



	<b>Experiment title:</b> <b>Block Allocation Group (Portugal)</b>	<b>Experiment number:</b> LS-1667
<b>Beamline:</b> ID14-1	<b>Date of experiment:</b> from: 21-06-00 to: 23-06-00	<b>Date of report:</b> 21-08-2000
<b>Shifts:</b> 6	<b>Local contact(s):</b> Dr. Germaine SAINZ	<i>Received at ESRF:</i>
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## Report:

### Adenylate kinase from *Desulfovibrio gigas* (native):

A data set was collected to 2.05 Å resolution. Overall statistics: R-merge = 11 %, completeness = 90.8%, I/σ(I) = 12.0, redundancy = 4.7. Highest resolution shell statistics (2.12 to 2.05 Å): R-merge = 32 %, completeness = 79.8%, I/σ(I) = 3.9, redundancy = 3.4. The solution of the structure is being tried by molecular replacement.

### Cytochrome c Peroxidase from *Pseudomonas nautica* (native):

A data set was collected to 2.82 Å resolution. Overall statistics: R-merge = 11.5 %, completeness = 100.0 %, I/σ(I) = 17.4, redundancy = 13. Highest resolution shell statistics (2.96 to 2.82 Å): R-merge = 30.7 %, completeness = 100.0 %, I/σ(I) = 11.4, redundancy = 13. The structure was solved by the molecular replacement method and is being refined with CNS. Current R-factor is 20.67 % and R-free is 21.65 %.

**Periplasmic Nitrate Reductase from *Desulfovibrio desulfuricans* ATCC 27774 (native) co-crystallised with cyanide:** A data set was collected to 1.80 Å resolution. Overall statistics: R-merge = 7.2 %, completeness = 99.8 %, I/σ(I) = 30.8, redundancy = 4. Highest resolution shell statistics (1.86 to 1.80 Å): R-merge = 23.5 %, completeness = 99.8 %, I/σ(I) = 5.5, redundancy = 4. The structure will be solved by the molecular replacement method.