Dr Andy M. C. Lau

07568 578021 - andy.m.lau@outlook.com

Personal Website: andymlau.com

Github: https://github.com/andymlau

Linkedin: https://www.linkedin.com/in/andymlau/

PROFILE

I am a Postdoctoral Research Associate currently based at King's College London.

My main research interests are in the characterisation of protein structure, dynamics and their interactions with other biomolecules using computational methods such as machine learning. I developed *Deuteros (publication 5)*, an easy to use GUI that performs analysis and visualisation of data from hydrogen-deuterium exchange mass spectrometry (HDX-MS).

EXPERIENCE

King's College London
Oct 2019 - current

Postdoctoral Research Associate

Developing software for processing of hydrogen deuterium exchange-mass spectrometry data.

Moleculomics Ltd.
Jan 2018 - May 2018

Researcher in Structural Bioinformatics

Developing machine learning methods for the automated prediction of protein-protein interfaces across the entire human genome for high-throughput screening of drug targets.

UCL
July 2014 - Feb 2015

Research Student

Supervisors: Dr Lindsay McDermott, Professor Stephen Perkins, Dr Alun Coker
Obtained the first crystal structure of zinc-a2-glycoprotein in complex with a fatty acid.
See publications 3 and 12.

EDUCATION

King's College London
Sep 2015 - Sep 2019

Doctor of Philosophy (pass with no corrections)

Supervisors: Dr Argyris Politis & Professor Franca Fraternali

Thesis title: "Dynamics of macromolecular complexes using computational modelling and structural mass spectrometry". Part of the BBSRC London Interdisciplinary Biosciences PhD Consortium led by University College London.

My research involves developing computational workflows for modelling of large and heterogeneous macromolecules such as antibodies and multi-subunit protein complexes.
Relevant publications: 1, 4, 5, 6, 10, 11.

King's College London
Sep 2012 - July 2015

Bachelor of Science in Biochemistry (First Class Honors)

Awarded the King's Experience Research Award (Nov, 2014) for research work within the competitive King's Undergraduate Research Fellow scheme.

Dr Andy M. C. Lau

07568 578021 - andy.m.lau@outlook.com

Personal Website: andymlau.com

Github: https://github.com/andymlau

Linkedin: https://www.linkedin.com/in/andymlau/

RESEARCH OUTPUT

1. **Lau, A. M. C**, Politis, A. Integrative mass spectrometry-based approaches for modelling macromolecular assemblies, ***Methods in Molecular Biology***, (in press)

2. Martens, C. et al. (2019) Integrating Hydrogen-Deuterium exchange mass spectrometry (HDX-MS) with Molecular Dynamics (MD) simulations to probe lipid-modulated conformational changes in membrane proteins, ***Nat. Protoc.***, DOI: 10.1038/s41596-019-0219-6.

3. **Lau, A. M. C.** et al. (2019) Crystal structure of zinc-a2-glycoprotein in complex with a fatty acid reveals multiple modes of lipid binding, ***Biochem. J.***, pii: BCJ20190354. doi: 10.1042/BCJ20190354

4. **Lau, A. M. C.** et al. (2019) Structural basis of Cullin 2-RING E3 ligase regulation by the COP9 signalosome. ***Nat. Comms.***, 10: 3814.

5. **Lau, A. M. C.** et al. (2019). Deuteros: software for rapid analysis and visualisation of data from differential hydrogen deuterium exchange-mass spectrometry. ***Bioinformatics***, btz022, http://doi.org/10.1093/bioinformatics/btz022

6. **Lau, A. M. C.** et al. (2018). A mass-spectrometry-based modelling workflow for accurate prediction of IgG antibody conformations in the gas phase. ***Angew. Chem.***, DOI: 10.1002/anie.201812018.

7. Martens, C. et al. (2018). Direct protein-lipid interactions shape the conformational landscape of secondary transporters, ***Nat. Comms.***, 9, 4151, 9 (1).

8. Ahdash, Z., **Lau, A. M. C.**, et al. (2018). Analysing protein architectures and protein- ligand complexes by integrative structural mass spectrometry. ***J. Vis. Exp.***, 140, 57966.

9. Pyle et al., (2018). Structural lipids enable the formation of functional oligomers of the eukaryotic purine symporter UapA. ***Cell Chem. Biol.*** 25 (7): 840-8.

10. Ahdash, Z., **Lau, A. M. C.**, et al. (2017). Mechanistic insight into the assembly of the HerA-NurA helicase-nuclease DNA end resection complex. ***Nucleic Acids Res.*** 45 (20): 12025-38.

11. Schmidt, C., **Lau, A. M. C.**, et al. (2017). Surface accessibility and dynamics of macromolecular assemblies captured by covalent labelling mass spectrometry and molecular simulations. ***Anal. Chem.***, 89 (3): 1459-1468.

12. Zahid, H., **Lau, A. M. C.**, et al., (2016). Zinc-induced oligomerisation of zinc a2 glycoprotein reveals multiple fatty acid binding sites. ***Biochem. J.***, 473 (1), 43-54.

SKILLS

Programming:	MATLAB, Python, Bash, experience with HPCs
Software:	MacOS, MD with GROMACS, very experienced with scientific figures
Languages:	English (Native Proficiency), Cantonese (Spoken)

REFERENCES

Dr Argyris Politis

Lecturer in Chemical Systems Biology, King's College London, UK
+44 (0)20 7848 7514 | argyris.politis@kcl.ac.uk

Professor Stephen Perkins

Professor of Structural Biochemistry, University College London, UK
+44 (0)20 7679 7048 | s.perkins@ucl.ac.uk