

Ultra-high resolution diffraction from the 'blue' copper protein amicyanin

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Introduction

Amicyanin is a cupredoxin of about 11.5 kDa molecular mass found in *Paracoccus denitrificans*. It is a one-electron carrier with a redox potential of +294 mV and is an obligatory intermediate in the transfer of electrons from methylamine dehydrogenase to cytochrome c551i [1]. The crystal structure of amicyanin is known at 1.3 Å resolution [2]. The protein has a β sandwich topology with nine β -strands forming two mixed β -sheets. The copper atom is located in a pocket between the β sheets and has four coordinating ligands, two histidines, one cysteine, and one methionine.

Methods and Materials

Amicyanin crystals are monoclinic, space group $P2_1$ and the cell dimensions at 110 K are $a = 28.58$, $b = 55.84$, $c = 27.16$ Å, and $\beta = 95.5^\circ$.

A four-pass data set at 19 keV was collected on beamline 19-ID-D at the Structural Biology Center (SBC) CAT. The diffraction for this crystal extended to a minimum d-spacing of 0.75 Å with an Rmerge of 5.0%.

Results

Extensive refinements of the structure of amicyanin against the 0.75 Å data set are currently underway, using the program SHELXL [3].

Acknowledgments

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References

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