Experimental report
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ID14-EH2
october 6 and 7 (6 shifts)

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The results obtained on ID14-EH3, allowed us to screen a large number of pSRII crystals with the optimal crystal handling protocol, in order to collect the highest resolution data set. 20 crystals were screened, one of which diffracted to better than 2.1 Å resolution. A complete data set to 2.1 Å was collected and integrated with an Rsym of 7.2%. The space group is $C222_1$, with a unit cell of a=84.8Å, b=128.7Å and c=50.7Å. The initial phases were determined by molecular replacement starting with the backbone of bacteriorhodopsin as a model. The complete model was then built from 2Fo-Fc electron density maps and refined. Additionally to the ground state experiment on pSRII, we started some preliminary measurements on excited states of pSRII in order to test the diffraction of illuminated crystals. Furthermore, crystals from five other membrane protein grown in lipidic cubic phases were tested. In total 26 crystals were screened, some of which diffracted to very low resolution, most of which did not diffract at all. Thses informations are crucial for optimizing the crystallization conditions.