bacteriovorus* tilt-series were collected using the continuous-tilting or fast-incremental methods  
235 with a total dosage of 100  $e^-/\text{\AA}^2$  and defocus values ranging from -2  $\mu$ m to -5  $\mu$ m.

#### 236 *The continuous-tilting method*

237 With the continuous-tilting method, the stage is continuously tilted in one direction as the camera  
238 simultaneously records and saves movie frames at a frame-rate of 20-40 frames per second (fps)  
239 using *SerialEM*'s TiltDuringRecord script command. This results in tilt-series containing hundreds  
240 to thousands of movie frames with very small angular intervals between each image, ranging from  
241 0.1°/image to 0.25°/image, depending on tilting speed and camera framerate. For bi-directional  
242 tilt-schemes, two separate movies were collected for each direction and combined using IMOD's  
243 *Newstack* command (Kremer et al., 1996). Stage tilting speeds were adjusted to meet the electron  
244 counting rate of the K2 Summit detector while maximizing SNR and minimizing radiation damage.  
245 Smaller pixel sizes deliver greater doses per  $\text{\AA}^2$ , allowing for greater tilting speeds.

#### 246 *The fast-incremental method*

247 We tested three types of tilt-schemes at 1°, 2°, and 3° tilt increments: the unidirectional scheme  
248 involves tilting the stage in a single direction, from -60° to +60°. The bidirectional scheme involves  
249 tilting the stage from -18° to +51° or +52°, then from -20° to -51° or -52°. Finally, the dose

250 symmetric scheme was adapted from Hagen et al. to maximize high-resolution information  
251 (Hagen et al., 2017) by starting at a low tilt angle and tilting the stage back and forth, starting at  
252 0 °, then 3°, -3°, 6°, -6°, and so on until -51° and +51°. All eucentricity measurements were done  
253 with 3-5 iterations for each tilt-scheme at different locations on the grid.

#### 254 *SerialEM scripts*

255 During the fast-incremental method, camera recording in *SerialEM* disables the user interface  
256 and prevents microscope control. We therefore used a second *SerialEM* program to control the  
257 stage and beam. The latest version of SerialEM has removed this limitation.

258

#### 259 ***Electron tomography data processing***

260 All tilt-series were processed and aligned using IMOD (Kremer et al., 1996). Defocus  
261 measurements were done using IMOD's *Ctfplotter*, EMAN2 (Tang et al., 2007, p. 2) or *CTFFIND4*  
262 (Rohou and Grigorieff, 2015), and contrast-transfer function (CTF) correction done by phase  
263 inversion using IMOD's *Ctfphaseflip*. Tomographic reconstructions by weighted back-projection  
264 were done using IMOD's *Tilt*, while SIRT reconstructions were produced using Tomo3D (Agulleiro  
265 and Fernandez, 2011). Subtomogram averaging was performed using Dynamo software  
266 (Castaño-Díez et al., 2012).

#### 267 *Alignment of low contrast frames obtained with continuous-tilting*

268 Because frames of continuous tilt-series have very low SNR, we developed *Neighbor-enhance*,  
269 a new script that increases SNR by averaging neighboring frames together. For each image in a  
270 raw tilt-series obtained with the continuous-tilting method, *Neighbor-enhance* uses IMOD  
271 functions to extract neighboring sets of frames. With the middle frame as a reference, each  
272 neighboring image is stretched by an amount equal to the ratio of the cosines of its tilt angle and

273 of the tilt angle of the reference frame. Stretched, motion-corrected sets of frames are finally  
274 averaged. This averaging greatly improves SNR and facilitates fiducial picking so a fine  
275 transformation matrix can be calculated and applied to the raw low contrast tilt-series (Figure 2).

276

#### 277 *Automated removal of blank frames obtained with the fast-incremental method*

278 The *removeblankframes* script first gain-normalizes, corrects defects, and runs IMOD's *Ccderaser*  
279 to remove deviant pixels on a raw fast-incremental tilt-series. It then extracts electron counts from  
280 each image of the tilt-series and excludes those with low electron counts, indicating a blank frame.  
281 Finally, the remaining non-blank movie frames are extracted and motion-corrected using IMOD's  
282 *Alignframes* to generate a final tilt stack for regular processing using a traditional workflow, such  
283 as IMOD's *Etomo*.

