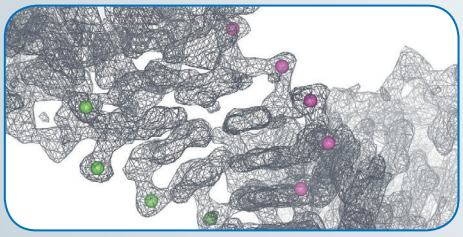
Dr. Dima Chirgadze, Head of The Crystallographic X-ray Facility at the Department of Biochemistry, University of Cambridge



Electron density map of a novel form of DNA solved using P-SAD (Raiber, E.-A., et al. (2015) *Nature Structural & Molecular Biology* **22**, 44–49)

Since we've acquired our Bruker system we have come on leaps and bounds in terms of the speed of data acquisition and ease of use of the machine and the software. It used to take us over 3 days to collect a single dataset on one of our older systems and now we can do the same data collection in just under 3 hours. This gave us a possibility to collect diffraction data from over 5,000 samples over the past 5 years.

The quality of the data coming off the machine is very high, easily beating anything we had collected ever before on an in-house X-ray source. This gave us the possibility to accurately measure the very small Sulphur anomalous signal for our SAD experiments. We now routinely use structure solution by SAD and have obtained *ab-initio* phases for over a dozen crystal structures, including a new form of DNA by P-SAD.

The system reliability and stability is also very good. We have not had any major breakdowns despite having the machine running at full power for >90% of the time. A few smaller issues were fixed promptly by experienced and qualified engineers; it is almost like having a 24-hour response from a personal engineer. The service costs are very reasonable considering the quality and the speed of the service one gets.

The data processing software PROTEUM2 that comes with the machine is very easy to use, well documented and designed with protein crystallographers´ needs in mind. Software updates are free of charge, can be easily downloaded and installed highlighting the fact that they were thoroughly tested before the release.

All in all we are very happy with our system. We call it our in-house synchrotron because the data that we can acquire on it can be on par with the synchrotron data, especially when used in conjunction with the highly-redundant datasets collection approach.

Exceptional Productivity

- A Fast and Efficient In-house Solution