

2020/08/31-2020/09/04

**CiCLE**

Cyclic Innovation for Clinical Empowerment

# Tutorial of Relion 3.1 : Innexin-6 pre-processing

Innexin-6を題材とした実習

Takeshi Kawabata (Institute for Protein Research, Osaka Univ.)

川端 猛 (大阪大学 蛋白質研究所)

2020/09/02



# Relionに必要なハードウェア・ソフトウェア

I am buying new GPUs, what do you recommend to run RELION on?

Our collaborator in Stockholm, Erik Lindahl, has made a useful [blog with GPU hardware recommendations](#). Briefly, you'll need an NVIDIA GPU with [a CUDA compute ability of at least 3.5](#), but you don't need the expensive double-precision NVIDIA cards, i.e. the high-end gamer cards will also do, but do see Erik's blog for details! Note that 3D auto-refine will benefit from 2 GPUs, while 2D and 3D classification can be run just as well with 1 GPU. Apart from your GPUs you'll need a decent amount of RAM on the CPU (at least 64Gb), and you may also benefit from a fast (e.g. a 400Gb SSD!) scratch disk, especially if your working directories will be mounted over the network connecting multiple machines.

OS : **Linux**。GPU用のライブラリとしてCUDAが必要。

GPU の種類: NVIDIA社製。ゲーム用の安価なカードでかまわない。GeForce 1080など。高価な倍精度のGPU(例えば、Tesla)は必要ない。

GPUの枚数: 2D分類は1枚でも動く。3D auto-refineは2枚以上必要。

主メモリ: できるだけ多く。最低でも64Gbyte。

ディスク: scratch領域にSSDがあるとよい。

CPU: CPUだけしか動かないタスクもあるので、コア数も多いほうがよい。



- CUDA (GPU計算のためのライブラリ)
- openmpi (ジョブ並列用のライブラリ)

• 以下のライブラリは無ければ、relionのコンパイラがインストール時にローカルにインストールする。

- FFTW (高速フーリエ変換のライブラリ)
- FLTK (GUIのライブラリ)

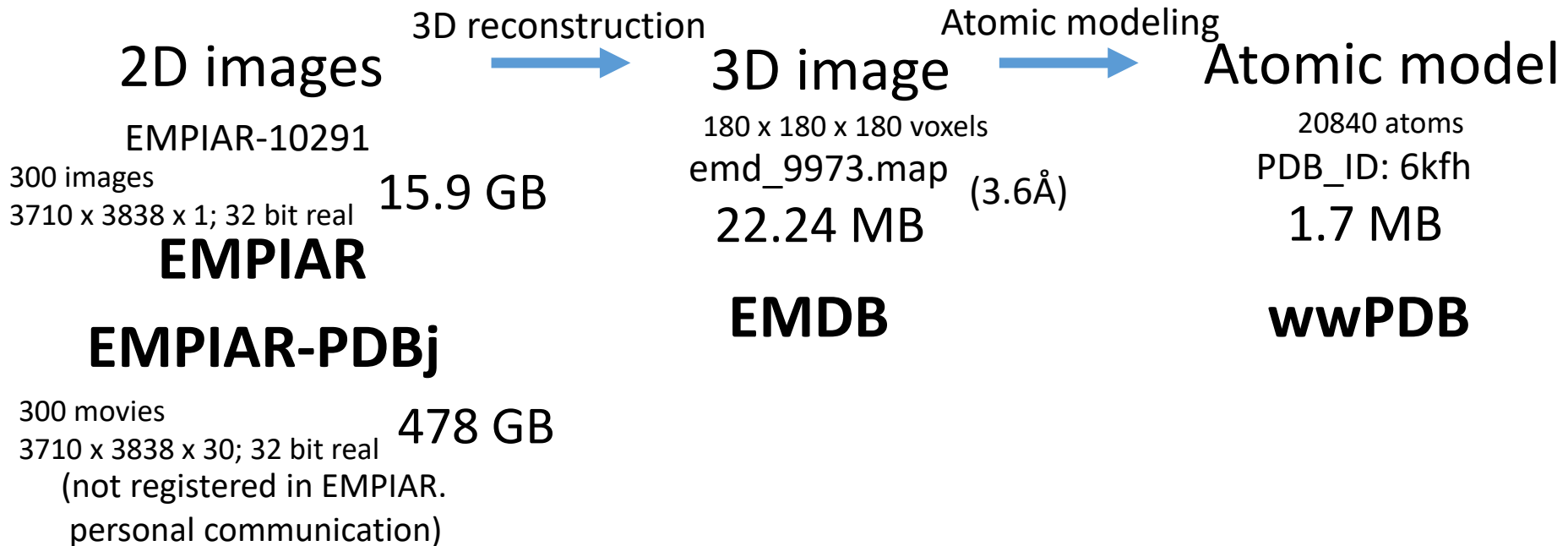
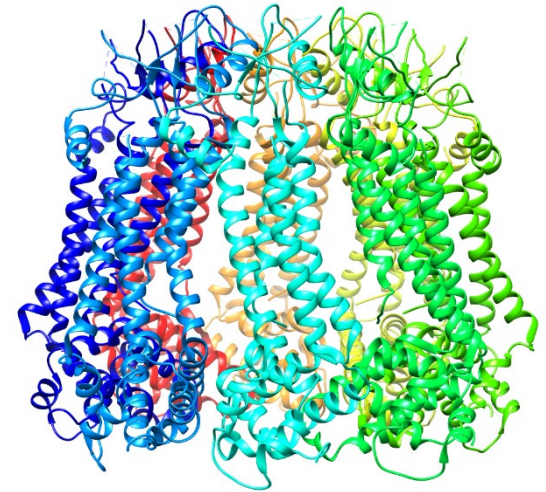
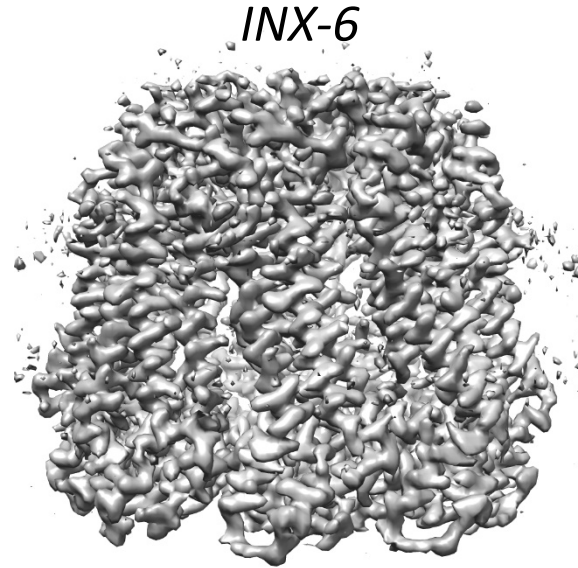
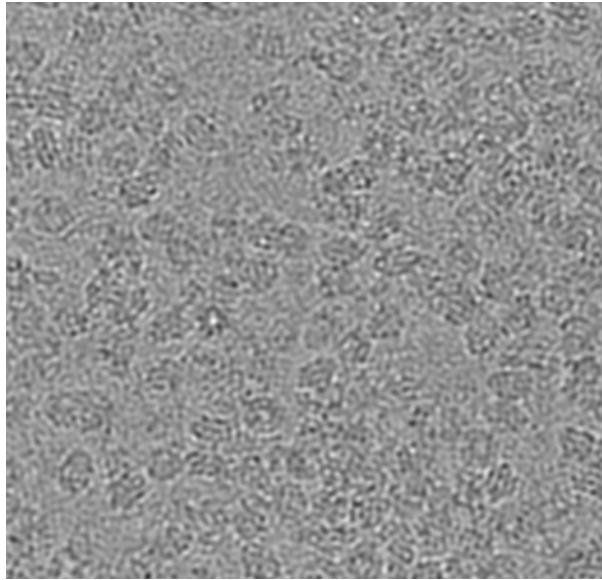


NVIDIA GeForce 1080 Ti



NVIDIA GeForce RTX™ 2080 Ti

# Data processing for EM Single Particle Analysis



# Summary of innexin-6 EM data

Batuujin Burendei, Ruriko Shinozaki, Masakatsu Watanabe, Tohru Terada, Kazutoshi Tani,\* , Yoshinori Fujiyoshi and Atsunori Oshima.  
Cryo-EM structures of undocked innexin-6 hemichannels in phospholipids. Science Advances 12 Feb 2020: Vol. 6, no. 7, eaax3157  
DOI: 10.1126/sciadv.aax3157

EMPIAR	EMDB	Resolution	PDB	molecules	Details of EMPIAR	Data size of EMPIAR entry
10289	9971	3.8 Å	6kff	WT INX-6 in a nanodisc	Motion corrected 2D projection images of innexin-6 gap junction hemichannels in nanodiscs.	<b>49.5 GB.</b> 933 *.mrc files. Each mrc files has 3710 x 3838 x 1 pixels.
10290	9972	3.8 Å	6kfg	WT INX-6 in a detergent	Motion corrected 2D projection images of innexin-6 gap junction hemichannels in detergent.	<b>26.4 GB.</b> 497 *.mrc files. Each mrc files has 3710 x 3838 x 1 pixels.
10291	9973	3.6 Å	6kfh	WT INX-6ΔN in a nanodisc	Motion corrected 2D projection images of N-terminal deleted innexin-6 gap junction hemichannels in nanodisc.	<b>15.9 GB.</b> 300 *.mrc files. Each mrc files has 3710 x 3838 x 1 pixels.

- EMPIARに登録されているのはMotionCorrection後の静止画像のみ
- undocked hemichannelはEMPIAR, EMDB, PDBで公開。Docked hemichannelは、EMDB (9570, 9571), PDB(5h1q, 5h1r)で公開されているが、EMPIARにはデータがない。



# JEM-3000SFF(JEOL)

The data were collected using a JEM-3000SFF (JEOL) electron microscope at 300 kV equipped with a K2 summit direct electron detector camera (Gatan).

Burendei, B.,Shinozaki, R.,Watanabe, M.,Terada, T.,Tani, K.,Fujiyoshi, Y.,Oshima, A. Sci Adv, 6:eaax3157-eaax3157, **2020**



Flagellar filament @9Å (1995)  
Flagellar filament @4.5Å (2003)

+

Gatan社製K2 Summit直接検出型カメラ



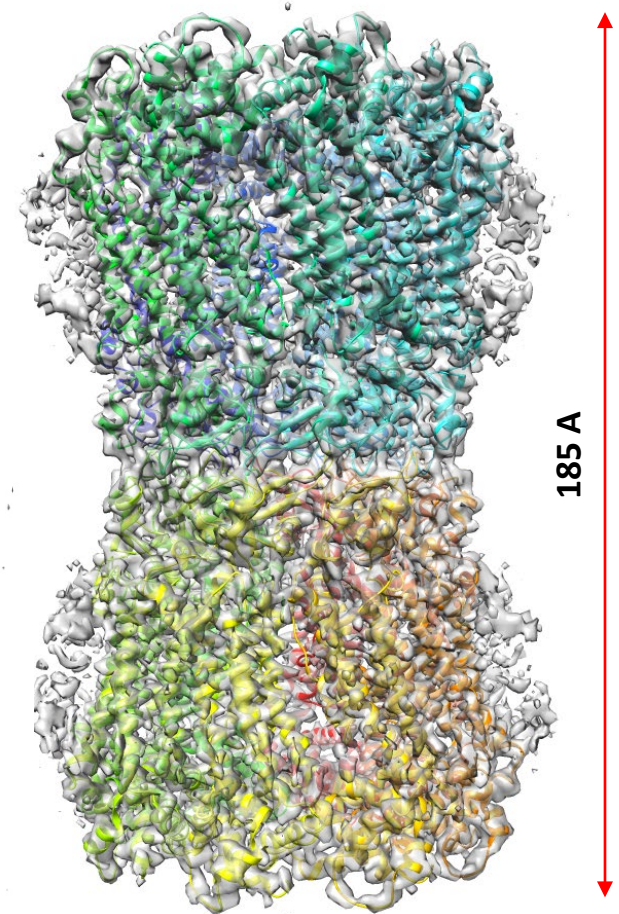
 GATAN

**JEOL JEM-3000SFF (G3)**  
Liq-He cooled specimen stage  
First FEG (Field Emission Gun)

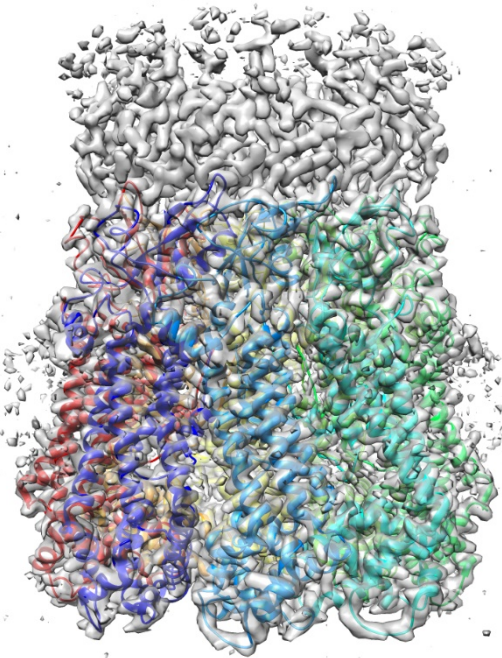
# Innexin-6 : docked and undocked states

Structural component of the gap junctions.

Docked innexin-6



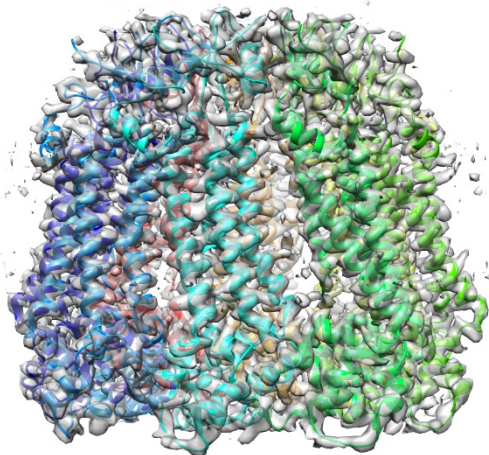
185 Å



117 Å

Undocked innexin-6  
hemichannel

EMPIAR-10291



117 Å

EMD-9973/PDB\_ID:6kfh

EMD-9570/PDB\_ID:5h1q

EMD-9571/PDB\_ID:5h1r

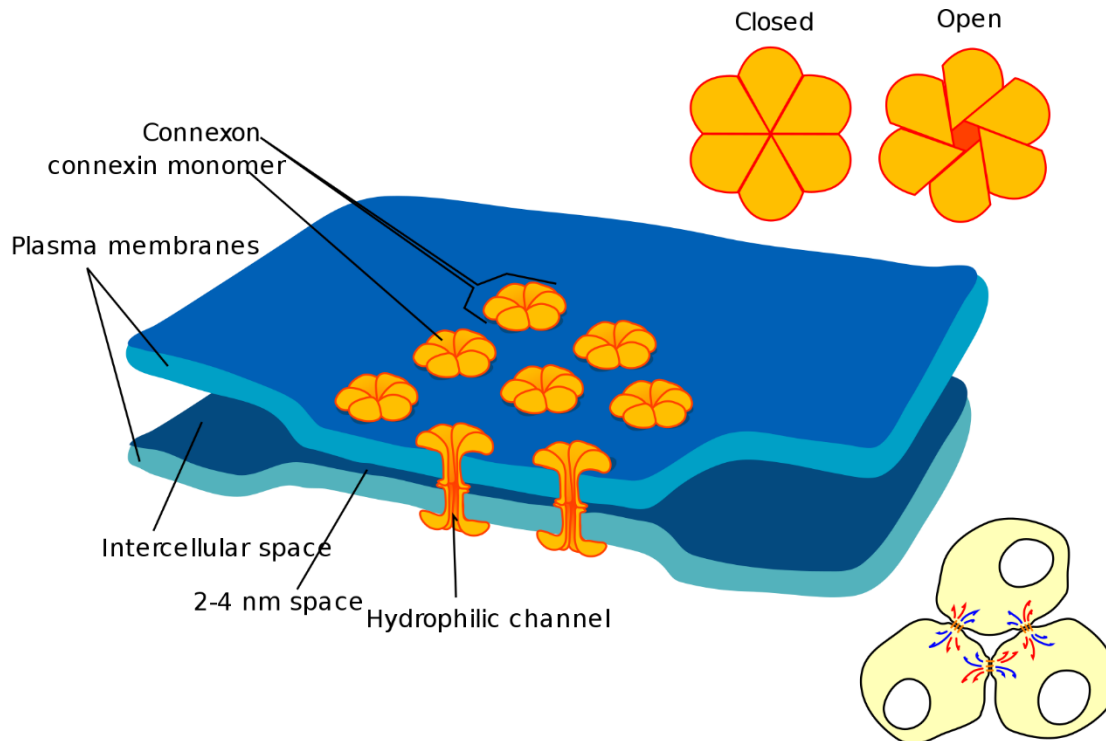
Burendei, B.,Shinozaki, R.,Watanabe,  
M.,Terada, T.,Tani, K.,Fujiyoshi, Y.,Oshima, A.  
Sci Adv, 6:eaax3157-eaax3157, 2020

Oshima, A.,Tani, K.,Fujiyoshi, Y.Nat Commun, 7:13681-13681,

# ギャップ結合 (gap junction)

ギャップ結合(ギャップけつごう、[英](#): Gap junction)は、隣り合う[上皮細胞](#)をつなぎ、水溶性の小さい[イオン](#)や[分子](#)を通過させる[細胞間結合](#)のこと。

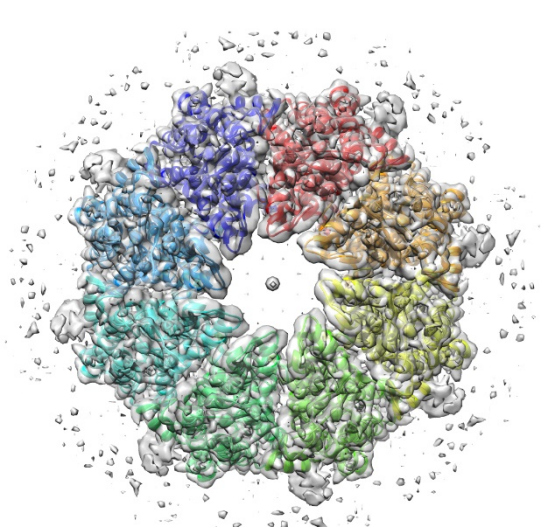
並んだ2つの[細胞](#)の[細胞膜](#)には[コネクソン](#)と呼ばれる[タンパク複合体](#)の末端が複数並んでおり、橋渡し構造をなしている。このコネクソンが[チャネル](#)となり、ここを通過して無機イオンや小さい水溶性分子が隣接細胞の[細胞質](#)から細胞質へと直接移動することができる。また、細胞同士を電氣的に結合するため、心筋組織などの興奮伝播にも関わっている。



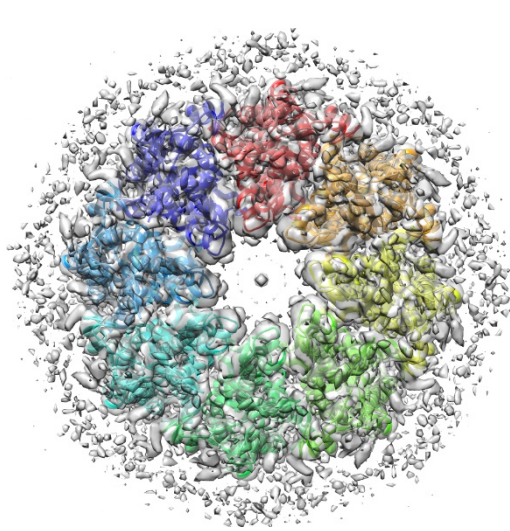
*Wikipediaからの引用*



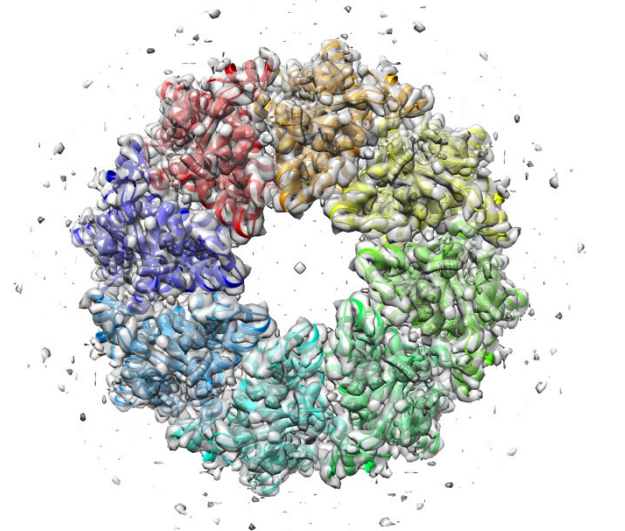
# Undocked innexin-6 hemichannel



EMD-9971/PDB\_ID:6kff  
EMPIAR-10289  
WT INX-6 in a nanodisc



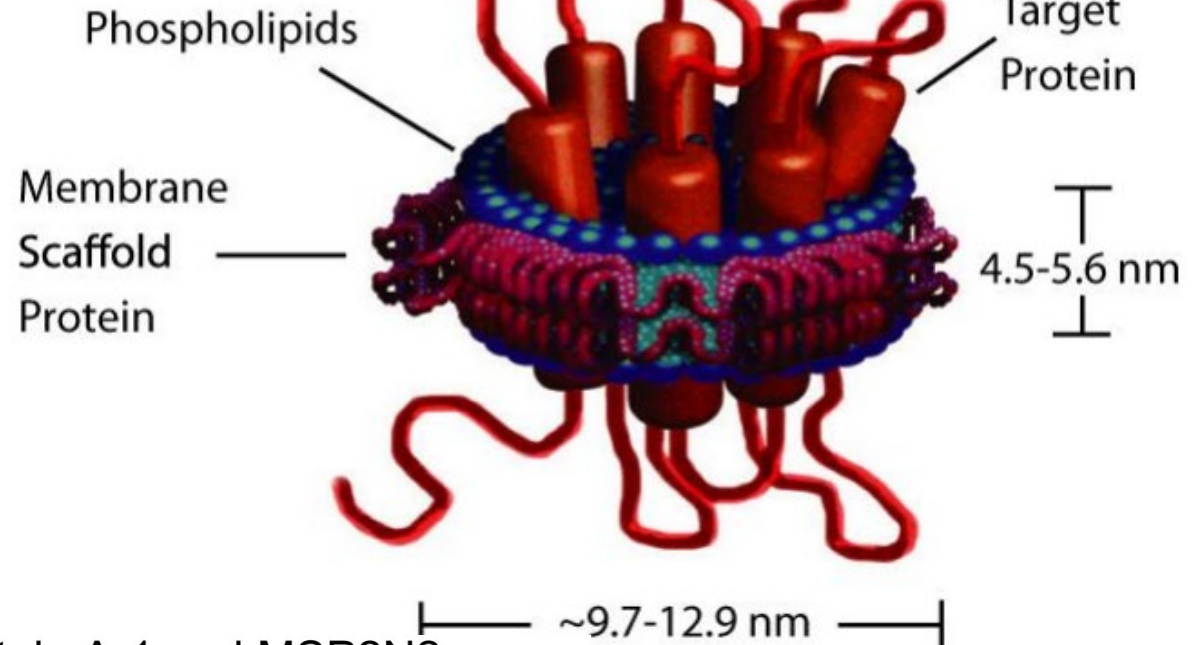
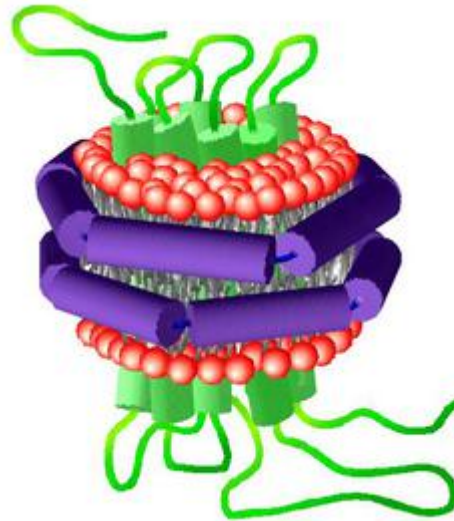
EMD-9972/PDB\_ID:6kfg  
EMPIAR-10290  
WT INX-6 in a detergent



