MS010.O03

Challenges and opportunities in structure determination of membrane proteins

Isabel Moraes[1]
[1]*Diamond Light Source, Didcot, United Kingdom*
E-mail: isabel.de-moraes@diamond.ac.uk

Over the years membrane proteins have fascinated scientists for playing a fundamental role in many critical biological processes. Located across the native cell membrane or mitochondria wall, integral membrane proteins perform a large diversity of vital functions. Mutations or improper folding of these proteins are associated with many known diseases such Alzheimer's, Parkinson's, cancer and many others. It is estimated that more than one quarter of the human genome codes integral membrane proteins and therefore imperative to investigate the role of these proteins in human health and diseases. Currently around 60% of the drugs on the market target membrane proteins.

At the present, around 680 unique membrane proteins structures are available in the Protein Data Bank. The advent of genomics and proteomics initiatives combined with high-throughput technologies such as automation, miniaturisation, integration, third-generation synchrotrons, the use of XFELs and EM have enhanced membrane protein structure determination rate.

X-ray crystallography is still the only method capable of providing detailed information on how ligands, co-factors and ions interact with proteins, therefore a powerful tool in biochemistry and drug discovery. Nevertheless the growth of membrane protein crystals suitable for X-ray diffraction studies amazingly remains a fine art and a major bottleneck in the field. Therefore it is often necessary to apply as many innovative approaches as possible. In this talk attention will be drawn to the latest methods and strategies for the production of suitable membrane protein crystals and data collection from such demanding crystals.

[1] Isabel Moraes (ed.) (2016). Springer, Advances in Experimental Medicine and Biology, Vol 922
[2] Moraes, J. & M. Archer (2014). Springer, Methods in Molecular Biology 2nd edition, Ray Owens (ed.)
[3] D. Axford et al. (2012) In situ macromolecular crystallography using microbeams. Acta Cryst. D68. 592-600

Keywords: Membrane Proteins