

Supplementary information 2 | Supplementary run command lists and parameter file. The commands are listed in sequence as they run, as well as associated parameter file and specific parameters chosen for each dataset. The commands are listed in the left column, parameter files in the middle column, and specific parameters chosen for the command in the right column.

List of commands in the order of execution for the HIV Gag T8I dataset

ctf estimate			
	emClarity ctf estimate param_ctf.m b2tilt20	param_ctf.m	nGPUs=4 nCpuCores=12 PIXEL_SIZE=1.179e-10 SuperResolution=0 Cs=2.7e-3 VOLTAGE=300e3 AMPCONT=0.1 beadDiameter=7e-9 defEstimate=2.3e-6 defWindow=1.5e-6 CUM_e_DOSE=123 doseAtMinTilt=3 oneOverCosineDose=0 startingAngle=0 startingDirection=pos doseSymmetricIncrement=1
	emClarity ctf estimate param_ctf.m b2tilt40		
	emClarity ctf estimate param_ctf.m b2tilt42		
	emClarity ctf estimate param_ctf.m b3tilt47		
	emClarity ctf estimate param_ctf.m b2tilt51		
	Update the startingAngle in param_ctf.m for each tilt-series		
template search at bin 8			
	emClarity templateSearch param_ts.m b2tilt20 1 emd_8403rescale.mrc C6 1	param_ts.m	Tmp_samplingRate=8 Tmp_threshold=1000 particleRadius=[66,66,56] Ali_mRadius=[116,116,72] Tmp_angleSearch= [180,9,35,7] symmetry=C6
	loop through all the sub-regions using a bash script		
initialize emClarity metadata			
	emClarity init param0.m	param0.m	subTomoMeta=gag fscGoldSplitOnTomos=1
generate bin6 tomogram			
	emClarity ctf 3d param0.m	param0.m	Ali_samplingRate=6
averaging and alignment (bin6)			
	emClarity avg param0.m 0 RawAlignment	param0.m	Ali_mCenter=[0,0,0] particleMass=1 Ali_mType=sphere Raw_className=0 FSC_bfactor=10
	emClarity alignRaw param0.m 0	param0.m	Raw_angleSearch=[0,0,30,6]
	emClarity avg param1.m 1 RawAlignment	param1.m	
	emClarity alignRaw param1.m 1	param1.m	Raw_angleSearch=[16,4,0,0]
	emClarity avg param2.m 2 RawAlignment	param2.m	
	emClarity alignRaw param2.m 2	param2.m	Raw_angleSearch=[0,0,9,3]
	emClarity removeDuplicates param2.m 2		
tilt-series refinement (bin6), generate newly aligned stacks, generate bin5 tomogram			
	emClarity tomoCPR param2.m 2	param2.m	

