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The Crystal Structure of *Bacillus subtilis* Lipase: A Minimal α/β Hydrolase Fold Enzyme†

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The X-ray structure of the lipase LipA from *Bacillus subtilis* has been determined at 1.5 Å resolution. It is the first structure of a member of homology family I.4 of bacterial lipases. The lipase shows a compact minimal α/β hydrolase fold with a six-stranded parallel β-sheet flanked by five α-helices, two on one side of the sheet and three on the other side. The catalytic triad residues, Ser77, Asp133 and His156, and the residues forming the oxyanion hole (backbone amide groups of Ile12 and Met78) are in positions very similar to those of other lipases of known structure. However, no lid domain is present and the active-site nucleophile Ser77 is solvent-exposed. A model of substrate binding is proposed on the basis of a comparison with other lipases with a covalently bound tetrahedral intermediate mimic. It explains the preference of the enzyme for substrates with C₈ fatty acid chains.

Keywords: *Bacillus subtilis*; lipase; X-ray crystallography; α/β hydrolase fold; esterase

Introduction

*Bacillus subtilis* is a Gram-positive, aerobic, spore-forming bacterium found in soil and water, and in association with plants. The organism is of substantial commercial interest because of its highly efficient protein secretion system.¹ It is used, for instance, for the production of bulk quantities of proteases and amylases.²

*B. subtilis* produces and excretes lipases, which catalyse both the hydrolysis and the synthesis of long-chain triacylglycerols. Because of their wide diversity in substrate specificity, lipases have found important industrial applications in the resolution of racemic mixtures, the synthesis of esters and in transesterification reactions. Moreover, they are used as an additive in laundry detergents.³,⁴

Extracellular lipolytic activity of *B. subtilis* was first observed in 1979.⁵ Molecular research started in 1992 when a lipase gene, *lipA*, was cloned, sequenced and overexpressed, and the protein was characterised.⁶–⁸ Later, a second gene, *lipB*, which is 68% identical with *lipA* at the nucleic acid level, was found as a result of the *B. subtilis* genome-sequencing project.⁹ This gene has been cloned and overexpressed as well, the protein was purified, and its substrate specificity has been determined.¹⁰

The *B. subtilis* lipase LipA is particularly interesting, since its molecular mass (19,348 Da, 181 amino acid residues) is much smaller than that of the lipases from other organisms. Furthermore, this enzyme represents one of the few examples of a lipase that does not show interfacial activation in the presence of oil-water interfaces.¹³ The absence of such an interfacial activation of *B. subtilis* lipase, together with its small size, suggests that...
it does not have a lid. Two other small α/β hydro-
olase fold enzymes without lids are known. They
are cutinase from Fusarium solani\textsuperscript{14,15} and acetylxy-
lan esterase from Penicillium purpurogenum.\textsuperscript{16} These
enzymes have an accessible active site, with an
intact preformed oxyanion hole, which stabilises
the negatively charged reaction intermediates.
However, their sequences do not show any hom-
ology to the \textit{B. subtilis} lipase sequence, and thus it
remained an open question whether the \textit{B. subtilis}
lipase active site resembles those of cutinase and
acetylxylan esterase.

Bacterial lipases are currently classified into
eight families,\textsuperscript{17} with true lipases forming family I,
the largest family, which contains six subfamilies.
\textit{Bacillus} lipases have been placed in subfamilies 4
and 5. These two subfamilies have in common that
alanine replaces the first glycine residue in the con-
served G-X-S-X-G pentapeptide around the active-
site serine residue. Subfamily 4 consists of only
three members, LipA and LipB from \textit{B. subtilis},
and a lipase from \textit{Bacillus pumilus}, which share 74-
77 \% sequence identity. With a mass of 19 kDa
they are the smallest true lipases known and share
very little sequence similarity (about 15 \%) with the
other, much larger, \textit{Bacillus} lipases that constitute
subfamily 5. Here, the first 3D structure of a mem-
ber of family I.4 is described.

