

## Application for a Macromolecular Crystallography Rolling Proposal at the ESRF - CryoEM Time

New proposal

General Information Scientific Area **Beamlines Request** Proposers Laboratory Support Facility Sample Environment Sample Description Safety Experience Publications

### Beamline Requirements

Beamline(s) requested: \*

Principal

CM01 (CryoEM) v

Number of shifts required \*

(1 shift is 8 hours)

Preferred starting time: Please select the period \*

Unacceptable dates

### Beam Requirements

16 Bunch Mode  4 x 10mA Mode  Multi Bunch

Circular polarization

White beam

Monochromatic beam

Fixed energy [keV]:

Tunable energy [keV]

from:

to:

Beam energy resolution [%]:

Spot size on sample [ $\mu\text{m}$ ]:

Comments:

Use this field to indicate if the Phase Plate is needed and how many images should be collected

Please complete information required under all Tabs before clicking on the 'Save' button.

Back

Save

View as PDF

Save Draft

Restore Draft

\* = Mandatory Field

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General Information Scientific Area Beamlines Request Proposers Laboratory Support Facility Sample Environment Sample Description **Safety** Experience Publications

### Safety

**Is the sample:** \*

Radioactive?  Contaminant?  Corrosive?  Oxidizing?  
 Explosive?  Biologic?  None of those

**Is there any danger** associated with the proposed sample, with any preparation at ESRF, or with sample equipment? \*

Yes  Uncertain  No

*If you have ticked Yes or Uncertain, you must give details of the associated risks in the box below:*

**Will you use live animals on site for your experiment (all kinds of animals are concerned)?**  Yes  No

**After the experiment, will the sample be:**  Removed by user?  Stored at ESRF?

**Are you coming with your sample: tick first box**  
**Do you plan to send your sample for an experiment later: tick 2<sup>nd</sup> box**

Please complete information required under all Tabs before clicking on the 'Save' button.

\* = Mandatory Field

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General Information	Scientific Area	Beamlines Request	Proposers	Laboratory Support Facility	Sample Environment	Sample Description	Safety	Experience	Publications																																				
<b>Sample Description</b>																																													
Substance and formula <span style="float:right">+</span>																																													
<div style="border: 1px solid red; height: 60px;"></div>																																													
Select if applicable <span style="float:right">+</span>																																													
<input type="checkbox"/> Single crystal <input type="checkbox"/> Powder <input type="checkbox"/> Polycrystalline <input type="checkbox"/> Multilayer <input type="checkbox"/> Liquid <input type="checkbox"/> Gas																																													
<input type="checkbox"/> Nanoparticles <input type="checkbox"/> Prepared at ESRF <input checked="" type="checkbox"/> <b>frozen grids</b>																																													
<table border="0" style="width:100%"> <tr> <td>Average size (nm)</td><td><input type="text"/></td> <td>Volume (mm<sup>3</sup>)</td><td><input type="text"/></td> <td>Surface area (mm<sup>2</sup>)</td><td><input type="text"/></td> </tr> <tr> <td>Mass (mol)</td><td><input type="text"/></td> <td>Matrix or solvent</td><td><input type="text"/></td> <td>Conc of absorb (mmol)</td><td><input type="text"/></td> </tr> <tr> <td>Molecular mass (Da)</td><td><input type="text"/></td> <td>Space group</td><td><input type="text"/></td> <td>Cell dimensions at T=</td><td><input type="text"/> K:</td> </tr> <tr> <td>a=</td><td><input type="text"/> Å</td> <td>b=</td><td><input type="text"/> Å</td> <td>c=</td><td><input type="text"/> Å</td> </tr> <tr> <td></td><td></td> <td>alpha=</td><td><input type="text"/> °</td> <td>beta=</td><td><input type="text"/> °</td> </tr> <tr> <td></td><td></td> <td></td><td></td> <td>gamma=</td><td><input type="text"/> °</td> </tr> </table>										Average size (nm)	<input type="text"/>	Volume (mm <sup>3</sup> )	<input type="text"/>	Surface area (mm <sup>2</sup> )	<input type="text"/>	Mass (mol)	<input type="text"/>	Matrix or solvent	<input type="text"/>	Conc of absorb (mmol)	<input type="text"/>	Molecular mass (Da)	<input type="text"/>	Space group	<input type="text"/>	Cell dimensions at T=	<input type="text"/> K:	a=	<input type="text"/> Å	b=	<input type="text"/> Å	c=	<input type="text"/> Å			alpha=	<input type="text"/> °	beta=	<input type="text"/> °					gamma=	<input type="text"/> °
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<p>Container (capillary, flat plate, type of pressure cell, grids (type) for CryoEM, etc.)</p> <p><b>!!!</b> Extra information required for cryoEM experiments: please add sufficient proof (raw images, 3D reconstruction, class averages etc.) to your application using the appropriate method of ESRF.</p> <p>Extra information required for Macromolecular Crystallography:</p> <p>Origin and expression system <input style="width:150px" type="text"/></p> <p>Previously observed diffraction (resolution, X-ray source, exposure")</p> <div style="border: 1px solid black; height: 60px; width:100%;"></div>																																													

This can be  
useful information.

Indicate which grid, pore size etc