284 Both *Neighbor-enhance* and *Removeblankframes* scripts are available for download at  
285 <https://jensenlab.caltech.edu/>.

286 Data Deposition: Tilt-series and tomographic reconstructions were deposited in the Electron  
287 Microscopy Data Bank (EMDB accession codes: EMD-9260 and EMD-9261), and the Electron  
288 Microscopy Public Image Archive (EMPIAR accession codes: EMPIAR-10225 and EMPIAR-  
289 10226)

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293 Electron Microscopy at Caltech.

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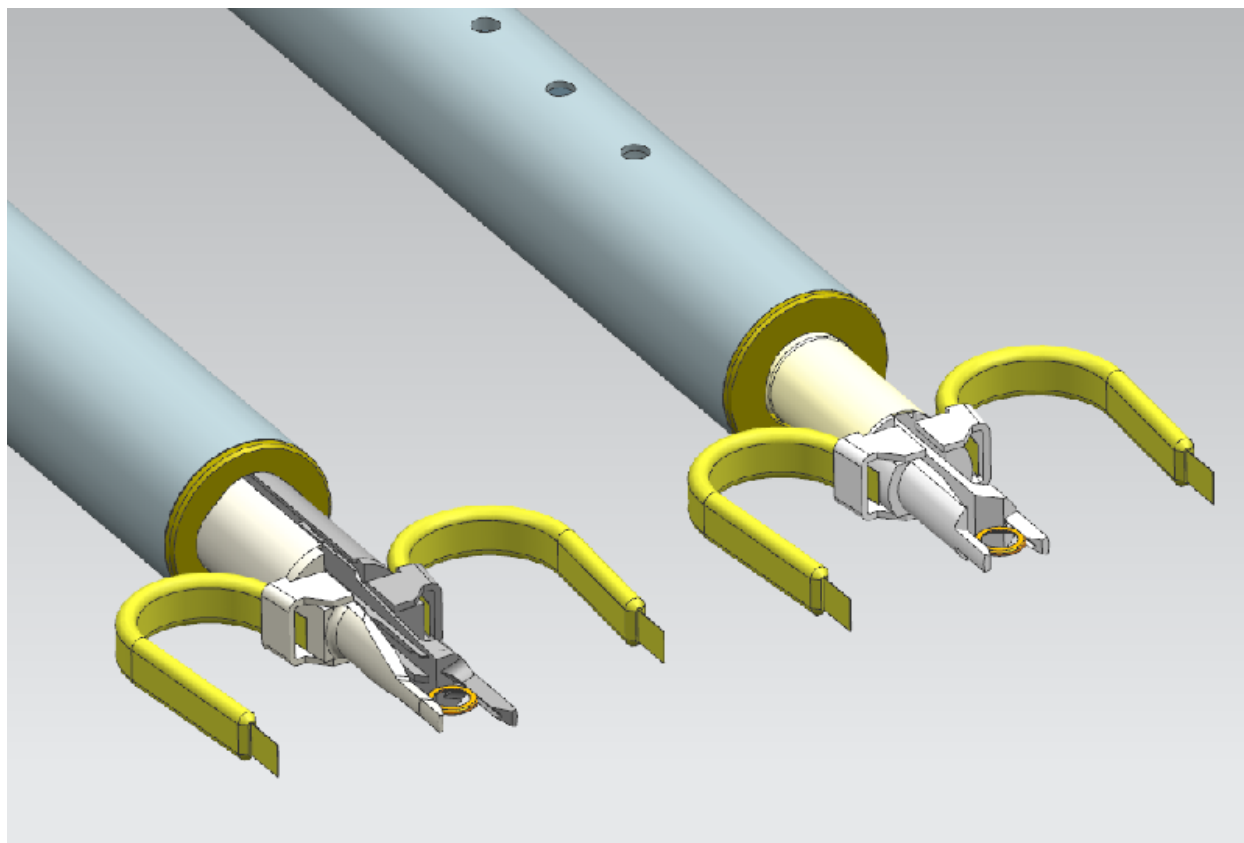
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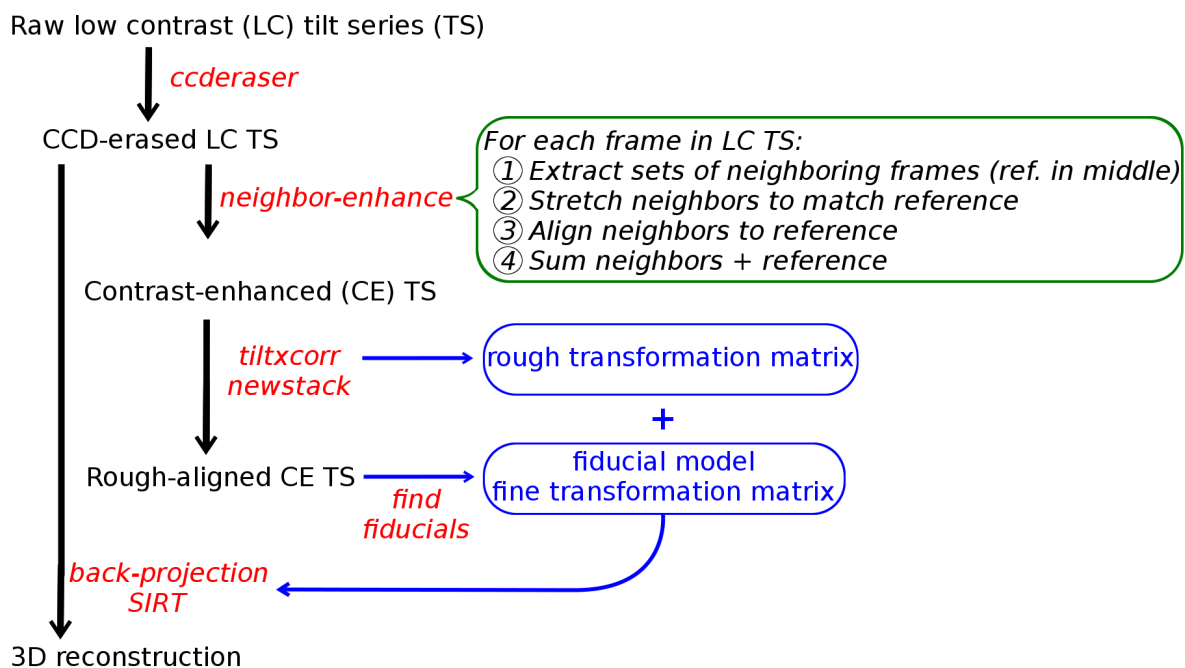
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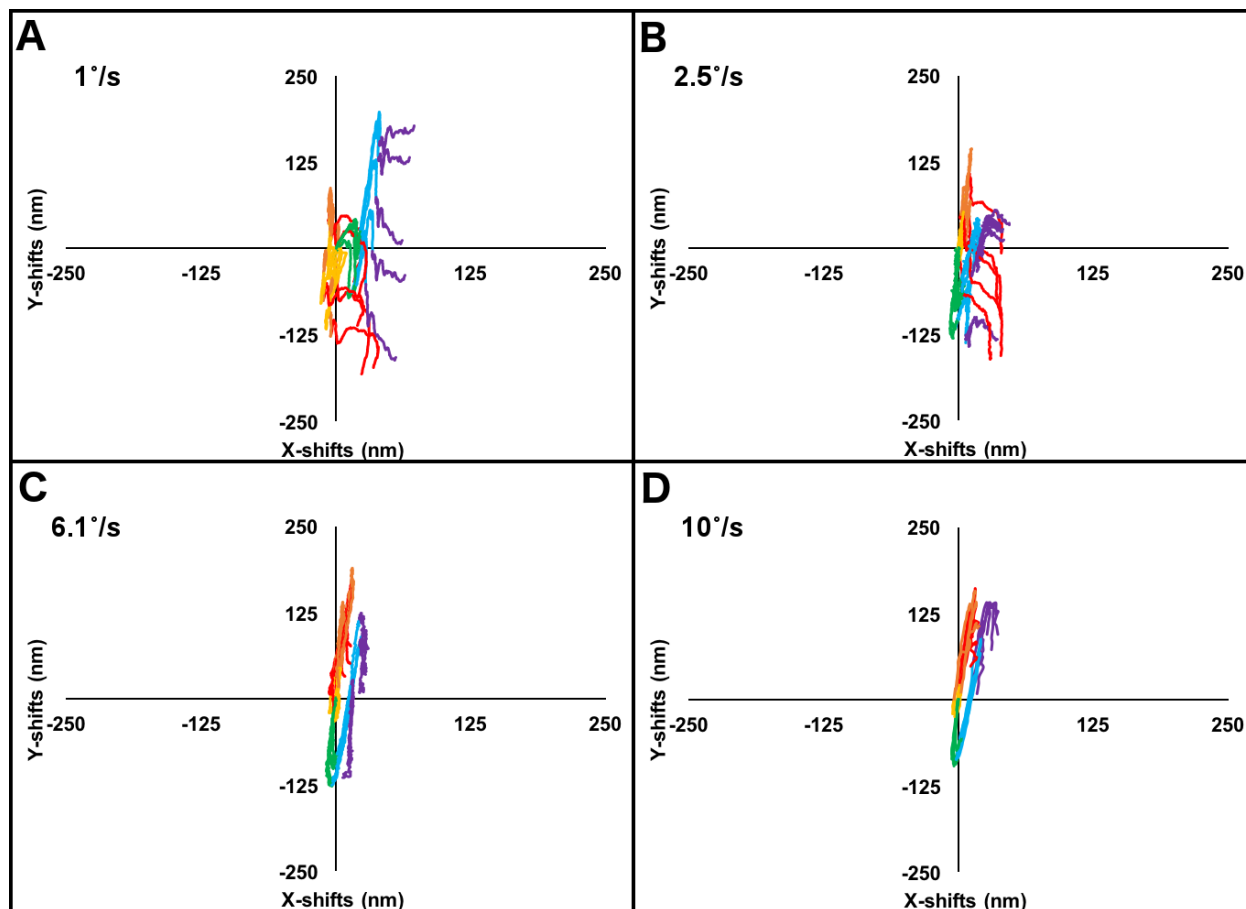
**Figure 1** - Diagram of traditional stage equipped with a dual-axis holder (left) and a stage equipped with a single-axis holder (right). Figure courtesy of Twan van den Oetelaar, Thermo Fisher Scientific.

