	Experiment title: Threonine synthase mutant	**Experiment number**: 30-01-402
Beamline: bm30	**Date of experiment**: from: 3-02-02 to: 4-02-02	**Date of report**: 22 mai 02
Shifts: 2	**Local contact(s)**: R. Kahn	*Received at ESRF:*

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Report:

The structures of apo- and holo- threonine synthase (TS) don't allow to find where the activator S-adenosyl methionine (SAM) binds. So we have tried to soak and cocrystallise a mutant of threonine synthase where the first 36 aminoacids have been truncated. This mutant is sensitive to SAM in a different way from the wild type enzyme.

5 crystals were tested and 3 data sets were collected.

The best came from crystals that had been obtained by co-crystallising the enzyme with SAM.

Space group is $P2_12_12_1$, unit cell is 75, 96, 107.5.

Data set name	Diffraction limit (highest resolution bin)	R-sym	Completeness	multiplicity
23c4	2.6 (2.8-2.6)	5.7% (19.7)	98.6 (91.2)	4.9 (3.5)
21a1	2.6 (2.8-2.6)	10.9 (43.3)	98.8 (98.8)	6.2 (4.1)

Crystal used for collecting data set 23c4 was cocrystallised with SAM and after molecular replacement the electron density map showed an extra density that could be attributed to SAM. Refinement is in process.
Crystal used for data set 21a1 was soaked with SAM and did not give any additional information regarding SAM binding.