Crystal Structure of Concanavalin B at 1.65 Å Resolution. An “Inactivated” Chitinase from Seeds of Canavalia ensiformis

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Seeds of Canavalia ensiformis (jack bean) contain besides large amounts of canavalin and concanavalin A, a protein with a molecular mass of 33,800 which has been named concanavalin B. Although concanavalin B shares about 40% sequence identity with plant chitinases belonging to glycosyl hydrolase family 18, no chitinase activity could be detected for this protein. To resolve this incongruity concanavalin B was crystallised and its three-dimensional structure determined at 1.65 Å (1 Å = 0.1 nm) resolution. The structure consists of a single domain with a (β/α)₈ topology. A 30 amino acid residue long loop occurs between the second β-strand of the barrel and the second α-helix. This extended loop is unusual for the (β/α)₈ topology, but appears in a similar conformation in the structures of the seed protein narbonin and several chitinases as well. Two non-proline cis-peptide bonds are present in the structure of concanavalin B: Ser34-Phe, and Trp265-Asn. This structural feature is rarely observed in proteins, but could also be identified in the three-dimensional structures of family 18 chitinases and narbonin in coincident positions. In the chitinases the aromatic residues of the non-proline cis-peptides have been proposed to have a function in the binding of the substrate. The region in concanavalin B, where in chitinases the active site is located, shows two significant differences. First, the catalytic glutamic acid is a glutamine in concanavalin B. Second, although part of the substrate binding cleft of the chitinases is present in concanavalin B, it is much shorter. From this we conclude that concanavalin B and family 18 chitinases are closely related, but that concanavalin B has lost its enzymatic function. It still may act as a carbohydrate binding protein, however.

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Keywords: (β/α)₈-barrel structure; chitinase; seed protein; X-ray crystallography; cis-peptide bonds

Introduction

A major fraction of the proteins in seeds of legumes has been classified as storage proteins. These proteins are synthesised during maturation of the seed, deposited in protein bodies and degraded during germination. Apparently, they are unable to catalyse any enzymatic reaction. One of these proteins is narbonin, a seed protein from Vicia narbonensis. Although the crystal structure of narbonin (Hennig et al., 1992, 1995) revealed that it has the “TIM-barrel” (β/α)₈-fold (Banner et al., 1975), which was found exclusively amongst enzymes, the three-dimensional structure did not give any clues to an enzymatic activity. In an effort to obtain additional information on the biological function of this seed protein, further narbonin-like proteins from various plant sources were purified to compare their biochemical and structural properties. The first such protein was narbonin from Vicia pannonica, which shows 85% sequence identity to narbonin from Vicia narbonensis and which also lacks enzymatic activity. X-ray crystallography to

Abbreviations used: Endo F₁, endo-β-N-acetylglucosaminidase F₁; r.m.s., root-mean-square.
1.9 Å (1 Å = 0.1 nm) resolution revealed close similarity between the three-dimensional structures of the two narbonins (M.H. and B.S., unpublished results). Both amino acid sequence and three-dimensional structure, are particularly well conserved between the two narbonins in that region of the molecule where the active site in (β/α)₈-barrel enzymes are generally found, i.e. the C-terminal ends of the β-strands in the barrel and the subsequent loops.

Concanavalin B from jack beans (*Canavalia ensiformis*) is biochemically similar to narbonin. It was originally purified by crystallisation from crude seed extracts by dialysis against water and, as narbonin, classified as a storage protein (Sumner, 1919). The crystallisation of this protein, with ammonium sulphate as precipitant, has been published (Morrison *et al.*, 1984). However, its three-dimensional structure has not been reported. The recently determined amino acid sequence of concanavalin B (Schlesier *et al.*, 1995) showed a striking homology of concanavalin B to several plant chitinases that belong to the glycosyl hydrolase family 18 (see Henrissat & Bairoch (1993) and Beintema (1994) for a classification of glycosyl hydrolases).

