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(54) Title: VARIANTS WITH ALTERED PROPERTIES

(57) Abstract: The present invention relates to variants (mutants) of polypeptides, in particular Termamyl-like alpha-amylases, which variant has alpha-amylase activity and exhibits an alteration in at least one of the following properties relative to said parent alpha-amylase: substrate specificity, substrate binding, substrate cleavage pattern, thermal stability, pH/activity profile, pH/stability profile, stability towards oxidation, Ca2+ dependency, specific activity, and solubility, in particular under production conditions.

Variants with altered properties

FIELD OF THE INVENTION

The present invention relates to variants (mutants) of parent Termamyl-like alpha-amylases, which variant has alpha-amylase activity and exhibits an alteration in at least one of the following properties relative to said parent alpha-amylase: substrate specificity, substrate binding, substrate cleavage pattern, thermal stability pH, /activity profile, pH/stability profile, stability towards oxidation, Ca^{2+} dependency, specific activity, and solubility in particular under production and application conditions.

BACKGROUND OF THE INVENTION

Alpha-Amylases (alpha-1,4-glucan-4-glucanohydrolases, E.C. 3.2.1.1) constitute a group of enzymes, which catalyze hydrolysis of starch and other linear and branched 1,4-glucosidic oligo- and polysaccharides.

In modern and industrial biotechnology high protein concentrations are achieved during fermentation, purification, recovery and in product formulation.

During the fermentation the protein concentration depend on the host cell used. In industrial processes the protein concentration typically lies from above 0.1g/liter fermentation broth. For high yield recombinant production of alpha-amylases in *Bacillus* sp. the protein concentration may be as high as 250g/liter fermentation broth. After purification the protein concentration may reach levels of about 1000 g/liter.

Such high concentrations leads to an undesirable precipitation resulting in lose of active protein. The tendency today is towards products of increasing strength, which make the ability to maintain the enzyme in solution of increasing importance. Often up-concentration of a protein solutions results in protein precipitates, which are difficult to dissolve into active protein.

Thus, it is the object of this application to provide alpha-amylases with altered properties as defined below, in particular

increased solubility.

BRIEF DISCLOSURE OF THE INVENTION

The object of the present invention is to provide Termamyl-like amylases which variants in comparison to the corresponding parent alpha-amylase, i.e., un-mutated alpha-amylase, has alpha-amylase activity and exhibits an alteration in at least one of the following properties relative to said parent alpha-amylase: substrate specificity, substrate binding, substrate cleavage pattern, thermal stability, pH/activity profile, pH/stability profile, stability towards oxidation, Ca^{2+} dependency, specific activity, and solubility, in particular increased solubility under production conditions.

Nomenclature

In the present description and claims, the conventional one-letter and three-letter codes for amino acid residues are used. For ease of reference, alpha-amylase variants of the invention are described by use of the following nomenclature:

Original amino acid(s): position(s): substituted amino acid(s)

According to this nomenclature, for instance the substitution of alanine for asparagine in position 30 is shown as:

Ala30Asn or A30N

a deletion of alanine in the same position is shown as:

Ala30* or A30*

and insertion of an additional amino acid residue, such as lysine, is shown as:

Ala30AlaLys or A30AK

A deletion of a consecutive stretch of amino acid residues, such as amino acid residues 30-33, is indicated as (30-33)* or Δ(A30-N33).

Where a specific alpha-amylase contains a "deletion" in comparison with other alpha-amylases and an insertion is made in such a position this is indicated as:

*36Asp or *36D

for insertion of an aspartic acid in position 36.

Multiple mutations are separated by plus signs, i.e.:

Ala30Asp + Glu34Ser or A30N+E34S

representing mutations in positions 30 and 34 substituting alanine and glutamic acid for asparagine and serine, respectively.

When one or more alternative amino acid residues may be inserted in a given position it is indicated as

A30N,E or

A30N or A30E

Furthermore, when a position suitable for modification is identified herein without any specific modification being suggested, it is to be understood that any amino acid residue may be substituted for the amino acid residue present in the position. Thus, for instance, when a modification of an alanine in position 30 is mentioned, but not specified, it is to be understood that the alanine may be deleted or substituted for any other amino acid, i.e., any one of:

R,N,D,A,C,Q,E,G,H,I,L,K,M,F,P,S,T,W,Y,V.

Further, "A30X" means any one of the following substitutions: A30R, A30N, A30D, A30C, A30Q, A30E, A30G, A30H, A30I, A30L, A30K, A30M, A30F, A30P, A30S, A30T, A30W, A30Y, or A30 V; or in short: A30R,N,D,C,Q,E,G,H,I,L,K,M,F,P,S,T,W,Y,V.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 is an alignment of the amino acid sequences of five parent Termamyl-like alpha-amylases. The numbers on the extreme left designate the respective amino acid sequences as follows:

1: SEQ ID NO: 4 (SP722)

2: SEQ ID NO: 2 (SP690)

3: SEQ ID NO: 10 (BAN)

4: SEQ ID NO: 8 (BLA)

5: SEQ ID NO: 6 (BSG).

Figure 2 shows a site-view of the unit cell of 4 enzyme molecules. Each molecule has 8 interacting zones.

Figure 3 shows a top-view of the unit cell of 4 enzyme molecules.

DETAILED DISCLOSURE OF THE INVENTION

The object of the present invention is to provide

polypeptides, such as enzymes, in particular alpha-amylases, with an alteration in at least one of the following properties relative to said parent polypeptide: substrate specificity, substrate binding, substrate cleavage pattern, thermal stability, pH/activity profile, pH/stability profile, stability towards oxidation, Ca^{2+} dependency, specific activity, and solubility, in particular under production conditions. The properties will be defined further below.

Polypeptide

Polypeptides according to the invention include proteins with biological activity, antimicrobial activity, and enzymatic activity.

Contemplated enzyme activities include proteases, amylases, CGTases, mannanases, maltogenic amylases, glucoamylases, carbohydrases, transferases, lyases, oxidoreductases, lipases.

In one prefered embodiment the enzyme is an alpha-amylase, in particular a *Bacillus* or *Aspergillus* alpha-amylase. In a preferred embodiment the *Bacillus* alpha-amylase is a Termamyl-like amylases.

Polypeptides with biological activity include, EPO, TPO, growth hormones, regulatory peptides, blood coagulation factores, antibodies etc.

Polypeptide with Altered Solubility

A protein (polypeptide) crystal is built up of systematic ordered identical units closely packed together in 3 dimensions. The unit cells may contain one or more protein molecules and a significant amount of water. Also ions like Calcium, Sodium, Chloride, Sulphate and larger molecules such as surfactants and substrates - present during crystal growth - can be identified in the tertiary structure. Although the single molecules and the single atoms are very small, the repeating array of identical units facilitates X-ray scattering and thus provide structure information, which can be used for protein engineering purposes.

Relative to crystals, precipitates and aggregates are smaller units and the single molecules are more disordered than

in the crystals. Nevertheless some of the intermolecular interactions are the same as is found in a well ordered crystals and thus can the tertiary structure (3D structure) and intermolecular information be used for designing protein engineered alpha-amylase variants with altered properties, in particular with reduced tendency of precipitating, i.e., variant with increased solubility.

Due to the spherical and often irregular surface structures of proteins, large holes in the unit cell exist, which are occupied by more disordered solvents like water. In fact, the large majority of the protein surface is covered with layers of water, which is one reason why structures of proteins solved by X-ray crystallography are the same as those for proteins in solution. Only at a few areas the protein molecules are in direct contact with each other, but also solvent mediated contacts function as the "glue" that binds the crystal together.

In general the solubility of proteins is affected by organic solvents, salts like ammonium sulphate, NaCl and $CaCl_2$, and by pH change altering the surface charge of the molecule. These factors are considered both for enzyme production to keep the enzyme in solution and for crystallography experiment to grow useful crystals. Large symmetric crystals are grown by slow increase in protein concentration or by altering the protein surface thereby enhancing the inter-molecular contacts.

Not all proteins crystallise in a form usefull for X-ray crystallography determination methods, but based on existing tertiary structure accurate models can be build if the homology between the template molecule and the molecule of interest is high enough.

When homologous polypeptides, such as enzymes, in particular Termamyl-like alpha-amylases (defined below), are compared on a tertiary structural basis, the large majority of differences are found on the surface of the molecule.

Despite that, the inventors found that surface residues identified to be involved - directly or indirectly through water molecules - in crystal formations for the Termamyl-like amylase (SP722 disclosed in SEQ ID NO: 4) is also playing a key role for

crystallisation of other Termamyl-like amylases (defined below).

Below is described one example of modelling a tertialy structure of one Termamyl-like alpha-alpha from another Termamyl-like alpha-amlase strauctur (SP722 strcutre disclosed in APPENDIX 1).

It is to be understood that the concept of the invention and the below described modelling method according to the invention can generally be extrapolated to all polypeptides, proteins, in particular enzymes, such as alpha-amylases.

The Tertiary Structure of SP722 and Modelling The Tertiary Structures of Another Termamyl-like alpha-amylase.

Mutants of alpha-amylases of the present invention have been found based on the tertiary structure shown in APPENDIX 1 of SP722 (SEQ ID NO: 4). Mutants of other polypeptides may be found based on other tertiary structures. Crystals of the alkaline Termamyl-like alpha-amylase (SP722) (shown in SEQ ID NO: 4 and also disclosed in US patent no. 5,824,531) were obtained by the hanging drop method (well-known in the art), and the tertiary structure (3D-structure) is disclosed in APPENDIX 1 herein.

The unit cell was found to contain 4 enzyme molecules and each molecule has 8 interacting zones (see Fig. 2 and 3). Two zones have been identified on the side of the enzyme surrounding the active site and one large area is found on the backside of the alpha-amylase relative to the active site. There are further two interaction zones on the sides and an interaction side at the bottom and one at the top of the molecule making top-to-bottom interactions.

As can be seen from Fig. 2 the two interaction zones surrounding the active site is interacting with the same two areas on an anti-parallel neighbour molecule. Likewise the backside zone is in contact with the backside zone on a third anti-parallel amylase molecule although all contacts here water mediated. It can also be seen from the Fig. 2 and 3 that the interacting areas are spread all over the molecule.

A model of another alkaline Termamyl-like amylase, AA560 has been build based on the SP722 tertiary structure disclosed in

APPENDIX 1. The AA560 alpha-amylase is about 87% identical to the template amylase (SP722) and the alignment contains no insertion or deletions. Due to the high homology (identity), the same symmetry and the same crystal interactions, the same interaction zones on the protein surface are involved in crystallization and precipitation at the increasing protein concentrations, which are reached during production, i.e., starting from fermentation stage through the purification stage (see Background section).

Mutations in these interaction zones were constructed, the enzyme expressed and purified, and the protein solubility was measured under different conditions as described in Example 8 and 9 using the method described in the "Materials and Methods" section.

The findings of the present invention may be applied on Termamyl-like amylases being at least 60% identical, preferably at least 70% identical, more preferably 80% identical, even more preferably 85% identical, even more preferably 90% identical, even more 95% identical, even more 97% identical, even more 99% identical to the Termamyl-like alpha-amylase shown in SEQ ID NO: 12. In a preferably the findings may be used on alkaline Termamyl-like alpha-amylases, especially alkaline alpha-amylases of the same length, without additional amino residues or gaps in an aligned primary structure in comparison to SP722 (SEQ ID NO: 4 shown as number 1 in the alignment in Fig. 1). Especially, the finding may be used on the following alkaline Termamyl-like alpha-amylases: SP690 (SEQ ID NO: 2), SP722 (SEQ ID NO: 4), AA560 (SEQ ID NO: 12), #707 alpha-amylase (SEQ ID NO: 13), the KSM APE 1378 alpha-amylase disclosed in KSM AP1378 alpha-amylase is disclosed in WO 97/00324, or fragment or truncated forms thereof. The latter mentioned alkaline alpha-amylases have very similar tertiary cryltal structure around the above-mentioned interactions zones, and have the same primary structure length 485 amino acids.

Contrary hereto, for instance, Termamyl (shown as sequence number 4 in the alignment in Fig. 1) lacks two amino acid residues (positions 1 and 2); has gaps in positions 174 and 181-

182; and has three additional amino acid residues in positions 378-381 when aligned with SP722.

BAN (shown as sequence number 3 in the alignment in Fig. 1) lacks five amino acid residues (positions 1-4 and 488); has gaps in positions 174 and 181-182; and has three additional amino acid residues in positions 378-381 if aligned with SP722.

BSG (shown as sequence number 5 in the alignment in Fig. 1) lacks one amino acid residues (position 1); and has 31 additional amino acid residues in positions 489-519 if aligned with SP722.

KSM-K36 and KSM-K38 (EP 1,022,334-A) lack five amino acid residues (positions 1 and 2) and has gaps in positions 174 and 181-182 when aligned with SP722.

AA180, AA20 and Amrk385 (Danish patent application no. PA 2000 00347 or PCT/DK01/00133) have one additional amino acid in position 261 when aligned with SP722.

Below it is described how to model a Termamyl-like alpha-amylase from another alpha-amylase. In Example 4 the modelling of AA560 from SP722 is described. This method can be exprepolated to other polypetides as for instance the above-mentioned.

Modelling of Termamyl-like Alpha-amylases

WO 96/23874 provides the tertiary structure (3D Structure), X-ray crystal structural data for a Termamyl-like alpha-amylase, which consists of the 300 N-terminal amino acid residues of the *B. amyloliquefaciens* alpha-amylase (BAN™) and amino acids 301-483 of the C-terminal end of the *B. licheniformis* alpha-amylase (SEQ ID NO: 8). WO 96/23874 further describes methodology for designing (modelling), on the basis of an analysis of the structure of a parent Termamyl-like alpha-amylase, variants of the parent Termamyl-like alpha-amylase which exhibit altered properties relative to the parent.

Other Termamyl-like structures may be modelled in accordance with WO 96/23874, which is hereby incorporated by reference.

In connection with obtaining variant of the present invention the AA560 tertiary structure was designed (modelled)

based on the tertiary structure of SP722 (disclosed in APPENDIX 1) as described in Example 1. The structure of other Termamyl-like alpha-amylases (*e.g.*, those disclosed herein) may be built analogously.

Termamyl-like alpha-amylases

A number of alpha-amylases produced by *Bacillus* spp. are highly homologous (identical) on the amino acid level. The identity of a number of *Bacillus* alpha-amylases can be found in the below Table 1:

Table 1

	Percent identity 707	AP1378	BAN	BSG	SP690	SP722	AA560	Termamyl
707	100.0	86.4	66.9	66.5	87.6	86.2	95.5	68.1
AP1378	86.4	100.0	67.1	68.1	95.1	86.6	86.0	69.4
BAN	66.9	67.1	100.0	65.6	67.1	68.8	66.9	80.7
BSG	66.5	68.1	65.6	100.0	67.9	67.1	66.3	65.4
SP690	87.6	95.1	67.1	67.9	100.0	87.2	87.0	69.2
SP722	86.2	86.6	68.8	67.1	87.2	100.0	86.8	70.8
AA560	95.5	86.0	66.9	66.3	87.0	86.8	100.0	68.3
Termamyl	68.1	69.4	80.7	65.4	69.2	70.8	68.3	100.0

For instance, the *B. licheniformis* alpha-amylase comprising the amino acid sequence shown in SEQ ID NO: 8 (commercially available as Termamyl™) has been found to be about 81% homologous with the *B. amyloliquefaciens* alpha-amylase comprising the amino acid sequence shown in SEQ ID NO: 10 and about 65% homologous with the *B. stearothermophilus* alpha-amylase comprising the amino acid sequence shown in SEQ ID NO: 6. Further homologous alpha-amylases include SP690 and SP722 disclosed in WO 95/26397 and further depicted in SEQ ID NO: 2 and SEQ ID NO: 4, respectively, herein. Other amylases are the AA560 alpha-amylase derived from *Bacillus* sp. and shown in SEQ ID NO: 12, and the #707 alpha-amylase derived from *Bacillus* sp., shown in SEQ ID NO: 13 and described by Tsukamoto et al., Biochemical and Biophysical Research Communications, 151 (1988), pp. 25-31.

The KSM AP1378 alpha-amylase is disclosed in WO 97/00324

(from KAO Corporation). Also the K38 and K38 alpha-amylases disclosed in EP 1,022,334 are contemplated according to the invention.

Still further homologous alpha-amylases include the alpha-amylase produced by the *B. licheniformis* strain described in EP 0252666 (ATCC 27811), and the alpha-amylases identified in WO 91/00353 and WO 94/18314. Other commercial Termamyl-like alpha-amylases are comprised in the products sold under the following tradenames: Optitherm™ and Takatherm™ (available from Solvay); Maxamyl™ (available from Gist-brocades/Genencor), Spezym AA™ and Spezyme Delta AA™ (available from Genencor), and Keistase™ (available from Daiwa), Purastar™ ST 5000E, PURASTRA™ HPAM L (from Genencor Int.).

Because of the substantial homology found between these alpha-amylases, they are considered to belong to the same class of alpha-amylases, namely the class of "Termamyl-like alpha-amylases".

Accordingly, in the present context, the term "Termamyl-like alpha-amylase" is intended to indicate an alpha-amylase, which, at the amino acid level, exhibits a substantial identity to Termamyl™, i.e., the *B. licheniformis* alpha-amylase having the amino acid sequence shown in SEQ ID NO: 8 herein.

In other words, all the following alpha-amylases, which has the amino acid sequences shown in SEQ ID NOS: 2, 4, 6, 8, 10, 12 and 13 herein are considered to be "Termamyl-like alpha-amylase". Other Termamyl-like alpha-amylases are alpha-amylases i) which displays at least 60%, such as at least 70%, e.g., at least 75%, or at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, at least 99% homology with at least one of said amino acid sequences shown in SEQ ID NOS: 2, 4, 6, 8, 10, 12, and 13, and/or ii) is encoded by a DNA sequence which hybridizes to the DNA sequences encoding the above-specified alpha-amylases which are apparent from SEQ ID NOS: 1, 3, 5, 7, 9 and of the present specification (which encoding sequences encode the amino acid sequences shown in SEQ ID NOS: 2, 4, 6, 8, 10 and 12 herein, respectively)

In connection with property i), the homology may be determined as the degree of identity between the two sequences indicating a derivation of the first sequence from the second. The homology may suitably be determined by means of computer programs known in the art such as GAP provided in the GCG program package (described above). Thus, Gap GCGv8 may be used with the following default parameters: GAP creation penalty of 5.0 and GAP extension penalty of 0.3, default scoring matrix, for nucleic sequences and 3.0 and 0.1, respectively, from protein sequences. GAP uses the method of Needleman/Wunsch/Sellers to make alignments.

A structural alignment between Termamyl (SEQ ID NO: 8) and another Termamyl-like alpha-amylase may be used to identify equivalent/corresponding positions in other Termamyl-like alpha-amylases. One method of obtaining said structural alignment is to use the Pile Up programme from the GCG package using default values of gap penalties, i.e., a gap creation penalty of 3.0 and gap extension penalty of 0.1. Other structural alignment methods include the hydrophobic cluster analysis (Gaboriaud et al., (1987), FEBS LETTERS 224, pp. 149-155) and reverse threading (Huber, T; Torda, AE, PROTEIN SCIENCE Vol. 7, No. 1 pp. 142-149 (1998).

Hybridisation

The oligonucleotide probe used in the characterisation of the polypeptide, such as the Termamyl-like alpha-amylase in accordance with property ii) above may suitably be prepared on the basis of the full or partial nucleotide or amino acid sequence of the alpha-amylase in question.

Suitable conditions for testing hybridisation involve pre-soaking in 5xSSC and prehybridizing for 1 hour at ~40°C in a solution of 20% formamide, 5xDenhardt's solution, 50mM sodium phosphate, pH 6.8, and 50mg of denatured sonicated calf thymus DNA, followed by hybridisation in the same solution supplemented with 100mM ATP for 18 hours at ~40°C, followed by three times washing of the filter in 2xSSC, 0.2% SDS at 40°C for 30 minutes (low stringency), preferred at 50°C (medium

stringency), more preferably at 65°C (high stringency), even more preferably at ~75°C (very high stringency). More details about the hybridisation method can be found in Sambrook et al., Molecular_Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor, 1989.

In the present context, "derived from" is intended not only to indicate an alpha-amylase produced or producible by a strain of the organism in question, but also an alpha-amylase encoded by a DNA sequence isolated from such strain and produced in a host organism transformed with said DNA sequence. Finally, the term is intended to indicate an alpha-amylase, which is encoded by a DNA sequence of synthetic and/or cDNA origin and which has the identifying characteristics of the alpha-amylase in question. The term is also intended to indicate that the parent alpha-amylase may be a variant of a naturally occurring alpha-amylase, i.e., a variant, which is the result of a modification (insertion, substitution, deletion) of one or more amino acid residues of the naturally occurring alpha-amylase.

Parent Termamyl-like Alpha-amylases

According to the invention all Termamy-like alpha-amylases, as defined above, may be used as the parent (i.e., backbone) alpha-amylase. In a preferred embodiment of the invention the parent alpha-amylase is derived from *B. licheniformis*, e.g., one of those referred to above, such as the *B. licheniformis* alpha-amylase having the amino acid sequence shown in SEQ ID NO: 10. Especially preferred parent alpha-amylases are the SP722 alpha-amylase and the AA560 alpha-amylases. In one embodiment the parent alpha-amyase has one or more of the followimng mutations/substitutions: Delta (R81-G182); Delta (D183-G184); Delta (D183-G184)+N195F; RR181Q+N445Q+K446N; Delta (D183-G184)+R181Q.

Parent hybrid Termamyl-like Alpha-amylases

The parent alpha-amylase (i.e., backbone alpha-amylase) may also be a hybrid alpha-amylase, i.e., an alpha-amylase, which comprises a combination of partial amino acid sequences derived from at least two alpha-amylases.

The parent hybrid alpha-amylase may be one, which on the basis of amino acid homology (identity) and/or DNA hybridization (as defined above) can be determined to belong to the Termamyl-like alpha-amylase family. In this case, the hybrid alpha-amylase is typically composed of at least one part of a Termamyl-like alpha-amylase and part(s) of one or more other alpha-amylases selected from Termamyl-like alpha-amylases or non-Termamyl-like alpha-amylases of microbial (bacterial or fungal) and/or mammalian origin.

Thus, the parent hybrid alpha-amylase may comprise a combination of partial amino acid sequences deriving from at least two Termamyl-like alpha-amylases, or from at least one Termamyl-like and at least one non-Termamyl-like bacterial alpha-amylase, or from at least one Termamyl-like and at least one fungal alpha-amylase. The Termamyl-like alpha-amylase from which a partial amino acid sequence derives, may be any of those specific Termamyl-like alpha-amylase referred to herein.

For instance, the parent alpha-amylase may comprise a C-terminal part of an alpha-amylase derived from a strain of *B. licheniformis*, and a N-terminal part of an alpha-amylase derived from a strain of *B. amyloliquefaciens* or from a strain of *B. stearothermophilus*. For instance, the parent α-amylase may comprise at least 430 amino acid residues of the C-terminal part of the *B. licheniformis* alpha-amylase, and may, *e.g.*, comprise a) an amino acid segment corresponding to the 37 N-terminal amino acid residues of the *B. amyloliquefaciens* alpha-amylase having the amino acid sequence shown in SEQ ID NO: 10 and an amino acid segment corresponding to the 445 C-terminal amino acid residues of the *B. licheniformis* alpha-amylase having the amino acid sequence shown in SEQ ID NO: 8, or a hybrid Termamyl-like alpha-amylase being identical to the Termamyl sequence, i.e., the *Bacillus licheniformis* alpha-amylase shown

in SEQ ID NO: 8, except that the N-terminal 35 amino acid residues (of the mature protein) has been replaced by the N-terminal 33 residues of BAN (mature protein), i.e., the *Bacillus amyloliquefaciens* alpha-amylase shown in SEQ ID NO: 10; or b) an amino acid segment corresponding to the 68 N-terminal amino acid residues of the *B. stearothermophilus* α-amylase having the amino acid sequence shown in SEQ ID NO: 6 and an amino acid segment corresponding to the 415 C-terminal amino acid residues of the *B. licheniformis* alpha-amylase having the amino acid sequence shown in SEQ ID NO: 8.

Another suitable parent hybrid alpha-amylase is the one previously described in WO 96/23874 (from Novo Nordisk) constituting the N-terminus of BAN, *Bacillus amyloliquefaciens* alpha-amylase (amino acids 1-300 of the mature protein) and the C-terminus from Termamyl (amino acids 301-483 of the mature protein).

Altered properties

The following discusses the relationship between mutations, which are present in variants of the invention, and desirable alterations in properties (relative to those a parent Termamyl-like alpha-amylase), which may result therefrom.

As mentioned above the invention relates to Termamyl-like alpha-amylases with altered properties, in particular under production conditions.

Parent Termamyl-like alpha-amylase specifically contemplated in connection with going through the specifically contemplated altered properties are the above mentioned parent Termamyl-like alpha-amylase and parent hydrid Termamyl-like alpha-amylases. The SP722 alpha-amylase is used as the starting point, but corresponding positions in, e.g., the Termamyl, BSG, BAN, AA560, SP690, AA180, KSM AP1378, and #707, K38, and K36 should be understood as disclosed too.

In a preferred embodiment the variant of the invention has increased solubility, in particular under washing or cleaning conditions.

In an aspect the invention relates to variant with altered

properties as mentioned above.

In the first aspect a variant of a parent Termamyl-like alpha-amylase, comprising an alteration at one or more positions (using SEQ ID NO: 12 for the amino acid numbering) selected from the group of:

R28, R118, N174; R181, G182, D183, G184, G186, W189, N195, M202, Y298, N299, K302, S303, N306, R310, N314; R320, H324, E345, Y396, R400, W439, R444, N445, K446, Q449, R458, N471, N484,

wherein

(a) the alteration(s) are independently

(i) an insertion of an amino acid downstream of the amino acid which occupies the position,

(ii) a deletion of the amino acid which occupies the position, or

(iii) a substitution of the amino acid which occupies the position with a different amino acid,

(b) the variant has alpha-amylase activity and (c) each position corresponds to a position of the amino acid sequence of the parent Termamyl-like alpha-amylase having the amino acid sequence of AA560 shown in SEQ ID NO: 12.

In SP722 (SEQ ID NO: 4) such corresponding positions are: R28; N94; L118; N125; Q174; R181; G182; D183; G184; A186; W189; N195, M202, Y298; N299; N302; S303; N306; A310; N314; K320; H324; Q345; F396, T400, W439, Q444; N445, K446, Q449, K458; N471, K484.

In a preferred embodiment the variant of the invention (using SEQ ID NO: 12 for the numbering) has one or more of the following mutations/substitutions:

Delta G184; Delta (R181-G182); Delta (D183-G184);
R28N,K; S94K; R118K; N125A,R,K; N174D; R181Q,E,K; G186R;
W189R,K; N195F; M202L; Y298H,F; N299A; K302R, S303Q,
N306G,D,R,K; R310A,K,Q,E,H,D,N; N314D; R320K; H324K;
E345R,D,K,N; Y396F; R400T,K; W439R; R444K; N445K,Q; K446N;
Q449E; R458K; N471E; N484Q.

Preferred double, triple and multi-mutations - using SEQ ID NO: 12 as the basis for the numbering - include:

Delta(D183-G184)+R181Q;

Delta(D183-G184)+G186R;
Delta(D183-G184)+N195F;
Delta(D183-G184)+M202L;
Delta(D183-G184)+G186R+N195F;
Delta(D183-G184)+N195F+R400T;
Delta(D183-G184)+N195F+W439R;
Delta(D183-G184)+N195F+Q449E;
Delta(D183-G184)+N195F+N484Q;
Delta(D183-G184)+N195F+K446N;
Delta(D183-G184)+N195F+N445Q+K446N+N484E;
Delta(D183-G184)+N195F+N445Q+K446N+Q449E;
Delta(D183-G184)+N195F+N471E;
Delta(D183-G184)+N195F+H324K;
Delta(D183-G184)+N195F+Y396F;
Delta(D183-G184)+N195F+K446D;
Delta(D183-G184)+N195F+R181Q;
Delta(D183-G184)+N195F+R181E;
Delta(D183-G184)+N195F+N445Q+K446N;
N445Q+K446N;
N445Q+K446N+N484E;
N445Q+K446N+Q449E;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N;
Delta (D183-G184)+N195F+R181Q+K446N;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+N484E;
Delta (D183-G184)+N195F+R181E+N445Q+K446N;
Delta (D183-G184)+N195F+R181E+K446N;
Delta (D183-G184)+N195F+R181E+N445Q+K446N+N484E;
Delta (D183-G184)+N195F+N445Q+K446N+Y243F;
Delta (D183-G184)+N195F+N445Q+K446N+V209I;
Delta (D183-G184)+N195F+E212R;
Delta (D183-G184)+N195F+M116R;
Delta (D183-G184)+N195F+K142H+D144H+R158H;
Delta (D183-G184)+N195F+K142H+D144H;
Delta (D183-G184)+N195F+R158H;
Delta (D183-G184)+N195F+E345R;
Delta (D183-G184)+N195F+W189R;
Delta (D183-G184)+N195F+Y298H;

Delta (D183-G184)+N195F+N299A;
Delta (D183-G184)+N195F+K302R+S303Q;
Delta (D183-G184)+N195F+N306G;
Delta (D183-G184)+N195F+Y298H+N299A+K302R+S303Q+N306G;
Delta (D183-G184)+N195F+N125A;
Delta (D183-G184)+N195F+N125R;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+R310A;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+R310A+Q311N;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+R320K;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+Q319K+R320D;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+N306A;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+K302N;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+E345N;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+Y298F;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+R28N;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+R28N+R310A;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+N128D+N306D;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+N128D;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+N306D;
N174D+N314D;
Delta (D183-G184)+N195F+N306D+R310H+E345D;
Delta(D183-G184)+R181Q+N195F+W189R+S94K;
Delta(D183-G184)+R181Q+W189R+S94K;
Delta(D183-G184)+N195F+R181Q+S94K;
Delta(D183-G184)+N195F+R181K+N125R;
Delta(D183-G184)+N195F+R181K+N125K;
Delta(D183-G184)+N195F+R118K+R320K+R458K;
Delta(D183-G184)+R181Q+N195F+R118K+R320K+R458K;
Delta(D183-G184)+N195F+R181Q+N306G;
Delta(D183-G184)+N195F+R181Q+W189R;
Delta(D183-G184)+R181Q+N195F+R118K+N125K+R444K+N445K
Delta(D183-G184)+R181Q+N195F+R118K+N125K+R320K+R458K;
Delta(D183-G184)+R181Q+N195F+R118K+N125R+R320K+R458K;
Delta(D183-G184)+R181Q+N195F+S94K+R118K+R320K+R458K;
Delta(D183-G184)+R181Q+N195F+R118K+N306R+R320K+R458K;
Delta(D183-G184)+N195F+R118K+R320K+R458K+R444K+N445K;
Delta(D183-G184)+N195F+S94K+R118K+N306R+R320K+R458K;

Contemplated variants include the specific ones mentioned in the examples and the above mention mutations in further combination with one or more of the mutations/substitution: Delta (D183-G184); N195F; R181Q; G186R; M202L; V206F,L,M; N193S,T,P

Increased solubility

All the above-mentioned mutations result in Termamyl-like alpha-amylase variants with altered solubility when used in any alpha-amylase within the group of Termamyl-like alpha-amylase as defined above.

Thus, in a preferred embodiment the variant of the invention is a variant of a parent Termamyl-like alpha-amylase, which has increased solubility (as defined) in comparison to the parent Termemyl-like alpha-amylase, comprising an alteration at one or more positions (using SEQ ID NO: 12 for the amino acid numbering) selected from the group of:
R28, R118, N174; R181, G182, D183, G184, G186, W189, N195, M202, Y298, N299, K302, S303, N306, R310, N314; R320, H324, E345, Y396, R400, W439, R444, N445, K446, Q449, R458, N471, N484,
wherein

(a) the alteration(s) are independently

(i) an insertion of an amino acid downstream of the amino acid which occupies the position,

(ii) a deletion of the amino acid which occupies the position, or

(iii) a substitution of the amino acid which occupies the position with a different amino acid,

(b) the variant has alpha-amylase activity and (c) each position corresponds to a position of the amino acid sequence of the parent Termamyl-like alpha-amylase having the amino acid sequence of AA560 shown in SEQ ID NO: 12.

In a preferred embodiment a variant of the invention with increased solubility in comparison to the parent alpha-amylase has one or more of the following substitutions:
Delta G184; Delta (R181-G182); Delta (D183-G184);
R28N,K; S94K; R118K; N125A,R,K; N174D; R181Q,E,K; G186R;

W189R,K; N195F; M202L; Y298H,F; N299A; K302R, S303Q, N306G,D,R,K; R310A,K,Q,E,H,D,N; N314D; R320K; H324K; E345R,D,K,N; Y396F; R400T,K; W439R; R444K; N445K,Q; K446N; Q449E; R458K; N471E; N484Q.

In a more preferred embodiment variant of the invention with increased solubility (determined using one of the methods described in the "Materials and Methods" section) - using SEQ ID NO: 12 as the basis for the numbering - include:

Delta(D183-G184)+R181Q;
Delta(D183-G184)+G186R;
Delta(D183-G184)+N195F;
Delta(D183-G184)+M202L;
Delta(D183-G184)+G186R+N195F;
Delta(D183-G184)+N195F+R400T;
Delta(D183-G184)+N195F+W439R;
Delta(D183-G184)+N195F+Q449E;
Delta(D183-G184)+N195F+N484Q;
Delta(D183-G184)+N195F+K446N;
Delta(D183-G184)+N195F+N445Q+K446N+N484E;
Delta(D183-G184)+N195F+N445Q+K446N+Q449E;
Delta(D183-G184)+N195F+N471E;
Delta(D183-G184)+N195F+H324K;
Delta(D183-G184)+N195F+Y396F;
Delta(D183-G184)+N195F+K446D;
Delta(D183-G184)+N195F+R181Q;
Delta(D183-G184)+N195F+R181E;
Delta(D183-G184)+N195F+N445Q+K446N;
N445Q+K446N;
N445Q+K446N+N484E;
N445Q+K446N+Q449E;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N;
Delta (D183-G184)+N195F+R181Q+K446N;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+N484E;
Delta (D183-G184)+N195F+R181E+N445Q+K446N;
Delta (D183-G184)+N195F+R181E+K446N;
Delta (D183-G184)+N195F+R181E+N445Q+K446N+N484E;
Delta (D183-G184)+N195F+N445Q+K446N+Y243F;

Delta (D183-G184)+N195F+N445Q+K446N+V209I;
Delta (D183-G184)+N195F+E212R;
Delta (D183-G184)+N195F+M116R;
Delta (D183-G184)+N195F+K142H+D144H+R158H;
Delta (D183-G184)+N195F+K142H+D144H;
Delta (D183-G184)+N195F+R158H;
Delta (D183-G184)+N195F+E345R;
Delta (D183-G184)+N195F+W189R;
Delta (D183-G184)+N195F+Y298H;
Delta (D183-G184)+N195F+N299A;
Delta (D183-G184)+N195F+K302R+S303Q;
Delta (D183-G184)+N195F+N306G;
Delta (D183-G184)+N195F+Y298H+N299A+K302R+S303Q+N306G;
Delta (D183-G184)+N195F+N125A;
Delta (D183-G184)+N195F+N125R;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+R310A;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+R310A+Q311N;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+R320K;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+Q319K+R320D;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+N306A;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+K302N;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+E345N;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+Y298F;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+R28N;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+R28N+R310A;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+N128D+N306D;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+N128D;
Delta (D183-G184)+N195F+R181Q+N445Q+K446N+N306D;
N174D+N314D;
Delta (D183-G184)+N195F+N306D+R310H+E345D;
Delta(D183-G184)+R181Q+N195F+W189R+S94K;
Delta(D183-G184)+R181Q+W189R+S94K;
Delta(D183-G184)+N195F+R181Q+S94K;
Delta(D183-G184)+N195F+R181K+N125R;
Delta(D183-G184)+N195F+R181K+N125K;
Delta(D183-G184)+N195F+R118K+R320K+R458K;
Delta(D183-G184)+R181Q+N195F+R118K+R320K+R458K;

Delta(D183-G184)+N195F+R181Q+N306G;
Delta(D183-G184)+N195F+R181Q+W189R;
Delta(D183-G184)+R181Q+N195F+R118K+N125K+R444K+N445K
Delta(D183-G184)+R181Q+N195F+R118K+N125K+R320K+R458K;
Delta(D183-G184)+R181Q+N195F+R118K+N125R+R320K+R458K;
Delta(D183-G184)+R181Q+N195F+S94K+R118K+R320K+R458K;
Delta(D183-G184)+R181Q+N195F+R118K+N306R+R320K+R458K;
Delta(D183-G184)+N195F+R118K+R320K+R458K+R444K+N445K;
Delta(D183-G184)+N195F+S94K+R118K+N306R+R320K+R458K;

Other combinations according to the invention include the specific one mentioned in the examples and one or more of the following substitutions: N195F; R181Q; G186R; M202L; V206F,L,M, N193P.

Stability

In the context of the present invention, mutations (including amino acid substitutions and deletions) of importance with respect to achieving altered stability, in particular improved stability (i.e., higher or lower), at especially high pH (*i.e.*, pH 8-10.5) include any of the mutations listed in the in "Altered properties" section.

Ca^{2+} stability

Altered Ca^{2+} stability means the stability of the enzyme under Ca^{2+} depletion has been improved, i.e., higher or lower stability. In the context of the present invention, mutations (including amino acid substitutions and deletions) of importance with respect to achieving altered Ca^{2+} stability, in particular improved Ca^{2+} stability, i.e., higher or lower stability, at especially high pH (*i.e.*, pH 8-10.5) include any of the mutations listed in the in "Altered properties" section.

Specific activity

In a further aspect of the present invention, important mutations (including amino acid substitutions and deletions) with respect to obtaining variants exhibiting altered specific activity, in particular increased or decreased specific

activity, especially at temperatures from 10-60°C, preferably 20-50°C, especially 30-40°C, include any of the mutations listed in the in "Altered properties" section.

General mutations in variants of the invention

The particularly interesting mutations (including amino acid substitutions and deletions) are those that increase the mobility around the active site of the enzyme. This is accomplished by changes that disrupt stabilizing interaction in the vicinity of the active site, *i.e.*, within preferably 10Å or 8Å or 6Å or 4Å from any of the residues constituting the active site.

Examples are mutations that reduce the size of side chains, such as

Ala to Gly,
Val to Ala or Gly,
Ile or Leu to Val, Ala, or Gly
Thr to Ser

Such mutations are expected to cause increased flexibility in the active site region either by the introduction of cavities or by the structural rearrangements that fill the space left by the mutation.

It may be preferred that a variant of the invention comprises one or more modifications in addition to those outlined above. Thus, it may be advantageous that one or more Proline residues present in the part of the alpha-amylase variant which is modified is/are replaced with a non-Proline residue which may be any of the possible, naturally occurring non-Proline residues, and which preferably is an Alanine, Glycine, Serine, Threonine, Valine or Leucine.

Analogously, it may be preferred that one or more Cysteine residues present among the amino acid residues with which the parent alpha-amylase is modified is/are replaced with a non-Cysteine residue such as Serine, Alanine, Threonine, Glycine, Valine or Leucine.

Furthermore, a variant of the invention may - either as the only modification or in combination with any of the above

outlined modifications - be modified so that one or more Asp and/or Glu present in an amino acid fragment corresponding to the amino acid fragment 185-209 of SEQ ID NO: 10 is replaced by an Asn and/or Gln, respectively. Also of interest is the replacement, in the Termamyl-like alpha-amylase, of one or more of the Lys residues present in an amino acid fragment corresponding to the amino acid fragment 185-209 of SEQ ID NO: 10 by an Arg.

It will be understood that the present invention encompasses variants incorporating two or more of the above outlined modifications.

Furthermore, it may be advantageous to introduce mutations in one or more of the following positions (using SEQ ID NO: 10 (Termamyl™) for the numbering):

M15, V128, A111, H133, W138, T149, M197, N188, A209, A210, H405, T412, in particular the following single, double or triple or multi mutations:

M15X, in particular M15T,L;

V128X, in particular V128E;

H133X, in particular H133Y;

N188X, in particular N188S,T,P;

M197X, in particular M197T,L;

A209X, in particular A209V;

M197T/W138F; M197T/W138Y; M15T/H133Y/N188S;

M15/V128E/H133Y/N188S; E119C/S130C; D124C/R127C; H133Y/T149I; G475R, H133Y/S187D; H133Y/A209V;

In AA560 this correspond to

L17X, in particular L17T;

E130X;

Y135X;

W140X, In particular W140F,Y;

T193X; in particular S,P;

M202X, in particular M202T,L;

V214X;

Contemplated combinations thereof, include

M202T/W140F; M202T/W140Y; L17T/T193S;

L17T/N193P; E121C/S132C; N126C/Q129C; T151I;

G480R.

Methods for preparing alpha-amylase variants of the invention

Several methods for introducing mutations into genes are known in the art. After a brief discussion of the cloning of alpha-amylase-encoding DNA sequences, methods for generating mutations at specific sites within the alpha-amylase-encoding sequence will be discussed.

Cloning a DNA sequence encoding an alpha-amylase

The DNA sequence encoding a parent alpha-amylase may be isolated from any cell or microorganism producing the alpha-amylase in question, using various methods well known in the art. First, a genomic DNA and/or cDNA library should be constructed using chromosomal DNA or messenger RNA from the organism that produces the alpha-amylase to be studied. Then, if the amino acid sequence of the alpha-amylase is known, homologous, labeled oligonucleotide probes may be synthesized and used to identify alpha-amylase-encoding clones from a genomic library prepared from the organism in question. Alternatively, a labeled oligonucleotide probe containing sequences homologous to a known alpha-amylase gene could be used as a probe to identify alpha-amylase-encoding clones, using hybridization and washing conditions of lower stringency.

Yet another method for identifying alpha-amylase-encoding clones would involve inserting fragments of genomic DNA into an expression vector, such as a plasmid, transforming alpha-amylase-negative bacteria with the resulting genomic DNA library, and then plating the transformed bacteria onto agar containing a substrate for alpha-amylase, thereby allowing clones expressing the alpha-amylase to be identified.

Alternatively, the DNA sequence encoding the enzyme may be prepared synthetically by established standard methods, e.g., the phosphoroamidite method described by S.L. Beaucage and M.H. Caruthers, Tetrahedron Letters 22, 1981, pp. 1859-1869 or the method described by Matthes et al., The EMBO J. 3, 1984, pp. 801-805. In the phosphoroamidite method, oligonucleotides are

synthesized, e.g., in an automatic DNA synthesizer, purified, annealed, ligated and cloned in appropriate vectors.

Finally, the DNA sequence may be of mixed genomic and synthetic origin, mixed synthetic and cDNA origin or mixed genomic and cDNA origin, prepared by ligating fragments of synthetic, genomic or cDNA origin (as appropriate, the fragments corresponding to various parts of the entire DNA sequence), in accordance with standard techniques. The DNA sequence may also be prepared by polymerase chain reaction (PCR) using specific primers, for instance as described in US 4,683,202 or R.K. Saiki et al., Science 239, 1988, pp. 487-491.

Expression of alpha-amylase variants

According to the invention, a DNA sequence encoding the variant produced by methods described above, or by any alternative methods known in the art, can be expressed, in enzyme form, using an expression vector which typically includes control sequences encoding a promoter, operator, ribosome binding site, translation initiation signal, and, optionally, a repressor gene or various activator genes.

The recombinant expression vector carrying the DNA sequence encoding an alpha-amylase variant of the invention may be any vector that may conveniently be subjected to recombinant DNA procedures, and the choice of vector will often depend on the host cell into which it is to be introduced. Thus, the vector may be an autonomously replicating vector, i.e., a vector which exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, e.g., a plasmid, a bacteriophage or an extrachromosomal element, minichromosome or an artificial chromosome. Alternatively, the vector may be one which, when introduced into a host cell, is integrated into the host cell genome and replicated together with the chromosome(s) into which it has been integrated.

In the vector, the DNA sequence should be operably connected to a suitable promoter sequence. The promoter may be any DNA sequence, which shows transcriptional activity in the host cell of choice and may be derived from genes encoding proteins either

homologous or heterologous to the host cell. Examples of suitable promoters for directing the transcription of the DNA sequence encoding an alpha-amylase variant of the invention, especially in a bacterial host, are the promoter of the *lac* operon of *E.coli*, the *Streptomyces coelicolor* agarase gene *dag*A promoters, the promoters of the *Bacillus licheniformis* alpha-amylase gene (*amyL*), the promoters of the *Bacillus stearothermophilus* maltogenic amylase gene (*amyM*), the promoters of the *Bacillus amyloliquefaciens* alpha-amylase (*amyQ*), the promoters of the *Bacillus subtilis* xylA and xylB genes etc. For transcription in a fungal host, examples of useful promoters are those derived from the gene encoding *A. oryzae* TAKA amylase, *Rhizomucor miehei* aspartic proteinase, *A. niger* neutral alpha-amylase, *A. niger* acid stable alpha-amylase, *A. niger* glucoamylase, *Rhizomucor miehei* lipase, *A. oryzae* alkaline protease, *A. oryzae* triose phosphate isomerase or *A. nidulans* acetamidase.

The expression vector of the invention may also comprise a suitable transcription terminator and, in eukaryotes, polyadenylation sequences operably connected to the DNA sequence encoding the alpha-amylase variant of the invention. Termination and polyadenylation sequences may suitably be derived from the same sources as the promoter.

The vector may further comprise a DNA sequence enabling the vector to replicate in the host cell in question. Examples of such sequences are the origins of replication of plasmids pUC19, pACYC177, pUB110, pE194, pAMB1 and pIJ702.

The vector may also comprise a selectable marker, e.g. a gene the product of which complements a defect in the host cell, such as the *dal* genes from *B. subtilis* or *B. licheniformis*, or one which confers antibiotic resistance such as ampicillin, kanamycin, chloramphenicol or tetracyclin resistance. Furthermore, the vector may comprise *Aspergillus* selection markers such as amdS, argB, niaD and sC, a marker giving rise to hygromycin resistance, or the selection may be accomplished by co-transformation, e.g., as described in WO 91/17243.

While intracellular expression may be advantageous in some

respects, e.g., when using certain bacteria as host cells, it is generally preferred that the expression is extracellular. In general, the *Bacillus* α-amylases mentioned herein comprises a preregion permitting secretion of the expressed protease into the culture medium. If desirable, this preregion may be replaced by a different preregion or signal sequence, conveniently accomplished by substitution of the DNA sequences encoding the respective preregions.

The procedures used to ligate the DNA construct of the invention encoding an alpha-amylase variant, the promoter, terminator and other elements, respectively, and to insert them into suitable vectors containing the information necessary for replication, are well known to persons skilled in the art (cf., for instance, Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Ed., Cold Spring Harbor, 1989).

The cell of the invention, either comprising a DNA construct or an expression vector of the invention as defined above, is advantageously used as a host cell in the recombinant production of an alpha-amylase variant of the invention. The cell may be transformed with the DNA construct of the invention encoding the variant, conveniently by integrating the DNA construct (in one or more copies) in the host chromosome. This integration is generally considered to be an advantage as the DNA sequence is more likely to be stably maintained in the cell. Integration of the DNA constructs into the host chromosome may be performed according to conventional methods, e.g., by homologous or heterologous recombination. Alternatively, the cell may be transformed with an expression vector as described above in connection with the different types of host cells.

The cell of the invention may be a cell of a higher organism such as a mammal or an insect, but is preferably a microbial cell, e.g., a bacterial or a fungal (including yeast) cell.

Examples of suitable bacteria are Gram-positive bacteria such as *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus lentus*, *Bacillus brevis*, *Bacillus stearothermophilus*, *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus coagulans*, *Bacillus circulans*, *Bacillus lautus*, *Bacillus megaterium*, *Ba-*

cillus thuringiensis, or *Streptomyces lividans* or *Streptomyces murinus*, or gramnegative bacteria such as *E.coli*. The transformation of the bacteria may, for instance, be effected by protoplast transformation or by using competent cells in a manner known *per se*.

The yeast organism may favorably be selected from a species of *Saccharomyces* or *Schizosaccharomyces*, e.g. *Saccharomyces cerevisiae*. The filamentous fungus may advantageously belong to a species of *Aspergillus*, e.g., *Aspergillus oryzae* or *Aspergillus niger*. Fungal cells may be transformed by a process involving protoplast formation and transformation of the protoplasts followed by regeneration of the cell wall in a manner known *per se*. A suitable procedure for transformation of *Aspergillus* host cells is described in EP 238 023.

In a yet further aspect, the present invention relates to a method of producing an alpha-amylase variant of the invention, which method comprises cultivating a host cell as described above under conditions conducive to the production of the variant and recovering the variant from the cells and/or culture medium.

The medium used to cultivate the cells may be any conventional medium suitable for growing the host cell in question and obtaining expression of the alpha-amylase variant of the invention. Suitable media are available from commercial suppliers or may be prepared according to published recipes (e.g., as described in catalogues of the American Type Culture Collection).

The alpha-amylase variant secreted from the host cells may conveniently be recovered from the culture medium by well-known procedures, including separating the cells from the medium by centrifugation or filtration, and precipitating proteinaceous components of the medium by means of a salt such as ammonium sulphate, followed by the use of chromatographic procedures such as ion exchange chromatography, affinity chromatography, or the like.

Industrial Applications

The alpha-amylase variants of this invention possess valuable properties allowing for a variety of industrial applications. In particular, enzyme variants of the invention are applicable as a component in washing, dishwashing and hard surface cleaning detergent compositions. Variant of the invention with altered properties may be used for starch processes, in particular starch conversion, especially liquefaction of starch (see, *e.g.*, US 3,912,590, EP patent publications Nos. 252 730 and 63 909, and WO 99/19467.

Further, variants of the invention are also particularly useful in the production of sweeteners and ethanol from starch, and/or for textile desizing

Composition

In an aspect the invention relates to a composition comprising a variant of the invention. In an embodiment the composition of the invention comprises one or more other enzymes, including one or more selected from the group of such as a lipase, cutinase, protease, cellulase, mannanase, maltogenic amylase, CGTase, glucoamylase, peroxidase or laccase, and/or another alpha-amylase.

Detergent compositions

As mentioned above, variants of the invention may suitably be incorporated in detergent compositions. Reference is made, for example, to WO 96/23874 and WO 97/07202 for further details concerning relevant ingredients of detergent compositions (such as laundry or dishwashing detergents), appropriate methods of formulating the variants in such detergent compositions, and for examples of relevant types of detergent compositions.

Detergent compositions comprising a variant of the invention may additionally comprise one or more other enzymes, such as a lipase, cutinase, protease, cellulase, mannanase, maltogenic amylase, CGTase, glucoamylase, peroxidase or laccase, and/or another alpha-amylase.

Alpha-amylase variants of the invention may be incorporated in detergents at conventionally employed concentrations. It is at present contemplated that a variant of the invention may be incorporated in an amount corresponding to 0.00001-10 mg (calculated as pure, active enzyme protein) of alpha-amylase per liter of wash/dishwash liquor using conventional dosing levels of detergent.

