GABBA AND MCBIOL PHD PROGRAMMES

STRUCTURAL BIOLOGY COURSE SCHEDULE

Monday (April 23th) **Meeting Room A**

10:00-10:20	Welcome address (S. M. R.)
10:20-12:00	Structural Biology and Protein Crystallography Overview (P. P.)
LUNCH	
14:00-15:00	Biological Small Angle X-ray Scattering: principles and applications (J.A.M.)
15:30-16:30	Natural anticoagulants (P.P.)
17:00-18:00	Polyglutamine disorders: more than simple repeats (S. M. R.)

Tuesday (April 24th) **Meeting Room B**

9:00-10:30	Structural and functional studies of membrane proteins (J. M. C.)
11:00-13:00	Computational Approaches to Predict and Refine the Structure of Proteins (J.C.)
LUNCH	
14:30-16:00	**PRACTICAL 1:** MODEL BUILDING (Groups I, II) – 115S2 **PRACTICAL 2:** How to read a Structural Biology paper; PDB AND PYMOL (Groups III, IV) – Room B
16:00-17:30	**PRACTICAL 1:** MODEL BUILDING (Group III, IV) – 115S2 **PRACTICAL 2:** How to read a Structural Biology paper; PDB AND PYMOL (Groups I, II) – Room B

Course Tutors:

Sandra de Macedo Ribeiro (Biomolecular Structure and Function Group, IBMC/i3S, Porto)
Pedro J. B. Pereira (Macromolecular Structure Group, IBMC/i3S, Porto)
José António Manso (Macromolecular Structure Group, IBMC/i3S, Porto)
João Morais Cabral (Structural Biochemistry Group, IBMC/i3S, Porto
João Coimbra (Dept. Química e Bioquímica, Fac. Ciências, Universidade do Porto)

Suggested Bibliography:
Protein crystallography and structure analysis

1 – A. L. Lamb, T. J. Kappock and N. R. Silvaggi (2015). You are lost without a map: Navigating the sea of protein structures. Biochim Biophys Acta 1854: 258–268. (https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5051661/)

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 Biol18:617-22. (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)

Protein Interactions and Computational Biology:

1 – Kastritis, P.L., Bonvin, A.M. (2013). On the binding affinity of macromolecular interactions: daring to ask why proteins interact. J R Soc Interface. 10:20120835. (http://www.ncbi.nlm.nih.gov/pubmed/23235262)

2- Moreira, IS; Fernandes, PA; Ramos, MJ (2010). Protein-Protein Docking: Dealing with the Unknown, J. Comput. Chem. 31: 317 (http://www.ncbi.nlm.nih.gov/pubmed/19462412)

3- Sousa, SF; Ribeiro AJM; Coimbra JTS; Neves, RPP; Martins, SA; Moorthy, NSHN ; Fernandes, PA; Ramos, MJ (2013). Protein-Ligand Docking in the New Millennium - A Retrospective of 10 Years in the Field, CURRENT MEDICINAL CHEMISTRY 20: 2296-2314 (http://www.ncbi.nlm.nih.gov/pubmed/23531220)

4 - Sousa, SF; Fernandes, PA; Ramos, MJ (2006). Protein-ligand docking: Current status and future challenges. Proteins 65: 15. (http://www.ncbi.nlm.nih.gov/pubmed/16862531)

5 – S. A. Adcock, and J. A. McCammon (2006). Molecular Dynamics: Survey of Methods for Simulating the Activity of Proteins. Chem. Rev. 106: 1589-1615. (https://pubs.acs.org/doi/abs/10.1021/cr040426m)

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

Protein crystallography for aspiring crystallographers or how to avoid pitfalls and traps in macromolecular structure determination
: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4080831/