Crystal Structure of the â-subunit of Acetyl-CoA Carboxylase in *C. Glutamicum.*

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Acetyl-CoA carboxylases (ACCs) catalyze the first committed step of fatty acid biosynthesis. Although ACC is an essential enzyme (complex) in every organism, the structure-function relationship of ACC remains to be unclear. As the first step for elucidating the structure-function relationship of ACC, we started the crystallographic analysis of DtsR1. DtsR1 is the β-subunit of ACC multisubunit complex in *Corynebacterium glutamicum*, which catalyzes the transcarboxylation between biotin and acetyl-CoA.

DtsR1 was over-expressed in *E. coli*, purified, and crystallized by the sitting-drop vapor diffusion method using PEG 6000 as a precipitant. The approximate dimensions of the obtained crystals were 0.07x0.07x0.03mm^3. Diffraction data of the crystals were collected at NW12 of the Photon Factory (Tsukuba), revealing that the crystals belong to the space group *R*32. The crystal structure of DtsR1 was solved at 3.2Å resolution by the molecular replacement method using single-subunit coordinates of the 12S transcarboxylase (PDB ID: 1ON3) as a search model. The obtained structure suggests that the biological unit of DtsR1 is a ring-shaped hexamer with the *32*-point group symmetry. Crystallographic refinement of DtsR1 is in progress at 2.7Å resolution.

Keywords: carboxylases, fatty acid biosynthesis, structure-function enzymes