| Requisition for PXRD Service | | | | | |
|--|----------------------|---------------|-------------|--|--|
| | _ | | | | |
| Name: | | | Date: | | |
| Email: | | | Supervisor: | | |
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| Sample Name: | | Sample no: Cl | | nemical Composition/Expected Elements: | |
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| If you enclose more than one sample make sure that they are labeled with the correct numbers | | | | | |
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| Data Collection: | | | | | |
| | ☐ Standard settings: | | | ☐ Personalized settings: | |
| | | | | | |
| | Start Angle (20) | 5 | | Start Angle (20) | |
| | End Angle (20) | 90 | | End Angle (20) | |
| | Time per step (s) | 40 | | Time per step (s) | |
| Step size (°) 0.026 A standard run takes ~10 min | | 0.026 | | Step size (°) | |
| A standard run takes - 10 mm | | | | | |
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| ☐ Return the sample after running it. | | | | | |
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Protocol for handling samples:

- Put your sample in a sample holder, wipe it with ethanol and put it in a zip-lock bag.
- Leave the bag in the tray outside the X-ray room.
- Email this requisition to Frederik Lund at fwl@sdu.dk with information about the sample and the desired settings for obtaining the diffractogram.
- All work is done with gloves and the sample holder is wiped with ethanol before it is returned to the zip-lock bag. If you do not want the sample back it will be discarded.
- Data is delivered via email.
- After the sample has been run it can be picked up in the tray outside the X-ray room.