**Table 1** - Time taken to record tilt series using the continuous tilting method with different pixel sizes. Files were saved without gain normalization as TIFF files with LZW compression.

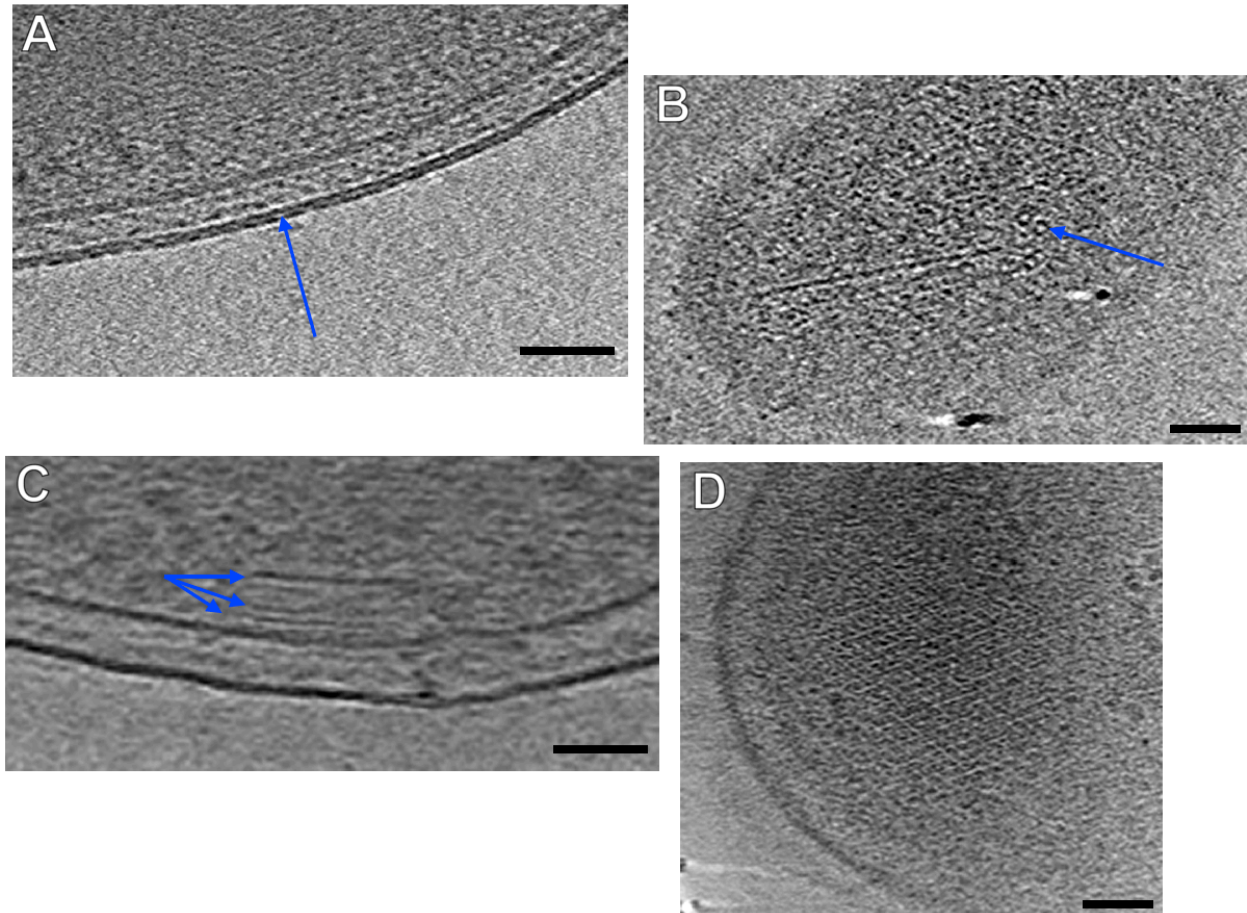
Nominal Magnification	Pixel Size (Å)	Exposure time (s)	Total frames	Total time per ts (min)
33kx	4.32	126	5040 or less	9.7
53kx	2.74	50	2000 or less	7.6
81kx	1.78	20	800	6.7
130kx	1.09	12	480	5.5



