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Broad antibiotic resistance profile of the subclass B3 metallo-β-lactamase GOB-1, a di-zinc enzyme

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Introduction

Metallo-β-lactamases (MBLs) belong to class B of the β-lactamases [1–3]. All MBLs exhibit the αββα sandwich fold [4] and unlike the enzymes of other classes (A, C and D), which all contain a nucleophilic serine residue in their active site, the MBLs utilize zinc to perform hydrolysis [5,6]. The heterogeneous class of MBLs is further divided into three groups (B1 and B3 MBL structures. Here we produced and studied the Q116A, Q116N and Q116H mutants. The substrate profiles were similar for each mutant, but with significantly reduced activity compared with that of the wild-type. In contrast to the Q116H enzyme, which bound two zinc ions just like the wild-type, only one zinc ion is present in Q116A and Q116N. These results suggest that the Q116 residue plays a role in the binding of the zinc ion in the QHH site.

The metallo-β-lactamase (MBL) GOB-1 was expressed via a T7 expression system in Escherichia coli BL21(DE3). The MBL was purified to homogeneity and shown to exhibit a broad substrate profile, hydrolyzing all the tested β-lactam compounds efficiently. The GOB enzymes are unique among MBLs due to the presence of a glutamine residue at position 116, a zinc-binding residue in all known class B1 and B3 MBL structures. Here we produced and studied the Q116A, Q116N and Q116H mutants. The substrate profiles were similar for each mutant, but with significantly reduced activity compared with that of the wild-type. In contrast to the Q116H enzyme, which bound two zinc ions just like the wild-type, only one zinc ion is present in Q116A and Q116N. These results suggest that the Q116 residue plays a role in the binding of the zinc ion in the QHH site.

Abbreviations

ICP, inductively coupled plasma; IPTG, isopropyl β-D-1-thiogalactopyranoside; LB, Luria–Bertani; MBL, metallo-β-lactamase; TB, terrific broth.
broadest substrate range of the MBLs and is uniquely tetrameric [9,24,25]. FEZ-1 shares 29.7% sequence identity with L1, but has a more limited substrate profile, with a strong preference for cephalosporins [16,26]. GOB-type enzymes include 18 variants, including GOB-1, the first isolated GOB enzyme [17]. GOB-1 is from *Elizabethkingia meningoseptica* (formerly *Chryseobacterium meningosepticum*), the pathogen responsible for neonatal meningitis, and also found to attack immunocompromised patients. It shares sequence identities of 28% with L1 and 43% with FEZ-1 (computation performed at the SIB using the BLAST network service). The GOB-18 variant studied by Moran-Barrio et al. [18] differs from GOB-1 by just three residues, Phe94, Ala137 and Asp282, far from the active site.

The three subclasses of MBLs also differ in their zinc dependency [7]. Subclass B1 enzymes can be active with one or two zinc ions in their active sites, whereas those of subclass B3 contain two zinc ions [27,28]. In contrast, subclass B2 enzymes are active with one zinc ion and are inhibited by the binding of a second zinc ion [29]. The crystal structures of the MBLs highlight two sites of zinc co-ordination. The first zinc site in classes B1 and B3 (HHH) is composed of residues His116, His118 and His196. The sole exceptions to this are the GOB enzymes, which have a glutamine at position 116. In subclass B2, position 116 is occupied by an asparagine residue [7] and this was previously thought to be one of the residues to which the inhibitory zinc binds. However, the recent structure of the subclass B2 CphA showed that the second inhibitory zinc ion was just bound to the two remaining histidines, His196 and His118 [30]. The second zinc site of subclass B1 is identical to the first site of subclass B2 and consists of Asp120, Cys221 and His 263 (DCH), whereas in subclass B3, Cys221 is replaced by His121 (DHH) as a zinc ligand [7,15,26].

Even though the GOB enzymes appear to have only one intact zinc-binding site, they were placed in subclass B3 on the basis of their amino acid sequences [17]. However, unlike L1 [24] they are monomeric and unlike FEZ-1 [18] show no preference for cephalosporins [17]. The crystal structures of both L1 and FEZ-1 have been published [15,26], whereas the structure of a GOB-type enzyme has yet to be solved. Recent work by Moran-Barrio et al. [18] suggests that the active form of the enzyme contains only one zinc ion, located in the DHH site. This is in contrast to all known B1 and B3 MBLs, with the possible exception of the mono-Co²⁺ form of BcII [31]. In the work described here, we produced the GOB-1 MBL in *Escherichia coli* from a T7-based expression vector. The results presented herein provide evidence for the presence of two zinc ions in the enzyme as purified. Therefore, in contrast to the GOB-18 variant [18], denaturing and refolding in the presence of zinc was not required. Although the outcome of the kinetic study, performed in the presence and absence of additional zinc, varied with the replacing residue, each Gln116 mutant showed a significant decrease in activity when compared with the wild-type enzyme.

