ESRF

Experiment title:

STRUCTURE DETERMINATION OF FTSY

Experiment number:

LS324

Beamline:

BL19

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3

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Received at ESRF :

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Report:

background:

FtsY is the receptor (or docking protein) for the signql recognition particle in E. coli. It has a molecular weight of about 54 kDa, but due to anunusual high content of glutamic acids in the N-terminal region it migrates with an apparent molecular weight of about 92 kDa on an SDSPAGE. We obtained small crystals of the full length protein which we could improve only by modifying the construct, so that we expressed only a “(kDa fragment containing the G-domain. This of main is homologous to other GTPases like p21 ras and efTU. However, the SRP related GTPases form a district subgroup of GTPases. No structure of any member of that family has been solved so far.

report:

The crystals of FtsY diffracted to beyond 2A, space group P21.

Cell dimensions: a=30, b=80, c=60 A, beta=95.5°

We collected a native and several putative derivative data sets using 100 K, lambda=lA. The native data were collected to 1.8A resolution, but diffraction was seen to at least 1.5A (couldn’t collect high resolution due to time limitation). We also collected a IrCl,

0s04, PtC14 and a AuCl data set. The completeness of the derivatives is about 91-962, the native about 88% complete. The problem turned out to be non-isomorphism, especially a change in the beta-angle to 1° and more. The Au and the Pt data could be used together with two other derivatives (collected at EMBL-Heidelberg). However, the phases were not good enough to solve the structure.

We have now replaced the Met by Se-Met and we will perform a MAD experiment - which should not suffer from the non-isomorphism.