\section*{Results and Discussion}

\textbf{General features of the structure}

The \textit{B. subtilis} lipase has a globular shape with
dimensions of 35 Å × 36 Å × 42 Å (see Figure 1).
The structure shows a single compact domain that
consists of six β-strands in a parallel β-sheet, sur-
rounded by α-helices. There are two α-helices on
one side of the β-sheet and three on the other side
(including a very small one of only four amino
acid residues).

The fold of \textit{B. subtilis} lipase resembles that of the
core of the α/β hydrolase fold enzymes,\textsuperscript{11} as do
the other lipases of which the 3D structure has
been elucidated. A comparison of the secondary
structure elements of \textit{B. subtilis} lipase and the cano-
nical α/β hydrolase fold (Figure 2(a) and (b))
shows that \textit{B. subtilis} lipase lacks the first two β-
strands (β1 and β2) of the canonical fold and that
helix αD is replaced by a small 3_{10} helix. Further-
more, helix αE is exceptionally small, with only
one helical turn, and several α-helices start or ter-
minate with 3_{10} helical turns (according to the pro-
gram DSSP,\textsuperscript{18} see Figure 2(b)). There is no separate
lid domain present, as for instance in the larger
lipases.\textsuperscript{13} Because of its small size and the absence
of a lid domain, \textit{B. subtilis} lipase can thus be con-
考sidered as a minimal α/β hydrolase fold enzyme.

\textbf{Two molecules in the asymmetric unit}

There are two lipase molecules in the asym-
metric unit of the \textit{P}_{2}\textsubscript{1},2,2_{1} space group, called A
and B. They are related by a rotation of 169° about
an axis in a general orientation. The N termini of
both molecules approach each other, but the elec-
tron density for the first N-terminal residues is not
unambiguously interpretable. Ala1 is not well
defined in both molecules, nor is Glu2 in molecule
A. In contrast, Glu2 of molecule B is clearly visible
in density, with its side-chain hydrogen bonded to
Lys170 and Asn174 of molecule A. Although the
electron density for the N-terminal residues (Ala1
and Glu2 of molecule A, and Ala1 of molecule B)
and blurred, it clearly extends towards a spherical
density. Since this latter density has a significant
level (>5σ), is spherical, is between the two mol-
ecules of the asymmetric unit, and since Cd\textsuperscript{2+}
(or Zn\textsuperscript{2+}) is essential for crystallization, it seems likely
that Cd\textsuperscript{2+} is bound to the N termini. Therefore, we
included a cadmium ion in the final model. How-
ever, the precise interactions of the N termini with
the ion remain elusive. The B-factor of this Cd\textsuperscript{2+}
is about 40 Å\textsuperscript{2}, while the B-factors of the nearest
amino acid residues (His3 of molecule A and Glu2
of molecule B) are about 25 Å\textsuperscript{2}. The higher B-factor
of the Cd\textsuperscript{2+} could indicate that the Cd\textsuperscript{2+}
position is not fully occupied in the crystal. This might
explain the blurred density for the N-terminal resi-
dues that are only partly bound and ordered when
Cd\textsuperscript{2+} is present. Since gel filtration and dynamic
light-scattering studies give no indications of oligo-
merisation (see Materials and Methods), molecules
A and B are unlikely to represent a functional dimer.

The r.m.s. difference in Cα positions of molecules A and B is 0.85 Å (residues 3 to 181). The largest differences occur in two neighbouring loops, Ile12-Ser16 and Lys44-Thr45. In molecule A, these loops are freely accessible from a solvent channel, while in molecule B they are involved in crystal contacts. This suggests that molecule A most likely represents the most abundant conformation in solution and that the conformations of the loops in molecule B are probably affected by the crystal packing.

