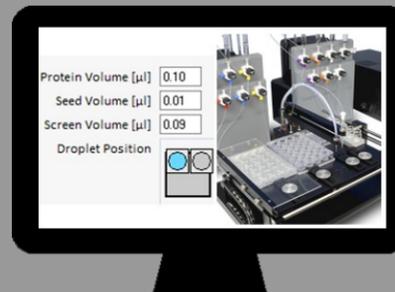


For more information

Request an online demonstration or
webinar for your lab

Carolyn@douglas.co.uk



Douglas Instruments
Success in protein crystallization

How to pre-screen your samples with in-plate DLS

Dear Crystallographer

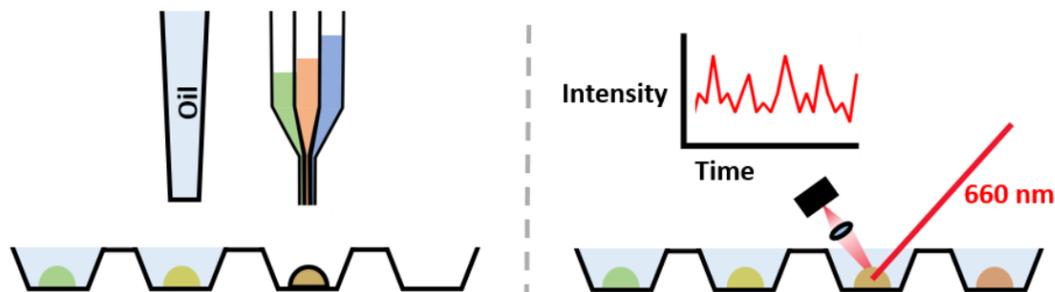
Screening with DLS

Dynamic light scattering provides a straightforward probe of protein quality in solution, particularly in relation to stability and aggregation (Kwan 2021). Nanoliter-sized drops are analysed in-plate using the **Spectrolight 600** from Xtal Concepts. Under-oil drops are accurately dispensed using a Douglas Instruments **Oryx4** or **Oryx8** robot.

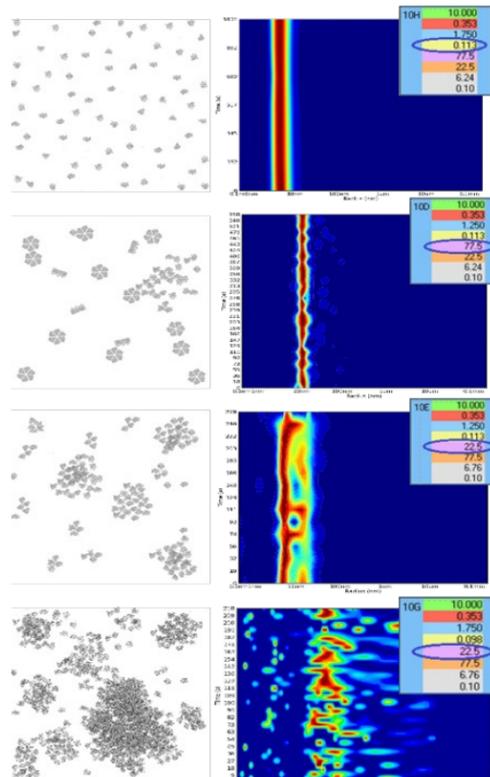
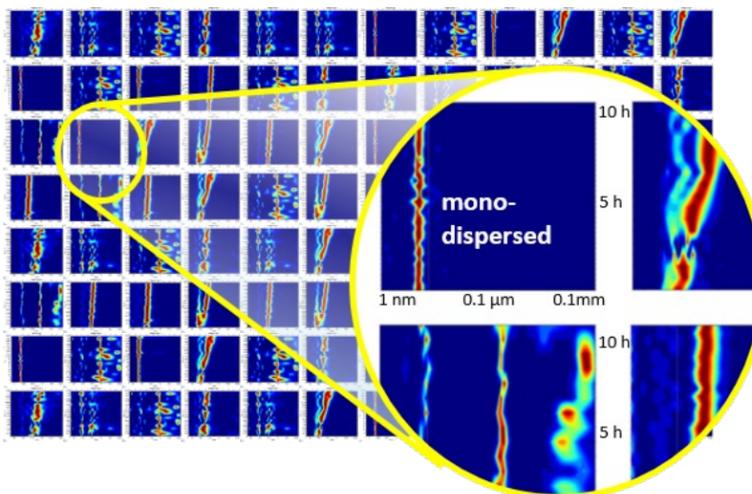
Typically drops from 140 nL total volume are dispensed by the robot before being automatically covered with 10 µL of paraffin oil. Readily available 96 well screens can be used including stability, buffer and detergent screens.

96 Well in-plate DLS

Measurements taken using the Spectrolight 600 are used to calculate the polydispersity of the sample.



Results from 96 well screens can be viewed as 'heat maps'.



The heat maps show radius on the x-axis and time on the y-axis.

- Characterization of biomolecules for further evaluation by CryoEM, NMR, SAXS or Crystallization
- Operates using Douglas Instruments **Vapor Batch plates** to perform high-throughput analysis.
- Assess homogeneity aggregation and assembly state
- Investigate protein interactions, e.g. oligomerization, aggregation, denaturation and receptor-ligand interactions
- Only 7.0 µL of protein required for a 96-well experiment (70 nL protein per drop)

Request more information

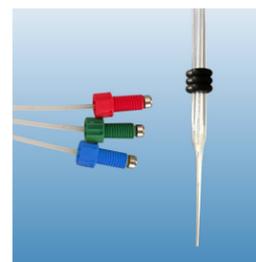
Douglas Instruments Products



Oryx Robots



Crystallization Plates



Oryx Microtips

Conferences:

Douglas Instruments is attending the following meetings:

BCA and BACG Joint Online Meeting 2021

29 March - 1 April 2021

IUCr 2021, Prague, Czech Republic

14 August - 22 August 2021

Recently published research using Oryx protein crystallization robots:

Diversity of Omega Glutathione Transferases in mushroom-forming fungi revealed by phylogenetic, transcriptomic, biochemical and structural approaches

Perrot, T., Schwartz, M., Derooy, A., Girardet, J.M., Kohler, A., Morel-Rouhier, M., Gelhaye, E. and Didierjean, C.

Fungal Genetics and Biology (2021): 103506.

Granulovirus PK-1 kinase activity relies on a side-to-side dimerization mode centered on the regulatory α C helix

Oliver, M.R., Horne, C.R., Shrestha, S., Keown, J.R., Liang, L.Y., Young, S.N., Sandow, J.J., Webb, A.I., Goldstone, D.C., Lucet, I.S. and Kannan, N.

Nature Communications 12.1 (2021): 1-11.

