

Preparation of large-volume crystals for structure analysis of human casein kinase-2 by neutron crystallography

Chie Shibazaki, Motoyasu Adachi, Takeshi Hiromoto, Rumi Shimizu and Ryota Kuroki

*Molecular Biology Research Division, Quantum Beam Science Center, JAEA, 2-4
Shirakata-shirane, Tokai, Ibaraki. 319-1195, Japan.*

a corresponding author: E-mail kuroki.ryota@jaea.go.jp

Casein kinase 2(CK2) is one of the ubiquitous Ser/Thr kinases and is involved in the cell cycle and the survival and proliferation of cells. CK2 is a heterotetrameric structure comprising two α - or α -subunits and two regulatory β -subunits, in which two β -subunits dimerize the two catalytic α - or α -subunits[1]. In order to understand the biological function of the alpha catalytic subunit of CK2 (CK2 α), we aim to analyze the structure of CK2 α including information of the hydrogen and hydrating water molecule by neutron crystallography.

The gene coding CK2 α was inserted into pET24a and expressed in *E. coli* strain BL21DE3, in which the mobile region (330-335) and chemically reactive thiols (Cys147 and Cys220) were removed by amino acid mutation. The recombinant CK2 α was successfully expressed in *E. coli* as a soluble protein and was purified by several steps of ion-exchange chromatography. A total of 150 mg protein was obtained from a 6 L culture, and was used for crystallization trials. The preparation of large crystals was performed using a macro seeding method specially developed for CK2 α . After mixing the protein solution (40 mg/mL) with the same portion of 25 mM Tris-HCl buffer (pH 8.5) containing 0.8 M ammonium sulfate, 1 mM dithiothreitol and 5 % acetonitrile, seed crystals were added to each well. Then, the concentration of ammonium sulfate was raised to 1.2 M over a period of several days by replacing the reservoir solution. Finally, a large crystal with a volume of approximately 2 mm³ was reproducibly obtained. From the X-ray diffraction study, we confirmed that the crystals obtained diffracted to approx. 1 Å resolution at 100K after soaking the crystal into the deuterated cryo protectant. The neutron diffraction data collection is planned to obtain a high resolution neutron structure of CK2 α .

Reference

[1] K. Niefind, B. Guerra, I. Ermakowa, O. G. Issinger, EMBO J. 20, 5320-5331. (2001)