EMD-9973/PDB\_ID:6kfh  
EMPIAR-10291  
WT INX-6 $\Delta$ N in a nanodisc

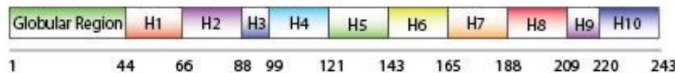
# nanodisc

Example of a Nanodisc containing a 7-transmembrane protein

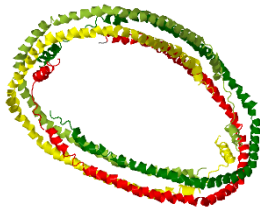
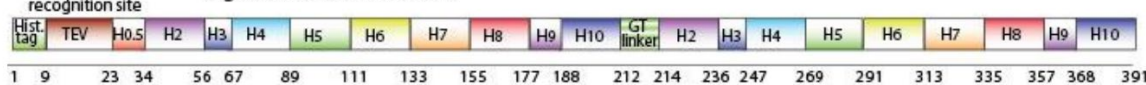


## Protein Maps of Apolipoprotein A-1 and MSP2N2

Apolipoprotein A1



Sigma MSP12 = MSP2N2



PDB\_ID: 1av1  
Apolipoprotein A-1  
(APOA1\_HUMAN)

To investigate the structure in a lipid bilayer, we reconstituted undocked WT INX-6 hemichannels in nanodiscs using the membrane scaffold protein 2N2 (**MSP2N2**) and 1-palmitoyl-2-oleoyl-sn-glycero-3-phosphocholine (POPC), as confirmed by Coomassie brilliant blue-stained gel and negatively stained electron micrographs (fig S1A).

Burendei, B., Shinozaki, R., Watanabe, M., Terada, T., Tani, K., Fujiyoshi, Y., Oshima, A.  
Sci Adv, 6:eaax3157-eaax3157, 2020



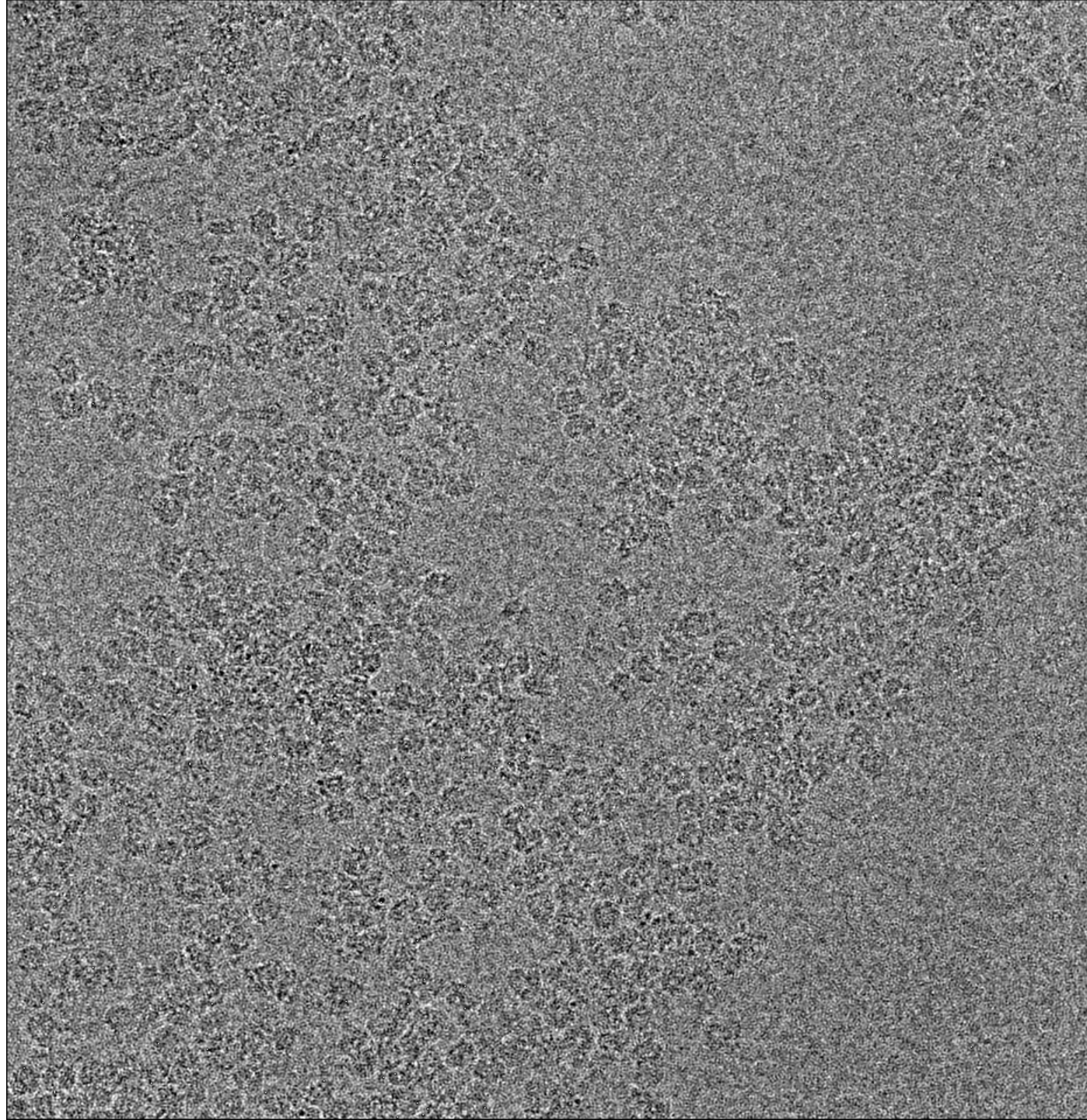
**EMPIAR-10289**  
**WT INX-6 in nanodisc**  
INX6hemiNano001

Pixel\_width: 1.232 Å

After CtfFind,  
SigmaContrast:3  
Lowpass filter 10 Å

These long circles  
are not proteins.  
micelle ? Nanodiscs ?

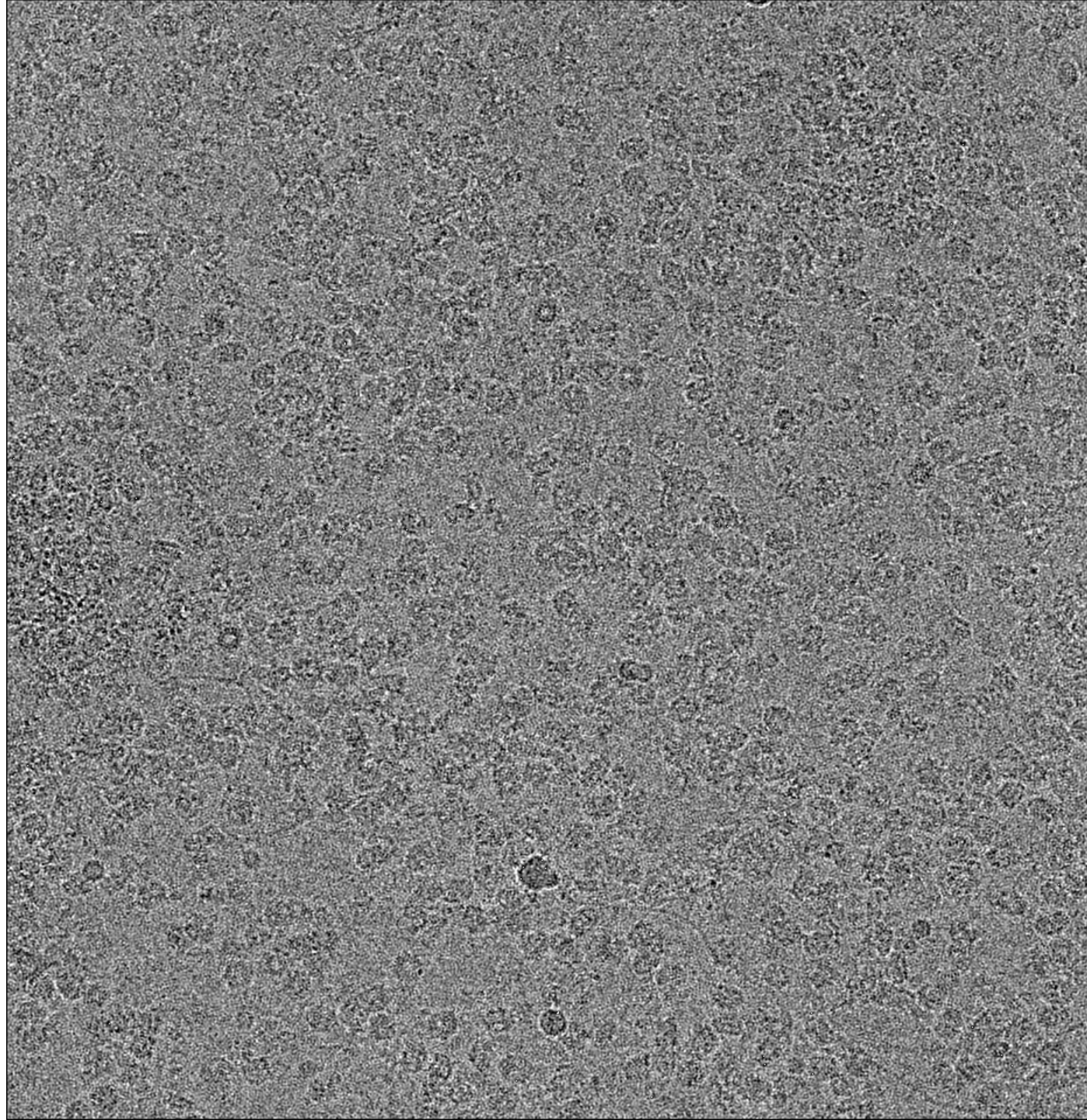




**EMPIAR-10290**  
**WT INX-6 in detergent**  
INX6hemiDet002

Pixel\_width: 1.232 Å

After CtfFind,  
SigmaContrast:3  
Lowpass filter 10 Å

A cryo-electron micrograph showing a dense field of small, dark, circular particles (nanodiscs) against a light gray background. The particles are distributed across the entire frame, with some appearing slightly more prominent than others.

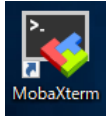
**EMPIAR-10291**  
**WT INX-6 $\Delta$ N in nanodisc**  
INX6hemiDet001

Pixel\_width: 1.232 Å

After CtfFind,  
SigmaContrast:3  
Lowpass filter 10 Å

# MobaXtermによるログインの方法

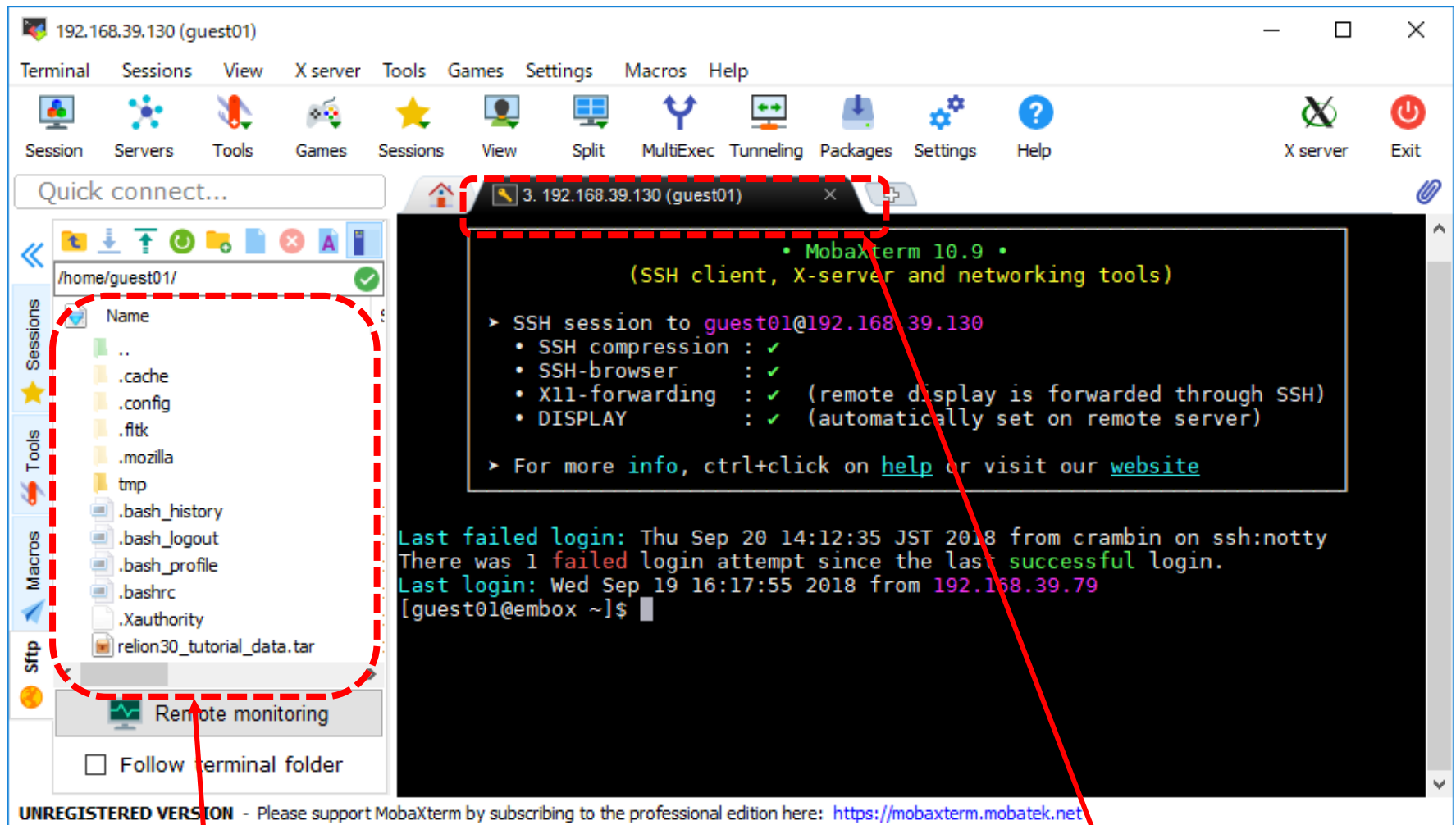
1) アイコン



をクリックして起動



# MobaXtermによるログイン画面



画面左にログイン先のファイルのリストが表示されます。

複数のログイン画面もタブで分けて表示できます。

※[Ctrl]キー＋マウスホイールで、フォントの大きさを変えることができます。



# Basic Unix Commands (1)

↑	前に使ったコマンドを表示	Show the previous command
↓	後に使ったコマンドを表示	Show the next command
<b>[Tab] key</b>	ファイル名の補間 例) <code>ls relion</code> <b>[Tab]</b> <code>ls relion30_tutorial</code>	Compensate file name (example) <code>ls relion</code> <b>[Tab]</b> <code>ls relion30_tutorial</code>
<b>[Ctrl]+[C]</b>	コマンド実行の中止	Quit the command
<b>[Ctrl]+[Z]</b>	コマンド実行の一時停止	Pause the command
<b>bg</b>	一時停止したコマンドをバックグラウンドで実行	Execute the paused command in background
<b>kill %%</b>	バックグラウンドで実行させた直前のコマンドの実行停止	Stop executing the latest background job
<b>pwd</b>	現在のディレクトリを表示	Print the current directory
<b>cd [directory]</b>	[directory]に移動	Go to [directory]
<b>cd ..</b>	一つ上のディレクトリに移動	Go to the upper directory
<b>cd</b>	ホームディレクトリに移動	Go to your home directory
<b>ls</b>	ファイルのリストの表示	Show a list of files
<b>ls -l</b>	ファイルのリストの表示。日付やファイルサイズも表示。	Show a list of files with their updated dates and file sizes.

# Basic Unix Commands (2)

<b>cat</b> [filename]	[filename]の内容を表示	Show the content of [filename]
<b>less</b> [filename]	[filename]の内容を表示 ↓:ダウン、↑:アップ、q:終了	Show the content of [filename] ↓:page down、↑:page up、q:exit
<b>vi</b> [filename]	[filename]を編集 [Esc]:コマンドモード [i]:入力モード [x]:削除 [:q!]:保存しないで終了 [ShiftZZ]:保存して終了	Edit [filename] [Esc]:command mode, [i]:insert, [x]:delete [:q!]:quit without save [Shift ZZ]:quit after save
<b>top</b>	実行中のジョブのリストを表示 [q]:終了 [1]:threadsを表示	Show a list of jobs. [q]:exit, [1]:show threads
<b>nvidia-smi</b>	GPUで実行中のジョブを表示	Show a list of GPU jobs
<b>kill</b> [processID]	[processID]のプロセスの実行中止	Stop executing the process [processID]

# 演習アカウントのホームディレクトリの内容

ホームディレクトリ /home/guest01の下に、以下のディレクトリがあります。

```
[guest01@embox2 ~]$ ls -lt
```

**演習用のデータの入ったディレクトリ**

```
drwxrwxr-x. 3 guest01 guest01          18   8月 26 19:48 EMPIAR-10291_100mic
```

```
[guest01@embox2 ~]$
```

```
[guest01@embox2 ~]$ ls -lt EMPIAR-10291_100mic
```

合計 16

```
-rw-rw-r--. 1 guest01 guest01 4501   8月 29 15:57 10291.xml
```

```
drwxrwxr-x. 2 guest01 guest01 4096   8月 26 19:52 data          ←empiarのメタデータファイル
```

```
[guest01@embox2 ~]$
```

**ディレクトリEMPIAR-10291\_100micの下のディレクトリdata/に100個のmrcファイルがあるはず。**

```
[guest01@embox2 ~]$ ls -lt EMPIAR-10291_100mic/data/
```

合計 5562400

```
-rw-rw-r--. 1 guest01 guest01 56956944   8月 26 19:52 INX6Ndelnano206.mrc
```

```
-rw-rw-r--. 1 guest01 guest01 56956944   8月 26 19:52 INX6Ndelnano234.mrc
```

```
-rw-rw-r--. 1 guest01 guest01 56956944   8月 26 19:52 INX6Ndelnano275.mrc
```

:

3710 x 3838 x 1; 32 bit real

```
-rw-rw-r--. 1 guest01 guest01 56956944   8月 26 19:52 INX6Ndelnano233.mrc
```

```
-rw-rw-r--. 1 guest01 guest01 56956944   8月 26 19:52 INX6Ndelnano248.mrc
```

```
-rw-rw-r--. 1 guest01 guest01 56956944   8月 26 19:52 INX6Ndelnano249.mrc
```

**ディレクトリEMPIAR-10291\_5movieの下のディレクトリmovie/に5個のmrcファイルがあるはず。**

```
[guest01@embox2 ~]$ ls -lt EMPIAR-10291_5movie/movie/
```

合計 8343160

```
-rwxrwxr-x. 1 guest01 guest01 1708678624   9月   1 21:02 INX6Ndelnano020.mrc  3710 x 3838 x 30; 32 bit real
```

```
-rwxrwxr-x. 1 guest01 guest01 1708678624   9月   1 21:02 INX6Ndelnano019.mrc
```

```
-rwxrwxr-x. 1 guest01 guest01 1708678624   9月   1 21:01 INX6Ndelnano010.mrc
```

```
-rwxrwxr-x. 1 guest01 guest01 1708678624   9月   1 21:01 INX6Ndelnano007.mrc
```

```
-rwxrwxr-x. 1 guest01 guest01 1708678624   9月   1 21:01 INX6Ndelnano006.mrc
```

# 1.1 Launch Relion

## Launch Relion from the “project directory”.

In this tutorial, the project directory is `~/EMPIAR-10291_100mic`.

Type following commands to launch relion:

```
$ cd
$ cd EMPIAR-10291_tutorial
$ relion
```

\*When you launch in the first time, you will be asked:  
*Only run the relion GUI from your ProjectDirectory. Do you want to start a new project here [y/n]?*  
answer ‘y’.