Crystal structures are known for several family 18 chitinases: the bacterial endo-β-N-acetylglucosaminidase F₁ (Endo F₁) secreted by *Flavobacterium meningosepticum* (Van Roey *et al.*, 1994) and chitinase A from *Serratia marcescens* (Perrakis *et al.*, 1994) were determined at 2.0 and 2.3 Å resolution, respectively. Hevamine, a plant chitinase from the latex of *Hevea brasiliensis* was analysed to 2.2 Å resolution (Terwisscha van Scheltinga *et al.*, 1994). All these enzymes show a (β/α)₈-folding topology in the functionally important domain. The putative catalytic residue is a glutamic acid located in the cleft formed by the loops connecting the parallel β-strands of the barrel with the subsequent α-helices (Beintema, 1994).

Here we report on the crystallisation and crystal structure analysis at 1.65 Å resolution of concanavalin B. Several novel structural arguments for

![Figure 1. (a) Ribbon representation of the folding of concanavalin B with the numbering of secondary structural elements as used in the text. The secondary structure elements were identified using the program DSSP (Kabsch & Sander, 1983) as follows: strand β₁, 6-11; helix α₁, 19-24; strand β₂, 30-36; strand β₂', 38-39; helix α₂, 66-74; strand β₃, 78-84; strand β₃', 89-90; helix α₃, 95-109; strand β₄, 125-129; helix α₄, 139-153; strand β₅, 158-161; helix α₅, 173-176; strand β₆, 183-187; helix α₆, 202-214; strand β₇, 222-227; helix α₇, 241-247; strand β₈, 259-265; helix α₈, 267-273; helix α₈', 275-282. The four disulphide bridges are shown in ball and stick representation with carbon atoms as open and sulphur atoms as filled circles. (b) Stereo view of the concanavalin B molecule rotated by 90°. The cleft formed by the β₂ loops is at the top (program MOLSCRIPT: Kraulis, 1991).](image-url)
the classification of “family 18” chitinases, like the identification of two conserved non-proline cis-peptide bonds and a characteristic extended loop following β-strand 2, are revealed. These features demonstrate that concanavalin B belongs to this family. However, the catalytic glutamic acid residue in chitinases is replaced by a glutamine residue in concanavalin B. This presumably is the main reason for its lack of catalytic activity. Possible functions for concanavalin B are discussed.

Results

Overall structure of the molecule

The overall structure of concanavalin B is shown in Figure 1. The molecule is very compact and shows no protrusions beyond an ellipsoid with dimensions of 30 Å × 40 Å × 50 Å. A total of 288 water molecules were identified in the asymmetric unit, but no electron density for metal ions or other ligands was detected. Concanavalin B consists of an eight-stranded parallel β-barrel surrounded by α-helices. Figure 1(a) illustrates the nomenclature of the α-helices and β-strands. The connecting loops will, in the following, be referred to as βₙαₙ for loops from β-strand n to α-helix n and αₓβₓ₊₁ for loops from α-helix x to β-strand x + 1, respectively. Four disulphide bridges (Cys41–Cys93, Cys54–Cys62, Cys23–Cys72, Cys165–Cys194) connect several βₓ loops (Figure 1).

Compared to the canonical (βₐ)₈-barrel (Brändén & Tooze, 1991) several βₓ loops contain insertions. The loop β₂α₂ resembles an antiparallel β-hairpin, although no direct hydrogen bonding is observed. The strands are connected by two hydrogen bonds mediated by water molecules. Figure 2 shows the backbones and hydrogen bonds

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**Figure 2.** Stereo view of parts of the loops β₂α₂ and β₃α₃ forming the parallel β-sheet [β²–β³]. Only backbone atoms are shown, except for residues Cys41, Ile43, Pro46 and Cys93. The disulphide bridge Cys41–Cys93 stabilises the conformation (program MOLSCRIPT: Kraulis, 1991).