The invention also relates to a method of providing alpha-amylases with altered properties relative to the parent alpha-amylase, in particular solubility, especially increased solubility, substrate specificity, substrate binding, substrate cleavage pattern, temperature stability, pH dependence of enzymatic activity, pH dependence of stability, stability towards oxidation, Ca^{2+}-dependency and specific activity, comprising the following steps:

(a) modelling the parent alpha-amylase on the three-dimensional structure of SEQ ID NO:4 depicted in the Appendix 1 to produce a three-dimensional structure of the parent alpha-amylase;

(b) identifying in the three-dimensional structure obtained in step (a) at least one structural part of the parent wherein an alteration in said structural part is predicted to result in said altered property;

(c) modifying the sequence of a nucleic acid encoding the parent alpha-amylase to produce a nucleic acid encoding a deletion, insertion, or substitution of one or more amino acids at a position corresponding to said structural part; and

(d) expressing the modified nucleic acid in a host cell to produce the variant alpha-amylase,

wherein the variant has alpha-amylase enzymatic activity and has at least one altered property relative to the parent.

In an embodiment the method is a method of constructing a variant of a parent alpha-amylase having an altered property relative to the parent, wherein the parent alpha-amylase has the sequence of SEQ ID Nos: 2, 4, 6, 8, 10, 12 or 13 or has a sequence at least 60 % identity (determined as described above) to said sequence, said method comprising:

(a) modelling the parent alpha-amylase on the three-dimensional structure of SEQ ID NO:4 depicted in the Appendix 1 to produce a three-dimensional structure of the parent alpha-amylase;

(b) comparing the three-dimensional structure obtained in step (a) with a three-dimensional structure of an unrelated alpha-amylase, wherein the unrelated alpha-amylase differs from the parent alpha-amylase in said property;

(c) identifying a structural part of the three-dimensional structure obtained in step (a) which is different from the three-dimensional structure of the unrelated alpha-amylase and which is predicted to be relevant to said property,

(d) modifying the sequence of a nucleic acid encoding the parent alpha-amylase to produce a nucleic acid encoding a deletion, insertion, or substitution of one or more amino acids at a position corresponding to said structural part; and

(e) expressing the modified nucleic acid in a host cell to produce the variant alpha-amylase,

wherein the variant has alpha-amylase activity and has one or more altered properties as compared to the parent alpha-amylase.

The Termamyl-like alpha-amylases contemplated are the ones described above.

Method of increasing the solubility of polypeptides

The present invention also relates to a method of increaning the solubility of polypeptides, such as enzymes, in particular Termamyl-like alpha-amylases.

The method of this invention comprises substitutions, insertions and/or deletion of one or more amino acid residue(s), which residue(s) hold a position close to a neighbour polypeptide molecule located in the protein crystal. In the context of this invention, a polypeptide amino acid residue holding a position close to the neighbour molecule indicates an amino acid residue located within the polypeptide in a way that it is within a potential intermolecular interactive distance from an amino acid residue located at a neighbour enzyme molecule in the crystal or precipitate.

Examples of potential intermolecular interactions include, but are not limited to hydrogen bonding, salt bridge formation, polar interactions, hydrophobic interactions and aromatic interactions.

The term "neighbouring" means in the context of the present invention the shortest distance between two positions in a crystal structure being prepared, e.g., as described in "Protein Crystallization Techniques, Strategies, and Tips", A Laboratory Manual by Terese M. Bergfors), or as describe on the Internet on the site: www.hamptonresearch.com.

Thus, in this aspect the invention relates to a method of increasing the solubility of enzyme crystals, wherein one or more amino acid residue(s),

1) located within a distance of 6.0 Å of a neighbouring polyptide molecule in the tertiary crystal structure, and

2) interacting with said neighbouring polypeptide molecule,

are mutated, e.g., by substitution or deletion.

In a preferred embodiment the amino acid residues to be mutated are located with 3.5 Å of a neighbouring polypeptide.

Contemplated polypeptides include antimicrobial polypeptides, polypeptides with biological activity, such as insulin, growth hormone, EPO, TPO, factor VII, Factor VIII.

Contemplated enzyme activities include protease, amylase, CGTase, carbohydrase, transferase, lyase, oxidoreductase, lipase, cellulase, cutinase, pectate lyase, mannanase, maltogenic amylase, glucoamylase, pectin lyase activity.

In a preferred embodiment the enzyme is an amylase, preferably an alpha-amylase, especially a Termamyl-like alpha-amylase as will be described further below.

An amino acid position "close" to the substrate indicates a distance less than 6 Å (angstrom) corresponding to a protein-protein interaction mediated by a single water molecule. In a preferred embodiment an amino acid position close to the substrate indicates a distance less than 3.5 Å (angstrom) corresponding to a direct protein-protein interaction.

Method of increasing the solubility of Termamyl-like alpha-aylases

In this aspect the invention relates to a method of increasing the solubility of Termamyl-like alpha-amylase crystals, wherein one or more amino acid residue(s),

1) located within a distance of 6.0 Å of a neighbouring Termamyl-like alpha-amylase molecule in the tertiary crystal structure, and

2) interacting with said neighbouring Termamyl-like alpha-amylase molecule,

are mutated, e.g., by substitution or deletion.

In a preferred embodiment the amino acid residues to be mutated are located with 3.5 Å of a neighbouring Termamyl-like alpha-amylase. The crystal structure of SP722 depicted in APPENDIX 1 may be used as the reference (fix-point) for determining the distance between neighbouring alpha-amylases.

However, it is within the scope of the invention that the reference (fix-point) crystal structure is a structure modelled (as described above or in WO 96/23874) from SP722 depicted in APPENDIX 1.

Preferred Termamyl-like alpha-amylases include *Bacillus* alpha-amylase selected from the group consisting of alpha-amylase derived from a strain of *B. licheniformis, B. amyloliquefaciens, B. stearothermophilus, Bacillus* sp. NCIB 12289, NCIB 12512, NCIB 12513 or DSM 9375, or DSMZ no. 12649, KSM AP1378. Termamyl-like alpha-amylase may be any of the alpha-amylases selected from the group depicted in SEQ ID NOS: 2, 4, 6, 8, 10, 12, and 13, or Termamyl-like alpha-amylase having an amino acid sequence which has a degree of identity to SEQ ID NO: 4 of at least 60%, preferably 70%, more preferably at least 80%, even more preferably at least about 90%, even more preferably at least 95%, even more preferably at least 97%, and even more preferably at least 99%, or Termamyl-like alpha-amylase encoded by a nucleic acid sequence, which hydridizes under low,

preferably medium, preferred high stringency conditions, with the nucleic acid sequence of SEQ ID NO: 11. The conditions are described in further details above.

Termamyl-like alpha-amylase amino acid residues being less than 6.0 Å from the nearest neighbour amylase molecule are the following (using the SP722 numbering):

19, 20, 21, 22, 25, 28, 29, 53, 76, 84, 87, 90, 93, 94, 124, 125, 126, 128, 142, 144, 156, 157, 158, 159, 160, 161, 170, 171, 172, 173, 174, 175, 183, 184, 185, 186, 187, 188, 189, 190, 193, 195, 196, 197, 209, 212, 226, 229, 256, 257, 258, 259, 280, 281, 298, 299, 300, 302, 303, 304, 305, 306, 310, 311, 314, 319, 320, 321, 322, 341, 345, 405, 406, 408, 444, 447, 448, 449, 463, 464, 465, 466, 467.

Termamyl-like alpha-amylase amino acid residues being less than 3.5 Å from the nearest neighbour amylase molecule are the following (using the SP722 numbering):

22, 25, 28, 76, 94, 125, 128, 158, 160, 171, 173, 174, 184, 189, 209, 226, 229, 298, 299, 302, 306, 310, 314, 320, 345, 405, 447, 466.

The amino acid residues being less than 6.0 Å from the nearest neighboring amylase molecule are the following positions identified in the model structure of the SP722 amylase:

ASN 19, ASP 20, GLY 21, GLN 22, ASN 25, ARG 28, ASP 29, GLN 53, ARG 76, GLN 84, SER 87, HIS 90, LYS 93, ASN 94, ASN 125, ASN 126, ASN 128, LYS 142, ASP 144, LYS 156, TRP 157, ARG 158, TRP 159, TYR 160, HIS 161, PHE 173, GLN 174, ASN 175, ASP 183, GLY 184, LYS 185, ALA 186, TRP 187, ASP 188, TRP 189, GLU 190, SER 193, GLY 196, ASN 197, ASP 209, GLU 212, ASN 226, ASN 229, ALA 256, THR 257, GLY 258, LYS 259, ASN 280, LYS 281, TYR 298, ASN 299, ALA 300, ASN 302, SER 303, GLY 304, GLY 305, ASN 306, ALA 310, ASN 314, GLN 319, LYS 320, HIS 321, PRO 322, GLU 341, GLN 345, PHE 405, ASP 406, HIS 408, GLN 444, ALA 447, GLY 448, GLN 449, THR 463, ILE 464, ASN 465, ALA 466, ASP 467.

The amino acid residues being less than 3.5 Å from the nearest neighboring amylase molecule are the following positions identified in the model structure of the SP722

amylase:
GLN 22, ASN 25, ARG 28, ARG 76, ASN 94, ASN 125, ASN 128, ARG 158, TYR 160, PHE 173, GLN 174, GLY 184, TRP 189, ASP 209, ASN 226, ASN 229, TYR 298, ASN 299, ASN 302, ASN 306, ASN 314, LYS 320, GLN 345, PHE 405, ALA 447, ALA 466.

The amino acid residues being less than 6.0 Å from the nearest neighboring amylase molecule are the following positions identified in the model structure of the AA560 amylase: ASN 19, ASP 20, ASN 22, ASN 25, ARG 28, SER 29, GLN 53, ARG 76, GLN 84, ALA 87, ASN 90, LYS 93, SER 94, PRO 124, ASN 125, ASN 126, ASN 128, LYS 142, ASP 144, LYS 156, TRP 157, ARG 158, TRP 159, TYR 160, HIS 161, SER 170, ARG 171, LYS 172, LEU 173, ASN 174, ASN 175, ASP 183, GLY 184, LYS 185, GLY 186, TRP 187, ASP 188, TRP 189, GLU 190, THR 193, ASN 195, GLY 196, ASN 197, ASP 209, GLU 212, ASN 226, GLY 229, ALA 256, THR 257, GLY 258, LYS 259, LYS 281, TYR 298, ASN 299, ALA 300, LYS 302, SER 303, GLY 304, ASN 306, ARG 310, GLN 311, ASN 314, GLN 319, ARG 320, HIS 321, PRO 322, GLU 341, GLU 345, LEU 405, HIS 408, ARG 444, ALA 447, GLY 448, GLN 449, THR 463, ILE 464, ASN 465, ALA 466, ASP 467.

The amino acid residues being less than 3.5 Å from the nearest neighboring amylase molecule are the following positions identified in the model structure of the AA560 amylase: ARG 28, ASN 125, ASN 128, ARG 158, TYR 160, ARG 171, LEU 173, ASN 174, GLY 184, TRP 189, GLY 196, ASP 209, ASN 226, TYR 298, ASN 299, LYS 302, ASN 306, ARG 310, ASN 314, ARG 320, GLU 345, ALA 447, ALA 466.

Substitutions in alpha-amylases leading to higher solubility and thus to higher performance.

In general, any substitutions disturbing or destroying a protein-protein interaction of any kind will lead to higher solubility and thus to higher performance in a particular application. An amino acid residue participating in protein-protein interaction may thus be changed to a larger, a smaller, more hydrophobic, more hydrophilic, to a charged or to an uncharged amino acid leading to higher solubility.

A larger amino acid residue is capable of making a steric hindance for the interaction and a smaller amino acid residue makes the distance between the interacting residues to large, weaking the interaction. Polar interaction and in particular saltbridges are destroyed by changing at least one of the involved residues to a hydrophobic residues, by changing at least one of the involved residues to a smaller residue making the distance for a strong interaction to large, or by changing at least one of the involved residues to a larger residue which make sterical hindrance. Hydrophobic interactions are effectively disturbed by changing one of the interacting amino acids to hydrophilic amino acid residues but also smaller or larger hydrophobic residues can destroy this kind of interaction. Aromatic interactions can be prevented by changing to a hydrophilic residue or to a small hydrophobic residue.

MATERIALS AND METHODS

Enzymes:

SP722: SEQ ID NO: 4, available from Novozymes, and disclosed in WO 95/26397.

AA560: SEQ ID NO: 12; disclosed in WO 00/60060 and available from Novozymes A/S; disclosed in Danish patent application no. PA 1999 00490; deposited on 25th January 1999 at DSMZ and assigned the DSMZ no. 12649.

AA560 were deposited by the inventors under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure at Deutshe Sammmlung von Microorganismen und Zellkulturen GmbH (DSMZ), Mascheroder Weg 1b, D-38124 Braunschweig DE.

Bacillus subtilis SHA273: see WO 95/10603

Plasmids

pJE1 contains the gene encoding a variant of SP722 alpha-amylase (SEQ ID NO: 4): viz. deletion of 6 nucleotides corresponding to amino acids D183-G184 in the mature protein. Transcription of the JE1 gene is directed from the *amyL* promoter. The plasmid further more contains the origin of replication and *cat*-gene conferring resistance towards kanamycin obtained from plasmid pUB110 (Gryczan, TJ et al. (1978), J. Bact. 134:318-329).

Methods:

Modelbuiling

Protein structure databases, such as "The Protein Data Bank (PDB) (<http://www.pdb.bnl.gov/>)" or "The Brookhaven databank at Brookhaven National Laboratory, US" are search for proteins similar to the molecule in question that a model are to be build of. The amino acid sequences are aligned taking structurally conserved regions into consideration and the coordinates are copied from the reference protein to the subject protein. The coordinates for regions with insertions and deletions are assigned either from other proteins having similar amino acid sequence, or by using the random structure generator function found in most 3D software packages, eg. in Homology from Biosym, MSI.

When coordinates have been assigned to all amino acids of the subjective protein and the fragments have been linked together, example by the cormands *END REPAIR* and *SPLICE REPAIR*, in the Discover program from from Biosym, MSI, the

model are to be refined. The energy of the model is minimised first by relaxing the molecule (RELAX command in the Discover program) and second minimised by molecular dynamics.

References can be found in and in the manuals of homology building software, eg. Homology from Biosym, MSI

Construction of library vector pDorK101

The *E. coli/Bacillus* shuttle vector pDorK101 (described below) can be used to introduce mutations without expression of alpha-amylase in *E. coli* and then be modified in such way that the alpha-amylase is active in Bacillus. The vector was constructed as follows: The JE1 encoding gene (SP722 with the deletion of D183-G184) was inactivated in pJE1 by gene interruption in the PstI site in the 5´coding region of the SEQ ID NO: 4: SP722 by a 1.2 kb fragment containing an *E. coli* origin of replication. This fragment was PCR amplified from the pUC19 (GenBank Accession #:X02514) using the forward primer: 5´-gacctgcagtcaggcaacta-3´ and the reverse primer: 5´-tagagtcgacctgcaggcat-3´. The PCR amplicon and the pJE1 vector were digested with PstI at 37°C for 2 hours. The pJE1 vector fragment and the PCR fragment were ligated at room temperature. for 1 hour and transformed in *E. coli* by electrotransformation. The resulting vector is designated pDorK101.

Filter screening assays

The assay can be used to screening of Termamyl-like α-amylase variants having an improved stability at high pH compared to the parent enzyme and Termamyl-like α-amylase variants having an improved stability at high pH and medium temperatures compared to the parent enzyme depending of the screening temperature setting

High pH filter assay

Bacillus libraries are plated on a sandwich of cellulose

acetate (OE 67, Schleicher & Schuell, Dassel, Germany) - and nitrocellulose filters (Protran-Ba 85, Schleicher & Schuell, Dassel, Germany) on TY agar plates with 10 μg/ml kanamycin at 37°C for at least 21 hours. The cellulose acetate layer is located on the TY agar plate.

Each filter sandwich is specifically marked with a needle after plating, but before incubation in order to be able to localize positive variants on the filter and the nitrocellulose filter with bound variants is transferred to a container with glycin-NaOH buffer, pH 8.6-10.6 and incubated at room temperature (can be altered from 10°-60°C) for 15 min. The cellulose acetate filters with colonies are stored on the TY-plates at room temperature until use. After incubation, residual activity is detected on plates containing 1% agarose, 0.2% starch in glycin-NaOH buffer, pH 8.6-10.6. The assay plates with nitrocellulose filters are marked the same way as the filter sandwich and incubated for 2 hours. at room temperature. After removal of the filters the assay plates are stained with 10% Lugol solution. Starch degrading variants are detected as white spots on dark blue background and then identified on the storage plates. Positive variants are rescreened twice under the same conditions as the first screen.

Low calcium filter assay

The *Bacillus* library are plated on a sandwich of cellulose acetate (OE 67, Schleicher & Schuell, Dassel, Germany) - and nitrocellulose filters (Protran-Ba 85, Schleicher & Schuell, Dassel, Germany) on TY agar plates with a relevant antibiotic, *e.g.*, kanamycin or chloramphenicol, at 37°C for at least 21 hours. The cellulose acetate layer is located on the TY agar plate.

Each filter sandwich is specifically marked with a needle after plating, but before incubation in order to be able to localize positive variants on the filter and the nitrocellulose filter with bound variants is transferred to a

container with carbonate/bicarbonate buffer pH 8.5-10 and with different EDTA concentrations (0.001 mM - 100 mM). The filters are incubated at room temperature for 1 hour. The cellulose acetate filters with colonies are stored on the TY-plates at room temperature until use. After incubation, residual activity is detected on plates containing 1% agarose, 0.2% starch in carbonate/bicarbonate buffer pH 8.5-10. The assay plates with nitrocellulose filters are marked the same way as the filter sandwich and incubated for 2 hours. at room temperature. After removal of the filters the assay plates are stained with 10% Lugol solution. Starch degrading variants are detected as white spots on dark blue background and then identified on the storage plates. Positive variants are rescreened twice under the same conditions as the first screen.

Method for obtaining the regions of interest:

There are three known 3D structures of bacterial α-amylases. Two of *B. licheniformis* α-amylase, Brookhaven database 1BPL (Machius et al. (1995), J. Mol. Biol. 246, p. 545-559) and 1VJS (Song et al. (1996), Enzymes for Carbohydrate 163 Engineering (Prog. Biotechnol. V 12). These two structures are lacking an important piece of the structure from the so-called B-domain, in the area around the two Calcium ions and one Sodium ion binding sites. We have therefore used a 3D structure of an alpha-amylase BA2 (WO 96/23874 which is a hybrid between BAN™ (SEQ ID NO. 5) and *B. licheniformis* alpha-amylase (SEQ ID NO. 4). On basis of the structure a model of *B. licheniformis* alpha amylase and the SP722 α-amylase has been build.

Fermentation and purification of α-amylase variants

Fermentation and purification may be performed by methods well known in the art.

Stability determination

All stability trials are made using the same set up. The method is as follows:
The enzyme is incubated under the relevant conditions (1-4). Samples are taken at various time points, e.g., after 0, 5, 10, 15 and 30 minutes and diluted 25 times (same dilution for all taken samples) in assay buffer (0.1M 50mM Britton buffer pH 7.3) and the activity is measured using the Phadebas assay (Pharmacia) under standard conditions pH 7.3, 37°C.

The activity measured before incubation (0 minutes) is used as reference (100%). The decline in percent is calculated as a function of the incubation time. The table shows the residual activity after, e.g., 30 minutes of incubation.

Specific activity determination

The specific activity is determined using the Phadebas assay (Pharmacia) as activity/mg enzyme. The manufactures instructions are followed (see also below under "Assay for α-amylase activity).

Solubility Determination I

Purified enzyme is dialyzed against a selected buffer overnight. Standard conditions are 0.02 M Tris-HCl, 0.15 M NaCl, pH 7.5, room temperature. A preparation, containing approximately 40 mg enzyme is concentrated on an amicon cell using Millepore ultrafiltration membranes, YM10, NMWL: 10,000. Measuring A_{280} before and during the process followed concentration of the enzyme. The concentration step is stopped when precipitation started to occur. Measurement of activity in the supernatant is made to ensure that the precipitate actually is amylase. The precipitate is then dissolved again by adding buffer at room temperature and the protein concentration is measured.

Solubility Determination II

Purified enzyme is dialyzed against a selected buffer overnight. Standard conditions are 0.01 M Boric acid, 0.01 M KCl, 0.002 M $CaCl_2$, 0.15M NaCl pH 7.5. A preparation,

containing approximately 40 mg enzyme is concentrated on an amicon cell using Millepore ultrafiltration membranes, YM10, NMWL: 10,000. Measuring A_{280} before and during the process followed concentration of the enzyme. The concentration step is stopped when precipitation started to occur. Measurement of activity in the supernatant is made to ensure that the precipitate actually is amylase. The precipitate is then dissolved again by adding buffer at room temperature and the protein concentration is measured.

Assays for Alpha-Amylase Activity

1. Phadebas assay

Alpha-amylase activity is determined by a method employing Phadebas® tablets as substrate. Phadebas tablets (Phadebas® Amylase Test, supplied by Pharmacia Diagnostic) contain a cross-linked insoluble blue-colored starch polymer, which has been mixed with bovine serum albumin and a buffer substance and tabletted.

For every single measurement one tablet is suspended in a tube containing 5 ml 50 mM Britton-Robinson buffer (50 mM acetic acid, 50 mM phosphoric acid, 50 mM boric acid, 0.1 mM $CaCl_2$, pH adjusted to the value of interest with NaOH). The test is performed in a water bath at the temperature of interest. The alpha-amylase to be tested is diluted in x ml of 50 mM Britton-Robinson buffer. 1 ml of this alpha-amylase solution is added to the 5 ml 50 mM Britton-Robinson buffer. The starch is hydrolyzed by the alpha-amylase giving soluble blue fragments. The absorbance of the resulting blue solution, measured spectrophotometrically at 620 nm, is a function of the alpha-amylase activity.

It is important that the measured 620 nm absorbance after 10 or 15 minutes of incubation (testing time) is in the range of 0.2 to 2.0 absorbance units at 620 nm. In this absorbance range there is linearity between activity and absorbance (Lambert-Beer law). The dilution of the enzyme must therefore be adjusted to fit this criterion. Under a specified set of conditions (temp., pH, reaction time, buffer conditions) 1 mg of a given alpha-

amylase will hydrolyze a certain amount of substrate and a blue colour will be produced. The colour intensity is measured at 620 nm. The measured absorbance is directly proportional to the specific activity (activity/mg of pure alpha-amylase protein) of the alpha-amylase in question under the given set of conditions.

2. Alternative method

Alpha-amylase activity is determined by a method employing the PNP-G7 substrate. PNP-G7 which is a abbreviation for p-nitrophenyl-alpha,D-maltoheptaoside is a blocked oligosaccharide which can be cleaved by an endo-amylase. Following the cleavage, the alpha-Glucosidase included in the kit digest the substrate to liberate a free PNP molecule which has a yellow colour and thus can be measured by visible spectophometry at λ=405nm. (400-420 nm.). Kits containing PNP-G7 substrate and alpha-Glucosidase is manufactured by Boehringer-Mannheim (cat. No. 1054635).

To prepare the substrate one bottle of substrate (BM 1442309) is added to 5 ml buffer (BM1442309). To prepare the α-Glucosidase one bottle of alpha-Glucosidase (BM 1462309) is added to 45 ml buffer (BM1442309). The working solution is made by mixing 5 ml alpha-Glucosidase solution with 0.5 ml substrate.

The assay is performed by transforming 20μl enzyme solution to a 96 well microtitre plate and incubating at 25°C. 200 μl working solution, 25°C is added. The solution is mixed and pre-incubated 1 minute and absorption is measured every 15 sec. over 3 minutes at OD 405 nm.

The slope of the time dependent absorption-curve is directly proportional to the specific activity (activity per mg enzyme) of the alpha-amylase in question under the given set of conditions.

<u>General method for random mutagenesis by use of the DOPE program</u>

The random mutagenesis may be carried out as follows:

1. Select regions of interest for modification in the parent enzyme

2. Decide on mutation sites and non-mutated sites in the selected region

3. Decide on which kind of mutations should be carried out, e.g. with respect to the desired stability and/or performance of the variant to be constructed

4. Select structurally reasonable mutations.

5. Adjust the residues selected by step 3 with regard to step 4.

6. Analyze by use of a suitable dope algorithm the nucleotide distribution.

7. If necessary, adjust the wanted residues to genetic code realism (e.g., taking into account constraints resulting from the genetic code (e.g. in order to avoid introduction of stop codons))(the skilled person will be aware that some codon combinations cannot be used in practice and will need to be adapted)

8. Make primers

9. Perform random mutagenesis by use of the primers

10. Select resulting α-amylase variants by screening for the desired improved properties.

Suitable dope algorithms for use in step 6 are well known in the art. One algorithm is described by Tomandl, D. et al., Journal of Computer-Aided Molecular Design, 11 (1997), pp. 29-38). Another algorithm, DOPE, is described in the following:

The dope program

The "DOPE" program is a computer algorithm useful to optimize the nucleotide composition of a codon triplet in such a way that it encodes an amino acid distribution which resembles most the wanted amino acid distribution. In order to assess which of the possible distributions is the most similar to the wanted amino acid distribution, a scoring function is needed. In the "Dope" program the following function was found to be suited:

$$s \equiv \prod_{i=1}^{N} \left(\frac{x_i^{y_i}}{y_i^{y_i}} \frac{(1-x_i)^{1-y_i}}{(1-y_i)^{1-y_i}} \right)^{w_i},$$

where the x_i's are the obtained amounts of amino acids and groups of amino acids as calculated by the program, y_i's are the wanted amounts of amino acids and groups of amino acids as defined by the user of the program (e.g. specify which of the 20 amino acids or stop codons are wanted to be introduced, e.g. with a certain percentage (e.g. 90% Ala, 3% Ile, 7% Val), and w_i's are assigned weight factors as defined by the user of the program (e.g., depending on the importance of having a specific amino acid residue inserted into the position in question). N is 21 plus the number of amino acid groups as defined by the user of the program. For purposes of this function 0^0 is defined as being 1.

A Monte-Carlo algorithm (one example being the one described by Valleau, J.P. & Whittington, S.G. (1977) A guide to Mont Carlo for statistical mechanics: 1 Highways. In "Stastistical Mechanics, Part A" Equlibrium Techniqeues ed. B.J. Berne, New York: Plenum) is used for finding the maximum value of this function. In each iteration the following steps are performed:

1. A new random nucleotide composition is chosen for each base, where the absolute difference between the current and the new composition is smaller than or equal to d for each of the four nucleotides G,A,T,C in all three positions of the codon (see below for definition of d).
2. The scores of the new composition and the current composition are compared by the use of the function s as described above. If the new score is higher or equal to the score of the current composition, the new composition is kept and the current composition is changed to the new one. If the new score is smaller, the probability of keeping the new composition is $\exp\left(1000\left(new_score - current_score\right)\right)$.

A cycle normally consists of 1000 iterations as described above in which d is decreasing linearly from 1 to 0. One hundred or more cycles are performed in an optimization process. The nucleotide composition resulting in the highest

score is finally presented.

EXAMPLES

EXAMPLE 1

Method of extracting important regions and amino acid residues for identifying SP722 alpha-amylase variants with altered properties.

The tertiary structure of the SP722 alpha-amylase was displayed on a UNIX computer station running Insight and all hydrogens and water molecules were deleted. For this minimized amylase structure, all the symetri related amylase molecules were displayed, according to the crystal parameters and the spacegroup determined in the pdb-structure file (Appendix 1). A small computer program was made to calculate the distance from each atom in the mother alpha-amylase to any atom in the symetri related amylase structures. Setting the distance cut-off to 3.5 Å and 6.0 Å, respectively resulted in the lists below:

The amino acid residues being less than 6.0 Å from the nearest neighboring amylase molecule are the following positions identified in the model structure of the SP722 amylase:

ASN 19, ASP 20, GLY 21, GLN 22, ASN 25, ARG 28, ASP 29, GLN 53, ARG 76, GLN 84, SER 87, HIS 90, LYS 93, ASN 94, ASN 125, ASN 126, ASN 128, LYS 142, ASP 144, LYS 156, TRP 157, ARG 158, TRP 159, TYR 160, HIS 161, PHE 173, GLN 174, ASN 175, ASP 183, GLY 184, LYS 185, ALA 186, TRP 187, ASP 188, TRP 189, GLU 190, SER 193, GLY 196, ASN 197, ASP 209, GLU 212, ASN 226, ASN 229, ALA 256, THR 257, GLY 258, LYS 259, ASN 280, LYS 281, TYR 298, ASN 299, ALA 300, ASN 302, SER 303, GLY 304, GLY 305, ASN 306, ALA 310, ASN 314, GLN 319, LYS 320, HIS 321, PRO 322, GLU 341, GLN 345, PHE 405, ASP 406, HIS 408, GLN 444, ALA 447, GLY 448, GLN 449, THR 463, ILE 464, ASN 465, ALA 466, ASP 467.

The amino acid residues being less than 3.5 Å from the nearest neighboring amylase molecule are the following positions identified in the model structure of the SP722 amylase:

GLN 22, ASN 25, ARG 28, ARG 76, ASN 94, ASN 125, ASN 128, ARG 158, TYR 160, PHE 173, GLN 174, GLY 184, TRP 189, ASP 209, ASN 226, ASN 229, TYR 298, ASN 299, ASN 302, ASN 306, ASN 314, LYS 320, GLN 345, PHE 405, ALA 447, ALA 466.

EXAMPLE 2

Alternative method of extracting important regions and amino acid residues for identifying SP722 alpha-amylase variants with altered properties.

The tertiary structure of the SP722 alpha-amylase was displayed on a UNIX computer station running Insight and all hydrogen and water molecules were deleted. This minimized amylase structure was imported ("getmol") into the WHAT IF software (G.Vriend, J. Mol. Graph.,(1990) 8, 52-56) and all the symmetry related amylase molecules within 6 angstrom were added to the soup ("symtry, symspg, sympar 6, soushl, soup). A new coordinate file for SP722 including the symmetry molecules was written (makmol, tot 0). The center SP722 amylase was then deleted from the structure file, and a new file including the surrounding molecules was written. A small computer program was made to calculate the distance from each atom in the mother alpha-amylase (original SP72 structure file without water molecules and Hydrogen atoms) to any atom in the symmetry related amylase file. Setting the distance cut-off to 3.5 Å and 6.0 Å, respectively resulted in identification of the position referred to in the description.

What If commands:

>>Whatif<<	Starts WHAT IF
>>Getmol sp722_HOH.pdb<<	import the water and H-depleted SP722 structure file into the WHAT IF sotware
>>symtry<<	Go to symmetry menu
>>symspg<<	Reads symmetry related information in structure file
>>sympar 6<<	Makes symmetry related residues within 6 A distance

>>soushl<< Adds the symmetry molecules to the soup
>>soup<< Go to soup menu

>>makmol, "sp722_wi6.pdb", tot 0<< writes the "sp722_wi6" pdb file including all atoms in the soup (SP722 and the symmetry molecules within 6 Å)

EXAMPLE 3

Homology building of AA560 from SP722 tertiary structure

The overall homology of the AA560 alpha-amylase (SEQ ID NO: 12) to SP722 (SEQ ID NO: 4) is about 87% as described above. Sequence alignment of AA560 and SP722 shows there to be no insertion or deletions, which can also be seen in Fig. 1.

The tertiary structure of the AA560 alpha-amylase was model build on the structure disclosed in Appendix 1 using the method "Modelbuiling" described in the "Materials & Methods"-section.

The structure of SP722 was displayed on a UNIX work staion running Insight and Homology software from BIOSYM, MSI. The amino acid sequences were aligned and the Sp722 coordinated assigned to the AA560 amino acids. The coordinates of the first four amino acids in AA560, which are missing in the SP722 structure, were assigned by the "END REPAIR" function.

The AA560 model was refined by first relaxing the amino acid side changes, using the "RELAX" command and then running molecular dynamics to minimise the energy of the 3D model. Default parameters from Insight 95, MSI were chosen for both relaxation molecular dynamics.

Finally the spacegroup and the unit cell dimentions are copied from the SP722 pdb file to the AA560 model file.

EXAMPLE 4

Method of extracting important regions for identifying AA560 alpha-amylase variants with altered altered properties

The model build structure of AA560 was subjected to the same calculations as was SP722 in Example 1. Because the homology of the two alpha-amylases is as high as about 87% identity, the crystal interactions of AA560 are expected to similar to those of SP722, i.e., AA560 crystalize in the same spacegroup as SP722 and with the similar unity cell parameter.

The tertiary structure of the AA560 alpha-amylase was displayed on a UNIX computer station running Insight and all hydrogens and water molecules were deleted. For this minimized amylase structure, all the symetri related amylase molecules were displayed, according to the crystal parameters and the spacegroup for SP722 (Appendix 1). A small computer program was made to calculate the distance from each atom in the "mother" alpha-amylase to any atom in the symetri related amylase structures. Setting the distance cut-off to 3.5 Å and 6.0 Å, respectively resulted in the lists below:

The amino acid residues being less than 6.0 Å from the nearest neighboring amylase molecule are the following positions identified in the model structure of the AA560 amylase: ASN 19, ASP 20, ASN 22, ASN 25, ARG 28, SER 29, GLN 53, ARG 76, GLN 84, ALA 87, ASN 90, LYS 93, SER 94, PRO 124, ASN 125, ASN 126, ASN 128, LYS 142, ASP 144, LYS 156, TRP 157, ARG 158, TRP 159, TYR 160, HIS 161, SER 170, ARG 171, LYS 172, LEU 173, ASN 174, ASN 175, ASP 183, GLY 184, LYS 185, GLY 186, TRP 187, ASP 188, TRP 189, GLU 190, THR 193, ASN 195, GLY 196, ASN 197, ASP 209, GLU 212, ASN 226, GLY 229, ALA 256, THR 257, GLY 258, LYS 259, LYS 281, TYR 298, ASN 299, ALA 300, LYS 302, SER 303, GLY 304, ASN 306, ARG 310, GLN 311, ASN 314, GLN 319, ARG 320, HIS 321, PRO 322, GLU 341, GLU 345, LEU 405, HIS 408, ARG 444, ALA 447, GLY 448, GLN 449, THR 463, ILE 464, ASN 465, ALA 466, ASP 467.

The amino acid residues being less than 3.5 Å from the nearest neighboring amylase molecule are the following positions identified in the model structure of the AA560 amylase: ARG 28, ASN 125, ASN 128, ARG 158, TYR 160, ARG 171, LEU 173, ASN 174, GLY 184, TRP 189, GLY 196, ASP 209, ASN 226, TYR 298, ASN 299, LYS 302, ASN 306, ARG 310, ASN 314, ARG 320, GLU 345, ALA 447, ALA 466.

EXAMPLE 5

Construction, by localized random, doped mutagenesis, of AA560 alpha-amylase variants having increased solubility in comparison to the parent enzyme

To increase the solubility of the AA560 alpha-amylase random mutagenesis in pre-selected region was performed as described in the following.

Region: Residue:
SAI: R181-W189

The DOPE software (see "Materials and Methods") was used to determine spiked codons for each suggested change in the SA1 region minimizing the amount of stop codons (see table 1). The exact distribution of nucleotides was calculated in the three positions of the codon to give the suggested population of amino acid changes. The doped regions were doped specifically in the indicated positions to have a high chance of getting the desired residues, but still allow other possibilities.

Table 1:
Distribution of amino acid residues for each position
R181: 72% R, 2% N, 7% Q, 4% H, 4%K, 11%S
G182: 73% G, 13% A, 12% S, 2% T
K185: 95% K, 5% R
G186: 50% A, 4% N, 6% D, 1%E, 1% G, 1% K, 5% S, 31% T
W187: 100% W
D188: 100% D
W189: 92% W, 8% S

The resulting doped oligonucleotide strand is shown in table 2 as sense strand: with the wild type nucleotide and amino acid sequences and the distribution of nucleotides for each doped position.

Table 2:

Position	181	182	185	186	187	188	189
Amino acid seq.	Arg	Gly	Lys	Gly	Trp	Asp	Trp
Wt nuc. seq.	aga	ggt	aaa	ggg	tgg	gat	tgg

Forward primer (SEQ ID NO: 14):
FSA: 5´-caa aat cgt atc tac aaa ttc 123 456 a7g 8910 tgg gat t11g gaa gta gat tcg gaa aat-3´

Distribution of nucleotides for each doped Position
1: 35% A, 65% C
2: 83% G, 17% A
3: 63% G, 37% T
4: 86% G, 14% A
5: 85% G, 15% C
6: 50% T, 50% C
7: 95% A, 5%G
8: 58% G, 37% A, 5% T
9: 86% C, 13% A, 1% G
10: 83% T, 17% G
11: 92% G, 8% C

Reverse primer (SEQ ID NO: 15):
RSA: 5´-gaa ttt gta gat acg att ttg-3'

Random mutagenesis

The spiked oligonucleotides apparent from Table 2 (which by a common term is designated FSA) and reverse primers RSA for the SA1 region and specific SEQ ID NO: 12: AA560 primers covering the SacII and the DraIII sites are used to generate PCR-library-fragments by the overlap extension method (Horton et al., Gene, 77 (1989), pp. 61-68) with an overlap of 21 base pairs. Plasmid pJE1 is template for the Polymerase Chain Reaction. The PCR fragments are cloned in the *E. coli/Bacillus* shuttle vector pDork101 (see "Materials and Methods" section) enabling mutagenesis in *E. coli* and immediate expression in *Bacillus subtilis* preventing lethal accumulation of amylases in *E. coli*. After establishing the cloned PCR fragments *in E. coli*, a modified pUC19 fragment is digested out of the plasmid and the promoter and the mutated Termamyl gene is physically connected and expression can take place in *Bacillus*.

Screening

The library may be screened in the low calcium filter

assays described in the "Material and Methods" section above.

EXAMPLE 6

Construction of variants of AA560 SEQ ID NO: 12

The gene encoding the AA560 alpha-amylase shown in SEQ ID NO: 12 is located in a plasmid pTVB223. The amylase is expressed from the amyL promoter in this construct in *Bacillus subtilis*.

A variant of the invention with delta(D183-G184) mutations was constructed by the mega-primer method as described by Sarkar and Sommer, (1990), BioTechniques 8: 404-407.

Gene specific primer B1 (SEQ ID NO: 16) and mutagenic primer 101458 (SEQ ID NO: 18) were used to amplify by PCR an approximately 645 bp DNA fragment from a pTVB223 plasmid encoding AA560 shown in SEQ ID NO: 12).

The 645 bp fragment was purified from an agarose gel and used as a mega-primer together with primer Y2 (SEQ ID NO: 17) in a second PCR carried out on the same template.

The resulting approximately 1080 bp fragment was digested with restriction enzymes BstEII and AflIII and the resulting approximately 510 bp DNA fragment was purified and ligated with the pTVB223 plasmid digested with the same enzymes. Competent *Bacillus subtilis* SHA273 (amylase and protease low) cells were transformed with the ligation and Chlorampenicol resistant transformants and was checked by DNA sequencing to verify the presence of the correct mutations on the plasmid.

primer B1: (SEQ ID NO: 16)

5' CGA TTG CTG ACG CTG TTA TTT GCG 3'

primer Y2: (SEQ ID NO: 17)

5' CTT GTT CCC TTG TCA GAA CCA ATG 3'

primer 101458 (SEQ ID NO: 18):

5' GT CAT AGT TGC CGA AAT CTG TAT CGA CTT C 3'

The resulting plasmid encoding the AA560 amylase with delta(D183-G184)+N195F was named pTVB232.

The construction of the other variants of the invention was carried out in a similar manner.

Example 7

Determination of solubility of AA560 and SP722 variants

AA560 variant was constructed as described above. The solubility was determined as descred in the "Material and Methods" section as Solubility Determination I

Variant	Solubility (mg/ml
Wild-type AA560	2 mg/ml
AA560 delta(D183-G184)+N195F+N445Q+N446N(AX23)	more than 6 mg/ml

0.02 M Tris-HCl, 0.15 M NaCl, pH 7.5, room temperature

The concentration step was started with a protein amount of 40 mg and in general, 50% of the amylases were lost during the process. This loss of protein occurred for all enzymes in the initial phase of the process and full recovery of the enzymes were obtained in the terminating phase where the volumes are become very limited. Loss of enzymes was due to adsorption to the membrane.

Example 8:

Determination of solubility of AA560 variants

AA560 variants were constructed as described above, using the wild-type AA560 as template. The solubility was determined as described in the "Material and Methods" section under Solubility Determination II

Mutations	**Solubility (g/L)**
Wild type AA560	2.8
AA560+N125A	9
AA560+N125R	9
AA560+N306R	7
AA560+Y298H+N299A+K302R+S303Q+N306G	12

AA560+delta(D183+G184)+R181Q+E345R	12
AA560+delta(D183+G184)+R181Q+W189R	4.5
AA560+delta(D183+G184)+R181Q+S94K+W189R	7
AA560+delta(D183+G184)+N195F+R118K+R320K+R458K	10
AA560+delta(D183+G184)+N195F+W189K+N306K+N445K	10
AA560+delta(D183+G184)+N195F+R118K+N125K+R444K+ N445K	3
AA560+delta(D183+G184)+N195F+W189K+N445K	12
AA560+delta(D183+G184)+N195F+R400T	4
AA560+delta(D183+G184)+N195F+W439R	5.5
AA560+delta(D183+G184)+N195F+Q449E	3.4
AA560+delta(D183+G184)+N195F+N484Q	4.3
AA560+delta(D183+G184)+N195F+R181Q+N445Q+K446N+ N484E	4.15
AA560+delta(D183+G184)+N195F+R181E+N445Q+K446N	3.5
AA560+delta(D183+G184)+N195F+R181E+K446N	5.2
AA560+delta(D183+G184)+N195F+R310A+R181Q+ N445Q+K446N	5
AA560+delta(D183+G184)+N195F+R320K+R181Q+ N445Q+K446N	6.9
AA560+delta(D183+G184)+N195F+Q319K+R320D+ R181Q+N445Q+K446N	4
AA560+delta(D183+G184)+N195F+N306A+R181Q+ N445Q+K446N	5.5
AA560+delta(D183+G184)+N195F+K302N+R181Q+ N445Q+K446N	8
AA560+delta(D183+G184)+N195F+E345N+R181Q+ N445Q+K446N	3.5

AA560+delta(D183+G184)+N195F+Y298F+R181Q+ N445Q+K446N	5
AA560+delta(D183+G184)+N195F+R28N+R181Q+ N445Q+K446N	4.5
AA560+delta(D183+G184)+N195F+R28N+R310A+ R181Q+N445Q+K446N	11
AA560+delta(D183+G184)+N195F+N128D+N306D+ R181Q+N445Q+K446N	5.3

APPENDIX 1

```
CRYST1   48.180   75.847  155.230  90.00  90.00  90.00 P 21 21 21
SCALE1    0.02076   0.00000   0.00000         0.00000
SCALE2    0.00000   0.01318   0.00000         0.00000
SCALE3    0.00000   0.00000   0.00644         0.00000
ATOM      1  N       THR A   5       7.992  45.862  57.008  1.00 44.97   7
ATOM      2  CA      THR A   5       9.424  45.847  57.375  1.00 44.28   6
ATOM      3  C       THR A   5       9.791  44.763  58.368  1.00 42.47   6
ATOM      4  O       THR A   5       9.118  44.516  59.385  1.00 44.78   8
ATOM      5  CB      THR A   5       9.859  47.256  57.794  1.00 53.11   6
ATOM      6  OG1     THR A   5       8.936  48.132  57.101  1.00 57.19   8
ATOM      7  CG2     THR A   5      11.285  47.524  57.327  1.00 53.46   6
ATOM      8  N       ASN A   6      10.798  43.965  58.016  1.00 37.90   7
ATOM      9  CA      ASN A   6      11.182  42.796  58.794  1.00 32.63   6
ATOM     10  C       ASN A   6      11.930  43.205  60.065  1.00 30.68   6
ATOM     11  O       ASN A   6      12.814  44.059  60.030  1.00 29.58   8
ATOM     12  CB      ASN A   6      12.053  41.919  57.914  1.00 30.63   6
ATOM     13  CG      ASN A   6      11.382  41.198  56.759  1.00 17.30   6
ATOM     14  OD1     ASN A   6      10.296  40.687  56.891  1.00 20.22   8
ATOM     15  ND2     ASN A   6      12.101  41.145  55.643  1.00 32.47   7
ATOM     16  N       GLY A   7      11.603  42.548  61.186  1.00 28.09   7
ATOM     17  CA      GLY A   7      12.292  42.881  62.451  1.00 22.75   6
ATOM     18  C       GLY A   7      13.597  42.146  62.640  1.00 19.14   6
ATOM     19  O       GLY A   7      13.695  40.965  62.333  1.00 16.06   8
ATOM     20  N       THR A   8      14.624  42.823  63.147  1.00 18.17   7
ATOM     21  CA      THR A   8      15.896  42.176  63.458  1.00 19.10   6
ATOM     22  C       THR A   8      16.482  42.662  64.779  1.00 17.43   6
ATOM     23  O       THR A   8      16.638  43.853  64.952  1.00 15.95   8
ATOM     24  CB      THR A   8      16.979  42.465  62.372  1.00 26.45   6
ATOM     25  OG1     THR A   8      16.351  42.055  61.153  1.00 24.27   8
ATOM     26  CG2     THR A   8      18.194  41.568  62.558  1.00 15.46   6
ATOM     27  N       MET A   9      16.841  41.711  65.650  1.00 16.99   7
ATOM     28  CA      MET A   9      17.410  42.149  66.957  1.00 16.54   6
ATOM     29  C       MET A   9      18.908  42.032  66.891  1.00 14.09   6
ATOM     30  O       MET A   9      19.450  41.117  66.285  1.00 16.28   8
ATOM     31  CB      MET A   9      16.903  41.092  67.986  1.00 20.39   6
ATOM     32  CG      MET A   9      17.005  41.347  69.462  1.00 34.30   6
ATOM     33  SD      MET A   9      16.749  39.831  70.439  1.00 29.87  16
ATOM     34  CE      MET A   9      15.299  39.172  69.801  1.00 10.47   6
ATOM     35  N       MET A  10      19.658  42.840  67.617  1.00 12.91   7
ATOM     36  CA      MET A  10      21.063  42.531  67.806  1.00 15.03   6
ATOM     37  C       MET A  10      21.371  42.281  69.316  1.00 15.55   6
ATOM     38  O       MET A  10      20.968  43.127  70.123  1.00 16.31   8
ATOM     39  CB      MET A  10      21.918  43.731  67.392  1.00  8.10   6
ATOM     40  CG      MET A  10      23.386  43.336  67.340  1.00 18.96   6
ATOM     41  SD      MET A  10      24.227  44.719  66.507  1.00 26.55  16
ATOM     42  CE      MET A  10      25.899  44.253  66.714  1.00 22.28   6
ATOM     43  N       GLN A  11      22.169  41.302  69.642  1.00 15.64   7
ATOM     44  CA      GLN A  11      22.676  41.141  70.997  1.00 16.62   6
ATOM     45  C       GLN A  11      23.900  42.031  71.121  1.00 14.80   6
ATOM     46  O       GLN A  11      24.973  41.754  70.591  1.00 15.68   8
ATOM     47  CB      GLN A  11      23.021  39.672  71.257  1.00 21.35   6
ATOM     48  CG      GLN A  11      23.790  39.566  72.563  1.00  9.63   6
ATOM     49  CD      GLN A  11      24.190  38.189  72.982  1.00 16.22   6
ATOM     50  OE1     GLN A  11      24.002  37.196  72.298  1.00 19.21   8
ATOM     51  NE2     GLN A  11      24.789  38.087  74.175  1.00 11.66   7
ATOM     52  N       TYR A  12      23.760  43.191  71.741  1.00 14.58   7
ATOM     53  CA      TYR A  12      24.863  44.157  71.774  1.00 14.52   6
ATOM     54  C       TYR A  12      25.913  43.966  72.861  1.00 16.45   6
ATOM     55  O       TYR A  12      26.204  44.903  73.648  1.00 18.06   8
ATOM     56  CB      TYR A  12      24.206  45.550  71.733  1.00 13.22   6
ATOM     57  CG      TYR A  12      25.138  46.568  71.112  1.00 19.25   6
ATOM     58  CD1     TYR A  12      25.099  46.777  69.714  1.00 21.72   6
ATOM     59  CD2     TYR A  12      26.042  47.309  71.833  1.00 21.37   6
ATOM     60  CE1     TYR A  12      25.939  47.688  69.119  1.00 23.24   6
ATOM     61  CE2     TYR A  12      26.857  48.237  71.237  1.00 25.94   6
ATOM     62  CZ      TYR A  12      26.807  48.431  69.845  1.00 25.18   6
ATOM     63  OH      TYR A  12      27.689  49.335  69.287  1.00 25.31   8
ATOM     64  N       PHE A  13      26.564  42.818  72.979  1.00 13.34   7
ATOM     65  CA      PHE A  13      27.685  42.656  73.887  1.00 16.82   6
ATOM     66  C       PHE A  13      28.274  41.290  73.605  1.00 14.75   6
ATOM     67  O       PHE A  13      27.546  40.479  73.068  1.00 14.38   8
```

