Sample Preparation for Routine and Advanced Structural Biology, Including Serial Data Collection, Microed, And Cryoem

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Serial data collection usually requires relatively small crystals that are well-ordered. Microseeding is an effective way to generate such samples. During the ten years since the random microseed matrix-screening (rMMS) method was published, understanding of the theoretical advantages of the method has increased [2 - 4], and several practical variations of the method have emerged. Moreover seeding can be carried out in a microbatch-under- oil setup, which is easy to scale up, volume-wise, and allows easy interpretation of phase diagrams. By combining these techniques, control can be increased and sample quality for both routine and advanced data collection improved.

Protein structure determination by cryoEM requires expensive equipment that has low throughput. It is therefore wasteful to examine samples that can be shown in advance to be aggregated, since such samples are unlikely to be suitable. We used a high-throughput screening approach with dynamic light scattering to explore 96 chemical conditions with as little as 10 µL of protein solution to identify conditions with reduced aggregation.

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