

To be completed ONLY for 'Solution-to-Structure' Rolling Access proposal:

SAMPLE:

1. Please provide evidence on sample purity and homogeneity (SEC, DLS, SEC-MALS, etc.)
2. What is the molecular weight (**in kDa**) of the sample as estimated by biophysical characterization (gel filtration, SEC-MALS, etc). If it is a complex of several proteins, also provide the MW of all the fragments of the complex.

3. What is the sample concentration (**in mg/ml**)? What technique (nanodrop, etc) was used to measure it?

4. What is the sample buffer? Please refer to the references below and CM01 website for buffer compatibility. Please provide at least 10ml of buffer (in 2ml aliquots) for potential dilutions.

5. Please choose if any of the below has been already performed?

Negative-stain Vitrification cryo-EM grid screening None

6. If Negative-stain is chosen in #5, please indicate which **stain** was used and the outcome. **Please provide a field-of-view from the NS-EM experiment.**

7. If Vitrification is chosen in #5, please indicate **the grid types** tried and the corresponding outcome.

| | Mesh (200/300/400) | 1.2/1.3 OR 2/1 OR 2/2 OR other (specify) | outcome |
|-----------------|-----------------------|--|---------|
| Quantifoil | | | |
| C-flat | | | |
| Ultrafoil | | | |
| Other (specify) | | | |

8. If cryo-EM grid screening has been chosen in #5, please indicate the outcome and related vitrification conditions (grid type, protein concentration). **Please provide a field-of-view from the cryo-EM experiment.**

Please keep in mind that the SOS pipeline for a successful experiment finishes with the collection of a data set. Image analysis is not included and the proposer should confirm that she/he is able to perform this task.

9. Which of the below computing infrastructure(s) you have access to?

GPU CPU cryo-EM software (RELION, cryo-SPARC, etc)

10. How many cryo-EM structures have been solved from your laboratory?

0 <5 >10

11. If #8 and #9 are not applicable, do you have collaboration with a cryo-EM lab for image analysis?

If yes, please give details.

REFERENCES:

1. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5140023/>
2. <https://www.sciencedirect.com/science/article/pii/S1046202316300330>
3. <https://www.jove.com/t/52311/do-s-don-ts-cryo-electron-microscopy-primer-on-sample-preparation>
4. <https://link.springer.com/article/10.1007/s12551-019-00571-w>