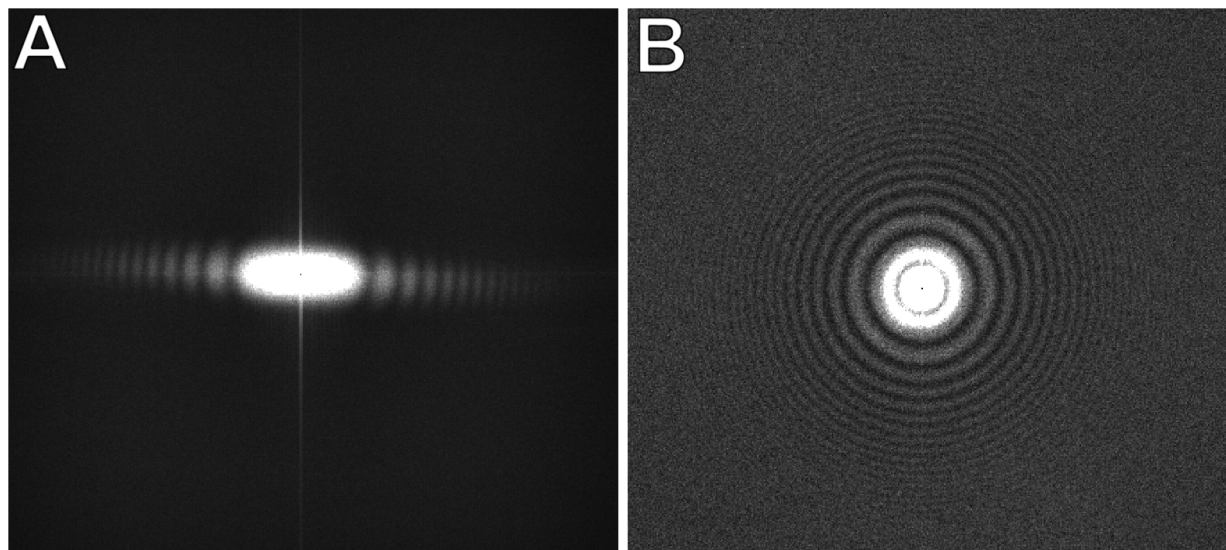
**Figure 2** - Workflow for processing data acquired using the continuous tilting method. Tilt-series data are depicted in black. Programs and scripts are depicted in red. Alignment transforms are depicted in blue. The green box contains a description of "neighbor-enhance", an IMOD script written to enhance the contrast of the fiducial markers (see methods section for details).



**Figure 3** - Stage eucentricity plots of XY shifts using the continuous tilting method at various