**Results**

**Construction of expression vector and preliminary expression experiments**

The pGB1 expression vector was constructed to include the enzyme’s own signal peptide and stop codon. The preliminary expression trials showed that the best yield was obtained in terrific broth (TB) medium in the absence of isopropyl β-D-1-thiogalactopyranoside (IPTG) with incubation at 28 °C for 24 h and showed no noticeable expression of the unprocessed precursor species. Under these conditions, GOB-1 represented only a low percentage of cell protein, but significantly more than with the pBS3 plasmid, previously described in Bellais et al. [17]. Unfortunately, with the crude extracts derived from the expression trials, activation by the substrate was observed, which made quantification difficult. This prevented an accurate determination of the quantity of GOB-1 present in the crude extract, but an estimate using the highest rate suggested that ~40 mg of GOB-1 was produced per litre of culture.

**Purification of wild-type GOB-1**

The reported purifications of several MBLs utilize an S-Sepharose column as the first purification step. When applied to GOB-1, this step yielded an enzyme with few contaminants. The second step was an UNO S12 column and allowed the removal of some impurity, but was not sufficient to reach homogeneity. A further purification step on a molecular sieve removed the two remaining contaminants of lower molecular masses. After the three purification steps, 7.6 mg of GOB-1 were produced, showing no contaminants by SDS/PAGE. The use of the molecular sieve column also confirmed a 30 kDa molecular mass and thus a monomeric structure, as shown by Bellais et al. [17].

**MS and N-terminal sequencing of wild-type GOB-1**

The ESI-TOF MS spectra of the denatured protein (data not shown) showed two peaks, indicating the
The presence of two proteins separated by 299 Da. The native ESI-TOF MS spectra (Fig. 1) also showed two peaks separated by 300 Da. This showed the presence of two proteins that could not be separated during purification and by SDS/PAGE and that contained the same amount of zinc. This implied that both proteins were GOB-1, although one was modified in some way, probably by incorrect cleavage of the signal peptide to create β-lactamase ragged ends.

The mass difference between the native and denatured spectra corresponds to the mass of zinc in the enzyme (Table 1). The result suggests that the native protein contains two zinc ions per wild-type molecule. The other members of subclass B3, both L1 and FEZ-1, also contain two zinc ions in their active sites [9,10].

To verify the hypothesis that GOB-1 has ragged ends (not a unique phenomenon with respect to MBLs [32]), the N-terminus of the enzyme was sequenced. The presence of two N-terminal sequences QVVKE and LNAQV confirmed that the signal peptide was cleaved at two positions.

### Table 1. Masses of the wild-type and mutant enzymes measured by ESI-TOF MS and calculated from their amino acid sequences.

<table>
<thead>
<tr>
<th>GOB-1 enzyme</th>
<th>Calculated</th>
<th>Denatured</th>
<th>Native</th>
<th>Difference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Wild-type</td>
<td>31196.5</td>
<td>31195.5</td>
<td>31321</td>
<td>125.5</td>
</tr>
<tr>
<td>Q116A</td>
<td>31139.0</td>
<td>31138.5</td>
<td>31202</td>
<td>63.5</td>
</tr>
<tr>
<td>Q116N</td>
<td>31182.0</td>
<td>31183.0</td>
<td>31243</td>
<td>60.0</td>
</tr>
<tr>
<td>Q116H</td>
<td>31205.5</td>
<td>31206.0</td>
<td>31331</td>
<td>125.0</td>
</tr>
</tbody>
</table>

In addition, a sample was digested using trypsin and the molecular mass of the resulting peptides was measured by MALDI-TOF MS (Fig. 2). A theoretical digestion of GOB-1 was performed using Peptide Mass on the expasy.org website. The sequence coverage given by the peptides produced by the tryptic digestion of GOB-1 is shown in Fig. S1. All the peaks detected by MALDI-TOF MS could be identified as peptides produced by the tryptic digestion, with three exceptions. The peak at 1598 (Fig. 2) is not a theoretical product of digestion. It does, however, correspond to the mass of the N-terminal peptide (1299 kDa) plus 298 Da, a value that in turn corresponds to the mass of the last three amino acids of the signal peptide, LNA. Another of the unidentified peptides, of mass 1282, is the mass of the N-terminal peptide less 17 Da, suggesting that the N-terminal glutamine residue has undergone cyclization into pyro-glutamate with the loss of NH₃. The third peak at 1453 kDa could not be explained and does not correspond to digestion of the enzyme or unprocessed precursor species.