ATOM	68	CB	PHE A	13	27.294	42.776	75.388	1.00	15.66	6
ATOM	69	CG	PHE A	13	26.320	41.755	75.919	1.00	12.49	6
ATOM	70	CD1	PHE A	13	24.961	41.920	75.789	1.00	13.73	6
ATOM	71	CD2	PHE A	13	26.743	40.643	76.601	1.00	14.47	6
ATOM	72	CE1	PHE A	13	24.033	41.007	76.282	1.00	12.15	6
ATOM	73	CE2	PHE A	13	25.835	39.720	77.121	1.00	19.40	6
ATOM	74	CZ	PHE A	13	24.466	39.875	76.958	1.00	11.64	6
ATOM	75	N	GLU A	14	29.485	41.003	74.010	1.00	14.36	7
ATOM	76	CA	GLU A	14	30.034	39.676	74.020	1.00	16.15	6
ATOM	77	C	GLU A	14	30.746	39.519	75.403	1.00	17.45	6
ATOM	78	O	GLU A	14	30.913	40.533	76.085	1.00	17.41	8
ATOM	79	CB	GLU A	14	31.054	39.352	72.923	1.00	16.10	6
ATOM	80	CG	GLU A	14	32.102	40.433	72.801	1.00	14.02	6
ATOM	81	CD	GLU A	14	33.463	39.876	73.166	1.00	19.45	6
ATOM	82	OE1	GLU A	14	33.542	38.730	73.659	1.00	17.76	8
ATOM	83	OE2	GLU A	14	34.460	40.577	72.944	1.00	24.92	8
ATOM	84	N	TRP A	15	31.209	38.352	75.765	1.00	16.89	7
ATOM	85	CA	TRP A	15	31.732	38.068	77.068	1.00	19.25	6
ATOM	86	C	TRP A	15	32.947	38.939	77.396	1.00	20.43	6
ATOM	87	O	TRP A	15	33.110	39.478	78.488	1.00	19.09	8
ATOM	88	CB	TRP A	15	32.101	36.576	77.206	1.00	20.93	6
ATOM	89	CG	TRP A	15	32.291	36.259	78.669	1.00	23.04	6
ATOM	90	CD1	TRP A	15	33.453	36.102	79.356	1.00	31.96	6
ATOM	91	CD2	TRP A	15	31.235	36.075	79.620	1.00	19.31	6
ATOM	92	NE1	TRP A	15	33.198	35.828	80.689	1.00	25.07	7
ATOM	93	CE2	TRP A	15	31.847	35.794	80.866	1.00	26.64	6
ATOM	94	CE3	TRP A	15	29.844	36.098	79.535	1.00	18.13	6
ATOM	95	CZ2	TRP A	15	31.099	35.552	82.018	1.00	22.00	6
ATOM	96	CZ3	TRP A	15	29.110	35.874	80.702	1.00	29.43	6
ATOM	97	CH2	TRP A	15	29.738	35.616	81.937	1.00	13.19	6
ATOM	98	N	HIS A	16	33.835	39.011	76.425	1.00	18.44	7
ATOM	99	CA	HIS A	16	35.061	39.722	76.562	1.00	17.90	6
ATOM	100	C	HIS A	16	35.149	41.187	76.257	1.00	17.37	6
ATOM	101	O	HIS A	16	36.293	41.637	76.074	1.00	19.01	8
ATOM	102	CB	HIS A	16	36.185	38.908	75.918	1.00	25.12	6
ATOM	103	CG	HIS A	16	36.354	37.568	76.564	1.00	22.79	6
ATOM	104	ND1	HIS A	16	36.995	37.436	77.791	1.00	31.80	7
ATOM	105	CD2	HIS A	16	35.974	36.324	76.195	1.00	30.13	6
ATOM	106	CE1	HIS A	16	37.007	36.145	78.108	1.00	36.35	6
ATOM	107	NE2	HIS A	16	36.391	35.434	77.169	1.00	28.59	7
ATOM	108	N	LEU A	17	34.102	41.977	76.290	1.00	16.37	7
ATOM	109	CA	LEU A	17	34.310	43.400	76.062	1.00	17.67	6
ATOM	110	C	LEU A	17	35.251	43.901	77.175	1.00	23.03	6
ATOM	111	O	LEU A	17	35.367	43.325	78.258	1.00	20.48	8
ATOM	112	CB	LEU A	17	32.998	44.133	76.231	1.00	19.00	6
ATOM	113	CG	LEU A	17	31.936	43.825	75.166	1.00	23.04	6
ATOM	114	CD1	LEU A	17	30.602	44.392	75.618	1.00	15.57	6
ATOM	115	CD2	LEU A	17	32.423	44.488	73.857	1.00	16.06	6
ATOM	116	N	PRO A	18	36.031	44.902	76.847	1.00	23.78	7
ATOM	117	CA	PRO A	18	36.979	45.490	77.777	1.00	24.94	6
ATOM	118	C	PRO A	18	36.187	46.159	78.903	1.00	24.27	6
ATOM	119	O	PRO A	18	35.132	46.765	78.711	1.00	23.28	8
ATOM	120	CB	PRO A	18	37.748	46.610	77.012	1.00	24.47	6
ATOM	121	CG	PRO A	18	36.813	46.841	75.862	1.00	25.71	6
ATOM	122	CD	PRO A	18	35.984	45.606	75.564	1.00	24.09	6
ATOM	123	N	ASN A	19	36.761	46.106	80.092	1.00	26.70	7
ATOM	124	CA	ASN A	19	36.172	46.812	81.251	1.00	27.71	6
ATOM	125	C	ASN A	19	36.645	48.255	81.184	1.00	28.45	6
ATOM	126	O	ASN A	19	37.608	48.592	81.900	1.00	28.72	8
ATOM	127	CB	ASN A	19	36.642	46.133	82.547	1.00	27.29	6
ATOM	128	CG	ASN A	19	36.225	46.903	83.794	1.00	29.44	6
ATOM	129	OD1	ASN A	19	35.232	47.640	83.776	1.00	22.52	8
ATOM	130	ND2	ASN A	19	37.044	46.750	84.839	1.00	25.06	7
ATOM	131	N	ASP A	20	35.986	49.096	80.377	1.00	28.38	7
ATOM	132	CA	ASP A	20	36.539	50.454	80.270	1.00	27.78	6
ATOM	133	C	ASP A	20	35.449	51.479	80.504	1.00	28.07	6
ATOM	134	O	ASP A	20	35.640	52.659	80.210	1.00	28.77	8
ATOM	135	CB	ASP A	20	37.177	50.655	78.893	1.00	26.77	6
ATOM	136	CG	ASP A	20	36.200	50.561	77.731	1.00	33.87	6
ATOM	137	OD1	ASP A	20	34.974	50.296	77.873	1.00	24.14	8
ATOM	138	OD2	ASP A	20	36.728	50.764	76.603	1.00	37.81	8
ATOM	139	N	GLY A	21	34.244	51.012	80.822	1.00	26.21	7
ATOM	140	CA	GLY A	21	33.162	51.940	81.081	1.00	27.22	6
ATOM	141	C	GLY A	21	32.691	52.722	79.860	1.00	26.93	6

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ATOM    142  O       GLY A  21      31.815  53.590  80.016  1.00 25.54   8
ATOM    143  N       GLN A  22      33.064  52.279  78.654  1.00 27.07   7
ATOM    144  CA      GLN A  22      32.703  53.030  77.462  1.00 27.36   6
ATOM    145  C       GLN A  22      31.641  52.404  76.590  1.00 27.67   6
ATOM    146  O       GLN A  22      31.360  52.911  75.502  1.00 28.65   8
ATOM    147  CB      GLN A  22      33.992  53.128  76.602  1.00 34.67   6
ATOM    148  CG      GLN A  22      34.972  54.171  77.137  1.00 48.07   6
ATOM    149  CD      GLN A  22      34.124  55.372  77.568  1.00 58.84   6
ATOM    150  OE1     GLN A  22      33.337  55.865  76.748  1.00 55.38   8
ATOM    151  NE2     GLN A  22      34.273  55.691  78.848  1.00 68.48   7
ATOM    152  N       HIS A  23      31.171  51.248  77.026  1.00 25.72   7
ATOM    153  CA      HIS A  23      30.218  50.491  76.306  1.00 24.66   6
ATOM    154  C       HIS A  23      28.930  51.227  76.079  1.00 26.24   6
ATOM    155  O       HIS A  23      28.425  51.142  74.940  1.00 26.09   8
ATOM    156  CB      HIS A  23      29.944  49.132  76.924  1.00 27.50   6
ATOM    157  CG      HIS A  23      29.459  48.262  75.783  1.00 30.42   6
ATOM    158  ND1     HIS A  23      28.124  47.891  75.695  1.00 26.32   7
ATOM    159  CD2     HIS A  23      30.139  47.735  74.731  1.00 18.69   6
ATOM    160  CE1     HIS A  23      28.009  47.109  74.625  1.00 24.30   6
ATOM    161  NE2     HIS A  23      29.197  46.996  74.051  1.00 25.74   7
ATOM    162  N       TRP A  24      28.389  51.936  77.058  1.00 24.06   7
ATOM    163  CA      TRP A  24      27.164  52.668  76.740  1.00 24.62   6
ATOM    164  C       TRP A  24      27.436  53.777  75.708  1.00 26.89   6
ATOM    165  O       TRP A  24      26.551  54.069  74.901  1.00 27.55   8
ATOM    166  CB      TRP A  24      26.500  53.227  77.983  1.00 23.57   6
ATOM    167  CG      TRP A  24      26.098  52.223  79.031  1.00 29.81   6
ATOM    168  CD1     TRP A  24      26.275  52.395  80.378  1.00 33.41   6
ATOM    169  CD2     TRP A  24      25.403  50.979  78.874  1.00 26.85   6
ATOM    170  NE1     TRP A  24      25.740  51.334  81.064  1.00 25.62   7
ATOM    171  CE2     TRP A  24      25.192  50.446  80.180  1.00 33.54   6
ATOM    172  CE3     TRP A  24      24.920  50.239  77.790  1.00 19.92   6
ATOM    173  CZ2     TRP A  24      24.573  49.204  80.388  1.00 20.29   6
ATOM    174  CZ3     TRP A  24      24.285  49.021  77.982  1.00 18.51   6
ATOM    175  CH2     TRP A  24      24.113  48.505  79.295  1.00 28.71   6
ATOM    176  N       ASN A  25      28.591  54.418  75.710  1.00 26.59   7
ATOM    177  CA      ASN A  25      28.968  55.488  74.809  1.00 26.82   6
ATOM    178  C       ASN A  25      29.058  54.937  73.374  1.00 26.47   6
ATOM    179  O       ASN A  25      28.457  55.583  72.526  1.00 27.54   8
ATOM    180  CB      ASN A  25      30.302  56.133  75.214  1.00 26.92   6
ATOM    181          ARG A  26      29.669  53.786  73.166  1.00 25.06   7
ATOM    185  CA      ARG A  26      29.742  53.064  71.909  1.00 24.34   6
ATOM    186  C       ARG A  26      28.350  52.795  71.364  1.00 26.26   6
ATOM    187  O       ARG A  26      27.987  53.129  70.211  1.00 28.46   8
ATOM    188  CB      ARG A  26      30.437  51.710  71.988  1.00 18.01   6
ATOM    189  CG      ARG A  26      31.918  51.719  72.254  1.00 30.32   6
ATOM    190  CD      ARG A  26      34.441  50.556  74.746  1.00 30.68   7
ATOM    194  NH2     ARG A  26      33.265  48.804  75.596  1.00 35.01   7
ATOM    195  N       LEU A  27      27.459  52.258  72.208  1.00 25.01   7
ATOM    196  CA    LEU A  27      25.274  51.387  72.868  1.00 15.58   6
ATOM    200  CG      LEU A  27      23.794  51.142  72.617  1.00 21.63   6
ATOM    201  CD1     LEU A  27      23.655  50.255  71.361  1.00 22.69   6
ATOM    202  CD2   ARG A  28      25.475  56.144  70.282  1.00 29.78   6
ATOM    206  O       ARG A  28      24.697  56.631  69.479  1.00 28.83   8
ATOM    207  CB      ARG A  28      25.466  56.807  72.651  1.00 31.86   6
ATOM    208  CG      ARG A  28      24.876  58.145  72.269  1.00 37.49   6
ATOM    209  CD      ARG A  28      25.164  59.255  73.228  1.00 44.67   6
ATOM    210  NE      ARG A  28      26.521  59.652  73.443  1.00 61.34   7
ATOM    211  CZ      ARG A  28      27.711  59.325  73.002  1.00 66.92   6
ATOM    212  NH1     ARG A  28      27.919  58.379  72.101  1.00 72.14   7
ATOM    213  NH2     ARG A  28      28.775  59.959  73.482  1.00 73.55   7
ATOM    214  N       ASP A  29      26.776  56.044  70.052  1.00 30.37   7
ATOM    215  CA      ASP A  29      27.415  56.397  68.797  1.00 31.81   6
ATOM    216  C       ASP A  29      26.957  55.556  67.596  1.00 31.24   6
ATOM    217  O       ASP A  29      26.834  56.080  66.507  1.00 32.51   8
ATOM    218  CB      ASP A  29      28.924  56.146  68.920  1.00 37.35   6
ATOM    219  CG      ASP A  29      29.654  57.288  69.578  1.00 59.15   6
ATOM    220  OD1     ASP A  29      29.044  58.378  69.658  1.00 70.33   8
ATOM    221  OD2     ASP A  29      30.815  57.073  70.001  1.00 68.87   8
ATOM    222  N       ASP A  30      26.669  54.287  67.733  1.00 29.14   7
ATOM    223  CA      ASP A  30      26.201  53.368  66.728  1.00 28.11   6
ATOM    224  C       ASP A  30      24.732  53.414  66.407  1.00 26.63   6
ATOM    225  O       ASP A  30      24.254  52.741  65.481  1.00 25.59   8
ATOM    226  CB      ASP A  30      26.522  51.957  67.270  1.00 28.11   6
ATOM    227  CG      ASP A  30      27.095  51.000  66.268  1.00 40.59   6
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ATOM    228  OD1  ASP A  30      27.215  51.364  65.080  1.00 36.45   8
ATOM    229  OD2  ASP A  30      27.418  49.858  66.666  1.00 33.26   8
ATOM    230  N    ALA A  31      23.951  54.167  67.177  1.00 26.99   7
ATOM    231  CA   ALA A  31      22.500  54.152  67.001  1.00 29.43   6
ATOM    232  C    ALA A  31      22.008  54.304  65.557  1.00 31.37   6
ATOM    233  O    ALA A  31      21.093  53.581  65.107  1.00 29.31   8
ATOM    234  CB   ALA A  31      21.876  55.193  67.930  1.00 24.51   6
ATOM    235  N    SER A  32      22.536  55.287  64.829  1.00 30.92   7
ATOM    236  CA   SER A  32      22.120  55.571  63.454  1.00 31.74   6
ATOM    237  C    SER A  32      22.581  54.499  62.471  1.00 30.97   6
ATOM    238  O    SER A  32      21.755  54.063  61.679  1.00 31.18   8
ATOM    239  CB   SER A  32      22.718  56.917  63.029  1.00 39.56   6
ATOM    240  OG   SER A  32      22.235  57.819  64.035  1.00 51.56   8
ATOM    241  N    ASN A  33      23.815  54.048  62.624  1.00 29.10   7
ATOM    242  CA   ASN A  33      24.326  52.942  61.839  1.00 31.79   6
ATOM    243  C    ASN A  33      23.438  51.724  61.953  1.00 31.25   6
ATOM    244  O    ASN A  33      22.833  51.264  60.966  1.00 33.18   8
ATOM    245  CB   ASN A  33      25.756  52.589  62.274  1.00 48.26   6
ATOM    246  CG   ASN A  33      26.695  53.755  62.031  1.00 68.29   6
ATOM    247  OD1  ASN A  33      27.868  53.733  62.424  1.00 77.59   8
ATOM    248  ND2  ASN A  33      26.213  54.813  61.370  1.00 73.87   7
ATOM    249  N    LEU A  34      23.210  51.247  63.171  1.00 30.16   7
ATOM    250  CA   LEU A  34      22.367  50.067  63.396  1.00 29.45   6
ATOM    251  C    LEU A  34      21.034  50.177  62.686  1.00 28.51   6
ATOM    252  O    LEU A  34      20.556  49.220  62.044  1.00 29.66   8
ATOM    253  CB   LEU A  34      22.161  49.834  64.927  1.00 27.74   6
ATOM    254  CG   LEU A  34      23.413  49.499  65.719  1.00 20.61   6
ATOM    255  CD1  LEU A  34      23.209  49.686  67.215  1.00 29.04   6
ATOM    256  CD2  LEU A  34      23.890  48.078  65.465  1.00 32.64   6
ATOM    257  N    ARG A  35      20.364  51.311  62.823  1.00 27.32   7
ATOM    258  CA   ARG A  35      19.081  51.557  62.189  1.00 29.35   6
ATOM    259  C    ARG A  35      19.214  51.455  60.657  1.00 30.45   6
ATOM    260  O    ARG A  35      18.392  50.762  60.059  1.00 29.83   8
ATOM    261  CB   ARG A  35      18.524  52.918  62.569  1.00 44.28   6
ATOM    262  CG   ARG A  35      17.495  53.521  61.643  1.00 57.02   6
ATOM    263  CD   ARG A  35      16.073  53.106  61.959  1.00 66.44   6
ATOM    264  NE   ARG A  35      15.900  51.741  62.407  1.00 70.16   7
ATOM    265  CZ   ARG A  35      15.357  50.735  61.742  1.00 79.55   6
ATOM    266  NH1  ARG A  35      14.861  50.835  60.517  1.00 84.75   7
ATOM    267  NH2  ARG A  35      15.301  49.545  62.326  1.00 84.97   7
ATOM    268  N    ASN A  36      20.248  52.071  60.108  1.00 30.64   7
ATOM    269  CA   ASN A  36      20.499  52.050  58.674  1.00 33.50   6
ATOM    270  C    ASN A  36      20.753  50.627  58.180  1.00 33.11   6
ATOM    271  O    ASN A  36      20.206  50.308  57.119  1.00 34.43   8
ATOM    272  CB   ASN A  36      21.733  52.898  58.251  1.00 33.25   6
ATOM    273  CG   ASN A  36      21.318  54.360  58.192  1.00 47.82   6
ATOM    274  OD1  ASN A  36      20.207  54.652  57.727  1.00 57.93   8
ATOM    275  ND2  ASN A  36      22.159  55.275  58.664  1.00 49.08   7
ATOM    276  N    ARG A  37      21.473  49.799  58.953  1.00 30.82   7
ATOM    277  CA   ARG A  37      21.675  48.412  58.544  1.00 28.45   6
ATOM    278  C    ARG A  37      20.462  47.517  58.755  1.00 27.29   6
ATOM    279  O    ARG A  37      20.537  46.312  58.476  1.00 28.02   8
ATOM    280  CB   ARG A  37      22.878  47.755  59.170  1.00 33.91   6
ATOM    281  CG   ARG A  37      24.277  48.255  58.983  1.00 48.35   6
ATOM    282  CD   ARG A  37      24.485  49.333  57.956  1.00 64.54   6
ATOM    283  NE   ARG A  37      25.152  48.953  56.738  1.00 78.70   7
ATOM    284  CZ   ARG A  37      24.836  48.073  55.801  1.00 90.48   6
ATOM    285  NH1  ARG A  37      23.749  47.306  55.840  1.00 91.76   7
ATOM    286  NH2  ARG A  37      25.672  47.941  54.763  1.00 96.24   7
ATOM    287  N    GLY A  38      19.312  47.981  59.205  1.00 26.89   7
ATOM    288  CA   GLY A  38      18.148  47.144  59.413  1.00 27.35   6
ATOM    289  C    GLY A  38      17.900  46.658  60.843  1.00 27.95   6
ATOM    290  O    GLY A  38      16.882  45.992  61.080  1.00 28.18   8
ATOM    291  N    ILE A  39      18.763  46.951  61.810  1.00 27.05   7
ATOM    292  CA   ILE A  39      18.517  46.493  63.191  1.00 24.22   6
ATOM    293  C    ILE A  39      17.353  47.254  63.782  1.00 22.57   6
ATOM    294  O    ILE A  39      17.452  48.494  63.788  1.00 22.56   8
ATOM    295  CB   ILE A  39      19.756  46.783  64.052  1.00 26.96   6
ATOM    296  CG1  ILE A  39      21.004  46.133  63.441  1.00 16.93   6
ATOM    297  CG2  ILE A  39      19.574  46.307  65.506  1.00 15.96   6
ATOM    298  CD1  ILE A  39      20.880  44.660  63.164  1.00 17.43   6
ATOM    299  N    THR A  40      16.295  46.579  64.216  1.00 21.17   7
ATOM    300  CA   THR A  40      15.193  47.336  64.794  1.00 21.79   6
ATOM    301  C    THR A  40      15.082  47.205  66.334  1.00 22.68   6
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ATOM    302  O     THR A  40      14.185  47.800  66.940  1.00 21.81   8
ATOM    303  CB    THR A  40      13.886  46.822  64.184  1.00 21.04   6
ATOM    304  OG1   THR A  40      13.789  45.438  64.408  1.00 24.12   8
ATOM    305  CG2   THR A  40      13.830  47.029  62.667  1.00 30.33   6
ATOM    306  N     PRO A  45      23.742  43.432  78.684  1.00 16.53   6
ATOM    343  C     PRO A  45      23.197  43.957  80.047  1.00 15.40   6
ATOM    344  O     PRO A  45      22.620  45.055  80.187  1.00 11.51   8
ATOM    345  CB    PRO A  45      25.283  43.566  78.614  1.00 15.61   6
ATOM    346  CG    PRO A  45      25.399  44.987  78.130  1.00 16.58   6
ATOM    347  CD    PRO A  45      24.258  45.220  77.138  1.00 17.71   6
ATOM    348  N     PRO A  46      23.250  43.079  81.026  1.00 15.72   7
ATOM    349  CA    PRO A  46      22.868  43.394  82.434  1.00 15.02   6
ATOM    350  C     PRO A  46      23.310  44.804  82.792  1.00 10.92   6
ATOM    351  O     PRO A  46      24.505  45.066  82.711  1.00 14.77   8
ATOM    352  CB    PRO A  46      23.553  42.319  83.299  1.00 15.77   6
ATOM    353  CG    PRO A  46      23.615  41.142  82.332  1.00 18.86   6
ATOM    354  CD    PRO A  46      23.898  41.758  80.967  1.00 15.86   6
ATOM    355  N     ALA A  47      22.400  45.735  83.008  1.00  8.30   7
ATOM    356  CA    ALA A  47      22.727  47.108  83.291  1.00 14.65   6
ATOM    357  C     ALA A  47      22.986  47.460  84.787  1.00 16.30   6
ATOM    358  O     ALA A  47      23.364  48.599  85.045  1.00 14.79   8
ATOM    359  CB    ALA A  47      21.507  47.957  82.916  1.00 11.00   6
ATOM    360  N     TRP A  48      22.763  46.486  85.681  1.00 18.56   7
ATOM    361  CA    TRP A  48      22.899  46.723  87.124  1.00 18.89   6
ATOM    362  C     TRP A  48      24.242  46.318  87.678  1.00 19.80   6
ATOM    363  O     TRP A  48      21.772  45.983  87.890  1.00 11.27   6
ATOM    365  CG    TRP A  48      21.837  44.535  87.479  1.00 14.85   6
ATOM    366  CD1   TRP A  48      22.781  43.612  87.768  1.00 15.96   6
ATOM    367  CD2   TRP A  48      20.934  43.899  86.561  1.00 12.45   6
ATOM    368  NE1   TRP A  48      22.512  42.415  87.101  1.00 17.91   7
ATOM    369  CE2   TRP A  48      21.398  42.608  86.343  1.00 19.48   6
ATOM    370  CE3   TRP A  48      19.826  44.347  85.840  1.00 20.02   6
ATOM    371  CZ2   TRP A  48      20.751  41.717  85.465  1.00 20.86   6
ATOM    372  CZ3   TRP A  48      19.175  43.484  84.997  1.00 16.49   6
ATOM    373  CH2   TRP A  48      19.632  42.176  84.845  1.00 16.15   6
ATOM    374  N     LYS A  49      24.416  46.571  88.985  1.00 19.67   7
ATOM    375  CA    LYS A  49      25.705  46.328  89.627  1.00 14.91   6
ATOM    376  C     LYS A  49      25.911  44.879  89.895  1.00 14.00   6
ATOM    377  O     LYS A  49      24.988  44.180  90.365  1.00 16.96   8
ATOM    378  CB    LYS A  49      25.709  47.263  90.876  1.00 18.57   6
ATOM    379  CG    LYS A  49      27.023  47.112  91.599  1.00  6.84   6
ATOM    380  CD    LYS A  49      28.243  47.753  91.027  1.00 18.29   6
ATOM    381  CE    LYS A  49      28.021  49.124  90.447  1.00 25.50   6
ATOM    382  NZ    LYS A  49      27.754  50.191  91.434  1.00 23.70   7
ATOM    383  N     GLY A  50      27.064  44.320  89.567  1.00 13.43   7
ATOM    384  CA    GLY A  50      27.330  42.896  89.765  1.00 15.74   6
ATOM    385  C     GLY A  50      28.336  42.721  90.912  1.00 19.14   6
ATOM    386  O     GLY A  50      28.528  43.669  91.705  1.00 21.31   8
ATOM    387  N     THR A  51      28.984  41.580  91.058  1.00 20.32   7
ATOM    388  CA    THR A  51      29.835  41.344  92.215  1.00 23.25   6
ATOM    389  C     THR A  51      31.107  42.157  92.218  1.00 25.68   6
ATOM    390  O     THR A  51      31.775  42.183  93.232  1.00 24.47   8
ATOM    391  CB    THR A  51      30.127  39.852  92.399  1.00 30.68   6
ATOM    392  OG1   THR A  51      30.831  39.427  91.237  1.00 28.77   8
ATOM    393  CG2   THR A  51      28.838  39.038  92.528  1.00 23.54   6
ATOM    394  N     SER A  52      31.491  42.737  91.084  1.00 24.37   7
ATOM    395  CA    SER A  52      32.625  43.577  90.915  1.00 24.00   6
ATOM    396  C     SER A  52      32.414  44.439  89.656  1.00 25.53   6
ATOM    397  O     SER A  52      31.411  44.331  88.931  1.00 24.62   8
ATOM    398  CB    SER A  52      33.937  42.839  90.870  1.00 25.10   6
ATOM    399  OG    SER A  52      34.166  42.313  89.577  1.00 36.64   8
ATOM    400  N     GLN A  53      33.327  45.385  89.473  1.00 25.22   7
ATOM    401  CA    GLN A  53      33.288  46.289  88.328  1.00 26.12   6
ATOM    402  C     GLN A  53      33.403  45.510  87.001  1.00 24.89   6
ATOM    403  O     GLN A  53      32.765  45.831  86.004  1.00 26.00   8
ATOM    404  CB    GLN A  53      34.544  47.217  88.329  1.00 20.73   6
ATOM    405  CG    GLN A  53      34.286  48.373  87.337  1.00 21.42   6
ATOM    406  CD    GLN A  53      35.441  49.355  87.321  1.00 19.77   6
ATOM    407  OE1   GLN A  53      35.253  50.545  87.603  1.00 32.66   8
ATOM    408  NE2   GLN A  53      36.620  48.900  86.998  1.00 18.17   7
ATOM    409  N     ASN A  54      34.237  44.495  86.953  1.00 23.60   7
ATOM    410  CA    ASN A  54      34.407  43.693  85.769  1.00 24.91   6
ATOM    411  C     ASN A  54      33.449  42.530  85.686  1.00 25.10   6
ATOM    412  O     ASN A  54      33.632  41.635  84.847  1.00 27.57   8
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ATOM    413  CB      ASN A  54      35.849  43.247  85.543  1.00 35.23    6
ATOM    414  CG      ASN A  54      36.394  42.608  86.793  1.00 50.63    6
ATOM    415  OD1     ASN A  54      36.661  43.330  87.761  1.00 67.24    8
ATOM    416  ND2   ASP A  55      30.145  42.704  84.859  1.00 23.09    8
ATOM    421  CB      ASP A  55      30.385  41.381  87.478  1.00 23.10    6
ATOM    422  CG      ASP A  55      29.678  40.060  87.574  1.00 23.18    6
ATOM    423  OD1     ASP A  55      30.133  39.153  88.301  1.00 45.89    8
ATOM    424  OD2     ASP A  55      28.671  39.779  86.928  1.00 23.98    8
ATOM    425  N       VAL A  56      30.427  40.542  84.263  1.00 20.61    7
ATOM    426  CA      VAL A  56      29.587  40.751  83.054  1.00 19.89    6
ATOM    427  C       VAL A  56      28.230  41.223  83.474  1.00 17.10    6
ATOM    428  O       VAL A  56      27.534  41.937  82.743  1.00 15.32    8
ATOM    429  CB      VAL A  56      29.576  39.529  82.118  1.00 22.64    6
ATOM    430  CG1     VAL A  56      28.492  39.655  81.068  1.00 22.70    6
ATOM    431  CG2     VAL A  56      30.972  39.455  81.519  1.00 17.09    6
ATOM    432  N       GLY A  57      27.754  40.807  84.660  1.00 16.15    7
ATOM    433  CA      GLY A  57      26.548  41.378  85.247  1.00 12.79    6
ATOM    434  C       GLY A  57      25.600  40.281  85.744  1.00 14.69    6
ATOM    435  O       GLY A  57      24.595  40.638  86.356  1.00 13.97    8
ATOM    436  N       TYR A  58      25.922  39.045  85.378  1.00 14.61    7
ATOM    437  CA      TYR A  58      25.135  37.900  85.760  1.00 17.45    6
ATOM    438  C       TYR A  58      25.379  37.525  87.257  1.00 19.31    6
ATOM    439  O       TYR A  58      24.514  36.826  87.790  1.00 16.95    8
ATOM    440  CB      TYR A  58      25.349  36.682  84.827  1.00 18.27    6
ATOM    441  CG      TYR A  58      24.758  37.019  83.439  1.00 17.30    6
ATOM    442  CD1     TYR A  58      23.415  37.075  83.197  1.00 12.56    6
ATOM    443  CD2     TYR A  58      25.650  37.402  82.418  1.00 20.54    6
ATOM    444  CE1     TYR A  58      22.896  37.482  81.965  1.00 16.37    6
ATOM    445  CE2     TYR A  58      25.148  37.764  81.159  1.00 19.89    6
ATOM    446  CZ      TYR A  58      23.788  37.799  80.934  1.00 19.27    6
ATOM    447  OH      TYR A  58      23.319  38.198  79.690  1.00 18.17    8
ATOM    448  N     TYR A  61      25.642  43.612  95.022  1.00 25.65    6
ATOM    463  CD1     TYR A  61      25.542  42.911  96.225  1.00 24.25    6
ATOM    464  CD2     TYR A  61      25.709  45.005  95.037  1.00 26.54    6
ATOM    465  CE1     TYR A  61      25.515  43.611  97.434  1.00 27.00    6
ATOM    466  CE2     TYR A  61      25.691  45.694  96.251  1.00 28.34    6
ATOM    467  CZ      TYR A  61      25.593  44.987  97.445  1.00 27.80    6
ATOM    468  OH      TYR A  61      25.575  45.686  98.624  1.00 28.01    8
ATOM    469  N       ASP A  62      22.987  44.124  93.011  1.00 18.28    7
ATOM    470  CA      ASP A  62      21.843  44.981  93.248  1.00 17.30    6
ATOM    471  C       ASP A  62      21.159  45.440  91.967  1.00 17.70    6
ATOM    472  O       ASP A  62      21.594  46.430  91.330  1.00 18.30    8
ATOM    473  CB      ASP A  62      22.379  46.196  94.092  1.00 12.40    6
ATOM    474  CG      ASP A  62      21.309  47.201  94.444  1.00 13.30    6
ATOM    475  OD1     ASP A  62      20.080  46.972  94.340  1.00 13.11    8
ATOM    476  OD2     ASP A  62      21.740  48.315  94.834  1.00 21.37    8
ATOM    477  N       LEU A  63      19.951  44.961  91.758  1.00 17.70    7
ATOM    478  CA      LEU A  63      19.104  45.322  90.647  1.00 20.95    6
ATOM    479  C       LEU A  63      18.646  46.775  90.591  1.00 22.88    6
ATOM    480  O       LEU A  63      18.114  47.141  89.515  1.00 22.24    8
ATOM    481  CB      LEU A  63      17.862  44.436  90.567  1.00 16.46    6
ATOM    482  CG      LEU A  63      18.088  42.925  90.539  1.00 20.24    6
ATOM    483  CD1     LEU A  63      16.765  42.178  90.480  1.00 15.13    6
ATOM    484  CD2     LEU A  63      18.994  42.499  89.388  1.00 16.31    6
ATOM    485  N       TYR A  64      18.800  47.552  91.680  1.00 18.58    7
ATOM    486  CA      TYR A  64      18.376  48.936  91.627  1.00 18.22    6
ATOM    487  C       TYR A  64      19.576  49.858  91.469  1.00 19.00    6
ATOM    488  O       TYR A  64      19.384  51.080  91.510  1.00 20.72    8
ATOM    489  CB      TYR A  64      17.549  49.422  92.809  1.00 18.99    6
ATOM    490  CG      TYR A  64      16.187  48.837  93.017  1.00 15.73    6
ATOM    491  CD1     TYR A  64      15.059  49.473  92.530  1.00 15.90    6
ATOM    492  CD2     TYR A  64      15.998  47.640  93.688  1.00 18.93    6
ATOM    493  CE1     TYR A  64      13.794  48.935  92.725  1.00 16.95    6
ATOM    494  CE2     TYR A  64      14.743  47.078  93.869  1.00 17.53    6
ATOM    495  CZ      TYR A  64      13.644  47.753  93.407  1.00 17.22    6
ATOM    496  OH      TYR A  64      12.375  47.252  93.591  1.00 20.36    8
ATOM    497  N       ASP A  65      20.780  49.347  91.314  1.00 17.16    7
ATOM    498  CA      ASP A  65      21.942  50.209  91.137  1.00 21.10    6
ATOM    499  C       ASP A  65      22.397  50.041  89.650  1.00 24.74    6
ATOM    500  O       ASP A  65      23.200  49.139  89.336  1.00 24.73    8
ATOM    501  CB      ASP A  65      23.067  49.696  92.045  1.00 11.90    6
ATOM    502  CG      ASP A  65      24.354  50.424  91.883  1.00 18.88    6
ATOM    503  OD1   LEU A  66      23.634  51.622  87.115  1.00 27.24    6
ATOM    508  O       LEU A  66      23.762  52.306  86.107  1.00 28.71    8
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ATOM    509  CB      LEU A  66      21.209  51.501  86.536  1.00 18.64   6
ATOM    510  CG      LEU A  66      19.816  50.978  86.851  1.00 22.36   6
ATOM    511  CD1     LEU A  66      18.686  51.757  86.184  1.00 20.71   6
ATOM    512  CD2     LEU A  66      19.690  49.492  86.541  1.00 20.39   6
ATOM    513  N       GLY A  67      24.664  51.443  87.921  1.00 27.26   7
ATOM    514  CA      GLY A  67      25.895  52.188  87.804  1.00 29.41   6
ATOM    515  C       GLY A  67      25.649  53.599  88.380  1.00 33.01   6
ATOM    516  O       GLY A  67      26.134  54.570  87.772  1.00 31.97   8
ATOM    517  N       GLU A  68      24.883  53.754  89.476  1.00 33.21   7
ATOM    518  CA      GLU A  68      24.760  55.102  90.026  1.00 35.92   6
ATOM    519  C       GLU A  68      25.245  55.205  91.479  1.00 37.18   6
ATOM    520  O       GLU A  68      25.462  56.313  91.959  1.00 37.26   8
ATOM    521  CB      GLU A  68      23.441  55.828  89.892  1.00 38.75   6
ATOM    522  CG      GLU A  68      22.257  55.179  90.540  1.00 34.11   6
ATOM    523  CD      GLU A  68      21.000  56.008  90.475  1.00 35.08   6
ATOM    524  OE1     GLU A  68      20.977  57.163  90.944  1.00 42.85   8
ATOM    525  OE2     GLU A  68      19.983  55.486  89.965  1.00 42.28   8
ATOM    526  N       PHE A  69      25.414  54.063  92.156  1.00 36.70   7
ATOM    527  CA      PHE A  69      25.849  54.029  93.531  1.00 34.43   6
ATOM    528  C       PHE A  69      27.229  53.434  93.693  1.00 33.96   6
ATOM    529  O       PHE A  69      21.909  55.783  94.626  1.00 21.63   6
ATOM    535  CE2     PHE A  69      21.194  53.860  93.385  1.00 26.02   6
ATOM    536  CZ      PHE A  69      20.928  55.108  93.931  1.00 26.60   6
ATOM    537  N       ASN A  70      27.922  53.932  94.703  1.00 32.25   7
ATOM    538  CA      ASN A  70      29.264  53.496  95.050  1.00 30.57   6
ATOM    539  C       ASN A  70      29.149  52.217  95.870  1.00 31.62   6
ATOM    540  O       ASN A  70      28.903  52.244  97.086  1.00 31.24   8
ATOM    541  CB      ASN A  70      29.904  54.618  95.879  1.00 35.22   6
ATOM    542  CG      ASN A  70      31.400  54.385  95.919  1.00 45.98   6
ATOM    543  OD1     ASN A  70      31.868  53.260  95.704  1.00 48.37   8
ATOM    544  ND2     ASN A  70      32.112  55.478  96.171  1.00 59.74   7
ATOM    545  N       GLN A  71      29.137  51.063  95.221  1.00 29.14   7
ATOM    546  CA      GLN A  71      28.967  49.769  95.816  1.00 27.72   6
ATOM    547  C       GLN A  71      29.890  48.785  95.102  1.00 27.35   6
ATOM    548  O       GLN A  71      30.129  48.954  93.897  1.00 28.50   8
ATOM    549  CB      GLN A  71      27.552  49.224  95.684  1.00 25.56   6
ATOM    550  CG      GLN A  71      26.447  50.165  95.980  1.00 28.71   6
ATOM    551  CD      GLN A  71      25.072  49.652  96.237  1.00 30.86   6
ATOM    552  OE1     GLN A  71      24.663  49.585  97.406  1.00 36.88   8
ATOM    553  NE2     GLN A  71      24.309  49.337  95.203  1.00 21.46   7
ATOM    554  N       LYS A  72      30.339  47.777  95.805  1.00 24.50   7
ATOM    555  CA      LYS A  72      31.272  46.797  95.290  1.00 27.35   6
ATOM    556  C       LYS A  72      32.568  47.381  94.790  1.00 28.76   6
ATOM    557  O       LYS A  72      33.281  46.720  94.029  1.00 32.25   8
ATOM    558  CB      LYS A  72      30.608  45.899  94.225  1.00 23.29   6
ATOM    559  CG      LYS A  72      29.407  45.149  94.803  1.00 28.84   6
ATOM    560  CD      LYS A  72      29.943  44.159  95.845  1.00 36.48   6
ATOM    561  CE      LYS A  72      28.888  43.822  96.892  1.00 35.12   6
ATOM    562  NZ      LYS A  72      29.356  42.633  97.676  1.00 38.56   7
ATOM    563  N       GLY A  73      33.040  48.526  95.263  1.00 28.49   7
ATOM    564  CA      GLY A  73      34.313  49.069  94.825  1.00 27.50   6
ATOM    565  C       GLY A  73      34.177  49.967  93.592  1.00 28.94   6
ATOM    566  O       GLY A  73      35.241  50.214  93.014  1.00 30.09   8
ATOM    567  N       THR A  74      32.977  50.387  93.152  1.00 27.05   7
ATOM    568  CA      THR A  74      32.928  51.157  91.915  1.00 26.78   6
ATOM    569  C       THR A  74      31.596  51.859  91.799  1.00 25.34   6
ATOM    570  O       THR A  74      30.631  51.367  92.386  1.00 24.37   8
ATOM    571  CB      THR A  74      33.103  50.222  90.664  1.00 31.26   6
ATOM    572  OG1     THR A  74      32.822  50.956  89.454  1.00 25.82   8
ATOM    573  CG2     THR A  74      32.107  49.060  90.679  1.00 26.69   6
ATOM    574  N       VAL A  75      31.535  52.982  91.075  1.00 24.66   7
ATOM    575  CA      VAL A  75      30.194  53.577  90.919  1.00 25.58   6
ATOM    576  C       VAL A  75      29.585  52.986  89.631  1.00 26.93   6
ATOM    577  O       VAL A  75      28.472  52.460  89.626  1.00 24.90   8
ATOM    578  CB    ARG A  76      30.395  53.124  88.553  1.00 25.83   7
ATOM    582  CA      ARG A  76      29.896  52.613  87.259  1.00 23.66   6
ATOM    583  C       ARG A  76      29.898  51.082  87.285  1.00 21.40   6
ATOM    584  O       ARG A  76      30.739  50.419  87.909  1.00 19.38   8
ATOM    585  CB      ARG A  76      30.853  53.148  86.159  1.00 13.83   6
ATOM    586  CG      ARG A  76      32.237  52.526  86.080  1.00 19.96   6
ATOM    587  CD      ARG A  76      36.104  50.868  84.274  1.00 16.75   7
ATOM    592  N       THR A  77      29.024  50.487  86.445  1.00 21.32   7
ATOM    593  CA      THR A  77      29.166  49.057  86.135  1.00 20.79   6
ATOM    594  C       THR A  77      30.312  48.886  85.128  1.00 21.29   6
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ATOM	595	O	THR	A	77	31.057	49.798	84.761	1.00	19.53	8
ATOM	596	CB	THR	A	77	27.910	48.519	85.446	1.00	22.75	6
ATOM	597	OG1	THR	A	77	27.781	49.215	84.171	1.00	22.39	8
ATOM	598	CG2	THR	A	77	26.698	48.832	86.297	1.00	14.11	6
ATOM	599	N	LYS	A	78	30.454	47.669	84.584	1.00	22.44	7
ATOM	600	CA	LYS	A	78	31.439	47.367	83.545	1.00	21.30	6
ATOM	601	C	LYS	A	78	31.304	48.242	82.284	1.00	19.80	6
ATOM	602	O	LYS	A	78	32.280	48.724	81.730	1.00	17.17	8
ATOM	603	CB	LYS	A	78	31.239	45.902	83.056	1.00	21.38	6
ATOM	604	CG	LYS	A	78	32.369	45.516	82.104	1.00	30.30	6
ATOM	605	CD	LYS	A	78	32.199	44.122	81.514	1.00	24.76	6
ATOM	606	CE	LYS	A	78	33.277	43.942	80.452	1.00	18.99	6
ATOM	607	NZ	LYS	A	78	33.410	42.535	80.068	1.00	18.31	7
ATOM	608	N	TYR	A	79	30.097	48.505	81.886	1.00	20.90	7
ATOM	609	CA	TYR	A	79	29.630	49.216	80.722	1.00	23.91	6
ATOM	610	C	TYR	A	79	29.582	50.734	80.798	1.00	26.85	6
ATOM	611	O	TYR	A	79	29.739	51.412	79.750	1.00	25.30	8
ATOM	612	CB	TYR	A	79	28.191	48.658	80.425	1.00	22.18	6
ATOM	613	CG	TYR	A	79	28.300	47.138	80.353	1.00	20.86	6
ATOM	614	CD1	TYR	A	79	29.177	46.490	79.495	1.00	20.37	6
ATOM	615	CD2	TYR	A	79	27.550	46.371	81.219	1.00	21.76	6
ATOM	616	CE1	TYR	A	79	29.277	45.109	79.469	1.00	19.56	6
ATOM	617	CE2	TYR	A	79	27.623	44.977	81.218	1.00	19.94	6
ATOM	618	CZ	TYR	A	79	28.487	44.359	80.347	1.00	18.41	6
ATOM	619	OH	TYR	A	79	28.545	42.993	80.361	1.00	14.29	8
ATOM	620	N	GLY	A	80	29.444	51.307	82.010	1.00	25.28	7
ATOM	621	CA	GLY	A	80	29.431	52.757	82.150	1.00	25.76	6
ATOM	622	C	GLY	A	80	28.537	53.169	83.321	1.00	26.75	6
ATOM	623	O	GLY	A	80	28.220	52.288	84.134	1.00	24.74	8
ATOM	624	N	THR	A	81	28.055	54.412	83.325	1.00	25.03	7
ATOM	625	CA	THR	A	81	27.175	54.853	84.404	1.00	26.29	6
ATOM	626	C	THR	A	81	25.734	54.946	83.930	1.00	27.39	6
ATOM	627	O	THR	A	81	25.500	55.049	82.731	1.00	26.45	8
ATOM	628	CB	THR	A	81	27.482	56.330	84.815	1.00	29.85	6
ATOM	629	OG1	THR	A	81	27.111	57.124	83.658	1.00	32.48	8
ATOM	630	CG2	THR	A	81	28.951	56.536	85.109	1.00	28.09	6
ATOM	631	N	ARG	A	82	24.808	55.096	84.880	1.00	26.31	7
ATOM	632	CA	ARG	A	82	23.417	55.253	84.557	1.00	27.17	6
ATOM	633	C	ARG	A	82	23.177	56.431	83.615	1.00	28.32	6
ATOM	634	O	ARG	A	82	22.235	56.296	82.817	1.00	30.27	8
ATOM	635	CB	ARG	A	82	22.522	55.403	85.777	1.00	18.09	6
ATOM	636	CG	ARG	A	82	21.204	56.100	85.672	1.00	17.36	6
ATOM	637	CD	ARG	A	82	20.177	55.821	86.717	1.00	24.02	6
ATOM	638	NE	ARG	A	82	18.880	56.374	86.434	1.00	32.87	7
ATOM	639	CZ	ARG	A	82	17.812	56.490	87.206	1.00	37.23	6
ATOM	640	NH1	ARG	A	82	17.809	56.078	88.472	1.00	40.74	7
ATOM	641	NH2	ARG	A	82	16.728	57.037	86.705	1.00	29.88	7
ATOM	642	N	SER	A	83	23.782	57.600	83.794	1.00	27.60	7
ATOM	643	CA	SER	A	83	23.411	58.673	82.846	1.00	29.66	6
ATOM	644	C	SER	A	83	23.908	58.301	81.423	1.00	27.02	6
ATOM	645	O	SER	A	83	23.185	58.587	80.470	1.00	27.16	8
ATOM	646	CB	SER	A	83	23.920	60.039	83.273	1.00	24.26	6
ATOM	647	OG	SER	A	83	25.337	59.906	83.317	1.00	35.47	8
ATOM	648	N	GLN	A	84	25.089	57.704	81.332	1.00	25.08	7
ATOM	649	CA	GLN	A	84	25.598	57.208	80.066	1.00	27.26	6
ATOM	650	C	GLN	A	84	24.624	56.198	79.473	1.00	28.38	6
ATOM	651	O	GLN	A	84	24.219	56.365	78.308	1.00	28.32	8
ATOM	652	CB	GLN	A	84	27.002	56.619	80.219	1.00	22.80	6
ATOM	653	CG	GLN	A	84	28.049	57.672	80.542	1.00	24.28	6
ATOM	654	CD	GLN	A	84	29.378	57.005	80.812	1.00	30.46	6
ATOM	655	OE1	GLN	A	84	30.478	57.520	80.610	1.00	40.53	8
ATOM	656	NE2	GLN	A	84	29.368	55.759	81.267	1.00	25.18	7
ATOM	657	N	LEU	A	85	24.097	55.230	80.250	1.00	27.63	7
ATOM	658	CA	LEU	A	85	23.109	54.315	79.712	1.00	26.47	6
ATOM	659	C	LEU	A	85	21.867	55.033	79.204	1.00	28.93	6
ATOM	660	O	LEU	A	85	21.284	54.664	78.164	1.00	29.54	8
ATOM	661	CB	LEU	A	85	22.654	53.270	80.708	1.00	22.28	6
ATOM	662	CG	LEU	A	85	21.488	52.356	80.351	1.00	23.99	6
ATOM	663	CD1	LEU	A	85	21.726	51.532	79.093	1.00	20.87	6
ATOM	664	CD2	LEU	A	85	21.261	51.347	81.489	1.00	28.27	6
ATOM	665	N	GLU	A	86	21.329	55.957	79.988	1.00	27.07	7
ATOM	666	CA	GLU	A	86	20.123	56.671	79.575	1.00	27.80	6
ATOM	667	C	GLU	A	86	20.374	57.493	78.302	1.00	27.01	6
ATOM	668	O	GLU	A	86	19.458	57.657	77.464	1.00	26.06	8

