**DATA ACQUISITION CRYOEM SESSION**

* Name of the PI and the scientist involved:
* Sample name/identifier:
* Sample components (protein/nucleic acids/ligands):
* Molecular weight (kDa):
* Sample preparation date and storage conditions:
* Concentration (µM) and method of measuring concentration:
* Sample volume and buffer composition:

CryoEM characterization

Cryo micrograph 1 Cryo micrograph 2 C2D averages from **500** images

(high defocus) (low defocus)

* Grid type and freezing parameters used for generating cryoEM grids:
* Number of images to generate C2D averages and average number of particles per image:

INFORMATION

* Particle concentration: Particles should populate the micrograph field of view completely. C2D averages derived from particles extracted from **500** images should exhibit discernable secondary structure features in multiple orientations.
* 3D reconstruction and particle orientation: A sub-nanometrical ( <10Å) 3D reconstruction should be obtained from **500** images with no preferential orientation issues. Map homogeneity and potential for high resolution will be considered necessary for long Krios collections.