Submitting a CMCF Proposal for Peer-Review

Calls for Proposals normally occur twice per year for peer-reviewed access to CLS beamlines. Once approved, the proposal becomes a project, and peer-reviewed CMCF projects are valid for 2 years. Beamtime is requested under the valid project as needed. Unless there is a significant change in the project, a new proposal need only be submitted when the current valid project is nearing expiry. Proposals are submitted through the CLS User Portal (user-portal.lightsource.ca).

This document provides general guidance for the spokesperson of a lab preparing a proposal for typical macromolecular crystallography (MX) work at the CMCF. Generally, one proposal is sufficient for all MX work that a PI's lab intends to perform, but it should include all areas of intended study. Required sections are largely self-explanatory, with the information provided on the form for each section. The following additional tips are provided for consistency and successful submission.

- **Scientific Description**
    - Describe the scientific background, the current stage of the project, and the goals.
    - A strong proposal will describe a targeted scientific inquiry and may consist of several sub-projects unified by a common theme. If this is not a suitable approach, sub-projects can be described in separate paragraphs within this section.
    - *It is important to give the peer review committee a sense of the current stage of the project, including the crystallographic aspects of the work. For example, if suitable protein samples are yet to be obtained, or if crystals are available.*
    - *It is also important to give a brief description of how the structures that will be determined will advance the overall research goals.*
    - You may include some key references that will help reviewers understand the science.
- **Capability & Productivity of Team**
    - The peer review committee must be convinced the group has the capability of using the requested beam time effectively. Factors that may be taken into account include; previous experience in MX, experience collecting MX data on synchrotron beamlines, size of the team compared to goals, and training such as the CLS Mx Data Collection School. Provide enough detail to convince the committee that you have planned carefully your experiment and will make optimal use of beam time.
    - A shortlist of recent PDB depositions and/or relevant publications can be included to help demonstrate productivity and capability in the MX field.
- **Beamline / Technique**
    - Normally, choose CMCF / MX, which will allow both CMCF-BM & CMCF-ID access.
    - *Note: for non-MX projects only, such as small molecule crystallography or powder diffraction, choose CMCF-BM.*

- **Shifts**
    - Do not request particular shifts at this stage. An estimate of the total number anticipated over a typical cycle (6-month period) can be provided.
- **Experimental Procedure**
    - Normally this is simply standard macromolecular crystallography data collection for high-resolution refinement and/or experimental phasing. Data collection can be Remote, On-Site, or Mail-In. It could also include other techniques available at CMCF for particular projects; S-SAD, metal identification on crystals, EXAFS on crystals, humidity control, etc.
- **Justification of Suitability**
    - The advantages of MX at a modern beamline include high flux, tunability, high throughput capabilities, and small beam sizes. Consider how such characteristics are necessary for successful completion of the proposed project (ex: high-resolution data, SAD/MAD, metal identification, etc). Capabilities of the CMCF beamlines are found in the beamline descriptions (cmcf.lightsource.ca).
- **Samples**
    - Unless there is a particular safety concern such as toxicity, radioactivity or biohazard, for which details should be provided, most non-hazardous protein MX samples can be described similar to the following example:

        i. Name: Protein Crystals
        ii. Type: Macromolecule
        iii. State: Crystal
        iv. Description: Cooled protein crystals mounted in standard sample holders
        v. Quantity: ~50 (ie: estimate an average shipment)
- **Sample Handling Procedure**
    - Usually samples are mounted, cooled, and loaded into standard containers in the home lab (Uni-Pucks for either beamline and/or cassettes for CMCF-BM). These are delivered in standard shippers to the CLS. Containers are loaded into the beamline automounters under liquid nitrogen conditions by staff with appropriate training. Unusual safe handling procedures should be described.
- **Waste Generation & Disposal**
    - Normally MX samples are prepared in the home lab and no waste is generated at the CLS. Samples and containers are returned to the home lab after experiments are complete and do not require disposal. If planning for on-site sample preparation, describe if waste generation is anticipated or if disposal considerations are needed.