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ATOM    669  CB   GLU A  86      19.696  57.582  80.748  1.00 40.30   6
ATOM    670  CG   GLU A  86      19.235  56.861  81.995  1.00 48.52   6
ATOM    671  CD   GLU A  86      18.760  57.679  83.176  1.00 52.20   6
ATOM    672  OE1  GLU A  86      19.624  58.224  83.903  1.00 61.23   8
ATOM    673  OE2  GLU A  86      17.545  57.797  83.458  1.00 49.66   8
ATOM    674  N    SER A  87      21.530  58.085  78.056  1.00 26.53   7
ATOM    675  CA   SER A  87      21.645  58.870  76.809  1.00 29.75   6
ATOM    676  C    SER A  87      21.731  57.901  75.618  1.00 30.32   6
ATOM    677  O    SER A  87      21.116  58.150  74.583  1.00 30.73   8
ATOM    678  CB   SER A  87      22.681  59.961  76.772  1.00 32.20   6
ATOM    679  OG   SER A  87      23.973  59.484  77.049  1.00 42.05   8
ATOM    680  N    ALA A  88      22.378  56.752  75.818  1.00 29.76   7
ATOM    681  CA   ALA A  88      22.413  55.724  74.788  1.00 27.74   6
ATOM    682  C    ALA A  88      20.985  55.297  74.496  1.00 26.48   6
ATOM    683  O    ALA A  88      20.561  55.293  73.334  1.00 26.88   8
ATOM    684  CB   ALA A  88      23.281  54.524  75.077  1.00 25.94   6
ATOM    685  N    ILE A  89      20.148  55.072  75.490  1.00 24.88   7
ATOM    686  CA   ILE A  89      18.768  54.692  75.217  1.00 23.52   6
ATOM    687  C    ILE A  89      18.053  55.828  74.481  1.00 25.44   6
ATOM    688  O    ILE A  89      17.120  55.529  73.701  1.00 24.83   8
ATOM    689  CB   ILE A  89      18.002  54.210  76.457  1.00 21.65   6
ATOM    690  CG1  ILE A  89      18.574  52.875  77.001  1.00 28.88   6
ATOM    691  CG2  ILE A  89      16.526  54.039  76.223  1.00 13.66   6
ATOM    692  CD1  ILE A  89      17.955  52.441  78.324  1.00 30.45   6
ATOM    693  N    HIS A  90      18.392  57.088  74.779  1.00 24.28   7
ATOM    694  CA   HIS A  90      17.727  58.199  74.112  1.00 28.25   6
ATOM    695  C    HIS A  90      18.037  58.199  72.591  1.00 26.88   6
ATOM    696  O    HIS A  90      17.173  58.406  71.747  1.00 25.73   8
ATOM    697  CB   HIS A  90      18.236  59.573  74.618  1.00 41.06   6
ATOM    698  CG   HIS A  90      17.378  60.661  74.031  1.00 59.86   6
ATOM    699  ND1  HIS A  90      16.033  60.458  73.761  1.00 65.74   7
ATOM    700  CD2  HIS A  90      17.648  61.935  73.657  1.00 65.92   6
ATOM    701  CE1  HIS A  90      15.520  61.574  73.267  1.00 67.17   6
ATOM    702  NE2  HIS A  90      16.477  62.487  73.190  1.00 67.40   7
ATOM    703  N    ALA A  91      19.333  58.038  72.335  1.00 27.28   7
ATOM    704  CA   ALA A  91      19.768  57.944  70.934  1.00 30.32   6
ATOM    705  C    ALA A  91      19.032  56.824  70.210  1.00 31.56   6
ATOM    706  O    ALA A  91      18.437  57.058  69.144  1.00 32.93   8
ATOM    707  CB   ALA A  91      21.267  57.723  70.921  1.00 33.17   6
ATOM    708  N    LEU A  92      18.930  55.617  70.792  1.00 30.95   7
ATOM    709  CA   LEU A  92      18.225  54.502  70.166  1.00 28.50   6
ATOM    710  C    LEU A  92      16.790  54.823  69.856  1.00 26.16   6
ATOM    711  O    LEU A  92      16.249  54.541  68.798  1.00 26.07   8
ATOM    712  CB   LEU A  92      18.264  53.207  71.008  1.00 26.14   6
ATOM    713  CG   LEU A  92      19.652  52.613  71.189  1.00 27.87   6
ATOM    714  CD1  LEU A  92      19.575  51.308  71.985  1.00 30.16   6
ATOM    715  CD2  LEU A  92      20.401  52.325  69.902  1.00 19.42   6
ATOM    716  N    LYS A  93      16.120  55.418  70.826  1.00 26.45   7
ATOM    717  CA   LYS A  93      14.704  55.754  70.718  1.00 26.60   6
ATOM    718  C    LYS A  93      14.539  56.842  69.633  1.00 27.98   6
ATOM    719  O    LYS A  93      13.541  56.873  68.916  1.00 25.59   8
ATOM    720  CB   LYS A  93      14.224  56.224  72.079  1.00 37.62   6
ATOM    721  CG   LYS A  93      13.149  55.529  72.860  1.00 39.22   6
ATOM    722  CD   LYS A  93      13.436  54.121  73.320  1.00 34.53   6
ATOM    723  CE   LYS A  93      12.624  53.763  74.546  1.00 36.60   6
ATOM    724  NZ   LYS A  93      11.468  52.873  74.376  1.00 34.30   7
ATOM    725  N    ASN A  94      15.511  57.730  69.524  1.00 30.08   7
ATOM    726  CA   ASN A  94      15.447  58.800  68.525  1.00 35.42   6
ATOM    727  C    ASN A  94      15.613  58.239  67.124  1.00 37.33   6
ATOM    728  O    ASN A  94      14.991  58.775  66.201  1.00 39.60   8
ATOM    729  CB   ASN A  94      16.419  59.943  68.838  1.00 44.84   6
ATOM    730  CG   ASN A  94      15.585  61.034  69.505  1.00 55.65   6
ATOM    731  OD1  ASN A  94      15.624  62.186  69.098  1.00 73.22   8
ATOM    732  ND2  ASN A  94      14.764  60.682  70.487  1.00 56.79   7
ATOM    733  N    ASN A  95      16.314  57.113  66.981  1.00 35.93   7
ATOM    734  CA   ASN A  95      16.458  56.453  65.701  1.00 33.37   6
ATOM    735  C    ASN A  95      15.482  55.332  65.486  1.00 32.25   6
ATOM    736  O    ASN A  95      15.761  54.421  64.693  1.00 34.32   8
ATOM    737  CB   ASN A  95      17.887  55.932  65.573  1.00 34.99   6
ATOM    738  CG   ASN A  95      18.799  57.098  65.245  1.00 45.21   6
ATOM    739  OD1  ASN A  95      19.110  57.368  64.085  1.00 46.20   8
ATOM    740  ND2  ASN A  95      19.235  57.795  66.278  1.00 40.71   7
ATOM    741  N    GLY A  96      14.357  55.277  66.188  1.00 31.16   7
ATOM    742  CA   GLY A  96      13.369  54.240  66.044  1.00 28.59   6
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ATOM	743	C	GLY	A	96	13.766	52.828	66.455	1.00	28.70	6
ATOM	744	O	GLY	A	96	13.023	51.874	66.136	1.00	29.32	8
ATOM	745	N	VAL	A	97	14.880	52.615	67.134	1.00	26.43	7
ATOM	746	CA	VAL	A	97	15.260	51.274	67.575	1.00	26.61	6
ATOM	747	C	VAL	A	97	14.691	50.959	68.959	1.00	27.97	6
ATOM	748	O	VAL	A	97	14.850	51.807	69.853	1.00	27.20	8
ATOM	749	CB	VAL	A	97	16.792	51.169	67.662	1.00	26.27	6
ATOM	750	CG1	VAL	A	97	17.244	49.754	67.987	1.00	14.11	6
ATOM	751	CG2	VAL	A	97	17.425	51.629	66.342	1.00	31.58	6
ATOM	752	N	GLN	A	98	14.104	49.795	69.159	1.00	27.95	7
ATOM	753	CA	GLN	A	98	13.575	49.334	70.448	1.00	25.14	6
ATOM	754	C	GLN	A	98	14.625	48.760	71.397	1.00	25.16	6
ATOM	755	O	GLN	A	98	15.696	48.353	70.944	1.00	22.76	8
ATOM	756	CB	GLN	A	98	12.539	48.251	70.157	1.00	17.49	6
ATOM	757	CG	GLN	A	98	11.170	48.854	69.932	1.00	29.35	6
ATOM	758	CD	GLN	A	98	10.184	47.795	69.503	1.00	42.26	6
ATOM	759	OE1	GLN	A	98	10.540	46.655	69.269	1.00	45.15	8
ATOM	760	NE2	GLN	A	98	8.924	48.192	69.376	1.00	56.07	7
ATOM	761	N	VAL	A	99	14.402	48.902	72.739	1.00	23.46	7
ATOM	762	CA	VAL	A	99	15.424	48.448	73.692	1.00	21.32	6
ATOM	763	C	VAL	A	99	14.917	47.330	74.598	1.00	19.22	6
ATOM	764	O	VAL	A	99	13.817	47.437	75.184	1.00	19.88	8
ATOM	765	CB	VAL	A	99	15.895	49.580	74.623	1.00	28.07	6
ATOM	766	CG1	VAL	A	99	17.158	49.135	75.360	1.00	27.17	6
ATOM	767	CG2	VAL	A	99	16.243	50.827	73.822	1.00	40.90	6
ATOM	768	N	TYR	A	100	15.590	46.194	74.586	1.00	17.68	7
ATOM	769	CA	TYR	A	100	15.261	45.045	75.395	1.00	17.15	6
ATOM	770	C	TYR	A	100	16.291	44.869	76.527	1.00	17.39	6
ATOM	771	O	TYR	A	100	17.483	44.789	76.233	1.00	15.80	8
ATOM	772	CB	TYR	A	100	15.270	43.716	74.633	1.00	20.33	6
ATOM	773	CG	TYR	A	100	14.287	43.618	73.496	1.00	23.97	6
ATOM	774	CD1	TYR	A	100	13.133	44.397	73.447	1.00	23.67	6
ATOM	775	CD2	TYR	A	100	14.564	42.732	72.441	1.00	24.39	6
ATOM	776	CE1	TYR	A	100	12.275	44.292	72.366	1.00	25.53	6
ATOM	777	CE2	TYR	A	100	13.704	42.635	71.358	1.00	23.58	6
ATOM	778	CZ	TYR	A	100	12.585	43.417	71.313	1.00	23.55	6
ATOM	779	OH	TYR	A	100	11.716	43.320	70.278	1.00	22.25	8
ATOM	780	N	GLY	A	101	15.790	44.787	77.780	1.00	17.34	7
ATOM	781	CA	GLY	A	101	16.727	44.623	78.906	1.00	14.59	6
ATOM	782	C	GLY	A	101	16.908	43.192	79.386	1.00	11.65	6
ATOM	783	O	GLY	A	101	15.973	42.408	79.355	1.00	12.65	8
ATOM	784	N	ASP	A	102	18.121	42.759	79.744	1.00	13.34	7
ATOM	785	CA	ASP	A	102	18.304	41.431	80.353	1.00	13.47	6
ATOM	786	C	ASP	A	102	17.648	41.507	81.777	1.00	15.09	6
ATOM	787	O	ASP	A	102	17.463	42.598	82.341	1.00	14.56	8
ATOM	788	CB	ASP	A	102	19.795	41.183	80.569	1.00	11.48	6
ATOM	789	CG	ASP	A	102	20.159	39.752	80.306	1.00	12.52	6
ATOM	790	OD1	ASP	A	102	19.384	38.867	80.788	1.00	15.17	8
ATOM	791	OD2	ASP	A	102	21.185	39.489	79.599	1.00	17.64	8
ATOM	792	N	VAL	A	103	17.229	40.390	82.280	1.00	14.82	7
ATOM	793	CA	VAL	A	103	16.493	40.167	83.502	1.00	14.92	6
ATOM	794	C	VAL	A	103	17.058	38.928	84.207	1.00	14.68	6
ATOM	795	O	VAL	A	103	16.849	37.788	83.790	1.00	13.55	8
ATOM	796	CB	VAL	A	103	15.005	39.890	83.261	1.00	18.86	6
ATOM	797	CG1	VAL	A	103	14.282	39.583	84.577	1.00	24.13	6
ATOM	798	CG2	VAL	A	103	14.338	41.114	82.610	1.00	23.58	6
ATOM	799	N	VAL	A	104	17.756	39.187	85.343	1.00	13.33	7
ATOM	800	CA	VAL	A	104	18.345	38.106	86.118	1.00	11.70	6
ATOM	801	C	VAL	A	104	17.667	38.025	87.518	1.00	14.62	6
ATOM	802	O	VAL	A	104	17.907	38.921	88.344	1.00	11.28	8
ATOM	803	CB	VAL	A	104	19.843	38.363	86.246	1.00	12.15	6
ATOM	804	CG1	VAL	A	104	20.493	37.200	87.026	1.00	15.28	6
ATOM	805	CG2	VAL	A	104	20.516	38.434	84.866	1.00	24.46	6
ATOM	806	N	MET	A	105	16.738	37.112	87.714	1.00	13.63	7
ATOM	807	CA	MET	A	105	15.988	36.987	88.961	1.00	15.45	6
ATOM	808	C	MET	A	105	16.313	35.668	89.656	1.00	15.72	6
ATOM	809	O	MET	A	105	15.681	35.344	90.656	1.00	16.37	8
ATOM	810	CB	MET	A	105	14.464	36.975	88.608	1.00	5.32	6
ATOM	811	CG	MET	A	105	14.085	38.454	88.115	1.00	9.60	6
ATOM	812	SD	MET	A	105	12.331	38.446	87.765	1.00	24.51	16
ATOM	813	CE	MET	A	105	11.881	39.900	88.682	1.00	45.97	6
ATOM	814	N	ASN	A	106	17.102	34.751	89.065	1.00	13.34	7
ATOM	815	CA	ASN	A	106	17.261	33.440	89.636	1.00	13.70	6
ATOM	816	C	ASN	A	106	18.025	33.465	91.013	1.00	14.43	6

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ATOM    817  O       ASN A 106      17.708  32.625  91.845  1.00 13.26   8
ATOM    818  CB      ASN A 106      18.066  32.548  88.719  1.00  6.27   6
ATOM    819  CG      ASN A 106      18.651  31.318  89.258  1.00  8.00   6
ATOM    820  OD1     ASN A 106      19.688  30.774  89.540  1.00 11.69   8
ATOM    821  ND2     ASN A 106      17.629  30.519  89.481  1.00  2.77   7
ATOM    822  N       HIS A 107      19.030  34.285  91.095  1.00 11.91   7
ATOM    823  CA      HIS A 107      19.986  34.236  92.154  1.00 10.48   6
ATOM    824  C       HIS A 107      20.535  35.624  92.397  1.00 12.08   6
ATOM    825  O       HIS A 107      20.227  36.573  91.672  1.00 11.45   8
ATOM    826  CB      HIS A 107      21.191  33.361  91.805  1.00 16.81   6
ATOM    827  CG      HIS A 107      21.832  33.780  90.505  1.00 26.29   6
ATOM    828  ND1     HIS A 107      21.509  33.126  89.312  1.00 25.26   7
ATOM    829  CD2     HIS A 107      22.724  34.735  90.199  1.00 25.06   6
ATOM    830  CE1     HIS A 107      22.215  33.687  88.353  1.00 22.21   6
ATOM    831  NE2     HIS A 107      22.945  34.679  88.842  1.00 20.55   7
ATOM    832  N       LEU A 108      21.234  35.733  93.529  1.00 12.42   7
ATOM    833  CA      LEU A 108      21.821  36.997  93.952  1.00 11.65   6
ATOM    834  C       LEU A 108      23.215  36.660  94.443  1.00 12.15   6
ATOM    835  O       LEU A 108      23.406  35.699  95.209  1.00 14.67   8
ATOM    836  CB      LEU A 108      21.042  37.746  95.003  1.00 21.94   6
ATOM    837  CG      LEU A 108      19.744  38.457  94.808  1.00 21.68   6
ATOM    838  CD1     LEU A 108      18.553  37.510  94.757  1.00 39.57   6
ATOM    839  CD2     LEU A 108      19.311  39.330  95.982  1.00 22.08   6
ATOM    840  N       GLY A 109      24.199  37.441  94.005  1.00 12.09   7
ATOM    841  CA      GLY A 109      25.565  37.136  94.430  1.00 11.56   6
ATOM    842  C       GLY A 109      26.202  38.357  95.083  1.00 12.72   6
ATOM    843  O       GLY A 109      25.681  39.484  95.013  1.00 13.88   8
ATOM    844  N       GLY A 110      27.383  38.153  95.652  1.00 13.11   7
ATOM    845  CA      GLY A 110      28.067  39.328  96.240  1.00 15.14   6
ATOM    846  C       GLY A 110      27.439  39.811  97.559  1.00 14.99   6
ATOM    847  O       GLY A 110      27.472  41.015  97.810  1.00 13.87   8
ATOM    848  N       ALA A 111      26.791  38.972  98.352  1.00 14.85   7
ATOM    849  CA      ALA A 111      26.179  39.445  99.591  1.00 18.80   6
ATOM    850  C       ALA A 111      27.108  40.326 100.430  1.00 18.06   6
ATOM    851  O       ALA A 111      28.296  40.106 100.516  1.00 18.52   8
ATOM    852  CB      ALA A 111      25.772  38.304 100.518  1.00 14.03   6
ATOM    853  N       ASP A 112      26.529  41.293 101.126  1.00 21.22   7
ATOM    854  CA      ASP A 112      27.346  42.122 102.035  1.00 23.75   6
ATOM    855  C       ASP A 112      27.869  41.314 103.234  1.00 23.71   6
ATOM    856  O       ASP A 112      28.969  41.671 103.682  1.00 23.18   8
ATOM    857  CB      ASP A 112      26.496  43.284 102.503  1.00 22.42   6
ATOM    858  CG      ASP A 112      26.071  44.169 101.348  1.00 20.14   6
ATOM    859  OD1     ASP A 112      26.995  44.523 100.598  1.00 27.30   8
ATOM    860  OD2     ASP A 112      24.879  44.509 101.271  1.00 20.89   8
ATOM    861  N       ALA A 113      27.194  40.251 103.702  1.00 24.00   7
ATOM    862  CA      ALA A 113      27.759  39.527 104.868  1.00 24.01   6
ATOM    863  C       ALA A 113      27.179  38.131 105.013  1.00 23.94   6
ATOM    864  O       ALA A 113      26.110  37.890 104.451  1.00 22.13   8
ATOM    865  CB      ALA A 113      27.342  40.331 106.122  1.00 26.22   6
ATOM    866  N       THR A 114      27.826  37.278 105.810  1.00 22.06   7
ATOM    867  CA      THR A 114      27.281  35.943 106.016  1.00 21.69   6
ATOM    868  C       THR A 114      26.312  35.843 107.186  1.00 22.01   6
ATOM    869  O       THR A 114      26.155  36.802 107.929  1.00 20.55   8
ATOM    870  CB      THR A 114      28.387  34.909 106.254  1.00 27.87   6
ATOM    871  OG1     THR A 114      28.996  35.251 107.512  1.00 29.11   8
ATOM    872  CG2   VAL A 117      21.913  29.028 108.776  1.00 20.64   6
ATOM    892  C       VAL A 117      21.937  27.532 108.893  1.00 17.39   6
ATOM    893  O       VAL A 117      22.915  26.888 108.527  1.00 19.05   8
ATOM    894  CB      VAL A 117      21.661  29.432 107.278  1.00 19.42   6
ATOM    895  CG1     VAL A 117      20.322  28.897 106.753  1.00 17.44   6
ATOM    896  CG2     VAL A 117      21.569  30.946 107.143  1.00 18.54   6
ATOM    897  N       THR A 118      20.829  27.010 109.358  1.00 17.83   7
ATOM    898  CA      THR A 118      20.756  25.536 109.467  1.00 19.80   6
ATOM    899  C       THR A 118      20.402  25.048 108.042  1.00 18.35   6
ATOM    900  O       THR A 118      19.399  25.534 107.507  1.00 16.70   8
ATOM    901  CB      THR A 118      19.548  25.042 110.320  1.00 17.44   6
ATOM    902  OG1     THR A 118      19.233  26.096 111.204  1.00 44.59   8
ATOM    903  CG2     THR A 118      19.779  23.693 110.989  1.00 22.04   6
ATOM    904  N       ALA A 119      21.103  24.023 107.604  1.00 19.84   7
ATOM    905  CA      ALA A 119      20.887  23.578 106.200  1.00 19.90   6
ATOM    906  C       ALA A 119      21.136  22.103 106.100  1.00 21.67   6
ATOM    907  O       ALA A 119      21.679  21.551 107.079  1.00 22.42   8
ATOM    908  CB      ALA A 119      22.069  24.322 105.517  1.00 19.05   6
ATOM    909  N       VAL A 120      20.764  21.406 105.044  1.00 20.76   7
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ATOM	910	CA	VAL	A	120	21.100	19.986	104.883	1.00	19.40	6
ATOM	911	C	VAL	A	120	21.803	19.899	103.514	1.00	21.46	6
ATOM	912	O	VAL	A	120	21.498	20.756	102.676	1.00	21.10	8
ATOM	913	CB	VAL	A	120	19.868	19.080	104.936	1.00	12.56	6
ATOM	914	CG1	VAL	A	120	18.742	19.485	104.021	1.00	15.21	6
ATOM	915	CG2	VAL	A	120	20.238	17.612	104.692	1.00	13.03	6
ATOM	916	N	GLU	A	121	22.737	19.042	103.259	1.00	20.32	7
ATOM	917	CA	GLU	A	121	23.390	18.922	101.980	1.00	22.51	6
ATOM	918	C	GLU	A	121	22.518	18.029	101.072	1.00	23.97	6
ATOM	919	O	GLU	A	121	21.864	17.068	101.531	1.00	23.54	8
ATOM	920	CB	GLU	A	121	24.754	18.289	102.125	1.00	22.70	6
ATOM	921	CG	GLU	A	121	25.819	19.157	102.767	1.00	26.10	6
ATOM	922	CD	GLU	A	121	27.114	18.370	102.881	1.00	33.79	6
ATOM	923	OE1	GLU	A	121	27.363	17.496	102.035	1.00	31.76	8
ATOM	924	OE2	GLU	A	121	27.912	18.621	103.804	1.00	33.28	8
ATOM	925	N	VAL	A	122	22.516	18.382	99.779	1.00	22.10	7
ATOM	926	CA	VAL	A	122	21.801	17.498	98.828	1.00	21.06	6
ATOM	927	C	VAL	A	122	22.809	16.962	97.815	1.00	20.23	6
ATOM	928	O	VAL	A	122	23.896	17.513	97.598	1.00	17.86	8
ATOM	929	CB	VAL	A	122	20.624	18.196	98.134	1.00	21.72	6
ATOM	930	CG1	VAL	A	122	19.599	18.610	99.182	1.00	12.05	6
ATOM	931	CG2	VAL	A	122	21.116	19.434	97.365	1.00	8.76	6
ATOM	932	N	ASN	A	123	22.387	15.895	97.128	1.00	20.00	7
ATOM	933	CA	ASN	A	123	23.253	15.301	96.107	1.00	20.45	6
ATOM	934	C	ASN	A	123	23.269	16.215	94.888	1.00	19.88	6
ATOM	935	O	ASN	A	123	22.211	16.559	94.335	1.00	19.99	8
ATOM	936	CB	ASN	A	123	22.661	13.917	95.794	1.00	17.50	6
ATOM	937	CG	ASN	A	123	23.481	13.213	94.706	1.00	32.28	6
ATOM	938	OD1	ASN	A	123	24.360	13.796	94.071	1.00	25.05	8
ATOM	939	ND2	ASN	A	123	23.208	11.935	94.490	1.00	31.02	7
ATOM	940	N	PRO	A	124	24.406	16.647	94.423	1.00	20.38	7
ATOM	941	CA	PRO	A	124	24.556	17.529	93.260	1.00	21.02	6
ATOM	942	C	PRO	A	124	23.926	16.947	92.001	1.00	20.97	6
ATOM	943	O	PRO	A	124	23.353	17.709	91.218	1.00	22.17	8
ATOM	944	CB	PRO	A	124	26.045	17.813	93.054	1.00	20.22	6
ATOM	945	CG	PRO	A	124	26.565	17.458	94.441	1.00	21.81	6
ATOM	946	CD	PRO	A	124	25.725	16.290	94.956	1.00	21.61	6
ATOM	947	N	ASN	A	125	23.881	15.634	91.873	1.00	20.24	7
ATOM	948	CA	ASN	A	125	23.325	14.948	90.722	1.00	22.34	6
ATOM	949	C	ASN	A	125	21.864	14.604	90.954	1.00	21.73	6
ATOM	950	O	ASN	A	125	21.226	14.008	90.082	1.00	21.29	8
ATOM	951	CB	ASN	A	125	24.077	13.632	90.428	1.00	22.86	6
ATOM	952	CG	ASN	A	125	25.505	13.887	89.964	1.00	30.09	6
ATOM	953	OD1	ASN	A	125	25.803	14.951	89.436	1.00	35.43	8
ATOM	954	ND2	ASN	A	125	26.467	12.978	90.138	1.00	38.09	7
ATOM	955	N	ASN	A	126	21.387	14.845	92.169	1.00	20.38	7
ATOM	956	CA	ASN	A	126	19.977	14.571	92.459	1.00	19.66	6
ATOM	957	C	ASN	A	126	19.575	15.450	93.620	1.00	21.05	6
ATOM	958	O	ASN	A	126	19.660	15.015	94.775	1.00	21.00	8
ATOM	959	CB	ASN	A	126	19.775	13.075	92.788	1.00	15.30	6
ATOM	960	CG	ASN	A	126	18.274	12.880	93.006	1.00	23.22	6
ATOM	961	OD1	ASN	A	126	17.452	13.810	93.032	1.00	26.30	8
ATOM	962	ND2	ASN	A	126	17.922	11.613	93.138	1.00	28.44	7
ATOM	963	N	ARG	A	127	19.221	16.720	93.401	1.00	19.57	7
ATOM	964	CA	ARG	A	127	18.962	17.676	94.443	1.00	17.56	6
ATOM	965	C	ARG	A	127	17.752	17.288	95.308	1.00	18.63	6
ATOM	966	O	ARG	A	127	17.461	18.065	96.243	1.00	16.95	8
ATOM	967	CB	ARG	A	127	18.856	19.092	93.904	1.00	12.51	6
ATOM	968	CG	ARG	A	127	20.138	19.752	93.386	1.00	14.72	6
ATOM	969	CD	ARG	A	127	20.547	19.160	92.023	1.00	14.85	6
ATOM	970	NE	ARG	A	127	21.631	19.938	91.401	1.00	14.09	7
ATOM	971	CZ	ARG	A	127	21.533	21.187	90.999	1.00	15.80	6
ATOM	972	NH1	ARG	A	127	20.374	21.834	91.097	1.00	16.14	7
ATOM	973	NH2	ARG	A	127	22.546	21.860	90.471	1.00	17.52	7
ATOM	974	N	ASN	A	128	17.002	16.258	94.938	1.00	17.64	7
ATOM	975	CA	ASN	A	128	15.857	15.806	95.706	1.00	20.96	6
ATOM	976	C	ASN	A	128	16.316	14.849	96.834	1.00	21.64	6
ATOM	977	O	ASN	A	128	15.520	14.474	97.658	1.00	21.03	8
ATOM	978	CB	ASN	A	128	14.855	14.998	94.847	1.00	20.92	6
ATOM	979	CG	ASN	A	128	13.982	15.912	94.008	1.00	25.08	6
ATOM	980	OD1	ASN	A	128	13.652	17.021	94.421	1.00	27.32	8
ATOM	981	ND2	ASN	A	128	13.692	15.454	92.798	1.00	25.22	7
ATOM	982	N	GLN	A	129	17.568	14.425	96.839	1.00	23.60	7
ATOM	983	CA	GLN	A	129	18.149	13.518	97.822	1.00	25.40	6

ATOM	984	C	GLN A 129	19.039	14.238	98.841	1.00	25.85	6
ATOM	985	O	GLN A 129	20.053	14.857	98.528	1.00	25.31	8
ATOM	986	CB	GLN A 129	18.969	12.476	97.065	1.00	30.26	6
ATOM	987	CG	GLN A 129	19.650	11.443	97.896	1.00	36.65	6
ATOM	988	CD	GLN A 129	20.688	10.589	97.220	1.00	50.60	6
ATOM	989	OE1	GLN A 129	21.389	10.920	96.262	1.00	50.90	8
ATOM	990	NE2	GLN A 129	20.789	9.382	97.783	1.00	59.68	7
ATOM	991	N	GLU A 130	18.617	14.169	100.106	1.00	26.25	7
ATOM	992	CA	GLU A 130	19.380	14.786	101.215	1.00	25.65	6
ATOM	993	C	GLU A 130	20.520	13.881	101.601	1.00	24.59	6
ATOM	994	O	GLU A 130	20.267	12.674	101.678	1.00	26.10	8
ATOM	995	CB	GLU A 130	18.439	15.032	102.378	1.00	24.08	6
ATOM	996	CG	GLU A 130	17.425	16.128	102.051	1.00	24.36	6
ATOM	997	CD	GLU A 130	16.469	16.440	103.190	1.00	29.99	6
ATOM	998	OE1	GLU A 130	16.642	15.811	104.263	1.00	27.95	8
ATOM	999	OE2	GLU A 130	15.583	17.309	103.034	1.00	26.77	8
ATOM	1000	N	ILE A 131	21.765	14.341	101.646	1.00	25.24	7
ATOM	1001	CA	ILE A 131	22.833	13.388	101.907	1.00	28.06	6
ATOM	1002	C	ILE A 131	23.624	13.682	103.171	1.00	29.97	6
ATOM	1003	O	ILE A 131	24.751	13.220	103.380	1.00	31.06	8
ATOM	1004	CB	ILE A 131	23.693	13.048	100.699	1.00	26.19	6
ATOM	1005	CG1	ILE A 131	24.647	14.095	100.166	1.00	28.34	6
ATOM	1006	CG2	ILE A 131	22.896	12.567	99.475	1.00	33.58	6
ATOM	1007	CD1	ILE A 131	24.858	15.364	100.874	1.00	35.74	6
ATOM	1008	N	SER A 132	23.082	14.483	104.080	1.00	30.13	7
ATOM	1009	CA	SER A 132	23.789	14.743	105.351	1.00	30.02	6
ATOM	1010	C	SER A 132	22.716	14.997	106.410	1.00	29.25	6
ATOM	1011	O	SER A 132	21.514	14.973	106.087	1.00	28.53	8
ATOM	1012	CB	SER A 132	24.781	15.922	105.207	1.00	19.90	6
ATOM	1013	OG	SER A 132	24.034	17.111	105.470	1.00	23.39	8
ATOM	1014	N	GLY A 133	23.137	15.175	107.666	1.00	29.91	7
ATOM	1015	CA	GLY A 133	22.164	15.515	108.732	1.00	27.01	6
ATOM	1016	C	GLY A 133	22.126	17.045	108.731	1.00	27.96	6
ATOM	1017	O	GLY A 133	22.988	17.643	108.055	1.00	28.15	8
ATOM	1018	N	ASP A 134	21.170	17.687	109.401	1.00	26.57	7
ATOM	1019	CA	ASP A 134	21.163	19.127	109.408	1.00	26.44	6
ATOM	1020	C	ASP A 134	22.423	19.663	110.046	1.00	28.36	6
ATOM	1021	O	ASP A 134	22.940	19.010	110.945	1.00	29.89	8
ATOM	1022	CB	ASP A 134	19.960	19.692	110.178	1.00	25.17	6
ATOM	1023	CG	ASP A 134	18.672	19.184	109.560	1.00	31.21	6
ATOM	1024	OD1	ASP A 134	18.758	18.348	108.637	1.00	33.74	8
ATOM	1025	OD2	ASP A 134	17.599	19.645	110.004	1.00	36.81	8
ATOM	1026	N	TYR A 135	22.883	20.858	109.733	1.00	27.86	7
ATOM	1027	CA	TYR A 135	24.017	21.450	110.430	1.00	27.39	6
ATOM	1028	C	TYR A 135	24.095	22.913	110.033	1.00	28.21	6
ATOM	1029	O	TYR A 135	23.466	23.263	109.032	1.00	27.76	8
ATOM	1030	CB	TYR A 135	25.310	20.707	110.279	1.00	28.84	6
ATOM	1031	CG	TYR A 135	26.031	20.662	108.957	1.00	24.62	6
ATOM	1032	CD1	TYR A 135	26.991	21.596	108.643	1.00	24.15	6
ATOM	1033	CD2	TYR A 135	25.761	19.660	108.042	1.00	25.71	6
ATOM	1034	CE1	TYR A 135	27.689	21.546	107.443	1.00	24.99	6
ATOM	1035	CE2	TYR A 135	26.442	19.601	106.829	1.00	24.95	6
ATOM	1036	CZ	TYR A 135	27.401	20.542	106.540	1.00	25.76	6
ATOM	1037	OH	TYR A 135	28.087	20.465	105.350	1.00	27.67	8
ATOM	1038	N	THR A 136	24.829	23.709	110.794	1.00	26.69	7
ATOM	1039	CA	THR A 136	24.874	25.132	110.547	1.00	25.35	6
ATOM	1040	C	THR A 136	26.030	25.509	109.642	1.00	24.11	6
ATOM	1041	O	THR A 136	27.142	25.073	109.831	1.00	21.73	8
ATOM	1042	CB	THR A 136	25.003	25.938	111.855	1.00	26.43	6
ATOM	1043	OG1	THR A 136	23.789	25.695	112.576	1.00	37.87	8
ATOM	1044	CG2	THR A 136	25.020	27.430	111.593	1.00	32.50	6
ATOM	1045	N	ILE A 137	25.684	26.380	108.659	1.00	23.93	7
ATOM	1046	CA	ILE A 137	26.723	26.842	107.737	1.00	21.01	6
ATOM	1047	C	ILE A 137	26.748	28.359	107.805	1.00	20.59	6
ATOM	1048	O	ILE A 137	25.781	28.967	108.272	1.00	22.54	8
ATOM	1049	CB	ILE A 137	26.471	26.381	106.280	1.00	20.65	6
ATOM	1050	CG1	ILE A 137	25.177	26.998	105.733	1.00	16.56	6
ATOM	1051	CG2	ILE A 137	26.437	24.861	106.202	1.00	17.98	6
ATOM	1052	CD1	ILE A 137	24.964	26.666	104.249	1.00	24.92	6
ATOM	1053	N	GLU A 138	27.858	28.918	107.332	1.00	20.50	7
ATOM	1054	CA	GLU A 138	27.921	30.389	107.257	1.00	21.16	6
ATOM	1055	C	GLU A 138	27.650	30.730	105.769	1.00	20.45	6
ATOM	1056	O	GLU A 138	28.464	30.333	104.916	1.00	21.84	8
ATOM	1057	CB	GLU A 138	29.342	30.790	107.636	1.00	17.31	6

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ATOM   1058  CG      GLU A 138      29.425  32.264 108.031  1.00 35.20   6
ATOM   1059  CD      GLU A 138      30.871  32.570 108.420  1.00 47.73   6
ATOM   1060  OE1     GLU A 138      31.483  31.664 109.037  1.00 46.82   8
ATOM   1061  OE2     GLU A 138      31.367  33.676 108.096  1.00 52.74   8
ATOM   1062  N       ALA A 139      26.496  31.293 105.485  1.00 19.42   7
ATOM   1063  CA      ALA A 139      26.047  31.439 104.093  1.00 18.49   6
ATOM   1064  C       ALA A 139      26.084  32.876 103.660  1.00 18.67   6
ATOM   1065  O       ALA A 139      25.783  33.763 104.485  1.00 15.46   8
ATOM   1066  CB      ALA A 139      24.628  30.904 103.958  1.00 13.24   6
ATOM   1067  N       TRP A 140      26.400  33.140 102.371  1.00 17.04   7
ATOM   1068  CA      TRP A 140      26.363  34.570 101.978  1.00 15.11   6
ATOM   1069  C       TRP A 140      24.968  34.964 101.565  1.00 17.06   6
ATOM   1070  O       TRP A 140      24.558  34.917 100.370  1.00 15.64   8
ATOM   1071  CB      TRP A 140      27.419  34.845 100.924  1.00 19.76   6
ATOM   1072  CG      TRP A 140      28.834  34.726 101.357  1.00 14.16   6
ATOM   1073  CD1     TRP A 140      29.615  33.616 101.329  1.00 20.68   6
ATOM   1074  CD2     TRP A 140      29.646  35.779 101.900  1.00 15.22   6
ATOM   1075  NE1     TRP A 140      30.859  33.908 101.820  1.00 22.96   7
ATOM   1076  CE2     TRP A 140      30.922  35.232 102.155  1.00 19.66   6
ATOM   1077  CE3     TRP A 140      29.419  37.116 102.209  1.00 17.43   6
ATOM   1078  CZ2     TRP A 140      31.966  35.972 102.715  1.00 19.26   6
ATOM   1079  CZ3     TRP A 140      30.454  37.880 102.709  1.00 17.26   6
ATOM   1080  CH2     TRP A 140      31.698  37.287 102.977  1.00 19.26   6
ATOM   1081  N       THR A 141      24.123  35.431 102.510  1.00 13.71   7
ATOM   1082  CA      THR A 141      22.735  35.685 102.263  1.00 12.75   6
ATOM   1083  C       THR A 141      22.279  37.074 102.694  1.00 13.45   6
ATOM   1084  O       THR A 141      21.144  37.474 102.421  1.00 11.95   8
ATOM   1085  CB      THR A 141      21.832  34.675 103.023  1.00 19.93   6
ATOM   1086  OG1     THR A 141      22.368  34.660 104.351  1.00 20.34   8
ATOM   1087  CG2     THR A 141      21.940  33.269 102.445  1.00 18.23   6
ATOM   1088  N       LYS A 142      23.237  37.833 103.243  1.00 14.14   7
ATOM   1089  CA      LYS A 142      22.803  39.127 103.724  1.00 13.25   6
ATOM   1090  C       LYS A 142      23.119  40.343 102.875  1.00 12.07   6
ATOM   1091  O       LYS A 142      24.272  40.602 102.715  1.00 12.38   8
ATOM   1092  CB      LYS A 142      23.366  39.384 105.167  1.00 22.24   6
ATOM   1093  CG      LYS A 142      22.617  40.641 105.665  1.00 24.68   6
ATOM   1094  CD      LYS A 142      23.632  41.559 106.331  1.00 47.57   6
ATOM   1095  CE      LYS A 142      23.167  41.885 107.765  1.00 41.52   6
ATOM   1096  NZ      LYS A 142      22.754  40.564 108.327  1.00 49.23   7
ATOM   1097  N       PHE A 143      22.058  41.048 102.474  1.00 12.20   7
ATOM   1098  CA      PHE A 143      22.273  42.185 101.586  1.00 15.87   6
ATOM   1099  C       PHE A 143      21.631  43.432 102.175  1.00 15.91   6
ATOM   1100  O       PHE A 143      20.429  43.476 102.346  1.00 17.13   8
ATOM   1101  CB      PHE A 143      21.581  41.919 100.181  1.00 17.78   6
ATOM   1102  CG      PHE A 143      22.117  40.744  99.384  1.00 15.53   6
ATOM   1103  CD1     PHE A 143      21.833  39.445  99.678  1.00 15.38   6
ATOM   1104  CD2     PHE A 143      22.904  40.993  98.248  1.00 21.45   6
ATOM   1105  CE1     PHE A 143      22.333  38.370  98.939  1.00 20.18   6
ATOM   1106  CE2     PHE A 143      23.401  39.957  97.489  1.00 13.29   6
ATOM   1107  CZ      PHE A 143      23.143  38.640  97.839  1.00 16.41   6
ATOM   1108  N       ASP A 144      22.452  44.460 102.391  1.00 18.78   7
ATOM   1109  CA      ASP A 144      21.878  45.710 102.908  1.00 23.30   6
ATOM   1110  C     ASP A 144      21.469  47.888 102.095  1.00 23.01   8
ATOM   1112  CB      ASP A 144      22.387  46.060 104.309  1.00 23.28   6
ATOM   1113  CG      ASP A 144      22.039  45.013 105.363  1.00 27.65   6
ATOM   1114  OD1     ASP A 144      20.865  44.750 105.635  1.00 25.54   8
ATOM   1115  OD2     ASP A 144      22.996  44.435 105.907  1.00 38.42   8
ATOM   1116  N       PHE A 145      23.045  46.682 100.963  1.00 25.63   7
ATOM   1117  CA      PHE A 145      23.195  47.725  99.925  1.00 24.68   6
ATOM   1118  C       PHE A 145      23.555  49.047 100.600  1.00 25.85   6
ATOM   1119  O       PHE A 145      22.898  50.077 100.518  1.00 25.95   8
ATOM   1120  CB      PHE A 145      21.868  47.911  99.141  1.00 12.40   6
ATOM   1121  CG      PHE A 145      21.212  46.667  98.629  1.00 17.44   6
ATOM   1122  CD1     PHE A 145      21.859  45.822  97.722  1.00 22.23   6
ATOM   1123  CD2     PHE A 145      19.941  46.319  99.032  1.00 21.70   6
ATOM   1124  CE1     PHE A 145      21.265  44.662  97.257  1.00 15.92   6
ATOM   1125  CE2     PHE A 145      19.311  45.171  98.552  1.00 26.05   6
ATOM   1126  CZ      PHE A 145      19.976  44.330  97.661  1.00 17.21   6
ATOM   1127  N       PRO A 146      24.698  49.038 101.255  1.00 27.30   7
ATOM   1128  CA      PRO A 146      25.269  50.166 101.962  1.00 29.33   6
ATOM   1129  C       PRO A 146      25.443  51.408 101.107  1.00 30.70   6
ATOM   1130  O       PRO A 146      25.143  52.508 101.576  1.00 29.79   8
ATOM   1131  CB      PRO A 146      26.732  49.809 102.381  1.00 28.88   6
ATOM   1132  CG      PRO A 146      26.943  48.518 101.641  1.00 30.07   6
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ATOM   1133  CD        PRO A 146      25.592  47.888 101.328  1.00 27.29   6
ATOM   1134  N   GLY A 147      25.957  51.200  99.866  1.00 29.98   7
ATOM   1135  CA  GLY A 147      26.215  52.382  99.045  1.00 29.30   6
ATOM   1136  C   GLY A 147      24.928  53.057  98.626  1.00 29.97   6
ATOM   1137  O   GLY A 147      24.919  54.261  98.349  1.00 32.02   8
ATOM   1138  N   ARG A 148      23.821  52.346  98.518  1.00 29.43   7
ATOM   1139  CA  ARG A 148      22.601  52.956  98.020  1.00 29.69   6
ATOM   1140  C   ARG A 148      21.630  53.394  99.118  1.00 31.82   6
ATOM   1141  O   ARG A 148      20.685  54.157  98.885  1.00 29.76   8
ATOM   1142  CB  ARG A 148      21.917  51.843  97.180  1.00 19.70   6
ATOM   1143  CG  ARG A 148      20.541  52.278  96.709  1.00 20.29   6
ATOM   1144  CD  ARG A 148      19.906  51.409  95.676  1.00 24.90   6
ATOM   1145  NE  ARG A 148      19.796  49.964  95.964  1.00 21.80   7
ATOM   1146  CZ  ARG A 148      18.704  49.454  96.514  1.00 12.63   6
ATOM   1147  NH1 ARG A 148      17.762  50.295  96.916  1.00 14.67   7
ATOM   1148  NH2 ARG A 148      18.590  48.144  96.715  1.00 17.35   7
ATOM   1149  N   GLY A 149      21.715  52.710 100.267  1.00 33.44   7
ATOM   1150  CA  GLY A 149      20.777  52.979 101.365  1.00 33.67   6
ATOM   1151  C   GLY A 149      19.397  52.506 100.928  1.00 33.52   6
ATOM   1152  O   GLY A 149      19.309  51.396 100.384  1.00 34.95   8
ATOM   1153  N   ASN A 150      18.362  53.307 101.158  1.00 31.50   7
ATOM   1154  CA  ASN A 150      17.027  52.915 100.732  1.00 29.53   6
ATOM   1155  C   ASN A 150      16.504  53.699  99.520  1.00 27.75   6
ATOM   1156  O   ASN A 150      15.287  53.760  99.281  1.00 25.07   8
ATOM   1157  CB  ASN A 150      16.070  53.058 101.922  1.00 40.30   6
ATOM   1158  CG  ASN A 150      16.456  52.237 103.138  1.00 55.09   6
ATOM   1159  OD1 ASN A 150      16.260  52.655 104.285  1.00 63.25   8
ATOM   1160  ND2 ASN A 150      17.016  51.048 102.957  1.00 53.95   7
ATOM   1161  N   THR A 151      17.389  54.302  98.720  1.00 28.99   7
ATOM   1162  CA  THR A 151      16.858  55.022  97.512  1.00 28.81   6
ATOM   1163  C   THR A 151      16.178  54.052  96.570  1.00 27.33   6
ATOM   1164  O   THR A 151      16.637  52.926  96.314  1.00 28.63   8
ATOM   1165  CB  THR A 151      18.044  55.679  96.808  1.00 36.51   6
ATOM   1166  OG1 THR A 151      18.794  56.322  97.830  1.00 35.60   8
ATOM   1167  CG2 THR A 151      17.618  56.610  95.680  1.00 30.56   6
ATOM   1168  N   TYR A 152      14.983  54.307  96.080  1.00 27.71   7
ATOM   1169  CA  TYR A 152      14.180  53.485  95.184  1.00 28.08   6
ATOM   1170  C   TYR A 152      13.577  52.275  95.869  1.00 27.94   6
ATOM   1171  O   TYR A 152      12.467  51.879  95.493  1.00 29.37   8
ATOM   1172  CB  TYR A 152      14.906  53.008  93.906  1.00 27.24   6
ATOM   1173  CG  TYR A 152      15.743  54.043  93.196  1.00 27.33   6
ATOM   1174  CD1 TYR A 152      15.198  55.276  92.854  1.00 29.84   6
ATOM   1175  CD2 TYR A 152      17.075  53.839  92.891  1.00 27.70   6
ATOM   1176  CE1 TYR A 152      15.959  56.239  92.210  1.00 30.71   6
ATOM   1177  CE2 TYR A 152      17.850  54.777  92.235  1.00 28.02   6
ATOM   1178  CZ  TYR A 152      17.275  55.985  91.899  1.00 30.18   6
ATOM   1179  OH  TYR A 152      18.007  56.985  91.276  1.00 31.59   8
ATOM   1180  N   SER A 153      14.308  51.601  96.769  1.00 26.11   7
ATOM   1181  CA  SER A 153      13.693  50.434  97.420  1.00 25.69   6
ATOM   1182  C   SER A 153      14.190  50.276  98.884  1.00 25.09   6
ATOM   1183  O   SER A 153      15.393  50.338  99.160  1.00 22.81   8
ATOM   1184  CB  SER A 153      14.088  49.186  96.606  1.00 24.66   6
ATOM   1185  OG  SER A 153      13.415  48.028  97.114  1.00 29.86   8
ATOM   1186  N   ASP A 154      13.273  49.927  99.793  1.00 24.96   7
ATOM   1187  CA  ASP A 154      13.817  49.687 101.156  1.00 28.71   6
ATOM   1188  C   ASP A 154      13.944  48.191 101.429  1.00 27.53   6
ATOM   1189  O   ASP A 154      14.252  47.821 102.561  1.00 26.49   8
ATOM   1190  CB  ASP A 154      12.991  50.404 102.222  1.00 34.87   6
ATOM   1191  CG  ASP A 154      11.563  49.912 102.224  1.00 39.14   6
ATOM   1192  OD1 ASP A 154      11.289  48.783 101.767  1.00 50.57   8
ATOM   1193  OD2 ASP A 154      10.674  50.664 102.696  1.00 55.34   8
ATOM   1194  N   PHE A 155      13.724  47.310 100.445  1.00 25.05   7
ATOM   1195  CA  PHE A 155      13.850  45.877 100.719  1.00 22.73   6
ATOM   1196  C   PHE A 155      15.243  45.408 101.069  1.00 20.67   6
ATOM   1197  O   PHE A 155      16.211  45.747 100.396  1.00 21.78   8
ATOM   1198  CB  PHE A 155      13.280  45.099  99.567  1.00 17.71   6
ATOM   1199  CG  PHE A 155      12.927  43.663  99.752  1.00 22.13   6
ATOM   1200  CD1 PHE A 155      11.632  43.319 100.096  1.00 20.02   6
ATOM   1201  CD2 PHE A 155      13.861  42.663  99.531  1.00 19.53   6
ATOM   1202  CE1 PHE A 155      11.252  41.995 100.217  1.00 24.70   6
ATOM   1203  CE2 PHE A 155      13.475  41.332  99.676  1.00 23.28   6
ATOM   1204  CZ  PHE A 155      12.174  40.989 100.006  1.00 20.40   6
ATOM   1205  N   LYS A 156      15.386  44.484 102.046  1.00 17.13   7
ATOM   1206  CA  LYS A 156      16.718  43.965 102.361  1.00 14.59   6
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ATOM   1207  C   LYS A 156      16.629  42.469 102.207  1.00 12.80   6
ATOM   1208  O   LYS A 156      15.512  41.997 102.422  1.00 15.89   8
ATOM   1209  CB  LYS A 156      17.168  44.274 103.807  1.00 20.78   6
ATOM   1210  CG  LYS A 156      17.086  45.757 104.093  1.00 21.02   6
ATOM   1211  CD  LYS A 156      18.251  46.516 103.515  1.00 23.93   6
ATOM   1212  CE  LYS A 156      17.953  48.016 103.618  1.00 30.28   6
ATOM   1213  NZ  LYS A 156      19.072  48.837 103.037  1.00 32.80   7
ATOM   1214  N   TRP A 157      17.695  41.778 101.877  1.00 11.89   7
ATOM   1215  CA  TRP A 157      17.454  40.339 101.625  1.00 13.27   6
ATOM   1216  C   TRP A 157      18.109  39.600 102.809  1.00  9.91   6
ATOM   1217  O   TRP A 157      19.144  40.070 103.255  1.00 10.57   8
ATOM   1218  CB  TRP A 157      18.172  39.893 100.292  1.00 12.07   6
ATOM   1219  CG  TRP A 157      17.439  40.438  99.052  1.00 20.71   6
ATOM   1220  CD1 TRP A 157      17.449  41.728  98.608  1.00 18.19   6
ATOM   1221  CD2 TRP A 157      16.566  39.735  98.161  1.00 15.04   6
ATOM   1222  NE1 TRP A 157      16.611  41.881  97.510  1.00 17.50   7
ATOM   1223  CE2 TRP A 157      16.083  40.660  97.218  1.00 18.56   6
ATOM   1224  CE3 TRP A 157      16.189  38.392  98.039  1.00 12.01   6
ATOM   1225  CZ2 TRP A 157      15.259  40.295  96.158  1.00 17.59   6
ATOM   1226  CZ3 TRP A 157      15.333  38.040  97.023  1.00 20.95   6
ATOM   1227  CH2 TRP A 157      14.871  38.981  96.079  1.00 22.76   6
ATOM   1228  N   ARG A 158      17.550  38.478 103.162  1.00 10.27   7
ATOM   1229  CA  ARG A 158      18.164  37.704 104.259  1.00 15.83   6
ATOM   1230  C   ARG A 158      18.104  36.234 103.874  1.00 15.51   6
ATOM   1231  O   ARG A 158      17.369  35.938 102.912  1.00 15.73   8
ATOM   1232  CB  ARG A 158      17.324  37.927 105.580  1.00 12.73   6
ATOM   1233  CG  ARG A 158      17.354  39.383 106.074  1.00 12.20   6
ATOM   1234  CD  ARG A 158      18.729  39.676 106.661  1.00 19.33   6
ATOM   1235  NE  ARG A 158      18.853  41.071 107.038  1.00 24.10   7
ATOM   1236  CZ  ARG A 158      19.328  42.154 106.473  1.00 32.65   6
ATOM   1237  NH1 ARG A 158      19.889  42.211 105.253  1.00 17.30   7
ATOM   1238  NH2 ARG A 158      19.249  43.300 107.168  1.00 28.36   7
ATOM   1239  N   TRP A 159      18.709  35.335 104.665  1.00 13.20   7
ATOM   1240  CA  TRP A 159      18.673  33.945 104.395  1.00 12.34   6
ATOM   1241  C   TRP A 159      17.282  33.431 104.062  1.00 15.51   6
ATOM   1242  O   TRP A 159      17.193  32.484 103.236  1.00 14.77   8
ATOM   1243  CB  TRP A 159      19.345  33.054 105.463  1.00 18.26   6
ATOM   1244  CG  TRP A 159      18.445  33.005 106.687  1.00 14.02   6
ATOM   1245  CD1 TRP A 159      18.397  33.991 107.651  1.00 16.36   6
ATOM   1246  CD2 TRP A 159      17.427  32.062 106.958  1.00 13.35   6
ATOM   1247  NE1 TRP A 159      17.416  33.645 108.558  1.00 23.93   7
ATOM   1248  CE2 TRP A 159      16.827  32.473 108.185  1.00 23.09   6
ATOM   1249  CE3 TRP A 159      16.985  30.884 106.376  1.00 12.10   6
ATOM   1250  CZ2 TRP A 159      15.771  31.777 108.765  1.00 24.07   6
ATOM   1251  CZ3 TRP A 159      15.964  30.168 106.964  1.00 22.85   6
ATOM   1252  CH2 TRP A 159      15.355  30.607 108.161  1.00 26.32   6
ATOM   1253  N   TYR A 160      16.211  33.902 104.731  1.00 15.24   7
ATOM   1254  CA  TYR A 160      14.917  33.287 104.520  1.00 15.26   6
ATOM   1255  C   TYR A 160      14.279  33.656 103.174  1.00 14.17   6
ATOM   1256  O   TYR A 160      13.291  33.045 102.816  1.00 12.44   8
ATOM   1257  CB  TYR A 160      13.917  33.558 105.687  1.00 14.38   6
ATOM   1258  CG  TYR A 160      13.860  34.993 106.096  1.00 15.35   6
ATOM   1259  CD1 TYR A 160      12.954  35.892 105.531  1.00 19.38   6
ATOM   1260  CD2 TYR A 160      14.712  35.464 107.096  1.00 16.13   6
ATOM   1261  CE1 TYR A 160      12.935  37.246 105.893  1.00 21.09   6
ATOM   1262  CE2 TYR A 160      14.711  36.795 107.507  1.00 15.66   6
ATOM   1263  CZ  TYR A 160      13.821  37.660 106.908  1.00 21.37   6
ATOM   1264  OH  TYR A 160      13.802  38.972 107.303  1.00 20.64   8
ATOM   1265  N   HIS A 161      14.814  34.621 102.434  1.00 16.14   7
ATOM   1266  CA  HIS A 161      14.328  34.887 101.056  1.00 16.93   6
ATOM   1267  C   HIS A 161      14.971  33.936 100.019  1.00 17.46   6
ATOM   1268  O   HIS A 161      14.654  33.984  98.823  1.00 15.86   8
ATOM   1269  CB  HIS A 161      14.750  36.316 100.683  1.00 10.99   6
ATOM   1270  CG  HIS A 161      14.061  37.316 101.550  1.00 16.42   6
ATOM   1271  ND1 HIS A 161      14.740  38.364 102.160  1.00 24.17   7
ATOM   1272  CD2 HIS A 161      12.765  37.417 101.916  1.00 15.95   6
ATOM   1273  CE1 HIS A 161      13.853  39.120 102.804  1.00 15.69   6
ATOM   1274  NE2 HIS A 161      12.666  38.565 102.667  1.00 16.91   7
ATOM   1275  N   PHE A 162      15.871  33.044 100.404  1.00 14.97   7
ATOM   1276  CA  PHE A 162      16.594  32.118  99.627  1.00 12.83   6
ATOM   1277  C   PHE A 162      16.376  30.671  99.966  1.00 14.26   6
ATOM   1278  O   PHE A 162      15.853  30.313 101.031  1.00 14.52   8
ATOM   1279  CB  PHE A 162      18.103  32.347  99.720  1.00  9.13   6
ATOM   1280  CG  PHE A 162      18.490  33.738  99.311  1.00 18.06   6
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ATOM	1281	CD1	PHE	A	162	18.476	34.088	97.949	1.00	21.87	6
ATOM	1282	CD2	PHE	A	162	18.892	34.689	100.208	1.00	13.90	6
ATOM	1283	CE1	PHE	A	162	18.826	35.366	97.541	1.00	13.60	6
ATOM	1284	CE2	PHE	A	162	19.271	35.961	99.824	1.00	15.51	6
ATOM	1285	CZ	PHE	A	162	19.241	36.321	98.470	1.00	23.43	6
ATOM	1286	N	ASP	A	163	16.546	29.790	98.981	1.00	10.90	7
ATOM	1287	CA	ASP	A	163	16.403	28.392	99.176	1.00	10.39	6
ATOM	1288	C	ASP	A	163	17.693	27.700	99.562	1.00	11.49	6
ATOM	1289	O	ASP	A	163	17.556	26.593	100.122	1.00	11.71	8
ATOM	1290	CB	ASP	A	163	15.857	27.587	97.983	1.00	12.96	6
ATOM	1291	CG	ASP	A	163	14.402	27.850	97.958	1.00	26.57	6
ATOM	1292	OD1	ASP	A	163	13.659	27.893	98.995	1.00	16.13	8
ATOM	1293	OD2	ASP	A	163	13.857	27.981	96.835	1.00	12.30	8
ATOM	1294	N	GLY	A	164	18.804	28.196	99.030	1.00	12.90	7
ATOM	1295	CA	GLY	A	164	20.030	27.375	99.336	1.00	12.98	6
ATOM	1296	C	GLY	A	164	21.179	28.077	98.628	1.00	13.37	6
ATOM	1297	O	GLY	A	164	20.969	29.133	97.996	1.00	12.18	8
ATOM	1298	N	VAL	A	165	22.384	27.600	98.870	1.00	12.35	7
ATOM	1299	CA	VAL	A	165	23.607	28.204	98.394	1.00	13.69	6
ATOM	1300	C	VAL	A	165	24.550	27.046	98.062	1.00	12.21	6
ATOM	1301	O	VAL	A	165	24.229	25.901	98.384	1.00	12.79	8
ATOM	1302	CB	VAL	A	165	24.355	29.033	99.478	1.00	14.33	6
ATOM	1303	CG1	VAL	A	165	23.590	30.310	99.744	1.00	12.75	6
ATOM	1304	CG2	VAL	A	165	24.616	28.170	100.718	1.00	15.74	6
ATOM	1305	N	ASP	A	166	25.713	27.351	97.518	1.00	12.34	7
ATOM	1306	CA	ASP	A	166	26.606	26.208	97.282	1.00	15.26	6
ATOM	1307	C	ASP	A	166	27.935	26.463	98.013	1.00	17.23	6
ATOM	1308	O	ASP	A	166	28.984	25.926	97.629	1.00	18.39	8
ATOM	1309	CB	ASP	A	166	26.875	26.081	95.788	1.00	18.07	6
ATOM	1310	CG	ASP	A	166	27.487	27.319	95.177	1.00	19.91	6
ATOM	1311	OD1	ASP	A	166	27.650	28.427	95.717	1.00	16.51	8
ATOM	1312	OD2	ASP	A	166	27.864	27.223	93.968	1.00	28.31	8
ATOM	1313	N	TRP	A	167	27.990	27.429	98.897	1.00	14.83	7
ATOM	1314	CA	TRP	A	167	29.294	27.690	99.508	1.00	17.67	6
ATOM	1315	C	TRP	A	167	29.108	27.944	101.013	1.00	18.96	6
ATOM	1316	O	TRP	A	167	28.289	28.817	101.338	1.00	17.91	8
ATOM	1317	CB	TRP	A	167	29.814	28.982	98.886	1.00	14.01	6
ATOM	1318	CG	TRP	A	167	31.187	29.314	99.401	1.00	19.38	6
ATOM	1319	CD1	TRP	A	167	31.570	30.362	100.163	1.00	18.10	6
ATOM	1320	CD2	TRP	A	167	32.367	28.539	99.143	1.00	25.35	6
ATOM	1321	NE1	TRP	A	167	32.927	30.286	100.393	1.00	27.77	7
ATOM	1322	CE2	TRP	A	167	33.437	29.185	99.790	1.00	24.31	6
ATOM	1323	CE3	TRP	A	167	32.622	27.366	98.417	1.00	27.58	6
ATOM	1324	CZ2	TRP	A	167	34.742	28.702	99.720	1.00	30.95	6
ATOM	1325	CZ3	TRP	A	167	33.909	26.871	98.349	1.00	28.47	6
ATOM	1326	CH2	TRP	A	167	34.956	27.554	98.988	1.00	28.98	6
ATOM	1327	N	ASP	A	168	29.877	27.216	101.797	1.00	20.19	7
ATOM	1328	CA	ASP	A	168	29.804	27.341	103.274	1.00	20.28	6
ATOM	1329	C	ASP	A	168	31.066	28.117	103.686	1.00	20.80	6
ATOM	1330	O	ASP	A	168	32.128	27.479	103.710	1.00	19.17	8
ATOM	1331	CB	ASP	A	168	29.928	25.971	103.959	1.00	24.57	6
ATOM	1332	CG	ASP	A	168	29.951	26.015	105.493	1.00	21.84	6
ATOM	1333	OD1	ASP	A	168	30.118	27.080	106.121	1.00	16.16	8
ATOM	1334	OD2	ASP	A	168	29.787	24.907	106.047	1.00	26.17	8
ATOM	1335	N	GLN	A	169	30.951	29.384	104.022	1.00	21.96	7
ATOM	1336	CA	GLN	A	169	32.157	30.143	104.321	1.00	25.62	6
ATOM	1337	C	GLN	A	169	33.047	29.549	105.412	1.00	28.23	6
ATOM	1338	O	GLN	A	169	34.271	29.681	105.365	1.00	27.18	8
ATOM	1339	CB	GLN	A	169	31.826	31.590	104.639	1.00	14.99	6
ATOM	1340	CG	GLN	A	169	33.097	32.409	104.761	1.00	25.50	6
ATOM	1341	CD	GLN	A	169	33.840	32.535	103.439	1.00	40.11	6
ATOM	1342	OE1	GLN	A	169	33.261	32.400	102.343	1.00	34.31	8
ATOM	1343	NE2	GLN	A	169	35.138	32.821	103.531	1.00	36.92	7
ATOM	1344	N	SER	A	170	32.454	28.854	106.387	1.00	30.01	7
ATOM	1345	CA	SER	A	170	33.267	28.219	107.409	1.00	30.93	6
ATOM	1346	C	SER	A	170	33.959	26.959	106.983	1.00	34.16	6
ATOM	1347	O	SER	A	170	34.930	26.640	107.695	1.00	36.58	8
ATOM	1348	CB	SER	A	170	32.410	28.039	108.667	1.00	20.08	6
ATOM	1349	OG	SER	A	170	31.551	26.927	108.481	1.00	22.36	8
ATOM	1350	N	ARG	A	171	33.630	26.158	105.981	1.00	33.63	7
ATOM	1351	CA	ARG	A	171	34.350	24.913	105.705	1.00	33.38	6
ATOM	1352	C	ARG	A	171	34.951	24.875	104.302	1.00	34.23	6
ATOM	1353	O	ARG	A	171	35.944	24.213	103.981	1.00	32.41	8
ATOM	1354	CB	ARG	A	171	33.468	23.695	105.939	1.00	27.27	6

