



Experiment title:
Bacteriophage phi29 connector (α)

Experiment number:
LS-1666

Beamline:
ID41EH4

Date of experiment:
from: 9 June 2000 to: 11 June 2000

Date of report:
17 Aug 2000

Shifts:
6

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Report:

During the assembly of the head of the double stranded DNA bacteriophages, a region called connector or portal plays an important role in the first steps of assembly and the packaging of DNA. This region is also involved in the process of DNA transfer into the host cell during viral infection. This region connects the head of the virus with the tail. Electron microscopy studies, based on two-dimensional projections, carried out by our collaborators at the Centro Nacional de Biotecnología (Madrid), show that the connector has a cylindrical shape with 12 subunits enclosing a 40Å diameter channel in the center. This has been already confirmed by us in a previous crystallographic study. Each subunit is formed by the 35KD p10 protein. The aim of this project is to solve the three-dimensional structure of the whole particle, using as starting point the electron microscopy model and, if possible, derivative data.

We tried to collect MAD datasets using SeMet as anomalous scatterer. Problems with beam line alignment prevented us from doing so. This was solved in the next allocation of time. See next report of LS1666 24-25 June 2000. Two MAD datasets using soaked TaBr clusters were then collected. Both diffracted better than 3 Å, but despite a signal in the fluorescence scan, no heavy ion positions could be localized.