	emClarity ctf update param3.m	param3.m	Ali_samplingRate=5
	emClarity ctf 3d param3.m	param3.m	
averaging and alignment (bin5)			
	emClarity avg param3.m 3 RawAlignment	param3.m	
	emClarity alignRaw param3.m 3	param3.m	Raw_angleSearch=[12,4,0,0]
	emClarity avg param4.m 4 RawAlignment	param3.m	
	emClarity alignRaw param4.m 4		Raw_angleSearch=[0,0,7.5,1.5]
	emClarity avg param5.m 5 RawAlignment	param5.m	
	emClarity alignRaw param5.m 5	param5.m	Raw_angleSearch=[7.5,2.5,0,0]
	emClarity removeDuplicates param5.m 5	param5.m	
tilt-series refinement (bin5), generate newly aligned stacks, generate bin4 tomogram			
	emClarity tomoCPR param5.m 5	param5.m	
	emClarity ctf update param6.m	param6.m	Ali_samplingRate=4
	emClarity ctf 3d param6.m	param6.m	
averaging and alignment (bin4)			
	emClarity avg param6.m 6 RawAlignment	param6.m	
	emClarity alignRaw param6.m 6	param6.m	Raw_angleSearch=[9,3,0,0]
	emClarity avg param7.m 7 RawAlignment	param7.m	
	emClarity alignRaw param7.m 7	param7.m	Raw_angleSearch=[0,0,9,1.5]
classification (bin4)			
	emClarity avg param8.m 8 RawAlignment	param8.m	flgClassify=1 Cls_mRadius=[92,92,76] Cls_mCenter=[0,0,0] Cls_mType=sphere Cls_samplingRate=4 symmetry=C1
	emClarity pca param8.m 8 0	param8.m	pcaScaleSpace=[10,20,40] Pca_randSubset=0 Pca_maxEigs=25
	emClarity cluster param8.m 8	param8.m	Pca_clusters=[9,12,16] Pca_coeffs=[zeros(1,12);7:18;7:18]
	emClarity avg param8.m 8 Cluster_cls	param8.m	Cls_className=9 Cls_classes_odd=[1:9;1.*ones(1,9)] Cls_classes_eve=[1:9;1.*ones(1,9)]
	emClarity geometry param8.m 8 Cluster_cls RemoveClasses cycle008_remove.mod STD	param8.m	
	emClarity skip param8.m 8	param8.m	
Further alignment (bin4)			
	emClarity avg param9.m 9 RawAlignment	param9.m	flgClassify=0 symmetry=C6 Ali_mRadius=[116,116,60]
	emClarity alignRaw param9.m 9	param9.m	Raw_angleSearch=[0,0,7.5,1.5]
	emClarity avg param10.m 10 RawAlignment	param10.m	
	emClarity alignRaw param10.m 10	param10.m	Raw_angleSearch=[6,1,0,0]
	emClarity removeDuplicates param10.m 10	param10.m	
tilt-series refinement (bin4), generate newly aligned stacks, generate bin3 tomogram			
	emClarity tomoCPR param10.m 10	param10.m	

	emClarity ctf update param11.m	param11.m	Ali_samplingRate=3
	emClarity ctf 3d param11.m	param11.m	Raw_angleSearch=[5,1.25,0,0]
averaging and alignment (bin3)			
	emClarity avg param11.m 11 RawAlignment	param11.m	
	emClarity alignRaw param11.m 11	param11.m	
	emClarity avg param12.m 12 RawAlignment	param12.m	Raw_angleSearch=[0,0,3,0.5]
	emClarity alignRaw param12.m 12	param12.m	
	emClarity avg param13.m 13 RawAlignment	param13.m	Raw_angleSearch=[3,1,0,0]
	emClarity alignRaw param13.m 13	param13.m	
	emClarity removeDuplicates param13.m 13	param13.m	
tilt-series refinement (bin3), generate newly aligned stacks, generate bin2 tomogram			
	emClarity tomoCPR param13.m 13	param13.m	
	emClarity ctf update param14.m	param14.m	Ali_samplingRate=2
	emClarity ctf 3d param14.m	param14.m	
averaging and alignment (bin2)			
	emClarity avg param14.m 14 RawAlignment	param14.m	
	emClarity alignRaw param14.m 14	param14.m	Raw_angleSearch=[0,0,3,0.5]
	emClarity avg param15.m 15 RawAlignment	param15.m	
	emClarity alignRaw param15.m 15	param15.m	Raw_angleSearch=[3,1,0,0]
	emClarity geometry param15.m 15 RawAlignment ShiftAll 0,0,20 STD		flgCenterRefCOM=0
	emClarity avg param16.m 16 RawAlignment	param16.m	
	emClarity alignRaw param16.m 16	param16.m	Raw_angleSearch=[0,0,2,0.5]
	emClarity removeDuplicates param16.m 16	Param16.m	
tilt-series refinement (bin2), generate newly aligned stacks, generate bin1 tomogram			
	emClarity tomoCPR param16.m 16	param16.m	
	emClarity ctf update param17.m	param17.m	Ali_samplingRate=1
	emClarity ctf 3d param17.m	param17.m	
averaging and alignment (bin1)			
	emClarity avg param17.m 17 RawAlignment	param17.m	
	emClarity alignRaw param17.m 17	param17.m	Raw_angleSearch=[0,0,1,0.25]
	emClarity avg param18.m 18 RawAlignment	param18.m	
	emClarity alignRaw param18.m 18	param18.m	Raw_angleSearch=[1,0.25,0,0]
Final average (subtomogram and cisTEM)			
	emClarity avg param19.m 19 RawAlignment	param19.m	
	emClarity avg param19.m 19 FinalAlignment	param19.m	
	emClarity reconstruct param18recon.m 18 gag60e C6 60	param18recon.m	particleRadius=[116,116,72]

*Note that only the parameters which are new to the cycle are updated at each step; the rest of parameters are inherited from the previous cycle.