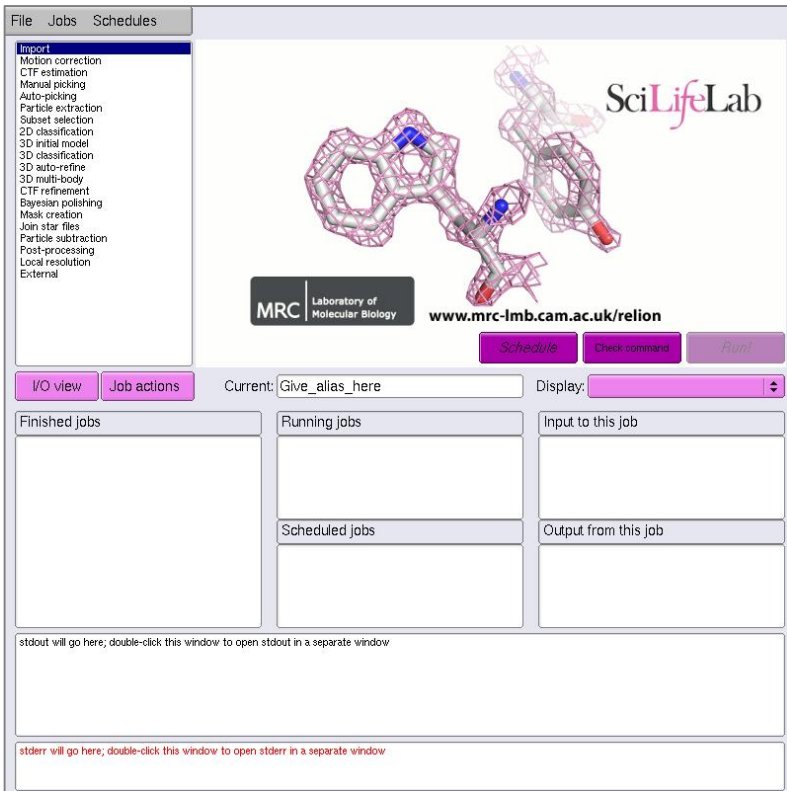
\* The file “default\_pipeline.star” is generated, which describes jobs you have done.

※Relionを起動したターミナルで、以下のキーを押すと、Relionがバックグラウンドで起動され、ターミナルとしてコマンド入力に使うことができる。

[Ctrl] + [Z] キーを押す  
`$ bg`

※Relionを二回目以降に起動する場合は、コマンドの最後に&をつけると、バックグラウンドでの起動となる。

```
$ relion &
```



# 1.1 Import micrographs / movies

Select “Import” from Job type browser.

Job type browser

File Jobs Schedules Movies/mics Others Running

Import  
Motion correction  
CTF estimation  
Manual picking  
Auto-picking  
Particle extraction  
Subset selection  
2D classification  
3D initial model  
3D classification  
3D auto-refine  
3D multi-body  
CTF refinement  
Bayesian polishing  
Mask creation  
Join star files  
Particle subtraction  
Post-processing  
Local resolution  
External

Import

Import raw movies/micrographs? Yes

Raw input files: data/\*.mrc

Are these multi-frame movies? No

Optics group: /usr/local/relion-3.1/data/mtf\_k2\_300kV.star

EMPIAR header file: MTF of the detector: -3.1/data/mtf\_k2\_300kV.star

Pixel size (Angstrom): 1.232

Voltage (kV): 300

Spherical aberration (mm): 1.6

Amplitude contrast: 0.1

Beamtilt in X (mrad): 0

Beamtilt in Y (mrad): 0

A value of spherical aberration 1.6 was obtained by personal communication with Prof. Oshima.

Schedule Check command Run!

I/O view Job actions

Current: Give\_alias\_here Display:

Click [Run!]

The directory “Import/job001” is generated. The file “movies.star” has a list of micrographs.

You can check it by the command: `less Import/job001/movies.star`



# 1.3 CTF estimation (< 1min)

The screenshot displays the MotionCorr software interface for CTF estimation. The top menu bar includes 'File', 'Jobs', 'Schedules', 'I/O', 'CTFFIND-4.1', 'Gctf', and 'Running'. The 'I/O' menu is open, showing options like 'Import', 'Motion correction', 'CTF estimation' (highlighted), 'Manual picking', and 'Auto-picking'. A callout box labeled 'CTF estimation' points to this menu item. The main window shows the 'Input micrographs STAR file' as 'ort/job001/micrographs.star' with a 'Browse' button. Below this, there are several settings: 'Use micrograph without dose-weighting?' (No), 'Estimate phase shifts?' (No), and 'Phase shift - Min, Max, Step (deg)' (0, 180, 10). The 'CTFFIND-4.1' tab is active, showing 'Use CTFFIND-4.1?' (Yes), 'CTFFIND-4.1 executable' (set to '/ctffind-4.1.5/bin/ctffind' with a 'Browse' button), 'Use power spectra from MotionCorr job?' (No), 'Use exhaustive search?' (No), 'Estimate CTF on window size (pix)' (set to -1 with a slider), 'FFT box size (pix)' (512), 'Minimum resolution (A)' (30), 'Maximum resolution (A)' (5), and 'Minimum defocus value (A)' (5000). The 'Running' tab is also visible, showing 'Number of MPI procs' (6), 'Submit to queue?' (No), 'Queue name' (openmpi), 'Queue submit command' (qsub), 'Standard submission script' (set to 'relion-3.1/scripts/qsub.csh' with a 'Browse' button), 'Minimum dedicated cores per node' (24), and 'Additional arguments'. A callout box labeled 'Click [Run !]' points to a 'Run!' button in the bottom right corner.

File Jobs Schedules I/O CTFFIND-4.1 Gctf Running MotionCorr/job001/micrographs.star

Import  
Motion correction  
CTF estimation  
Manual picking  
Auto-picking

CTF estimation

2D classification  
3D initial model  
3D classification  
3D auto-refine  
3D multi-body  
CTF refinement  
Bayesian polishing  
Mask creation  
Join star files  
Particle subtraction  
Post-processing  
Local resolution  
External

I/O view Job actions Cur

I/O CTFFIND-4.1 Gctf Running

Input micrographs STAR file: ort/job001/micrographs.star ? Browse

Use micrograph without dose-weighting? No ?

Estimate phase shifts? No ?

Phase shift - Min, Max, Step (deg) 0 180 10 ?

I/O CTFFIND-4.1 Gctf Running

Use CTFFIND-4.1? Yes Yes ?

CTFFIND-4.1 executable: /ctffind-4.1.5/bin/ctffind" ? Browse

Use power spectra from MotionCorr job? No ?

Use exhaustive search? No ?

Estimate CTF on window size (pix) -1 ?

FFT box size (pix): 512 ?

Minimum resolution (A): 30 ?

Maximum resolution (A): 5 ?

Minimum defocus value (A): 5000 ?

Number of MPI procs: 6 6 ?

Submit to queue? No ?

Queue name: openmpi ?

Queue submit command: qsub ?

Standard submission script: relion-3.1/scripts/qsub.csh ? Browse

Minimum dedicated cores per node: 24 ?

Additional arguments: ?

Click [Run !] Run!

# Check the results of CTF estimation

**File** **Jobs** **Autorun**

**Re-read pipeline** Alt+R

Edit project note Alt+E

Print all notes Alt+P

Remake .Nodes/ Alt+N

Display Alt+D

Show initial screen Alt+Z

Empty trash Alt+T

About

Quit Alt+Q

3D auto-refine

3D multi-body

CTF refinement

**File** **Jobs** **Schedules**

Import

Motion correction

**CTF estimation**

Manual picking

Auto-picking

Particle extraction

Subset selection

**CTF estimation**

3D multi-body

CTF refinement

Bayesian polishing

Mask creation

Join star files

Particle subtraction

Post-processing

Local resolution

External

**I/O** **CTFFIND-4.1** **Gctf** **Running**

Use Gctf instead? Yes

Gctf executable: /6/bin/Gctf-v1.06\_sm\_30\_cu8.0\_x86\_64 Browse

Ignore 'Searches' parameters? Yes

Perform equi-phase averaging? No

Other Gctf options:

Which GPUs to use: 0

*Schedule* *Check command* *Continue!*

*I/O view* *Job actions* Current: 003: CtfFind/job003/

Display: out: micrographs\_ctf.star

micrographs\_ctf.star

Scale: 0.5 Min: 0 Max: 0

Sigma contrast: 0 Color: greyscale

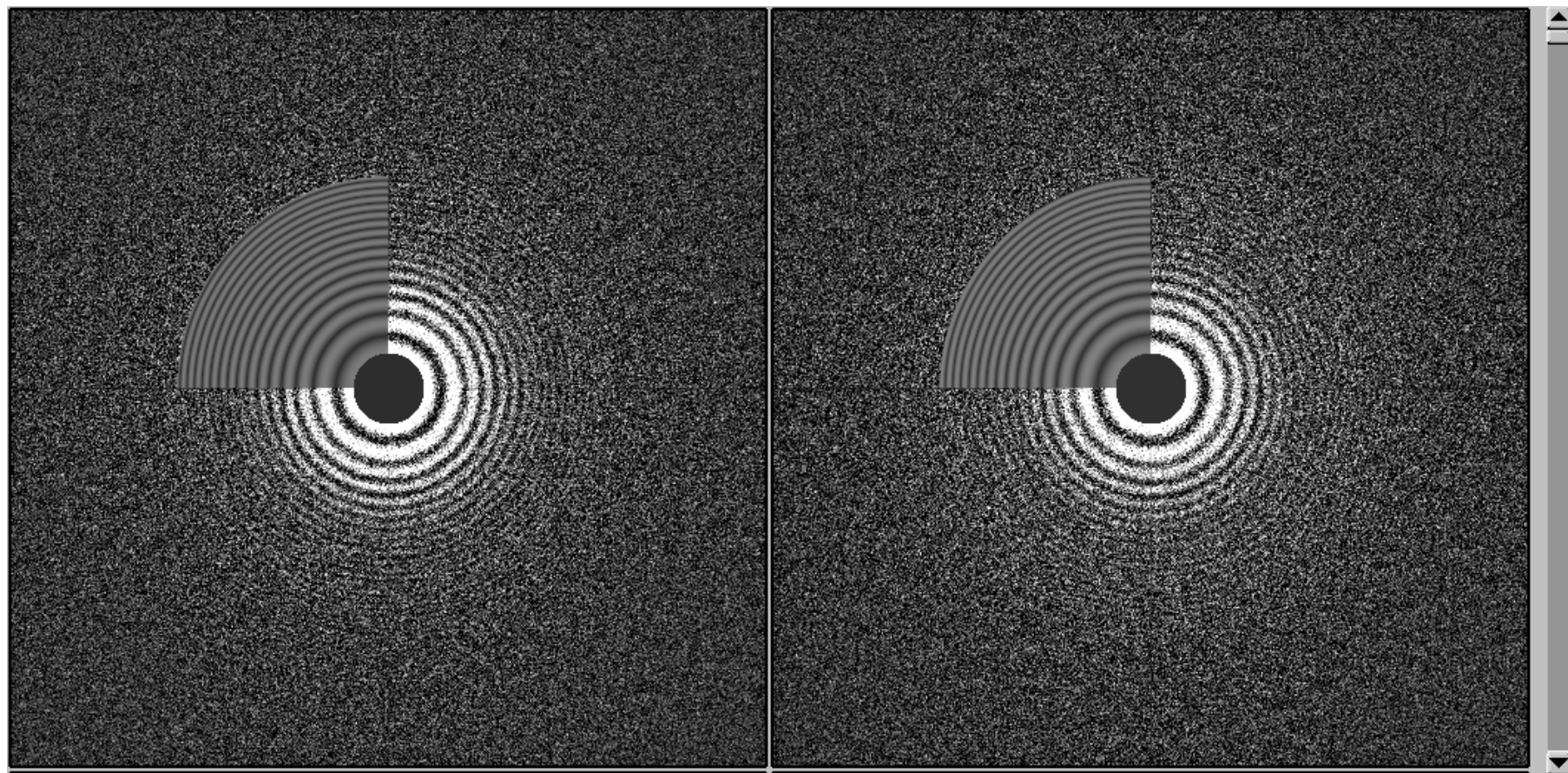
Display: rlnCtfImage

☐ Sort images on: rlnOpticsGroup

☐ Reverse sort? ☐ Apply orientations? ☐ Read whole stacks?

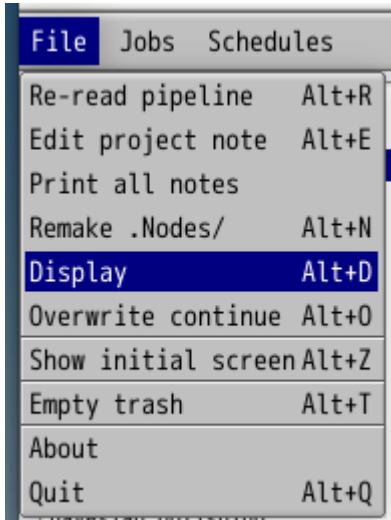
Nr. columns: 5 Ori scale: 1 Max. nr. images: 1000

Display!

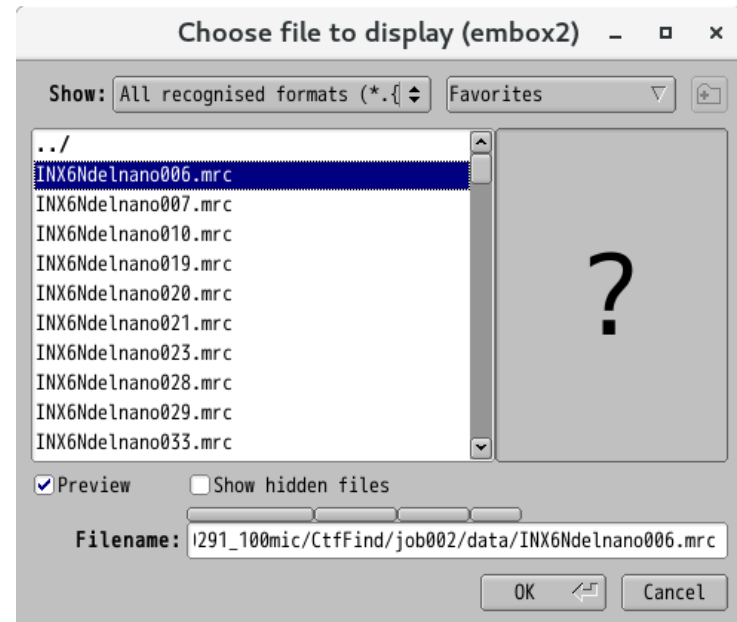


# Check CTF-corrected micrographs

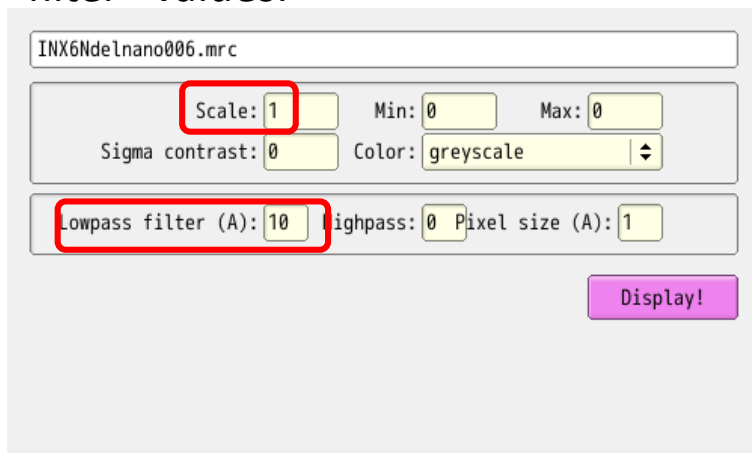
(1) Select [File] -> [Display]



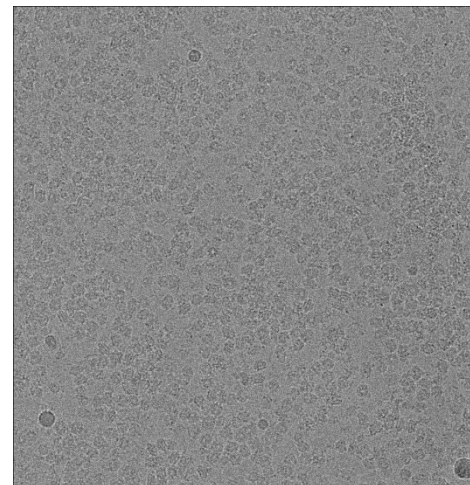
(2) Select one of the file in CtfFind/job002/data



(3) Input your favorite “scale” and “Low pass filter” values.



(4) You can see the CTF-corrected micrograph





INX6Ndelnano006.mrc

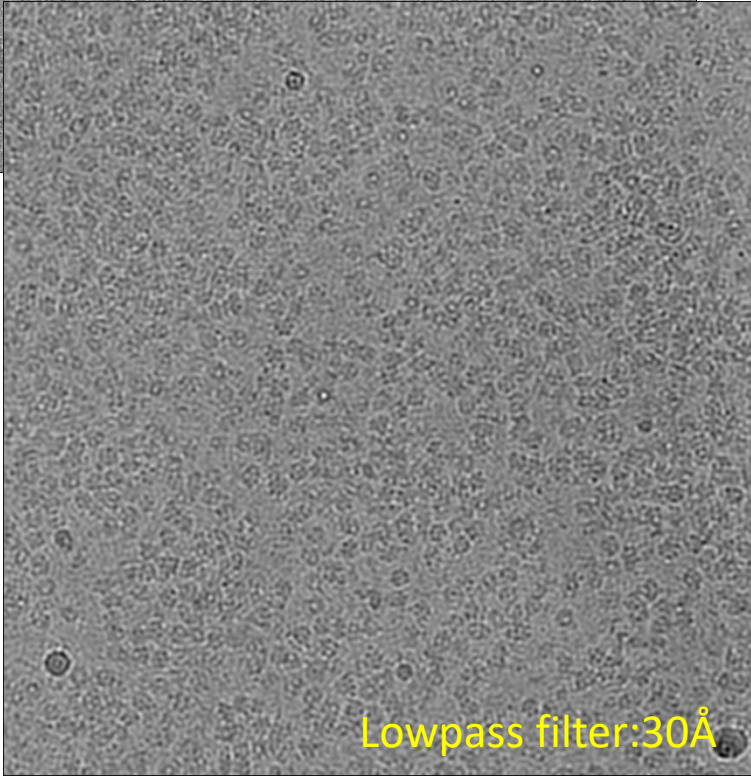
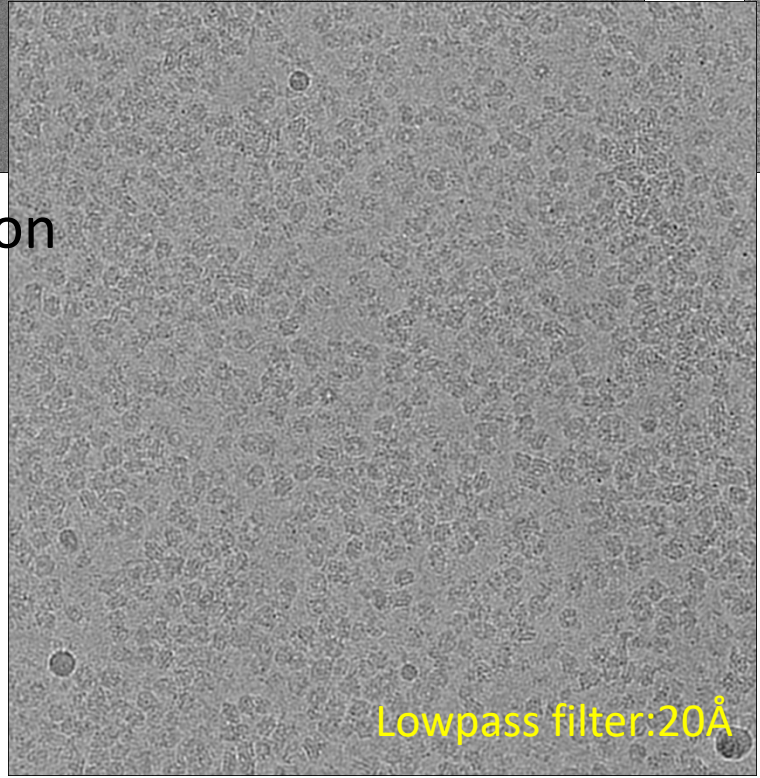
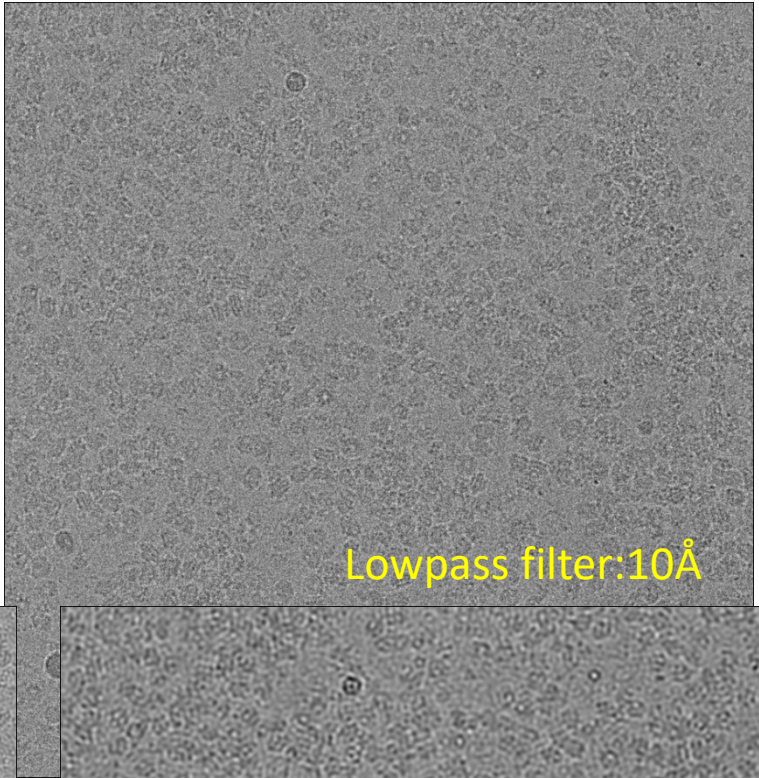
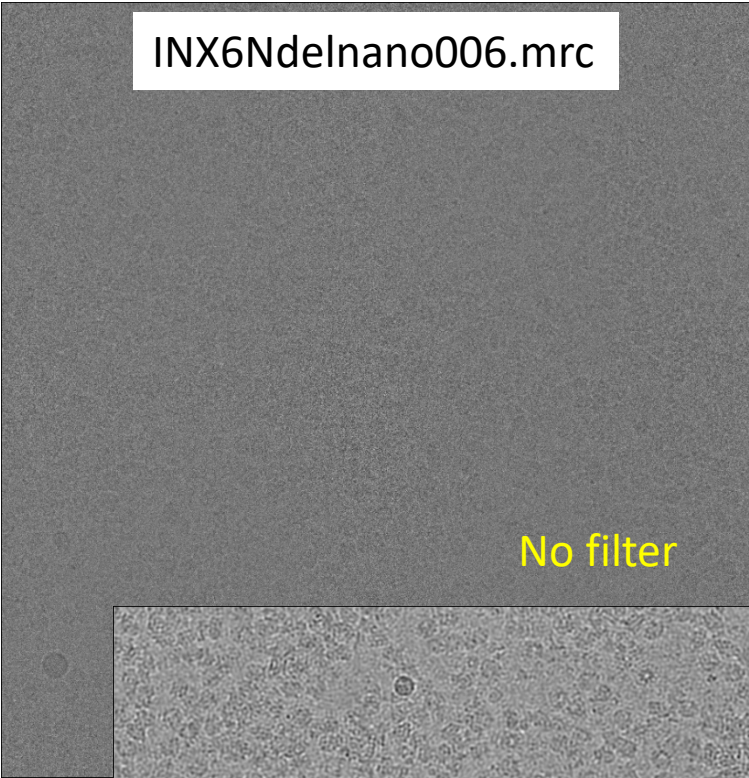
No filter

