

## Crystal structure analysis of Hmc

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High molecular mass cytochrome  $c_3$  (Hmc) from *Desulfovibrio vulgaris* Miyazaki F is an electron transfer protein composed of a single polypeptide and 16 heme  $c$  groups (total molecular weight is 67 kDa). Primary and tertiary structures of Hmc have not been reported but Hmc may have four cytochrome  $c_3$  domains since the primary structure of Hmc from Hildenborough strain indicates that Hmc is divided into four cytochrome  $c_3$  units.

The function of Hmc *in vivo* remains unclear but the protein must transport electrons because cytochrome  $c_3$  is an electron transfer protein. Redox potentials of heme groups are from positive ( $E = 60$  mV) to negative ( $E = -260$  mV), which cover the redox potentials of other electron transfer proteins, such as cytochrome  $c_3$ , cytochrome  $c_{553}$ , ferredoxins I and II, and rubredoxin. Hmc may receive electrons from hydrogenase.

Data sets for native crystals were collected at BL41XU equipped with the Rigaku R-AXIS IV imaging plate detector system. A wavelength of an incident beam

was 0.708 Å and a crystal-to-detector distance was 400 mm. The crystals diffracted to 3.0 Å for the first frame, but we could not complete the data collection because of immediate radiation damage of Hmc crystals.

The image data were processed by using the programs *DENZO* and *SCALEPACK*. The programs indicates that the crystals belong to an orthorhombic space group of  $P2_12_12_1$  with unit cell dimensions of  $a=60.5$  Å,  $b=85.2$  Å,  $c=127.6$  Å.

The crystals subjected to the data collections were weak for radiation damage. We have searched new crystallization conditions to improve the quality of the crystals and then we have obtained a new Hmc crystal using a precipitant solution containing 20 % glycerol. It may improve the quality of the crystals and we will collect a complete data set at 100 K using the new crystal. We hope we can complete the data collection at SPring-8 using the new crystals if the occasion arises.