**Mutation of the Gln116 residue**

At position 116, GOB-1 has a glutamine rather than a histidine residue like other members of subclass B3 (or indeed subclass B1). To investigate the effect of this residue it was mutated to histidine, asparagine (the amino acid at position 116 in subclass B2) and, as a control, alanine, giving the Q116H, Q116N and Q116A mutants, respectively.

The best purification method found for the mutant enzymes was to use the S-Sepharose column, followed by a 5 mL Econo-Pac CHT-II cartridge. The remaining
impurities were removed in a third purification step on an S-Source column. This last step produced two elution peaks for each enzyme. In each case, the mass difference between the two elution peaks was found to be 18 Da by ESI-TOF MS (Fig. 3) and the highest peak corresponded to the theoretically calculated mass. As a consequence, the N-terminal residue of the mutants has undergone partial cyclization. The protein of highest molecular mass (Table 1) was used in all experiments.

**MS of GOB-1 mutants**

Native ESI-TOF MS spectra of the mutants were obtained. Although Fig. 4 reveals the presence of many salt peaks, the spectra suggest that both Q116N and Q116A contain one zinc ion per molecule. This was confirmed by the inductively coupled plasma (ICP)/MS results (see below). Therefore, the mutation of the glutamine residue at position 116 results in the loss of zinc from the corresponding site of the enzyme under MS conditions. Q116H, like the wild-type, contains two zinc ions (Tables 1, 2).

**Determination of the zinc and iron contents using ICP/MS**

In contrast to the wild-type and Q116H enzymes, ICP/MS failed to highlight the binding of two zinc ions by the Q116A and Q116N enzymes (Table 2). Moreover, the ICP/MS discarded the presence of bound iron in all the enzymes.

**Kinetic study**

Before the kinetic characterization of GOB-1, the optimum concentration of ZnCl₂ in the buffer was determined. At the three concentrations of imipenem tested, the addition of Zn²⁺ in the buffer did not significantly modify the activity. However, 50 μM ZnCl₂ gave a slightly higher rate of hydrolysis. Consequently, 50 μM ZnCl₂ was thereafter added to the buffer.

The steady-state kinetic parameters of the wild-type and mutant GOB-1 enzymes were measured with the β-lactam substrates benzylpenicillin, cefoxitin, cephalothin, imipenem, meropenem and nitrocefin, both in the
presence and the absence of added zinc. The results are shown in Table 3. The wild-type enzyme hydrolysed all the substrates very efficiently, almost independently of the zinc concentration in the buffer, showing no strong preference for any type of β-lactam. Our results support those previously reported for GOB-1 [17], with the enzyme showing the highest rate of substrate turnover with penicillin ($k_{cat}$ = 630 s$^{-1}$) and the highest $k_{cat}/K_M$ value with meropenem (8.0 μM$^{-1}$s$^{-1}$).

The mutations of Gln116 significantly affected the catalytic ability of the enzyme, as would be expected for a zinc-binding residue. In the absence of added zinc, the activity was decreased 60–600-fold when the residue was mutated to the nonchelating alanine (Q116A). However, the resulting enzyme was not completely inactive and although the $k_{cat}$ values were dramatically decreased, the $K_M$ values were very similar. Activity was not restored by the addition of 50 μM zinc. Indeed, although $k_{cat}$ values slightly increased (e.g. 4.6-fold for imipenem), the $k_{cat}/K_M$ values slightly decreased due to the large increase in $K_M$ values (34-fold for imipenem).