List of commands in the order of execution for the HIV Gag WT dataset, EMPIAR-10164

ctf estimate			
	emClarity ctf estimate param0.m TS_001	param0.m	nGPUs=4
	emClarity ctf estimate param0.m TS_003		nCpuCores=12
	emClarity ctf estimate param0.m TS_043		PIXEL_SIZE=1.35e-10
	emClarity ctf estimate param0.m TS_045		SuperResolution=0
	emClarity ctf estimate param0.m TS_054		Cs=2.7e-3
	Update the startingAngle in param0.m for each tilt-series		VOLTAGE=300e3
			AMPCONT=0.1
			beadDiameter=10e-9
			defEstimate=3.5e-6
			defWindow=2e-6
			CUM_e_DOSE=123
			doseAtMinTilt=3
			oneOverCosineDose=0
			startingAngle=0
			startingDirection=pos
			doseSymmetricIncrement=-2
template search at bin 6			
	emClarity rescale EMD-8403.mrc EMD-8403_rescale.mrc 3.62 1.35 cpu		
	emClarity templateSearch param_ts.m TS_001 1 EMD-8403_rescale.mrc C6 1	param0.m	Tmp_samplingRate=6
	loop through all the sub-regions using a bash script		Tmp_threshold=2000
			particleRadius=[66,66,56]
			Ali_mRadius=[116,116,72]
			Tmp_angleSearch= [180,9,35,7]
			Symmetry=C6
initialize emClarity metadata			
	emClarity init param0.m	param0.m	subTomoMeta=gag
			fscGoldSplitOnTomos=1
generate bin4 tomogram			
	emClarity ctf 3d param0.m	param0.m	Ali_samplingRate=6
averaging and alignment (bin4)			
	emClarity avg param0.m 0 RawAlignment	param0.m	Ali_mCenter=[0,0,0]
			particleMass=1
			Ali_mType=sphere
			Raw_className=0
			FSC_bfactor=10
			shape_mask_lowpass=18
			shape_mask_threshold=2.4
	emClarity alignRaw param0.m 0	param0.m	Raw_angleSearch=[0,0,30,5]
	emClarity avg param1.m 1 RawAlignment	param1.m	
	emClarity alignRaw param1.m 1	param1.m	Raw_angleSearch=[30,5,0,0]
	emClarity avg param2.m 2 RawAlignment	param2.m	
	emClarity alignRaw param2.m 2	param2.m	Raw_angleSearch=[0,0,24,3]
	emClarity avg param3.m 3 RawAlignment	param3.m	
	emClarity alignRaw param3.m 3	param3.m	Raw_angleSearch=[12,3,0,0]
	emClarity removeDuplicates param3.m 3		

