**Life Science BAG Science Case**

***Please keep to the advised word count in the sections mentioned below***

***Help text can be removed before attaching the science case to the proposal.***

***Your research should demonstrate it follows the Code of best Practice in Scientific Research as described*** [***here***](https://www.diamond.ac.uk/Home/Legal-and-Compliance/Codes-of-Conduct/Code-of-Best-Practice-in-the-Conduct-of-Scientific-Research.html)***, and note that Diamond supports research that is for peaceful and humane purposes.***

***Please delete questions/information not relevant to your proposal.***

For guidance on the BAG process please [see here](https://www.diamond.ac.uk/Users/Apply-for-Beamtime/BAG-Access.html)

For XChem BAGs: please use the document found on the [XChem web-site here](https://www.diamond.ac.uk/Instruments/Mx/Fragment-Screening/XChem-Applications/BAG-Access.html)

1. **Resubmitted proposal**

If this is a resubmission of a previously rejected proposal, you must address the review panel’s previous comments here. Please make it clear why your proposal should be reconsidered.

Add Text if relevant

1. **Beamtime Requirement Summary**

Please summarise the PIs and their time required for the next 6 months in the table below.

*For MX proposals please ensure you request time on all available instruments (****MX, I24, I23, VMXi****) in anticipation that you may have projects that arise in which these beamlines would be advantageous to use during this allocation period and to provide operational flexibility to meet your needs.*

|  |  |
| --- | --- |
| **PI, Organisation** | **Beamtime Required**  (1 shift = 8 hours, please list request by instrument) |
| **Lead PI (name/affiliation)** |  |
| **Other PIs on the proposal (name/affiliation)**  A PI is defined as a group leader directing their own line of research  *(please make sure this list matches the one in UAS and any PIs no longer on the project are removed from the proposal in UAS)* |  |
|  |  |
| Add more rows if required |  |
|  |  |
| **Proposal reference number (if related to another proposal)** |  |
| **Date of proposal** |  |
| **Number of EMDB/PDB submissions in last 2 years from data on Diamond beamlines** |  |
| **Number of publications in last 2 years from data on Diamond beamlines** |  |
| **Shifts requested for 6 months: *name instrument and number of shifts*** | Are these in the proposal summary too? |
| **Shifts requested for 6 months: *name instrument and number of shifts*** | Are these in the proposal summary too? |
| **Shifts requested for 6 months: *name instrument and number of shifts (B21 requests[[1]](#footnote-2))*** |  |
| **Shifts requested: *name instrument and number of shifts (VMXi requests[[2]](#footnote-3))*** |  |

**eBIC proposals** (can be deleted if proposal is not related to eBIC)

|  |  |
| --- | --- |
| **Please indicate the number of shifts required for specific techniques** | |
| SPA/tomography |  |
| cryoFIB/SEM Lamella preparation (*please select the Aquilos instrument in UAS*) |  |
|  |  |

**B21 beamtime requests** (can be deleted if proposal is not related to B21)

|  |  |
| --- | --- |
| **Please indicate the type of sample to be investigated** (examples provided) | |
| **Name** | **Composition** |
| *Ex.* DNA repair proteins | DNA and protein (150 kDa) |
| *Ex.* Membrane channels | Protein and lipids (62 kDa) |
|  |  |
|  |  |

**VMXi beamtime requests** (can be deleted if proposal is not related to VMXi)

|  |  |
| --- | --- |
| **Please indicate the type of data to be collected** | |
| **Name** | **Yes/No** |
| Room temperature data collection |  |
| Crystallisation plate screening (grid scans) |  |

**Scientific context**

Using the headings below (3-6), cover the beamtime used and outputs from previous use of Diamond (if relevant), and the scientific case and justification for the proposed project.

1. **Scientific case for proposed project(s), including experimental plan** *(please update the science case if this is a continuation BAG - only for new BAG proposal or new projects that are not listed in the original BAG science case- up to up to a maximum of* 2000 words)

*(For projects requesting eBIC time: for either or both SPA/tomography and cryoFIB-SEM lamella preparation should include as much detail as reasonably possible, with associated preliminary data, to ensure reviewers can accurately assess them. In particular for cryoFIB-SEM lamella preparation PI requests should include data such as cryoLM/TEM atlases of cells grown on grids showing a reasonable distribution of cells. In addition, if the target protein is fluorescently labelled then cryoFM or room temperature confocal data should also be provided)*

Add text here

1. **Justification for beamtime request** *(All requests: up to 300 words per beamline requested. For B21 (bioSAXS) requests*[[3]](#footnote-4) *and VMXi requests[[4]](#footnote-5) please see the relevant footnotes)*

Add text here.

1. **Publications**

*It is essential that details are given of relevant publications (and PDB (protein databank)) depositions in case of structural biology experiments) produced in the last 2 years from work carried out at Diamond or elsewhere. (Can be deleted/omitted, if this is already reported on separately in this submission)*

Add Text

1. For *B21 requests* please consider: A typical SEC-SAXS experiments requires minimum 2 hours, 1.5 hours for equilibration and calibration and 0.5 hours for sample measurement.  Each subsequent sample will be 0.5 hours. For example: If 3 different groups are submitting 1 sample each with each in a different running buffer, that would require at least 6 hours thereby consuming a single 8 hour shift.  Batch mode experiments are approximately 3 minutes per sample. [↑](#footnote-ref-2)
2. For VMXi requests please consider the number of anticipated crystallisation plates for in situ data collection or grid screening. We anticipate around 5-8 full plates (96 well) per 8 hr shift although actual data collection time will vary depending on sample density and experimental plan. [↑](#footnote-ref-3)
3. BioSAXS (B21): please provide a separate paragraph stating justification, could be as simple as validating the crystal or cryo-EM structure proposed in the structure determination; or modelling larger complexes, determining the full-length solution structure, assessing conformational changes or testing small molecule binding.  BioSAXS is a highly complementary technique that strengthens a structural biology program. [↑](#footnote-ref-4)
4. VMXi: please provide a separate paragraph stating justification for room temperature in situ VMXi experiments. Examples could include optimisation of crystallisation conditions, room temperature data collection, assessment of intrinsic crystal quality. [↑](#footnote-ref-5)