The effects of the Q116N mutation were slightly different. The results in Table 2 show an important loss of activity in the absence of zinc (160–1500 times), mainly due to a decrease in $k_{cat}$ values. The $K_M$ values remained quite similar (meropenem, cefoxitin), slightly (imipenem, benzylpenicillin) or significantly increased (nitrocefin, cephalothin). In contrast to the Q116A mutant, the activity of the Q116N mutant increased when 50 μM zinc was present in the buffer (Q116N is then only 1.3–110-fold less active than the wild-type). $K_M$ values were similar to that of the wild-type (with the exception of nitrocefin). Initial hydrolysis rates of 100 μM nitrocefin were measured in the presence of increasing zinc concentrations (0, 1, 2.5, 5, 10, 25, 50, 100, 250, 500 and 1000 μM). This experiment showed that the maximal rate is obtained at 50 μM zinc concentration and is constant up to the highest tested concentration. The apparent dissociation constant for the second zinc ion ($K_D$) determined from this graph was 2.5 ± 0.3 μM (Fig. S2).

The effects of the Q116H mutation were less drastic. The activity decrease in comparison with the wild-type enzyme was only 2.1–74-fold. The $k_{cat}$ values decreased only 1.9- (for benzylpenicillin) to 50-fold (for imipenem). The $K_M$ values significantly increased for all the substrates but meropenem and cefoxitin. Q116H showed similar $k_{cat}$ and $K_M$ values in the presence of 50 μM zinc.

Table 2. Summary of zinc binding for wild-type and mutants GOB-1. Standard deviation values were below 10%.

<table>
<thead>
<tr>
<th>Protein</th>
<th>Zn$^{2+}$ content in a buffer containing less than 0.4 μM of free zinc</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>MS</td>
</tr>
<tr>
<td>Wild-type</td>
<td>2</td>
</tr>
<tr>
<td>Q116A</td>
<td>1</td>
</tr>
<tr>
<td>Q116N</td>
<td>1</td>
</tr>
<tr>
<td>Q116H</td>
<td>2</td>
</tr>
</tbody>
</table>

**Apo-GOB-1 and the remetallated form**

The GOB-1 apoprotein was devoid of β-lactamase activity that could be recovered by the addition of Zn(II). Remetallated GOB-1 bound 2 equivalents of zinc, as shown by ICP/MS and MS (Fig. S3). However, its activity was only 60% of that of the enzyme as isolated. The addition of zinc (50 μM, 100 μM or 1 mM) to the reaction medium did not significantly modify this activity.
Inactivation by metal chelator

EDTA inactivated GOB-1 and its mutants in a time-dependent manner. The \( k_i \) was independent of chelator concentration for the wild-type and mutant enzymes (Fig. S4). This suggests that EDTA acts by scavenging the free metal, with the \( k_i \) value representing the rate of zinc dissociation from the enzyme. The \( k_i \) value of wild-type GOB-1 was measured in the concentration range 0.5–50 \( \mu M \), similar to those used to inactivate the other B3 enzymes L1 [24] and FEZ-1 [10] (up to 200 \( \mu M \) and 0.5–10 \( \mu M \), respectively), indicating \( k_i \) values of \( \sim 0.0053 \) s\(^{-1}\). This result is not very different from that obtained with FEZ-1 (0.025 s\(^{-1}\)) [10]. By comparison, incubation of IMP-1 (subclass B1) with 10 mM EDTA for 1 h only inactivated the enzyme by 10% [33]. The mutants behaved in a similar manner and the following \( k_i \) values were obtained: Q116A, 0.0044 s\(^{-1}\); Q116H, 0.0068 s\(^{-1}\) and Q116N 0.011 s\(^{-1}\).

In the cases of the di-zinc species (i.e. the wild-type and Q116H), these rather similar apparent \( k_i \) values might correspond to the loss of the most tightly bound Zn\( ^{++} \).

Discussion

The MBL GOB-1 is a very efficient enzyme that hydrolyses the six tested \( \beta \)-lactams with \( k_{cat}/K_M \) values above \( 10^6 \) M\(^{-1}\)s\(^{-1}\). All the \( k_{cat}/K_M \) values reported here are slightly higher (between 1.5- and 10-fold) than those previously published by Bellais et al. [17], probably because of the higher protein purity. The kinetic parameters determined here for the GOB-1 enzyme are also similar to those previously determined for the GOB-18 variant [18].

