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Microlytic MCSG Suite

The MCSG Suite has been developed at the Midwest Center for Structural Genomics. As part of the Protein Structure Initiative, MCSG has been instrumental in the development of rapid, integrated, and cost-effective methods for protein structure determination via X-ray crystallography.

- ★ Most up-to-date set of crystallization conditions for initial screening
- ★ Contains the highest number of crystallization conditions from deposited structures in the PDB[1]
- ★ 384 crystallization conditions, optimized through high-throughput validation
- ★ Non-redundant conditions constitute the broadest coverage of crystallization space of any commercially available screen
- ★ Screen has crystallized proteins from both prokaryotic and eukaryotic organisms

The 384 conditions of the MCSG Suite comprises 4 screens of 96 unique conditions that are available in either 1.7 ml deep well block, or 10 ml tube format.

How does the Microlytic MCSG Suite improve your current vapor diffusion pipeline?

The last two decades have seen a rapid expansion in the number of commercially available screens, each with distinguishing design rationales. In most laboratories, multiple crystallization screens are kept on hand without the following:

- a clearly defined workflow to establish the order in which screens should be used
- guidance in differences of design rational or coverage of crystallization space
- an easy reference to determine the level of redundancy between two reagent sets

As a result, much of the crystallization screening becomes highly redundant, increasing the protein requirements without a commensurate increase in crystallization outcome.

To support preferred vapor diffusion workflows, we introduced the MCSG Crystallization Suite, developed at the Midwest Center for Structural Genomics at Argonne National Laboratories through Phases I and II of the Protein Structure Initiative. The MCSG Suite has been developed as a single, comprehensive set of crystallization conditions to be used in a stand-alone manner.

The end result is the best, first-pass screening suite possible, with:

- data-driven selection of individual conditions based on crystallization experiments at the MCSG to yield the most productive crystallization conditions
- superior organization: conditions are ranked by productivity
- the broadest coverage of crystallization space within a reasonable amount of conditions
- applicability to unique and difficult proteins

Reference:

1. Fazio, Vincent J., Peat, Thomas, S. and Newman, Janet (2014) in *Acta Crystallographica Section F, Structural Biology Communications*, International Union of Crystallography, **F70**, 1303–1311.

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