

W0111

Protein Crystallization Conditions Database, Crystal T.B. – A Farewell to Random Screening. Jose Martin Ciloy², Shigeru Sugiyama¹, Fujiko Shibata¹, Yoshiko Kobayashi¹, Shigekazu Masumoto², Yoko Sato², Junya Ohori², Kaoru Sugimori², Masato Kitajima², Takako Sakamaki², Koji Inaka¹, ¹Maruwa Food Industry Ltd., ²Fujitsu Kyushu System Engineering Ltd.

The first known successful crystallization of a protein was recorded more than 150 years ago. Since then, introduction of new technologies as well as advances in analytical techniques and the speed of the computers significantly reduced the amount of time to analyze a crystal structure. On the other hand, protein crystallization still unavoidably relies on tedious “trial and error” screening, making it a bottleneck in the entire structural analysis process. Speeding up the whole process requires a more rational approach to protein crystallization. Our team has developed Crystal T.B., a database that summarizes all information in the literature relevant to successful crystallization. It contains recipes for preparing good crystals that are suitable for diffraction analysis. The use of the database eliminates the need to rely on random screening, and introduces a new rational approach of narrowing down crystallization parameters to more highly successful conditions beforehand. We will focus on our actual experience in using the database by showing examples on how it was applied to accelerate our crystallization process.