tilting speeds (inset). The tilt axis is parallel to the x-axis. Each curve is depicted with a rainbow color gradient from red to violet, with red being  $-51^\circ$  and violet being  $+51^\circ$  tilt.



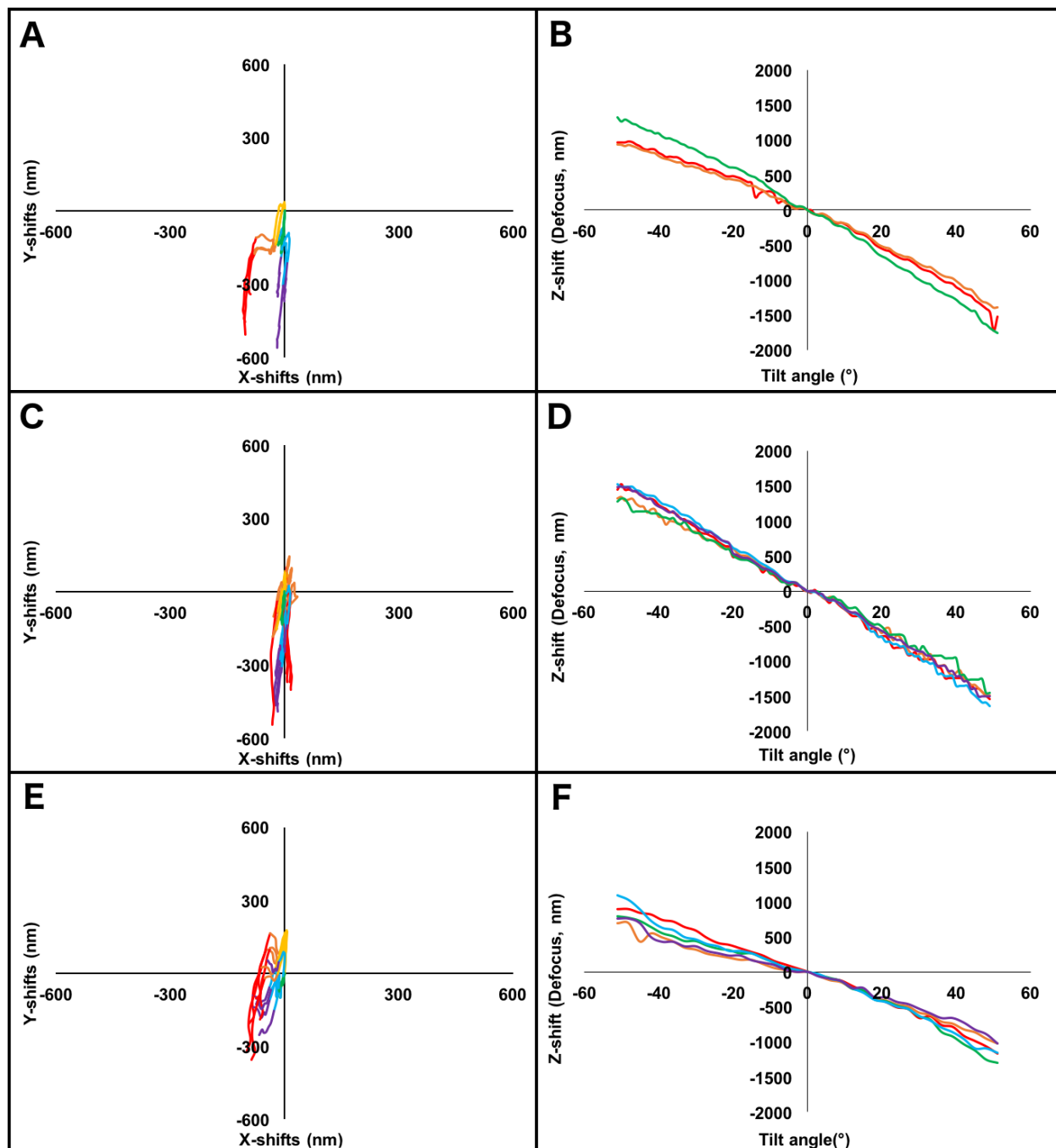
**Figure 4** - Observable features in several tomograms of *Bdellovibrio bacteriovorus* collected using the continuous tilting method. A) Double leaflets of the outer membrane lipid bilayer. B) Secretin pores, C) Side-view of MCP array. D) Top view of MCP array (Scale bars: 50nm).



