# Protein Structure Laboratory -- Work Request Form

## Instructions

Please provide the following information, which is intended to provide us with the necessary information for the project. If requested, acost estimate will be provided based on this information.

* **Type directly** onto to this Microsoft Word document; **it will expand as you type**, but please be concise, and please use 10 point Arial font for readability. **Please complete ALL sections.**
* Save the document as “Lastname - PSL Work Request” (without quotes) and submit it *electronically* to Dr. Scott Lovell, Director, Protein Structure and X-ray Crystallography Laboratory ([swlovell@ku.edu](mailto:swlovell@ku.edu))

## Work Request Parameters

| **Submission date:** |  |
| --- | --- |
| **PSL Work Request # (leave blank)** |  |
| **Project Cost Estimate: (leave blank)** |  |

## Submitter Information

| **Name** |  |
| --- | --- |
| **Department** |  |
| **Institution** |  |
| **Phone** |  |
| **Email** |  |

## Laboratory Contact

| **Name** |  |
| --- | --- |
| **Department** |  |
| **Phone** |  |
| **Email** |  |

## Work Request Information

1. **Description of work requested:** Tell us exactly what you want us to provide (i.e. define the "deliverable" or "product" you expect to receive from this work request. *Examples might include: consultation, training, protein crystallization, cocrystallization with ligands, ligand soaking of crystals, X-ray data collection and/or structure solution.*
2. **Methods.** Are there any specific methods that you recommend or request? Please provide relevant background and/or specific literature references **(attach PDF copies if available)**. Mention special precautions, if any.
3. **Will personnel from your lab be involved** in any of the work being requested? If so, please explain how:
4. **Materials to be provided by Requestor.** List materials that will be provided to us from your lab (eg. protein, buffers, etc). Explain if any of these items are "precious" (extremely costly or in very limited supply). **NOTE:** It is recommended that protein samples are concentrated between 8 to 12 mg/mL. The standard screening protocol includes four screens (384 drops) incubated at a single temperature and would minimally require of 48 L of the concentrated protein sample. If this sample volume is not available, the minimum volume necessary for crystallization screening is 12 L of the concentrated protein sample. This would provide enough of the sample for a single 96-condition crystallization screen. Protein purity is crucial for crystallization experiments. If available, please submit a picture of the SDS-PAGE gel for your final purified sample along with this work request form.
5. **Protein Information:** Please give the name and exact amino acid sequence of protein sample that will be used for crystallization: (**List ALL residues including those resulting from cloning and/or purification tags**).
   1. **Protein Name:**
   2. **Complete Amino Acid Sequence for your sample:**
   3. **Protein Purification Method.** Please describe the methods used for purification of the submitted sample. Include any chemical components such as salts, buffers, reducing agents, etc. that were utilized in the purification steps from initial lysis to delivery of the final purified sample. This is important as sometimes these materials show up in the crystal structure.
   4. **Protein Concentration (mg/mL) :**
   5. **Protein Storage Buffer, pH, concentration:**
   6. **Sample Volume (L)**
   7. **Additional Information:**  *(i.e., stability issues, disulfides, multimeric state, etc.)*
   8. **Structural Information:** If requesting a crystal structure, is the structure of your protein or a homologous protein known? If yes, please provide any relevant Protein Databank accession codes.
6. **Ligand Information:** Please provide the following information for any small molecule compounds that will be used for cocrystallization and/or crystal soaking experiments. If a solution of a particular small molecule is supplied, please provide the concentration and solvent information if applicable.

| Ligand Name / ID | Molecular Weight (g/mol) | Concentration (mM) | Solvent |
| --- | --- | --- | --- |
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Billing Information

| **Address Invoice(s) to (name)** |  |
| --- | --- |
| **Institution/Department** |  |
| **Mailing address/zip** |  |
| **Area code and phone #** |  |
| **Email** |  |

## Terms and Conditions

1. **Timing**. Requests are generally processed in the order received. If there is any "special" urgency or timing consideration, such as a looming grant application deadline, please explain here in detail.
2. **Authorship and acknowledgement policies.** Core Lab Directors and staff members often make significant intellectual or otherwise enabling contributions to the success of a research project, and recognition of these contributions is important. In such cases, it is expected that such individual(s) will be included as co-author(s) of all publications arising from or making use of the results obtained by the Protein Structure Laboratory.
3. **Research support and billing information:**  The Protein Structure and X-Ray Crystallography Laboratory operates on a fee-for-service basis. Core Lab rates are the same for all clients. In other cases, F&A surcharges may apply. Acknowledgement and authorship are not substitutes for payment of the costs of the research/service that the cores provide.
4. **Guarantee**: The PSL guarantees to perform the work requested (i.e., to execute the client-provided or client-approved protocol) competently and faithfully, and to document steps accurately, but gives no guarantee of specific outcomes on research-like projects (defined as not a repeat of a known successful protocol). The Core Lab Director will notify the Client when the project will start, and will furnish brief email updates at significant milestone events, plus a complete report at completion of the project.