ESRF	**Experiment title:** Crystal structure of the small nuclear GTP-binding protein Ran in complex with its Guanine nucleotide Exchange Factor RCC1	**Experiment number:** LS 1322
Beamline: ID02B	**Date of experiment:** BAG allocation – LS1322 from: 16/7/99 to: 19/7/99	**Date of report:** 31/8/99
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Names and affiliations of applicants (* indicates experimentalists):

Louis RENAULT
Max-Planck Institut für molekulare Physiologie
Postfach 50 02 47
44 202 Dortmund, GERMANY

Report:

We have collected data sets from small Ran-RCC1 crystals on ID02B at ESRF on july 99. Two small crystal forms were available. Several cryo-protectant solutions were tried for the first crystal form which constitutes very narrow and fragile plates with a typical size of 250*250*3 micrometer but we could not obtained any good diffraction pattern. The second crystal form is constituted of crystals sometimes twinned with a typical size of 80*80*30 micrometer. The best single crystals diffracted at resolution higher than 1.95 Å on ID02B. Crystals belong to space group P1 with unit cell dimensions of

$a = 50.27$ $b = 71.52$ $c = 77.83$ $\alpha = 100.93$ $\beta = 91.86$ $\gamma = 104.53$

at 100K. These crystals are very sensitive to radiation damage and no complete data set could be collected from a single crystal. We collected therefore different low and high resolution data sets from several crystals. Data sets were processed and merged using XDS and XSCALE from W. Kabsch [KABSCH, W. Automatic processing of rotation diffraction data from crystals of initially unknown symmetry and cell constants. J. Appl. Cryst. 26, 795, 1993]. The table above summarize the best data sets which could be merged together with correlation coefficients higher than 0.88 in XSCALE. Data sets producing lower correlation coefficients were excluded.

Crystal Number	Number of degrees collected	Resolution Range (Å)	Measured reflections	Unique reflections	completeness at I/σ >1 (%)	R_{sym} (%)	R_{meas} (%)	I/σ
Crystal 1	147	17-2.1	77 150	46 767	72.2	4.7	6.3	11.3
					(13.3)	(11.0)	(21.0)	(4.6)
Crystal 2	130	15-1.82	113 517	73 242	73.7	5.0	7.0	10.7
					(56.1)	(18.1)	(23.1)	(3.6)
Crystal 3	74	15-1.88	57 172	42 278	47.6	7.4	10.4	8.11
					(51.0)	(16.6)	(23.1)	(3.1)
Merge of the 3 data sets		17-1.82	247 886	87 827	85.1	11.2	13.5	8.1
					(53.3)	(13.8)	(19.5)	(2.4)

Table 1: data collection statistics for data sets collected at beam line ID02B, ESRF.
Values in parenthesis concern the last resolution shell, respectively 2.2-2.1 Å, 1.88-1.82 Å, 1.95-1.88 Å and 1.88-1.82 Å for data sets of crystal 1, crystal 2, crystal 3 and the merge.

The molecular replacement method by using the moldels of Ran and RCC1 has been initiated with these data by using AMORE from G. NAVAZA (Acta Cryst. A50,157-163, 1994) and is still in process. In parallel, we are attempting to improve the completeness and redundancy of our merged data set by using local scaling with MAXSCALE from M. ROULD to merge data sets of lower quality, especially one low resolution data set and a high resolution data set with correlation coefficient equal or higher than 0.7 in XSCALE.