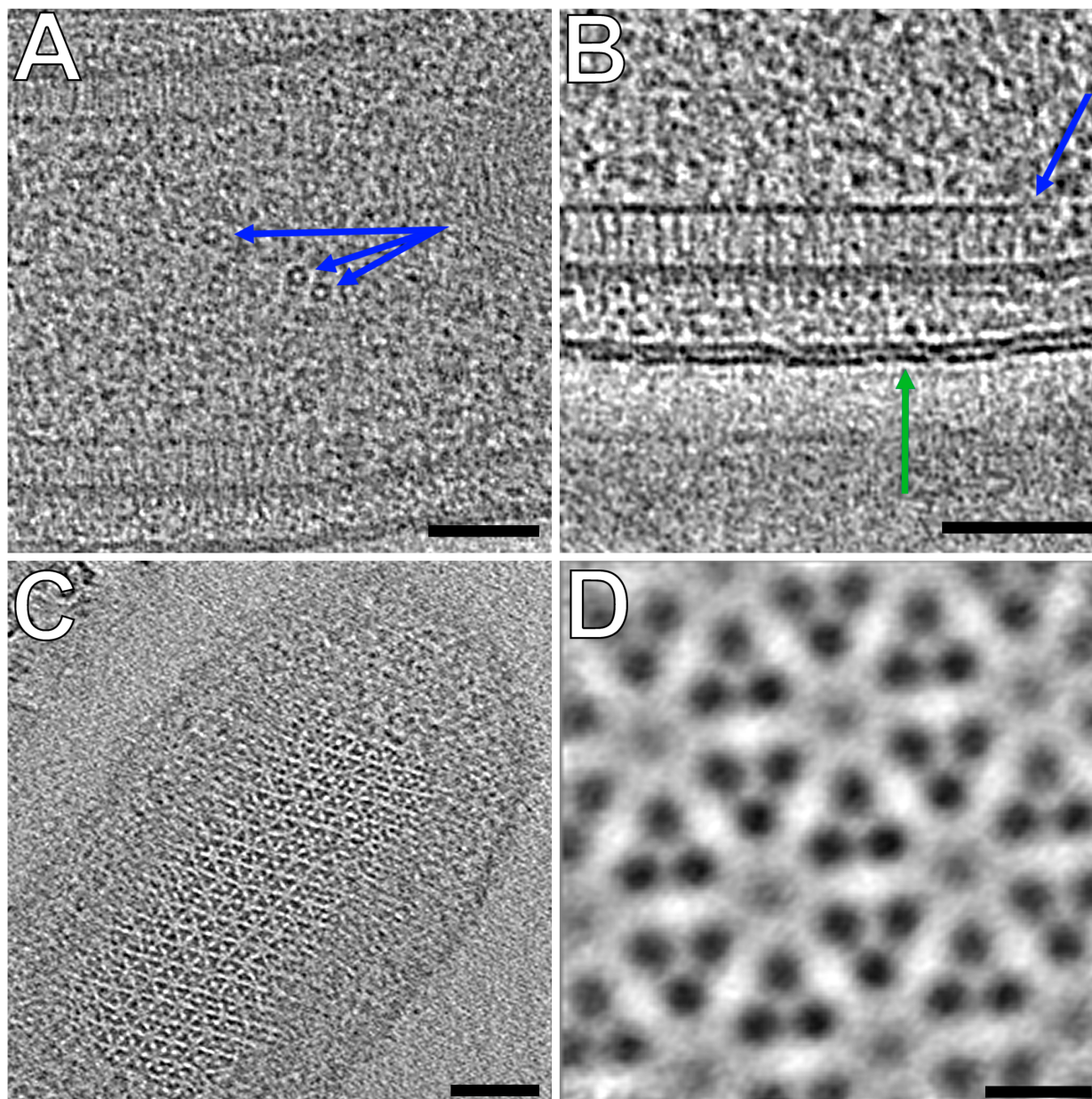
**Figure 5** - A) Power spectrum of high-dose continuous tilt-series taken of cross-gratings to show partial Thon rings along the tilt axis. B) Power spectrum of 0 degree tilt angle after fast-incremental tilting (tilting to 0 and immediately unblinking beam with no added delay time). Nyquist frequency is depicted at the edge of each image.