The mutants of GOB-1 generated by site-directed mutagenesis of Gln116 exhibit a loss of activity that cannot be corrected by the addition of zinc. The Q116H mutant and the wild-type enzyme both contain two zinc ions in the active site and therefore show little difference upon the addition of further zinc. However, the mutant exhibited significantly less activity than the
wild-type GOB-1 (\(k_{\text{cat}}\) shows a two- to 50-fold decrease, dependent upon which substrate is examined) and increased \(K_m\) values, suggesting that the steric effect of the larger, less flexible histidine residue hinders the positioning of the substrates in the active site. Another possibility would be the creation of a modified zinc position in the recreated HHH site leading to a decreased efficiency. However, as all other B1 and B3 enzymes include a histidine at position 116, this will remain speculation until the structure of the GOB-1 active site is directly determined.

In contrast to the Q116H mutant, the presence of an alanine or an asparagine residue at position 116 decreased the ability of the latter mutants to chelate a zinc ion in the AHH or NHH site. Indeed, in the absence of added zinc ([Zn] < 0.5 \(\mu\)M), these mutants were under a mono-zinc form, whereas the wild-type GOB-1 is already in a di-zinc form. The \(K_m\) values determined in these conditions for the Q116A mutant are very similar to those corresponding to the wild-type enzyme. This suggests that the Q116A mutation, which affects the metal content, does not affect the binding of the substrates. A similar behaviour is observed for the carboxamidase activity of the Q116N mutant.

This decreased ability to chelate a second zinc is also reflected by the \(K_D\) value determined for the Q116N mutant. These results prove that Q116 plays a role in the binding of the zinc ion in the QHH site. The \(k_{\text{cat}}\) and \(k_{\text{cat}}/K_m\) values of the Q116A and Q116N mutants were strongly decreased (\(k_{\text{cat}}\) shows an 11–284-fold decrease for Q116A and a 23–227-fold decrease for Q116N compared with that of the wild-type) and cannot be restored by the addition of zinc. Nevertheless, the activity of the Q116N mutant increased with increasing zinc concentration in the buffer. This contrasts with the subclass B2 enzymes, which also have an asparagine residue at this position [7], as they are inhibited upon binding of a second zinc ion. However, it was demonstrated by Bebrone et al. [30] that this inhibition results from immobilization of the catalytically important His118 and His196 residues.

Our results differ from those obtained for the GOB-1 variant, which is supposed to be fully active with a single zinc ion in the DHH zinc-binding site [18]. GOB-1 and GOB-18 enzymes only differ by three single amino acid changes, if this is a zinc-binding residue. However, as all other B1 and B3 enzymes include a histidine at position 116, this will remain speculation until the structure of the GOB-1 active site is directly determined.

Materials and methods

**Chemicals**

Buffers and BSA were purchased from BDH Chemicals (Poole, UK) or Sigma-Aldrich (Steinheim, Germany); IPTG from Eurogentech (Liége, Belgium) and kanamycin, dimethylsulfoxide and ZnCl₂ from Merck (Darmstadt, Germany). Meropenem (\(\Delta\varepsilon_{300} = -6500 \ M^{-1} \cdot \text{cm}^{-1}\)) was a gift from ICI Pharmaceuticals (Macclesfield, UK). Imipenem (\(\Delta\varepsilon_{300} = -9000 \ M^{-1} \cdot \text{cm}^{-1}\)) was a gift from Merck Sharpe and Dohme Research Laboratories (Rahway, NJ, USA). Benzylpenicillin (\(\Delta\varepsilon_{235} = -775 \ M^{-1} \cdot \text{cm}^{-1}\)) was a gift from Rhône-Poulenc (Paris, France). Chloramphenicol, cefoxitin (\(\Delta\varepsilon_{260} = -6600 \ M^{-1} \cdot \text{cm}^{-1}\)), cephalothin (\(\Delta\varepsilon_{273} = -6300 \ M^{-1} \cdot \text{cm}^{-1}\)) and EDTA were purchased from Sigma (St Louis, MO, USA) and nitrocef (\(\Delta\varepsilon_{432} = 15 000 \ M^{-1} \cdot \text{cm}^{-1}\)) from Unipath Oxoid (Basingstoke, UK). Sequencing grade modified trypsin was obtained from Promega (Madison, WI, USA) and \(\alpha\)-cyano-4-hydroxycinnamic acid was from Aldrich (Taufkirchen, Germany). The peptide standard mixture was purchased from Applied Biosystems (Foster City, CA, USA).