Lowpass filter:10Å

After  
CTF estimation

Lowpass filter:20Å

Lowpass filter:30Å



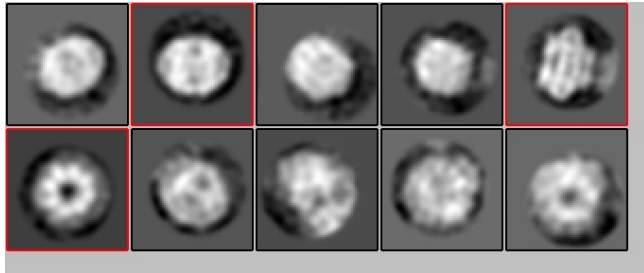
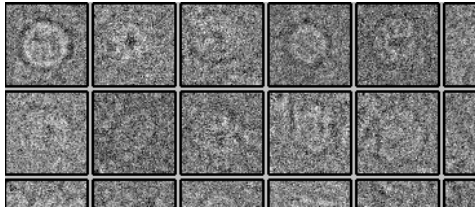
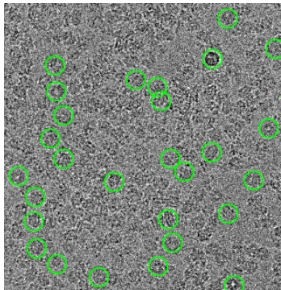


# Picking by Relion

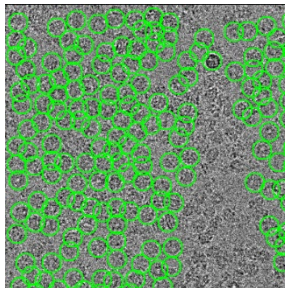
*For a few  
micrographs*

Manual picking

Auto-picking: LoG-based



*For many  
micrographs*

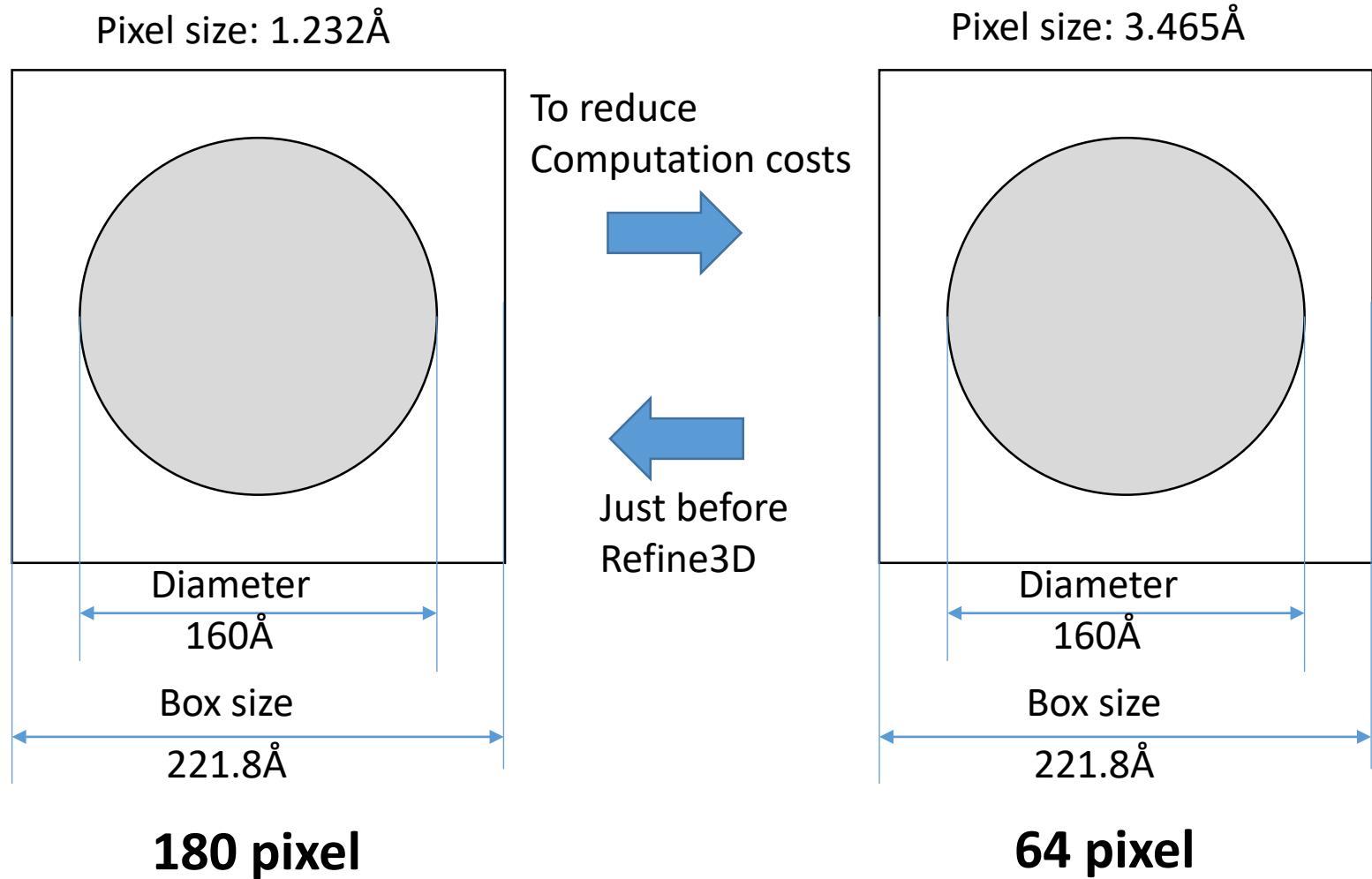


Class2D

Select Good Classes for reference

Auto-picking: reference-based

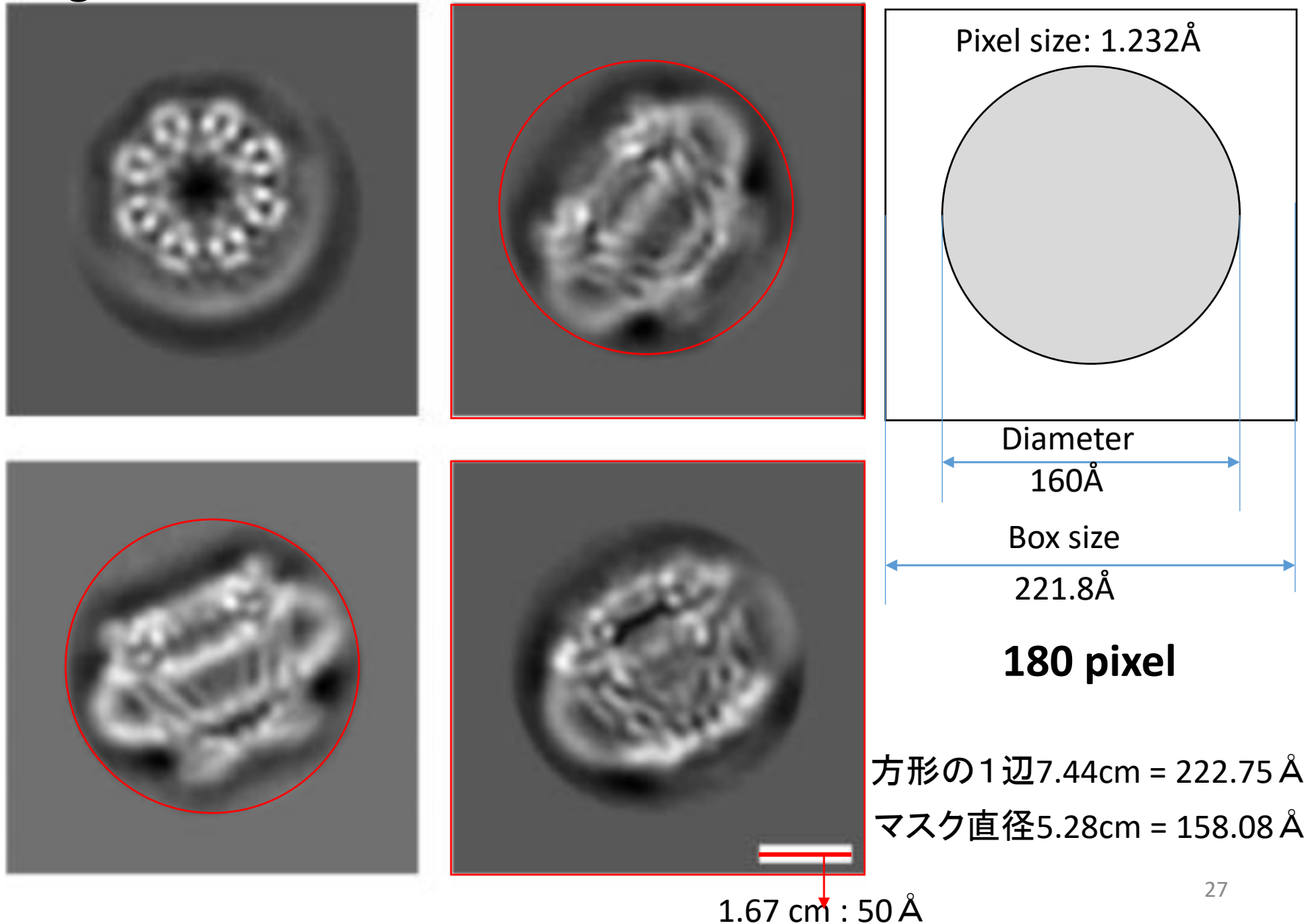
# Box size of particles



# 2D Class average images from the original article

Fig.S3c

Burendei et al. Science Advances. 2020. DOI: 10.1126/sciadv.aax3157





# 1.4 Manual Particle Picking

The screenshot shows the manual particle picking workflow in a software interface. The main window has tabs for File, Jobs, Schedules, I/O, Display, Colors, and Running. The I/O tab is selected, showing the input micrographs path: CtfFind/job003/micrographs\_ctf.star. The Display tab is also selected, showing various parameters for particle picking, including Particle diameter (A), Scale for micrographs, Sigma contrast, White value, Black value, Lowpass filter (A), Highpass filter (A), Pixel size (A), Pick start-end coordinates helices?, and Scale for CTF image. The Lowpass filter (A) is set to 10. The Alias is set to 5mic, and the Current is also 5mic. The Run button is highlighted with a red box and the text "をクリック!".

Manual picking

File

File	pick	0	CTF	
data/INX6NdeInano006.mrc	pick	0	CTF	198
data/INX6NdeInano007.mrc	pick	0	CTF	192
data/INX6NdeInano010.mrc	pick	0	CTF	189
data/INX6NdeInano019.mrc	pick	0	CTF	211
data/INX6NdeInano020.mrc	pick	0	CTF	202
data/INX6NdeInano021.mrc	pick	0	CTF	199
data/INX6NdeInano022.mrc	pick	0	CTF	202
data/INX6NdeInano023.mrc	pick	0	CTF	181

上から順に[pick]を選び、  
粒子をピックする。  
上から5つの画像に対して  
手動ピックを行う。

※[Shift]キーを押しながら  
クリックすると、○が消える！

ManualPick/Many/Movies/\*\_manualpick.starに保存される。

Alias: 5mic

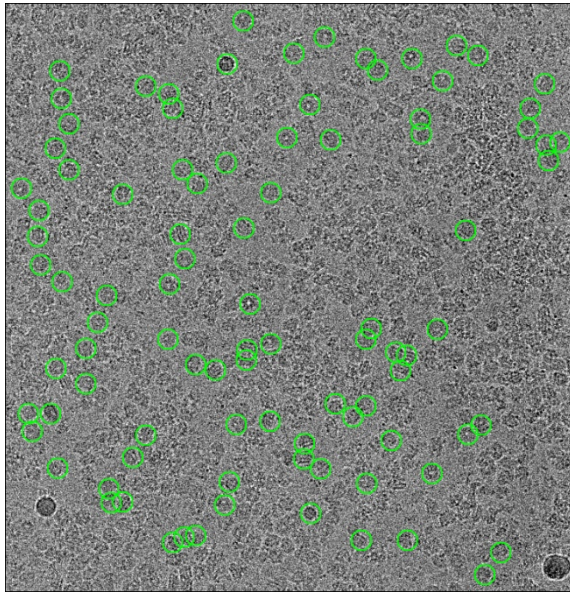
Current: 5mic

Run! をクリック!

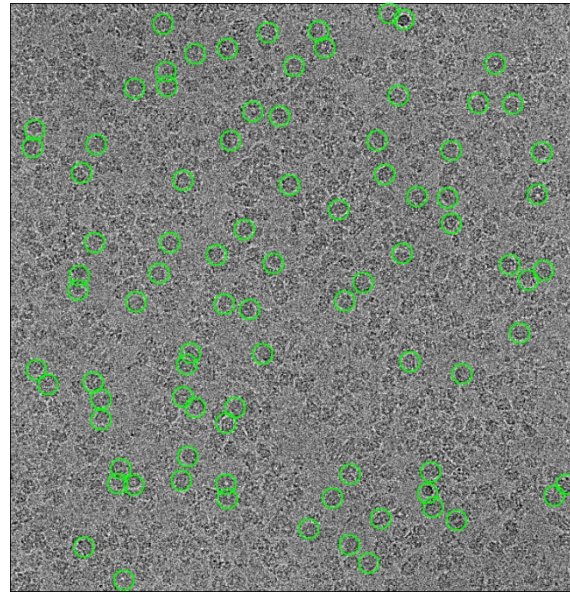
Save STAR with coordinates  
Load coordinates  
Reload coordinates  
Clear coordinates  
Help  
Quit



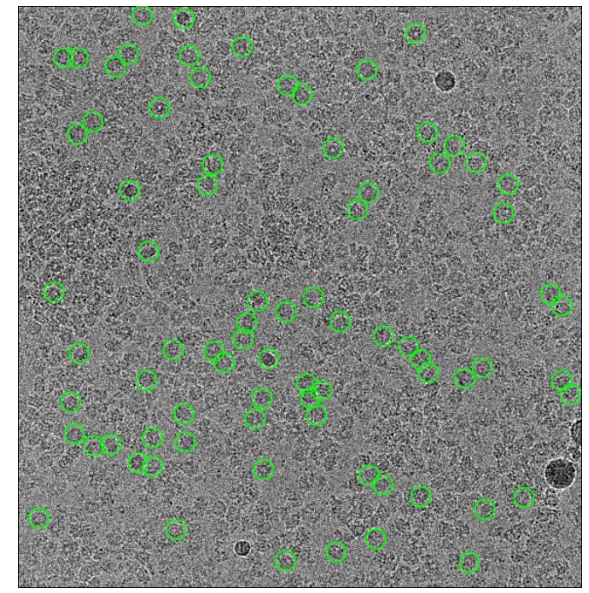
# Manual Particle Picking



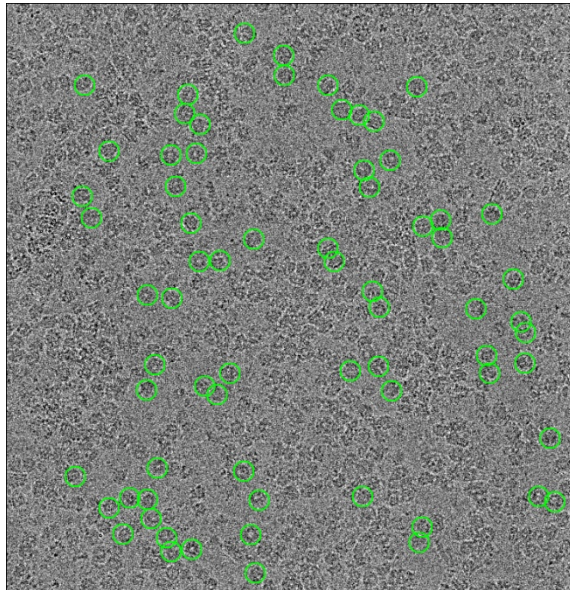
006 : 94 particles



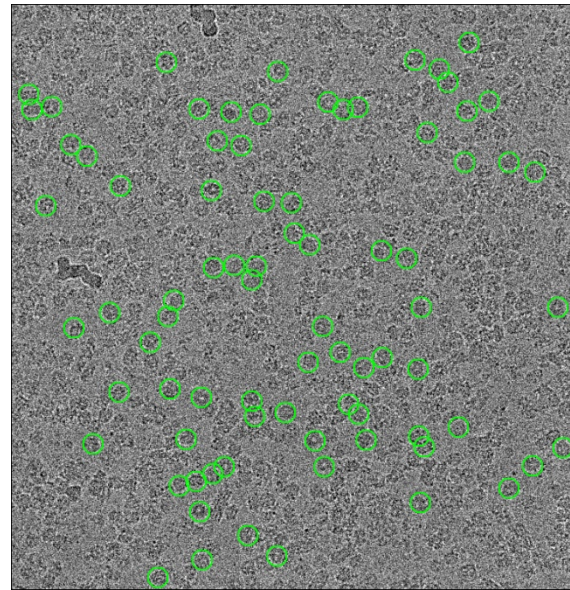
007 : 87 particles



010 : 79 particles



0019 : 70 particles



0020 : 80 particles

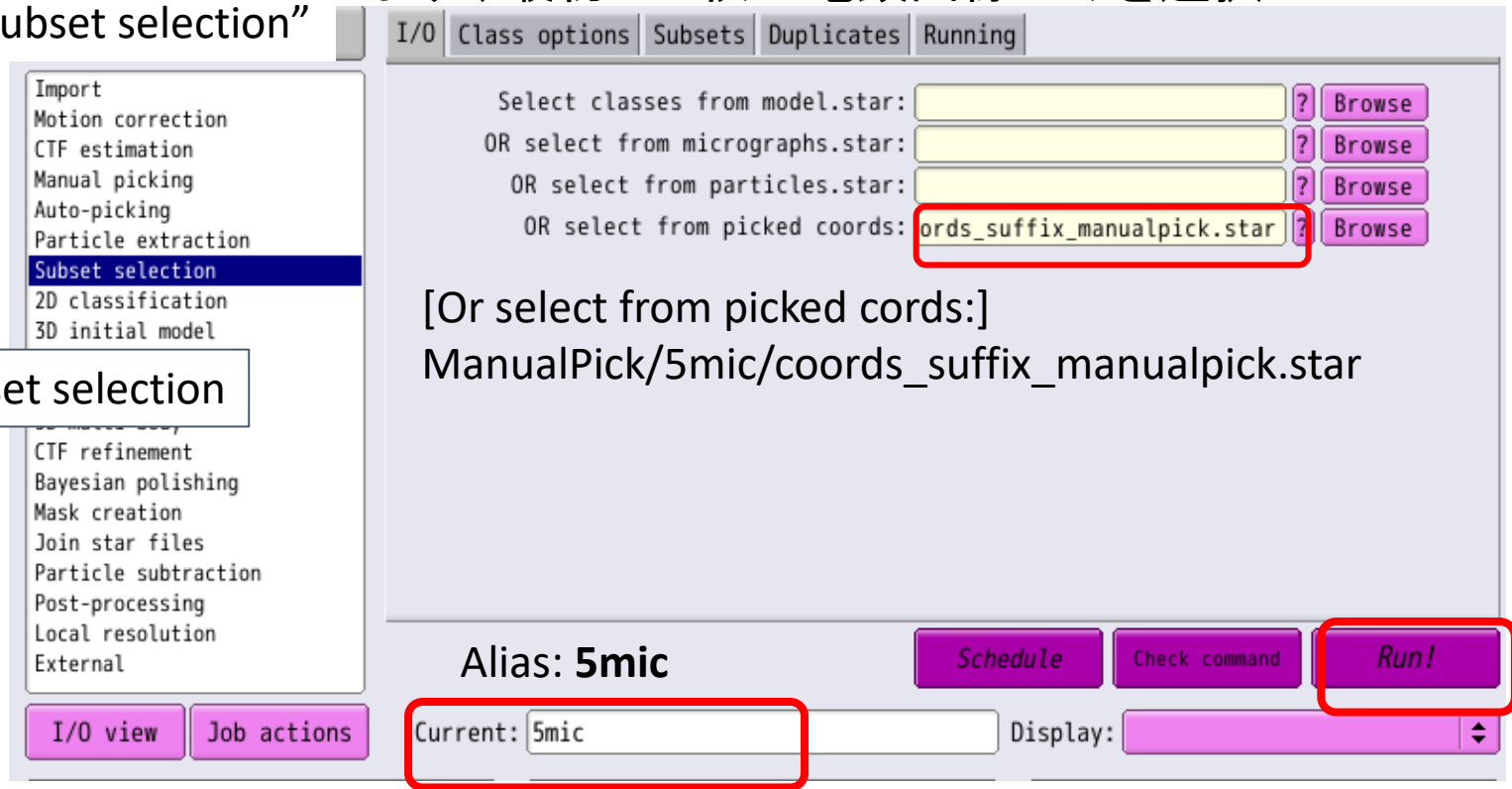
File			
data/INX6NdeInano006.mrc	pick	94	CTF
data/INX6NdeInano007.mrc	pick	87	CTF
data/INX6NdeInano010.mrc	pick	79	CTF
data/INX6NdeInano019.mrc	pick	70	CTF
data/INX6NdeInano020.mrc	pick	80	CTF
data/INX6NdeInano021.mrc	pick	0	CTF
data/INX6NdeInano023.mrc	pick	0	CTF
data/INX6NdeInano028.mrc	pick	0	CTF



