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Supporting information for article:

Single-particle XFEL three-dimensional Reconstruction of Ribosome-size Particles based on Fourier Slice Matching: Requirements to Reach Subnanometer Resolution

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Table S1 Angle search parameters for slice matching

Iteration#	Number of reference slices	Angle sampling interval [degree]	Angle search range [degree] [*]
1-10	1692	5	All
11-20	10242	2	± 10
21-30	39692	1	± 10

^{*}Angle search range from the angle assigned at the previous iteration.

Table S2 Parameters for phase retrieval

Trial number for phase retrievals	10
Number of iterations for each trial	500
Parameter beta for HIO method	0.8
Over-sampling ratio	4
Radius of support region [nm]	16

Table S3 Relationship between slice matching parameters, angle errors, e , and the corresponding error in the position of diffraction pattern pixels at q_{out} in 3D volume, $d=2\pi q_{out} e/360^\circ$.

beam intensity	number of patterns	q_{in}	q_{out}	α	η	average angle error, e [degree]	position error at q_{out} , d [pixels]
strong	10242	20	30	15	2	0.89	0.46
strong	1692	20	30	15	2	1.04	0.54
strong	362	10	20	10	2	2.42	0.84
medium	10242	10	20	5	2	4.24	1.47
medium	1692	10	20	5	2	4.21	1.46
medium	362	10	20	5	2	6.89	2.40
weak	10242	5	10	5	2	46.22	8.06
weak	1692	5	10	5	2	57.87	10.09
weak	362	5	10	5	2	36.57	6.38