When these loops are left out of the comparison, the r.m.s. difference in Cα positions of the remaining 172 amino acid residues is reduced to 0.46 Å. However, Luzzati and SigmaA plots19,20 indicate that the statistically expected r.m.s. difference would be between 0.15 and 0.20 Å. The largest variations in Cα positions occur in the α-helices and loops, but not in the central β-sheet. This indicates that the residues away from the core β-sheet have some conformational freedom.

The catalytic triad

In lipases, the active-site residues are Ser, Asp/Glu and His.11 They always occur in this order in the amino acid sequence, with Ser being the nucleophile. On the basis of a multiple sequence alignment of several microbial lipases, Ser77 was suggested to be the nucleophile in B. subtilis lipase6 and Asp133 was proposed as the catalytic acid.21 The S77C and D133N mutants were indeed devoid of lipase activity.22 For the active-site histidine residue, two candidates were present initially, His152 and His156. As an H152N mutant showed activity comparable to that of wild-type lipase A, it was concluded that His156 is most likely the catalytic histidine residue.22,23 These assignments are in agreement with our 3D structure. Ser77, Asp133 and His156 are arranged in a catalytic triad-like configuration. Ser77 is positioned at a very sharp turn between strand β5 and helix αC, the so-called nucleophile elbow. Its main chain φ,ψ angles are outside the favoured regions of the Ramachandran plot (52°, −127° and 51°, −122° for molecules A and B, respectively), as is common for the nucleophile in α/β hydrolase fold enzymes.13 Asp133 is located at the end of strand β7, and His156 is situated in the loop following strand β8. These locations and the relative orientations of the side-chains are similar to those found in other lipases.

Ala75, which occurs instead of the first Gly in the G-X-S-X-G consensus sequence around the active-site Ser77, has a conformation very similar to that of the Gly residues in other lipases. Its φ,ψ angles are −126°, 140° and −118°, 143° for molecules A and B, respectively. They are typical φ,ψ angles for a β-strand conformation. An alanine instead of a glycine residue does therefore not

![Figure 2. Secondary structure topology of (a) the canonical α/β hydrolase fold, (b) B. subtilis lipase, (c) F. solani cutinase and (d) P. purpurogenum acetylxylan esterase. The broken lines in (a) indicate loops of variable length.](image-url)
greatly affect the main-chain conformation of the nucleophile elbow.

Comparison with other α/β hydrolases

From a DALI structure alignment, it appears that B. subtilis lipase is most similar in structure to the core of the much larger lipase B from the yeast Candida antarctica. The r.m.s. difference of the 163 aligned C atoms is 1.9 Å. It could be considered remarkable that B. subtilis lipase resembles more closely a fungal lipase than other bacterial lipases, although these organisms are phylogenetically quite distinct. One possible explanation could be that, similar to B. subtilis LipA, the C. antarctica lipase B has the first glycine residue in the Gly-X-Ser-X-Gly lipase consensus motif replaced. The threonine residue in C. antarctica lipase B at this position and the alanine residue in B. subtilis LipA restrict the close approach of strand β5 and helix αC, the secondary structure elements flanking the nucleophile elbow. Compared to other lipases, helix αC in these two enzymes is more bent away from strand β5, thus rationalising the structural agreement between the B. subtilis and C. antarctica lipases.

So far, the 3D structures of two other small (~20 kDa) α/β hydrolase fold enzymes without lid have been elucidated, cutinase and acetylxylan esterase. Figures 3 and 4 show a DALI structural comparison of B. subtilis lipase with these enzymes. Although the structures appear similar, the C atoms of B. subtilis lipase superimpose with a rather high r.m.s. difference of 2.8 Å (145 out of 197 C atoms for cutinase), and 2.9 Å (148 out of 207 for acetylxylan esterase), respectively. Nevertheless, five β-strands (β3 to β7) are common in the three structures as well as four α-helices (αA, αB, αC and αF).