# Subset selection

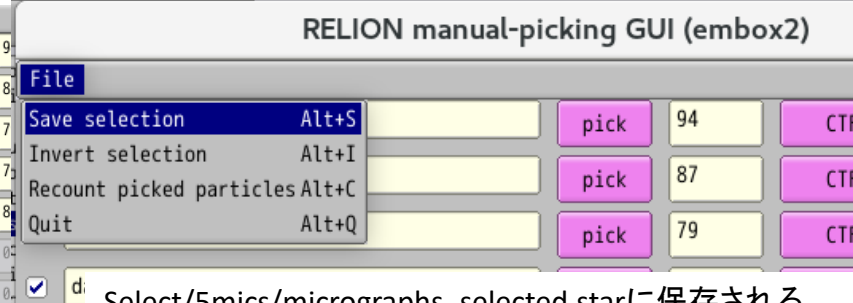
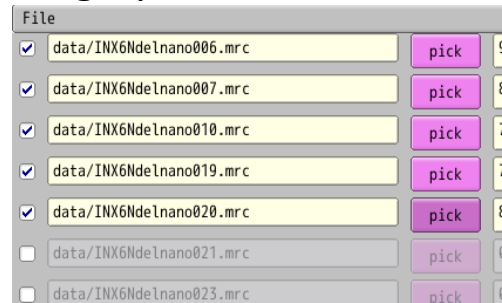
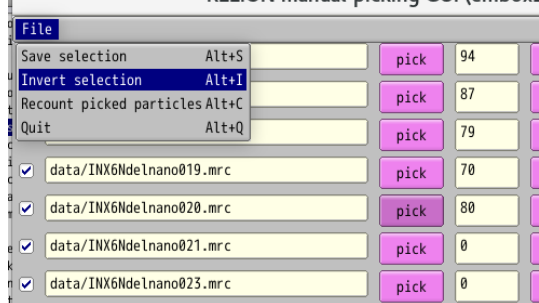
まず、最初の5枚の電顕画像だけを選択

Select "Subset selection"



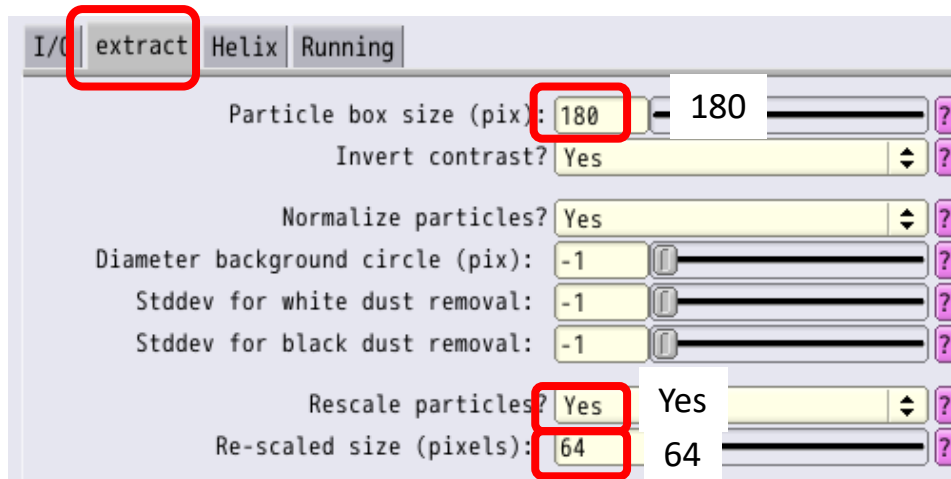
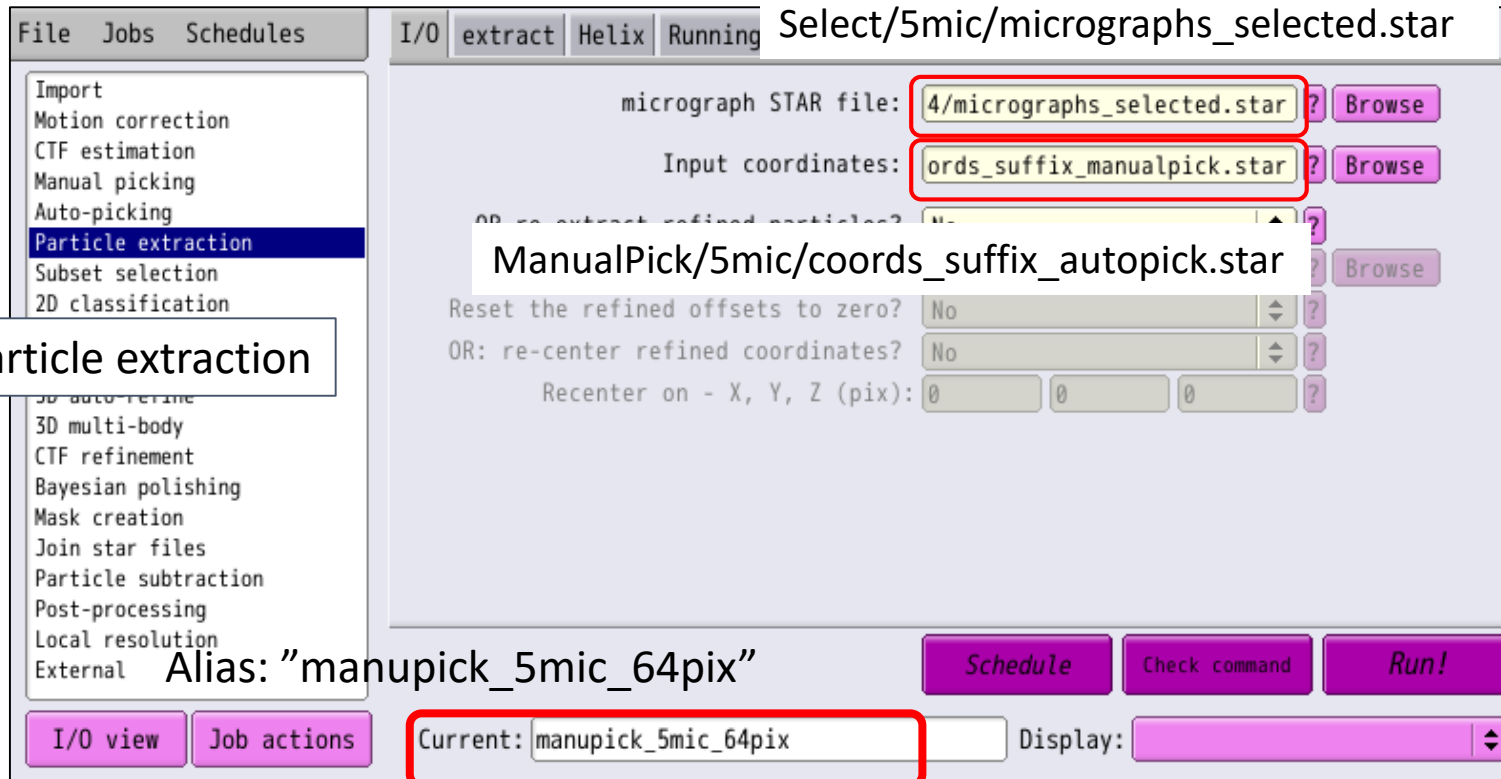
[File]⇒[Invert selection] Check ☒ for the top 5  
To uncheck ☒ Micrographs

[File]から、[Save selection]を選ぶ





# 1.6 Particle extraction



\*Box size: 180 pixel x 1.232=221.7 Å

\*Box size of the particle has to be even number.

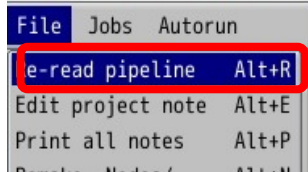
\*To reduce computational costs, we rescale 180 pixel into 64 pixel.

Click [Run !]



# 1.6 Particle extraction

RELION-3.0.5: /home/guest01/tmp/relion



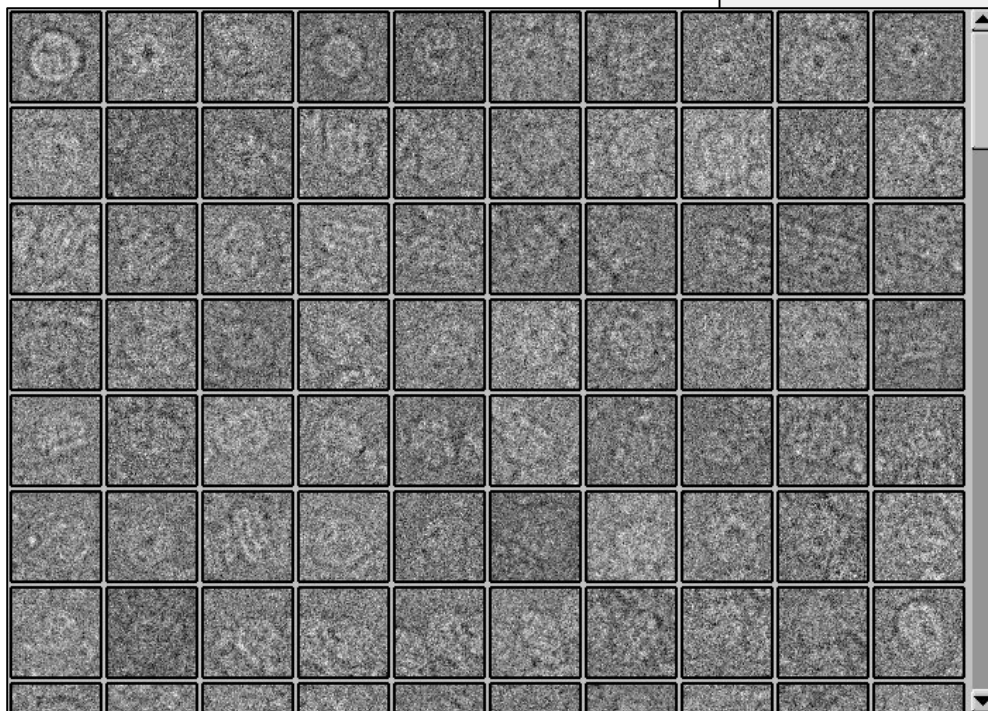
particles.star

Scale: 1 Min: 0 Max: 0  
Sigma contrast: 0 Color: greyscale

Display: rlnImageName  
☐ Sort images on: rlnCoordinateX  
☐ Reverse sort? ☐ Apply orientations? ☐ Read whole stacks?

Nr. columns: 10 Ori scale: 1 Max. nr. images: 1000

Display!



# 1.7 2D Classification : to make templates for autopick

[1GPU, 1 min]

File Jobs Schedules I/O CTF Optimisation

Extract/manupick\_5mic\_64pix/particles.star

Input images STAR file:  Browse

Continue from here:  Browse

I/O CTF **Optimisation** Sampling Helix Compute Running

Number of classes:  10

Regularisation parameter T:  2

Number of iterations:  25

Use fast subsets (for large data sets)?  No

Mask diameter (A)  160

Mask individual particles with zeros?  Yes

Limit resolution E-step to (A):  -1

2D classification

3D multi-body  
CTF refinement  
Bayesian polishing  
Mask creation  
Join star files  
Particle subtraction  
Post-processing  
Local resolution  
External

Alias: "manupick\_5mic\_64pix"

I/O view Job actions  Display:

I/O CTF **Optimisation** Sampling Helix **Compute** Running

Use parallel disc I/O?  Yes

Number of pooled particles:  3

Pre-read all particles into RAM?  No

Copy particles to scratch directory:

Combine iterations through disc?  No

Yes CPU acceleration?  Yes

Which GPUs to use:  0

I/O CTF Optimisation Sampling Helix Compute **Running**

Number of MPI procs:  1

Number of threads:  4

Submit to queue?  No

Queue name:  openmpi

Queue submit command:  qsub

Standard submission script:  relion-3.1/scripts/qsub.csh

Minimum dedicated cores per node:  24

Additional arguments:

33

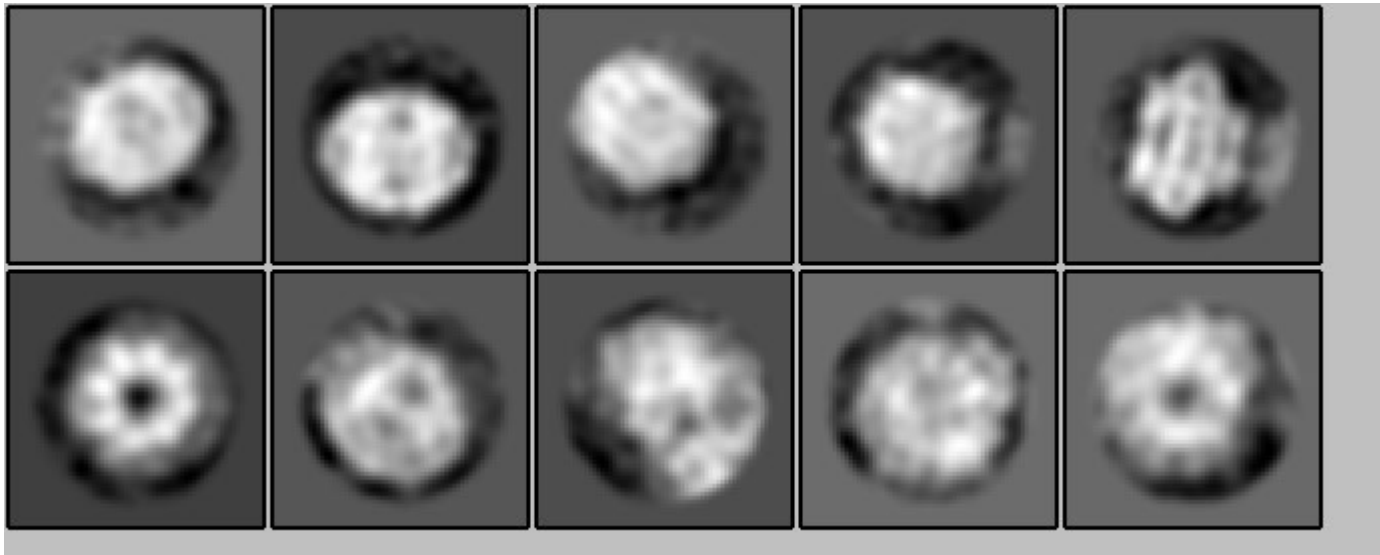
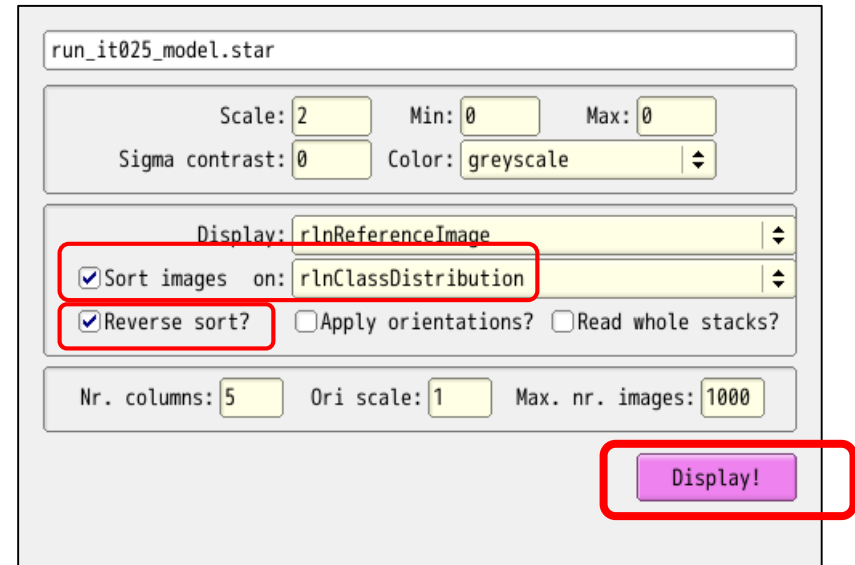
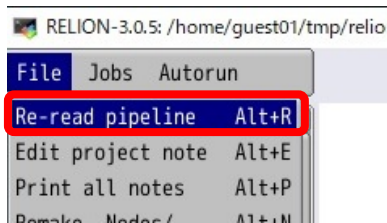
各受講者のGPU番号  
(0,1,2,3のどれか)を入力

※relion\_refineというプログラムが実行される。

1MPI, 4 threads, 1GPUでメモリ VIRT 47.6GB RES 492MB使用。



# 1.7 2D Classification : to make templates for autopick



# 1.8 Selecting templates for auto-picking

File Jobs Schedules **I/O** Class options Subsets Class2D/manupick\_5mic\_64pix/run\_it025\_model.star

Import  
Motion correction  
CTF estimation  
Manual picking  
Auto-picking  
Particle extraction  
**Subset selection**  
2D classification  
3D initial model

CTF refinement  
Bayesian polishing  
Mask creation  
Join star files  
Particle subtraction  
Post-processing  
Local resolution  
External

Select classes from model.star: **job006/run\_it025\_model.star** ? Browse  
OR select from micrographs.star: ? Browse  
OR select from particles.star: ? Browse  
OR select from picked coords: ords\_suffix\_manualpick.star ? Browse

Alias: "manupick\_5mic\_64pix"

Schedule Check command **Run!**

I/O view Job actions Current: **manupick\_5mic\_64pix** Display: ?

☒ Sort images on: rlnClassDistribution  
Sorted by number of particles belong to the class

run\_it025\_model.star

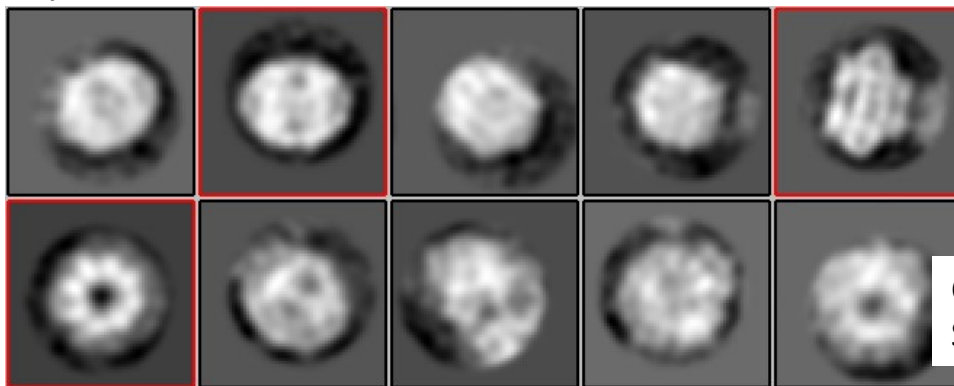
Scale: 1 Min: 0 Max: 0  
Sigma contrast: 0 Color: greyscale

Display: rlnReferenceImage  
☒ Sort images on: rlnClassDistribution  
☐ Reverse sort? ☐ Apply orientations? ☐ Read whole stacks?

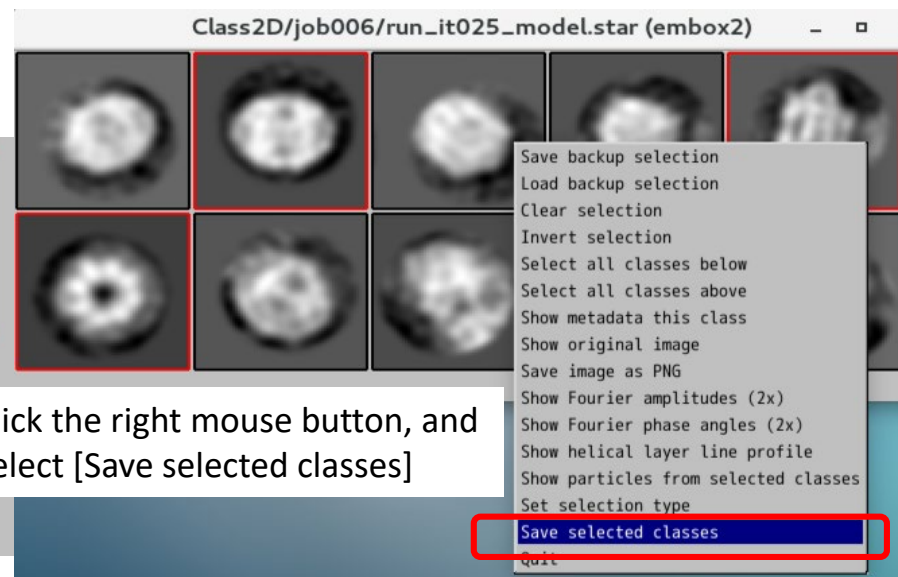
Nr. columns: 10 Ori scale: 1 Max. nr. images: 1000  
Max nr selected parts per class: -1

Display!

Among the 10 classes, select a few nice-looking classes, by the left button of the mouse.



Click the right mouse button, and Select [Save selected classes]



# Auto-picking;reference-based; for 5mic

Four parameters have to be optimized : 1. Picking threshold, 2. Min.inter-particle dis, 3. Max. stddev noise 4. Min. avg\_noise. Repeating ref-based picking for the 5 micrographs help us to optimized them.

[1GPU, < 1min]

File Jobs Schedules **I/O** Laplacian Ref Select/5mic/micrographs\_selected.star

Import  
Motion correction  
CTF estimation  
Manual picking  
**Auto-picking**  
Particle extraction  
Subset selection

3D auto-refine  
3D multi-body  
CTF refinement  
Bayesian polishing  
Mask creation  
Join star files  
Particle subtraction  
Post-processing  
Local resolution  
External

Input micrographs for autopick: 4/micrographs\_selected.star ? Browse  
Pixel size in micrographs (A) -1 ?  
2D references: /job007/class\_averages.star ? Browse  
OR: provide a 3D reference? No ?  
3D angular sampling: 30 de ?  
OR: use Laplacian-of-Gaussian? No No ?

Select/manu\_5mic\_64pix/class\_averages.star

Alias:"manu\_5mic\_64pix"

I/O view Job actions current: manu\_5mic\_64pix

Schedule Check command Run!

These four parameters have to be optimized.

I/O Laplacian **References** autopicking Helix Running

Lowpass filter references (A) 20 ?  
Highpass filter (A) -1 ?  
Pixel size in references (A) 3.465 ?  
160 ?  
5 ?

References have inverted contrast? Yes ?  
Are References CTF corrected? Yes ?  
Ignore CTFs until first peak? No ?