tilt-series refinement (bin4), generate newly aligned stacks, generate bin3 tomogram			
	emClarity tomoCPR param3.m 3	param3.m	
	emClarity ctf update param4.m	param4.m	Ali_samplingRate=3
	emClarity ctf 3d param4.m	param4.m	
averaging and alignment (bin3)			
	emClarity avg param4.m 4 RawAlignment	param4.m	
	emClarity alignRaw param4.m 4	param4.m	Raw_angleSearch=[0,0,12,3]
	emClarity avg param5.m 5 RawAlignment	param5.m	
	emClarity alignRaw param5.m 5	param5.m	Raw_angleSearch=[12,3,0,0]
	emClarity avg param6.m 6 RawAlignment	param6.m	
	emClarity alignRaw param6.m 6	param6.m	Raw_angleSearch=[0,0,6,1.5]
	emClarity avg param7.m 7 RawAlignment	param7.m	
	emClarity alignRaw param7.m 7	param7.m	Raw_angleSearch=[6,1.5,0,0]
	emClarity removeDuplicates param7.m 7	param7.m	
tilt-series refinement (bin3), generate newly aligned stacks, generate bin2 tomogram			
	emClarity tomoCPR param7.m 7	param7.m	
	emClarity ctf update param8.m	param8.m	Ali_samplingRate=2
	emClarity ctf 3d param8.m	param8.m	
averaging and alignment (bin2)			
	emClarity avg param8.m 8 RawAlignment	param8.m	
	emClarity alignRaw param8.m 8	param8.m	Raw_angleSearch=[0,0,6,1.5]
	emClarity avg param9.m 9 RawAlignment	param9.m	
	emClarity alignRaw param9.m 9	param9.m	Raw_angleSearch=[6,1.5,0,0]
	emClarity avg param10.m 10 RawAlignment	param10.m	
	emClarity alignRaw param10.m 10	param10.m	Raw_angleSearch=[0,0,3,0.75]
	emClarity avg param11.m 11 RawAlignment	param11.m	
	emClarity alignRaw param11.m 11	param11.m	Raw_angleSearch=[3,0.75,0,0]
	emClarity removeDuplicates param11.m 11	param11.m	
tilt-series refinement (bin2), generate newly aligned stacks, generate bin1 tomogram			
	emClarity tomoCPR param11.m 11	param11.m	
	emClarity ctf update param12.m	param12.m	Ali_samplingRate=1
	emClarity ctf 3d param12.m	param12.m	
averaging and alignment (bin1)			
	emClarity avg param12.m 12 RawAlignment	param12.m	
	emClarity alignRaw param12.m 12	param12.m	Raw_angleSearch=[0,0,4,1]
	emClarity avg param13.m 13 RawAlignment	param13.m	
	emClarity alignRaw param13.m 13	param13.m	Raw_angleSearch=[4,1,0,0]
	emClarity avg param14.m 14 RawAlignment	param14.m	
	emClarity alignRaw param14.m 14	param14.m	Raw_angleSearch=[0,0,2,0.25]
	emClarity avg param15.m 15 RawAlignment	param15.m	
	emClarity alignRaw param15.m 15	param15.m	Raw_angleSearch=[2,0.25,0,0]
	emClarity avg param16.m 16 RawAlignment	param16.m	Ali_mRadius=[88,88,72]
	emClarity alignRaw param16.m 16	param16.m	Raw_angleSearch=[0,0,2,0.25]

	emClarity avg param17.m 17 RawAlignment	param17.m	
	emClarity alignRaw param17.m 17	param17.m	Raw_angleSearch=[1,0.25,0,0]
	emClarity avg param18.m 18 RawAlignment	param18.m	
	emClarity alignRaw param18.m 18	param18.m	Raw_angleSearch=[0,0,0.5,0.125]
Final average			
	emClarity avg param19.m 19 RawAlignment	param19.m	FSC_bfactor=[10,25,50,75,100,250]
	emClarity avg param19.m 19 FinalAlignment	param19.m	

List of commands in the order of execution for the apoferritin dataset, EMPIAR-10304