B. subtilis is the smallest (181 amino acid residues) of these three enzymes. The additional amino acid residues of cutinase (197 amino acid residues) form an N-terminal extension at the position of the canonical α/β hydrolase fold strand β2 (Figure 2(c)) and the loops are generally longer, also in the lid region. On the other hand, cutinase lacks the canonical αE and β8 secondary structure elements, which are present in B. subtilis lipase (Figures 2(b) and (c), and 3).

Acetylxylan esterase has 207 amino acid residues. The additional residues are located in longer loop regions, between strand β4 and helix αB, and between helix αC and strand β6. The C-terminal region of acetylxylan esterase is folded differently, with a β-strand at position β8 inserted between strands β6 and β7 (Figures 2(b) and (d), and 4).

The active-site cleft

Because no lid is present, the active site of B. subtilis lipase is solvent-exposed. It is located at the bottom of a small cleft between two loops consisting of residues 10 to 15 and 131 to 137. Compared to the active sites of cutinase and acetylxylan esterase, the cleft is shallower and wider, because the loops lining the cleft are shorter and do not extend as much from the core of the protein (Figures 3 and 4).

To obtain insight into substrate binding, substrate preference and enantioselectivity of B. subtilis lipase, we compared its structure with those of lipases with a covalently bound inhibitor in the active site. There are three structures known of lipases with a covalently bound triglyceride analogue. These inhibitors (Figure 5(a) and (b)) bind covalently with their phosphoryl group to the active-site serine residue, mimicking the first tetrahedral intermediate in the cleavage reaction of the natural triacylglycerol substrates (Figure 5(c)). The binding mode of these inhibitors in the various lipases is remarkably similar. One of the phosphoryl oxygen atoms is bound in the so-called oxyanion hole by two peptide NH groups. The catalytic histidine N is at hydrogen bonding distance from the active-site serine O and the ester oxygen atom between the phosphorus atom and the glycerol backbone (Figure 5(d)). The sn-moiety of the inhibitor points in the same direction in all three lipases, away from the glycerol backbone. In contrast, further away from the phosphoryl group, the positions and directions of the sn-1, sn-2 and sn-3 chains vary.

A superposition of the active sites of B. subtilis lipase and the lipases with a covalently bound substrate analogue shows that the B. subtilis lipase active-site residues (Ser77, Asp133 and His156) are in very similar positions and orientations compared to those in the inhibitor bound lipases. This is true also for the oxyanion hole, which is formed by the backbone nitrogen atoms of the residue immediately following the nucleophile and a residue located between strand β3 and helix αA. Although in B. subtilis lipase no substrate analogue is bound, the oxyanion hole seems to be present intact at the conserved position. It is formed by the peptide NH atoms of Met78 and Ile12. This shows that B. subtilis lipase has a pre-formed oxyanion hole like cutinase, but in contrast to e.g. the lipase from Burkholderia cepacia (formerly named Pseudomonas cepacia), which needs a conformational change upon lid opening to form the oxyanion hole.

In the three inhibited lipases, the phosphoryl group of the tetrahedral intermediate mimic is bound in a very similar way and orientation (Figure 5(d)). Assuming that this will also be the case for B. subtilis lipase, we made a model of B. subtilis lipase with a covalently bound inhibitor. We retained the position and interactions of the phosphoryl group. The directions of the sn-1, sn-2 and sn-3 chains away from the phosphoryl group were optimised manually to fit in the hydrophobic grooves on the surface of the B. subtilis lipase molecule.
The result is shown in Figure 6. The hydrophobic residues Leu108, Leu140, Ala105, Met78, Ile135 and Ile12 are close to the $sn$-3 chain in this model. Ile157, Leu160, Tyr161, Asn18, Ala15, Phe17, Ile135, Gly155 and Met134 are residues that are likely to play a role in $sn$-1 and $sn$-2 binding. As can be seen from Figure 6, the $B.\ subtilis$ lipase surface easily accommodates lipid molecules with fatty acid chains of up to eight carbon atoms. Longer chains would probably stick out of the pro-