I/O Laplacian References **autopicking** Helix Running

Picking threshold: 0.05 0.0  
Minimum inter-particle distance (A): 100 100  
Maximum stddev noise: 1.1 1.1  
Minimum avg noise: -999 -999

Write FOM maps? No  
Read FOM maps? No

Shrink factor: 0

Use GPU acceleration? Yes Yes

Which GPUs to use: 0

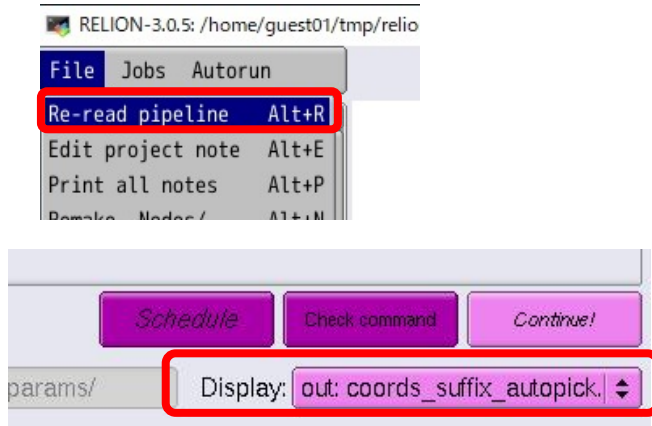
Run!

3.465 Å  
(=1.232 Å \* 180 pixel /64 pixel)

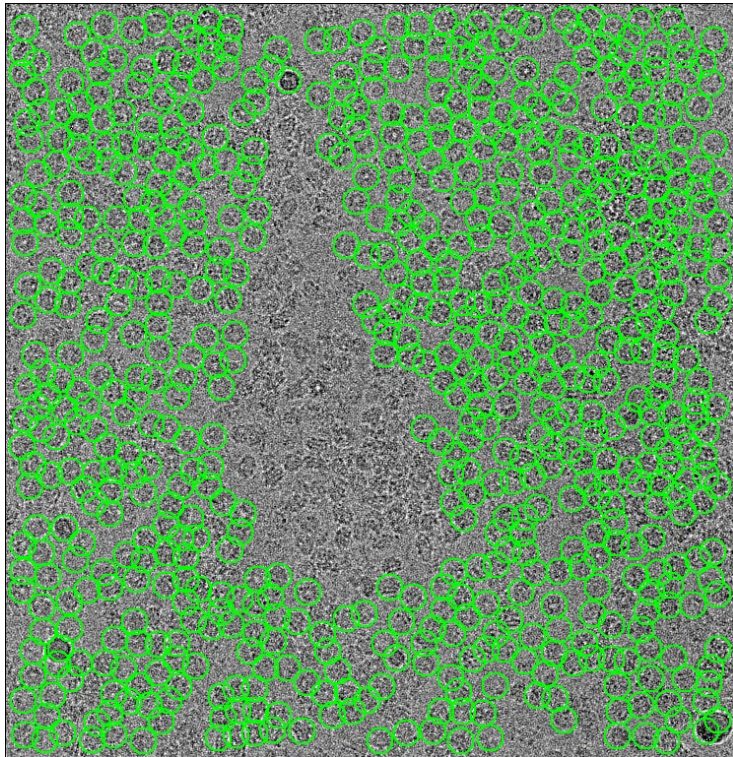
Input your GPU number (0,1,2,3)



# Auto-picking;reference-based; for 5mic



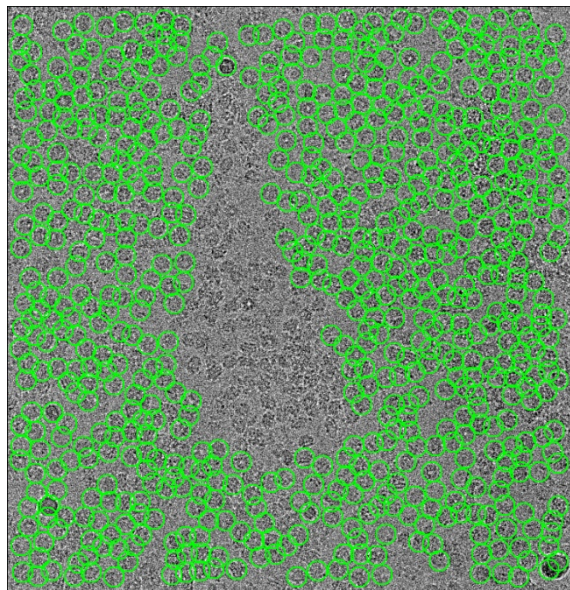
✓	data/INX6NdeInano006.mrc	pick	674	CTF	19895.3
✓	data/INX6NdeInano007.mrc	pick	638	CTF	19207.3
✓	data/INX6NdeInano010.mrc	pick	686	CTF	18995.4
✓	data/INX6NdeInano019.mrc	pick	655	CTF	21145.6
✓	data/INX6NdeInano020.mrc	pick	600	CTF	20288.3



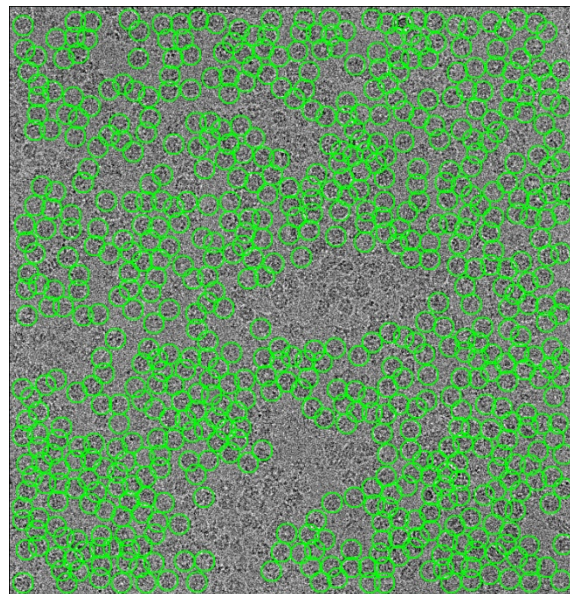
Total number of particles from 100 micrographs is 3253  
i.e. on average there were 651 particles per micrograph.



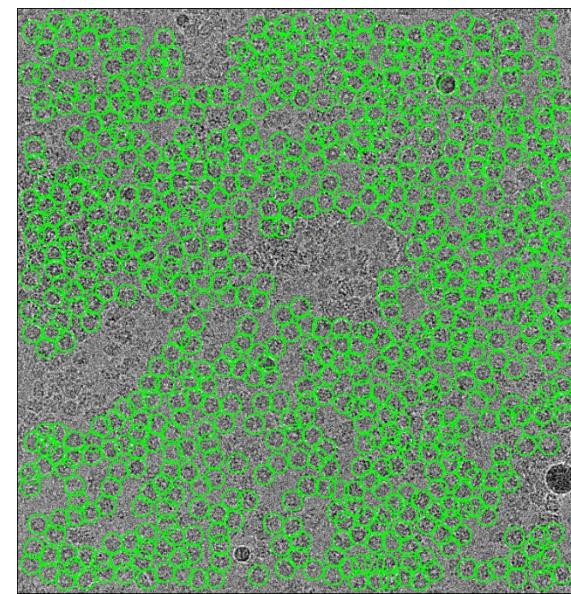
# Auto Picking



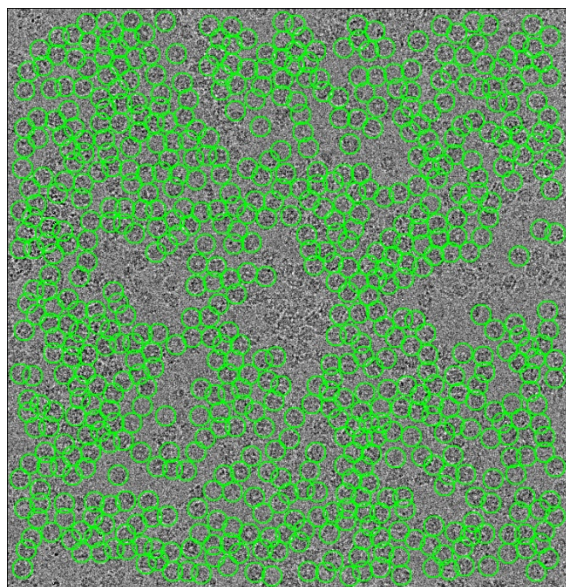
006 : 674 particles



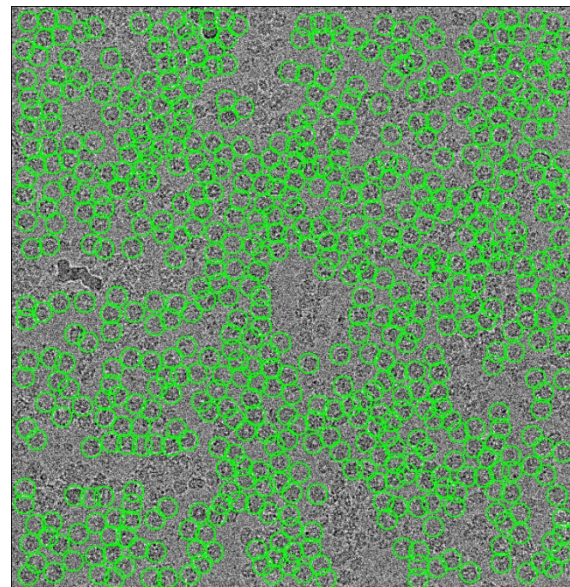
007 : 638 particles



010 : 686 particles



019 : 655 particles



020 : 600 particles

Ndelnano006.mrc	pick	674	CTF	19895.3
Ndelnano007.mrc	pick	638	CTF	19207.3
Ndelnano010.mrc	pick	686	CTF	18995.4
Ndelnano019.mrc	pick	655	CTF	21145.6
Ndelnano020.mrc	pick	600	CTF	20288.3



# Auto-picking;reference-based; for 100mic

Four parameters have to be optimized : 1. Picking threshold, 2. Min.inter-particle dis, 3. Max. stddev noise 4. Min. avg\_noise. Repeating ref-based picking for the 5 micrographs help us to optimized them.

[1GPU, < 1min]

Auto-picking

File Jobs Schedules **I/O** Laplacian Ref CtfFind/job002/micrographs\_ctf.star

Import  
Motion correction  
CTF estimation  
Manual picking  
**Auto-picking**  
Particle extraction  
Subset selection

Input micrographs for autopick:  Browse

Pixel size in micrographs (A)  ?

2D references:  Browse

OR: provide a 3D reference? No ?

Select/manu\_5mic\_64pix/class\_averages.star

3D angular sampling: 30 de ?

OR: use Laplacian-of-Gaussian?  No ?

Alias:"manu\_100mic\_64pix"

Current: manu\_100mic\_64pix

Use the optimized four parameters.

**I/O** Laplacian **References** autopicking Helix Running

Lowpass filter references (A)  ?

Highpass filter (A)  ?

Pixel size in references (A)  ?

?

?

References have inverted contrast? Yes ?

Are References CTF corrected? Yes ?

Ignore CTFs until first peak? No ?

**I/O** Laplacian References **autopicking** Helix Running

Picking threshold:  0.0

Minimum inter-particle distance (A):  100

Maximum stddev noise:  1.1

Minimum avg noise:  -999

Write FOM maps? No

Read FOM maps? No

Shrink factor:

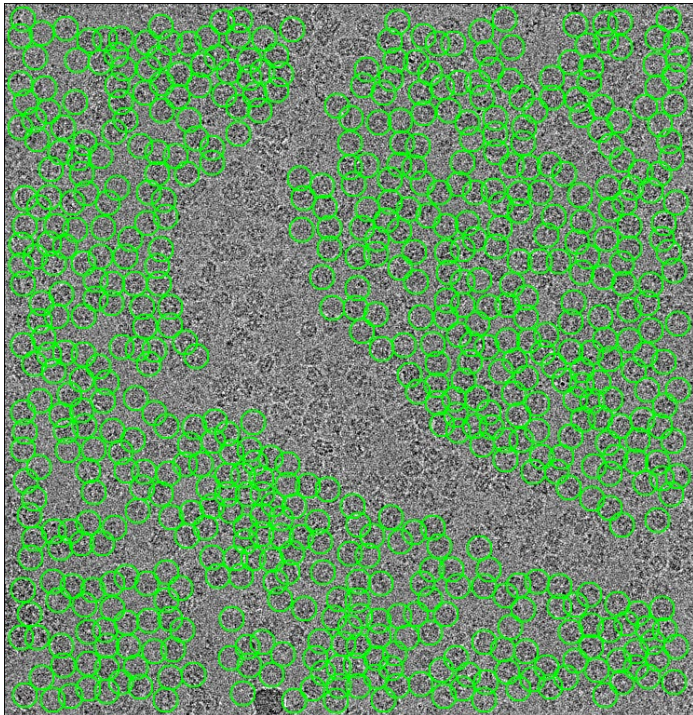
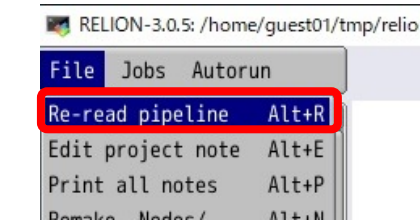
Use GPU acceleration?  Yes

Which GPUs to use:

3.465 Å  
(=1.232 Å \* 180 pixel /64 pixel)

Input your GPU number (0,1,2,3)

# Auto-picking;reference-based; for 100mic

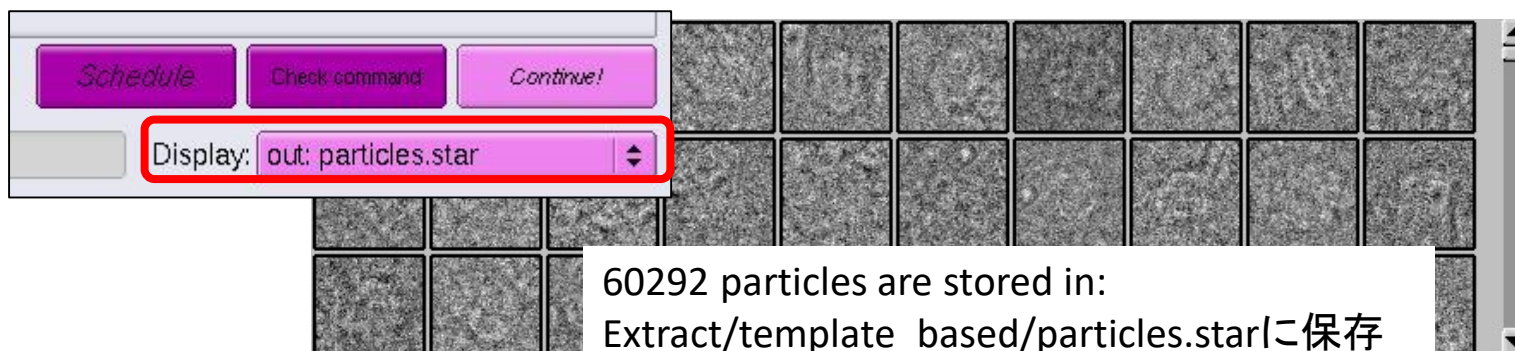
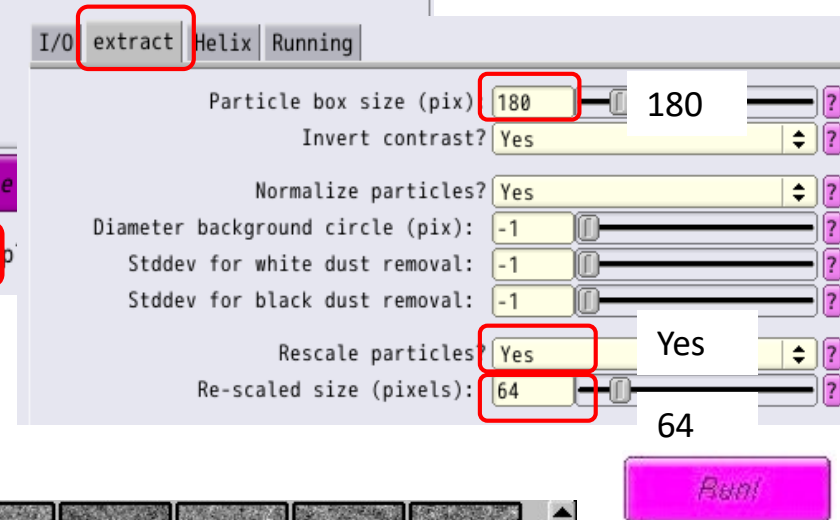
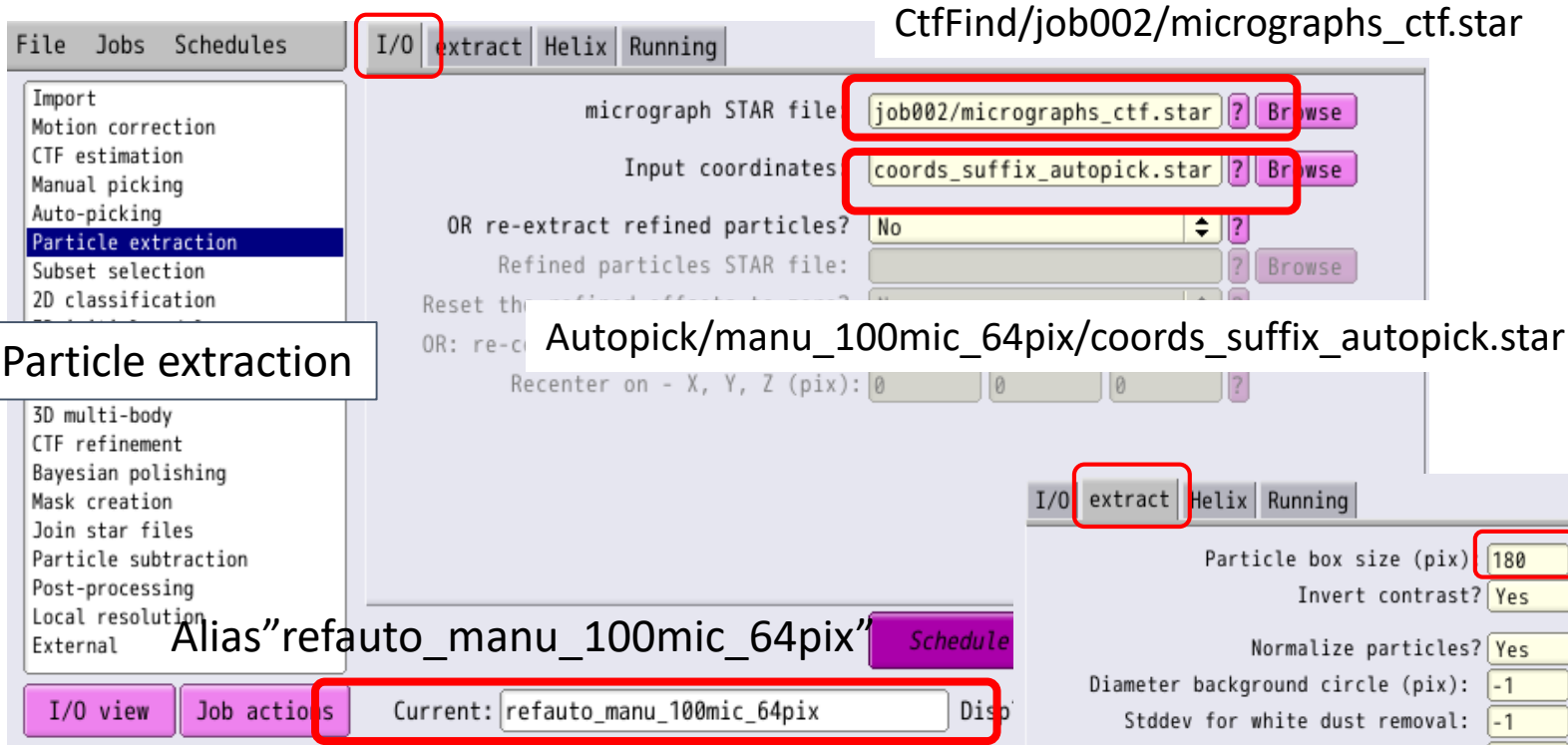


File				
✓ data/INX6Ndelnano006.mrc	pick	674	CTF	19895.3
✓ data/INX6Ndelnano007.mrc	pick	638	CTF	19207.3
✓ data/INX6Ndelnano010.mrc	pick	686	CTF	18995.4
✓ data/INX6Ndelnano019.mrc	pick	655	CTF	21145.6
✓ data/INX6Ndelnano020.mrc	pick	600	CTF	20288.3
✓ data/INX6Ndelnano021.mrc	pick	711	CTF	19941.8
✓ data/INX6Ndelnano023.mrc	pick	655	CTF	20295.9
✓ data/INX6Ndelnano028.mrc	pick	659	CTF	18192.1
File				
✓ data/INX6Ndelnano248.mrc	pick	487	CTF	21312.2
✓ data/INX6Ndelnano249.mrc	pick	541	CTF	20736.9
✓ data/INX6Ndelnano261.mrc	pick	617	CTF	21737.5
✓ data/INX6Ndelnano272.mrc	pick	587	CTF	22592.9
✓ data/INX6Ndelnano275.mrc	pick	504	CTF	23313.2
✓ data/INX6Ndelnano282.mrc	pick	512	CTF	19622.1
✓ data/INX6Ndelnano283.mrc	pick	512	CTF	20057
✓ data/INX6Ndelnano296.mrc	pick	625	CTF	18982

Total number of particles from 100 micrographs is 60292  
i.e. on average there were 603 particles per micrograph.



# 1.9 Particle extraction



# Appendix: Motion Correction

# Import movie/\*.mrc

Launch “relion” in the directory “EMPIAR-10291\_5movie/”.

Job type browser

File Jobs Schedules

Movies/mics Others Running

Import

Motion correction

CTF estimation

Manual picking

Auto-picking

Particle extraction

Subset selection

2D classification

3D initial model

3D classification

3D auto-refine

3D multi-body

CTF refinement

Bayesian polishing

Mask creation

Join star files

Particle subtraction

Post-processing

Local resolution

External

Import

Import raw movies/micrographs? Yes

Raw input files: movie/\*.mrc

Are these multi-frame movies? Yes

Optics: /usr/local/relion-3.1/data/mtf\_k2\_300kV.star

MTF of the detector: /usr/local/relion-3.1/data/mtf\_k2\_300kV.star

Pixel size (Angstrom): 1.232

Voltage (kV): 300

Spherical aberration (mm): 1.6

Amplitude contrast: 0.1

Beamtilt in X (mrad): 0

Beamtilt in Y (mrad): 0

Pixel size 0.495 Å is described in EMPIAR header file: 10291.xml.

