

STRUCTURAL BIOLOGY COURSE SCHEDULE

Mon (Apr 17th) Meeting Room B

09:30-09:45 Welcome address (S. M. R.)

09:45-10:45 Structural Biology: Overview (S. M. R.)

11:00-12:00 CryoEM (C. T.)

12:00-13:00 Structural analysis of RNA polymerases (C. T.)

LUNCH

14:30-15:30 Protein Crystallography: Overview (P. P.)

16:00-17:30 Recombinant protein expression and purification (F. F. S.)

Tue (Apr 18th) Meeting Room B

09:30-11:00 Principles of X-ray Crystallography (D. d. S.)

11:15-12:45 Model Building and Refinement (U. B.)

LUNCH

14:00-15:00 Laser Diffraction Practical (P.P)

15:30-17:00 PDB and PyMOL (S.M.R.)

Wed (Apr 19th) Meeting Room B

9:30-10:45 A tale of two metals (D. d. S.)

11:15-12:30 The Collagen Chaperone HSP47 in Health and Disease (U. B.)

LUNCH

15:00-16:30 Q&A Open Session

Thu (Apr 20th) Meeting Room B

09:30-11:00 Synchrotron Radiation in Structural Biology (D. d. S.)

11:15-12:30 Natural anticoagulants (P. P.)

LUNCH

Mariano Gago Auditorium

14:00-16:00 Remote synchrotron data collection practical (D. d. S.)

16:00-18:00 Data processing, structure solution, and model building (D. d. S.)

Fri (Apr 21st) Meeting Room B

9:30-10:45 Regulation of the activity of K⁺ channels and transporters (J. M. C.)

11:00-12:15 Protein folding and misfolding in neurodegenerative diseases (S. M. R.)

LUNCH

14:30-16:30 Evaluation exercise

Course Tutors:

Sandra de Macedo Ribeiro (Protein Crystallography Group, IBMC/i3S, Porto)

Pedro J. B. Pereira (Biomolecular Structure Group, IBMC/i3S, Porto)

João Morais Cabral (Structural Biochemistry Group, IBMC/i3S, Porto)

Frederico Ferreira da Silva (B2Tech – Biochemical and Biophysical Technologies, IBMC/i3S, Porto)
Carlos Fernández Tornero (Structure of Macromolecular Assemblies Group, Centro de Investigaciones Biológicas – CIB, Madrid)
Daniele de Sanctis (Structural Biology Group, ESRF – European Synchrotron Radiation Facility, Grenoble)
Ulrich Baumann (Department für Chemie, Universität zur Köln, Köln)

Suggested Bibliography:

Protein crystallography and structure analysis

1 - *International Tables for Crystallography* (2006). Vol. F, Chapter 1.1, pp. 1–63

2 - G. Rhodes (2006). *Crystallography Made Crystal Clear: A Guide for Users of Macromolecular Models*. Academic Press, Burlington. ISBN 9780125870733.

3- Minor Jr., D.L. (2007). The Neurobiologist's Guide to Structural Biology: A Primer on Why Macromolecular Structure Matters and How to Evaluate Structural Data. *Neuron* 54: 511–533 (<http://www.ncbi.nlm.nih.gov/pubmed/17521566>)

4 - Cowieson, N.P., Kobe, B., Martin, J.L. (2008). United we stand: combining structural methods. *Curr Opin Struct Biol* 18:617-22. (<http://www.ncbi.nlm.nih.gov/pubmed/18755272>)

5 - Lander, G.C., Saibil, HR., Nogales. E. (2012). Go hybrid: EM, crystallography, and beyond. *Curr Opin Struct Biol*. 22:627-35. (<http://www.ncbi.nlm.nih.gov/pubmed/22835744>)

6 - Dyer, K.N., Hammel, M., Rambo, R.P., Tsutakawa, S.E., Rodic, I., Classen, S., Tainer, J.A., Hura, G.L. (2014). High-throughput SAXS for the characterization of biomolecules in solution: a practical approach. *Methods Mol Biol*. 1091:245-58. (<http://www.ncbi.nlm.nih.gov/pubmed/24203338>).

7 - Petoukhov, M.V., Svergun, D.I. (2013). Applications of small-angle X-ray scattering to biomacromolecular solutions. *Int J Biochem Cell Biol*. 45:429-37. (<http://www.ncbi.nlm.nih.gov/pubmed/23235262>)

Additional Reading:

History of Crystallography: <http://onlinelibrary.wiley.com/doi/10.1111/febs.12796/full>

Protein Crystallography for non-crystallographers:
<http://www.ncbi.nlm.nih.gov/pubmed/18034855>

Software (to be installed on students' machines):

CCP4 (<http://www.ccp4.ac.uk/download/index.php> ; OS X users must have X11 installed – see <https://www.xquartz.org/>)

COOT (http://www.yesbl.york.ac.uk/~lohkamp/coot/wincoot_newest_download.php (for Windows), <http://psbmini.ucsc.edu/~wgscott/coot/stablereleases/> (for OS X), <https://www2.mrc-lmb.cam.ac.uk/personal/pemsley/coot/binaries/release/> (for Linux))

PyMOL (<http://pymol.org/edu/?q=educational/>)