

Structural studies of the outer membrane heme receptor from *Shigella dysenteriae*

Several crystals (frozen at the Lab and frozen on the beamline) were tested, more than 100.

One of those ([SeMet]) diffracted X-ray at low resolution, around 7 Å. The crystal belongs to the C2 space group ($a=145.61$, $b=211.38$, $c=144.98$ Å, $\beta=115.67^\circ$). A SAD dataset has been collected, even if the resolution is low. These crystal belongs to a new space group and its analysis could be interesting to discuss about the loop conformations (avoid the effect of the crystal packing when describing a structure. It is better to have several crystal forms).

Another crystal of the native protein diffracted X-rays at 4 Å resolution. The crystal belongs to the orthorhombic system ($a=78.67$, $b=116.35$, $c=117.12$ Å) and the space group is $P2_12_12_1$. 1 molecule is in the ua. The crystal was saved to collect data to a better resolution on ID beamline.

In the same time, we collected data for a protein which binds to membrane proteins. The space group is $P3_221$ and 1 molecule is in the ua ($a=b=56.65$ Å, $c=46.68$ Å). The crystals diffracted to 3 Å resolution.