A value of spherical aberration 1.6 was obtained by personal communication with Prof. Oshima.

Schedule Check command Run!

I/O view Job actions

Current: Give\_alias\_here Display:

Click [Run!]



# Motion Correction

No GPU, 2min for 5 movies

File Jobs Schedules I/O Motion Running Import/job001/movies.star

Import  
Motion correction  
CTF estimation  
Manual picking  
Auto-picking  
Particle extraction  
Subset selection  
2D classification  
3D initial model  
3D classification  
3D auto-refine  
3D multi-body  
CTF refinement  
Bayesian polishing  
Mask creation  
Join star files  
Particle subtraction  
Post-processing  
Local resolution  
External

Motion correction

Input movies STAR file: Import/job001/movies.star ? Browse

First frame for corrected sum: 1 ?

Last frame for corrected sum: -1 ?

Dose per frame (e/A2): 0.2 0.2 ?

Pre-exposure (e/A2): 0 ?

Do dose-weighting? Yes ?

Save non-dose weighted as well? No ?

Save sum of power spectra? No ?

Sum power spectra every e/A2: 4 ?

A value of "Dose per frame (e/A2)" 0.2 was obtained by personal communication with Prof. Oshima.

Schedule Check command Run!

I/O view Job actions

Current: Give\_alias\_here

I/O Motion Running

I/O Motion Running

Number of patches X, Y: 5 5 5 5 ?

Group frames: 1 ?

Binning factor: 1 ?

Gain-reference image: ? Browse

Gain rotation: No rotation (0) ?

Gain flip: No flipping (0) ?

Defect file: ? Browse

Use RELION's own implementation? Yes Yes ?

MOTIONCOR2 executable: InCor2-1.1.0/MotionCor2\_1.1.0-Cuda80 ? Browse

Which GPUs to use: 0 ?

Number of MPI procs: 1 1 ?

Number of threads: 6 6 ?

Submit to queue? No ?

Queue name: openmpi ?

Queue submit command: qsub ?

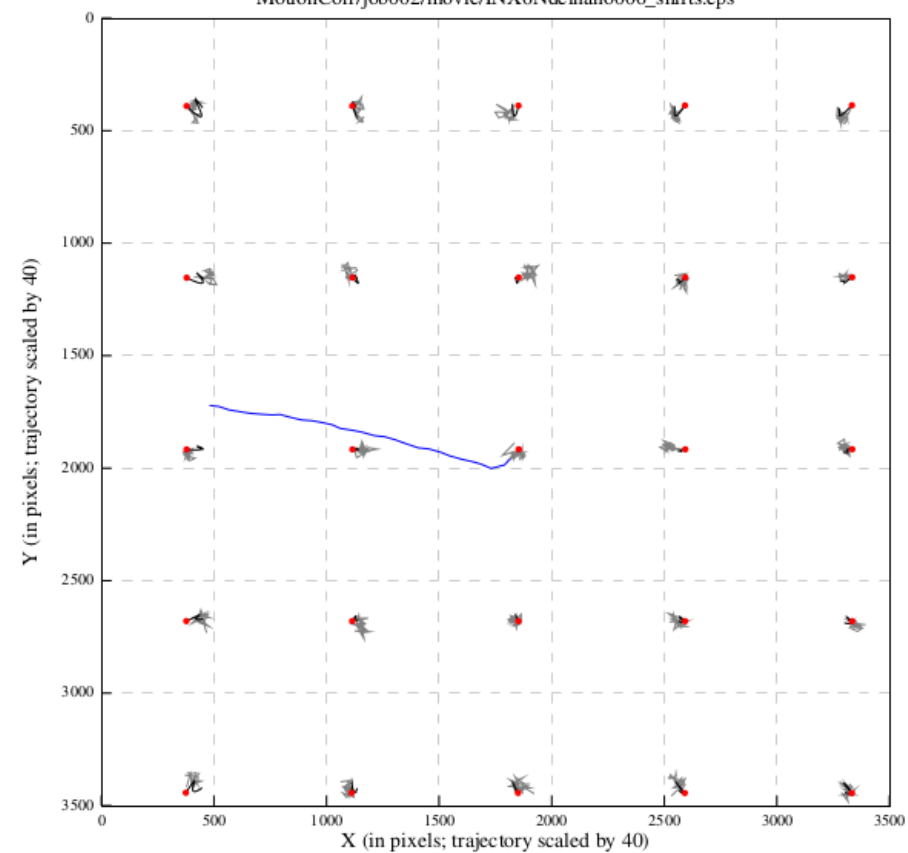
Standard submission script: /usr/local/relion-3.1/scripts/qsub.csh ? Browse

Minimum dedicated cores per node: 24 ?

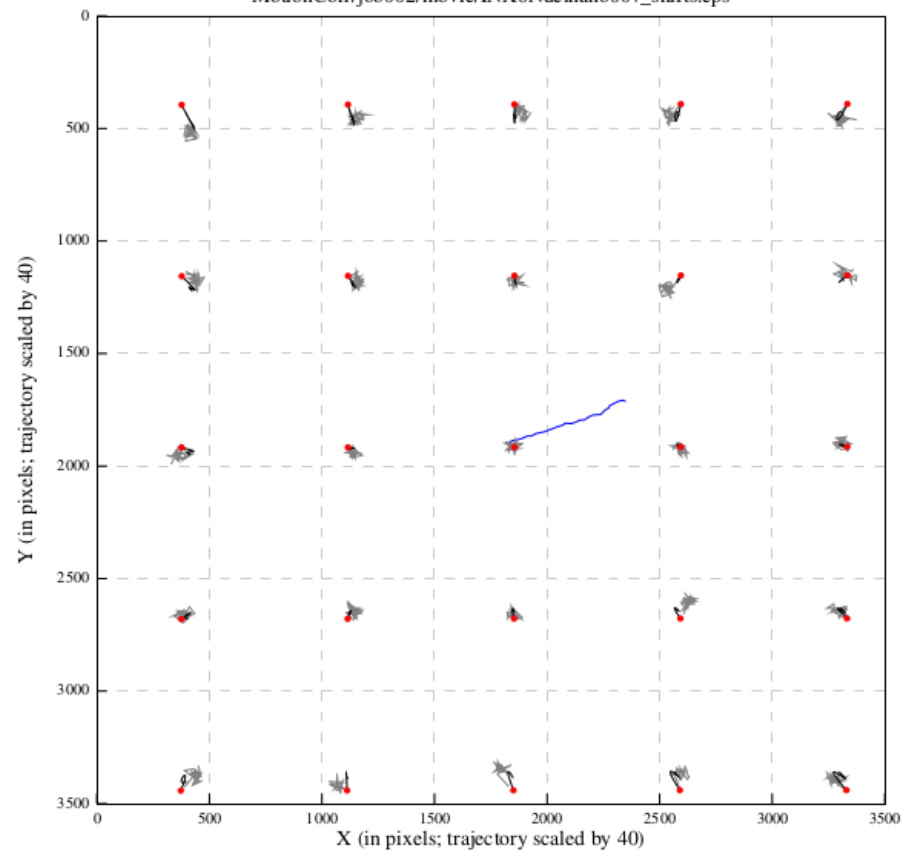
Additional arguments: ?

Click [Run!]

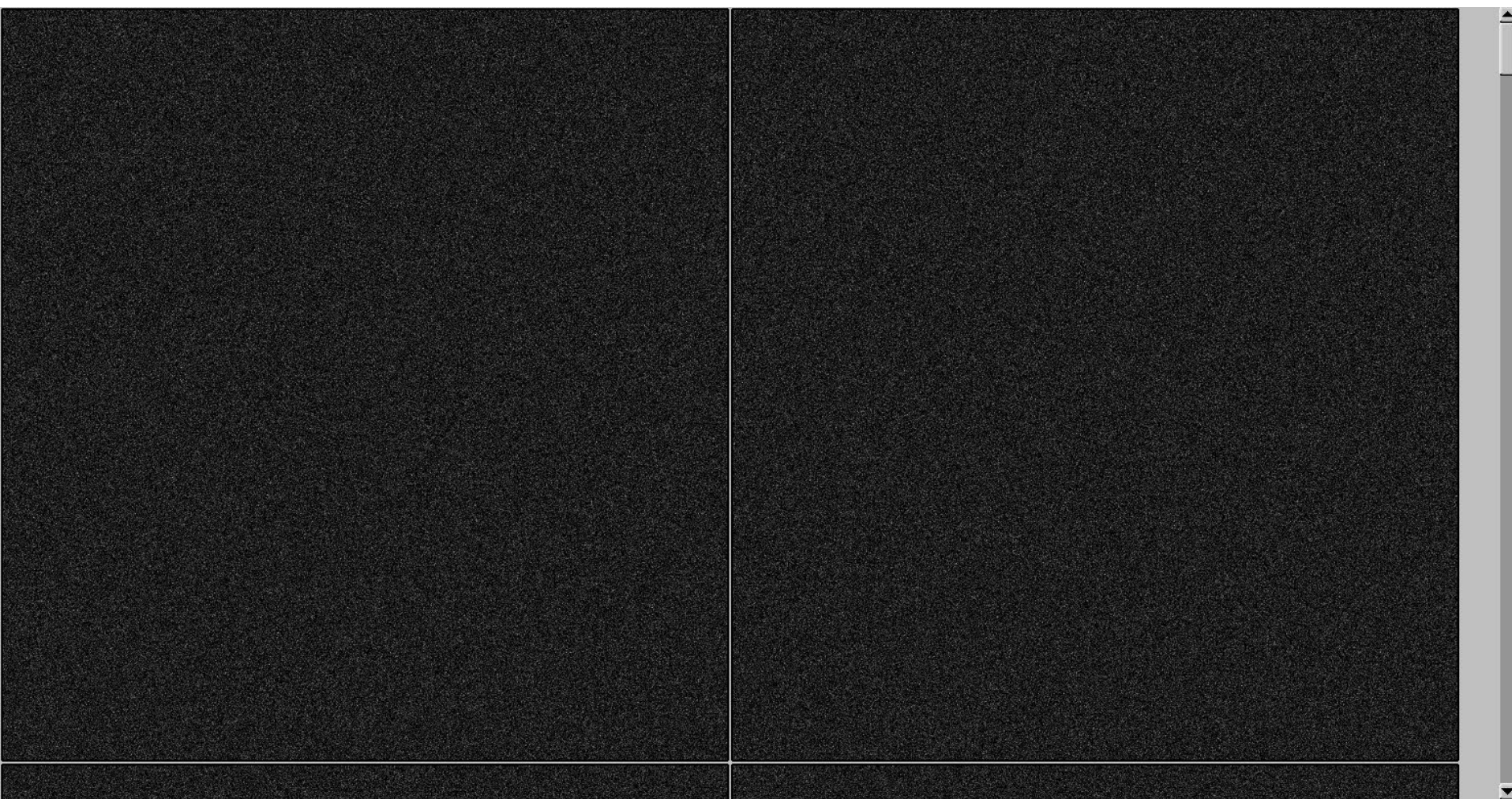
MotionCorr/job002/movie/INX6NdeInano006\_shifts.eps



MotionCorr/job002/movie/INX6NdeInano007\_shifts.eps



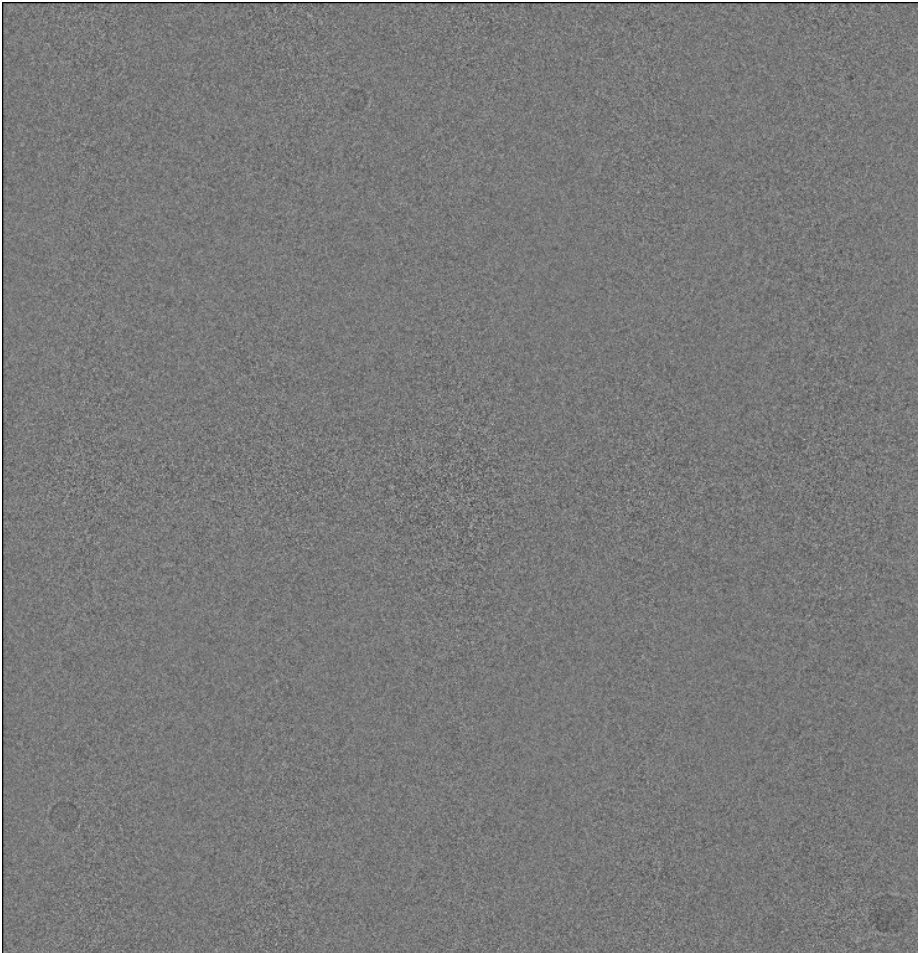
movie/INX6Ndelnano006.mrc



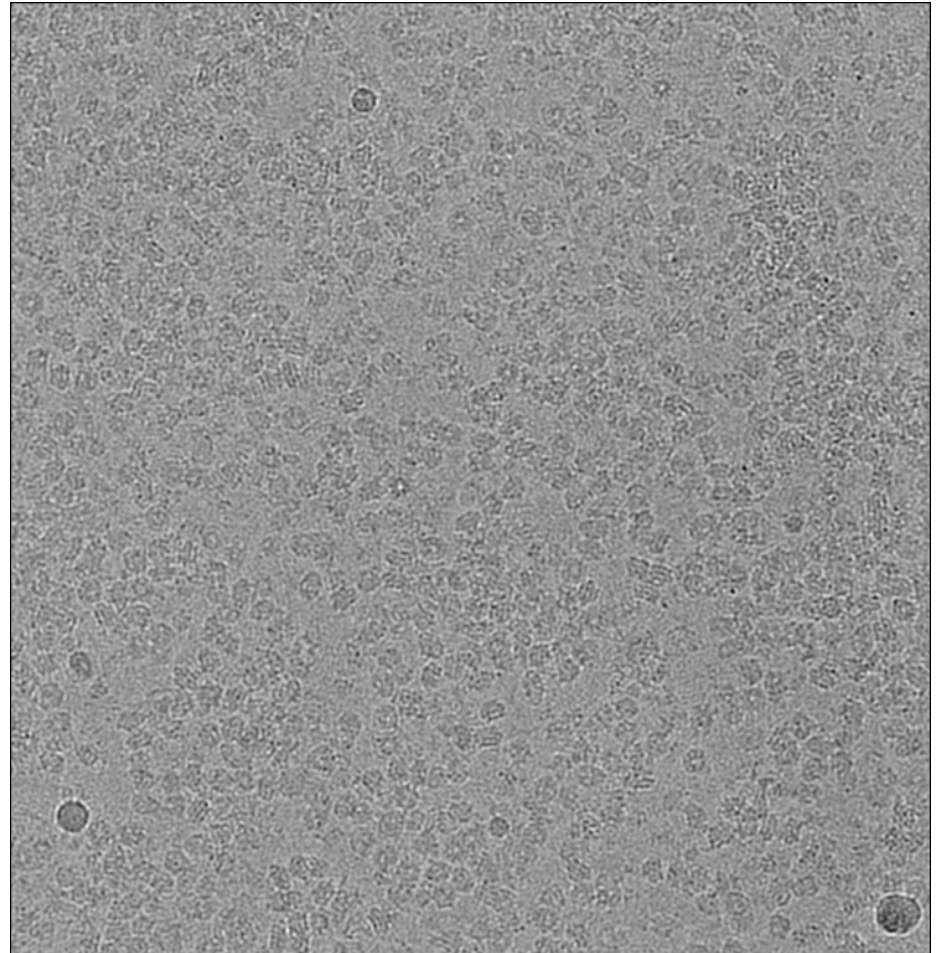
First two frames among 30 frames



MotionCorr/job002/movie/INX6Ndelnano006.mrc



Motion Corrected microraph



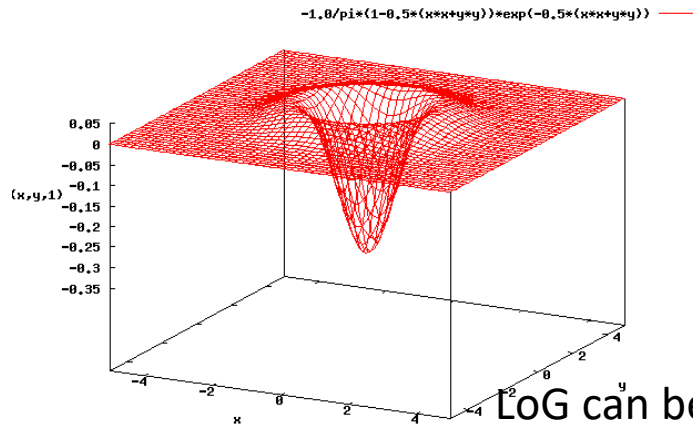
20 low pass filtered

# Appendix:

## LoG-based autopicking

# “Blob” detection using LoG filter

LoG : Laplacian of Gaussian



$$\phi(\mathbf{r}) = \frac{1}{2\pi\sigma^2} \exp\left[-\frac{\mathbf{r}^2}{2\sigma^2}\right]$$

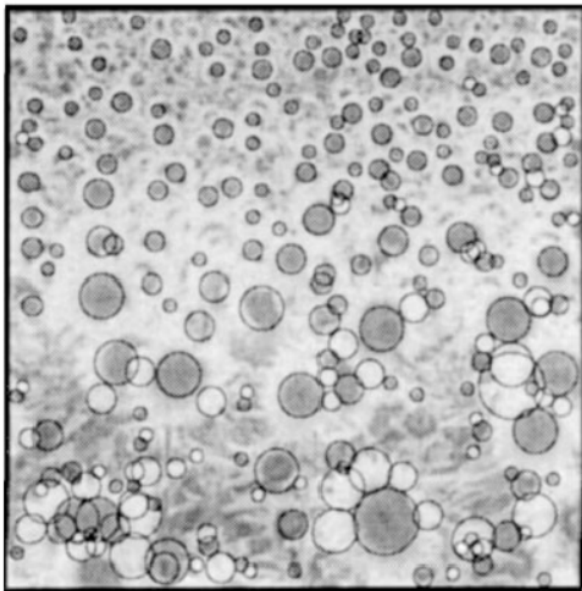
$$\text{LoG}(\mathbf{r}) = \frac{\partial^2 \phi}{\partial x^2} + \frac{\partial^2 \phi}{\partial y^2} = -\frac{2}{\sigma^2} \left(1 - \frac{x^2 + y^2}{2\sigma^2}\right) \phi(\mathbf{r})$$

[Big Gauss] – [normal Gauss]

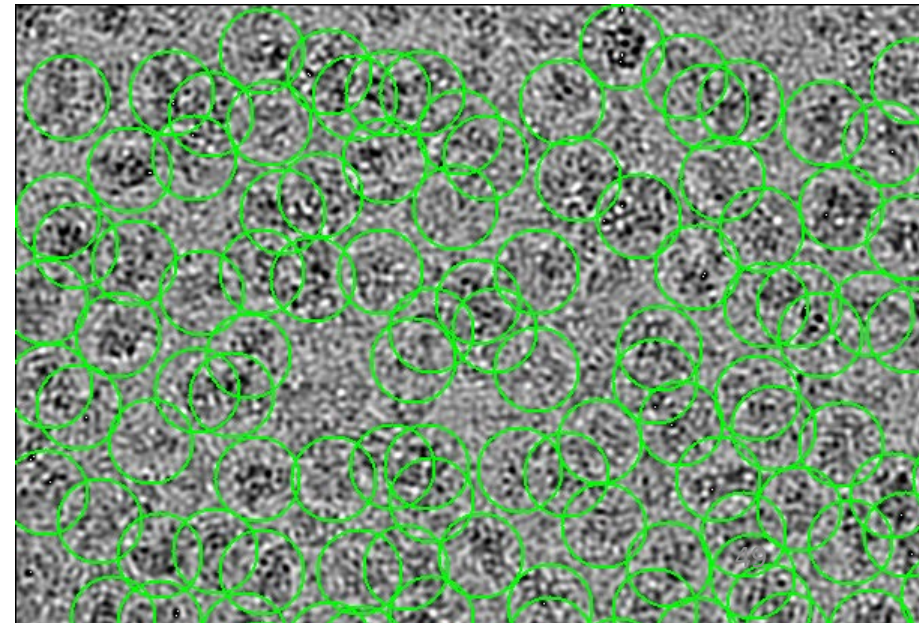
$$\text{LoG}(\mathbf{r}) \cong \text{DoG}(\mathbf{r}) = \phi(\mathbf{r}|k\sigma) - \phi(\mathbf{r}|\sigma)$$

LoG can be approximated as DoG (Difference of Gaussians)

