Optimized Crystallization Solution Analyzed from JAXA Cryoprotectant Database

<u>Sachiko Takahashi</u>^a, Hiroaki Tanaka^a, Masaru Sato^b, Moritoshi Motohara^b, Satoshi Sano^b, Tomoyuki Kobayashi^b, Susumu Yoshitomi^b, *^aJapan Space Forum.* ^b*Japan Aerospace Exploration Agency.* E-mail: s-takahashi@jsforum.or.jp

Techniques for cryofreezing protein crystals are essential for Xray diffraction experiment to reduce radiation-induced damages caused by X-ray beam in synchrotron facility. However, even though high optical quality crystals are obtained, inappropriate way of adding cryoprotectant to mother liquor often causes deterioration of crystal quality.

If the mother liquor is also suitable for cryoprotectant, the damage caused by soaking in artificial mother liquor before diffraction analysis could be avoided. Therefore, we picked up data from International Space Environment Utilization Research Data Base (ISRDB) (http://idb.exst.jaxa.jp/) constructed by Japan Aerospace Exploration Agency (JAXA) and analyzed crystallization solution data which are effective both in crystallization and cryoprotection. We will show the results which will be useful both for crystallizing and for cryofreezing protein crystals without any damages.

Keywords: cryoprotectant database, x-ray diffraction, statistical analysis experimental data