**Bacterial strains and vectors**

The plasmid pBS3 has been described previously. *Escherichia coli* DH5α was used as the host for recombinant plas-
mids during the construction of the expression vectors. *Escherichia coli* BL21-DE3 and *E. coli* BL21-DE3 (pLysS) (Novagen, Madison, WI, USA) were both tested as the hosts for the expression plasmids. The expression vector pET28a (Novagen) was used for the construction of the T7-based expression factor.

**Construction of the expression vector and preliminary expression experiments**

*Bam*HI and *XhoI* restriction sites were introduced at either end of the *bla*GOB-1 gene by PCR using the oligonucleotide primers (5'-GGGGGGAATCCATGAGAAATTTTGCTA CACTGTTTTTCATG-3') and (5'-CCCCCCCCCTCGAGTTAACATTTTGCTGCTTACTT-3'), where the restriction sites generated are underlined. The PCR conditions were: incubation at 95 °C for 5 min; 30 cycles of amplification that involved denaturation for 1 min at 95 °C, annealing for 1 min at 58 °C and extension for 1 min at 68 °C; and 5 min at 68 °C after the cycling. *Pfu* and *taq* polymerase (Promega) were used for the PCR. The PCR products were cloned into the pET28a vector to obtain the recombinant plasmid pGB1, which was then transformed into *E. coli* DH5α. The gene was sequenced to verify that no unwanted mutations had taken place during the PCR.

The pGB1 vector was transformed into *E. coli* BL21-DE3 and BL21-DE3 (pLysS). Preliminary expression trials involved single colonies of *E. coli* BL21-DE3 and BL21-DE3 (pLysS) containing pGB1 used to inoculate 100 mL Luria–Bertani (LB), containing 50 μg mL⁻¹ kanamycin. The cultures were incubated overnight at 37 °C with orbital shaking at 250 r.p.m. before 2 mL samples were removed and added to 100 mL medium. Three types of medium, 2XYT (16 g L⁻¹ tryptone, 10 g L⁻¹ yeast extract, 5 g L⁻¹ sodium chloride), TB and LB, supplemented with 50 μg mL⁻¹ kanamycin were tested. After selection of the best medium, additional conditions were studied: two temperatures (28 and 37 °C), when the culture reached an absorbance of 0.6 at 600 nm and three different IPTG concentrations (0, 0.1 and 1 mM). Aliquots (2 mL) of the various cultures were sampled after 2, 4, 6, 24, 33 and 48 h. After centrifugation for 1 min at 15 000 g, the bacterial pellet was resuspended in 500 μL buffer (Hepes; 20 mM at pH 6.5 containing 50 μM ZnCl₂). Cells were lysed by sonication on ice, which involved 5 × 15 s pulses with 30 s delays. The cell debris was removed by centrifugation at 15 000 g for 10 min at 4 °C. A 15 μL sample from each aliquot was analysed by SDS/PAGE.

The enzyme activity in each sample was determined by following the hydrolysis of 100 μM imipenem at 300 nm in 20 mM Hepes at pH 6.5 containing 50 μM ZnCl₂ using a Uvikon XL spectrophotometer and 10 mm path length cells.

**Mutagenesis**

The Quick Change site-directed mutagenesis kit (Stratagene, La Jolla, CA, USA) was used to perform the mutagenesis on the pGB1 plasmid. The primers used for this experiment were as follows:

For the Q116A mutant forward and reverse:

(5'-GATCTTGCTTTACTGGGCTCACTACGACC ATACAGG-3')
(5'-GCACCTGTATGGTGTTAGTGAGCAGCAATTTTGTC-3'),

For the Q116N mutant forward and reverse:

(5'-GATCTTGCTTTACTAACGCTCAGTACGACC ATACAGG-3')
(5'-GCACCTGTATGGTGTTAGTGAGCAGCGTTAGTAAG CAGC-3')

For the Q116H mutant forward and reverse:

(5'-GATCTTGCTTTACTCATCAGTACGACC ATACAGG-3')
(5'-GCACCTGTATGGTGTTAGTGAGCAGCGTTAGTAAG CAGC-3')

