X	**Experiment title:**	**Experiment number**: LS-2083
Beamline: ID-29	**Date of experiment**: from: September 6 2001 to: September 7 2001	**Date of report**: July 25, 2005
Shifts: 3	**Local contact(s)**: Bill Sheppard	*Received at ESRF:*
Names and affiliations of applicants (* indicates experimentalists):		

Report:

We tried to collect data on two proteins: a carbonic anhydrase from a salt-tolerant alga *D. salina*, and human cerezyme, which is implicated in Gaucher's Disease. While we were able to collect what seemed to be good MAD data (three wavelengths) using the zinc cation in the active site of the carbonic anhydrase, MOSFLM could not scale the data, and we could get no useful patterson maps. Bill Sheppard spent an enormous amount of time trying to get MOSFLM to process the data, which did finally succeed in producing some very poor patterson maps. As data collection was proceeding, we assessed that problem lay in the shutter, but a replacement was not available, and so could not improve the situation. Back at home, I tried using DENZO, which could easily integrate the data, but SCALEPACK could not scale the frames, confirming our suspicions. Data were deemed useless, and we applied for rapid access time to BM-14 (experiment 14-U-28). We were granted a slot, and collected excellent MAD data on Nov 19, 2001, just over two months after our time on ID-29. These data were used to solve the structure.

We tried 9 cerezyme crystals, none of which diffracted well.