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**Figure 3.** Ramachandran φ,ψ diagram for the refined structure of concanavalin B. Glycine residues are represented by triangles. Dark areas correspond to the energetically most favourable φ,ψ regions (see the text). This diagram was produced using the PROCHECK suite of programs (Laskowski, 1993).
of the β2α2 and β3α3 loops. These two loops are partially in β-strand conformation (β2 and β3, respectively) and together they form a two-stranded parallel β-sheet. Cys41 lies in a type I β-turn which is followed by a bulge containing the residues Ile43 to Pro46. A disulphide bridge, Cys41–Cys93, stabilises the loops β2α2 and β3α3. Cys93 is the only residue with unfavourable dihedral angles (φ = 65°, ψ = −65°), but has well defined electron density (Figures 3 and 4).

Figure 4. Stereo view on the additional disulphide bridge of concanavalin B and its environment. Cys93 is the only residue with φ,ψ angles in a “forbidden” region of the Ramachandran plot (Figure 3). The electron density, contoured at 1.5σ (blue) and 5.0σ (red), was calculated with coefficients (2Fo − Fc) and α, phases from the refined 1.65 Å structure.

Figure 5. Stereo view of the non-proline cis-peptide bonds Ser34-Phe (Top) and Trp265-Asn in concanavalin B. The electron density in blue (contoured at 3σ) was calculated with coefficients (Fo − Fc) and α, phases from the refined 1.65 Å structure with the residues involved in the cis-peptide bond as well as water molecules (Top) and residues Pro227-Ala228 omitted. Atoms are shown in stick representation coloured yellow, red and blue for carbons, oxygens and nitrogens, respectively. Water molecules are depicted as red spheres (Program “O”, Jones et al., 1991).
After helix $a2$ the typical $b_2$b folding topology is only interrupted by an additional short $a$-helix $a8'$ in the loop $b8$$a8$. The additional $a$-helix seems to be a common feature of several ($b/\alpha$)$_8$ barrel proteins (Farber, 1993). In two proteins involved in tryptophan biosynthesis, indoleglycerolphosphate synthase and phosphoribosylanthranilate isomerase, a phosphate binding site is located at the N terminus of this helix $a8'$ (Wilmanns et al., 1992). It is part of the substrate binding site. In concanavalin B this charge compensation is achieved by the side-chain of residue Asp16 from the neighbouring loop $b1z1$ and a main-chain hydrogen bond of the peptide NH of Arg267 ($a8'$) and the main-chain carbonyl group of Tyr10 ($b1$). The close proximity to loop $b1z1$ leaves no room for the binding of a ligand at the N terminus of helix $a8'$. In concanavalin B this helix is present as well, but as in concanavalin B a ligand binding can be excluded (Hennig et al., 1995; Terwisscha van Scheltinga et al., 1994). In order to estimate the structural similarity of concanavalin B and hevamine the r.m.s. differences in 254 C$\alpha$ positions after optimal superposition of the ($b/\alpha$)$_8$-molecule were calculated to be 1.4 Å (Program “O”, Jones et al., 1991).

At four locations the electron density distribution could only be interpreted in terms of cis-peptide bonds. In the refinement the $\omega$-angles converged to values close to 0°. Only two of these conformations involve proline residues (Ser167-Pro and Tyr216-Pro). The other two cis-peptide conformations are found in the positions Ser34-Phe35 and Trp265-Asn266 (Figure 5).