**Production and purification of the zinc β-lactamase**

LB medium (100 mL) containing 50 μg mL⁻¹ kanamycin was inoculated with a colony of *E. coli* BL21-DE3 carrying the pGB1 plasmid and incubated overnight at 37 °C with orbital shaking at 250 r.p.m. Twenty millilitres of preculture were added to 2 L LB medium and incubated at 28 °C for 24 h under orbital shaking. Cells were harvested by centrifugation at 14 500 g for 20 min at 4 °C. The pellet was resuspended in 200 mL buffer A (20 mM sodium cacodylate, pH 6.5) before the cells were disrupted (Basic Z model; Constant Systems Ltd, Warwick, UK). Cell debris was removed by centrifugation at 14 300 g for 40 min at 4 °C and the supernatant dialysed overnight against buffer A at 4 °C. The crude extract was then loaded on to an S-Sepharose FF column (2.6 × 34 cm; Pharmacia, Uppsala, Sweden) equilibrated in buffer A. The column was washed with buffer A before a salt gradient of 0–0.5 M NaCl in five column volumes was used to elute the GOB-1 protein. The active fractions were pooled and dialysed overnight against buffer A to remove the salt. The sample was loaded on to an UNO S-12 column equilibrated with buffer A and eluted with a 0–0.5 M NaCl gradient in five column volumes. The fractions that showed β-lactamase activity were then loaded on to a Sephacryl-100 molecular sieve column (1.5 × 56 cm) previously equilibrated in buffer B (buffer A with 0.25 M NaCl). For molecular mass determination on this column, the following proteins were used for calibration; BSA 66.2 kDa, ovalbumin 45 kDa, soybean trypsin inhibitor 21.5 kDa, lysozyme 14.4 kDa. Active fractions were pooled, dialysed against buffer A and concentrated to a final concentration of approximately 1 mg mL⁻¹, before being stored at −20 °C.
The mutant plasmids were transformed into *E. coli* BL21-DE3 and production was carried out as described above for the wild-type. Purification was performed as described for the wild-type with the following modifications. The second column used was a 5 mL ceramic hydroxyapatite Econo-Pac CHT-II cartridge (Bio-Rad, Hercules, CA, USA). The purification was carried out as suggested in the manufacturer’s instructions. The third column, an S-Source column from Amersham Biosciences (Piscataway, NJ, USA), was used to separate the desired mutants from the variant of the enzyme with an N-terminal pyro-glutamate residue. The enzyme was loaded and the column was washed in 20 mM sodium cacodylate pH 6.5 before a salt gradient of 0–0.5 M NaCl in 10 column volumes was used to elute the GOB-1 mutant.

**MS and the determination of the N-terminal sequence**

**Native or denatured intact enzyme**

Enzyme samples were desalted using Microcon YM-10 (10 kDa) centrifugal filters (Millipore, Billerica, MA, USA) in 15 mM ammonium acetate (pH 7.5). Seven dilution/concentration steps were performed at 4 °C and 14 000 g. This yielded a 100 μM stock enzyme solution in ammonium acetate pH 7.5. The experimental samples were then prepared by diluting the enzyme to a final concentration of 15 μM in 15 mM ammonium acetate pH 7.5 directly in a 96-well plate. ESI-MS analyses used a Q-TOF MS (Q-TOFmicro Micromass, Altrincham, UK) interfaced with a NanoMate™ chip-based nano-ESI source (Advion Biosciences, Ithaca, NY, USA). Samples were infused through the Q-TOF through the ESI chip (estimated flow rate 100 nL·min⁻¹). Typically, a spraying voltage of 1.70 kV ± 0.1 kV, depending on the ‘sprayability’ of the sample, and a sample pressure of 1.70 kV ± 0.1 kV, depending on the cooling.

**Peptide mapping**

After denaturation at 100 °C for 15 min, 10 μg of GOB-1 was digested with 0.5 μg trypsin in 50 mM NH₄HCO₃ (pH 8) for 4 h at 37 °C. The digestion was stopped by adding 0.1% trifluoroacetic acid. Digested protein (10 μL) was loaded on to a ZipTip C18 (Millipore). Elution was performed with a 10 μL matrix solution (α-cyano-4-hydroxycinnamic acid in 50% acetonitrile, 0.1% trifluoroacetic acid) on a MALDI plate and dried before the MALDI measurement.

