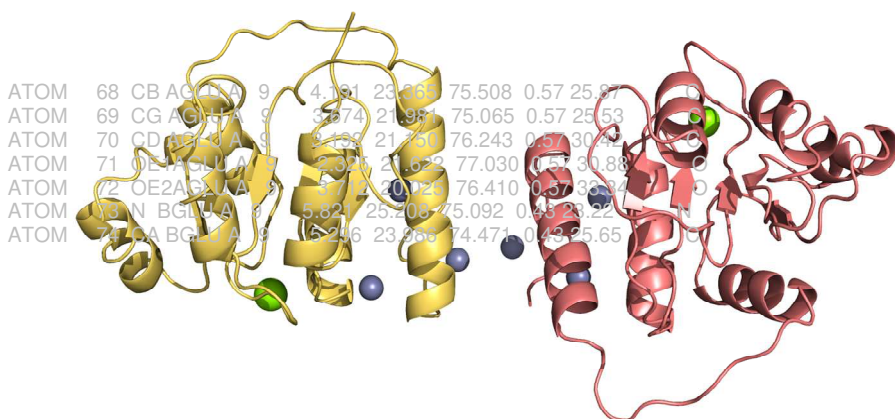


EC²/BIG-NSE workshop Microbiology at Atomic Resolution (M@AR)

January 13-16, 2020: M/T/W/Th 13:00-16:00

Instructor: Professor Katrina Forest, forest@bact.wisc.edu

Venue: Seminar room BEL301, Villa BELL, TU-Berlin



Many of us appreciate the value of three-dimensional structures of proteins and nucleic acids but are you really prepared to harvest all you can from an x-ray crystal structure without being seduced into interpreting more than you should from it?

Are you familiar with other options for gaining structural information when a crystal structure is unavailable, including electron microscopy?

Do you wish you knew how to make compelling images of three-dimensional structures using molecular graphics programs?

Would you like to get your hands on some x-ray diffraction data and see if you can solve a structure yourself?

M@AR may be the workshop you are looking for to augment your formal coursework.

Open to **senior undergraduates and graduate students in the fields of Microbiology, Genetics, Biochemistry, Biophysics, Chemical Engineering**, etc. in this course you will have opportunity for guided reading of structural biology literature, learn how structures are solved, assess structure quality, and become competent with the PyMOL molecular graphics program.

Seats are available in this small course and your participation is welcomed. You will need to bring a laptop, and install some software before the class starts (see below).

Questions? lonlon@win.tu-berlin.de for logistics, forest@bact.wisc.edu for content.

Topics and Learning Outcomes

3-dimensional crystal structures will be the basis for discussions of molecular processes that are critical to microbiology in particular, but have direct relevance to all biological systems. By studying selected proteins and nucleic acids in detail we'll learn how specific problems are solved with given protein architectures and chemistries as well as more generally how successful themes of protein structure are modified and recycled.

There will be four 3-hour meetings. We will make extensive use of computer graphics programs (especially PyMol) for 3-D emphasis as well as of databases and programs available on the World Wide Web for retrieving and manipulating structural information.

By the end of the week, you will be able to critically evaluate the quality of published structural models for biological macromolecules. Students will be competent in use of PyMol for visualizing 3D structures. Moreover, you will have a working knowledge of some common themes in structural biology which you will be able to rely on when pursuing laboratory research or reading structural biology literature outside class.

Text Book/References

Most critical: Original journal articles available via TUB electronic subscriptions.

Texts you might find useful:

Introduction to Protein Structure, Bränden and Tooze, 2nd edition (1999) Garland Publishing.

Crystal structure analysis: a primer, Glusker and Trueblood. 2nd edition (1985) Oxford University Press.

Introduction to Macromolecular Crystallography, A. McPherson. 2002, Wiley and Sons.

Proteins Structure and Function David Whitford, 2005, Wiley and Sons

On line resources you may want to make use of:

PDB (options for accessing include www.rcsb.org www.ebi.ac.uk/pdbe/ and wwpdb.org), Pymol, Swiss PDB-Viewer, Molprobability, Dyndom, Phyre2, Coot, Phenix.

To get the most out of this 4-day workshop:

Install software (Pymol, Phenix, Coot) on your own laptop in advance (*instructions will be provided*). Prepare yourself for each class. Read the papers critically, understand the background and the important knowledge gaps that lead up to a structure, and plan questions for those things you don't understand yet. Augment your reading by using PyMOL to examine structures and/or Coot to look at electron density maps. As the week goes on, remember to try to put each new structure in the context of what we may have learned already. Are there conserved folds or similar active site geometries? Are there equivalent structure determination challenges?





Instructor



Professor Katrina Forest

University of Wisconsin-Madison
Einstein Visiting Fellow at UniSysCat/EC²/BIG-NSE
forest@bact.wisc.edu

Katrina Forest is a professor of Bacteriology and Biophysics at the University of Wisconsin-Madison, USA. Currently she is as well Einstein Visiting Fellow at Technische Universität Berlin, and in particular at the Cluster of Excellence UniSysCat and the Einstein Center of Catalysis EC²/BIG-NSE.

There she is currently working on a new research project on **light-driven biocatalysis**. The highly interdisciplinary project is directed to elucidate structure-function relationships of a novel photoreceptor, a rhodopsin from abundant freshwater microbes. For two more years she will continue working together with the groups of Prof. P. Hildebrandt (TU Berlin), Prof. T. Friedrich (TU Berlin), Prof. M. A. Mroginiski (TU Berlin), Dr. P. Scheerer (Charité Universitätsmedizin Berlin), and Prof. P. Hegemann (HU Berlin), who support the project with methodological expertise in spectroscopy, theory, structural biology, and electrophysiology. The investigations will add novel components to the optogenetic tool kit for light-driven neurobiological signalling.

Professor Forest is an internationally renowned scientist who significantly advanced the field of photoreceptor research in the past years, i.e., by the first high-resolution structure determination of phytochrome, the generation of far-red fluorophores with applications in imaging, and substantial contributions towards understanding formation and stability of the unusual knot in the phytochrome typology.



Tentative Schedule

Monday 13.1.20

Theory

Protein structure whirlwind overview

Crystallography Concepts I: Macromolecular crystals – why are they useful and how are they obtained?

Practice

PyMOL Installation Check and Tutorial

Reading: Structure Determination Review and a Classic Oligomeric Motor Protein

Wlodawer review article, FEBS 2013

The Walker A motif in RecA & motor proteins

Tuesday 14.1.20

Theory

Crystallography Concepts II: Crystallographic data

Practice

Verify *PHENIX* and *COOT* software installation, public data bases.

Readings: Large and Small, High and Low Resolution

Low resolution but informative

Extremely high resolution

Wednesday 15.1.20

Theory

Crystallography Concepts III: The Phase Problem

Practice

DIY structure solution: Phenix and molecular replacement

Readings: Signaling and Catalysis

Light-regulated cyclase

Superoxide dismutase

Thursday 16.1.20

Theory

Crystallography Concepts IV: Structure Refinement and Analysis

Practice

DIY structure solution: fitting electron density and refinement

Readings: Membrane Proteins

Inner membrane helical proteins – rhodopsin

Outer membrane beta barrel proteins – maltoporin

