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Shifts: 3	Local contact(s): Dr . E. Gordon	<i>Received at ESRF:</i>
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Report:

Study of pathways involving kinases and tRNA methyltransferase.

We have tested 50 crystals from 3 different projects.

CapO - We collected 2 SAD data sets at 9.9 keV (1.252Å) with Europium derivatives of the UDP-acetyl-mannosamine dehydrogenase CapO, the substrate of the *S. aureus* tyrosine kinase CapB : 1 SAD data set in P65 at 2.8Å resolution and 1 data set in P212121 at to 2.5Å resolution. We also collected 3 native data sets in P65 up to 2.5Å resolution. These data allowed us to solve the structure of CapO which is now under refinement. These results will be published in 2009.

CapB - We collected 3 native data sets with crystals of cytoplasmic domain of the *E. coli* tyrosine kinase Wzc. They diffract up to 3.8 Å resolution in space group C2. These data allowed us to solve the structure of Wzc by molecular replacement using our CapAB structure as initial model. These results will be published in 2009.

RTrmlp – The crystal structure of the tRNA m1A58 methyltransferase of *Pyrococcus abyssi* is known at a resolution of 3.4Å. In order to compare it to other tRNA m1A58 methyltransferases, we would like to improve this resolution. Thus we found another crystallisation condition (2.4M Ammonium Sulfate, 0.2M Ammonium acetate) and we obtained a data set to a maximum resolution of 2.5Å. The refinement is in progress.