Figure 3. Stereo view of the $C^\alpha$ traces of the $B.\ subtilis$ lipase in black (top) and $F.\ solani$ cutinase in grey (bottom). The C termini (C), N termini (N) and active sites (AS) are indicated. A superposition of $B.\ subtilis$ lipase and $F.\ solani$ cutinase is given in the middle.40
tein surface into the solvent and would not be stabilised by hydrophobic residues on the surface of the molecule. In this way, it can be rationalised that the *B. subtilis* lipase has its highest activity on triacylglycerol molecules with C₈-chains.⁷,¹⁰

**Stereospecificity**

*B. subtilis* lipase shows a very small difference in reactivity towards C₂-glycerol backbone stereoisomers.¹⁰ In *B. cepacia* lipase with a bound inhibitor, the experimentally determined stereospecificity

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**Figure 4.** Stereo view of the C² traces of the *B. subtilis* lipase in black (top) and *P. purpurogenum* acetylxylan esterase in grey (bottom). The C termini (C), N termini (N) and active sites (AS) are indicated. A superposition of *B. subtilis* lipase and *P. purpurogenum* acetylxylan esterase is given in the middle.⁴⁰
around the C-2 glycerol backbone atom could be explained by a specific hydrogen bonding interaction of Thr18 with the carbonyl oxygen atom of the sn-2 chain. In agreement with the low stereoselectivity of B. subtilis lipase, there is no such hydrophilic amino acid residue present at a position equivalent to Thr18 in B. cepacia lipase. Instead, Asn18 of B. subtilis lipase (which occupies a position different from Thr18 in B. cepacia lipase) is at interacting distance from the scissile bond carbonyl oxygen atom of both substrate enantiomers. This residue might therefore contribute to the stereoselectivity of B. subtilis lipase. However, the observed stereoselectivity of B. subtilis lipase towards natural triacylglycerols is very low, and the contribution of Asn18 to the stereoselectivity must be minor. Nevertheless, Asn18 might contribute to the stereoselectivity on other substrates. Recently, it was observed that B. subtilis LipA hydrolysed benzyl, naphthyl and menthyl esters with high enantioselectivity, albeit at a low reaction rate (M.T Reetz et al., unpublished results). Since these substrates are industrially important, the B. subtilis lipase may prove to be a valuable biocatalyst for biotechnological applications.

Comparison of lipases A and B from B. subtilis

The second B. subtilis lipase, LipB, consists of 182 amino acid residues, and is 74% identical with LipA (see Figure 7 for the sequence alignment). The one additional amino acid residue precedes Ala1 of LipA. The 45 residues that are different are generally located on the surface of the molecule and not clustered at a particular spot. Two substitutions are located in the core of the protein: Val96 of LipA into Ile97 in LipB, and Met8 of LipA into Leu9 in LipB. These two residues are >10 Å apart, and the small differences in size of their side-chains can probably be accommodated by slight adjustments of nearby residues. A view of the active-site cleft (Figure 8) shows that the amino acid differences between LipA and LipB are not close to the active site, but occur mainly at the edge of the active-site surface region. Gly13 of LipA (Ser14 in LipB) and Met134 of LipA (Gln135 in LipB) are closest to the active-site serine residue at a distance of about 9 Å.

Like LipA, LipB has the highest specific activity on C8 triacylglycerol substrates, but its activity is about 40% higher than that of LipA. LipB, however, is unable to hydrolyse long (C18) triacylglycerol substrates, which LipA can hydrolyse. Since LipA and LipB have the same size, and since the hydrophobic surfaces around the active site are very similar, this can explain the preference for C8 substrates of both LipA and LipB, but the inability of LipB to hydrolyse long triacylglycerol substrates is more difficult to explain. As a hypothesis, we suggest that the variation in amino acids at the rim of the active-site surface could contribute to the different behaviour of LipA and LipB towards long (C18) substrates. These differences in amino acids could have an effect on both the binding of single substrate molecules in the active site or on the interaction of the enzyme with substrate-water interfaces.

