<b>ESRF</b>	Experiment title: Bacterial sugar transporter, integral membrane.	Experiment number: MX 1239						
Beamline:	Date of experiment:	Date of report:						
ID23-1	from: 11/4/2011 to: 12/4/2011	16/5/2011						
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## **Report:**

- We collected images from ~40 crystals (frozen at 100K) from which we collected 6 complete datasets (see Table below).

- We improved the resolution from 10.5 Å (BM16 Feb 2011) to 8.8 Å, the data were indexed and integrated in XDS and scaled with SCALA (CCP4), using quite strict data quality requirements.

p242: The best crystal diffracts to 8.8 Å (Detector distance=622.129 mm;  $\Delta\Phi=2^{\circ}$ ;  $\lambda=0.9724$  Å; t=2 s) Space group: P622, one monomer per au (solvent content=72%; Vm=4.4) or two monomers per au (s=45%; Vm=2.2) (Vm values are quite larger in membrane proteins than for soluble proteins).

- Although a bit far-fetched, we are currently trying molecular replacement with a structure that has 19 % seq. identity.

- We also tried the dehydration techniques (HC1, together with Silvia Russi) on 2-3 crystals, but apparently the crystals are extremely fragile and sensitive to osmotic/pressure differences and they would dissolve even in their own mother liquor (without even dehydrating the crystal). So, no data were collected from the dehydration experiments. Although further work needs to be done on this technique.

CRYST.	RUN	# IMG (# PROC)	MAX. RESOL. (Á)	RMERG (LAST SHELL)	I/SIG (LAST SHELL)	MULT.	COMPL. % (LAST SHELL)	SG	CELL PARAM. (Á)	BL
32_3	1	90(60)	10.5	0.11(0.36)	7.6(3.5)	3.6(3.6)	95.0(94.7)	P6	a=b=215.0 c= 132.0	BM16
p132	1	50 (50)	9.1	0.11 (0.44)	2.5 (1.5)	5.0 (4.7)	97.2(100.0)	P6	a=b=215.3 c=132.9	ID23-1
	3	50 (50)	bad							ID23-1
p242	5	190 (30)	8.8	0.12 (0.46)	10.8 (3.7)	6.3 (6.6)	99.3 (100.0)	P622	a=b=213.8 c=130.8	ID23-1
	7	190 (190)	bad							ID23-1
p243	10	190 (60)	9.2	0.12 (0.43)	8.8 (4.0)	5.2 (5.3)	98.2(100.0)	P321	a=b=221.2 c=132.1	ID23-1
p244	5	190 (40)	9.2	0.09 (0.52)	12.4 (3.1)	4.0 (4.2)	98.6(100.0)	P321	a=b=216.9 c=132.0	ID23-1