T. Lindeberg (1998). Feature detection with automatic scale selection. Int. J. Computer Vision. 30 (2): 77–116

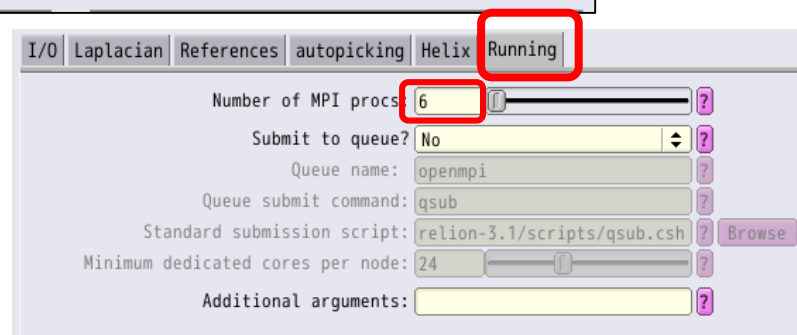
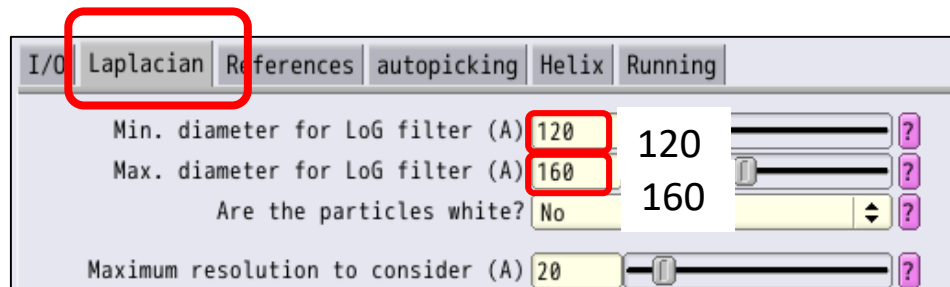
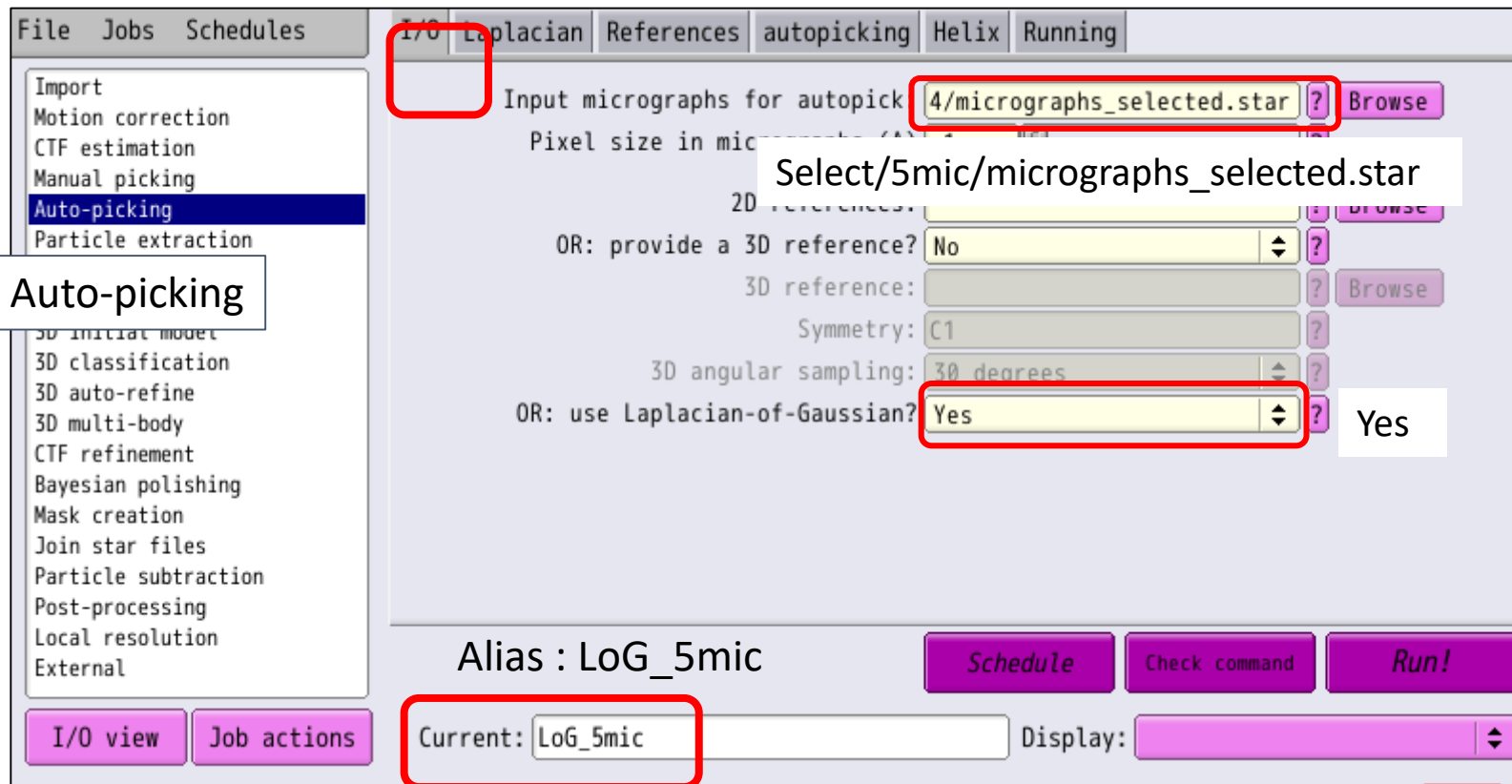


CryoEM particle picking by Relion 3.0





# 1.5 LoG-based autopicking (1分以下)

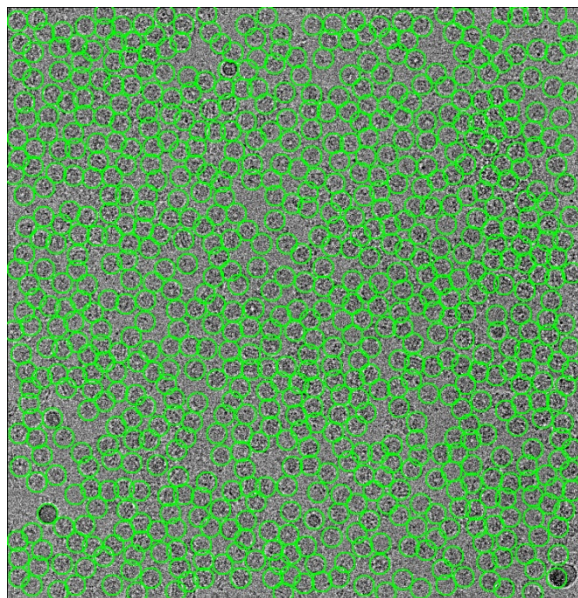


※dmin,dmaxをユーザーが指定。それらをもとに全部で4+3+4=11通りのdを試す。  
dmin/5, dmin/4, dmin/3, dmin/2, dmin, (dmin+dmax)/2, dmax, 2dmax, 3dmax, 4dmax, 5dmax

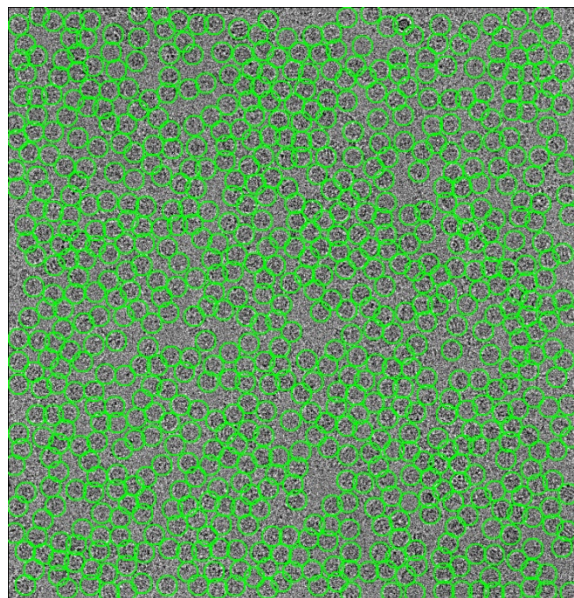




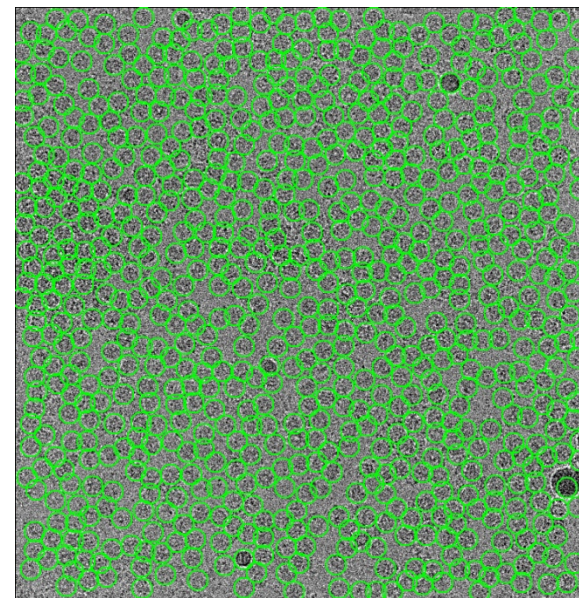
# LoGbased Auto Picking



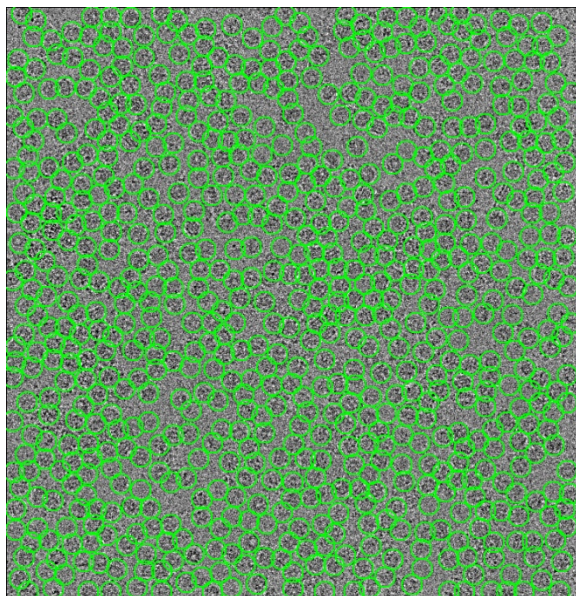
006 : 726 particles



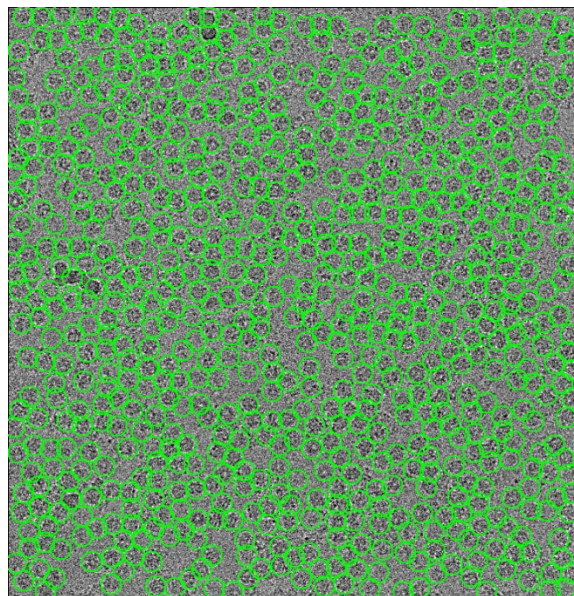
007 : 726 particles



0010 : 733 particles



0019 : 713 particles



0020 : 708 particles

a/INX6NdeInano006.mrc	<input type="button" value="pick"/>	726	<input type="button" value="CTF"/>	19895.3
a/INX6NdeInano007.mrc	<input type="button" value="pick"/>	726	<input type="button" value="CTF"/>	19207.3
a/INX6NdeInano010.mrc	<input type="button" value="pick"/>	733	<input type="button" value="CTF"/>	18995.4
a/INX6NdeInano019.mrc	<input type="button" value="pick"/>	713	<input type="button" value="CTF"/>	21145.6
a/INX6NdeInano020.mrc	<input type="button" value="pick"/>	708	<input type="button" value="CTF"/>	20288.3



# 1.6 Particle extraction

File Jobs Schedules I/O extract Helix Running Select/5mic/micrographs\_selected.star

Import  
Motion correction  
CTF estimation  
Manual picking  
Auto-picking  
**Particle extraction**  
Subset selection  
2D classification

3D auto-refine  
3D multi-body  
CTF refinement  
Bayesian polishing  
Mask creation  
Join star files  
Particle subtraction  
Post-processing  
Local resolution  
External

micrograph STAR file: 4/micrographs\_selected.star ? Browse

Input coordinates: coords\_suffix\_autopick.star ? Browse

0 AutoPick/LoG\_5mic/coords\_suffix\_autopick.star

Reset the refined offsets to zero? No ?

OR: re-center refined coordinates? No ?

Recenter on - X, Y, Z (pix): 0 0 0 ?

Alias : LoG\_5mic\_64pix

Schedule Check command Run!

I/O view Job actions Current: LoG\_5mic\_64pix Display:

I/O extract Helix Running

Particle box size (pix): 180 180 ?

Invert contrast? Yes ?

Normalize particles? Yes ?

Diameter background circle (pix): -1 ?

Stddev for white dust removal: -1 ?

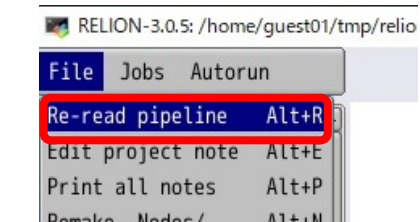
Stddev for black dust removal: -1 ?

Rescale particles? Yes Yes ?

Re-scaled size (pixels): 64 64 ?

Run!

# 1.6 Particle extraction



particles.star

Scale: 1 Min: 0 Max: 0

Sigma contrast: 0 Color: greyscale

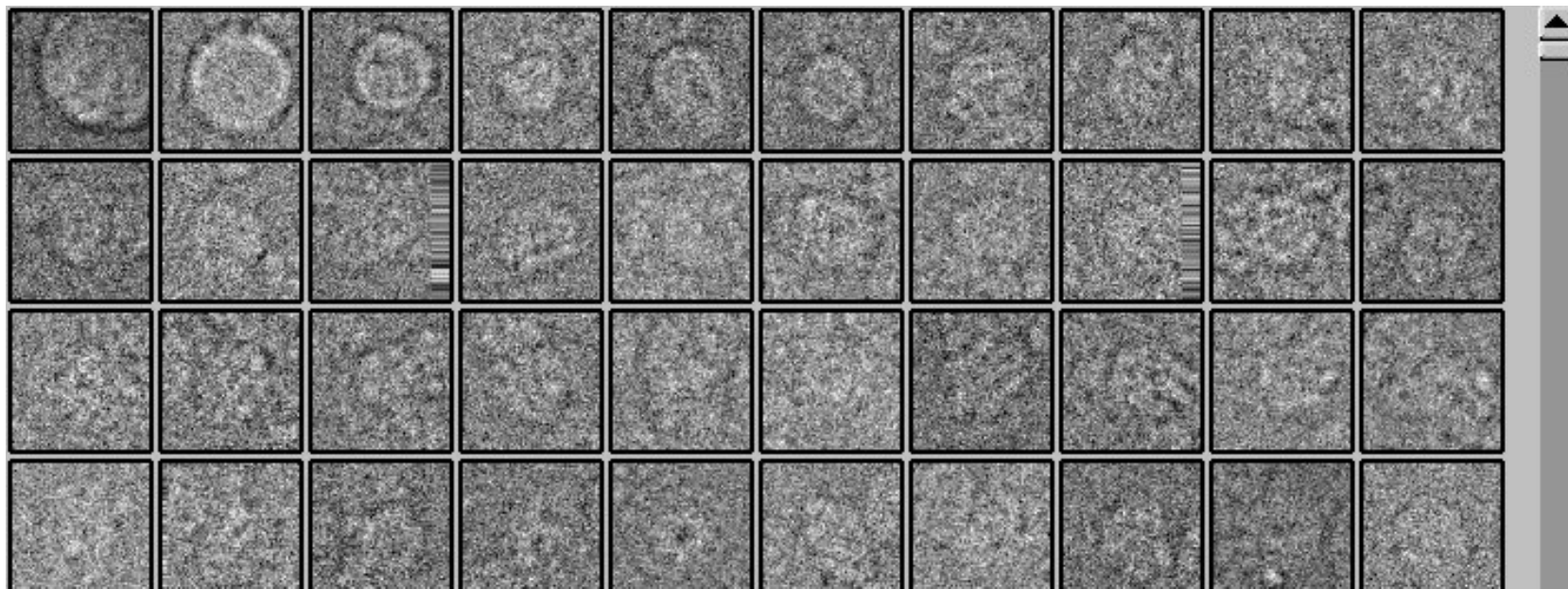
Display: rlnImageName

☐ Sort images on: rlnCoordinateX

☐ Reverse sort? ☐ Apply orientations? ☐ Read whole stacks?

Nr. columns: 10 Ori scale: 1 Max. nr. images: 1000

Display!





# 1.7 Making templates for autopicking (1分)

[2 GPU;]

File Jobs Schedules I/O CTF Optimisation Sampling Helix Compute Running

Extract/LoG\_5mic\_64pix/particles.star

Input images STAR file:  Browse

Continue from here:  Browse

2D classification

2D classification

Alias : LoG\_5mic\_64pix

Current:  Display:

Optimisation

Number of classes:  10

Regularisation parameter T:  2

Number of iterations:  25

Use fast subsets (for large data sets)?  No

Mask diameter (A):  160

Mask individual particles with zeros?  Yes

Limit resolution E-step to (A):  -1

Schedule Check command Run!

I/O CTF Optimisation Sampling Helix Compute Running

Use parallel disc I/O?  Yes

Number of pooled particles:  3

Pre-read all particles into RAM?  No

Copy particles to scratch directory:

Combine iterations through disc?  No

Use GPU acceleration?  Yes

Which GPUs to use:  0:1

I/O CTF Optimisation Sampling Helix Compute Running

Number of MPI procs:  3

Number of threads:  2

Submit to queue?  No

Queue name:  openmpi

Queue submit command:  qsub

Standard submission script:  relion-3.1/scripts/qsub.csh Browse

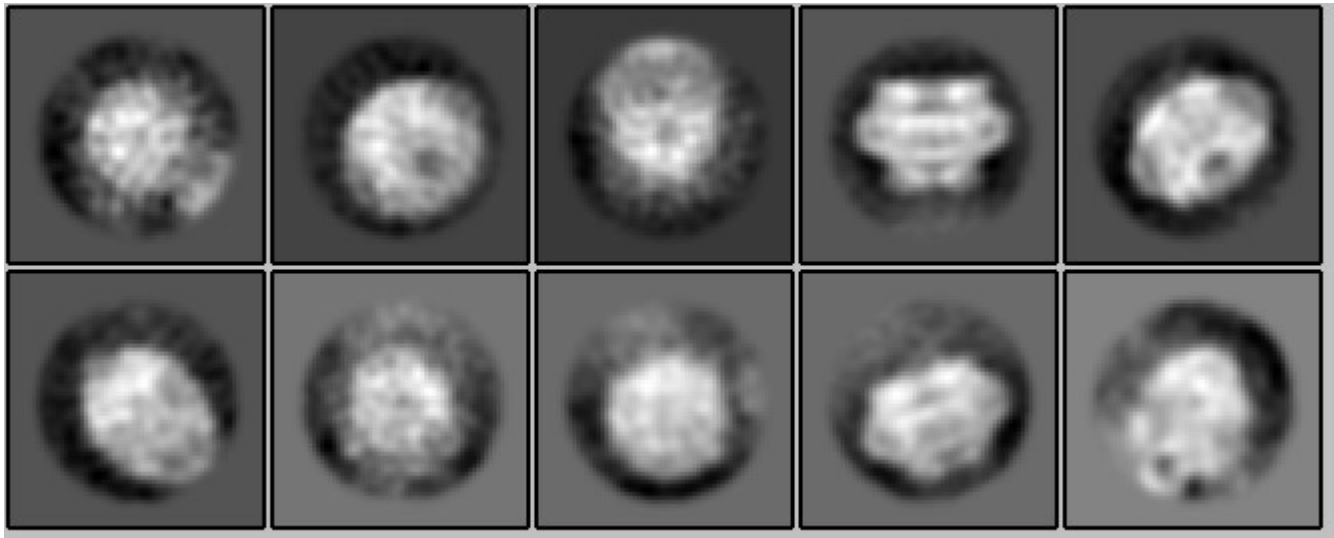
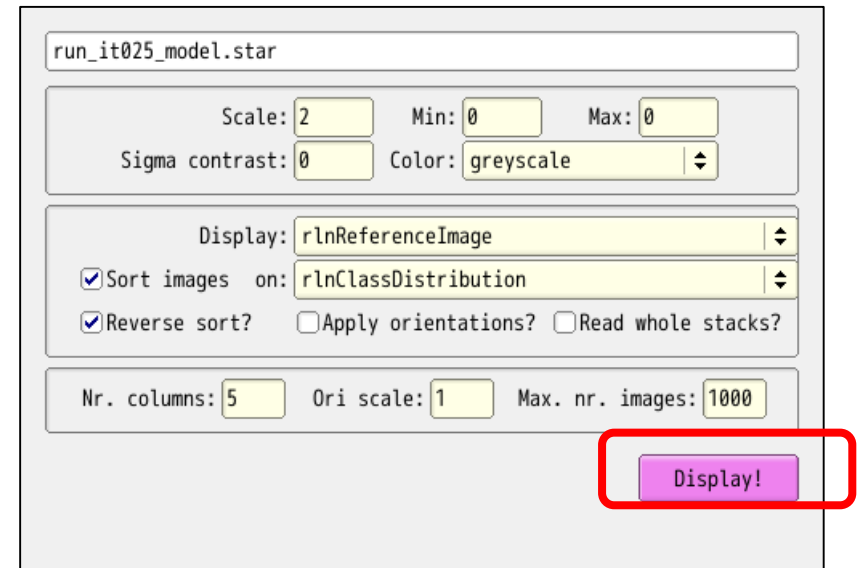
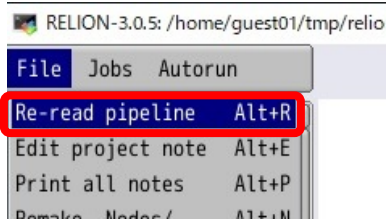
Minimum dedicated cores per node:  24

Additional arguments:

Input your GPU numbers.  
Let's use 2 GPUs !

Run!

# 1.7 Making templates for autopicking



No C8 top view....