ATOM	1355	CG	ARG	A	171	33.012	23.494	107.353	1.00	33.00	6
ATOM	1356	CD	ARG	A	171	31.872	22.500	107.407	1.00	39.19	6
ATOM	1357	NE	ARG	A	171	31.388	22.325	108.770	1.00	39.85	7
ATOM	1358	CZ	ARG	A	171	30.408	23.012	109.340	1.00	43.41	6
ATOM	1359	NH1	ARG	A	171	29.725	23.983	108.734	1.00	29.35	7
ATOM	1360	NH2	ARG	A	171	30.110	22.693	110.606	1.00	44.37	7
ATOM	1361	N	GLN	A	172	34.304	25.642	103.410	1.00	33.77	7
ATOM	1362	CA	GLN	A	172	34.824	25.847	102.066	1.00	33.35	6
ATOM	1363	C	GLN	A	172	35.157	24.625	101.241	1.00	31.96	6
ATOM	1364	O	GLN	A	172	36.210	24.583	100.568	1.00	33.96	8
ATOM	1365	CB	GLN	A	172	36.076	26.747	102.222	1.00	42.50	6
ATOM	1366	CG	GLN	A	172	35.640	28.090	102.820	1.00	49.13	6
ATOM	1367	CD	GLN	A	172	36.811	28.995	103.127	1.00	58.31	6
ATOM	1368	OE1	GLN	A	172	36.603	30.173	103.425	1.00	58.18	8
ATOM	1369	NE2	GLN	A	172	38.009	28.427	103.051	1.00	62.72	7
ATOM	1370	N	PHE	A	173	34.269	23.659	101.211	1.00	30.25	7
ATOM	1371	CA	PHE	A	173	34.431	22.480	100.363	1.00	29.08	6
ATOM	1372	C	PHE	A	173	33.761	22.758	99.013	1.00	28.52	6
ATOM	1373	O	PHE	A	173	32.782	23.518	99.080	1.00	26.08	8
ATOM	1374	CB	PHE	A	173	33.523	21.401	100.979	1.00	34.67	6
ATOM	1375	CG	PHE	A	173	33.945	20.938	102.338	1.00	35.82	6
ATOM	1376	CD1	PHE	A	173	35.268	20.654	102.612	1.00	36.63	6
ATOM	1377	CD2	PHE	A	173	33.012	20.769	103.335	1.00	33.85	6
ATOM	1378	CE1	PHE	A	173	35.662	20.221	103.872	1.00	45.83	6
ATOM	1379	CE2	PHE	A	173	33.378	20.336	104.594	1.00	39.40	6
ATOM	1380	CZ	PHE	A	173	34.709	20.058	104.868	1.00	38.34	6
ATOM	1381	N	GLN	A	174	34.128	22.107	97.888	1.00	28.71	7
ATOM	1382	CA	GLN	A	174	33.196	22.333	96.794	1.00	29.82	6
ATOM	1383	C	GLN	A	174	32.546	21.071	96.280	1.00	29.35	6
ATOM	1384	O	GLN	A	174	32.603	20.035	96.933	1.00	30.96	8
ATOM	1385	CB	GLN	A	174	33.216	23.494	95.843	1.00	53.27	6
ATOM	1386	CG	GLN	A	174	31.939	24.362	95.817	1.00	60.86	6
ATOM	1387	CD	GLN	A	174	30.996	24.108	96.976	1.00	55.96	6
ATOM	1388	OE1	GLN	A	174	30.235	23.170	97.136	1.00	47.07	8
ATOM	1389	NE2	GLN	A	174	31.083	25.001	97.961	1.00	62.44	7
ATOM	1390	N	ASN	A	175	31.699	21.302	95.282	1.00	27.07	7
ATOM	1391	CA	ASN	A	175	30.822	20.245	94.812	1.00	26.14	6
ATOM	1392	C	ASN	A	175	29.838	19.874	95.936	1.00	23.99	6
ATOM	1393	O	ASN	A	175	29.386	18.733	96.097	1.00	23.58	8
ATOM	1394	CB	ASN	A	175	31.616	19.093	94.213	1.00	29.32	6
ATOM	1395	CG	ASN	A	175	30.663	18.073	93.581	1.00	36.03	6
ATOM	1396	OD1	ASN	A	175	29.890	18.446	92.704	1.00	43.41	8
ATOM	1397	ND2	ASN	A	175	30.695	16.832	94.049	1.00	40.76	7
ATOM	1398	N	ARG	A	176	29.402	20.871	96.719	1.00	20.65	7
ATOM	1399	CA	ARG	A	176	28.335	20.697	97.680	1.00	20.93	6
ATOM	1400	C	ARG	A	176	27.188	21.654	97.362	1.00	18.46	6
ATOM	1401	O	ARG	A	176	27.458	22.800	96.980	1.00	18.62	8
ATOM	1402	CB	ARG	A	176	28.690	21.084	99.142	1.00	31.62	6
ATOM	1403	CG	ARG	A	176	30.003	20.520	99.625	1.00	34.75	6
ATOM	1404	CD	ARG	A	176	29.901	19.018	99.769	1.00	36.13	6
ATOM	1405	NE	ARG	A	176	31.137	18.503	100.325	1.00	47.87	7
ATOM	1406	CZ	ARG	A	176	31.416	18.089	101.543	1.00	49.61	6
ATOM	1407	NH1	ARG	A	176	30.563	18.063	102.550	1.00	46.30	7
ATOM	1408	NH2	ARG	A	176	32.658	17.662	101.749	1.00	55.95	7
ATOM	1409	N	ILE	A	177	25.981	21.182	97.672	1.00	16.68	7
ATOM	1410	CA	ILE	A	177	24.860	22.144	97.505	1.00	16.11	6
ATOM	1411	C	ILE	A	177	24.091	22.054	98.836	1.00	15.68	6
ATOM	1412	O	ILE	A	177	23.828	20.927	99.235	1.00	16.63	8
ATOM	1413	CB	ILE	A	177	23.940	21.719	96.337	1.00	13.12	6
ATOM	1414	CG1	ILE	A	177	24.667	22.007	94.985	1.00	23.05	6
ATOM	1415	CG2	ILE	A	177	22.629	22.507	96.345	1.00	10.60	6
ATOM	1416	CD1	ILE	A	177	23.895	21.379	93.831	1.00	18.83	6
ATOM	1417	N	TYR	A	178	23.727	23.189	99.412	1.00	16.89	7
ATOM	1418	CA	TYR	A	178	23.017	23.203	100.683	1.00	16.31	6
ATOM	1419	C	TYR	A	178	21.599	23.740	100.577	1.00	15.83	6
ATOM	1420	O	TYR	A	178	21.432	24.909	100.222	1.00	18.10	8
ATOM	1421	CB	TYR	A	178	23.741	24.169	101.700	1.00	14.58	6
ATOM	1422	CG	TYR	A	178	25.224	23.899	101.776	1.00	18.47	6
ATOM	1423	CD1	TYR	A	178	25.713	22.976	102.686	1.00	19.67	6
ATOM	1424	CD2	TYR	A	178	26.159	24.534	100.966	1.00	21.12	6
ATOM	1425	CE1	TYR	A	178	27.055	22.694	102.824	1.00	19.76	6
ATOM	1426	CE2	TYR	A	178	27.519	24.286	101.077	1.00	22.80	6
ATOM	1427	CZ	TYR	A	178	27.959	23.343	102.006	1.00	23.23	6
ATOM	1428	OH	TYR	A	178	29.301	23.045	102.135	1.00	22.73	8

ATOM	1429	N	LYS	A	179	20.602	22.972	100.926	1.00	13.95	7
ATOM	1430	CA	LYS	A	179	19.229	23.456	101.016	1.00	15.91	6
ATOM	1431	C	LYS	A	179	18.979	23.979	102.441	1.00	18.32	6
ATOM	1432	O	LYS	A	179	19.390	23.307	103.414	1.00	18.01	8
ATOM	1433	CB	LYS	A	179	18.376	22.221	100.747	1.00	13.64	6
ATOM	1434	CG	LYS	A	179	16.890	22.544	100.722	1.00	14.01	6
ATOM	1435	CD	LYS	A	179	16.131	21.266	100.433	1.00	19.62	6
ATOM	1436	CE	LYS	A	179	16.270	20.192	101.483	1.00	16.36	6
ATOM	1437	NZ	LYS	A	179	15.227	19.138	101.260	1.00	18.20	7
ATOM	1438	N	PHE	A	180	18.404	25.143	102.594	1.00	17.85	7
ATOM	1439	CA	PHE	A	180	18.139	25.718	103.920	1.00	20.43	6
ATOM	1440	C	PHE	A	180	16.959	25.011	104.598	1.00	21.42	6
ATOM	1441	O	PHE	A	180	15.986	24.567	103.955	1.00	21.98	8
ATOM	1442	CB	PHE	A	180	17.857	27.203	103.751	1.00	10.99	6
ATOM	1443	CG	PHE	A	180	19.005	28.092	103.351	1.00	11.27	6
ATOM	1444	CD1	PHE	A	180	20.321	27.717	103.401	1.00	14.93	6
ATOM	1445	CD2	PHE	A	180	18.756	29.383	102.939	1.00	10.08	6
ATOM	1446	CE1	PHE	A	180	21.351	28.581	103.081	1.00	14.29	6
ATOM	1447	CE2	PHE	A	180	19.747	30.272	102.622	1.00	15.90	6
ATOM	1448	CZ	PHE	A	180	21.064	29.862	102.681	1.00	17.25	6
ATOM	1449	N	ARG	A	181	17.043	24.843	105.932	1.00	22.19	7
ATOM	1450	CA	ARG	A	181	15.904	24.275	106.697	1.00	20.04	6
ATOM	1451	C	ARG	A	181	14.961	25.397	107.043	1.00	18.91	6
ATOM	1452	O	ARG	A	181	15.339	26.564	107.084	1.00	20.54	8
ATOM	1453	CB	ARG	A	181	16.414	23.589	107.966	1.00	20.73	6
ATOM	1454	CG	ARG	A	181	17.128	22.268	107.640	1.00	15.66	6
ATOM	1455	CD	ARG	A	181	16.076	21.326	107.101	1.00	19.94	6
ATOM	1456	NE	ARG	A	181	16.565	19.949	107.059	1.00	22.50	7
ATOM	1457	CZ	ARG	A	181	16.137	19.042	106.182	1.00	31.69	6
ATOM	1458	NH1	ARG	A	181	15.269	19.370	105.222	1.00	29.02	7
ATOM	1459	NH2	ARG	A	181	16.662	17.820	106.294	1.00	31.49	7
ATOM	1460	N	GLY	A	182	13.697	25.174	107.337	1.00	20.46	7
ATOM	1461	CA	GLY	A	182	12.859	26.345	107.675	1.00	21.18	6
ATOM	1462	C	GLY	A	182	11.452	25.903	107.256	1.00	24.79	6
ATOM	1463	O	GLY	A	182	11.256	24.957	106.480	1.00	24.88	8
ATOM	1464	N	ASP	A	183	10.517	26.696	107.733	1.00	24.99	7
ATOM	1465	CA	ASP	A	183	9.120	26.406	107.485	1.00	28.22	6
ATOM	1466	C	ASP	A	183	8.757	26.520	106.019	1.00	26.65	6
ATOM	1467	O	ASP	A	183	8.862	27.603	105.453	1.00	27.60	8
ATOM	1468	CB	ASP	A	183	8.295	27.420	108.313	1.00	56.42	6
ATOM	1469	CG	ASP	A	183	7.075	26.720	108.892	1.00	70.56	6
ATOM	1470	OD1	ASP	A	183	7.167	25.516	109.215	1.00	75.66	8
ATOM	1471	OD2	ASP	A	183	6.041	27.413	109.000	1.00	82.78	8
ATOM	1472	N	GLY	A	184	8.311	25.397	105.455	1.00	26.42	7
ATOM	1473	CA	GLY	A	184	7.963	25.502	104.021	1.00	25.46	6
ATOM	1474	C	GLY	A	184	9.233	25.707	103.182	1.00	23.60	6
ATOM	1475	O	GLY	A	184	9.093	26.357	102.155	1.00	22.86	8
ATOM	1476	N	LYS	A	185	10.408	25.261	103.568	1.00	21.74	7
ATOM	1477	CA	LYS	A	185	11.597	25.434	102.800	1.00	20.76	6
ATOM	1478	C	LYS	A	185	11.734	24.222	101.877	1.00	20.17	6
ATOM	1479	O	LYS	A	185	11.787	23.114	102.397	1.00	18.16	8
ATOM	1480	CB	LYS	A	185	12.914	25.617	103.556	1.00	18.80	6
ATOM	1481	CG	LYS	A	185	13.105	27.046	103.982	1.00	18.48	6
ATOM	1482	CD	LYS	A	185	13.381	27.981	102.791	1.00	17.41	6
ATOM	1483	CE	LYS	A	185	13.007	29.383	103.057	1.00	14.81	6
ATOM	1484	NZ	LYS	A	185	13.385	30.535	102.205	1.00	19.47	7
ATOM	1485	N	ALA	A	186	11.700	24.509	100.556	1.00	17.48	7
ATOM	1486	CA	ALA	A	186	11.900	23.396	99.598	1.00	15.05	6
ATOM	1487	C	ALA	A	186	12.364	23.870	98.205	1.00	14.06	6
ATOM	1488	O	ALA	A	186	12.093	25.012	97.975	1.00	10.55	8
ATOM	1489	CB	ALA	A	186	10.652	22.577	99.407	1.00	16.40	6
ATOM	1490	N	TRP	A	187	12.960	23.127	97.305	1.00	12.54	7
ATOM	1491	CA	TRP	A	187	13.290	23.693	95.969	1.00	13.33	6
ATOM	1492	C	TRP	A	187	11.974	24.064	95.287	1.00	9.00	6
ATOM	1493	O	TRP	A	187	10.955	23.363	95.437	1.00	8.49	8
ATOM	1494	CB	TRP	A	187	13.985	22.535	95.204	1.00	8.05	6
ATOM	1495	CG	TRP	A	187	15.346	22.215	95.750	1.00	5.34	6
ATOM	1496	CD1	TRP	A	187	15.790	20.949	96.045	1.00	8.08	6
ATOM	1497	CD2	TRP	A	187	16.448	23.098	96.034	1.00	2.71	6
ATOM	1498	NE1	TRP	A	187	17.107	20.983	96.478	1.00	6.12	7
ATOM	1499	CE2	TRP	A	187	17.495	22.305	96.483	1.00	6.57	6
ATOM	1500	CE3	TRP	A	187	16.632	24.476	95.993	1.00	4.12	6
ATOM	1501	CZ2	TRP	A	187	18.734	22.815	96.917	1.00	13.17	6
ATOM	1502	CZ3	TRP	A	187	17.858	24.993	96.414	1.00	4.12	6

ATOM	1503	CH2	TRP	A	187	18.895	24.160	96.868	1.00	5.94	6
ATOM	1504	N	ASP	A	188	11.914	25.155	94.566	1.00	9.68	7
ATOM	1505	CA	ASP	A	188	10.697	25.489	93.799	1.00	11.71	6
ATOM	1506	C	ASP	A	188	10.263	24.423	92.812	1.00	10.59	6
ATOM	1507	O	ASP	A	188	11.039	23.569	92.427	1.00	11.68	8
ATOM	1508	CB	ASP	A	188	10.994	26.753	93.006	1.00	11.90	6
ATOM	1509	CG	ASP	A	188	11.305	27.859	93.976	1.00	17.27	6
ATOM	1510	OD1	ASP	A	188	10.635	27.762	95.013	1.00	16.53	8
ATOM	1511	OD2	ASP	A	188	11.952	28.884	93.890	1.00	11.59	8
ATOM	1512	N	TRP	A	189	9.004	24.449	92.380	1.00	11.75	7
ATOM	1513	CA	TRP	A	189	8.438	23.580	91.387	1.00	12.99	6
ATOM	1514	C	TRP	A	189	7.283	24.372	90.753	1.00	16.78	6
ATOM	1515	O	TRP	A	189	6.721	25.203	91.463	1.00	16.54	8
ATOM	1516	CB	TRP	A	189	7.896	22.310	91.974	1.00	10.02	6
ATOM	1517	CG	TRP	A	189	7.311	21.334	90.992	1.00	17.66	6
ATOM	1518	CD1	TRP	A	189	5.989	21.060	90.752	1.00	13.06	6
ATOM	1519	CD2	TRP	A	189	8.081	20.530	90.096	1.00	15.06	6
ATOM	1520	NE1	TRP	A	189	5.911	20.076	89.785	1.00	14.69	7
ATOM	1521	CE2	TRP	A	189	7.178	19.753	89.365	1.00	14.15	6
ATOM	1522	CE3	TRP	A	189	9.445	20.394	89.843	1.00	20.41	6
ATOM	1523	CZ2	TRP	A	189	7.606	18.856	88.380	1.00	18.86	6
ATOM	1524	CZ3	TRP	A	189	9.857	19.518	88.861	1.00	15.20	6
ATOM	1525	CH2	TRP	A	189	8.945	18.745	88.151	1.00	12.94	6
ATOM	1526	N	GLU	A	190	7.110	24.333	89.431	1.00	16.45	7
ATOM	1527	CA	GLU	A	190	7.843	23.484	88.501	1.00	14.15	6
ATOM	1528	C	GLU	A	190	9.100	24.138	87.965	1.00	11.80	6
ATOM	1529	O	GLU	A	190	9.100	25.327	87.614	1.00	13.59	8
ATOM	1530	CB	GLU	A	190	6.913	23.273	87.234	1.00	18.03	6
ATOM	1531	CG	GLU	A	190	7.561	22.319	86.234	1.00	15.34	6
ATOM	1532	CD	GLU	A	190	6.635	21.758	85.154	1.00	18.34	6
ATOM	1533	OE1	GLU	A	190	5.430	22.032	85.206	1.00	11.63	8
ATOM	1534	OE2	GLU	A	190	7.130	21.043	84.278	1.00	18.43	8
ATOM	1535	N	VAL	A	191	10.153	23.337	87.867	1.00	13.43	7
ATOM	1536	CA	VAL	A	191	11.424	23.766	87.270	1.00	13.29	6
ATOM	1537	C	VAL	A	191	11.901	22.612	86.373	1.00	12.80	6
ATOM	1538	O	VAL	A	191	11.352	21.515	86.481	1.00	11.36	8
ATOM	1539	CB	VAL	A	191	12.556	24.142	88.261	1.00	15.48	6
ATOM	1540	CG1	VAL	A	191	12.244	25.469	88.971	1.00	7.91	6
ATOM	1541	CG2	VAL	A	191	12.830	23.000	89.226	1.00	9.01	6
ATOM	1542	N	ASP	A	192	12.973	22.785	85.599	1.00	13.22	7
ATOM	1543	CA	ASP	A	192	13.508	21.670	84.807	1.00	12.54	6
ATOM	1544	C	ASP	A	192	13.923	20.545	85.728	1.00	14.99	6
ATOM	1545	O	ASP	A	192	14.443	20.794	86.838	1.00	16.15	8
ATOM	1546	CB	ASP	A	192	14.729	22.142	83.981	1.00	14.61	6
ATOM	1547	CG	ASP	A	192	15.256	21.039	83.073	1.00	12.27	6
ATOM	1548	OD1	ASP	A	192	14.462	20.560	82.244	1.00	18.65	8
ATOM	1549	OD2	ASP	A	192	16.369	20.590	83.300	1.00	16.21	8
ATOM	1550	N	SER	A	193	13.822	19.303	85.306	1.00	13.14	7
ATOM	1551	CA	SER	A	193	14.074	18.138	86.116	1.00	14.27	6
ATOM	1552	C	SER	A	193	15.416	17.506	85.990	1.00	17.10	6
ATOM	1553	O	SER	A	193	15.652	16.494	86.634	1.00	18.48	8
ATOM	1554	CB	SER	A	193	12.952	17.115	85.914	1.00	26.77	6
ATOM	1555	OG	SER	A	193	12.955	16.710	84.539	1.00	29.00	8
ATOM	1556	N	GLU	A	194	16.299	18.056	85.164	1.00	18.40	7
ATOM	1557	CA	GLU	A	194	17.659	17.525	85.057	1.00	19.32	6
ATOM	1558	C	GLU	A	194	18.328	17.724	86.447	1.00	19.49	6
ATOM	1559	O	GLU	A	194	18.132	18.756	87.087	1.00	17.74	8
ATOM	1560	CB	GLU	A	194	18.473	18.378	84.026	1.00	14.77	6
ATOM	1561	CG	GLU	A	194	19.922	17.922	84.051	1.00	16.84	6
ATOM	1562	CD	GLU	A	194	20.843	18.632	83.071	1.00	36.83	6
ATOM	1563	OE1	GLU	A	194	20.344	19.311	82.168	1.00	24.18	8
ATOM	1564	OE2	GLU	A	194	22.098	18.522	83.150	1.00	39.46	8
ATOM	1565	N	ASN	A	195	19.075	16.714	86.868	1.00	18.99	7
ATOM	1566	CA	ASN	A	195	19.645	16.590	88.199	1.00	20.82	6
ATOM	1567	C	ASN	A	195	18.522	16.398	89.230	1.00	20.55	6
ATOM	1568	O	ASN	A	195	18.638	16.891	90.350	1.00	23.35	8
ATOM	1569	CB	ASN	A	195	20.448	17.811	88.628	1.00	13.63	6
ATOM	1570	CG	ASN	A	195	21.625	18.101	87.712	1.00	25.71	6
ATOM	1571	OD1	ASN	A	195	21.858	19.253	87.318	1.00	28.78	8
ATOM	1572	ND2	ASN	A	195	22.329	17.039	87.388	1.00	19.03	7
ATOM	1573	N	GLY	A	196	17.370	15.874	88.887	1.00	18.63	7
ATOM	1574	CA	GLY	A	196	16.252	15.689	89.806	1.00	15.28	6
ATOM	1575	C	GLY	A	196	15.410	16.927	89.909	1.00	13.09	6
ATOM	1576	O	GLY	A	196	14.229	16.925	89.587	1.00	15.77	8

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ATOM   1577  N   ASN A 197      15.969  18.061  90.274  1.00 13.90   7
ATOM   1578  CA  ASN A 197      15.287  19.333  90.380  1.00 14.20   6
ATOM   1579  C   ASN A 197      16.363  20.345  90.053  1.00 13.47   6
ATOM   1580  O   ASN A 197      17.331  20.320  90.804  1.00 14.96   8
ATOM   1581  CB  ASN A 197      14.726  19.574  91.793  1.00 11.86   6
ATOM   1582  CG  ASN A 197      14.107  20.947  91.973  1.00  9.73   6
ATOM   1583  OD1 ASN A 197      14.848  21.955  91.990  1.00  9.97   8
ATOM   1584  ND2 ASN A 197      12.788  21.059  92.111  1.00  7.43   7
ATOM   1585  N   TYR A 198      16.193  21.192  89.041  1.00 11.73   7
ATOM   1586  CA  TYR A 198      17.310  22.082  88.700  1.00 13.36   6
ATOM   1587  C   TYR A 198      17.075  23.499  89.136  1.00 10.84   6
ATOM   1588  O   TYR A 198      17.564  24.522  88.641  1.00 10.06   8
ATOM   1589  CB  TYR A 198      17.596  22.046  87.168  1.00 13.55   6
ATOM   1590  CG  TYR A 198      19.009  22.282  86.714  1.00 14.34   6
ATOM   1591  CD1 TYR A 198      20.016  22.855  87.492  1.00 13.73   6
ATOM   1592  CD2 TYR A 198      19.362  21.779  85.436  1.00 11.59   6
ATOM   1593  CE1 TYR A 198      21.321  23.013  87.038  1.00 13.97   6
ATOM   1594  CE2 TYR A 198      20.642  21.931  84.962  1.00 11.79   6
ATOM   1595  CZ  TYR A 198      21.597  22.557  85.726  1.00 12.84   6
ATOM   1596  OH  TYR A 198      22.864  22.651  85.193  1.00 13.95   8
ATOM   1597  N   ASP A 199      16.285  23.625  90.222  1.00 11.61   7
ATOM   1598  CA  ASP A 199      16.082  25.006  90.757  1.00  6.05   6
ATOM   1599  C   ASP A 199      17.423  25.461  91.157  1.00  4.34   6
ATOM   1600  O   ASP A 199      17.699  26.673  90.916  1.00  8.06   8
ATOM   1601  CB  ASP A 199      15.078  24.839  91.949  1.00 11.81   6
ATOM   1602  CG  ASP A 199      14.739  26.085  92.655  1.00 21.25   6
ATOM   1603  OD1 ASP A 199      14.885  27.212  92.094  1.00  5.27   8
ATOM   1604  OD2 ASP A 199      14.254  26.128  93.823  1.00 17.12   8
ATOM   1605  N   TYR A 200      18.435  24.875  91.732  1.00  7.57   7
ATOM   1606  CA  TYR A 200      19.631  25.578  92.190  1.00  7.08   6
ATOM   1607  C   TYR A 200      20.625  25.573  90.999  1.00  9.10   6
ATOM   1608  O   TYR A 200      20.853  24.522  90.402  1.00 10.97   8
ATOM   1609  CB  TYR A 200      20.304  24.756  93.389  1.00  8.94   6
ATOM   1610  CG  TYR A 200      21.515  25.582  93.795  1.00 10.82   6
ATOM   1611  CD1 TYR A 200      21.350  26.662  94.650  1.00  8.86   6
ATOM   1612  CD2 TYR A 200      22.779  25.369  93.222  1.00 10.54   6
ATOM   1613  CE1 TYR A 200      22.420  27.501  94.957  1.00  9.83   6
ATOM   1614  CE2 TYR A 200      23.827  26.217  93.513  1.00 10.73   6
ATOM   1615  CZ  TYR A 200      23.645  27.284  94.377  1.00 11.56   6
ATOM   1616  OH  TYR A 200      24.685  28.169  94.657  1.00  8.88   8
ATOM   1617  N   LEU A 201      21.244  26.706  90.779  1.00 10.58   7
ATOM   1618  CA  LEU A 201      22.265  26.813  89.730  1.00  9.44   6
ATOM   1619  C   LEU A 201      23.521  27.412  90.320  1.00  6.35   6
ATOM   1620  O   LEU A 201      24.590  26.823  90.208  1.00  9.88   8
ATOM   1621  CB  LEU A 201      21.772  27.860  88.683  1.00 10.07   6
ATOM   1622  CG  LEU A 201      22.848  28.119  87.567  1.00  8.98   6
ATOM   1623  CD1 LEU A 201      23.129  26.765  86.878  1.00 11.75   6
ATOM   1624  CD2 LEU A 201      22.175  29.082  86.583  1.00 11.24   6
ATOM   1625  N   MET A 202      23.451  28.635  90.847  1.00  8.21   7
ATOM   1626  CA  MET A 202      24.653  29.206  91.458  1.00  9.75   6
ATOM   1627  C   MET A 202      24.369  30.318  92.473  1.00  7.69   6
ATOM   1628  O   MET A 202      23.255  30.785  92.622  1.00  9.81   8
ATOM   1629  CB  MET A 202      25.514  29.878  90.308  1.00 12.10   6
ATOM   1630  CG  MET A 202      24.611  30.882  89.567  1.00 10.97   6
ATOM   1631  SD  MET A 202      25.654  31.671  88.182  1.00 21.46  16
ATOM   1632  CE  MET A 202      26.028  30.134  87.333  1.00 16.25   6
ATOM   1633  N   TYR A 203      25.406  30.811  93.167  1.00 11.04   7
ATOM   1634  CA  TYR A 203      25.192  31.876  94.200  1.00 11.53   6
ATOM   1635  C   TYR A 203      24.131  31.534  95.262  1.00 10.29   6
ATOM   1636  O   TYR A 203      23.917  30.362  95.584  1.00 11.59   8
ATOM   1637  CB  TYR A 203      24.766  33.119  93.372  1.00 13.34   6
ATOM   1638  CG  TYR A 203      26.015  33.736  92.767  1.00 19.37   6
ATOM   1639  CD1 TYR A 203      27.047  34.149  93.618  1.00 20.46   6
ATOM   1640  CD2 TYR A 203      26.203  33.879  91.379  1.00 17.82   6
ATOM   1641  CE1 TYR A 203      28.208  34.722  93.123  1.00 22.58   6
ATOM   1642  CE2 TYR A 203      27.365  34.450  90.885  1.00 19.42   6
ATOM   1643  CZ  TYR A 203      28.366  34.856  91.734  1.00 24.00   6
ATOM   1644  OH  TYR A 203      29.553  35.431  91.281  1.00 23.69   8
ATOM   1645  N   ALA A 204      23.329  32.520  95.669  1.00 11.94   7
ATOM   1646  CA  ALA A 204      22.206  32.292  96.570  1.00 10.93   6
ATOM   1647  C   ALA A 204      20.929  32.206  95.736  1.00 10.49   6
ATOM   1648  O   ALA A 204      20.477  33.172  95.131  1.00  9.71   8
ATOM   1649  CB  ALA A 204      22.068  33.473  97.589  1.00  9.30   6
ATOM   1650  N   ASP A 205      20.254  31.078  95.797  1.00  9.32   7
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ATOM	1651	CA	ASP	A	205	19.056	30.845	95.020	1.00	9.79	6
ATOM	1652	C	ASP	A	205	17.797	31.470	95.540	1.00	14.23	6
ATOM	1653	O	ASP	A	205	17.369	31.145	96.701	1.00	13.37	8
ATOM	1654	CB	ASP	A	205	18.907	29.308	95.034	1.00	11.48	6
ATOM	1655	CG	ASP	A	205	17.997	29.001	93.864	1.00	17.50	6
ATOM	1656	OD1	ASP	A	205	18.477	29.186	92.710	1.00	14.51	8
ATOM	1657	OD2	ASP	A	205	16.831	28.644	94.068	1.00	7.75	8
ATOM	1658	N	VAL	A	206	17.146	32.307	94.734	1.00	11.30	7
ATOM	1659	CA	VAL	A	206	15.945	32.995	95.132	1.00	9.20	6
ATOM	1660	C	VAL	A	206	14.815	32.084	95.466	1.00	12.62	6
ATOM	1661	O	VAL	A	206	14.566	31.138	94.683	1.00	11.57	8
ATOM	1662	CB	VAL	A	206	15.540	34.120	94.202	1.00	13.76	6
ATOM	1663	CG1	VAL	A	206	14.245	34.804	94.653	1.00	13.90	6
ATOM	1664	CG2	VAL	A	206	16.684	35.101	94.179	1.00	11.36	6
ATOM	1665	N	ASP	A	207	14.092	32.323	96.581	1.00	10.69	7
ATOM	1666	CA	ASP	A	207	12.992	31.406	96.913	1.00	11.90	6
ATOM	1667	C	ASP	A	207	11.718	31.981	96.310	1.00	13.90	6
ATOM	1668	O	ASP	A	207	11.131	32.928	96.871	1.00	12.71	8
ATOM	1669	CB	ASP	A	207	12.836	31.346	98.443	1.00	15.17	6
ATOM	1670	CG	ASP	A	207	11.726	30.503	98.952	1.00	22.74	6
ATOM	1671	OD1	ASP	A	207	10.964	29.956	98.108	1.00	19.17	8
ATOM	1672	OD2	ASP	A	207	11.521	30.286	100.169	1.00	20.54	8
ATOM	1673	N	MET	A	208	11.225	31.367	95.216	1.00	13.35	7
ATOM	1674	CA	MET	A	208	10.079	31.963	94.507	1.00	15.70	6
ATOM	1675	C	MET	A	208	8.768	31.646	95.201	1.00	17.50	6
ATOM	1676	O	MET	A	208	7.700	32.148	94.848	1.00	18.55	8
ATOM	1677	CB	MET	A	208	9.976	31.477	93.030	1.00	17.03	6
ATOM	1678	CG	MET	A	208	11.197	31.966	92.202	1.00	12.28	6
ATOM	1679	SD	MET	A	208	11.381	33.711	92.110	1.00	23.21	16
ATOM	1680	CE	MET	A	208	12.944	34.091	91.430	1.00	20.00	6
ATOM	1681	N	ASP	A	209	8.827	30.719	96.163	1.00	16.74	7
ATOM	1682	CA	ASP	A	209	7.640	30.466	96.979	1.00	20.55	6
ATOM	1683	C	ASP	A	209	7.425	31.556	98.040	1.00	19.95	6
ATOM	1684	O	ASP	A	209	6.318	31.628	98.566	1.00	21.59	8
ATOM	1685	CB	ASP	A	209	7.690	29.136	97.686	1.00	17.97	6
ATOM	1686	CG	ASP	A	209	7.557	27.883	96.835	1.00	31.63	6
ATOM	1687	OD1	ASP	A	209	6.800	28.001	95.847	1.00	31.19	8
ATOM	1688	OD2	ASP	A	209	8.251	26.896	97.233	1.00	32.40	8
ATOM	1689	N	HIS	A	210	8.380	32.411	98.375	1.00	20.52	7
ATOM	1690	CA	HIS	A	210	8.186	33.429	99.385	1.00	18.61	6
ATOM	1691	C	HIS	A	210	7.420	34.626	98.888	1.00	19.89	6
ATOM	1692	O	HIS	A	210	7.830	35.435	98.052	1.00	19.58	8
ATOM	1693	CB	HIS	A	210	9.561	33.808	99.938	1.00	19.59	6
ATOM	1694	CG	HIS	A	210	9.481	34.653	101.178	1.00	27.83	6
ATOM	1695	ND1	HIS	A	210	9.945	34.202	102.414	1.00	32.20	7
ATOM	1696	CD2	HIS	A	210	8.970	35.884	101.394	1.00	20.96	6
ATOM	1697	CE1	HIS	A	210	9.736	35.153	103.327	1.00	23.85	6
ATOM	1698	NE2	HIS	A	210	9.169	36.180	102.716	1.00	34.38	7
ATOM	1699	N	PRO	A	211	6.289	34.918	99.532	1.00	22.38	7
ATOM	1700	CA	PRO	A	211	5.376	35.976	99.137	1.00	21.41	6
ATOM	1701	C	PRO	A	211	6.026	37.320	99.125	1.00	22.35	6
ATOM	1702	O	PRO	A	211	5.636	38.134	98.241	1.00	24.85	8
ATOM	1703	CB	PRO	A	211	4.089	35.908	99.974	1.00	22.59	6
ATOM	1704	CG	PRO	A	211	4.546	34.989	101.059	1.00	22.80	6
ATOM	1705	CD	PRO	A	211	5.670	34.076	100.574	1.00	21.75	6
ATOM	1706	N	GLU	A	212	7.058	37.600	99.904	1.00	19.19	7
ATOM	1707	CA	GLU	A	212	7.541	38.984	99.779	1.00	20.41	6
ATOM	1708	C	GLU	A	212	8.578	39.110	98.673	1.00	19.26	6
ATOM	1709	O	GLU	A	212	8.905	40.204	98.189	1.00	17.10	8
ATOM	1710	CB	GLU	A	212	7.888	39.558	101.141	1.00	29.62	6
ATOM	1711	CG	GLU	A	212	9.158	39.175	101.818	1.00	44.14	6
ATOM	1712	CD	GLU	A	212	9.381	39.713	103.232	1.00	53.86	6
ATOM	1713	OE1	GLU	A	212	8.401	40.209	103.827	1.00	61.45	8
ATOM	1714	OE2	GLU	A	212	10.514	39.666	103.781	1.00	32.90	8
ATOM	1715	N	VAL	A	213	9.160	37.972	98.313	1.00	19.73	7
ATOM	1716	CA	VAL	A	213	10.109	37.977	97.173	1.00	20.44	6
ATOM	1717	C	VAL	A	213	9.278	38.201	95.886	1.00	18.35	6
ATOM	1718	O	VAL	A	213	9.541	39.130	95.138	1.00	18.56	8
ATOM	1719	CB	VAL	A	213	10.799	36.605	97.149	1.00	21.92	6
ATOM	1720	CG1	VAL	A	213	11.469	36.366	95.797	1.00	22.74	6
ATOM	1721	CG2	VAL	A	213	11.799	36.623	98.297	1.00	25.64	6
ATOM	1722	N	VAL	A	214	8.200	37.480	95.732	1.00	18.19	7
ATOM	1723	CA	VAL	A	214	7.316	37.633	94.592	1.00	20.51	6
ATOM	1724	C	VAL	A	214	6.928	39.081	94.441	1.00	23.51	6

ATOM	1725	O	VAL	A	214	7.049	39.704	93.356	1.00	24.81	8
ATOM	1726	CB	VAL	A	214	6.053	36.773	94.667	1.00	22.40	6
ATOM	1727	CG1	VAL	A	214	5.078	37.088	93.544	1.00	32.00	6
ATOM	1728	CG2	VAL	A	214	6.399	35.293	94.639	1.00	21.53	6
ATOM	1729	N	ASN	A	215	6.490	39.701	95.540	1.00	22.11	7
ATOM	1730	CA	ASN	A	215	6.067	41.089	95.499	1.00	20.65	6
ATOM	1731	C	ASN	A	215	7.195	42.036	95.194	1.00	19.24	6
ATOM	1732	O	ASN	A	215	7.027	43.008	94.446	1.00	19.17	8
ATOM	1733	CB	ASN	A	215	5.269	41.478	96.761	1.00	35.08	6
ATOM	1734	CG	ASN	A	215	3.881	40.869	96.604	1.00	35.00	6
ATOM	1735	OD1	ASN	A	215	3.164	41.271	95.689	1.00	58.96	8
ATOM	1736	ND2	ASN	A	215	3.472	39.903	97.402	1.00	52.78	7
ATOM	1737	N	GLU	A	216	8.377	41.768	95.716	1.00	17.10	7
ATOM	1738	CA	GLU	A	216	9.466	42.704	95.478	1.00	17.74	6
ATOM	1739	C	GLU	A	216	9.882	42.652	93.964	1.00	17.58	6
ATOM	1740	O	GLU	A	216	10.301	43.672	93.415	1.00	13.53	8
ATOM	1741	CB	GLU	A	216	10.640	42.358	96.358	1.00	17.67	6
ATOM	1742	CG	GLU	A	216	11.948	43.068	96.105	1.00	28.42	6
ATOM	1743	CD	GLU	A	216	11.838	44.580	96.017	1.00	23.80	6
ATOM	1744	OE1	GLU	A	216	10.776	45.098	96.371	1.00	30.40	8
ATOM	1745	OE2	GLU	A	216	12.804	45.270	95.617	1.00	31.36	8
ATOM	1746	N	LEU	A	217	9.935	41.444	93.443	1.00	17.03	7
ATOM	1747	CA	LEU	A	217	10.411	41.180	92.084	1.00	19.84	6
ATOM	1748	C	LEU	A	217	9.412	41.774	91.079	1.00	20.75	6
ATOM	1749	O	LEU	A	217	9.832	42.493	90.189	1.00	21.48	8
ATOM	1750	CB	LEU	A	217	10.653	39.700	91.932	1.00	11.86	6
ATOM	1751	CG	LEU	A	217	12.078	39.172	91.888	1.00	19.48	6
ATOM	1752	CD1	LEU	A	217	13.209	39.933	92.505	1.00	16.47	6
ATOM	1753	CD2	LEU	A	217	12.099	37.703	92.249	1.00	12.39	6
ATOM	1754	N	ARG	A	218	8.112	41.741	91.333	1.00	21.19	7
ATOM	1755	CA	ARG	A	218	7.147	42.417	90.508	1.00	22.98	6
ATOM	1756	C	ARG	A	218	7.344	43.914	90.478	1.00	25.87	6
ATOM	1757	O	ARG	A	218	7.189	44.576	89.450	1.00	25.87	8
ATOM	1758	CB	ARG	A	218	5.699	42.152	90.944	1.00	18.95	6
ATOM	1759	CG	ARG	A	218	5.394	40.694	90.636	1.00	10.41	6
ATOM	1760	CD	ARG	A	218	3.962	40.385	91.065	1.00	12.60	6
ATOM	1761	NE	ARG	A	218	3.837	38.941	90.836	1.00	23.07	7
ATOM	1762	CZ	ARG	A	218	2.659	38.338	90.698	1.00	30.77	6
ATOM	1763	NH1	ARG	A	218	1.556	39.063	90.731	1.00	41.73	7
ATOM	1764	NH2	ARG	A	218	2.630	37.025	90.508	1.00	34.53	7
ATOM	1765	N	ARG	A	219	7.633	44.448	91.669	1.00	26.91	7
ATOM	1766	CA	ARG	A	219	7.809	45.891	91.779	1.00	25.88	6
ATOM	1767	C	ARG	A	219	9.097	46.275	91.108	1.00	23.84	6
ATOM	1768	O	ARG	A	219	9.172	47.352	90.497	1.00	23.41	8
ATOM	1769	CB	ARG	A	219	7.666	46.341	93.233	1.00	37.02	6
ATOM	1770	CG	ARG	A	219	8.704	47.268	93.798	1.00	55.61	6
ATOM	1771	CD	ARG	A	219	8.297	48.719	93.748	1.00	79.18	6
ATOM	1772	NE	ARG	A	219	9.295	49.624	93.196	1.00	96.62	7
ATOM	1773	CZ	ARG	A	219	9.203	50.951	93.059	1.00	104.91	6
ATOM	1774	NH1	ARG	A	219	8.132	51.621	93.451	1.00	111.12	7
ATOM	1775	NH2	ARG	A	219	10.236	51.611	92.543	1.00	106.48	7
ATOM	1776	N	TRP	A	220	10.149	45.464	91.279	1.00	21.44	7
ATOM	1777	CA	TRP	A	220	11.404	45.840	90.635	1.00	21.83	6
ATOM	1778	C	TRP	A	220	11.138	45.866	89.093	1.00	21.82	6
ATOM	1779	O	TRP	A	220	11.533	46.795	88.420	1.00	21.38	8
ATOM	1780	CB	TRP	A	220	12.599	44.973	91.041	1.00	13.52	6
ATOM	1781	CG	TRP	A	220	13.727	45.208	90.059	1.00	21.56	6
ATOM	1782	CD1	TRP	A	220	14.642	46.203	90.022	1.00	22.24	6
ATOM	1783	CD2	TRP	A	220	13.998	44.369	88.926	1.00	14.67	6
ATOM	1784	NE1	TRP	A	220	15.508	46.024	88.940	1.00	16.13	7
ATOM	1785	CE2	TRP	A	220	15.125	44.887	88.286	1.00	21.21	6
ATOM	1786	CE3	TRP	A	220	13.387	43.195	88.444	1.00	25.00	6
ATOM	1787	CZ2	TRP	A	220	15.653	44.325	87.109	1.00	17.63	6
ATOM	1788	CZ3	TRP	A	220	13.914	42.622	87.289	1.00	23.47	6
ATOM	1789	CH2	TRP	A	220	15.016	43.208	86.660	1.00	20.65	6
ATOM	1790	N	GLY	A	221	10.446	44.915	88.545	1.00	20.99	7
ATOM	1791	CA	GLY	A	221	9.967	44.762	87.199	1.00	24.79	6
ATOM	1792	C	GLY	A	221	9.384	46.035	86.595	1.00	24.57	6
ATOM	1793	O	GLY	A	221	9.942	46.595	85.643	1.00	22.41	8
ATOM	1794	N	GLU	A	222	8.413	46.611	87.304	1.00	25.64	7
ATOM	1795	CA	GLU	A	222	7.801	47.881	86.928	1.00	23.20	6
ATOM	1796	C	GLU	A	222	8.796	49.012	86.978	1.00	24.03	6
ATOM	1797	O	GLU	A	222	8.879	49.889	86.109	1.00	24.03	8
ATOM	1798	CB	GLU	A	222	6.774	48.279	87.985	1.00	22.11	6