**Structure of the cleft formed by the $b/\alpha$ loops**

In ($b/\alpha$)$_8$-barrel enzymes the active site is always located in a cavity at the C-terminal end of the parallel $b$-barrel, with the $b\alpha$-$x$ loops giving the enzyme its substrate and reaction specificity. In concanavalin B a cleft is also present (Figure 1(b)). It is rather flat and about 7 Å deep, 8 Å wide and 30 Å long (Figure 6). The loops $b3z3$ and $b7z7$ are diametrically opposite and form the side walls of the cleft. They both have a proline residue at the top (Pro86 and Pro234). Loop $b5z5$ shapes the major part of the bottom of the cleft with the backbone and side-chains of the residues Gly164 to Tyr171. This loop is stabilised by a disulphide bridge Cys165–Cys195. In addition, several side-chains from other loops delineate the cleft such as Gln131 and Arg187, which lie in close proximity in the central region of its bottom (Figure 6). An aromatic cluster formed by the side-chains of Trp265, Phe35 and Tyr189 borders the cleft at one end. The indole of Trp265 is accessible to the solvent and divides the cleft in two sections. Phe35 and Trp265 seem to require distinct structural constraints, because they are involved in cis-peptide bonds connecting Ser34 with Phe35 and Trp265 with Asn266. The other end of the cleft is a flat depression only. It is bordered by the backbone atoms of loop $b2z2$ and by the side-chains of Gln13, Thr32, Asn266 and Gln268 (Figure 6).
Table 1. Alignment of the two conserved regions in family 18 chitinases for proteins with known three-dimensional structure

<table>
<thead>
<tr>
<th>Secondary structure</th>
<th>β3→</th>
<th>β4→</th>
</tr>
</thead>
<tbody>
<tr>
<td>Concanavalin B</td>
<td>VKVFLALGGF</td>
<td>122</td>
</tr>
<tr>
<td>Hevamine</td>
<td>1KVMLSLOGGI</td>
<td>118</td>
</tr>
<tr>
<td>Narbonin</td>
<td>VKVVISGGRG</td>
<td>123</td>
</tr>
<tr>
<td>Chitinase A</td>
<td>LKILPSGWWT</td>
<td>206</td>
</tr>
<tr>
<td>Endo-F1</td>
<td>1KIVSLISILNH</td>
<td>123</td>
</tr>
</tbody>
</table>

Sequences shown are from *Canavalia ensiformis* concanavalin B (sequence Schlesier et al., 1995, structure this paper), *Hevea brasiliensis* hevamine (Jekel et al., 1991; Terwisscha van Scheltinga et al., 1994), *Vicia narbonensis* narbonin (Nong et al., 1993; Hennig et al., 1995, Flavobacterium meningosepticum endo-β-acetylglucosaminidase F1 (Tarentino et al., 1992, Van Roey et al., 1994). Conserved residues are drawn in bold. The residue numbers and the secondary structure assignment correspond to the concanavalin B sequence and structure, respectively. The proposed catalytic residue in hevamine, chitinase A and endo-β-acetylglucosaminidase F1 is highlighted with an arrow.

Discussion

Concanavalin B is yet another member of the fast-growing family of structures having (β/α)₅-barrel topology (Farber, 1993). In addition to narbonin from the seeds of *Vicia narbonensis* and *Vicia pannonica* it is the second representative of the family with no demonstrated catalytic activity. The structures of the plant proteins concanavalin B and narbonin are highly similar to that of hevamine, a plant enzyme with both lysozyme and chitinase activity (Beintema, 1994; Terwisscha van Scheltinga et al., 1994). All these plant proteins and the bacterial members of family 18 chitinases such as endo-β-N-acetylglucosaminidase F1 (Van Roey et al., 1994) and chitinase A (Perrakis et al., 1994) have (β/α)₅ topology and an extended β₂α₂-loop. These structural features can therefore be considered common characteristics. On the other hand there are also clear differences between these proteins. The bacterial enzyme chitinase A has two additional domains and endo-β-N-acetylglucosaminidase F1 lacks helices α5, α6 and α8'.

