Centre for Cryo-electron Microscopy of Membrane Proteins

SEMINAR SERIES 2022

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Michelle Dunstone is a former ARC Future Fellow who has recently moved to a teaching and research role in the Department of Biochemistry and Molecular Biology, Biomedical Discovery Institute, Monash University. She obtained her Honours degree in Biochemistry (Monash University) and her PhD in the lab of Prof Michael Parker (St Vincent's Institute/University of Melbourne) (2005). In her PhD she studied the MACPF class of pore forming proteins of the human immune system.
While the project did not yield any published results during her PhD, she was able to make a breakthrough in 2007 with the first representative structure of a MACPF pore forming protein (Science (2007)) followed by cryo-EM structures of the many different MACPF/CDC proteins: pleurotolysin, MAC and MPEG1 (PLoS Biology (2015), and Nature communications (2016, 2018, 2019)).

Michelle's expertise was recently recognised in the award of a 2020 Georgina Sweet Award for Women in Quantitative Biomedical Science. She passionately believes in the promotion of the niche pore forming protein community and, to this end, co-founded and led the Prato Pores conferences series, the only international conference dedicated to pore forming proteins.

Discovering how pore forming proteins evolve different assembly and targeting mechanisms

Pore forming proteins are proteins that can literally punch holes (pores) into target cell membranes. There are over 30 different types of pore forming proteins that have evolved independently but one of the most fascinating is the MACPF/CDC superfamily. The MACPF/CDC proteins can oligomerise into a ring-shaped transmembrane beta-barrel pore capable of either direct cell lysis or the passive transport other large protein toxins. Members of the MACPF/CDC superfamily are found in all kingdoms of life with a range of functions including as immune effectors, pathogenicity factors, parasite egress, fungal defence and marine toxins. Whilst current structural biology research on the MACPF/CDC family suggest there is a common domain and a common pore structure for the family, there is a wide variation in the assembly pathways observed. Recent research using combinations of structure and single molecule imaging methods explains how and why different members have evolved different assembly pathways to suit their evolved function.