

1) In order to overcome earlier problems encountered with twinned crystals a new crystal form of *Pseudomonas* TACII 18 (psychrophilic) Alkaline protease was grown and cryo data were collected on 1 crystal.

These data led to the determination of the 3D structure even in the absence of the primary structure, due to the very high quality data. However data to a resolution of 1.9 Å have been collected since then, and these results have been submitted.

2) *Alteromonas haloplantidis* (psychrophilic)  $\alpha$ -amylase mutant K300R : cryo data were collected. Unfortunately these are not complete. An electron density map has been calculated. The map is readily interpretable, but due to the low completeness and a more complete set of data collected later, no continuation of the treatment of these data has been done.

---

#### Diffraction data and refinement statistics for the data

---

	<b>mutant K300R</b>	<b>Protease</b>
Space group	C222 <sub>1</sub>	R3 (hexagonal setting used)
Cell dimensions, Å	a=70.12 b=135.67 c=113.20	a=b=184.59 c=37.85 $\alpha=\beta=90^\circ$ and $\gamma=120^\circ$
Measurements, <i>n</i>	22453	32123
Unique reflections	12544	17980
Resolution, Å	2.38	2.38
Completeness, %	65.0	93.2
Compl. outermost shell, %	66.6	59.0
R <sub>merge</sub> , %	2.9	4.0
I/ $\sigma$ (I) > 2, %	86.4	80.5
I/ $\sigma$ (I) > 2 outermost shell, %	81.4	58.9
R <sub>factor</sub> , %	20.03*	18.70
R <sub>free</sub> , %	23.21*	25.66