In view of the 39% sequence identity and the close similarity in three-dimensional structure between concanavalin B and hevamine, the question arises whether concanavalin B could have any chitinase activity. All (β/α)₅ barrel enzymes for which catalytic activity has been observed, have their active sites positioned in a cleft formed by the βα loops of the molecule. Surprisingly, this is also the region where the highest sequence identity between concanavalin B, hevamine and narbonin is observed (Coulson, 1994). However, if we look at essential residues for chitinase activity then it appears that these have been replaced in concanavalin B (Table 1). For instance, mutagenesis analysis identified Glu204 as an essential residue for activity in chitinase A1 of *Bacillus circulans*. The mutation Glu204-Gln completely inactivated chitinase A1 (Watanabe et al., 1993). The three-dimensional structure of hevamine assigned Glu127, which is equivalent to Glu204 of the *B. circulans* chitinase A1, as a catalytic residue (Beintema, 1994; Terwisscha van Scheltinga et al., 1994). The corresponding residue in concanavalin B is Glu131 (Figure 7). This replacement might explain why concanavalin B has no chitinase activity. In narbonin a glutamate (Glu132) is present in an equivalent position to the catalytic glutamate in hevamine and chitinase A (Table 1). However, it is involved in a salt bridge with Arg87, an interaction which seems to be incompatible with catalysis. In agreement with
solution studies it is thus unlikely that concanavalin B and narbonin have chitinase activity. Nevertheless, these proteins may still have a function in binding chitin or other carbohydrates. Another conserved residue in chitinases (Gln181 in hevamine) was originally proposed to bind a putative catalytic water molecule for an inverting mechanism (Terwisscha van Scheltinga et al., 1994). However, recent results show unambiguously that hevamine acts via a retaining mechanism (Terwisscha van Scheltinga et al., unpublished results), refuting a catalytic role for the water molecule bound to Gln181.

How similar are the potential substrate binding regions in hevamine, concanavalin B and narbonin? In hevamine, the side walls of the substrate binding cleft are formed by the glycine-rich loops β3β3' and β7α7. In concanavalin B, either loop contains one proline (Pro86 and Pro234, Figure 6). Such Gly-Pro replacements will certainly have an effect on the flexibility of these loops, and they affect substrate binding, but they do not necessarily prevent binding of carbohydrates. In narbonin, the loops that form the side walls of the cleft are connected by a salt bridge formed by Arg87 (β3α3), Asp231 (β7α7) and Glu132 (β4α4) (Hennig et al., 1992, 1995). This salt bridge has to be disrupted to make the cleft accessible for oligosaccharides. Presumably, this salt bridge prevents narbonin from acting as a chitinase, in spite of the presence of a catalytic glutamic acid.

However, there are also several residues that are fully conserved. For example, the aromatic cluster Trp265, Phe35, Tyr190 and Tyr189 in both proteins have almost identical conformations in concanavalin B, hevamine and narbonin. Two of these residues, Phe35 and Trp265, are involved in cis-peptide bonds in concanavalin B (Figures 6 and 7). This unusual geometry normally involves proline residues. Non-proline cis-peptide bonds have rarely been reported for proteins. Examination of the Brookhaven Protein Data Bank revealed only 0.05% of the non-proline peptide bonds to be cis (Stewart et al., 1990). Interestingly, in narbonin the Gly30–Phe31 and Trp261–Asn262 peptide bonds have this geometry as well, while recent further refinement of hevamine identified exactly the same feature there (A.C.T.S. & B.W.D., unpublished data). Moreover, also for the chitinase A from Serratia marcescens, the occurrence of three cis-peptide bonds has been reported (Perrakis et al., 1994). Two of these correspond to those described above. In another

Table 2. Local sequences around residues involved in non-proline cis-peptide bonds

<table>
<thead>
<tr>
<th>Secondary structure</th>
<th>Non-proline cis-peptide bonds</th>
<th>Position of cis-peptide bond</th>
</tr>
</thead>
<tbody>
<tr>
<td>Concavalin B</td>
<td>SFL 264 LWN</td>
<td>β2–β8</td>
</tr>
<tr>
<td>Hevamine</td>
<td>APL 254 LWS</td>
<td></td>
</tr>
<tr>
<td>Narbonin</td>
<td>GPA 260 FWI</td>
<td></td>
</tr>
<tr>
<td>Chitinase A</td>
<td>GFF 538 SWI</td>
<td></td>
</tr>
<tr>
<td>Position of cis-peptide bond</td>
<td>↑</td>
<td>↑</td>
</tr>
</tbody>
</table>