Conclusions

The crystal structure of B. subtilis lipase A is the first 3D structure of a member of homology family
I.4 of bacterial lipases. The molecule has a compact globular shape and has no lid domain. It can be considered as a minimal α/β hydrolase fold enzyme. The active-site residues, Ser77, Asp133 and His156, and the backbone amide groups of residues Ile12 and Met78 forming the oxyanion hole are in positions very similar to those of other known lipase structures. From a comparison with other lipases, which have a covalently bound substrate mimic in the active site, we suggest that the C₈ acyl chains of a substrate are bound on the protein surface, and stabilised by hydrophobic interactions with protein residues. Since the terminal methyl groups of the C₈ chains reach the rim of the hydrophobic surface, it can be rationalised that trioctylglycerol is the preferred substrate of *B. subtilis* lipase. The known 3D-structure of this lipase, and the fact that it can easily be overexpressed and purified from *E. coli*, make this enzyme a very interesting candidate for optimisation by directed evolution.

**Materials and Methods**

**Optimisation of purification**

The gene of *B. subtilis* lipase (lipA) has been cloned, and the protein has been overexpressed, purified and crystallized.

To obtain better yields (30 mg of pure protein from one litre of culture), the production and purification procedure was adapted as follows. *B. subtilis* BCL1051 was grown aerobically for seven hours at 37°C in three 5-l Erlenmeyer flasks, each containing 0.5 l of medium as described, but with 0.1 M instead of 1 M KH₂PO₄/K₂HPO₄ buffer (pH 7.0). The culture medium was inoculated at 2% (v/v) with 10 ml pre-cultures. After growth and centrifugation of the cells, the culture supernatant was loaded directly onto a hydrophobic interaction col-
umn (30 ml Phenyl Sepharose 6 FF (low sub), Pharma-

cia) pre-equilibrated with 0.1 M potassium phosphate
(pH 8.0), at 5°C. After washing with 10 mM potassium
phosphate buffer (pH 8.0), and with 30% (v/v) ethylene
glycol in 10 mM potassium phosphate buffer (pH 8.0),
the lipase was eluted with 50% ethylene glycol in
10 mM potassium phosphate buffer (pH 8.0). Fractions
containing lipase activity against p-nitrophenylpalmitate
were pooled (85 ml). The pooled fractions were diluted
1:1 (v/v) with 50 mM bicine buffer (pH 8.5), prior to
loading onto a cation-exchange column (Hitrap SP, Phar-
macia) at 9°C. Maximally, 40 ml was loaded onto a 5 ml
column. The column was washed with 50 mM bicine
buffer (pH 8.5), and the lipase was eluted with a linear
gradient from 0 to 300 mM NaCl in 50 mM bicine buffer
(pH 8.5). The fractions containing the lipase were pooled
and dialysed overnight against 2 mM glycine buffer
(pH 10.0), at 5°C and concentrated to approximately
6 mg ml⁻¹ in a Macrosep (10 K) centrifugal concentrator
(Filtron) for use in crystallization experiments. The lipase
was stored at −20°C. The lipase was pure, as judged
from a silver-stained SDS-PAGE gel (data not shown).

Determination of the N-terminal sequence of the puri-
fied lipase revealed the predicted amino acid sequence.
To check whether the pure lipase was not aggregated, an
analytical gel-filtration column (Superdex 200 HR 10/30,
Pharmacia) was run with 20 mM glycine, 150 mM NaCl
(pH 10.0). The lipase eluted as one sharp peak at a
volume that corresponded to an apparent molecular
mass that is smaller (<10 kDa) than expected (19 kDa),
but with no aggregates in the void volume. In addition,
dynamic light-scattering measurements were carried out
with a solution of 6 mg/ml protein in 2 to 6 mM glycine
buffer (pH 10). These experiments showed only mono-
meric protein. It is therefore unlikely that LipA forms
multimers in solution at pH 10.