**Table 2** - Time taken to collect fast-incremental tilt series. Files were saved without gain normalization in MRC format.

Collection Scheme	Tilt Increment	Total number of frames	Exposure time per tilt	Total record time	Total time per ts
Unidirectional	3°	1050	1 sec	97 sec	2.6 min
Bidirectional	3°	950	1 sec	89 sec	2.7 min
Bidirectional	1°	3440	0.7 sec	190 sec	6 min
Dose Symmetric	3°	1450	1 sec	138 sec	4 min



**Figure 6** - Stage eucentricity displayed as plots of X, Y, and Z shifts using the fast-incremental method and various collection schemes: A) Unidirectional XY shifts,  $-51^\circ$  to  $+51^\circ$ ,  $1^\circ$  increment B) Z shifts for the data in A. C) Bidirectional XY shifts from  $-18^\circ$  to  $\pm 52^\circ$ ,  $1^\circ$  increment. D) Z shifts for the data in C. E) Dose Symmetric XY shifts to  $\pm 51^\circ$ ,  $3^\circ$  increment. F) Z shifts for the data in E. The tilt axis is parallel to the x-axis. Each curve is depicted with a rainbow color gradient from red to violet, with red being  $-51^\circ$  and violet being  $+51^\circ$  tilt. Note that the scale here is 2.4x larger than depicted in Fig. 2.



**Figure 7** –A, B and C) Observable features in a tomogram of *Bdellovibrio bacteriovorus* collected using the fast-incremental method, bi-directional scheme with 1° tilt increment. (Scale bars: 50nm). A) Side view of MCP array (blue arrow) and double leaflets of the outer membrane lipid bilayer (green arrow). B) Barrel-shaped protein complexes (blue arrows) C) Top view of MCP array D) Subtomogram average of MCP array shown in C (Scale bar: 5nm).