The proteins listed are identical to those of Table 1. The secondary structure corresponds to concanavalin B. Arrows show the positions of the cis bonds. A cis-peptide bond between Phe45 and Ser46 (β2 region), but none for the β8 region, have been reported for endo-β-acetylglucosaminidase F1.
Future work will be focused on systematic investigations of the carbohydrate binding properties of concanavalin B and narbonin. In addition, heterologous expression and purification of the proteins pave the way for site-directed mutagenesis to exchange tentative active site residues to those observed in glycohydrolases in order to determine the catalytic and carbohydrate binding properties of such mutants.

Materials and Methods

Enzymatic characterisation

Chitinase activity was assayed spectrophotometrically with CM-Chitin-RBV (Loewe Biochemica, München) as a substrate (Wirth & Wolf, 1990) using McIlvaine buffer (McIlvaine, 1921), 0.1 M Tris-HCl and 0.1 M acetate at pH values between 3.0 and 9.5 at 40°C (McIlvaine, 1921), 0.1 M Tris-HCl and 0.1 M acetate at pH 7.5-8.0 (Wirth & Wolf, 1990) using McIlvaine buffer. Lysozyme activity was determined by monitoring the values between 3.0 and 9.5 at 40°C (McIlvaine, 1921), 0.1 M Tris-HCl and 0.1 M acetate at pH 7.5-8.0 (Wirth & Wolf, 1990) using McIlvaine buffer. The catalytic and carbohydrate binding properties of observed in glycohydrolases in order to determine the catalytic and carbohydrate binding properties of such mutants.

Purification and crystallisation

Concanavalin B was purified as described (Schlesier et al., 1995). Briefly, flour from mature seeds was stirred for 30 minutes at room temperature with 2.5 parts (v/w) of 0.1 M Tris-HCl buffer (pH 9.5) containing 0.5 M NaCl. After centrifugation for 30 minutes at 6000g, microcrystals of concanavalin B were collected by sedimentation. The crystals were dissolved in 0.1 M citric acid and subsequently the pH was increased from pH 3.0 to pH 5.0 at 4°C in steps of 0.5 pH unit by dialysis against McIlvaine buffer. Crystallisation by pH-shift is a suitable method for the growth of well-diffracting crystals for high resolution X-ray analysis (Hennig & Schlesier, 1994). Crystals with a maximum size of 4 mm × 0.3 mm × 0.3 mm grew within a week. The crystals diffract to better than 1.4 Å resolution. The structural analysis revealed that they belong to space group P61, with unit cell parameters a = b = 81.4 Å, c = 102.2 Å, α = β = 90°, γ = 120°. One molecule in the asymmetric unit corresponds to a Vv value of 2.88 Å3/Da and a solvent content of about 57% using the sequence derived molecular mass of 33,828 (Matthews, 1968).

Data collection and processing

A needle-shaped crystal was mounted in a glass capillary and X-ray diffraction data to 1.65 Å resolution were measured on a MAR-Research image plate area detector system mounted on a modified Elliott GX-20 rotating anode generator (CuKα, 40 kV and 50 mA). Data evaluation was performed with the XDS program package (Kabsch, 1988). The integrated intensities were converted into CCP4 format by ROTAPREP, scaled with the program ROTAVATA and merged using AGROVATA. The reflection intensities were finally converted to structure factor amplitudes using TRUNCATE (SERC, 1994). The excellent quality of the diffraction data is indicated by an Rsym of 4.2% for the entire data set. Details on data collection parameters and statistics of the measured data are summarised in Table 3.