Crystalization and data collection

Previous crystallization conditions yielded crystals in
space group C2, which diffracted to 2 Å resolution.22,30
A better-diffracting crystal form (space group P2₁2₁2₁)
was obtained by omitting the n-octyl-β-D-glucoside, but
adding 3 mM CdCl₂ or 10 mM ZnCl₂ to the reservoir
(containing 35% PEG4000, 0.1 M ethanol amine
(pH 10.0), and 20 mM Na₂SO₄). Drops were made by
mixing 3 ml of lipase solution with 3 ml of reservoir. This
new crystal form diffracts to 1.5 Å resolution using syn-
chrotron radiation (see Table 1, native) when flash-frozen
in liquid nitrogen directly from the drop in which it was
grown.

All data were processed and scaled using the
programs DENZO and SCALEPACK.31 Reduction to
structure factor amplitudes was performed with
TRUNCATE.32

Table 1. Data collection

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Figure 7. Sequence alignment of LipA and LipB. Identical residues are boxed in yellow and the catalytic triad resi-
dues are highlighted in green. Secondary structure elements occurring in LipA are indicated. G1 to G5 are 3₁₀ helices.
Heavy-atom derivatives, phasing and density modification

Heavy-atom derivatives were prepared by soaking crystals grown in the presence of Cd\(^{2+}\) overnight in 42% PEG4000, 0.1 M ethanol amine (pH 10.0), 20 mM Na\(_2\)SO\(_4\), 5 mM K\(_2\)PtCl\(_4\) or 5 mM HgCl\(_2\), and flash-frozen in liquid nitrogen. Data were collected at the EMBL outstation at DESY, Hamburg (Table 1). The anomalous Patterson map of the Pt derivative showed one consistent very clear peak in each of the three Harker sections. It was obvious that this was a derivative. A cross-Fourier of the initial Pt phases with the Hg derivative data gave two potential Hg sites. With the program SHARP\(^{33}\) and the MIRAS method, the heavy-atom positions were refined. Additional heavy-atom sites present in the residual maps were added (see Table 2). The overall figure of merit for the acentric reflections was 0.54 using all data to 2.5 Å resolution. Solvent flattening with 38% solvent was done with DM.\(^{34}\) In the resulting electron density map, a β-sheet and several α-helices were recognisable.

Model building, refinement and analysis

With the program wARP,\(^{35,36}\) the phases were improved and extended to 1.5 Å resolution. The model was auto traced,\(^{37}\) including most of the side-chains. Of the 362 amino acid residues (two molecules of 181 amino acid residues each in the asymmetric unit), 344 were positioned correctly. After changing a few side-chains and adding a few amino acid residues, the model was refined with CNS\(^{38}\) until the structure did not converge further. The \(R\) factor is 18.1% (1.5 Å native) and \(R_{free}\) is 20.6%. After a final refinement step including the \(R_{free}\) set, the \(R\)-factor became 17.7%. The final model contains residues 3-181 of molecule A and residues 2-181 of molecule B, 518 water molecules and one Cd\(^{2+}\) in the asymmetric unit. Residues Ala1 and Glu2 (of molecule A), and Ala1 and residues 13 to 17 (of molecule B) are not clear in density, but the rest of the model is fully covered by electron density.

The geometry of the final model was analysed using PROCHECK.\(^{39}\) 90% of the residues are in the most favoured regions of the Ramachandran plot and no residues are in disallowed regions. The r.m.s. deviation from ideality in bond length is 0.005 Å and in bond angles 1.2°.

Protein Data Bank accession code

The co-ordinates have been deposited with the RCSB Protein Data Bank with accession code 1I6W.

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References


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