



	<b>Experiment title:</b> PROTEIN CRYSTALLOGRAPHY AT AFMB-CNRS, MARSEILLE	<b>Experiment number:</b> LS1657
<b>Beamline:</b> ID14-1/2	<b>Date of experiment:</b> from: 03.03.00                      to: 04.03.00	<b>Date of report:</b> Aug00  <i>Received at ESRF:</i>
<b>Shifts:</b> 3	<b>Local contact(s):</b> Stephanie Monaco, Ed MITCHELL	
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## Report:

Protein name: VHH CAB07 anti amylase

Size: 14552 daltons, 136 aa

.Data collection of complex amylase and VHH CAB07

Crystals of the complex amylase with VHH CAB07 were frozen with 10% glycerol as cryoprotectant.

These crystals were of the space group P21 with cell dimensions a=52.7 Å, b=286.8 Å; c=65.9, beta= 93.73. Two data set were collected to 100K, with exposures time of 5 and 20 s per degree to resolution of 2.0 Å.

.The 3\_D structure of the scFV was determined by molecular replacement, using as the search model Amylase (F.Payan) and xxxxxxxx  
The refinement is in progress.

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Total number of observation	456505
number of unique reflections	78282
overall % data > 1sigma (last shell)	80.0(72.9)
overall R-merge (%) (last shell)	7.0(5.6)
overall I/sigma(I) (last shell)	8.0(8.)
resolution	29.0-2.0 A

Data will be processed with IDL and PROW

refinement resolution: 20 - 2.0 A	
final Rfactor/Rfree	20.0/23.5
total number of refl. in resol. range:	1310131 (100%)
total number of reflections used:	65658 (50%)
number of reflections in working set:	64043
number of reflections in test set:	1655
number of protein atoms:	16172

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