Structure determination

Co-ordinates of the structures of narbonin (R-factor 15.9% for data between 10.0 and 1.8 Å, r.m.s. deviations from ideal bond length 0.015 Å, Brookhaven PDB code 1NAR) and hevamine (R-factor 16.9% for data between 10.0 and 2.2 Å, r.m.s. deviations from ideal bond length 0.014 Å, Brookhaven PDB code 1HVM) were used as models in molecular replacement. Several search models were tried for cross-rotation function calculations using AMoRe (Navaza, 1994). Cross-rotation calculation gave no

Table 4. Statistics of the final model

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
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<tr>
<td>No. of protein atoms</td>
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<tr>
<td>No. of water molecules</td>
<td>288</td>
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<tr>
<td>r.m.s. deviation from ideal distances (1–2) (Å)</td>
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<tr>
<td>r.m.s. deviation from ideal bond angles (°)</td>
<td>1.8</td>
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<td>Mean B-factor for protein atoms (Å²)</td>
<td>15.1</td>
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<tr>
<td>Mean B-factor for water molecules (Å²)</td>
<td>39.0</td>
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<tr>
<td>R-factor* (10.0–1.65 Å, all data) (%)</td>
<td>17.2</td>
</tr>
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</table>

* R-factor = \( \sum_{i} \frac{|F(hkl)| - F(hkl)|}{\sum_{i} F(hkl)} \).

Table 3. Data collection statistics

<table>
<thead>
<tr>
<th>Parameter</th>
<th>Value</th>
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<tr>
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</tr>
<tr>
<td>Measured reflections</td>
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</tr>
<tr>
<td>Unique reflections</td>
<td>40,387</td>
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<td>Resolution ranges (Å)</td>
<td>15.0–1.65 (all data) 15.0–2.0 1.74–1.65</td>
</tr>
<tr>
<td>Redundancy</td>
<td>3.6 4.1 2.9</td>
</tr>
<tr>
<td>Relections with I &gt; 3σ (%)</td>
<td>82.2 92.8 63.3</td>
</tr>
<tr>
<td>Completeness (%)</td>
<td>85.9 94.7 64.1</td>
</tr>
<tr>
<td>Rsym</td>
<td>0.041 0.032 0.230</td>
</tr>
</tbody>
</table>

\[ R_{sym} = \frac{\sum_{hkl} |I(hkl)| - \langle I(hkl) \rangle}{\sum_{hkl} I(hkl)} \]
significant solution, neither for narbonin nor hevamine models. The orientations of the molecule corresponding to 50 cross-rotation peaks with the highest correlation were tried in a translation search. The highest signal-to-noise ratio for the correlation coefficient and lowest R-factor were observed with a modified hevamine structure in which the residues 40 to 58 and 107 to 112 (hevamine numbering) had been removed and residues non-identical to concanavalin B had been substituted for serine residues (alanine or glycine residues in hevamine were not changed). The overall sequence identity between hevamine and concanavalin B is about 39% (Schlesier et al., 1995). A Patterson integration radius of 15 Å and a resolution range 15 to 4.5 Å gave the best signal-to-noise ratio in the rotation function calculation. A clear maximum in the translation search using data from 12.0 to 4.0 Å was found. The search model, placed accordingly in the unit cell, gave an initial R-factor for all data in this resolution range of 51.3%.

Refinement

The position and orientation of the molecule, as a single rigid entity, were refined for ten cycles with X-PLOR (Brünger, 1992a) using reflections in the resolution range of 10.0 to 6.0 Å. This rigid body refinement reduced the R-factor from 49.0 to 45.2%. Extension of the resolution to 3.0 Å and further refinement of 21 rigid segments of the molecule (each segment containing at least one strand or helix or loop region) lowered the R-factor to 43.6%. The free R-factor (Brünger, 1992b), for 10% of the observed X-ray data not used in the refinement, was 47.1% after this step confirming the correctness of the solution.

After energy minimisation of the model (preparation step) and determination of a suitable weighting scheme a simulated annealing run was carried out. An initial temperature of 3000 K was lowered to 300 K by 25 K per simulated annealing run was carried out. An initial step) and determination of a suitable weighting scheme a

Acknowledgement

We thank Professor Kasper Kirschner for discussions and critical reading of the manuscript.

References


of hydrogen-bonded and geometrical features. 

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