ATOM	1799	CG	GLU	A	222	5.405	47.683	87.787	1.00	40.46	6
ATOM	1800	CD	GLU	A	222	4.516	48.274	88.906	1.00	50.60	6
ATOM	1801	OE1	GLU	A	222	4.478	49.528	88.896	1.00	48.94	8
ATOM	1802	OE2	GLU	A	222	3.974	47.454	89.687	1.00	46.61	8
ATOM	1803	N	TRP	A	223	9.563	49.070	88.069	1.00	22.02	7
ATOM	1804	CA	TRP	A	223	10.507	50.196	88.175	1.00	22.34	6
ATOM	1805	C	TRP	A	223	11.543	50.187	87.046	1.00	24.50	6
ATOM	1806	O	TRP	A	223	11.997	51.232	86.571	1.00	24.43	8
ATOM	1807	CB	TRP	A	223	11.280	49.965	89.495	1.00	23.32	6
ATOM	1808	CG	TRP	A	223	12.332	50.997	89.722	1.00	12.36	6
ATOM	1809	CD1	TRP	A	223	12.096	52.257	90.194	1.00	12.65	6
ATOM	1810	CD2	TRP	A	223	13.730	50.898	89.482	1.00	14.74	6
ATOM	1811	NE1	TRP	A	223	13.307	52.928	90.308	1.00	14.71	7
ATOM	1812	CE2	TRP	A	223	14.307	52.121	89.855	1.00	13.39	6
ATOM	1813	CE3	TRP	A	223	14.567	49.910	88.959	1.00	17.71	6
ATOM	1814	CZ2	TRP	A	223	15.675	52.408	89.749	1.00	18.37	6
ATOM	1815	CZ3	TRP	A	223	15.913	50.186	88.851	1.00	17.26	6
ATOM	1816	CH2	TRP	A	223	16.469	51.401	89.250	1.00	21.97	6
ATOM	1817	N	TYR	A	224	12.142	49.020	86.780	1.00	22.93	7
ATOM	1818	CA	TYR	A	224	13.196	48.885	85.759	1.00	22.60	6
ATOM	1819	C	TYR	A	224	12.620	49.271	84.357	1.00	20.78	6
ATOM	1820	O	TYR	A	224	13.238	50.024	83.644	1.00	20.47	8
ATOM	1821	CB	TYR	A	224	13.618	47.428	85.695	1.00	23.16	6
ATOM	1822	CG	TYR	A	224	14.692	46.916	84.770	1.00	21.12	6
ATOM	1823	CD1	TYR	A	224	15.898	47.567	84.607	1.00	20.00	6
ATOM	1824	CD2	TYR	A	224	14.491	45.716	84.087	1.00	20.21	6
ATOM	1825	CE1	TYR	A	224	16.909	47.056	83.812	1.00	19.68	6
ATOM	1826	CE2	TYR	A	224	15.489	45.203	83.293	1.00	19.23	6
ATOM	1827	CZ	TYR	A	224	16.668	45.880	83.143	1.00	19.19	6
ATOM	1828	OH	TYR	A	224	17.629	45.330	82.336	1.00	20.77	8
ATOM	1829	N	THR	A	225	11.445	48.786	84.040	1.00	21.36	7
ATOM	1830	CA	THR	A	225	10.767	49.090	82.822	1.00	26.04	6
ATOM	1831	C	THR	A	225	10.585	50.602	82.698	1.00	30.55	6
ATOM	1832	O	THR	A	225	11.111	51.175	81.742	1.00	30.61	8
ATOM	1833	CB	THR	A	225	9.427	48.372	82.725	1.00	23.52	6
ATOM	1834	OG1	THR	A	225	9.726	46.984	82.687	1.00	26.82	8
ATOM	1835	CG2	THR	A	225	8.707	48.745	81.418	1.00	31.34	6
ATOM	1836	N	ASN	A	226	9.974	51.244	83.704	1.00	31.50	7
ATOM	1837	CA	ASN	A	226	9.766	52.676	83.718	1.00	31.16	6
ATOM	1838	C	ASN	A	226	11.026	53.473	83.808	1.00	32.12	6
ATOM	1839	O	ASN	A	226	11.188	54.509	83.143	1.00	33.63	8
ATOM	1840	CB	ASN	A	226	8.840	53.077	84.891	1.00	29.40	6
ATOM	1841	CG	ASN	A	226	7.454	52.571	84.563	1.00	30.15	6
ATOM	1842	OD1	ASN	A	226	7.237	52.230	83.399	1.00	39.98	8
ATOM	1843	ND2	ASN	A	226	6.524	52.463	85.483	1.00	41.24	7
ATOM	1844	N	THR	A	227	11.990	53.011	84.593	1.00	33.58	7
ATOM	1845	CA	THR	A	227	13.179	53.871	84.732	1.00	34.37	6
ATOM	1846	C	THR	A	227	13.950	54.002	83.429	1.00	34.33	6
ATOM	1847	O	THR	A	227	14.624	55.022	83.187	1.00	33.24	8
ATOM	1848	CB	THR	A	227	13.993	53.466	85.970	1.00	33.49	6
ATOM	1849	OG1	THR	A	227	15.097	54.351	86.173	1.00	47.56	8
ATOM	1850	CG2	THR	A	227	14.627	52.095	85.722	1.00	53.36	6
ATOM	1851	N	LEU	A	228	13.989	52.951	82.599	1.00	34.32	7
ATOM	1852	CA	LEU	A	228	14.809	52.959	81.387	1.00	31.35	6
ATOM	1853	C	LEU	A	228	13.954	52.937	80.121	1.00	32.12	6
ATOM	1854	O	LEU	A	228	14.487	52.726	79.028	1.00	33.07	8
ATOM	1855	CB	LEU	A	228	15.697	51.732	81.399	1.00	19.92	6
ATOM	1856	CG	LEU	A	228	16.872	51.635	82.343	1.00	28.23	6
ATOM	1857	CD1	LEU	A	228	17.626	50.347	82.084	1.00	22.94	6
ATOM	1858	CD2	LEU	A	228	17.793	52.837	82.321	1.00	28.36	6
ATOM	1859	N	ASN	A	229	12.652	53.106	80.259	1.00	30.09	7
ATOM	1860	CA	ASN	A	229	11.717	53.072	79.147	1.00	31.01	6
ATOM	1861	C	ASN	A	229	11.965	51.870	78.238	1.00	29.35	6
ATOM	1862	O	ASN	A	229	12.074	52.027	77.024	1.00	29.88	8
ATOM	1863	CB	ASN	A	229	11.753	54.401	78.392	1.00	35.74	6
ATOM	1864	CG	ASN	A	229	10.564	54.629	77.480	1.00	44.56	6
ATOM	1865	OD1	ASN	A	229	9.494	54.024	77.526	1.00	48.29	8
ATOM	1866	ND2	ASN	A	229	10.739	55.572	76.547	1.00	47.22	7
ATOM	1867	N	LEU	A	230	11.969	50.651	78.747	1.00	26.34	7
ATOM	1868	CA	LEU	A	230	12.151	49.434	77.963	1.00	24.98	6
ATOM	1869	C	LEU	A	230	10.985	49.012	77.078	1.00	23.59	6
ATOM	1870	O	LEU	A	230	9.815	49.179	77.394	1.00	24.27	8
ATOM	1871	CB	LEU	A	230	12.478	48.268	78.919	1.00	25.61	6
ATOM	1872	CG	LEU	A	230	13.741	48.428	79.759	1.00	18.62	6

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ATOM   1873  CD1 LEU A 230      14.014  47.133  80.513  1.00 27.61   6
ATOM   1874  CD2 LEU A 230      14.967  48.696  78.877  1.00 28.13   6
ATOM   1875  N   ASP A 231      11.278  48.365  75.924  1.00 21.79   7
ATOM   1876  CA  ASP A 231      10.246  47.835  75.043  1.00 20.65   6
ATOM   1877  C   ASP A 231      10.110  46.339  75.292  1.00 20.30   6
ATOM   1878  O   ASP A 231       9.103  45.756  74.891  1.00 20.54   8
ATOM   1879  CB  ASP A 231      10.618  48.043  73.528  1.00 21.94   6
ATOM   1880  CG  ASP A 231      10.901  49.525  73.367  1.00 13.94   6
ATOM   1881  OD1 ASP A 231       9.942  50.286  73.503  1.00 24.69   8
ATOM   1882  OD2 ASP A 231      12.054  49.949  73.183  1.00 20.63   8
ATOM   1883  N   GLY A 232      11.122  45.727  75.946  1.00 18.68   7
ATOM   1884  CA  GLY A 232      10.932  44.300  76.199  1.00 16.67   6
ATOM   1885  C   GLY A 232      12.089  43.727  76.991  1.00 15.71   6
ATOM   1886  O   GLY A 232      12.953  44.439  77.478  1.00 16.01   8
ATOM   1887  N   PHE A 233      12.086  42.394  77.129  1.00 14.55   7
ATOM   1888  CA  PHE A 233      13.180  41.803  77.919  1.00 13.86   6
ATOM   1889  C   PHE A 233      13.750  40.550  77.278  1.00 12.54   6
ATOM   1890  O   PHE A 233      13.006  39.820  76.615  1.00 12.13   8
ATOM   1891  CB  PHE A 233      12.440  41.134  79.160  1.00 12.94   6
ATOM   1892  CG  PHE A 233      11.624  42.107  79.987  1.00  4.98   6
ATOM   1893  CD1 PHE A 233      12.212  43.177  80.588  1.00  6.42   6
ATOM   1894  CD2 PHE A 233      10.279  41.877  80.166  1.00 15.69   6
ATOM   1895  CE1 PHE A 233      11.475  44.065  81.375  1.00 15.76   6
ATOM   1896  CE2 PHE A 233       9.528  42.742  80.945  1.00 25.06   6
ATOM   1897  CZ  PHE A 233      10.115  43.834  81.532  1.00 14.14   6
ATOM   1898  N   ARG A 234      14.941  40.227  77.730  1.00 12.74   7
ATOM   1899  CA  ARG A 234      15.505  38.901  77.488  1.00 12.43   6
ATOM   1900  C   ARG A 234      15.587  38.314  78.928  1.00 14.55   6
ATOM   1901  O   ARG A 234      16.230  38.935  79.814  1.00 14.89   8
ATOM   1902  CB  ARG A 234      16.899  39.022  76.882  1.00  5.93   6
ATOM   1903  CG  ARG A 234      17.586  37.656  76.732  1.00 10.20   6
ATOM   1904  CD  ARG A 234      18.540  37.408  77.899  1.00 15.00   6
ATOM   1905  NE  ARG A 234      19.404  36.232  77.692  1.00 14.34   7
ATOM   1906  CZ  ARG A 234      20.182  35.688  78.615  1.00 24.46   6
ATOM   1907  NH1 ARG A 234      20.160  36.173  79.871  1.00 13.27   7
ATOM   1908  NH2 ARG A 234      20.930  34.647  78.289  1.00 12.67   7
ATOM   1909  N   ILE A 235      14.928  37.217  79.185  1.00 14.15   7
ATOM   1910  CA  ILE A 235      14.874  36.653  80.533  1.00 12.69   6
ATOM   1911  C   ILE A 235      15.873  35.548  80.793  1.00 12.06   6
ATOM   1912  O   ILE A 235      15.773  34.464  80.203  1.00 12.54   8
ATOM   1913  CB  ILE A 235      13.446  36.187  80.820  1.00 10.54   6
ATOM   1914  CG1 ILE A 235      12.504  37.385  80.567  1.00  9.10   6
ATOM   1915  CG2 ILE A 235      13.310  35.831  82.331  1.00 16.58   6
ATOM   1916  CD1 ILE A 235      11.115  36.763  80.407  1.00 15.58   6
ATOM   1917  N   ASP A 236      16.776  35.785  81.749  1.00  9.36   7
ATOM   1918  CA  ASP A 236      17.781  34.796  82.093  1.00 10.49   6
ATOM   1919  C   ASP A 236      17.441  33.558  82.860  1.00 12.64   6
ATOM   1920  O   ASP A 236      16.607  33.534  83.759  1.00 15.01   8
ATOM   1921  CB  ASP A 236      18.886  35.533  82.806  1.00 10.07   6
ATOM   1922  CG  ASP A 236      20.154  34.798  83.084  1.00 20.01   6
ATOM   1923  OD1 ASP A 236      20.882  34.542  82.112  1.00 14.97   8
ATOM   1924  OD2 ASP A 236      20.455  34.555  84.310  1.00 22.16   8
ATOM   1925  N   ALA A 237      18.050  32.429  82.484  1.00 11.95   7
ATOM   1926  CA  ALA A 237      18.011  31.158  83.169  1.00 12.87   6
ATOM   1927  C   ALA A 237      16.653  30.687  83.598  1.00 16.11   6
ATOM   1928  O   ALA A 237      16.440  30.225  84.762  1.00 15.77   8
ATOM   1929  CB  ALA A 237      18.924  31.424  84.407  1.00 13.46   6
ATOM   1930  N   VAL A 238      15.677  30.602  82.687  1.00  9.31   7
ATOM   1931  CA  VAL A 238      14.320  30.328  83.035  1.00  7.91   6
ATOM   1932  C   VAL A 238      14.133  28.877  83.391  1.00  9.01   6
ATOM   1933  O   VAL A 238      13.113  28.602  84.037  1.00 10.54   8
ATOM   1934  CB  VAL A 238      13.212  30.742  82.045  1.00 14.17   6
ATOM   1935  CG1 VAL A 238      13.273  32.240  81.788  1.00 13.29   6
ATOM   1936  CG2 VAL A 238      13.486  29.997  80.712  1.00 15.01   6
ATOM   1937  N   LYS A 239      15.066  27.991  83.077  1.00  5.59   7
ATOM   1938  CA  LYS A 239      14.711  26.629  83.448  1.00 10.08   6
ATOM   1939  C   LYS A 239      14.865  26.363  85.008  1.00  7.29   6
ATOM   1940  O   LYS A 239      14.529  25.276  85.419  1.00  7.91   8
ATOM   1941  CB  LYS A 239      15.636  25.685  82.762  1.00 12.33   6
ATOM   1942  CG  LYS A 239      17.092  25.584  82.801  1.00 25.74   6
ATOM   1943  CD  LYS A 239      17.278  24.453  81.732  1.00 25.18   6
ATOM   1944  CE  LYS A 239      18.708  24.141  81.578  1.00 26.14   6
ATOM   1945  NZ  LYS A 239      19.049  22.792  81.090  1.00 29.06   7
ATOM   1946  N   HIS A 240      15.615  27.232  85.621  1.00  8.92   7
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ATOM	1947	CA	HIS	A	240	15.904	27.175	87.047	1.00	14.13	6
ATOM	1948	C	HIS	A	240	14.880	28.058	87.743	1.00	15.09	6
ATOM	1949	O	HIS	A	240	15.029	28.277	88.936	1.00	10.80	8
ATOM	1950	CB	HIS	A	240	17.327	27.746	87.264	1.00	10.84	6
ATOM	1951	CG	HIS	A	240	18.312	27.095	86.328	1.00	7.11	6
ATOM	1952	ND1	HIS	A	240	18.625	25.766	86.369	1.00	6.30	7
ATOM	1953	CD2	HIS	A	240	18.997	27.608	85.226	1.00	9.29	6
ATOM	1954	CE1	HIS	A	240	19.524	25.452	85.416	1.00	10.25	6
ATOM	1955	NE2	HIS	A	240	19.767	26.568	84.761	1.00	6.19	7
ATOM	1956	N	ILE	A	241	13.855	28.688	87.174	1.00	11.07	7
ATOM	1957	CA	ILE	A	241	12.949	29.591	87.887	1.00	9.64	6
ATOM	1958	C	ILE	A	241	11.555	29.021	87.800	1.00	14.21	6
ATOM	1959	O	ILE	A	241	11.114	28.540	86.713	1.00	9.89	8
ATOM	1960	CB	ILE	A	241	13.014	30.983	87.274	1.00	10.12	6
ATOM	1961	CG1	ILE	A	241	14.389	31.615	87.488	1.00	7.20	6
ATOM	1962	CG2	ILE	A	241	11.921	31.942	87.733	1.00	13.70	6
ATOM	1963	CD1	ILE	A	241	14.592	32.912	86.714	1.00	8.67	6
ATOM	1964	N	LYS	A	242	10.790	29.009	88.919	1.00	11.24	7
ATOM	1965	CA	LYS	A	242	9.482	28.353	88.886	1.00	11.43	6
ATOM	1966	C	LYS	A	242	8.667	28.791	87.642	1.00	11.92	6
ATOM	1967	O	LYS	A	242	8.506	29.992	87.454	1.00	12.59	8
ATOM	1968	CB	LYS	A	242	8.805	28.706	90.226	1.00	9.80	6
ATOM	1969	CG	LYS	A	242	7.375	28.212	90.391	1.00	14.60	6
ATOM	1970	CD	LYS	A	242	6.822	28.881	91.688	1.00	23.88	6
ATOM	1971	CE	LYS	A	242	5.656	28.032	92.185	1.00	30.29	6
ATOM	1972	NZ	LYS	A	242	5.228	28.446	93.546	1.00	51.79	7
ATOM	1973	N	TYR	A	243	8.207	27.886	86.794	1.00	12.14	7
ATOM	1974	CA	TYR	A	243	7.591	28.335	85.513	1.00	12.18	6
ATOM	1975	C	TYR	A	243	6.430	29.283	85.699	1.00	13.50	6
ATOM	1976	O	TYR	A	243	6.349	30.392	85.138	1.00	10.33	8
ATOM	1977	CB	TYR	A	243	7.177	27.155	84.639	1.00	11.39	6
ATOM	1978	CG	TYR	A	243	8.272	26.205	84.196	1.00	8.33	6
ATOM	1979	CD1	TYR	A	243	9.605	26.506	84.310	1.00	9.57	6
ATOM	1980	CD2	TYR	A	243	7.937	24.971	83.661	1.00	6.42	6
ATOM	1981	CE1	TYR	A	243	10.610	25.624	83.980	1.00	7.83	6
ATOM	1982	CE2	TYR	A	243	8.937	24.099	83.234	1.00	6.98	6
ATOM	1983	CZ	TYR	A	243	10.260	24.446	83.402	1.00	7.87	6
ATOM	1984	OH	TYR	A	243	11.213	23.503	83.006	1.00	8.46	8
ATOM	1985	N	SER	A	244	5.514	28.975	86.659	1.00	12.18	7
ATOM	1986	CA	SER	A	244	4.381	29.873	86.861	1.00	11.90	6
ATOM	1987	C	SER	A	244	4.708	31.236	87.348	1.00	12.87	6
ATOM	1988	O	SER	A	244	4.008	32.267	87.088	1.00	15.15	8
ATOM	1989	CB	SER	A	244	3.275	29.152	87.666	1.00	25.44	6
ATOM	1990	OG	SER	A	244	3.751	28.984	88.988	1.00	28.03	8
ATOM	1991	N	PHE	A	245	5.861	31.370	88.033	1.00	11.37	7
ATOM	1992	CA	PHE	A	245	6.246	32.688	88.460	1.00	11.43	6
ATOM	1993	C	PHE	A	245	6.616	33.538	87.223	1.00	13.09	6
ATOM	1994	O	PHE	A	245	6.337	34.745	87.182	1.00	13.56	8
ATOM	1995	CB	PHE	A	245	7.424	32.575	89.450	1.00	3.88	6
ATOM	1996	CG	PHE	A	245	8.040	33.938	89.664	1.00	9.47	6
ATOM	1997	CD1	PHE	A	245	7.518	34.846	90.543	1.00	15.08	6
ATOM	1998	CD2	PHE	A	245	9.205	34.267	89.009	1.00	10.42	6
ATOM	1999	CE1	PHE	A	245	8.111	36.094	90.721	1.00	18.19	6
ATOM	2000	CE2	PHE	A	245	9.788	35.507	89.127	1.00	19.59	6
ATOM	2001	CZ	PHE	A	245	9.257	36.439	90.015	1.00	20.86	6
ATOM	2002	N	THR	A	246	7.457	32.964	86.332	1.00	13.88	7
ATOM	2003	CA	THR	A	246	7.914	33.765	85.147	1.00	12.92	6
ATOM	2004	C	THR	A	246	6.725	34.265	84.322	1.00	9.66	6
ATOM	2005	O	THR	A	246	6.471	35.411	84.043	1.00	11.86	8
ATOM	2006	CB	THR	A	246	8.840	32.888	84.303	1.00	18.73	6
ATOM	2007	OG1	THR	A	246	10.005	32.537	85.091	1.00	14.92	8
ATOM	2008	CG2	THR	A	246	9.307	33.704	83.074	1.00	18.81	6
ATOM	2009	N	ARG	A	247	5.796	33.383	84.079	1.00	12.73	7
ATOM	2010	CA	ARG	A	247	4.532	33.626	83.444	1.00	17.39	6
ATOM	2011	C	ARG	A	247	3.756	34.764	84.072	1.00	19.55	6
ATOM	2012	O	ARG	A	247	3.361	35.700	83.384	1.00	17.62	8
ATOM	2013	CB	ARG	A	247	3.709	32.309	83.590	1.00	15.50	6
ATOM	2014	CG	ARG	A	247	2.457	32.504	82.725	1.00	22.20	6
ATOM	2015	CD	ARG	A	247	1.449	31.398	82.962	1.00	25.17	6
ATOM	2016	NE	ARG	A	247	0.951	31.529	84.344	1.00	24.49	7
ATOM	2017	CZ	ARG	A	247	0.495	30.539	85.084	1.00	29.19	6
ATOM	2018	NH1	ARG	A	247	0.442	29.281	84.679	1.00	27.83	7
ATOM	2019	NH2	ARG	A	247	0.116	30.825	86.338	1.00	43.27	7
ATOM	2020	N	ASP	A	248	3.532	34.712	85.422	1.00	19.59	7

ATOM	2021	CA	ASP	A	248	2.722	35.793	86.019	1.00	17.00	6
ATOM	2022	C	ASP	A	248	3.558	36.996	86.271	1.00	15.85	6
ATOM	2023	O	ASP	A	248	3.007	38.103	86.247	1.00	19.31	8
ATOM	2024	CB	ASP	A	248	2.006	35.325	87.287	1.00	22.99	6
ATOM	2025	CG	ASP	A	248	1.126	34.143	86.996	1.00	24.92	6
ATOM	2026	OD1	ASP	A	248	0.595	33.975	85.867	1.00	34.48	8
ATOM	2027	OD2	ASP	A	248	0.997	33.283	87.871	1.00	26.88	8
ATOM	2028	N	TRP	A	249	4.881	36.900	86.402	1.00	14.97	7
ATOM	2029	CA	TRP	A	249	5.636	38.154	86.525	1.00	15.57	6
ATOM	2030	C	TRP	A	249	5.437	39.001	85.260	1.00	17.82	6
ATOM	2031	O	TRP	A	249	5.272	40.222	85.230	1.00	17.70	8
ATOM	2032	CB	TRP	A	249	7.110	37.767	86.721	1.00	15.81	6
ATOM	2033	CG	TRP	A	249	8.030	38.925	86.795	1.00	12.74	6
ATOM	2034	CD1	TRP	A	249	8.260	39.669	87.926	1.00	21.36	6
ATOM	2035	CD2	TRP	A	249	8.874	39.499	85.786	1.00	23.21	6
ATOM	2036	NE1	TRP	A	249	9.177	40.677	87.677	1.00	19.21	7
ATOM	2037	CE2	TRP	A	249	9.555	40.598	86.353	1.00	19.38	6
ATOM	2038	CE3	TRP	A	249	9.075	39.225	84.427	1.00	21.80	6
ATOM	2039	CZ2	TRP	A	249	10.457	41.403	85.647	1.00	18.58	6
ATOM	2040	CZ3	TRP	A	249	9.946	40.033	83.699	1.00	21.96	6
ATOM	2041	CH2	TRP	A	249	10.635	41.099	84.319	1.00	25.93	6
ATOM	2042	N	LEU	A	250	5.564	38.362	84.084	1.00	19.80	7
ATOM	2043	CA	LEU	A	250	5.504	39.085	82.783	1.00	18.64	6
ATOM	2044	C	LEU	A	250	4.123	39.711	82.615	1.00	16.90	6
ATOM	2045	O	LEU	A	250	4.040	40.899	82.268	1.00	21.03	8
ATOM	2046	CB	LEU	A	250	5.720	38.052	81.682	1.00	20.74	6
ATOM	2047	CG	LEU	A	250	6.535	38.290	80.438	1.00	36.99	6
ATOM	2048	CD1	LEU	A	250	7.712	39.215	80.654	1.00	30.25	6
ATOM	2049	CD2	LEU	A	250	6.983	36.903	79.940	1.00	36.20	6
ATOM	2050	N	THR	A	251	3.090	38.984	82.947	1.00	16.98	7
ATOM	2051	CA	THR	A	251	1.733	39.547	82.859	1.00	21.47	6
ATOM	2052	C	THR	A	251	1.536	40.765	83.748	1.00	25.19	6
ATOM	2053	O	THR	A	251	1.017	41.836	83.338	1.00	24.99	8
ATOM	2054	CB	THR	A	251	0.710	38.482	83.236	1.00	25.31	6
ATOM	2055	OG1	THR	A	251	0.819	37.400	82.317	1.00	19.58	8
ATOM	2056	CG2	THR	A	251	-0.704	39.048	83.064	1.00	35.15	6
ATOM	2057	N	HIS	A	252	2.109	40.616	84.975	1.00	25.52	7
ATOM	2058	CA	HIS	A	252	2.076	41.706	85.938	1.00	26.37	6
ATOM	2059	C	HIS	A	252	2.714	42.971	85.388	1.00	24.27	6
ATOM	2060	O	HIS	A	252	2.183	44.083	85.511	1.00	22.81	8
ATOM	2061	CB	HIS	A	252	2.821	41.311	87.262	1.00	30.15	6
ATOM	2062	CG	HIS	A	252	2.744	42.478	88.218	1.00	26.03	6
ATOM	2063	ND1	HIS	A	252	3.699	43.461	88.309	1.00	23.15	7
ATOM	2064	CD2	HIS	A	252	1.767	42.804	89.089	1.00	25.20	6
ATOM	2065	CE1	HIS	A	252	3.343	44.369	89.189	1.00	23.46	6
ATOM	2066	NE2	HIS	A	252	2.176	43.970	89.685	1.00	31.78	7
ATOM	2067	N	VAL	A	253	3.935	42.813	84.862	1.00	22.82	7
ATOM	2068	CA	VAL	A	253	4.628	43.984	84.345	1.00	23.83	6
ATOM	2069	C	VAL	A	253	3.928	44.549	83.089	1.00	25.77	6
ATOM	2070	O	VAL	A	253	3.866	45.775	82.954	1.00	24.97	8
ATOM	2071	CB	VAL	A	253	6.097	43.672	84.050	1.00	24.83	6
ATOM	2072	CG1	VAL	A	253	6.804	44.884	83.495	1.00	20.28	6
ATOM	2073	CG2	VAL	A	253	6.788	43.156	85.302	1.00	31.84	6
ATOM	2074	N	ARG	A	254	3.387	43.673	82.241	1.00	26.27	7
ATOM	2075	CA	ARG	A	254	2.661	44.167	81.068	1.00	29.21	6
ATOM	2076	C	ARG	A	254	1.428	44.949	81.521	1.00	30.40	6
ATOM	2077	O	ARG	A	254	1.295	46.102	81.106	1.00	31.03	8
ATOM	2078	CB	ARG	A	254	2.312	43.037	80.111	1.00	30.34	6
ATOM	2079	CG	ARG	A	254	3.530	42.557	79.251	1.00	20.49	6
ATOM	2080	CD	ARG	A	254	3.130	41.213	78.623	1.00	18.72	6
ATOM	2081	NE	ARG	A	254	4.228	40.726	77.790	1.00	21.16	7
ATOM	2082	CZ	ARG	A	254	4.369	39.491	77.347	1.00	21.93	6
ATOM	2083	NH1	ARG	A	254	3.498	38.564	77.689	1.00	19.85	7
ATOM	2084	NH2	ARG	A	254	5.415	39.197	76.567	1.00	24.23	7
ATOM	2085	N	ASN	A	255	0.576	44.394	82.369	1.00	31.01	7
ATOM	2086	CA	ASN	A	255	-0.566	45.115	82.915	1.00	31.98	6
ATOM	2087	C	ASN	A	255	-0.178	46.372	83.672	1.00	33.52	6
ATOM	2088	O	ASN	A	255	-0.792	47.422	83.476	1.00	33.39	8
ATOM	2089	CB	ASN	A	255	-1.418	44.249	83.838	1.00	35.19	6
ATOM	2090	CG	ASN	A	255	-1.980	43.048	83.118	1.00	43.21	6
ATOM	2091	OD1	ASN	A	255	-1.921	42.986	81.887	1.00	59.02	8
ATOM	2092	ND2	ASN	A	255	-2.520	42.052	83.792	1.00	50.05	7
ATOM	2093	N	ALA	A	256	0.861	46.351	84.513	1.00	34.99	7
ATOM	2094	CA	ALA	A	256	1.219	47.546	85.250	1.00	36.39	6

ATOM	2095	C	ALA	A	256	1.742	48.650	84.363	1.00	39.16	6
ATOM	2096	O	ALA	A	256	1.546	49.803	84.753	1.00	39.92	8
ATOM	2097	CB	ALA	A	256	2.275	47.346	86.325	1.00	36.68	6
ATOM	2098	N	THR	A	257	2.486	48.360	83.303	1.00	39.44	7
ATOM	2099	CA	THR	A	257	3.051	49.482	82.545	1.00	40.36	6
ATOM	2100	C	THR	A	257	2.098	49.887	81.428	1.00	40.85	6
ATOM	2101	O	THR	A	257	2.331	50.920	80.803	1.00	42.44	8
ATOM	2102	CB	THR	A	257	4.397	49.077	81.893	1.00	39.97	6
ATOM	2103	OG1	THR	A	257	4.124	47.852	81.178	1.00	37.26	8
ATOM	2104	CG2	THR	A	257	5.472	48.822	82.927	1.00	34.15	6
ATOM	2105	N	GLY	A	258	1.130	49.050	81.085	1.00	40.80	7
ATOM	2106	CA	GLY	A	258	0.263	49.337	79.965	1.00	41.62	6
ATOM	2107	C	GLY	A	258	0.931	49.107	78.618	1.00	43.26	6
ATOM	2108	O	GLY	A	258	0.382	49.531	77.591	1.00	44.58	8
ATOM	2109	N	LYS	A	259	2.064	48.436	78.539	1.00	43.07	7
ATOM	2110	CA	LYS	A	259	2.812	48.174	77.323	1.00	42.68	6
ATOM	2111	C	LYS	A	259	2.834	46.694	76.956	1.00	41.44	6
ATOM	2112	O	LYS	A	259	2.890	45.847	77.845	1.00	41.40	8
ATOM	2113	CB	LYS	A	259	4.276	48.563	77.540	1.00	48.99	6
ATOM	2114	CG	LYS	A	259	4.585	50.028	77.728	1.00	52.01	6
ATOM	2115	CD	LYS	A	259	5.936	50.184	78.421	1.00	53.13	6
ATOM	2116	CE	LYS	A	259	7.023	50.603	77.455	1.00	53.64	6
ATOM	2117	NZ	LYS	A	259	8.088	51.407	78.132	1.00	54.27	7
ATOM	2118	N	GLU	A	260	2.914	46.352	75.682	1.00	41.04	7
ATOM	2119	CA	GLU	A	260	2.959	44.974	75.194	1.00	39.46	6
ATOM	2120	C	GLU	A	260	4.157	44.136	75.641	1.00	35.90	6
ATOM	2121	O	GLU	A	260	4.059	42.918	75.735	1.00	36.93	8
ATOM	2122	CB	GLU	A	260	2.927	45.027	73.650	1.00	62.65	6
ATOM	2123	CG	GLU	A	260	3.452	43.824	72.907	1.00	77.65	6
ATOM	2124	CD	GLU	A	260	4.228	44.064	71.627	1.00	84.79	6
ATOM	2125	OE1	GLU	A	260	4.274	45.218	71.142	1.00	87.14	8
ATOM	2126	OE2	GLU	A	260	4.814	43.082	71.092	1.00	81.45	8
ATOM	2127	N	MET	A	261	5.306	44.722	75.855	1.00	32.24	7
ATOM	2128	CA	MET	A	261	6.527	44.101	76.247	1.00	29.42	6
ATOM	2129	C	MET	A	261	6.721	42.716	75.616	1.00	27.28	6
ATOM	2130	O	MET	A	261	6.291	41.663	76.054	1.00	28.96	8
ATOM	2131	CB	MET	A	261	6.747	44.016	77.743	1.00	27.19	6
ATOM	2132	CG	MET	A	261	6.436	45.227	78.605	1.00	31.84	6
ATOM	2133	SD	MET	A	261	7.576	46.582	78.418	1.00	42.23	16
ATOM	2134	CE	MET	A	261	9.138	45.895	78.957	1.00	31.14	6
ATOM	2135	N	PHE	A	262	7.510	42.703	74.566	1.00	24.48	7
ATOM	2136	CA	PHE	A	262	7.943	41.467	73.921	1.00	22.71	6
ATOM	2137	C	PHE	A	262	8.924	40.804	74.917	1.00	19.54	6
ATOM	2138	O	PHE	A	262	9.719	41.573	75.440	1.00	21.34	8
ATOM	2139	CB	PHE	A	262	8.837	41.850	72.694	1.00	12.70	6
ATOM	2140	CG	PHE	A	262	9.496	40.626	72.136	1.00	12.10	6
ATOM	2141	CD1	PHE	A	262	8.740	39.641	71.535	1.00	18.73	6
ATOM	2142	CD2	PHE	A	262	10.846	40.436	72.243	1.00	10.21	6
ATOM	2143	CE1	PHE	A	262	9.330	38.481	71.012	1.00	15.61	6
ATOM	2144	CE2	PHE	A	262	11.454	39.326	71.738	1.00	12.87	6
ATOM	2145	CZ	PHE	A	262	10.691	38.352	71.125	1.00	11.25	6
ATOM	2146	N	ALA	A	263	8.997	39.482	74.973	1.00	19.06	7
ATOM	2147	CA	ALA	A	263	10.069	38.925	75.791	1.00	18.90	6
ATOM	2148	C	ALA	A	263	10.522	37.600	75.167	1.00	14.30	6
ATOM	2149	O	ALA	A	263	9.720	36.809	74.716	1.00	16.72	8
ATOM	2150	CB	ALA	A	263	9.538	38.600	77.231	1.00	16.61	6
ATOM	2151	N	VAL	A	264	11.809	37.352	75.318	1.00	14.17	7
ATOM	2152	CA	VAL	A	264	12.291	36.027	74.899	1.00	13.57	6
ATOM	2153	C	VAL	A	264	13.018	35.448	76.120	1.00	12.86	6
ATOM	2154	O	VAL	A	264	13.840	36.092	76.773	1.00	12.22	8
ATOM	2155	CB	VAL	A	264	13.259	36.200	73.695	1.00	7.10	6
ATOM	2156	CG1	VAL	A	264	14.352	37.209	73.955	1.00	4.19	6
ATOM	2157	CG2	VAL	A	264	13.796	34.868	73.266	1.00	4.85	6
ATOM	2158	N	ALA	A	265	12.840	34.168	76.346	1.00	12.26	7
ATOM	2159	CA	ALA	A	265	13.451	33.519	77.500	1.00	13.87	6
ATOM	2160	C	ALA	A	265	14.544	32.577	77.071	1.00	13.85	6
ATOM	2161	O	ALA	A	265	14.370	31.837	76.071	1.00	14.15	8
ATOM	2162	CB	ALA	A	265	12.349	32.652	78.180	1.00	9.68	6
ATOM	2163	N	GLU	A	266	15.639	32.607	77.821	1.00	10.52	7
ATOM	2164	CA	GLU	A	266	16.711	31.664	77.669	1.00	6.70	6
ATOM	2165	C	GLU	A	266	16.463	30.382	78.430	1.00	14.18	6
ATOM	2166	O	GLU	A	266	16.733	30.218	79.665	1.00	12.91	8
ATOM	2167	CB	GLU	A	266	18.058	32.279	78.038	1.00	6.87	6
ATOM	2168	CG	GLU	A	266	19.243	31.294	77.841	1.00	10.70	6

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ATOM   2169  CD  GLU A 266      20.193  31.084  79.001  1.00 28.43   6
ATOM   2170  OE1 GLU A 266      19.858  31.387  80.192  1.00 24.40   8
ATOM   2171  OE2 GLU A 266      21.365  30.604  78.811  1.00 16.24   8
ATOM   2172  N   PHE A 267      15.916  29.380  77.736  1.00 13.24   7
ATOM   2173  CA  PHE A 267      15.792  28.055  78.292  1.00 11.67   6
ATOM   2174  C   PHE A 267      16.843  27.158  77.636  1.00 14.76   6
ATOM   2175  O   PHE A 267      16.573  26.528  76.597  1.00 15.16   8
ATOM   2176  CB  PHE A 267      14.383  27.547  78.026  1.00 13.42   6
ATOM   2177  CG  PHE A 267      14.035  26.272  78.734  1.00 13.78   6
ATOM   2178  CD1 PHE A 267      14.609  25.058  78.433  1.00  9.97   6
ATOM   2179  CD2 PHE A 267      13.051  26.337  79.737  1.00  8.86   6
ATOM   2180  CE1 PHE A 267      14.232  23.901  79.124  1.00 21.47   6
ATOM   2181  CE2 PHE A 267      12.702  25.188  80.435  1.00 10.17   6
ATOM   2182  CZ  PHE A 267      13.271  23.954  80.167  1.00  7.77   6
ATOM   2183  N   TRP A 268      18.024  27.031  78.178  1.00 11.88   7
ATOM   2184  CA  TRP A 268      19.092  26.287  77.557  1.00 13.36   6
ATOM   2185  C   TRP A 268      19.051  24.789  77.661  1.00 16.10   6
ATOM   2186  O   TRP A 268      19.582  24.124  78.545  1.00 18.52   8
ATOM   2187  CB  TRP A 268      20.484  26.773  77.869  1.00  7.98   6
ATOM   2188  CG  TRP A 268      21.559  26.333  76.900  1.00 11.23   6
ATOM   2189  CD1 TRP A 268      22.226  25.165  76.785  1.00 14.63   6
ATOM   2190  CD2 TRP A 268      22.016  27.154  75.816  1.00 13.22   6
ATOM   2191  NE1 TRP A 268      23.116  25.210  75.736  1.00 12.62   7
ATOM   2192  CE2 TRP A 268      22.988  26.427  75.134  1.00 14.70   6
ATOM   2193  CE3 TRP A 268      21.658  28.452  75.390  1.00 17.12   6
ATOM   2194  CZ2 TRP A 268      23.644  26.942  74.005  1.00 18.35   6
ATOM   2195  CZ3 TRP A 268      22.311  28.963  74.259  1.00 19.48   6
ATOM   2196  CH2 TRP A 268      23.317  28.208  73.619  1.00  8.78   6
ATOM   2197  N   LYS A 269      18.447  24.173  76.643  1.00 16.93   7
ATOM   2198  CA  LYS A 269      18.410  22.732  76.582  1.00 15.46   6
ATOM   2199  C   LYS A 269      18.213  22.360  75.088  1.00 15.49   6
ATOM   2200  O   LYS A 269      17.316  22.923  74.471  1.00 12.29   8
ATOM   2201  CB  LYS A 269      17.182  22.267  77.362  1.00 14.40   6
ATOM   2202  CG  LYS A 269      17.499  20.809  77.692  1.00 18.39   6
ATOM   2203  CD  LYS A 269      16.292  20.205  78.426  1.00 27.57   6
ATOM   2204  CE  LYS A 269      17.007  19.267  79.381  1.00 35.05   6
ATOM   2205  NZ  LYS A 269      17.031  17.880  78.885  1.00 41.79   7
ATOM   2206  N   ASN A 270      18.983  21.413  74.623  1.00 15.03   7
ATOM   2207  CA  ASN A 270      18.845  20.988  73.226  1.00 15.62   6
ATOM   2208  C   ASN A 270      17.758  19.943  73.144  1.00 14.07   6
ATOM   2209  O   ASN A 270      18.024  18.769  72.933  1.00 13.60   8
ATOM   2210  CB  ASN A 270      20.181  20.434  72.746  1.00 14.33   6
ATOM   2211  CG  ASN A 270      20.143  20.084  71.245  1.00 23.70   6
ATOM   2212  OD1 ASN A 270      19.220  20.565  70.577  1.00 17.65   8
ATOM   2213  ND2 ASN A 270      21.079  19.263  70.787  1.00 10.70   7
ATOM   2214  N   ASP A 271      16.511  20.338  73.307  1.00 16.99   7
ATOM   2215  CA  ASP A 271      15.453  19.319  73.432  1.00 18.25   6
ATOM   2216  C   ASP A 271      14.144  20.076  73.255  1.00 19.23   6
ATOM   2217  O   ASP A 271      13.662  20.828  74.109  1.00 18.38   8
ATOM   2218  CB  ASP A 271      15.525  18.727  74.853  1.00 26.80   6
ATOM   2219  CG  ASP A 271      14.461  17.665  75.102  1.00 39.25   6
ATOM   2220  OD1 ASP A 271      13.251  17.922  75.022  1.00 39.03   8
ATOM   2221  OD2 ASP A 271      14.814  16.512  75.402  1.00 53.52   8
ATOM   2222  N   LEU A 272      13.528  19.745  72.113  1.00 16.74   7
ATOM   2223  CA  LEU A 272      12.307  20.447  71.735  1.00 17.19   6
ATOM   2224  C   LEU A 272      11.143  20.097  72.672  1.00 13.55   6
ATOM   2225  O   LEU A 272      10.339  20.973  72.944  1.00 12.34   8
ATOM   2226  CB  LEU A 272      12.023  20.131  70.241  1.00 14.98   6
ATOM   2227  CG  LEU A 272      10.672  20.700  69.831  1.00 13.62   6
ATOM   2228  CD1 LEU A 272      10.649  22.196  69.942  1.00 16.93   6
ATOM   2229  CD2 LEU A 272      10.343  20.272  68.393  1.00 27.80   6
ATOM   2230  N   GLY A 273      11.102  18.845  73.111  1.00 13.14   7
ATOM   2231  CA  GLY A 273      10.087  18.437  74.095  1.00 17.42   6
ATOM   2232  C   GLY A 273      10.111  19.307  75.393  1.00 16.23   6
ATOM   2233  O   GLY A 273       9.098  19.859  75.857  1.00 13.91   8
ATOM   2234  N   ALA A 274      11.308  19.525  75.958  1.00 15.44   7
ATOM   2235  CA  ALA A 274      11.404  20.360  77.165  1.00 14.48   6
ATOM   2236  C   ALA A 274      10.928  21.766  76.900  1.00 16.65   6
ATOM   2237  O   ALA A 274      10.285  22.449  77.719  1.00 13.98   8
ATOM   2238  CB  ALA A 274      12.880  20.359  77.568  1.00 10.97   6
ATOM   2239  N   LEU A 275      11.280  22.296  75.666  1.00 14.39   7
ATOM   2240  CA  LEU A 275      10.893  23.652  75.329  1.00 10.53   6
ATOM   2241  C   LEU A 275       9.398  23.814  75.156  1.00 11.28   6
ATOM   2242  O   LEU A 275       8.797  24.824  75.571  1.00 11.68   8
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ATOM	2243	CB	LEU	A	275	11.657	24.168	74.087	1.00	15.03	6
ATOM	2244	CG	LEU	A	275	13.161	24.299	74.333	1.00	21.33	6
ATOM	2245	CD1	LEU	A	275	14.000	24.218	73.048	1.00	20.57	6
ATOM	2246	CD2	LEU	A	275	13.353	25.663	74.996	1.00	13.26	6
ATOM	2247	N	GLU	A	276	8.752	22.794	74.582	1.00	10.24	7
ATOM	2248	CA	GLU	A	276	7.289	22.892	74.457	1.00	12.93	6
ATOM	2249	C	GLU	A	276	6.595	22.784	75.843	1.00	14.28	6
ATOM	2250	O	GLU	A	276	5.521	23.356	76.036	1.00	15.27	8
ATOM	2251	CB	GLU	A	276	6.761	21.730	73.572	1.00	13.24	6
ATOM	2252	CG	GLU	A	276	7.260	21.889	72.130	1.00	34.25	6
ATOM	2253	CD	GLU	A	276	6.825	20.834	71.145	1.00	39.49	6
ATOM	2254	OE1	GLU	A	276	6.737	19.619	71.394	1.00	36.50	8
ATOM	2255	OE2	GLU	A	276	6.546	21.221	69.992	1.00	45.71	8
ATOM	2256	N	ASN	A	277	7.169	21.984	76.749	1.00	14.65	7
ATOM	2257	CA	ASN	A	277	6.571	21.916	78.128	1.00	12.73	6
ATOM	2258	C	ASN	A	277	6.602	23.281	78.737	1.00	10.71	6
ATOM	2259	O	ASN	A	277	5.607	23.931	79.099	1.00	13.72	8
ATOM	2260	CB	ASN	A	277	7.313	20.778	78.849	1.00	15.75	6
ATOM	2261	CG	ASN	A	277	6.865	20.857	80.335	1.00	26.77	6
ATOM	2262	OD1	ASN	A	277	5.702	20.667	80.586	1.00	15.27	8
ATOM	2263	ND2	ASN	A	277	7.699	21.168	81.300	1.00	10.18	7
ATOM	2264	N	TYR	A	278	7.743	23.963	78.681	1.00	11.83	7
ATOM	2265	CA	TYR	A	278	7.915	25.320	79.150	1.00	12.29	6
ATOM	2266	C	TYR	A	278	6.889	26.262	78.575	1.00	14.54	6
ATOM	2267	O	TYR	A	278	6.217	27.109	79.227	1.00	13.66	8
ATOM	2268	CB	TYR	A	278	9.369	25.831	78.890	1.00	9.85	6
ATOM	2269	CG	TYR	A	278	9.561	27.264	79.336	1.00	11.93	6
ATOM	2270	CD1	TYR	A	278	9.700	27.581	80.725	1.00	12.91	6
ATOM	2271	CD2	TYR	A	278	9.590	28.306	78.440	1.00	10.42	6
ATOM	2272	CE1	TYR	A	278	9.854	28.897	81.123	1.00	11.06	6
ATOM	2273	CE2	TYR	A	278	9.690	29.636	78.833	1.00	10.81	6
ATOM	2274	CZ	TYR	A	278	9.864	29.912	80.198	1.00	13.63	6
ATOM	2275	OH	TYR	A	278	9.989	31.239	80.563	1.00	13.37	8
ATOM	2276	N	LEU	A	279	6.749	26.175	77.201	1.00	15.84	7
ATOM	2277	CA	LEU	A	279	5.837	27.144	76.541	1.00	12.10	6
ATOM	2278	C	LEU	A	279	4.398	26.841	76.957	1.00	10.12	6
ATOM	2279	O	LEU	A	279	3.590	27.755	77.102	1.00	13.43	8
ATOM	2280	CB	LEU	A	279	5.957	26.966	75.033	1.00	27.35	6
ATOM	2281	CG	LEU	A	279	6.798	27.756	74.077	1.00	19.86	6
ATOM	2282	CD1	LEU	A	279	7.360	29.080	74.426	1.00	14.50	6
ATOM	2283	CD2	LEU	A	279	7.884	26.930	73.416	1.00	19.52	6
ATOM	2284	N	ASN	A	280	4.056	25.581	77.114	1.00	12.52	7
ATOM	2285	CA	ASN	A	280	2.674	25.297	77.551	1.00	16.58	6
ATOM	2286	C	ASN	A	280	2.448	25.814	78.985	1.00	18.62	6
ATOM	2287	O	ASN	A	280	1.569	26.632	79.240	1.00	19.40	8
ATOM	2288	CB	ASN	A	280	2.527	23.766	77.511	1.00	17.54	6
ATOM	2289	CG	ASN	A	280	2.154	23.278	76.119	1.00	30.66	6
ATOM	2290	OD1	ASN	A	280	2.550	22.183	75.708	1.00	34.93	8
ATOM	2291	ND2	ASN	A	280	1.390	24.095	75.409	1.00	33.44	7
ATOM	2292	N	LYS	A	281	3.394	25.467	79.887	1.00	18.75	7
ATOM	2293	CA	LYS	A	281	3.305	25.918	81.293	1.00	17.49	6
ATOM	2294	C	LYS	A	281	3.343	27.395	81.418	1.00	16.48	6
ATOM	2295	O	LYS	A	281	2.771	27.964	82.380	1.00	20.69	8
ATOM	2296	CB	LYS	A	281	4.433	25.289	82.127	1.00	13.25	6
ATOM	2297	CG	LYS	A	281	4.497	23.774	82.206	1.00	13.95	6
ATOM	2298	CD	LYS	A	281	3.243	23.306	82.907	1.00	17.14	6
ATOM	2299	CE	LYS	A	281	2.970	21.830	82.684	1.00	7.97	6
ATOM	2300	NZ	LYS	A	281	4.215	21.104	83.039	1.00	13.19	7
ATOM	2301	N	THR	A	282	3.902	28.186	80.512	1.00	16.82	7
ATOM	2302	CA	THR	A	282	3.872	29.638	80.592	1.00	13.27	6
ATOM	2303	C	THR	A	282	2.761	30.179	79.680	1.00	13.92	6
ATOM	2304	O	THR	A	282	2.734	31.369	79.367	1.00	13.05	8
ATOM	2305	CB	THR	A	282	5.199	30.321	80.271	1.00	25.12	6
ATOM	2306	OG1	THR	A	282	5.667	29.872	78.968	1.00	20.09	8
ATOM	2307	CG2	THR	A	282	6.215	29.936	81.369	1.00	17.02	6
ATOM	2308	N	ASN	A	283	1.899	29.294	79.218	1.00	14.25	7
ATOM	2309	CA	ASN	A	283	0.798	29.771	78.374	1.00	19.43	6
ATOM	2310	C	ASN	A	283	1.131	30.541	77.089	1.00	20.89	6
ATOM	2311	O	ASN	A	283	0.380	31.442	76.680	1.00	19.32	8
ATOM	2312	CB	ASN	A	283	-0.077	30.671	79.255	1.00	29.96	6
ATOM	2313	CG	ASN	A	283	-0.989	29.957	80.214	1.00	49.27	6
ATOM	2314	OD1	ASN	A	283	-2.037	30.523	80.557	1.00	63.24	8
ATOM	2315	ND2	ASN	A	283	-0.657	28.762	80.704	1.00	57.30	7
ATOM	2316	N	TRP	A	284	2.209	30.262	76.387	1.00	19.27	7