**MS analysis** was performed using a 4800 MALDI TOF/TOF™ analyser (Applied Biosystems/MDS SCIEX) equipped with a 200 Hz Nd:YAG-Laser (λ = 355 nm, 3–7 ns pulse width). MS data were acquired in the positive ion reflectron mode with 470 ns delayed extraction, accumulating 500 laser shots using the 4000 Series EXPLORER™ remote access client software (version 3.5.1). External mass calibration was performed in the mass range m/z of 800–3500. The calibration mixture consisted of the following compounds: des-Arg¹-bradykinin (904.4681), angiotensin I (1296.6853), Glu¹-fibrinopeptide B (1570.6774), adrenocorticotropic hormone fragments 1–17 (2093.0867), adrenocorticotropic hormone fragments 18–39 (2465.1989), adrenocorticotropic hormone fragments 7–38 (3557.9294). For MS/MS measurements, the acceleration voltage was 8 kV, the laser energy 4090 and 4000 laser shots were accumulated.

**N-terminal sequence**

The N-terminal sequence was determined using a gas-phase sequencer (Prosite 492 protein sequencer; Applied Biosystems).

**Determination of the zinc and iron content using ICP/MS**

Protein samples were dialysed against 20 mM sodium cacodylate, pH 6.5. Protein concentrations were then determined by standard colorimetric assays (BCA; Pierce, Rockford, IL, USA). Zinc and iron concentrations were measured by ICP MS at the Malvoz Institute (Province de Liège, Belgium). The metal/enzyme ratio was calculated from the differences in metal concentration between the enzyme sample and the dialysis buffer.

**Determination of kinetic parameters**

Hydrolysis of antibiotics by the wild-type and mutant GOB-1 was monitored by following the variation in absorbance using a Uvikon 860 spectrophotometer connected to a microcomputer via an RS232 serial interface or a Uvikon XL spectrophotometer. Reactions were performed in thermostatically controlled 10 and 2 mm path length cells at 30 °C and using 20 mM sodium cacodylate buffer pH 6.5, containing 20 μg·mL⁻¹ BSA (and 50 μM ZnCl₂ when indicated). The steady-state kinetic parameters were determined under initial rate conditions using the Hanes linearization of the Henri–Michaelis–Menten equation. Low KM values were determined as KM using meropenem as the reporter...
substrate. In these cases, the $k_{cat}$ values were obtained from initial hydrolysis rates measured at saturating substrate concentrations. All data were analysed using Microsoft Excel and the KALEIDAGRAPH 3.5 programme [36].

Enzymatic measurement in the presence of increasing concentrations of zinc and the determination of $K_{D2}$

Activity was measured in the presence of increasing concentrations of zinc at 30 °C in 20 mM sodium cacodylate buffer pH 6.5, containing 20 μg mL$^{-1}$ BSA, as previously described. The binding of the second zinc ion resulted in an increase in activity and equation 1 was used:

$$RA = \frac{\left[\{\text{Zn}\} \nabla \right]}{\left(\left[\text{Zn}\right] + K_{D2}\right)}$$

where $\nabla$ represents the ratio of activity at saturating zinc concentration versus activity in the absence of added zinc (Act. [Zn]=$\nabla$/Act. [Zn](0)).

Experimental data were fitted to equation 1 by nonlinear regression analysis with the help of the SIGMA PLOT software.

Preparation of the GOB-1 apoenzyme and the remetallated form

The GOB-1 apoprotein was prepared by treating ~40 μM enzyme samples in 10 mM Tris/HCl, pH 7.0, with chelating agents in mild denaturing conditions, as previously described for GOB-18 [18]. The remetallated form was obtained by dialysing the apo-GOB-1 against 100 volumes of 10 mM Tris/HCl, pH 7.0, 50 mM NaCl, with 40 μM ZnSO$_4$.

Inactivation by chelating agents

The inactivation of wild-type and mutant GOB-1 by the chelating agent EDTA was followed using imipenem as a reporter substrate and measuring the initial rates of hydrolysis at varying EDTA concentrations (0.5–50 μM), in the same buffer as that used for the other kinetic experiments, without the addition of zinc. The dependence of $k_i$ on the concentration of chelating agent was investigated.

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References


Supporting information

The following supplementary material is available:

Fig. S1. GOB-1 sequence, including the LNA from the signal peptide. Peptides from the tryptic digestion identified by MALDI-TOF MS are highlighted to show the sequence coverage. Peptides either have one or no sites of missed cleavage; no peptides with two or more missed cleavage sites were identified.

Fig. S2. Relative activity of the Q116N mutant measured in the presence of increasing concentrations of zinc.

Fig. S3. Native ESI-TOF MS of the remetallated GOB-1.

Fig. S4. Graph showing the effect of varying EDTA concentration on the $k_i$ of the GOB-1 enzymes.

This supplementary material can be found in the online version of this article.

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