

**Phenix User Workshop**

**Missoula, MT**

**Thursday, June 27 – Friday, June 28, 2024**

The Center for Biomolecular Structure and Dynamics at the University of Montana, together with the Phenix team, is hosting a Phenix software package workshop. Composed of lectures and hands-on tutorials, this in-person workshop will provide comprehensive training in the use of Phenix software for macromolecular structure determination from crystallographic and cryo-electron microscopy experimental data.

[**Registration**](https://umt.co1.qualtrics.com/jfe/form/SV_8H2gBXr3plfv8tE)

[**Website**](https://www.umt.edu/center-biomolecular-structure-dynamics/default.php)

**Instructors:** Pavel Afonine, Dorothee Liebschner, Nigel Moriarty, Oleg Sobolev and Christopher Williams

**Location:** Skaggs Building Room 169 on the University of Montana Campus in Missoula, MT

**Date:** Thursday, June 27, 2024, 8:30 am - 5:00 pm, Crystallography

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| **Time** | **Agenda** | **Instructor** |
| 8:30 am | Welcome/Introduction to Phenix | DL |
| 8:40 | Lecture: Steps in Crystallography (overview of Xtallography tools) | DL |
| 8:50 | Lecture: Xtriage / Data analysis (35 min) | PVA |
| 9:25 | Lecture: AlphaFold (35 min) | CJW |
| 10:00 | 15 min break |  |
| 10:15 | Tutorial: AlphaFold prediction (15 min) | OS |
| 10:30 | Lecture: SAD/MAD phasing in Phenix (40 min) | DL |
| 11:10 | Tutorial: SAD phasing (20 min) | DL |
| 11:30 | MR (lecture and tutorial) (30 min) | DL |
| 12:00 pm | 1h lunch break |  |
| 13:00 | Lecture: Refinement (60 min) | PVA |
| 14:00 | Tutorial: Refinement (30 min) | PVA |
| 14:30 pm | 15 min break |  |
| 14:45 | Lecture: Model validation (45 min) | CJW |
| 15:30 | Tutorial: Model validation (30 min) | CJW |
| 16:00 | Q/A - 1:1 session with the Phenix team | everyone |
| 17:00 pm | End |  |

**Date:** Friday, June 28, 2024, 8:30 am - 5:00 pm, cryo-EM

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| **Time** | **Agenda (cryo-EM)** | **Instructor** |
| 8:30 am | Lecture: Ligands (45 min) | NWM |
| 9:15 am | Tutorial: Ligands (45 min) | NWM |
| 10:00 am | 15 min break |  |
| 10:15 | Tutorial: Ligands continued (30 min) | NWM |
| 10:45 | Lecture: Steps in cryo-EM (20 min) | PVA |
| 11:05 | Lecture: Mtriage + map improvement (25 min) | PVA |
| 11:30 | Tutorial: map improvement + Docking + apply symmetry (30 min) | DL |
| 12:00 pm | 1h lunch break |  |
| 13:00 | Tutorial: Docking in ChimeraX (20 min) | DL |
| 13:20 | Lecture: Real-space-refine (40 min) | PVA |
| 14:00 | Tutorial: Real-space-refine (20 min) | PVA |
| 14:50 | 15 min break |  |
| 14:20 | Lecture: Advanced restraints, selection editor (30 min) | OS |
| 15:05 | Tutorial: Advanced restraints, selection editor (25 min) | OS |
| 15:30 | Tutorial: pdbtools (15 min) | CJW |
| 15:45 | Tutorial: PDB deposition (15 min) | PVA/OS |
| 16:00 pm | Q/A - 1:1 session with the Phenix team | everyone |
| 17:00 | End |  |

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A logo for a medical science company

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