ATOM	2317	CA	TRP	A	284	2.582	30.844	75.117	1.00	21.66	6
ATOM	2318	C	TRP	A	284	2.641	32.329	75.187	1.00	21.59	6
ATOM	2319	O	TRP	A	284	2.435	32.954	74.157	1.00	23.14	8
ATOM	2320	CB	TRP	A	284	1.556	30.421	73.978	1.00	15.89	6
ATOM	2321	CG	TRP	A	284	1.629	28.927	73.876	1.00	17.98	6
ATOM	2322	CD1	TRP	A	284	0.841	28.047	74.594	1.00	32.38	6
ATOM	2323	CD2	TRP	A	284	2.516	28.115	73.125	1.00	21.72	6
ATOM	2324	NE1	TRP	A	284	1.202	26.742	74.328	1.00	22.08	7
ATOM	2325	CE2	TRP	A	284	2.216	26.766	73.416	1.00	17.99	6
ATOM	2326	CE3	TRP	A	284	3.547	28.397	72.221	1.00	23.27	6
ATOM	2327	CZ2	TRP	A	284	2.905	25.687	72.839	1.00	21.96	6
ATOM	2328	CZ3	TRP	A	284	4.225	27.313	71.658	1.00	27.52	6
ATOM	2329	CH2	TRP	A	284	3.917	25.987	71.965	1.00	25.63	6
ATOM	2330	N	ASN	A	285	2.958	32.939	76.338	1.00	20.45	7
ATOM	2331	CA	ASN	A	285	2.889	34.381	76.427	1.00	14.22	6
ATOM	2332	C	ASN	A	285	4.222	35.004	76.135	1.00	13.71	6
ATOM	2333	O	ASN	A	285	4.360	36.215	76.292	1.00	16.62	8
ATOM	2334	CB	ASN	A	285	2.266	34.837	77.754	1.00	23.77	6
ATOM	2335	CG	ASN	A	285	3.180	34.903	78.970	1.00	27.16	6
ATOM	2336	OD1	ASN	A	285	4.369	34.524	78.933	1.00	16.54	8
ATOM	2337	ND2	ASN	A	285	2.672	35.424	80.111	1.00	21.01	7
ATOM	2338	N	HIS	A	286	5.253	34.220	75.778	1.00	15.57	7
ATOM	2339	CA	HIS	A	286	6.501	34.895	75.381	1.00	12.65	6
ATOM	2340	C	HIS	A	286	7.300	33.916	74.506	1.00	11.98	6
ATOM	2341	O	HIS	A	286	6.854	32.804	74.345	1.00	14.13	8
ATOM	2342	CB	HIS	A	286	7.264	35.443	76.587	1.00	19.68	6
ATOM	2343	CG	HIS	A	286	7.742	34.382	77.537	1.00	17.05	6
ATOM	2344	ND1	HIS	A	286	6.887	33.754	78.456	1.00	16.46	7
ATOM	2345	CD2	HIS	A	286	8.948	33.817	77.703	1.00	18.10	6
ATOM	2346	CE1	HIS	A	286	7.630	32.868	79.117	1.00	17.83	6
ATOM	2347	NE2	HIS	A	286	8.870	32.870	78.693	1.00	17.71	7
ATOM	2348	N	SER	A	287	8.426	34.322	73.915	1.00	12.20	7
ATOM	2349	CA	SER	A	287	9.164	33.385	73.059	1.00	14.12	6
ATOM	2350	C	SER	A	287	10.374	32.782	73.741	1.00	14.82	6
ATOM	2351	O	SER	A	287	10.774	33.248	74.825	1.00	17.15	8
ATOM	2352	CB	SER	A	287	9.754	34.254	71.893	1.00	16.58	6
ATOM	2353	OG	SER	A	287	8.684	34.771	71.102	1.00	17.00	8
ATOM	2354	N	VAL	A	288	11.054	31.840	73.121	1.00	12.79	7
ATOM	2355	CA	VAL	A	288	12.250	31.203	73.563	1.00	14.52	6
ATOM	2356	C	VAL	A	288	13.371	31.262	72.497	1.00	16.11	6
ATOM	2357	O	VAL	A	288	13.084	31.296	71.293	1.00	14.78	8
ATOM	2358	CB	VAL	A	288	12.044	29.731	73.950	1.00	13.45	6
ATOM	2359	CG1	VAL	A	288	11.129	29.540	75.214	1.00	8.20	6
ATOM	2360	CG2	VAL	A	288	11.456	28.913	72.829	1.00	13.24	6
ATOM	2361	N	PHE	A	289	14.620	31.197	72.912	1.00	11.88	7
ATOM	2362	CA	PHE	A	289	15.732	31.147	71.988	1.00	14.18	6
ATOM	2363	C	PHE	A	289	15.709	29.767	71.359	1.00	13.88	6
ATOM	2364	O	PHE	A	289	15.346	28.776	72.043	1.00	9.88	8
ATOM	2365	CB	PHE	A	289	17.087	31.415	72.599	1.00	9.88	6
ATOM	2366	CG	PHE	A	289	17.309	32.868	72.865	1.00	13.13	6
ATOM	2367	CD1	PHE	A	289	17.630	33.713	71.811	1.00	10.95	6
ATOM	2368	CD2	PHE	A	289	17.268	33.384	74.167	1.00	18.20	6
ATOM	2369	CE1	PHE	A	289	17.900	35.050	72.049	1.00	17.86	6
ATOM	2370	CE2	PHE	A	289	17.561	34.726	74.383	1.00	16.59	6
ATOM	2371	CZ	PHE	A	289	17.877	35.587	73.336	1.00	16.81	6
ATOM	2372	N	ASP	A	290	16.003	29.722	70.036	1.00	11.93	7
ATOM	2373	CA	ASP	A	290	15.918	28.405	69.381	1.00	10.84	6
ATOM	2374	C	ASP	A	290	17.241	27.703	69.580	1.00	13.22	6
ATOM	2375	O	ASP	A	290	18.127	27.521	68.720	1.00	11.57	8
ATOM	2376	CB	ASP	A	290	15.592	28.596	67.882	1.00	17.74	6
ATOM	2377	CG	ASP	A	290	15.165	27.305	67.203	1.00	8.50	6
ATOM	2378	OD1	ASP	A	290	15.413	26.178	67.665	1.00	10.35	8
ATOM	2379	OD2	ASP	A	290	14.479	27.377	66.115	1.00	14.66	8
ATOM	2380	N	VAL	A	291	17.338	26.969	70.722	1.00	11.25	7
ATOM	2381	CA	VAL	A	291	18.561	26.296	71.086	1.00	5.98	6
ATOM	2382	C	VAL	A	291	18.871	25.107	70.214	1.00	6.18	6
ATOM	2383	O	VAL	A	291	20.044	24.846	69.880	1.00	7.63	8
ATOM	2384	CB	VAL	A	291	18.627	26.021	72.658	1.00	11.65	6
ATOM	2385	CG1	VAL	A	291	19.839	25.216	72.998	1.00	9.12	6
ATOM	2386	CG2	VAL	A	291	18.797	27.390	73.361	1.00	5.15	6
ATOM	2387	N	PRO	A	292	17.960	24.206	69.956	1.00	6.90	7
ATOM	2388	CA	PRO	A	292	18.131	23.122	68.992	1.00	8.93	6
ATOM	2389	C	PRO	A	292	18.692	23.624	67.645	1.00	7.94	6
ATOM	2390	O	PRO	A	292	19.613	22.995	67.165	1.00	11.81	8

ATOM	2391	CB	PRO	A	292	16.749	22.501	68.809	1.00	9.92	6
ATOM	2392	CG	PRO	A	292	16.058	22.934	70.114	1.00	8.69	6
ATOM	2393	CD	PRO	A	292	16.537	24.373	70.327	1.00	7.60	6
ATOM	2394	N	LEU	A	293	18.247	24.714	67.062	1.00	10.68	7
ATOM	2395	CA	LEU	A	293	18.737	25.213	65.763	1.00	11.10	6
ATOM	2396	C	LEU	A	293	20.192	25.650	65.885	1.00	12.31	6
ATOM	2397	O	LEU	A	293	21.080	25.293	65.104	1.00	13.69	8
ATOM	2398	CB	LEU	A	293	17.883	26.394	65.252	1.00	8.55	6
ATOM	2399	CG	LEU	A	293	18.529	27.085	64.005	1.00	8.91	6
ATOM	2400	CD1	LEU	A	293	18.547	26.028	62.889	1.00	14.47	6
ATOM	2401	CD2	LEU	A	293	17.697	28.283	63.570	1.00	6.40	6
ATOM	2402	N	HIS	A	294	20.584	26.306	66.998	1.00	10.78	7
ATOM	2403	CA	HIS	A	294	21.999	26.615	67.259	1.00	8.98	6
ATOM	2404	C	HIS	A	294	22.834	25.349	67.238	1.00	8.37	6
ATOM	2405	O	HIS	A	294	23.918	25.401	66.617	1.00	10.24	8
ATOM	2406	CB	HIS	A	294	22.216	27.414	68.575	1.00	14.04	6
ATOM	2407	CG	HIS	A	294	23.648	27.309	69.026	1.00	9.37	6
ATOM	2408	ND1	HIS	A	294	24.571	28.222	68.589	1.00	10.24	7
ATOM	2409	CD2	HIS	A	294	24.315	26.446	69.840	1.00	10.07	6
ATOM	2410	CE1	HIS	A	294	25.764	27.943	69.105	1.00	11.91	6
ATOM	2411	NE2	HIS	A	294	25.671	26.832	69.818	1.00	8.31	7
ATOM	2412	N	TYR	A	295	22.438	24.229	67.818	1.00	7.59	7
ATOM	2413	CA	TYR	A	295	23.272	23.041	67.767	1.00	10.71	6
ATOM	2414	C	TYR	A	295	23.301	22.399	66.331	1.00	12.73	6
ATOM	2415	O	TYR	A	295	24.343	21.839	65.992	1.00	11.33	8
ATOM	2416	CB	TYR	A	295	22.815	21.988	68.830	1.00	12.97	6
ATOM	2417	CG	TYR	A	295	23.371	22.374	70.208	1.00	16.51	6
ATOM	2418	CD1	TYR	A	295	24.687	22.187	70.543	1.00	15.81	6
ATOM	2419	CD2	TYR	A	295	22.540	22.989	71.154	1.00	18.65	6
ATOM	2420	CE1	TYR	A	295	25.220	22.604	71.752	1.00	17.42	6
ATOM	2421	CE2	TYR	A	295	23.019	23.388	72.373	1.00	19.62	6
ATOM	2422	CZ	TYR	A	295	24.355	23.197	72.675	1.00	22.11	6
ATOM	2423	OH	TYR	A	295	24.804	23.591	73.924	1.00	21.14	8
ATOM	2424	N	ASN	A	296	22.173	22.434	65.605	1.00	8.29	7
ATOM	2425	CA	ASN	A	296	22.141	21.907	64.219	1.00	10.41	6
ATOM	2426	C	ASN	A	296	23.189	22.685	63.414	1.00	6.38	6
ATOM	2427	O	ASN	A	296	24.030	22.072	62.803	1.00	7.68	8
ATOM	2428	CB	ASN	A	296	20.748	22.243	63.617	1.00	7.49	6
ATOM	2429	CG	ASN	A	296	19.773	21.165	63.988	1.00	9.99	6
ATOM	2430	OD1	ASN	A	296	20.061	20.282	64.830	1.00	12.42	8
ATOM	2431	ND2	ASN	A	296	18.578	21.090	63.424	1.00	13.13	7
ATOM	2432	N	LEU	A	297	23.235	23.991	63.539	1.00	6.28	7
ATOM	2433	CA	LEU	A	297	24.228	24.816	62.913	1.00	7.26	6
ATOM	2434	C	LEU	A	297	25.651	24.549	63.305	1.00	12.65	6
ATOM	2435	O	LEU	A	297	26.574	24.474	62.450	1.00	11.73	8
ATOM	2436	CB	LEU	A	297	23.906	26.290	63.098	1.00	3.62	6
ATOM	2437	CG	LEU	A	297	22.496	26.762	62.637	1.00	13.98	6
ATOM	2438	CD1	LEU	A	297	22.357	28.272	62.977	1.00	5.32	6
ATOM	2439	CD2	LEU	A	297	22.424	26.576	61.117	1.00	10.90	6
ATOM	2440	N	TYR	A	298	25.892	24.420	64.642	1.00	9.91	7
ATOM	2441	CA	TYR	A	298	27.252	24.121	65.117	1.00	8.20	6
ATOM	2442	C	TYR	A	298	27.660	22.763	64.599	1.00	6.55	6
ATOM	2443	O	TYR	A	298	28.803	22.585	64.123	1.00	9.41	8
ATOM	2444	CB	TYR	A	298	27.099	24.033	66.689	1.00	9.28	6
ATOM	2445	CG	TYR	A	298	28.271	23.362	67.349	1.00	8.40	6
ATOM	2446	CD1	TYR	A	298	29.502	23.971	67.360	1.00	8.56	6
ATOM	2447	CD2	TYR	A	298	28.121	22.138	67.959	1.00	12.60	6
ATOM	2448	CE1	TYR	A	298	30.595	23.359	68.011	1.00	11.66	6
ATOM	2449	CE2	TYR	A	298	29.186	21.534	68.612	1.00	12.63	6
ATOM	2450	CZ	TYR	A	298	30.390	22.159	68.624	1.00	12.14	6
ATOM	2451	OH	TYR	A	298	31.461	21.534	69.222	1.00	18.26	8
ATOM	2452	N	ASN	A	299	26.803	21.744	64.652	1.00	6.95	7
ATOM	2453	CA	ASN	A	299	27.263	20.456	64.134	1.00	9.55	6
ATOM	2454	C	ASN	A	299	27.468	20.453	62.571	1.00	13.82	6
ATOM	2455	O	ASN	A	299	28.443	19.870	62.073	1.00	11.91	8
ATOM	2456	CB	ASN	A	299	26.080	19.553	64.517	1.00	12.01	6
ATOM	2457	CG	ASN	A	299	26.192	19.058	65.973	1.00	18.94	6
ATOM	2458	OD1	ASN	A	299	27.318	18.757	66.382	1.00	13.12	8
ATOM	2459	ND2	ASN	A	299	25.118	18.927	66.739	1.00	11.91	7
ATOM	2460	N	ALA	A	300	26.608	21.178	61.829	1.00	10.90	7
ATOM	2461	CA	ALA	A	300	26.728	21.193	60.341	1.00	13.38	6
ATOM	2462	C	ALA	A	300	28.063	21.837	60.015	1.00	11.55	6
ATOM	2463	O	ALA	A	300	28.877	21.283	59.284	1.00	9.92	8
ATOM	2464	CB	ALA	A	300	25.627	22.057	59.713	1.00	5.87	6

ATOM	2465	N	SER	A	301	28.416	22.908	60.779	1.00	10.29	7
ATOM	2466	CA	SER	A	301	29.669	23.576	60.587	1.00	8.35	6
ATOM	2467	C	SER	A	301	30.917	22.770	60.935	1.00	11.77	6
ATOM	2468	O	SER	A	301	31.982	23.182	60.431	1.00	9.86	8
ATOM	2469	CB	SER	A	301	29.730	24.937	61.305	1.00	16.73	6
ATOM	2470	OG	SER	A	301	30.179	24.745	62.651	1.00	16.74	8
ATOM	2471	N	ASN	A	302	30.797	21.642	61.635	1.00	9.53	7
ATOM	2472	CA	ASN	A	302	31.979	20.871	61.987	1.00	12.86	6
ATOM	2473	C	ASN	A	302	31.981	19.582	61.175	1.00	12.44	6
ATOM	2474	O	ASN	A	302	32.842	18.715	61.393	1.00	12.66	8
ATOM	2475	CB	ASN	A	302	31.833	20.448	63.536	1.00	10.96	6
ATOM	2476	CG	ASN	A	302	32.455	21.559	64.362	1.00	12.81	6
ATOM	2477	OD1	ASN	A	302	33.671	21.716	64.316	1.00	10.84	8
ATOM	2478	ND2	ASN	A	302	31.695	22.416	65.059	1.00	11.91	7
ATOM	2479	N	SER	A	303	30.990	19.419	60.303	1.00	9.65	7
ATOM	2480	CA	SER	A	303	30.905	18.161	59.584	1.00	11.59	6
ATOM	2481	C	SER	A	303	31.581	18.096	58.201	1.00	11.60	6
ATOM	2482	O	SER	A	303	31.515	17.032	57.607	1.00	11.47	8
ATOM	2483	CB	SER	A	303	29.469	17.674	59.486	1.00	21.93	6
ATOM	2484	OG	SER	A	303	28.928	17.533	60.790	1.00	20.56	8
ATOM	2485	N	GLY	A	304	32.374	19.057	57.832	1.00	14.77	7
ATOM	2486	CA	GLY	A	304	33.210	19.066	56.618	1.00	17.32	6
ATOM	2487	C	GLY	A	304	32.397	18.788	55.312	1.00	17.00	6
ATOM	2488	O	GLY	A	304	32.911	18.072	54.447	1.00	17.50	8
ATOM	2489	N	GLY	A	305	31.166	19.213	55.226	1.00	14.82	7
ATOM	2490	CA	GLY	A	305	30.290	18.985	54.094	1.00	15.48	6
ATOM	2491	C	GLY	A	305	29.588	17.703	54.314	1.00	16.63	6
ATOM	2492	O	GLY	A	305	28.693	17.463	53.504	1.00	16.11	8
ATOM	2493	N	ASN	A	306	29.788	16.819	55.278	1.00	15.13	7
ATOM	2494	CA	ASN	A	306	28.948	15.624	55.355	1.00	15.73	6
ATOM	2495	C	ASN	A	306	27.640	15.815	56.075	1.00	14.60	6
ATOM	2496	O	ASN	A	306	26.890	14.812	56.192	1.00	16.40	8
ATOM	2497	CB	ASN	A	306	29.730	14.515	56.100	1.00	27.81	6
ATOM	2498	CG	ASN	A	306	30.761	13.901	55.189	1.00	33.85	6
ATOM	2499	OD1	ASN	A	306	30.662	14.051	53.980	1.00	27.05	8
ATOM	2500	ND2	ASN	A	306	31.756	13.197	55.701	1.00	27.79	7
ATOM	2501	N	TYR	A	307	27.215	16.978	56.472	1.00	12.08	7
ATOM	2502	CA	TYR	A	307	25.952	17.035	57.241	1.00	14.18	6
ATOM	2503	C	TYR	A	307	24.781	16.883	56.264	1.00	16.05	6
ATOM	2504	O	TYR	A	307	24.907	17.587	55.299	1.00	12.72	8
ATOM	2505	CB	TYR	A	307	25.858	18.413	57.926	1.00	11.27	6
ATOM	2506	CG	TYR	A	307	24.701	18.546	58.899	1.00	15.63	6
ATOM	2507	CD1	TYR	A	307	24.883	18.120	60.218	1.00	17.92	6
ATOM	2508	CD2	TYR	A	307	23.486	19.084	58.561	1.00	16.39	6
ATOM	2509	CE1	TYR	A	307	23.853	18.253	61.133	1.00	22.23	6
ATOM	2510	CE2	TYR	A	307	22.444	19.219	59.444	1.00	19.66	6
ATOM	2511	CZ	TYR	A	307	22.642	18.802	60.759	1.00	23.46	6
ATOM	2512	OH	TYR	A	307	21.642	18.869	61.695	1.00	25.41	8
ATOM	2513	N	ASP	A	308	23.591	16.418	56.401	1.00	13.94	7
ATOM	2514	CA	ASP	A	308	22.531	16.460	55.437	1.00	13.17	6
ATOM	2515	C	ASP	A	308	21.776	17.751	55.543	1.00	14.66	6
ATOM	2516	O	ASP	A	308	20.839	17.941	56.332	1.00	15.00	8
ATOM	2517	CB	ASP	A	308	21.684	15.233	55.628	1.00	9.65	6
ATOM	2518	CG	ASP	A	308	20.585	15.152	54.567	1.00	16.73	6
ATOM	2519	OD1	ASP	A	308	20.400	16.065	53.758	1.00	16.88	8
ATOM	2520	OD2	ASP	A	308	19.891	14.137	54.693	1.00	14.99	8
ATOM	2521	N	MET	A	309	22.105	18.682	54.620	1.00	12.06	7
ATOM	2522	CA	MET	A	309	21.479	19.984	54.669	1.00	10.03	6
ATOM	2523	C	MET	A	309	19.995	19.925	54.496	1.00	11.61	6
ATOM	2524	O	MET	A	309	19.380	20.906	54.955	1.00	12.12	8
ATOM	2525	CB	MET	A	309	22.080	20.994	53.681	1.00	20.14	6
ATOM	2526	CG	MET	A	309	23.601	21.176	53.875	1.00	17.95	6
ATOM	2527	SD	MET	A	309	23.869	22.451	55.168	1.00	17.26	16
ATOM	2528	CE	MET	A	309	23.532	23.967	54.322	1.00	10.92	6
ATOM	2529	N	ALA	A	310	19.391	18.896	53.908	1.00	10.05	7
ATOM	2530	CA	ALA	A	310	17.926	18.938	53.854	1.00	14.66	6
ATOM	2531	C	ALA	A	310	17.317	18.815	55.281	1.00	17.97	6
ATOM	2532	O	ALA	A	310	16.133	19.091	55.442	1.00	15.37	8
ATOM	2533	CB	ALA	A	310	17.404	17.690	53.130	1.00	7.97	6
ATOM	2534	N	LYS	A	311	18.097	18.340	56.246	1.00	18.30	7
ATOM	2535	CA	LYS	A	311	17.577	18.186	57.613	1.00	21.21	6
ATOM	2536	C	LYS	A	311	17.995	19.322	58.542	1.00	20.93	6
ATOM	2537	O	LYS	A	311	17.689	19.170	59.721	1.00	22.60	8
ATOM	2538	CB	LYS	A	311	18.134	16.857	58.122	1.00	17.90	6

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ATOM   2539  CG  LYS A 311      17.596  15.669  57.320  1.00 27.66   6
ATOM   2540  CD  LYS A 311      17.919  14.390  58.048  1.00 40.46   6
ATOM   2541  CE  LYS A 311      18.018  13.147  57.187  1.00 53.31   6
ATOM   2542  NZ  LYS A 311      19.293  12.385  57.486  1.00 60.95   7
ATOM   2543  N   LEU A 312      18.546  20.444  58.086  1.00 18.62   7
ATOM   2544  CA  LEU A 312      18.952  21.512  58.957  1.00 16.83   6
ATOM   2545  C   LEU A 312      17.889  22.045  59.932  1.00 16.10   6
ATOM   2546  O   LEU A 312      18.314  22.536  61.000  1.00 16.57   8
ATOM   2547  CB  LEU A 312      19.465  22.772  58.296  1.00 14.38   6
ATOM   2548  CG  LEU A 312      20.877  23.279  58.342  1.00 20.88   6
ATOM   2549  CD1 LEU A 312      20.864  24.762  58.061  1.00 20.98   6
ATOM   2550  CD2 LEU A 312      21.681  22.941  59.568  1.00 25.82   6
ATOM   2551  N   LEU A 313      16.642  22.116  59.613  1.00 13.56   7
ATOM   2552  CA  LEU A 313      15.615  22.672  60.475  1.00 14.51   6
ATOM   2553  C   LEU A 313      14.935  21.585  61.308  1.00 15.32   6
ATOM   2554  O   LEU A 313      14.075  21.927  62.129  1.00 14.10   8
ATOM   2555  CB  LEU A 313      14.525  23.397  59.644  1.00 12.48   6
ATOM   2556  CG  LEU A 313      15.077  24.595  58.877  1.00 21.20   6
ATOM   2557  CD1 LEU A 313      13.988  25.262  58.044  1.00 17.97   6
ATOM   2558  CD2 LEU A 313      15.715  25.619  59.844  1.00 16.09   6
ATOM   2559  N   ASN A 314      15.293  20.315  61.111  1.00 14.54   7
ATOM   2560  CA  ASN A 314      14.549  19.306  61.859  1.00 18.06   6
ATOM   2561  C   ASN A 314      14.791  19.401  63.387  1.00 18.92   6
ATOM   2562  O   ASN A 314      15.930  19.568  63.824  1.00 15.49   8
ATOM   2563  CB  ASN A 314      14.974  17.893  61.401  1.00 23.05   6
ATOM   2564  CG  ASN A 314      14.330  17.460  60.071  1.00 29.52   6
ATOM   2565  OD1 ASN A 314      13.468  18.106  59.463  1.00 23.14   8
ATOM   2566  ND2 ASN A 314      14.787  16.326  59.564  1.00 22.18   7
ATOM   2567  N   GLY A 315      13.721  19.262  64.155  1.00 19.24   7
ATOM   2568  CA  GLY A 315      13.833  19.187  65.610  1.00 17.88   6
ATOM   2569  C   GLY A 315      14.003  20.576  66.173  1.00 16.97   6
ATOM   2570  O   GLY A 315      14.437  20.709  67.319  1.00 20.46   8
ATOM   2571  N   THR A 316      13.686  21.634  65.428  1.00 13.17   7
ATOM   2572  CA  THR A 316      13.939  22.972  65.936  1.00 10.52   6
ATOM   2573  C   THR A 316      12.657  23.638  66.379  1.00 11.28   6
ATOM   2574  O   THR A 316      11.548  23.166  66.032  1.00 13.19   8
ATOM   2575  CB  THR A 316      14.583  23.888  64.845  1.00 16.57   6
ATOM   2576  OG1 THR A 316      13.639  23.868  63.748  1.00 13.69   8
ATOM   2577  CG2 THR A 316      15.886  23.264  64.400  1.00 11.29   6
ATOM   2578  N   VAL A 317      12.808  24.754  67.083  1.00  9.48   7
ATOM   2579  CA  VAL A 317      11.615  25.465  67.500  1.00 10.33   6
ATOM   2580  C   VAL A 317      11.073  26.218  66.265  1.00 11.64   6
ATOM   2581  O   VAL A 317       9.860  26.352  66.100  1.00 12.12   8
ATOM   2582  CB  VAL A 317      11.883  26.544  68.593  1.00 10.20   6
ATOM   2583  CG1 VAL A 317      10.551  27.181  69.018  1.00 10.92   6
ATOM   2584  CG2 VAL A 317      12.568  25.916  69.807  1.00 10.14   6
ATOM   2585  N   VAL A 318      11.985  26.824  65.488  1.00 10.03   7
ATOM   2586  CA  VAL A 318      11.498  27.594  64.324  1.00 12.79   6
ATOM   2587  C   VAL A 318      10.720  26.750  63.334  1.00 12.26   6
ATOM   2588  O   VAL A 318       9.691  27.169  62.821  1.00 14.96   8
ATOM   2589  CB  VAL A 318      12.579  28.500  63.750  1.00 10.04   6
ATOM   2590  CG1 VAL A 318      13.618  27.626  63.021  1.00  3.78   6
ATOM   2591  CG2 VAL A 318      11.948  29.590  62.919  1.00 17.99   6
ATOM   2592  N   GLN A 319      10.935  25.467  63.190  1.00 14.71   7
ATOM   2593  CA  GLN A 319      10.195  24.610  62.319  1.00 17.78   6
ATOM   2594  C   GLN A 319       8.783  24.386  62.812  1.00 22.17   6
ATOM   2595  O   GLN A 319       7.802  24.453  62.056  1.00 19.34   8
ATOM   2596  CB  GLN A 319      10.980  23.316  62.105  1.00 12.50   6
ATOM   2597  CG  GLN A 319      10.253  22.339  61.198  1.00 13.69   6
ATOM   2598  CD  GLN A 319      10.889  20.989  61.098  1.00 22.01   6
ATOM   2599  OE1 GLN A 319      11.040  20.278  62.086  1.00 27.91   8
ATOM   2600  NE2 GLN A 319      11.344  20.567  59.900  1.00 26.90   7
ATOM   2601  N   LYS A 320       8.644  24.072  64.113  1.00 22.53   7
ATOM   2602  CA  LYS A 320       7.369  23.743  64.731  1.00 20.27   6
ATOM   2603  C   LYS A 320       6.600  24.914  65.270  1.00 20.25   6
ATOM   2604  O   LYS A 320       5.387  24.879  65.097  1.00 22.65   8
ATOM   2605  CB  LYS A 320       7.557  22.758  65.878  1.00 28.06   6
ATOM   2606  CG  LYS A 320       6.854  21.444  65.592  1.00 41.77   6
ATOM   2607  CD  LYS A 320       5.644  21.334  66.488  1.00 50.06   6
ATOM   2608  CE  LYS A 320       5.485  19.947  67.110  1.00 53.75   6
ATOM   2609  NZ  LYS A 320       4.273  19.915  67.987  1.00 53.30   7
ATOM   2610  N   HIS A 321       7.185  25.939  65.872  1.00 17.78   7
ATOM   2611  CA  HIS A 321       6.451  27.070  66.406  1.00 17.78   6
ATOM   2612  C   HIS A 321       7.193  28.343  66.059  1.00 19.94   6
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ATOM	2613	O	HIS	A	321	7.826	29.049	66.885	1.00	20.97	8
ATOM	2614	CB	HIS	A	321	6.440	27.016	67.996	1.00	17.17	6
ATOM	2615	CG	HIS	A	321	5.844	25.741	68.489	1.00	7.99	6
ATOM	2616	ND1	HIS	A	321	6.584	24.678	68.967	1.00	21.64	7
ATOM	2617	CD2	HIS	A	321	4.569	25.292	68.428	1.00	12.69	6
ATOM	2618	CE1	HIS	A	321	5.763	23.670	69.234	1.00	18.85	6
ATOM	2619	NE2	HIS	A	321	4.530	24.013	68.913	1.00	20.43	7
ATOM	2620	N	PRO	A	322	7.113	28.801	64.817	1.00	18.84	7
ATOM	2621	CA	PRO	A	322	7.857	29.919	64.297	1.00	16.35	6
ATOM	2622	C	PRO	A	322	7.495	31.214	64.937	1.00	15.92	6
ATOM	2623	O	PRO	A	322	8.327	32.103	65.048	1.00	17.57	8
ATOM	2624	CB	PRO	A	322	7.551	30.051	62.767	1.00	18.11	6
ATOM	2625	CG	PRO	A	322	6.291	29.215	62.690	1.00	19.63	6
ATOM	2626	CD	PRO	A	322	6.391	28.081	63.734	1.00	19.70	6
ATOM	2627	N	MET	A	323	6.270	31.375	65.380	1.00	15.79	7
ATOM	2628	CA	MET	A	323	5.946	32.674	65.999	1.00	18.66	6
ATOM	2629	C	MET	A	323	6.503	32.728	67.439	1.00	19.54	6
ATOM	2630	O	MET	A	323	6.450	33.810	68.009	1.00	18.49	8
ATOM	2631	CB	MET	A	323	4.417	32.838	65.991	1.00	24.07	6
ATOM	2632	CG	MET	A	323	3.940	33.170	64.565	1.00	52.61	6
ATOM	2633	SD	MET	A	323	2.249	33.780	64.474	1.00	69.72	16
ATOM	2634	CE	MET	A	323	1.332	32.252	64.705	1.00	60.17	6
ATOM	2635	N	HIS	A	324	7.050	31.633	67.964	1.00	18.53	7
ATOM	2636	CA	HIS	A	324	7.611	31.719	69.331	1.00	17.80	6
ATOM	2637	C	HIS	A	324	9.089	31.424	69.336	1.00	19.06	6
ATOM	2638	O	HIS	A	324	9.603	31.068	70.408	1.00	18.98	8
ATOM	2639	CB	HIS	A	324	6.895	30.630	70.147	1.00	19.82	6
ATOM	2640	CG	HIS	A	324	5.495	31.084	70.453	1.00	24.52	6
ATOM	2641	ND1	HIS	A	324	4.404	30.648	69.731	1.00	29.89	7
ATOM	2642	CD2	HIS	A	324	5.038	31.953	71.384	1.00	30.43	6
ATOM	2643	CE1	HIS	A	324	3.321	31.243	70.218	1.00	34.69	6
ATOM	2644	NE2	HIS	A	324	3.667	32.032	71.226	1.00	30.63	7
ATOM	2645	N	ALA	A	325	9.753	31.465	68.169	1.00	17.22	7
ATOM	2646	CA	ALA	A	325	11.175	31.186	68.083	1.00	15.46	6
ATOM	2647	C	ALA	A	325	11.989	32.439	67.872	1.00	16.14	6
ATOM	2648	O	ALA	A	325	11.688	33.248	66.983	1.00	15.68	8
ATOM	2649	CB	ALA	A	325	11.517	30.230	66.918	1.00	13.81	6
ATOM	2650	N	VAL	A	326	13.053	32.650	68.662	1.00	14.07	7
ATOM	2651	CA	VAL	A	326	14.017	33.699	68.433	1.00	11.09	6
ATOM	2652	C	VAL	A	326	15.268	32.951	67.941	1.00	12.79	6
ATOM	2653	O	VAL	A	326	15.707	32.027	68.603	1.00	13.69	8
ATOM	2654	CB	VAL	A	326	14.411	34.668	69.512	1.00	10.21	6
ATOM	2655	CG1	VAL	A	326	15.622	35.512	69.255	1.00	5.75	6
ATOM	2656	CG2	VAL	A	326	13.181	35.529	69.857	1.00	15.88	6
ATOM	2657	N	THR	A	327	15.643	33.230	66.653	1.00	10.18	7
ATOM	2658	CA	THR	A	327	16.738	32.402	66.088	1.00	5.75	6
ATOM	2659	C	THR	A	327	18.036	33.115	66.280	1.00	2.58	6
ATOM	2660	O	THR	A	327	18.105	34.346	66.171	1.00	7.39	8
ATOM	2661	CB	THR	A	327	16.477	32.120	64.556	1.00	11.93	6
ATOM	2662	OG1	THR	A	327	16.120	33.376	63.955	1.00	8.64	8
ATOM	2663	CG2	THR	A	327	15.247	31.232	64.436	1.00	6.52	6
ATOM	2664	N	PHE	A	328	19.092	32.256	66.427	1.00	4.68	7
ATOM	2665	CA	PHE	A	328	20.356	33.009	66.544	1.00	5.31	6
ATOM	2666	C	PHE	A	328	21.426	32.064	66.018	1.00	4.46	6
ATOM	2667	O	PHE	A	328	21.174	30.887	66.007	1.00	7.88	8
ATOM	2668	CB	PHE	A	328	20.729	33.361	68.040	1.00	10.06	6
ATOM	2669	CG	PHE	A	328	20.892	32.177	68.973	1.00	8.83	6
ATOM	2670	CD1	PHE	A	328	19.810	31.411	69.353	1.00	7.17	6
ATOM	2671	CD2	PHE	A	328	22.110	31.846	69.500	1.00	11.93	6
ATOM	2672	CE1	PHE	A	328	19.952	30.319	70.200	1.00	12.02	6
ATOM	2673	CE2	PHE	A	328	22.292	30.785	70.376	1.00	6.08	6
ATOM	2674	CZ	PHE	A	328	21.166	30.014	70.717	1.00	4.49	6
ATOM	2675	N	VAL	A	329	22.618	32.516	65.776	1.00	3.61	7
ATOM	2676	CA	VAL	A	329	23.689	31.561	65.419	1.00	6.19	6
ATOM	2677	C	VAL	A	329	24.612	31.281	66.621	1.00	8.45	6
ATOM	2678	O	VAL	A	329	25.080	30.150	66.823	1.00	5.56	8
ATOM	2679	CB	VAL	A	329	24.559	32.288	64.293	1.00	9.54	6
ATOM	2680	CG1	VAL	A	329	25.572	31.346	63.707	1.00	3.85	6
ATOM	2681	CG2	VAL	A	329	23.621	32.666	63.148	1.00	8.28	6
ATOM	2682	N	ASP	A	330	25.071	32.366	67.289	1.00	9.42	7
ATOM	2683	CA	ASP	A	330	25.997	32.213	68.400	1.00	11.97	6
ATOM	2684	C	ASP	A	330	25.663	33.266	69.475	1.00	11.48	6
ATOM	2685	O	ASP	A	330	24.962	34.225	69.185	1.00	9.81	8
ATOM	2686	CB	ASP	A	330	27.485	32.325	68.053	1.00	9.87	6

ATOM	2687	CG	ASP	A	330	28.078	31.041	67.577	1.00	21.67	6
ATOM	2688	OD1	ASP	A	330	27.916	30.053	68.325	1.00	12.86	8
ATOM	2689	OD2	ASP	A	330	28.713	30.985	66.479	1.00	13.95	8
ATOM	2690	N	ASN	A	331	26.186	33.083	70.706	1.00	13.63	7
ATOM	2691	CA	ASN	A	331	25.883	34.116	71.729	1.00	12.71	6
ATOM	2692	C	ASN	A	331	27.005	34.153	72.747	1.00	13.53	6
ATOM	2693	O	ASN	A	331	28.031	33.495	72.513	1.00	13.75	8
ATOM	2694	CB	ASN	A	331	24.491	33.935	72.300	1.00	7.36	6
ATOM	2695	CG	ASN	A	331	24.423	32.664	73.177	1.00	16.83	6
ATOM	2696	OD1	ASN	A	331	25.399	32.003	73.561	1.00	15.71	8
ATOM	2697	ND2	ASN	A	331	23.214	32.296	73.527	1.00	14.16	7
ATOM	2698	N	HIS	A	332	26.851	34.918	73.819	1.00	14.73	7
ATOM	2699	CA	HIS	A	332	27.992	35.058	74.772	1.00	16.51	6
ATOM	2700	C	HIS	A	332	28.287	33.755	75.481	1.00	15.53	6
ATOM	2701	O	HIS	A	332	29.413	33.627	75.940	1.00	23.15	8
ATOM	2702	CB	HIS	A	332	27.751	36.178	75.772	1.00	15.38	6
ATOM	2703	CG	HIS	A	332	26.554	35.863	76.594	1.00	18.78	6
ATOM	2704	ND1	HIS	A	332	25.280	35.846	76.055	1.00	26.51	7
ATOM	2705	CD2	HIS	A	332	26.427	35.519	77.907	1.00	16.53	6
ATOM	2706	CE1	HIS	A	332	24.394	35.521	77.003	1.00	21.51	6
ATOM	2707	NE2	HIS	A	332	25.084	35.316	78.122	1.00	18.42	7
ATOM	2708	N	ASP	A	333	27.425	32.794	75.583	1.00	13.82	7
ATOM	2709	CA	ASP	A	333	27.648	31.483	76.118	1.00	14.31	6
ATOM	2710	C	ASP	A	333	28.355	30.563	75.119	1.00	15.52	6
ATOM	2711	O	ASP	A	333	29.083	29.676	75.561	1.00	13.90	8
ATOM	2712	CB	ASP	A	333	26.325	30.770	76.388	1.00	13.27	6
ATOM	2713	CG	ASP	A	333	25.254	31.297	77.309	1.00	44.51	6
ATOM	2714	OD1	ASP	A	333	25.641	31.795	78.383	1.00	22.07	8
ATOM	2715	OD2	ASP	A	333	24.000	31.244	77.004	1.00	51.59	8
ATOM	2716	N	SER	A	334	28.022	30.614	73.775	1.00	15.01	7
ATOM	2717	CA	SER	A	334	28.678	29.600	72.897	1.00	12.67	6
ATOM	2718	C	SER	A	334	29.996	30.054	72.336	1.00	13.90	6
ATOM	2719	O	SER	A	334	30.756	29.295	71.664	1.00	15.43	8
ATOM	2720	CB	SER	A	334	27.670	29.290	71.743	1.00	13.31	6
ATOM	2721	OG	SER	A	334	27.467	30.528	71.037	1.00	7.52	8
ATOM	2722	N	GLN	A	335	30.391	31.294	72.559	1.00	15.37	7
ATOM	2723	CA	GLN	A	335	31.655	31.863	72.059	1.00	15.42	6
ATOM	2724	C	GLN	A	335	32.828	31.146	72.696	1.00	19.12	6
ATOM	2725	O	GLN	A	335	32.726	30.487	73.733	1.00	18.06	8
ATOM	2726	CB	GLN	A	335	31.759	33.374	72.246	1.00	15.85	6
ATOM	2727	CG	GLN	A	335	31.874	33.849	73.727	1.00	21.14	6
ATOM	2728	CD	GLN	A	335	31.977	35.359	73.825	1.00	14.14	6
ATOM	2729	OE1	GLN	A	335	30.999	36.082	73.978	1.00	15.97	8
ATOM	2730	NE2	GLN	A	335	33.183	35.919	73.666	1.00	20.22	7
ATOM	2731	N	PRO	A	336	33.988	31.195	72.045	1.00	18.66	7
ATOM	2732	CA	PRO	A	336	35.141	30.422	72.427	1.00	21.11	6
ATOM	2733	C	PRO	A	336	35.535	30.541	73.910	1.00	21.47	6
ATOM	2734	O	PRO	A	336	35.630	31.632	74.463	1.00	20.06	8
ATOM	2735	CB	PRO	A	336	36.315	30.898	71.533	1.00	21.26	6
ATOM	2736	CG	PRO	A	336	35.498	31.327	70.307	1.00	22.42	6
ATOM	2737	CD	PRO	A	336	34.207	31.946	70.824	1.00	21.11	6
ATOM	2738	N	GLY	A	337	35.756	29.389	74.519	1.00	23.46	7
ATOM	2739	CA	GLY	A	337	36.227	29.335	75.895	1.00	25.50	6
ATOM	2740	C	GLY	A	337	35.071	29.447	76.884	1.00	25.73	6
ATOM	2741	O	GLY	A	337	35.352	29.084	78.031	1.00	27.95	8
ATOM	2742	N	GLU	A	338	33.917	29.999	76.559	1.00	22.43	7
ATOM	2743	CA	GLU	A	338	32.827	30.090	77.484	1.00	22.33	6
ATOM	2744	C	GLU	A	338	32.125	28.786	77.828	1.00	22.91	6
ATOM	2745	O	GLU	A	338	32.358	27.685	77.351	1.00	22.68	8
ATOM	2746	CB	GLU	A	338	31.812	31.168	77.168	1.00	17.78	6
ATOM	2747	CG	GLU	A	338	32.440	32.564	77.270	1.00	22.34	6
ATOM	2748	CD	GLU	A	338	32.952	32.755	78.715	1.00	29.04	6
ATOM	2749	OE1	GLU	A	338	32.114	32.805	79.623	1.00	27.92	8
ATOM	2750	OE2	GLU	A	338	34.187	32.810	78.861	1.00	19.42	8
ATOM	2751	N	SER	A	339	31.197	28.939	78.777	1.00	24.21	7
ATOM	2752	CA	SER	A	339	30.450	27.883	79.434	1.00	24.36	6
ATOM	2753	C	SER	A	339	29.691	26.926	78.538	1.00	21.82	6
ATOM	2754	O	SER	A	339	29.675	25.711	78.789	1.00	24.25	8
ATOM	2755	CB	SER	A	339	29.444	28.501	80.457	1.00	32.53	6
ATOM	2756	OG	SER	A	339	30.214	29.253	81.421	1.00	35.18	8
ATOM	2757	N	LEU	A	340	29.040	27.416	77.495	1.00	20.02	7
ATOM	2758	CA	LEU	A	340	28.344	26.458	76.592	1.00	18.17	6
ATOM	2759	C	LEU	A	340	29.104	26.412	75.236	1.00	19.43	6
ATOM	2760	O	LEU	A	340	28.447	26.384	74.171	1.00	15.42	8

ATOM	2761	CB	LEU	A	340	26.916	26.987	76.489	1.00	21.01	6
ATOM	2762	CG	LEU	A	340	26.161	27.034	77.864	1.00	22.85	6
ATOM	2763	CD1	LEU	A	340	24.807	27.708	77.681	1.00	29.12	6
ATOM	2764	CD2	LEU	A	340	25.934	25.631	78.372	1.00	20.86	6
ATOM	2765	N	GLU	A	341	30.410	26.644	75.257	1.00	15.17	7
ATOM	2766	CA	GLU	A	341	31.187	26.743	74.028	1.00	16.51	6
ATOM	2767	C	GLU	A	341	30.716	25.775	72.914	1.00	13.73	6
ATOM	2768	O	GLU	A	341	30.620	24.575	73.046	1.00	12.93	8
ATOM	2769	CB	GLU	A	341	32.678	26.615	74.252	1.00	15.92	6
ATOM	2770	CG	GLU	A	341	33.532	26.518	72.994	1.00	34.72	6
ATOM	2771	CD	GLU	A	341	35.022	26.565	73.226	1.00	38.23	6
ATOM	2772	OE1	GLU	A	341	35.568	25.733	73.968	1.00	49.78	8
ATOM	2773	OE2	GLU	A	341	35.730	27.429	72.683	1.00	51.54	8
ATOM	2774	N	SER	A	342	30.307	26.343	71.767	1.00	13.62	7
ATOM	2775	CA	SER	A	342	29.800	25.498	70.610	1.00	12.16	6
ATOM	2776	C	SER	A	342	29.630	26.518	69.453	1.00	9.95	6
ATOM	2777	O	SER	A	342	28.516	26.840	69.089	1.00	10.55	8
ATOM	2778	CB	SER	A	342	28.487	24.856	71.014	1.00	11.64	6
ATOM	2779	OG	SER	A	342	27.526	25.740	71.578	1.00	10.33	8
ATOM	2780	N	PHE	A	343	30.743	27.112	69.096	1.00	8.26	7
ATOM	2781	CA	PHE	A	343	30.845	28.273	68.243	1.00	14.28	6
ATOM	2782	C	PHE	A	343	30.727	27.865	66.752	1.00	14.09	6
ATOM	2783	O	PHE	A	343	31.490	26.977	66.427	1.00	15.10	8
ATOM	2784	CB	PHE	A	343	32.150	29.020	68.461	1.00	7.83	6
ATOM	2785	CG	PHE	A	343	32.130	30.489	68.111	1.00	18.35	6
ATOM	2786	CD1	PHE	A	343	31.135	31.324	68.579	1.00	13.69	6
ATOM	2787	CD2	PHE	A	343	33.124	31.041	67.314	1.00	15.40	6
ATOM	2788	CE1	PHE	A	343	31.095	32.664	68.242	1.00	12.25	6
ATOM	2789	CE2	PHE	A	343	33.113	32.400	67.009	1.00	10.93	6
ATOM	2790	CZ	PHE	A	343	32.119	33.211	67.491	1.00	10.68	6
ATOM	2791	N	VAL	A	344	29.802	28.461	66.025	1.00	15.94	7
ATOM	2792	CA	VAL	A	344	29.677	28.038	64.592	1.00	13.97	6
ATOM	2793	C	VAL	A	344	30.922	28.436	63.790	1.00	11.82	6
ATOM	2794	O	VAL	A	344	31.366	29.575	63.779	1.00	13.31	8
ATOM	2795	CB	VAL	A	344	28.406	28.592	63.990	1.00	17.29	6
ATOM	2796	CG1	VAL	A	344	28.214	28.200	62.492	1.00	14.50	6
ATOM	2797	CG2	VAL	A	344	27.178	28.056	64.744	1.00	4.23	6
ATOM	2798	N	GLN	A	345	31.557	27.472	63.108	1.00	11.93	7
ATOM	2799	CA	GLN	A	345	32.791	27.751	62.371	1.00	13.62	6
ATOM	2800	C	GLN	A	345	32.641	28.845	61.303	1.00	15.48	6
ATOM	2801	O	GLN	A	345	31.579	29.089	60.695	1.00	14.28	8
ATOM	2802	CB	GLN	A	345	33.410	26.543	61.726	1.00	16.29	6
ATOM	2803	CG	GLN	A	345	33.398	25.247	62.466	1.00	28.74	6
ATOM	2804	CD	GLN	A	345	34.757	24.688	62.741	1.00	41.22	6
ATOM	2805	OE1	GLN	A	345	34.914	23.475	62.547	1.00	52.69	8
ATOM	2806	NE2	GLN	A	345	35.721	25.561	62.976	1.00	49.90	7
ATOM	2807	N	GLU	A	346	33.742	29.587	61.162	1.00	12.40	7
ATOM	2808	CA	GLU	A	346	33.672	30.778	60.332	1.00	14.26	6
ATOM	2809	C	GLU	A	346	33.214	30.541	58.876	1.00	14.02	6
ATOM	2810	O	GLU	A	346	32.423	31.331	58.393	1.00	13.79	8
ATOM	2811	CB	GLU	A	346	35.068	31.404	60.394	1.00	14.25	6
ATOM	2812	CG	GLU	A	346	35.121	32.681	59.551	1.00	32.42	6
ATOM	2813	CD	GLU	A	346	36.535	33.237	59.460	1.00	48.94	6
ATOM	2814	OE1	GLU	A	346	37.450	32.689	60.123	1.00	55.69	8
ATOM	2815	OE2	GLU	A	346	36.723	34.230	58.719	1.00	52.71	8
ATOM	2816	N	TRP	A	347	33.609	29.456	58.224	1.00	12.79	7
ATOM	2817	CA	TRP	A	347	33.170	29.294	56.818	1.00	16.92	6
ATOM	2818	C	TRP	A	347	31.661	29.131	56.734	1.00	17.45	6
ATOM	2819	O	TRP	A	347	31.046	29.639	55.787	1.00	17.59	8
ATOM	2820	CB	TRP	A	347	33.884	28.078	56.211	1.00	8.52	6
ATOM	2821	CG	TRP	A	347	33.437	26.750	56.724	1.00	17.57	6
ATOM	2822	CD1	TRP	A	347	33.897	26.140	57.885	1.00	16.50	6
ATOM	2823	CD2	TRP	A	347	32.447	25.874	56.186	1.00	20.29	6
ATOM	2824	NE1	TRP	A	347	33.231	24.958	58.076	1.00	15.01	7
ATOM	2825	CE2	TRP	A	347	32.352	24.755	57.043	1.00	23.63	6
ATOM	2826	CE3	TRP	A	347	31.625	25.925	55.052	1.00	25.23	6
ATOM	2827	CZ2	TRP	A	347	31.490	23.692	56.784	1.00	22.24	6
ATOM	2828	CZ3	TRP	A	347	30.765	24.880	54.811	1.00	18.80	6
ATOM	2829	CH2	TRP	A	347	30.708	23.754	55.639	1.00	19.24	6
ATOM	2830	N	PHE	A	348	31.008	28.439	57.686	1.00	13.89	7
ATOM	2831	CA	PHE	A	348	29.580	28.185	57.685	1.00	12.21	6
ATOM	2832	C	PHE	A	348	28.777	29.372	58.138	1.00	13.54	6
ATOM	2833	O	PHE	A	348	27.569	29.424	57.920	1.00	15.25	8
ATOM	2834	CB	PHE	A	348	29.253	26.982	58.612	1.00	13.35	6

