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**The High Resolution X-Ray Structure of Taka-Amylase; The Crystal Grown in Microgravity Environment.**

Akifumi Higashiura<sup>1</sup>, Hiroaki Tanaka<sup>2</sup>, Koji Inaka<sup>4</sup>, Masaru Sato<sup>3</sup>, Shigeru Sugiyama<sup>4</sup>, Sachiko Takahashi<sup>2</sup>, Mari Yamanaka<sup>2</sup>, Moritoshi Motohara<sup>3</sup>, Satoshi Sano<sup>3</sup>, Tomoyuki Kobayashi<sup>3</sup>, Mamoru Suzuki<sup>1</sup>, Tetsuo Tanaka<sup>3</sup>, Atsushi Nakagawa<sup>1</sup>, <sup>1</sup>Inst. for Protein Research, Osaka Univ., <sup>2</sup>Japan Space Forum, <sup>3</sup>Japan Aerospace Exploration Agency, <sup>4</sup>Maruwa Food Ind., Inc.

Recently, high brilliance and highly focused synchrotron beam lines, X-ray data collection at low temperature and technical advances in crystallographic analysis have significantly improved the resolution of X-ray crystallography. A crystallization in microgravity environment is one of the technique for the determination of high resolution structure. In this study Taka-amylase, a glycoprotein derived from *Aspergillus oryzae*, was used as a model protein for high resolution X-ray crystal structure analysis. The space crystals were produced in the JAXA-GCF (Japan Aerospace Exploration Agency –Granada Crystallization Facility) project. Taka-amylase structure was refined against X-ray data recorded on beamline BL44XU of SPring-8 to resolution of 1.0Å. This high resolution structure was providing us with a more reliable picture of the geometric and conformational properties of proteins and implied the necessity to improve bond length and angle restraints.