



Experiment title:

TCR / peptide / MHC complexes

Experiment number:

Beamline:
ID14 eh2

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Shifts:
2

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Report:

During spring 2000, we have obtained new crystals of putative TCR/pMHC complexes involved 2 different TCRs (BM3.3 and KB5-C20) and different peptides. Experiments on ID14-eh2 beamline have allowed us to test them for diffraction.

For the first TCR (BM3.3, viral peptide), crystals have shown weak diffraction intensity up to 8Å resolution. Nevertheless, we have been able to collect a few diffraction images ($\Delta_{\theta} = 0.93\text{\AA}$, $\Delta_{\omega} = 0.5^{\circ}$, $t = 60\text{s}$). Owing to this restricted data set, we have determined a unit cell in a monoclinic lattice: $a = 168\text{\AA}$, $b = 95\text{\AA}$, $c = 186\text{\AA}$, $\beta = 110^{\circ}$.

Crystals of potential complex between the second TCR (KB5-C20) and a new peptide bound to murin MHC molecule have been tested too. We have collected 360 images ($\Delta_{\theta} = 0.93\text{\AA}$, $\Delta t = 30\text{s}$, $\Delta_{\omega} = 0.5^{\circ}$) on a single crystal at 2.1Å resolution. A complete data set has been obtained (Space group: $P2_1$, unit cell $a = 66\text{\AA}$, $b = 81\text{\AA}$, $c = 89\text{\AA}$, $\beta = 111^{\circ}$) with a Rmerge of 19%. This quite high Rmerge is due to the rapid decay of the diffraction intensity after the 180 images. Unfortunately, the crystal unit cell corresponds to a pMHC crystal one. The molecular replacement solution has confirmed the absence of the TCR moiety.

However, these results are encouraging and lead us to make new crystallization tests for future runs during the fall.