Classical Crystal Growth Screening

Molecular Dimensions

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Structure Screens™

The classic screens began with the original publication by Jancarik & Kim in 1991[1]. A later extension to the screen was based on further conditions found to be successful in the crystallization of biological macromolecules[2]. Further work a decade later led to a minimal redundancy sparse matrix screen of only 24 reagents[4]. Heavy plus light approaches allow for separation of nucleation from crystal growth[5].

- The original sparse matrix screen [1].
- An extension[2] with novel precipitants and combinations.
- Enhanced buffer selection[3].
- Sparse matrix formula efficiently samples salts, polymers, organics & pH.
- Proven effective with more than 1,000 biological macromolecules.
- Minimal redundancy version optimises probability of successfully obtaining a crystal[4].
- Separate nucleation from crystal growth[5] with a heavy plus light approach to obtain larger, better diffracting crystals compared to conventional methods[5].

References

1. Jancarik, J. & Kim, S.H. J. Appl. Cryst. (1991), **24**, 409-411.
2. Cudney, R., Patel, S., Weisgraber, K., Newhouse, Y., and McPherson, A., Acta Cryst. (1994) **D50**, 414-423.
3. Wooh *et al* Acta Cryst. (2003) **D59**, 769 – 772.
4. Kimber M.S. *et al.*, (2003), Proteins: Structure, Function, and Genetics **51**, 562-568.
5. Saradakis & Chayen, (Protein Science (2000) **9**:755-757.

The Solubility Tool Kit™

A systematic alternative to sparse matrices to determine the solubility and crystallization potential of protein salts [1 - 4].
The Solubility Tool Kit is manufactured under an exclusive license from CNRS/ Université René Descartes (Paris V), France.

- Provides the best starting conditions for the right buffer, pH and salt.
- Rapidly identifies likely crystallization reagents and their suitable range of concentration.
- Locate the nucleation zone of a protein and prepare phase diagrams.
- Can be performed with batch, vapour diffusion or dialysis technique.
- Provides detailed information on the solubility profile of a protein.

References

1. Riès-Kautt M, Ducruix A,. Methods Enzymol 1997, **276**:23-59.
2. Riès-Kautt M, Ducruix A, In *"Crystallization of Nucleic acids and proteins: A practical approach"*. (Ducruix A and Giegé R. ed.) IRL/Oxford Press.
3. Riès-Kautt M Strategy 2, In *"Protein Crystallization Techniques, Strategies, and Tips"* (Bergfors T. ed) IUL Biotechnology Series International University Line, La Jolla, California.
4. Vaney M. C. *et al*, Acta Cryst D (2001), **D57**, 929-940.

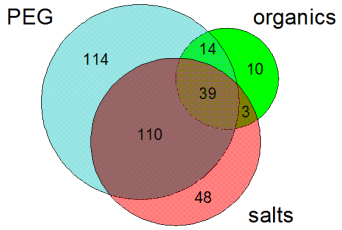
Clear Strategy™ Screens

Two complimentary 6 x 4 matrix screens developed by Brzozowski and Walton[1] from the Laboratory of Structural Biology at York University. Originally tested on a number of proteins which had not been crystallized previously and yielded diffraction quality crystals. Now these are amongst our most popular products because of their simplicity of use.
These products are manufactured under an exclusive license from University of York.

- Limit number of trials.
- Aid rational design of subsequent trials.
- User defined pH.
- Use protein information.
- Maintain 'folding homogeneity' of protein.
- Interchangeable components.
- Potential anomalous scattering centres[2].

References

1. Brzozowski A. M. and Walton J., (2001) J. Appl. Cryst. **34**, 97-101.
2. Dauter Z., Dauter M. & Rajashankar K. R. (2000), *Acta Cryst.* **D56**, 232-237.
3. Selmer *et al*, (2006), Science **313**, 1935-1442.



Ven diagram of reduced redundancy classic screening conditions

Stura FootPrint Screens

The footprint screens are based on the concept of screening the protein precipitant solubility curve.

- Screen the protein precipitant solubility curve rather than a crystallization trial[1].
- Test the relative protein solubility with precipitants that have been used successfully in the crystallization of many proteins[2].
- Once initial crystals or crystalline aggregates are obtained from the initial screening, streak seeding is recommended to determine the ranges of conditions under which crystal growth can proceed[3].

References

1. Stura E.A., Nemerow G.R., Wilson I.A, (1992),. Journal of Crystal Growth **122**, 273-285.
2. Stura E.A. (1999) Strategy 3: Reverse Screening. In *"Crystallization of Proteins: Techniques, Strategies and Tips. A laboratory manual"* (Bergfors T. ed.) International University Line pp113-124.
3. Stura E.A, Satterthwait A.C., Calvo J.C., Kaslow D.C., Wilson I.A. (1994) Reverse Screening. Acta Cryst. **D50**: 448-455.