Previous attempts along these lines had produced little new information because of the limited resolution. Seal myoglobin and lamprey haemoglobin were shown to be close structural relatives of sperm whale myoglobin. Slightly more information was gained about carboxypeptidase B, which was shown in a study at 5.5 Å resolution to lack electron density at the N-terminus by comparison with carboxypeptidase A, which has four extra N-terminal amino acids (Schmid *et al.*, *J. molec. Biol.*, **84**, 97; 1974).

Although these methods served to confirm that one structure was like another, they were unable to provide detailed information about the new structure. Bode *et al.* show such information can be gained if one works at sufficiently high resolution.

The Munich group had already worked out one structure involving the trypsin molecule. This was the complex of pancreatic trypsin inhibitor with trypsin (Huber *et al.*, *J. molec. Biol.*, **89**, 73; 1974). They used isomorphous replacement to give an electron density map, and then used a computer method to orient the inhibitor structure, which they had worked out separately, to give the best fit to the map. For the trypsin part of the complex, a previously determined trypsin structure did not fit well, but the coordinates for chymotrypsin, edited to account for known chemical differences, could be rotated to a correct orientation and refined. During refinement, the phase angles obtained

Brightly shines the X-ray quasar

from John Gribbin

A NEW candidate for the title "intrinsically the strongest X-ray source known" has been put forward by Schreier *et al.* on the basis of observations made by the Astronomical Netherlands Satellite (ANS) and a timely revision of an old Uhuru error box (*Astrophys. J. Lett.*, **201**, L137; 1975). If the identification is correct, and if the QSO NAB0137-01 which is the subject of the identification is at the cosmological distance implied by its redshift of 0.33, then the source radiates about 2×10^{46} erg s⁻¹ at X-ray frequencies, four times as much as 3C273 and 50 times as much as its own optical luminosity.

But there must remain some doubt about the identification of the Uhuru source 3U0138-01 with this QSO, even though the evidence is suggestive. A tentative identification had already been made on the basis of the original Uhuru data, and this now looks better since the Uhuru error box first published turns out to have been too short in one direction; the stretch in the box implied by subsequent revisions brings one edge almost out to include the QSO. The strip of sky scanned by ANS definitely includes the QSO, but the triangular error box resulting from a combination of Uhuru and ANS observations still does not quite include this object at the 90% level.

The QSO was originally found by Bahcall *et al.* (*Astrophys. J. Lett.*, **199**,

L9; 1975) during an optical search of the sky near 10 Uhuru high latitude sources. They estimate that 0.7 QSOs would be found among the 10 boxes by chance, and the location of NAB0137-01 just outside the 90% error box for 3U0138-01 seems to fit this estimate rather well. Schreier *et al.*, however, point out that with the ANS data this particular error box is now much smaller, and say that the statistical chance of finding Bahcall *et al.*'s 0.7 of a QSO in this particular box out of the 10 is much smaller. The combined ANS/Uhuru box covers 0.02 square degrees, while the other nine Uhuru boxes of this search range from 0.14 to 0.52 square degrees in size. The probability that a QSO would be found by chance in a box of 0.02 square degrees is only 0.005; but the statistical argument remains unsatisfactory, as is usually the case for samples of one, and further identifications of high latitude X-ray sources with QSOs are needed before this can be taken at face value.

Even so, the possibility that NAB0137-01 has such a large X-ray to optical luminosity ratio is interesting in view of the lack of other identifications. It suggests that the optical objects associated with such X-ray sources may be very faint, and highlights the need for searches down to limiting magnitudes of at least 18—as well, of course, as emphasising the need for better X-ray positions.

THERE has just been placed in Westminster Abbey a marble scroll bearing an appropriate inscription to the memory of Jeremiah Horrocks. The movement for such a memorial was commenced some time ago, and is referred to in *NATURE*, vol. x. p. 190, and xi. p. 31. The inscription is as follows:—

In Memory of
JEREMIAH HORROCKS,
Curate of Hoole, in Lancashire,
Who died on the 3d of January, 1641,
in or near his 22d year;
Having in so short a life
Detected the long inequality in the mean
motion of Jupiter and Saturn;
Discovered the orbit of the Moon
to be an ellipse;
Determined the motion of the lunar apse;
Suggested the physical cause of its revolution;
And predicted from his own observations
the Transit of Venus,
Which was seen by himself and his friend
William Crabtree
On Sunday the 24th of November (O.S.) 1639:
This Tablet, facing the Monument of Newton,
Was raised after the lapse of more than
two centuries. December 9, 1874.
from *Nature*, 13, 112, Dec. 9, 1875.

from isomorphous replacement were abandoned in favour of phase angles calculated from the partly refined structure.

This is the key point of the whole operation. At lower resolution, the insertion of calculated phase angles would firmly fix the structure at that assumed in the phase calculation. This work was done at 2.3 Å resolution, where there is sufficient detail in the electron density map to require every atom to be in the right place.

In the latest work, the trypsin structure obtained from the complex was used as a starting point. Instead of isomorphous replacement, a search was made for the best orientation of the trypsin molecule to fit the diffraction data. This orientation was used to provide calculated phases, and the procedure continues as before, this time at 1.8 Å resolution.

The results show a remarkable consistency. The two trypsin structures have a mean difference of 0.25 Å (though due to error in the reorientation of the trypsin molecule, the start-

ing orientation averaged 0.44 Å away). Main chain atoms common to chymotrypsin and trypsin differ on average by 0.75 Å, and most side chains and internally bound water molecules are in similar conformations. Considering the different conditions, and the fact that these comparisons must include experimental error, they indicate that the polypeptide chain of these enzymes has evolved considerable rigidity.

Working at a lower resolution of 3.5 Å, Ward *et al.* (*J. molec. Biol.*, **98**, 161; 1975) have determined the structure of new crystal forms of human deoxyhaemoglobin A and S, using similar techniques. At this resolution no refinement was possible, and the authors are rightly cautious in interpreting apparent differences between their structures (crystallised in polyethylene glycol solutions) and the normal form. The particular interest of these structures is that they may provide a clue to the mechanism by which sickle cell haemoglobin aggregates into fibres.

These techniques mean that a new