sptlabtech

Team interviews – **chameleon**

Tim Booth

CryoEM Business Development Manager

01 What is it that excites you about working with a new product like chameleon?

There is a lot about the chameleon that is different from any other plunge freeze device on the market or otherwise. It introduces chameleon-specific concepts and experimental control unavailable elsewhere. Because of that it represents a shift in how to think about sample preparation and how it relates to the rest of the workflow. Traditionally in cryoEM we've engaged with lots of iterative trial and error methods to deal with challenging specimen or the negative effects of blotting. With chameleon we have a platform to experimentally determine how each unique specimen behaves during vitrification and then can optimize for ideal specimen around that behavior. It has been exciting working with customers as they relearn sample preparation and how to use chameleon to optimize the vitrification process for their specimen instead of optimizing the specimen to work on a standard device.

02 How does chameleon support the future of cryo-EM?

Structure determination is becoming an integral part of the process to answer biological questions and less as an endpoint to confirm biochemistry. As we see the technological landscape evolve further to include more affordable and local cryoEM screening microscope resources, the need for improved sample quality and a reproducible sample preparation platform available at the bench becomes increasingly important. chameleon moves the goal posts of the screening process towards better specimen and higher resolutions, improving the practicality of preliminary structure determination that can feedback into biochemical optimization workflows.

03 What benefits do you see chameleon delivering to the bench scientist?

The most challenging aspect of structural biology today remains to be obtaining well-behaved protein samples that are stable enough to undergo structural characterization. The foundation of a high resolution cryoEM structure is biochemical optimization with each unique sample requiring gel filtration, SDS-PAGE analysis, mass spectrometry, and functional assays to determine purity ahead of freezing. This optimization happens at the bench while traditional sample prep for cryoEM happens at the microscope in expert hands. Providing a resource to capture timely biochemistry in ice at the bench with reduced variability due to handling can minimize unnecessarily long initial research cycles and open pathways to preliminary data needed for centralized cryoEM resource applications.

04 How do the advantages gained from chameleon differ across a range of labs and facilities?

There is no doubt that the facility models of academic institutions, large government centralized resources, and pharma differ drastically. Even so, the future of CryoEM depends on all three to meet the needs of a growing diverse research community. The efficient operation of each model depends heavily on specimen quality. The less resources allocated to specimen screening on high end infrastructure, the more time available for high quality data collection. The faster initial research cycles are completed, the more effort can be placed on better biochemical optimization. With the high quality and reproducible samples prepared by chameleon, shared community resources often overcome by iterative trial and error workflows are made available to more projects and users.

To learn more about chameleon and our team of experts click here