ctf estimate			
	emClarity ctf estimate param_ctf.m TS1	param_ctf.m	nGPUs=4
	emClarity ctf estimate param_ctf.m TS2		nCpuCores=20
	emClarity ctf estimate param_ctf.m TS3		PIXEL_SIZE=1.34e-10
	emClarity ctf estimate param_ctf.m TS4		SuperResolution=0
	emClarity ctf estimate param_ctf.m TS5		Cs=2.7e-3
	emClarity ctf estimate param_ctf.m TS6		VOLTAGE=300e3
	Update the startingAngle in param0.m for each tilt-series		AMPCONT=0.1
			beadDiameter=10e-9
			defEstimate=3.5e-6
			defWindow=2.0e-6
			CUM_e_DOSE=102
			doseAtMinTilt=2.5
			oneOverCosineDose=0
			startingAngle=0
			startingDirection=pos
			doseSymmetricIncrement=2
template search at bin 6			
	emClarity templateSearch param_ts.m TS1 1 ApoF_Template_2.mrc O 1	param_ts.m	Tmp_samplingRate=6
	loop through all the sub-regions using a bash script		Tmp_threshold=800
			particleRadius=[65,65,65]
			Ali_mRadius=[70,70,70]
			Tmp_angleSearch= [180,15,180,15]
			Symmetry=O
initialize emClarity metadata			
	emClarity init param0.m	param0.m	subTomoMeta=ApoF
			fscGoldSplitOnTomos=1
generate bin4 tomogram			
	emClarity ctf 3d param0.m	param0.m	Ali_samplingRate=4
averaging and alignment (bin4)			
	emClarity avg param0.m 0 RawAlignment	param0.m	Ali_mCenter=[0,0,0]
			particleMass=0.5
			Ali_mType=sphere
			Raw_className=0
			FSC_bfactor=10
	emClarity alignRaw param0.m 0	param0.m	Raw_angleSearch=[0,0,45,5]
	emClarity avg param1.m 1 RawAlignment	param1.m	
	emClarity alignRaw param1.m 1	param1.m	Raw_angleSearch=[45,5,0,0]
	emClarity avg param2.m 2 RawAlignment	param2.m	
	emClarity alignRaw param2.m 2	param2.m	Raw_angleSearch=[0,0,24,4]
	emClarity avg param3.m 3 RawAlignment	param3.m	
	emClarity alignRaw param3.m 3	param3.m	Raw_angleSearch=[24,4,0,0]
	emClarity avg param4.m 4 RawAlignment	param4.m	
	emClarity alignRaw param4.m 4	param4.m	Raw_angleSearch=[0,0,15,3]
	emClarity avg param5.m 5 RawAlignment	param5.m	
	emClarity alignRaw param5.m 5	param5.m	Raw_angleSearch=[15,3,0,0]
	emClarity removeDuplicates param5.m 5	param5.m	
tilt-series refinement (bin4), generate newly aligned stacks, generate bin2 tomogram			

	emClarity tomoCPR param5.m 5	param5.m	
	emClarity ctf update param6.m	param6.m	Ali_samplingRate=2
	emClarity ctf 3d param6.m	param6.m	
averaging and alignment (bin2)			
	emClarity avg param6.m 6 RawAlignment	param6.m	
	emClarity alignRaw param6.m 6	param6.m	Raw_angleSearch=[0,0,12,3]
	emClarity avg param7.m 7 RawAlignment	param7.m	
	emClarity alignRaw param7.m 7	param7.m	Raw_angleSearch=[12,3,0,0]
	emClarity avg param8.m 8 RawAlignment	param8.m	
	emClarity alignRaw param8.m 8	param8.m	Raw_angleSearch=[0,0,8,2]
	emClarity avg param9.m 9 RawAlignment	param9.m	
	emClarity alignRaw param9.m 9	param9.m	Raw_angleSearch=[8,2,0,0]
	emClarity removeDuplicates param9.m 9	param9.m	
tilt-series refinement (bin2), generate newly aligned stacks, generate bin1 tomogram			
	emClarity tomoCPR param9.m 9	param9.m	
	emClarity ctf update param10.m	param10.m	Ali_samplingRate=1
	emClarity ctf 3d param10.m	param10.m	
averaging and alignment (bin1)			
	emClarity avg param10.m 10 RawAlignment	param10.m	
	emClarity alignRaw param10.m 10	param10.m	Raw_angleSearch=[0,0,9,3]
	emClarity avg param11.m 11 RawAlignment	param11.m	
	emClarity alignRaw param11.m 11	param11.m	Raw_angleSearch=[9,3,0,0]
	emClarity avg param12.m 12 RawAlignment	param12.m	
	emClarity alignRaw param12.m 12	param12.m	Raw_angleSearch=[0,0,8,2]
	emClarity avg param13.m 13 RawAlignment	param13.m	
	emClarity alignRaw param13.m 13	param13.m	Raw_angleSearch=[8,2,0,0]
	emClarity avg param14.m 14 RawAlignment	param14.m	
	emClarity alignRaw param14.m 14	param14.m	Raw_angleSearch=[0,0,4,1]
	emClarity avg param15.m 15 RawAlignment	param15.m	
	emClarity alignRaw param15.m 15	param15.m	Raw_angleSearch=[4,1,0,0]
	emClarity avg param16.m 16 RawAlignment	param16.m	
	emClarity alignRaw param16.m 16	param16.m	Raw_angleSearch=[0,0,3,0.5]
	emClarity avg param17.m 17 RawAlignment	param17.m	
	emClarity alignRaw param17.m 17	param17.m	Raw_angleSearch=[3,0.5,0,0]
	emClarity avg param18.m 18 RawAlignment	param18.m	
	emClarity alignRaw param18.m 18	param18.m	Raw_angleSearch=[0,0,4,0.25]
	emClarity avg param19.m 19 RawAlignment	param19.m	
	emClarity alignRaw param19.m 19	param19.m	Raw_angleSearch=[4,0.25,0,0]
	emClarity avg param20.m 20 RawAlignment	param20.m	
	emClarity alignRaw param20.m 20	param20.m	Raw_angleSearch=[0,0,3,0.5]
Final average (subtomogram and cisTEM)			
	emClarity avg param21.m 21 RawAlignment	param21.m	
	emClarity avg param21.m 21 FinalAlignment	param21.m	

