Protein Crystallization Conditions Database, Crystal T.B.

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In the past 10 years, technical improvements in protein crystallography have been quite remarkable. Especially, with the improvements in hardware for the collection of diffraction data and in software for structure analysis and refinement, it is now possible to solve the protein structure within a few days of receiving a protein crystal. However, since these ordinary crystallization methods are based on a trial and error screening technique, a great amount of time and sample is necessary. We have developed a database that will help guide the user to a rational crystallization method. This database is composed of all the elements that are essential for protein crystallization experiments. The database contains not only detailed crystallization conditions data extracted from published reports of crystallization and structural analysis, but also biological information for each biological macromolecule. Crystallization conditions related to a specific target protein can be easily searched with the help of just a few keywords. Comparison of the search results readily reveals common parameters that provide an estimate to possible crystallization conditions before any screening experiment is started. It is an efficient approach to crystallization since it helps reduce unnecessary screenings in the process. The database also provides homology searching which is helpful in finding the crystallization conditions for unknown proteins where only the amino acid sequence is known.

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