Parameter file:

```
% This is a comment; Inline comments will break the parser.
% String to name the structure that contains all of the metadata, projectName
subTomoMeta=gag
fastScratchDisk=
% Number of GPUS
nGPUs=4
nCpuCores=12
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%% Mask parameters %%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
% The particle radius in x,y,z Angstrom, smallest value to contain particle.
% For particles in a lattice, neighboring particles can be used in alignment
% by specifying a larger mask size, but this paramter must correspond to your
% target, a cetral hexamer of capsid proteins for example.
particleRadius=[66,66,56]
particleMass=1
Ali_mType=sphere
Cls_mType=sphere
% For special cases where repeated motifs are present which might cause one
% subtomo to drift to a neighbor. This allows a larger alignment mask to be used
% for the rotational search (Ali_m...) but limits the translational peak search.
%Peak_mType=sphere
%Peak_mRadius=[100,100,100]
% mask radius and center - and center in Angstrom. Mask size is determined
% large enough to contain delocalized signal, proper apodization, and to
% avoid wraparound error in cross-correlation.
Ali_mRadius=[116,116,72]
Ali_mCenter=[ 0,0,0 ]
Cls_mRadius=[92,92,76]
Cls_mCenter=[ 0,0,0 ]
% Sampling rate
Ali_samplingRate=6
Cls_samplingRate=6
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%% Tomo-constrained projection refinement parameters %%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
% I advise to avoid using this experimental feature for now.
tomoCprDefocusRefine=0
tomoCprDefocusRange=500e-9;
tomoCprDefocusStep=20e-9;
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%% subTomogram alignment %%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
Raw_className=0
% Second row specifies C6 symmetry, old parameter convention
Raw_classes_odd=[0;6.*ones(2,1)]
Raw_classes_eve=[0;6.*ones(2,1)]
symmetry=C6
Raw_angleSearch=[0,0,30,6]
```

[illegible]

```

%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%% Parameters for CTF all si (meters, volts)%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%% Microscope parameters %%%%%%%%%
% pixel size Of the data saved in fixed stacks in meter - MUST match header
PIXEL_SIZE=1.179e-10
% Currently any super-resolution data is cropped in Fourier Space after alignment
% allowing for finer sampling when interpolating the stacks, while then
% filtering out noise due to aliasing.
SuperResolution=0
% Spherical abberation in meter
Cs=2.7e-3
% Accelerating voltage in Volt
VOLTAGE=300e3
% Percent amplitude contrast
AMPCONT=0.10
% search range in meter - generally safe to test a wide range
defEstimate=3.5e-6
defWindow=2e-6
% The PS is considered from the lower resolution inflection point
% past the first zero to this cutoff resolution (unit: meter)
defCutOff=7e-10
% Total dose in electron/A^2, assumed constant rate
CUM_e_DOSE=122
% Gold fiducial diameter in meter
beadDiameter=7e-9

```