ATOM	2835	CG	PHE	A	348	27.920	26.338	58.393	1.00	17.24	6
ATOM	2836	CD1	PHE	A	348	27.774	25.380	57.390	1.00	16.47	6
ATOM	2837	CD2	PHE	A	348	26.798	26.653	59.153	1.00	10.80	6
ATOM	2838	CE1	PHE	A	348	26.581	24.725	57.137	1.00	16.99	6
ATOM	2839	CE2	PHE	A	348	25.594	26.042	58.880	1.00	15.47	6
ATOM	2840	CZ	PHE	A	348	25.468	25.067	57.898	1.00	17.41	6
ATOM	2841	N	LYS	A	349	29.441	30.318	58.853	1.00	12.58	7
ATOM	2842	CA	LYS	A	349	28.736	31.427	59.451	1.00	14.41	6
ATOM	2843	C	LYS	A	349	27.853	32.265	58.554	1.00	14.28	6
ATOM	2844	O	LYS	A	349	26.689	32.562	58.876	1.00	13.07	8
ATOM	2845	CB	LYS	A	349	29.685	32.253	60.351	1.00	11.83	6
ATOM	2846	CG	LYS	A	349	28.973	33.313	61.209	1.00	18.84	6
ATOM	2847	CD	LYS	A	349	29.688	33.532	62.566	1.00	15.69	6
ATOM	2848	CE	LYS	A	349	29.183	32.553	63.636	1.00	18.65	6
ATOM	2849	NZ	LYS	A	349	30.124	32.604	64.865	1.00	14.15	7
ATOM	2850	N	PRO	A	350	28.313	32.630	57.340	1.00	13.75	7
ATOM	2851	CA	PRO	A	350	27.479	33.386	56.384	1.00	9.95	6
ATOM	2852	C	PRO	A	350	26.302	32.527	55.993	1.00	6.14	6
ATOM	2853	O	PRO	A	350	25.181	33.057	55.892	1.00	9.02	8
ATOM	2854	CB	PRO	A	350	28.425	33.760	55.209	1.00	11.63	6
ATOM	2855	CG	PRO	A	350	29.789	33.521	55.791	1.00	13.93	6
ATOM	2856	CD	PRO	A	350	29.690	32.450	56.896	1.00	12.47	6
ATOM	2857	N	LEU	A	351	26.423	31.209	55.890	1.00	5.76	7
ATOM	2858	CA	LEU	A	351	25.254	30.399	55.544	1.00	7.58	6
ATOM	2859	C	LEU	A	351	24.179	30.374	56.632	1.00	11.79	6
ATOM	2860	O	LEU	A	351	22.931	30.395	56.432	1.00	8.84	8
ATOM	2861	CB	LEU	A	351	25.666	28.953	55.261	1.00	7.39	6
ATOM	2862	CG	LEU	A	351	26.395	28.531	53.988	1.00	17.59	6
ATOM	2863	CD1	LEU	A	351	27.764	29.180	53.897	1.00	16.27	6
ATOM	2864	CD2	LEU	A	351	26.526	27.034	53.789	1.00	9.25	6
ATOM	2865	N	ALA	A	352	24.724	30.316	57.908	1.00	9.34	7
ATOM	2866	CA	ALA	A	352	23.722	30.269	59.053	1.00	6.62	6
ATOM	2867	C	ALA	A	352	23.055	31.607	59.170	1.00	2.63	6
ATOM	2868	O	ALA	A	352	21.823	31.709	59.309	1.00	7.27	8
ATOM	2869	CB	ALA	A	352	24.615	30.028	60.331	1.00	8.00	6
ATOM	2870	N	TYR	A	353	23.733	32.721	58.894	1.00	4.31	7
ATOM	2871	CA	TYR	A	353	23.040	34.002	58.912	1.00	6.40	6
ATOM	2872	C	TYR	A	353	21.981	34.202	57.823	1.00	10.05	6
ATOM	2873	O	TYR	A	353	20.862	34.755	58.003	1.00	11.41	8
ATOM	2874	CB	TYR	A	353	24.034	35.166	58.976	1.00	9.62	6
ATOM	2875	CG	TYR	A	353	24.455	35.483	60.418	1.00	14.53	6
ATOM	2876	CD1	TYR	A	353	23.589	36.097	61.305	1.00	18.62	6
ATOM	2877	CD2	TYR	A	353	25.726	35.177	60.886	1.00	17.29	6
ATOM	2878	CE1	TYR	A	353	23.950	36.375	62.629	1.00	17.02	6
ATOM	2879	CE2	TYR	A	353	26.111	35.447	62.213	1.00	19.57	6
ATOM	2880	CZ	TYR	A	353	25.209	36.032	63.088	1.00	16.24	6
ATOM	2881	OH	TYR	A	353	25.568	36.289	64.398	1.00	12.95	8
ATOM	2882	N	ALA	A	354	22.242	33.544	56.647	1.00	11.17	7
ATOM	2883	CA	ALA	A	354	21.279	33.699	55.500	1.00	9.08	6
ATOM	2884	C	ALA	A	354	20.072	32.896	55.874	1.00	5.76	6
ATOM	2885	O	ALA	A	354	18.942	33.293	55.634	1.00	6.50	8
ATOM	2886	CB	ALA	A	354	21.964	33.141	54.255	1.00	8.32	6
ATOM	2887	N	LEU	A	355	20.293	31.740	56.476	1.00	7.26	7
ATOM	2888	CA	LEU	A	355	19.114	30.958	56.901	1.00	8.15	6
ATOM	2889	C	LEU	A	355	18.208	31.687	57.869	1.00	13.11	6
ATOM	2890	O	LEU	A	355	16.961	31.630	57.758	1.00	14.67	8
ATOM	2891	CB	LEU	A	355	19.670	29.630	57.456	1.00	11.74	6
ATOM	2892	CG	LEU	A	355	18.601	28.784	58.187	1.00	18.51	6
ATOM	2893	CD1	LEU	A	355	17.767	28.021	57.175	1.00	23.46	6
ATOM	2894	CD2	LEU	A	355	19.293	27.745	59.047	1.00	20.77	6
ATOM	2895	N	ILE	A	356	18.803	32.427	58.881	1.00	12.17	7
ATOM	2896	CA	ILE	A	356	17.858	33.039	59.827	1.00	12.67	6
ATOM	2897	C	ILE	A	356	17.463	34.402	59.307	1.00	13.33	6
ATOM	2898	O	ILE	A	356	16.406	34.878	59.760	1.00	14.98	8
ATOM	2899	CB	ILE	A	356	18.478	33.139	61.284	1.00	11.08	6
ATOM	2900	CG1	ILE	A	356	19.683	34.049	61.369	1.00	11.75	6
ATOM	2901	CG2	ILE	A	356	18.899	31.710	61.679	1.00	5.59	6
ATOM	2902	CD1	ILE	A	356	20.169	34.327	62.846	1.00	12.46	6
ATOM	2903	N	LEU	A	357	18.239	35.098	58.466	1.00	9.14	7
ATOM	2904	CA	LEU	A	357	17.765	36.443	58.112	1.00	10.92	6
ATOM	2905	C	LEU	A	357	16.851	36.483	56.874	1.00	11.65	6
ATOM	2906	O	LEU	A	357	16.159	37.475	56.724	1.00	13.44	8
ATOM	2907	CB	LEU	A	357	18.970	37.362	57.908	1.00	15.64	6
ATOM	2908	CG	LEU	A	357	19.863	37.520	59.155	1.00	23.64	6

ATOM	2909	CD1	LEU	A	357	21.206	38.149	58.863	1.00	9.34	6
ATOM	2910	CD2	LEU	A	357	19.129	38.400	60.180	1.00	9.22	6
ATOM	2911	N	THR	A	358	16.853	35.476	56.009	1.00	13.41	7
ATOM	2912	CA	THR	A	358	16.047	35.618	54.767	1.00	15.69	6
ATOM	2913	C	THR	A	358	14.855	34.712	54.671	1.00	17.67	6
ATOM	2914	O	THR	A	358	14.114	34.871	53.669	1.00	18.83	8
ATOM	2915	CB	THR	A	358	16.892	35.503	53.488	1.00	6.92	6
ATOM	2916	OG1	THR	A	358	17.493	34.198	53.338	1.00	9.85	8
ATOM	2917	CG2	THR	A	358	18.016	36.551	53.490	1.00	6.29	6
ATOM	2918	N	ARG	A	359	14.629	33.807	55.632	1.00	15.05	7
ATOM	2919	CA	ARG	A	359	13.414	33.009	55.653	1.00	12.87	6
ATOM	2920	C	ARG	A	359	12.342	33.824	56.365	1.00	15.49	6
ATOM	2921	O	ARG	A	359	12.628	34.769	57.122	1.00	15.95	8
ATOM	2922	CB	ARG	A	359	13.597	31.645	56.291	1.00	14.00	6
ATOM	2923	CG	ARG	A	359	14.651	30.824	55.541	1.00	15.78	6
ATOM	2924	CD	ARG	A	359	14.643	29.396	56.080	1.00	11.69	6
ATOM	2925	NE	ARG	A	359	13.411	28.697	56.026	1.00	18.91	7
ATOM	2926	CZ	ARG	A	359	12.387	27.893	55.960	1.00	18.82	6
ATOM	2927	NH1	ARG	A	359	12.470	26.638	55.555	1.00	37.09	7
ATOM	2928	NH2	ARG	A	359	11.134	28.231	56.128	1.00	35.48	7
ATOM	2929	N	GLU	A	360	11.075	33.508	56.124	1.00	13.34	7
ATOM	2930	CA	GLU	A	360	10.009	34.272	56.766	1.00	16.87	6
ATOM	2931	C	GLU	A	360	9.797	33.905	58.272	1.00	17.41	6
ATOM	2932	O	GLU	A	360	9.164	34.657	58.978	1.00	17.91	8
ATOM	2933	CB	GLU	A	360	8.753	33.701	56.089	1.00	22.63	6
ATOM	2934	CG	GLU	A	360	7.507	34.543	56.320	1.00	43.72	6
ATOM	2935	CD	GLU	A	360	6.319	33.647	55.944	1.00	53.59	6
ATOM	2936	OE1	GLU	A	360	6.476	32.823	55.022	1.00	33.23	8
ATOM	2937	OE2	GLU	A	360	5.274	33.777	56.616	1.00	69.43	8
ATOM	2938	N	GLN	A	361	10.024	32.680	58.690	1.00	16.57	7
ATOM	2939	CA	GLN	A	361	9.823	32.228	60.052	1.00	20.85	6
ATOM	2940	C	GLN	A	361	10.894	32.729	61.033	1.00	18.61	6
ATOM	2941	O	GLN	A	361	12.109	32.718	60.781	1.00	15.15	8
ATOM	2942	CB	GLN	A	361	9.981	30.674	60.070	1.00	15.83	6
ATOM	2943	CG	GLN	A	361	8.810	30.118	59.253	1.00	20.02	6
ATOM	2944	CD	GLN	A	361	9.143	29.897	57.778	1.00	26.16	6
ATOM	2945	OE1	GLN	A	361	10.184	30.238	57.224	1.00	15.02	8
ATOM	2946	NE2	GLN	A	361	8.253	29.232	57.073	1.00	22.71	7
ATOM	2947	N	GLY	A	362	10.387	33.010	62.256	1.00	19.95	7
ATOM	2948	CA	GLY	A	362	11.266	33.294	63.385	1.00	16.72	6
ATOM	2949	C	GLY	A	362	11.673	34.720	63.504	1.00	19.34	6
ATOM	2950	O	GLY	A	362	11.589	35.495	62.537	1.00	19.82	8
ATOM	2951	N	TYR	A	363	12.132	35.159	64.678	1.00	17.12	7
ATOM	2952	CA	TYR	A	363	12.640	36.516	64.902	1.00	13.85	6
ATOM	2953	C	TYR	A	363	14.118	36.349	65.165	1.00	14.95	6
ATOM	2954	O	TYR	A	363	14.576	35.736	66.157	1.00	15.51	8
ATOM	2955	CB	TYR	A	363	11.833	37.074	66.067	1.00	16.66	6
ATOM	2956	CG	TYR	A	363	12.145	38.458	66.549	1.00	17.64	6
ATOM	2957	CD1	TYR	A	363	12.827	39.352	65.739	1.00	18.51	6
ATOM	2958	CD2	TYR	A	363	11.702	38.910	67.805	1.00	18.47	6
ATOM	2959	CE1	TYR	A	363	13.111	40.649	66.129	1.00	21.67	6
ATOM	2960	CE2	TYR	A	363	11.970	40.197	68.233	1.00	19.85	6
ATOM	2961	CZ	TYR	A	363	12.665	41.058	67.408	1.00	20.59	6
ATOM	2962	OH	TYR	A	363	12.963	42.342	67.782	1.00	17.62	8
ATOM	2963	N	PRO	A	364	14.971	36.846	64.285	1.00	14.44	7
ATOM	2964	CA	PRO	A	364	16.376	36.602	64.232	1.00	12.94	6
ATOM	2965	C	PRO	A	364	17.157	37.600	65.050	1.00	10.83	6
ATOM	2966	O	PRO	A	364	16.828	38.782	65.173	1.00	12.01	8
ATOM	2967	CB	PRO	A	364	16.861	36.777	62.728	1.00	12.52	6
ATOM	2968	CG	PRO	A	364	15.821	37.780	62.253	1.00	13.06	6
ATOM	2969	CD	PRO	A	364	14.522	37.501	63.016	1.00	17.02	6
ATOM	2970	N	SER	A	365	18.303	37.060	65.467	1.00	12.81	7
ATOM	2971	CA	SER	A	365	19.177	37.955	66.264	1.00	13.83	6
ATOM	2972	C	SER	A	365	20.617	37.834	65.836	1.00	13.08	6
ATOM	2973	O	SER	A	365	21.186	36.734	65.692	1.00	15.72	8
ATOM	2974	CB	SER	A	365	19.016	37.409	67.724	1.00	19.64	6
ATOM	2975	OG	SER	A	365	19.975	38.079	68.550	1.00	28.22	8
ATOM	2976	N	VAL	A	366	21.271	38.967	65.698	1.00	12.55	7
ATOM	2977	CA	VAL	A	366	22.671	38.974	65.280	1.00	13.77	6
ATOM	2978	C	VAL	A	366	23.538	39.159	66.526	1.00	15.58	6
ATOM	2979	O	VAL	A	366	23.215	40.017	67.353	1.00	14.42	8
ATOM	2980	CB	VAL	A	366	22.890	40.239	64.373	1.00	17.08	6
ATOM	2981	CG1	VAL	A	366	24.327	40.304	63.919	1.00	11.12	6
ATOM	2982	CG2	VAL	A	366	21.942	40.159	63.185	1.00	23.07	6

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ATOM   2983  N   PHE A 367      24.638  38.457  66.594  1.00 14.78   7
ATOM   2984  CA  PHE A 367      25.533  38.506  67.717  1.00 14.70   6
ATOM   2985  C   PHE A 367      26.613  39.550  67.502  1.00 17.61   6
ATOM   2986  O   PHE A 367      27.427  39.578  66.556  1.00 16.79   8
ATOM   2987  CB  PHE A 367      26.178  37.117  67.871  1.00 13.83   6
ATOM   2988  CG  PHE A 367      27.171  36.983  69.000  1.00 17.14   6
ATOM   2989  CD1 PHE A 367      26.912  37.575  70.245  1.00 21.47   6
ATOM   2990  CD2 PHE A 367      28.314  36.224  68.836  1.00 10.74   6
ATOM   2991  CE1 PHE A 367      27.811  37.426  71.295  1.00 17.03   6
ATOM   2992  CE2 PHE A 367      29.219  36.070  69.893  1.00 20.19   6
ATOM   2993  CZ  PHE A 367      28.970  36.675  71.138  1.00 11.94   6
ATOM   2994  N   TYR A 368      26.770  40.425  68.478  1.00 16.71   7
ATOM   2995  CA  TYR A 368      27.823  41.428  68.486  1.00 18.35   6
ATOM   2996  C   TYR A 368      29.182  40.803  68.219  1.00 19.12   6
ATOM   2997  O   TYR A 368      30.029  41.415  67.524  1.00 21.05   8
ATOM   2998  CB  TYR A 368      27.806  42.189  69.810  1.00 17.30   6
ATOM   2999  CG  TYR A 368      28.846  43.292  69.966  1.00 17.20   6
ATOM   3000  CD1 TYR A 368      30.183  43.012  70.185  1.00 14.16   6
ATOM   3001  CD2 TYR A 368      28.424  44.628  69.933  1.00 15.05   6
ATOM   3002  CE1 TYR A 368      31.098  44.049  70.329  1.00 16.57   6
ATOM   3003  CE2 TYR A 368      29.321  45.670  70.080  1.00 14.72   6
ATOM   3004  CZ  TYR A 368      30.641  45.354  70.276  1.00 18.79   6
ATOM   3005  OH  TYR A 368      31.554  46.387  70.443  1.00 24.91   8
ATOM   3006  N   GLY A 369      29.470  39.650  68.835  1.00 16.89   7
ATOM   3007  CA  GLY A 369      30.779  39.052  68.692  1.00 19.01   6
ATOM   3008  C   GLY A 369      31.071  38.607  67.249  1.00 21.56   6
ATOM   3009  O   GLY A 369      32.237  38.589  66.852  1.00 20.31   8
ATOM   3010  N   ASP A 370      30.001  38.233  66.530  1.00 20.90   7
ATOM   3011  CA  ASP A 370      30.203  37.856  65.119  1.00 21.19   6
ATOM   3012  C   ASP A 370      30.346  39.143  64.279  1.00 21.90   6
ATOM   3013  O   ASP A 370      31.190  39.176  63.390  1.00 20.14   8
ATOM   3014  CB  ASP A 370      29.024  37.062  64.591  1.00 15.54   6
ATOM   3015  CG  ASP A 370      28.821  35.687  65.177  1.00 11.32   6
ATOM   3016  OD1 ASP A 370      29.755  34.957  65.507  1.00 14.67   8
ATOM   3017  OD2 ASP A 370      27.644  35.274  65.227  1.00 14.90   8
ATOM   3018  N   TYR A 371      29.527  40.158  64.522  1.00 19.84   7
ATOM   3019  CA  TYR A 371      29.508  41.372  63.764  1.00 20.87   6
ATOM   3020  C   TYR A 371      30.777  42.214  63.872  1.00 24.06   6
ATOM   3021  O   TYR A 371      31.488  42.507  62.853  1.00 22.38   8
ATOM   3022  CB  TYR A 371      28.249  42.138  64.122  1.00 20.00   6
ATOM   3023  CG  TYR A 371      27.931  43.235  63.129  1.00 22.37   6
ATOM   3024  CD1 TYR A 371      27.170  42.920  61.978  1.00 20.86   6
ATOM   3025  CD2 TYR A 371      28.342  44.537  63.356  1.00 23.52   6
ATOM   3026  CE1 TYR A 371      26.846  43.910  61.073  1.00 22.15   6
ATOM   3027  CE2 TYR A 371      28.028  45.531  62.449  1.00 27.44   6
ATOM   3028  CZ  TYR A 371      27.291  45.201  61.302  1.00 26.41   6
ATOM   3029  OH  TYR A 371      27.020  46.192  60.406  1.00 25.92   8
ATOM   3030  N   TYR A 372      31.113  42.576  65.113  1.00 20.55   7
ATOM   3031  CA  TYR A 372      32.343  43.299  65.392  1.00 20.27   6
ATOM   3032  C   TYR A 372      33.540  42.457  65.762  1.00 19.46   6
ATOM   3033  O   TYR A 372      34.585  43.086  65.922  1.00 19.22   8
ATOM   3034  CB  TYR A 372      32.138  44.358  66.485  1.00 22.02   6
ATOM   3035  CG  TYR A 372      31.116  45.411  66.145  1.00 25.43   6
ATOM   3036  CD1 TYR A 372      31.414  46.287  65.077  1.00 29.79   6
ATOM   3037  CD2 TYR A 372      29.907  45.563  66.768  1.00 25.19   6
ATOM   3038  CE1 TYR A 372      30.523  47.274  64.698  1.00 29.82   6
ATOM   3039  CE2 TYR A 372      29.007  46.561  66.415  1.00 27.56   6
ATOM   3040  CZ  TYR A 372      29.335  47.410  65.383  1.00 30.90   6
ATOM   3041  OH  TYR A 372      28.494  48.412  64.971  1.00 33.96   8
ATOM   3042  N   GLY A 373      33.569  41.146  65.801  1.00 20.64   7
ATOM   3043  CA  GLY A 373      34.745  40.352  66.120  1.00 21.67   6
ATOM   3044  C   GLY A 373      34.897  40.097  67.649  1.00 23.24   6
ATOM   3045  O   GLY A 373      34.142  40.563  68.495  1.00 22.78   8
ATOM   3046  N   ILE A 374      35.796  39.198  68.001  1.00 21.63   7
ATOM   3047  CA  ILE A 374      36.132  38.841  69.367  1.00 23.49   6
ATOM   3048  C   ILE A 374      37.666  38.724  69.375  1.00 21.40   6
ATOM   3049  O   ILE A 374      38.398  37.741  69.231  1.00 19.77   8
ATOM   3050  CB  ILE A 374      35.265  37.898  70.159  1.00 31.39   6
ATOM   3051  CG1 ILE A 374      36.097  36.914  71.011  1.00 30.19   6
ATOM   3052  CG2 ILE A 374      34.048  37.123  69.642  1.00 20.15   6
ATOM   3053  CD1 ILE A 374      35.843  37.222  72.468  1.00 43.36   6
ATOM   3054  N   PRO A 375      38.261  39.908  69.563  1.00 21.92   7
ATOM   3055  CA  PRO A 375      39.697  40.117  69.418  1.00 24.23   6
ATOM   3056  C   PRO A 375      40.527  39.315  70.387  1.00 28.10   6
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ATOM	3057	O	PRO	A	375	41.627	38.900	69.995	1.00	30.20	8
ATOM	3058	CB	PRO	A	375	40.001	41.594	69.537	1.00	23.29	6
ATOM	3059	CG	PRO	A	375	38.651	42.217	69.774	1.00	22.77	6
ATOM	3060	CD	PRO	A	375	37.565	41.183	69.739	1.00	20.77	6
ATOM	3061	N	THR	A	376	39.963	39.027	71.557	1.00	26.59	7
ATOM	3062	CA	THR	A	376	40.694	38.305	72.571	1.00	29.38	6
ATOM	3063	C	THR	A	376	40.912	36.901	72.077	1.00	31.17	6
ATOM	3064	O	THR	A	376	41.922	36.294	72.423	1.00	32.53	8
ATOM	3065	CB	THR	A	376	39.882	38.365	73.888	1.00	34.99	6
ATOM	3066	OG1	THR	A	376	38.559	37.905	73.570	1.00	33.12	8
ATOM	3067	CG2	THR	A	376	39.737	39.808	74.366	1.00	29.78	6
ATOM	3068	N	HIS	A	377	39.924	36.317	71.381	1.00	31.46	7
ATOM	3069	CA	HIS	A	377	40.107	34.949	70.876	1.00	32.11	6
ATOM	3070	C	HIS	A	377	40.481	35.154	69.425	1.00	33.61	6
ATOM	3071	O	HIS	A	377	40.760	36.367	69.170	1.00	35.65	8
ATOM	3072	CB	HIS	A	377	38.872	34.112	71.176	1.00	27.76	6
ATOM	3073	CG	HIS	A	377	38.794	33.981	72.680	1.00	31.06	6
ATOM	3074	ND1	HIS	A	377	38.521	35.079	73.472	1.00	34.60	7
ATOM	3075	CD2	HIS	A	377	38.993	32.924	73.497	1.00	36.91	6
ATOM	3076	CE1	HIS	A	377	38.556	34.685	74.739	1.00	45.06	6
ATOM	3077	NE2	HIS	A	377	38.832	33.386	74.790	1.00	43.40	7
ATOM	3078	N	SER	A	378	40.550	34.303	68.425	1.00	34.63	7
ATOM	3079	CA	SER	A	378	41.010	35.069	67.178	1.00	36.89	6
ATOM	3080	C	SER	A	378	39.918	35.297	66.174	1.00	35.75	6
ATOM	3081	O	SER	A	378	40.081	34.897	65.027	1.00	38.61	8
ATOM	3082	CB	SER	A	378	42.341	34.526	66.711	1.00	43.48	6
ATOM	3083	OG	SER	A	378	43.304	35.530	67.068	1.00	56.38	8
ATOM	3084	N	VAL	A	379	38.787	35.882	66.582	1.00	34.79	7
ATOM	3085	CA	VAL	A	379	37.590	36.026	65.778	1.00	32.09	6
ATOM	3086	C	VAL	A	379	37.439	37.399	65.148	1.00	30.08	6
ATOM	3087	O	VAL	A	379	37.076	38.373	65.789	1.00	29.50	8
ATOM	3088	CB	VAL	A	379	36.301	35.708	66.561	1.00	31.07	6
ATOM	3089	CG1	VAL	A	379	35.102	35.593	65.619	1.00	22.44	6
ATOM	3090	CG2	VAL	A	379	36.468	34.420	67.358	1.00	29.31	6
ATOM	3091	N	PRO	A	380	37.638	37.423	63.830	1.00	28.72	7
ATOM	3092	CA	PRO	A	380	37.614	38.627	63.017	1.00	25.27	6
ATOM	3093	C	PRO	A	380	36.213	39.177	62.905	1.00	20.31	6
ATOM	3094	O	PRO	A	380	35.288	38.402	63.071	1.00	21.62	8
ATOM	3095	CB	PRO	A	380	38.136	38.219	61.599	1.00	26.88	6
ATOM	3096	CG	PRO	A	380	37.929	36.723	61.630	1.00	28.41	6
ATOM	3097	CD	PRO	A	380	38.033	36.231	63.057	1.00	28.36	6
ATOM	3098	N	ALA	A	381	36.031	40.454	62.723	1.00	18.38	7
ATOM	3099	CA	ALA	A	381	34.731	41.051	62.525	1.00	21.39	6
ATOM	3100	C	ALA	A	381	34.134	40.531	61.198	1.00	23.08	6
ATOM	3101	O	ALA	A	381	34.852	40.306	60.231	1.00	21.90	8
ATOM	3102	CB	ALA	A	381	34.872	42.548	62.522	1.00	21.51	6
ATOM	3103	N	MET	A	382	32.870	40.142	61.151	1.00	20.95	7
ATOM	3104	CA	MET	A	382	32.283	39.562	59.957	1.00	19.68	6
ATOM	3105	C	MET	A	382	31.243	40.480	59.371	1.00	19.80	6
ATOM	3106	O	MET	A	382	30.361	40.117	58.575	1.00	20.42	8
ATOM	3107	CB	MET	A	382	31.720	38.171	60.316	1.00	12.09	6
ATOM	3108	CG	MET	A	382	32.901	37.210	60.460	1.00	22.27	6
ATOM	3109	SD	MET	A	382	32.198	35.595	60.910	1.00	34.94	16
ATOM	3110	CE	MET	A	382	33.716	34.885	61.572	1.00	45.83	6
ATOM	3111	N	LYS	A	383	31.326	41.739	59.837	1.00	17.95	7
ATOM	3112	CA	LYS	A	383	30.428	42.787	59.377	1.00	20.66	6
ATOM	3113	C	LYS	A	383	30.348	42.796	57.822	1.00	20.83	6
ATOM	3114	O	LYS	A	383	29.264	42.891	57.272	1.00	22.65	8
ATOM	3115	CB	LYS	A	383	31.099	44.109	59.793	1.00	15.20	6
ATOM	3116	CG	LYS	A	383	30.330	45.327	59.325	1.00	24.36	6
ATOM	3117	CD	LYS	A	383	30.986	46.580	59.956	1.00	30.19	6
ATOM	3118	CE	LYS	A	383	30.647	47.797	59.077	1.00	33.69	6
ATOM	3119	NZ	LYS	A	383	29.187	47.850	58.718	1.00	27.34	7
ATOM	3120	N	ALA	A	384	31.506	42.740	57.175	1.00	21.38	7
ATOM	3121	CA	ALA	A	384	31.504	42.788	55.685	1.00	24.86	6
ATOM	3122	C	ALA	A	384	30.684	41.650	55.106	1.00	21.91	6
ATOM	3123	O	ALA	A	384	29.954	41.867	54.128	1.00	23.76	8
ATOM	3124	CB	ALA	A	384	32.911	42.774	55.106	1.00	20.64	6
ATOM	3125	N	LYS	A	385	30.746	40.467	55.665	1.00	19.75	7
ATOM	3126	CA	LYS	A	385	29.909	39.379	55.191	1.00	19.30	6
ATOM	3127	C	LYS	A	385	28.495	39.409	55.687	1.00	18.88	6
ATOM	3128	O	LYS	A	385	27.640	38.802	55.031	1.00	21.08	8
ATOM	3129	CB	LYS	A	385	30.574	38.054	55.561	1.00	24.42	6
ATOM	3130	CG	LYS	A	385	31.939	38.084	54.864	1.00	38.35	6

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ATOM   3131  CD  LYS A 385      32.421  36.669  54.612  1.00 40.27   6
ATOM   3132  CE  LYS A 385      33.732  36.479  55.365  1.00 50.29   6
ATOM   3133  NZ  LYS A 385      34.643  35.513  54.703  1.00 54.83   7
ATOM   3134  N   ILE A 386      28.190  40.107  56.801  1.00 17.18   7
ATOM   3135  CA  ILE A 386      26.800  39.977  57.253  1.00 12.72   6
ATOM   3136  C   ILE A 386      26.013  41.132  56.711  1.00  9.20   6
ATOM   3137  O   ILE A 386      24.798  41.064  56.507  1.00 11.51   8
ATOM   3138  CB  ILE A 386      26.814  40.000  58.848  1.00 16.85   6
ATOM   3139  CG1 ILE A 386      27.322  38.670  59.349  1.00 18.12   6
ATOM   3140  CG2 ILE A 386      25.402  40.258  59.352  1.00  9.70   6
ATOM   3141  CD1 ILE A 386      27.992  38.666  60.715  1.00 26.94   6
ATOM   3142  N   ASP A 387      26.634  42.281  56.488  1.00 11.30   7
ATOM   3143  CA  ASP A 387      25.911  43.440  55.965  1.00 12.22   6
ATOM   3144  C   ASP A 387      25.032  43.227  54.750  1.00 14.02   6
ATOM   3145  O   ASP A 387      23.879  43.635  54.731  1.00 14.95   8
ATOM   3146  CB  ASP A 387      26.911  44.587  55.788  1.00 20.41   6
ATOM   3147  CG  ASP A 387      26.987  45.457  57.041  1.00 23.19   6
ATOM   3148  OD1 ASP A 387      26.206  45.313  58.002  1.00 22.62   8
ATOM   3149  OD2 ASP A 387      27.865  46.315  57.094  1.00 20.44   8
ATOM   3150  N   PRO A 388      25.495  42.550  53.702  1.00 16.26   7
ATOM   3151  CA  PRO A 388      24.708  42.265  52.502  1.00 17.21   6
ATOM   3152  C   PRO A 388      23.527  41.400  52.894  1.00 16.18   6
ATOM   3153  O   PRO A 388      22.461  41.604  52.289  1.00 14.98   8
ATOM   3154  CB  PRO A 388      25.603  41.521  51.492  1.00 17.18   6
ATOM   3155  CG  PRO A 388      26.974  41.824  52.028  1.00 20.47   6
ATOM   3156  CD  PRO A 388      26.869  42.092  53.538  1.00 16.83   6
ATOM   3157  N   ILE A 389      23.678  40.499  53.878  1.00 15.35   7
ATOM   3158  CA  ILE A 389      22.493  39.668  54.265  1.00 14.27   6
ATOM   3159  C   ILE A 389      21.456  40.476  55.004  1.00 15.37   6
ATOM   3160  O   ILE A 389      20.251  40.367  54.778  1.00 17.64   8
ATOM   3161  CB  ILE A 389      22.904  38.411  55.012  1.00 13.28   6
ATOM   3162  CG1 ILE A 389      24.171  37.860  54.393  1.00 14.11   6
ATOM   3163  CG2 ILE A 389      21.798  37.398  55.185  1.00 10.66   6
ATOM   3164  CD1 ILE A 389      24.689  36.568  54.999  1.00 13.92   6
ATOM   3165  N   LEU A 390      21.928  41.446  55.822  1.00 18.10   7
ATOM   3166  CA  LEU A 390      20.977  42.349  56.488  1.00 18.21   6
ATOM   3167  C   LEU A 390      20.268  43.216  55.426  1.00 18.49   6
ATOM   3168  O   LEU A 390      19.086  43.509  55.556  1.00 16.37   8
ATOM   3169  CB  LEU A 390      21.820  43.232  57.443  1.00 16.56   6
ATOM   3170  CG  LEU A 390      22.135  42.516  58.799  1.00 19.93   6
ATOM   3171  CD1 LEU A 390      23.073  43.419  59.554  1.00 17.20   6
ATOM   3172  CD2 LEU A 390      20.845  42.259  59.575  1.00 16.58   6
ATOM   3173  N   GLU A 391      21.007  43.665  54.386  1.00 16.17   7
ATOM   3174  CA  GLU A 391      20.325  44.465  53.303  1.00 16.48   6
ATOM   3175  C   GLU A 391      19.263  43.652  52.609  1.00 12.13   6
ATOM   3176  O   GLU A 391      18.139  44.102  52.465  1.00 16.96   8
ATOM   3177  CB  GLU A 391      21.446  44.917  52.361  1.00 25.49   6
ATOM   3178  CG  GLU A 391      21.100  45.488  51.018  1.00 51.51   6
ATOM   3179  CD  GLU A 391      20.006  46.533  51.042  1.00 69.83   6
ATOM   3180  OE1 GLU A 391      20.195  47.596  51.682  1.00 77.21   8
ATOM   3181  OE2 GLU A 391      18.946  46.275  50.422  1.00 80.47   8
ATOM   3182  N   ALA A 392      19.503  42.363  52.322  1.00 12.95   7
ATOM   3183  CA  ALA A 392      18.482  41.499  51.727  1.00 13.47   6
ATOM   3184  C   ALA A 392      17.251  41.328  52.577  1.00 14.57   6
ATOM   3185  O   ALA A 392      16.079  41.279  52.174  1.00 12.14   8
ATOM   3186  CB  ALA A 392      19.080  40.082  51.469  1.00  5.69   6
ATOM   3187  N   ARG A 393      17.527  41.153  53.924  1.00 16.57   7
ATOM   3188  CA  ARG A 393      16.368  41.005  54.818  1.00 13.88   6
ATOM   3189  C   ARG A 393      15.605  42.315  54.841  1.00 11.43   6
ATOM   3190  O   ARG A 393      14.382  42.370  54.754  1.00 11.77   8
ATOM   3191  CB  ARG A 393      16.836  40.691  56.266  1.00 24.03   6
ATOM   3192  CG  ARG A 393      15.660  40.832  57.246  1.00 15.55   6
ATOM   3193  CD  ARG A 393      16.104  40.214  58.625  1.00 20.25   6
ATOM   3194  NE  ARG A 393      14.888  39.976  59.386  1.00 11.48   7
ATOM   3195  CZ  ARG A 393      13.997  39.041  59.398  1.00 15.02   6
ATOM   3196  NH1 ARG A 393      14.119  37.965  58.629  1.00 12.91   7
ATOM   3197  NH2 ARG A 393      12.987  39.202  60.267  1.00 11.47   7
ATOM   3198  N   GLN A 394      16.302  43.425  54.960  1.00 14.50   7
ATOM   3199  CA  GLN A 394      15.572  44.692  55.025  1.00 18.94   6
ATOM   3200  C   GLN A 394      14.768  45.107  53.787  1.00 20.87   6
ATOM   3201  O   GLN A 394      13.698  45.710  53.936  1.00 21.23   8
ATOM   3202  CB  GLN A 394      16.626  45.777  55.292  1.00 19.73   6
ATOM   3203  CG  GLN A 394      15.997  47.166  55.327  1.00 34.13   6
ATOM   3204  CD  GLN A 394      17.033  48.146  55.868  1.00 42.94   6
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ATOM	3205	OE1	GLN	A	394	18.211	48.045	55.527	1.00	48.00	8
ATOM	3206	NE2	GLN	A	394	16.567	49.063	56.694	1.00	38.78	7
ATOM	3207	N	ASN	A	395	15.315	44.868	52.605	1.00	22.35	7
ATOM	3208	CA	ASN	A	395	14.704	45.340	51.349	1.00	22.62	6
ATOM	3209	C	ASN	A	395	14.155	44.303	50.380	1.00	22.55	6
ATOM	3210	O	ASN	A	395	13.227	44.631	49.640	1.00	22.44	8
ATOM	3211	CB	ASN	A	395	15.829	46.048	50.584	1.00	24.25	6
ATOM	3212	CG	ASN	A	395	15.991	47.421	51.208	1.00	29.25	6
ATOM	3213	OD1	ASN	A	395	17.120	47.874	51.307	1.00	42.49	8
ATOM	3214	ND2	ASN	A	395	14.890	48.003	51.618	1.00	34.43	7
ATOM	3215	N	PHE	A	396	14.625	43.069	50.419	1.00	20.24	7
ATOM	3216	CA	PHE	A	396	14.178	42.018	49.532	1.00	23.30	6
ATOM	3217	C	PHE	A	396	13.431	40.810	50.076	1.00	25.23	6
ATOM	3218	O	PHE	A	396	12.770	40.125	49.265	1.00	21.78	8
ATOM	3219	CB	PHE	A	396	15.501	41.489	48.876	1.00	21.33	6
ATOM	3220	CG	PHE	A	396	16.123	42.583	48.037	1.00	19.57	6
ATOM	3221	CD1	PHE	A	396	15.499	42.952	46.846	1.00	26.52	6
ATOM	3222	CD2	PHE	A	396	17.292	43.195	48.406	1.00	20.67	6
ATOM	3223	CE1	PHE	A	396	16.057	43.949	46.042	1.00	22.29	6
ATOM	3224	CE2	PHE	A	396	17.856	44.204	47.632	1.00	29.18	6
ATOM	3225	CZ	PHE	A	396	17.230	44.580	46.437	1.00	24.68	6
ATOM	3226	N	ALA	A	397	13.570	40.513	51.400	1.00	24.28	7
ATOM	3227	CA	ALA	A	397	12.981	39.290	51.968	1.00	22.16	6
ATOM	3228	C	ALA	A	397	11.557	39.399	52.386	1.00	21.58	6
ATOM	3229	O	ALA	A	397	11.171	39.620	53.587	1.00	23.05	8
ATOM	3230	CB	ALA	A	397	13.901	38.838	53.134	1.00	19.19	6
ATOM	3231	N	TYR	A	398	10.619	39.421	51.435	1.00	18.06	7
ATOM	3232	CA	TYR	A	398	9.191	39.615	51.630	1.00	17.56	6
ATOM	3233	C	TYR	A	398	8.372	38.762	50.656	1.00	20.75	6
ATOM	3234	O	TYR	A	398	8.866	38.357	49.598	1.00	20.32	8
ATOM	3235	CB	TYR	A	398	8.789	41.079	51.316	1.00	19.32	6
ATOM	3236	CG	TYR	A	398	9.471	42.075	52.213	1.00	23.94	6
ATOM	3237	CD1	TYR	A	398	8.899	42.359	53.471	1.00	25.13	6
ATOM	3238	CD2	TYR	A	398	10.683	42.646	51.885	1.00	23.28	6
ATOM	3239	CE1	TYR	A	398	9.562	43.213	54.347	1.00	25.33	6
ATOM	3240	CE2	TYR	A	398	11.333	43.489	52.764	1.00	25.72	6
ATOM	3241	CZ	TYR	A	398	10.750	43.770	53.999	1.00	25.29	6
ATOM	3242	OH	TYR	A	398	11.394	44.636	54.841	1.00	23.06	8
ATOM	3243	N	GLY	A	399	7.142	38.444	50.960	1.00	19.46	7
ATOM	3244	CA	GLY	A	399	6.211	37.716	50.120	1.00	18.92	6
ATOM	3245	C	GLY	A	399	6.307	36.226	50.292	1.00	19.52	6
ATOM	3246	O	GLY	A	399	7.169	35.751	51.061	1.00	18.13	8
ATOM	3247	N	THR	A	400	5.450	35.527	49.577	1.00	15.63	7
ATOM	3248	CA	THR	A	400	5.372	34.072	49.637	1.00	16.69	6
ATOM	3249	C	THR	A	400	6.760	33.457	49.556	1.00	17.74	6
ATOM	3250	O	THR	A	400	7.607	33.929	48.761	1.00	19.47	8
ATOM	3251	CB	THR	A	400	4.500	33.578	48.455	1.00	20.78	6
ATOM	3252	OG1	THR	A	400	3.266	34.312	48.565	1.00	26.31	8
ATOM	3253	CG2	THR	A	400	4.170	32.117	48.502	1.00	18.82	6
ATOM	3254	N	GLN	A	401	6.904	32.347	50.264	1.00	13.87	7
ATOM	3255	CA	GLN	A	401	8.207	31.693	50.327	1.00	12.58	6
ATOM	3256	C	GLN	A	401	8.072	30.316	49.725	1.00	10.72	6
ATOM	3257	O	GLN	A	401	7.025	29.726	49.886	1.00	12.72	8
ATOM	3258	CB	GLN	A	401	8.623	31.511	51.823	1.00	14.98	6
ATOM	3259	CG	GLN	A	401	9.983	30.844	52.002	1.00	16.56	6
ATOM	3260	CD	GLN	A	401	10.397	31.000	53.497	1.00	22.68	6
ATOM	3261	OE1	GLN	A	401	10.340	30.068	54.312	1.00	15.75	8
ATOM	3262	NE2	GLN	A	401	10.753	32.220	53.780	1.00	12.60	7
ATOM	3263	N	HIS	A	402	9.083	29.893	48.969	1.00	10.91	7
ATOM	3264	CA	HIS	A	402	9.047	28.533	48.421	1.00	11.66	6
ATOM	3265	C	HIS	A	402	10.348	27.899	48.924	1.00	12.41	6
ATOM	3266	O	HIS	A	402	11.410	28.518	48.690	1.00	14.47	8
ATOM	3267	CB	HIS	A	402	9.181	28.627	46.865	1.00	16.44	6
ATOM	3268	CG	HIS	A	402	7.932	29.307	46.340	1.00	11.10	6
ATOM	3269	ND1	HIS	A	402	6.775	28.628	46.139	1.00	18.89	7
ATOM	3270	CD2	HIS	A	402	7.695	30.590	46.062	1.00	20.41	6
ATOM	3271	CE1	HIS	A	402	5.858	29.486	45.718	1.00	18.34	6
ATOM	3272	NE2	HIS	A	402	6.396	30.678	45.646	1.00	20.72	7
ATOM	3273	N	ASP	A	403	10.248	26.705	49.441	1.00	12.64	7
ATOM	3274	CA	ASP	A	403	11.402	26.031	49.997	1.00	14.92	6
ATOM	3275	C	ASP	A	403	11.920	24.881	49.174	1.00	14.87	6
ATOM	3276	O	ASP	A	403	11.074	24.144	48.698	1.00	17.16	8
ATOM	3277	CB	ASP	A	403	11.065	25.382	51.362	1.00	17.08	6
ATOM	3278	CG	ASP	A	403	10.991	26.379	52.508	1.00	20.75	6

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ATOM   3279  OD1 ASP A 403      11.378  27.559  52.450  1.00 25.42   8
ATOM   3280  OD2 ASP A 403      10.539  25.965  53.602  1.00 34.57   8
ATOM   3281  N   TYR A 404      13.246  24.771  49.068  1.00 14.04   7
ATOM   3282  CA  TYR A 404      13.823  23.629  48.376  1.00 16.23   6
ATOM   3283  C   TYR A 404      14.855  22.957  49.295  1.00 16.89   6
ATOM   3284  O   TYR A 404      16.072  23.055  49.023  1.00 15.20   8
ATOM   3285  CB  TYR A 404      14.474  24.048  47.005  1.00 15.62   6
ATOM   3286  CG  TYR A 404      13.484  24.770  46.102  1.00 18.51   6
ATOM   3287  CD1 TYR A 404      13.259  26.145  46.273  1.00 18.46   6
ATOM   3288  CD2 TYR A 404      12.733  24.110  45.148  1.00 21.41   6
ATOM   3289  CE1 TYR A 404      12.335  26.804  45.500  1.00 22.55   6
ATOM   3290  CE2 TYR A 404      11.801  24.768  44.339  1.00 21.59   6
ATOM   3291  CZ  TYR A 404      11.619  26.115  44.527  1.00 23.32   6
ATOM   3292  OH  TYR A 404      10.723  26.830  43.779  1.00 23.96   8
ATOM   3293  N   PHE A 405      14.372  22.256  50.326  1.00 17.74   7
ATOM   3294  CA  PHE A 405      15.284  21.492  51.238  1.00 19.60   6
ATOM   3295  C   PHE A 405      15.320  20.072  50.710  1.00 19.93   6
ATOM   3296  O   PHE A 405      14.661  19.205  51.267  1.00 21.69   8
ATOM   3297  CB  PHE A 405      14.731  21.454  52.680  1.00 17.01   6
ATOM   3298  CG  PHE A 405      15.069  22.753  53.375  1.00 20.75   6
ATOM   3299  CD1 PHE A 405      14.317  23.873  53.178  1.00 22.73   6
ATOM   3300  CD2 PHE A 405      16.177  22.858  54.197  1.00 21.89   6
ATOM   3301  CE1 PHE A 405      14.612  25.070  53.790  1.00 21.02   6
ATOM   3302  CE2 PHE A 405      16.495  24.046  54.781  1.00 16.66   6
ATOM   3303  CZ  PHE A 405      15.713  25.174  54.597  1.00 17.73   6
ATOM   3304  N   ASP A 406      16.014  19.845  49.577  1.00 21.98   7
ATOM   3305  CA  ASP A 406      15.832  18.590  48.897  1.00 21.63   6
ATOM   3306  C   ASP A 406      17.093  17.945  48.411  1.00 22.94   6
ATOM   3307  O   ASP A 406      16.984  17.020  47.609  1.00 24.02   8
ATOM   3308  CB  ASP A 406      14.872  18.811  47.699  1.00 28.49   6
ATOM   3309  CG  ASP A 406      15.357  19.804  46.665  1.00 32.06   6
ATOM   3310  OD1 ASP A 406      16.509  20.304  46.657  1.00 21.32   8
ATOM   3311  OD2 ASP A 406      14.537  20.124  45.779  1.00 37.10   8
ATOM   3312  N   HIS A 407      18.235  18.336  48.921  1.00 20.46   7
ATOM   3313  CA  HIS A 407      19.494  17.723  48.573  1.00 15.99   6
ATOM   3314  C   HIS A 407      20.365  17.772  49.847  1.00 19.29   6
ATOM   3315  O   HIS A 407      20.206  18.636  50.728  1.00 16.32   8
ATOM   3316  CB  HIS A 407      20.180  18.592  47.501  1.00 21.88   6
ATOM   3317  CG  HIS A 407      21.382  17.950  46.905  1.00 17.78   6
ATOM   3318  ND1 HIS A 407      22.682  18.370  47.145  1.00 14.44   7
ATOM   3319  CD2 HIS A 407      21.478  16.898  46.048  1.00 28.23   6
ATOM   3320  CE1 HIS A 407      23.533  17.609  46.464  1.00 25.92   6
ATOM   3321  NE2 HIS A 407      22.824  16.714  45.771  1.00 24.79   7
ATOM   3322  N   HIS A 408      21.342  16.884  49.880  1.00 19.10   7
ATOM   3323  CA  HIS A 408      22.188  16.822  51.064  1.00 21.16   6
ATOM   3324  C   HIS A 408      23.186  17.947  51.022  1.00 21.67   6
ATOM   3325  O   HIS A 408      23.680  18.158  52.121  1.00 19.33   8
ATOM   3326  CB  HIS A 408      22.930  15.491  51.221  1.00 20.31   6
ATOM   3327  CG  HIS A 408      23.579  15.023  49.970  1.00 26.72   6
ATOM   3328  ND1 HIS A 408      24.932  15.179  49.722  1.00 31.57   7
ATOM   3329  CD2 HIS A 408      23.034  14.426  48.883  1.00 26.74   6
ATOM   3330  CE1 HIS A 408      25.217  14.677  48.544  1.00 28.79   6
ATOM   3331  NE2 HIS A 408      24.084  14.213  48.021  1.00 30.92   7
ATOM   3332  N   ASN A 409      23.506  18.620  49.903  1.00 19.79   7
ATOM   3333  CA  ASN A 409      24.478  19.678  50.007  1.00 14.82   6
ATOM   3334  C   ASN A 409      23.838  20.998  49.635  1.00 15.23   6
ATOM   3335  O   ASN A 409      24.086  22.012  50.289  1.00 15.13   8
ATOM   3336  CB  ASN A 409      25.696  19.563  49.120  1.00 13.46   6
ATOM   3337  CG  ASN A 409      26.628  18.428  49.204  1.00 27.43   6
ATOM   3338  OD1 ASN A 409      27.478  17.977  48.416  1.00 28.86   8
ATOM   3339  ND2 ASN A 409      26.555  17.756  50.319  1.00 10.65   7
ATOM   3340  N   ILE A 410      23.027  20.967  48.535  1.00 13.15   7
ATOM   3341  CA  ILE A 410      22.604  22.283  48.031  1.00  9.70   6
ATOM   3342  C   ILE A 410      21.166  22.552  48.400  1.00  7.63   6
ATOM   3343  O   ILE A 410      20.320  21.757  48.041  1.00 11.50   8
ATOM   3344  CB  ILE A 410      22.820  22.291  46.474  1.00 16.75   6
ATOM   3345  CG1 ILE A 410      24.299  22.086  46.177  1.00 22.85   6
ATOM   3346  CG2 ILE A 410      22.352  23.604  45.889  1.00  9.39   6
ATOM   3347  CD1 ILE A 410      24.632  21.694  44.755  1.00 31.95   6
ATOM   3348  N   ILE A 411      20.922  23.736  48.999  1.00  4.35   7
ATOM   3349  CA  ILE A 411      19.476  23.883  49.370  1.00  7.35   6
ATOM   3350  C   ILE A 411      19.118  25.312  49.101  1.00  6.74   6
ATOM   3351  O   ILE A 411      20.055  26.094  48.964  1.00 10.01   8
ATOM   3352  CB  ILE A 411      19.566  23.505  50.873  1.00 24.68   6
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ATOM	3353	CG1	ILE	A	411	18.497	22.504	51.187	1.00	28.54	6
ATOM	3354	CG2	ILE	A	411	19.819	24.485	52.000	1.00	14.86	6
ATOM	3355	CD1	ILE	A	411	19.176	21.170	51.304	1.00	29.46	6
ATOM	3356	N	GLY	A	412	17.853	25.708	49.136	1.00	10.56	7
ATOM	3357	CA	GLY	A	412	17.632	27.154	48.948	1.00	12.21	6
ATOM	3358	C	GLY	A	412	16.127	27.373	49.061	1.00	9.86	6
ATOM	3359	O	GLY	A	412	15.436	26.448	49.462	1.00	13.72	8
ATOM	3360	N	TRP	A	413	15.781	28.635	48.939	1.00	9.03	7
ATOM	3361	CA	TRP	A	413	14.392	29.000	49.050	1.00	11.26	6
ATOM	3362	C	TRP	A	413	14.236	30.311	48.290	1.00	10.42	6
ATOM	3363	O	TRP	A	413	15.203	31.062	48.143	1.00	12.22	8
ATOM	3364	CB	TRP	A	413	13.888	29.200	50.524	1.00	12.93	6
ATOM	3365	CG	TRP	A	413	14.834	30.062	51.320	1.00	5.97	6
ATOM	3366	CD1	TRP	A	413	14.787	31.409	51.517	1.00	7.37	6
ATOM	3367	CD2	TRP	A	413	15.978	29.574	52.035	1.00	8.67	6
ATOM	3368	NE1	TRP	A	413	15.856	31.803	52.275	1.00	12.54	7
ATOM	3369	CE2	TRP	A	413	16.582	30.676	52.625	1.00	4.92	6
ATOM	3370	CE3	TRP	A	413	16.509	28.294	52.238	1.00	6.88	6
ATOM	3371	CZ2	TRP	A	413	17.769	30.633	53.367	1.00	9.92	6
ATOM	3372	CZ3	TRP	A	413	17.718	28.227	52.969	1.00	14.87	6
ATOM	3373	CH2	TRP	A	413	18.292	29.378	53.503	1.00	5.74	6
ATOM	3374	N	THR	A	414	12.972	30.623	47.991	1.00	10.08	7
ATOM	3375	CA	THR	A	414	12.807	31.960	47.345	1.00	14.05	6
ATOM	3376	C	THR	A	414	11.677	32.691	48.030	1.00	14.13	6
ATOM	3377	O	THR	A	414	10.869	32.066	48.655	1.00	14.72	8
ATOM	3378	CB	THR	A	414	12.364	31.788	45.853	1.00	13.44	6
ATOM	3379	OG1	THR	A	414	11.181	30.986	45.841	1.00	7.59	8
ATOM	3380	CG2	THR	A	414	13.352	30.897	45.066	1.00	5.57	6
ATOM	3381	N	ARG	A	415	11.632	33.992	47.813	1.00	15.54	7
ATOM	3382	CA	ARG	A	415	10.563	34.849	48.279	1.00	16.88	6
ATOM	3383	C	ARG	A	415	10.036	35.572	47.003	1.00	17.79	6
ATOM	3384	O	ARG	A	415	10.822	36.251	46.335	1.00	17.94	8
ATOM	3385	CB	ARG	A	415	11.217	35.912	49.217	1.00	7.42	6
ATOM	3386	CG	ARG	A	415	11.958	35.313	50.482	1.00	8.31	6
ATOM	3387	CD	ARG	A	415	11.024	34.333	51.205	1.00	3.61	6
ATOM	3388	NE	ARG	A	415	9.971	35.182	51.854	1.00	13.50	7
ATOM	3389	CZ	ARG	A	415	10.214	35.932	52.957	1.00	19.07	6
ATOM	3390	NH1	ARG	A	415	11.382	35.996	53.591	1.00	13.77	7
ATOM	3391	NH2	ARG	A	415	9.241	36.682	53.478	1.00	12.34	7
ATOM	3392	N	GLU	A	416	8.749	35.703	46.821	1.00	19.68	7
ATOM	3393	CA	GLU	A	416	8.147	36.400	45.693	1.00	20.64	6
ATOM	3394	C	GLU	A	416	8.104	37.905	45.754	1.00	24.26	6
ATOM	3395	O	GLU	A	416	7.873	38.542	44.689	1.00	23.56	8
ATOM	3396	CB	GLU	A	416	6.754	35.864	45.394	1.00	16.78	6
ATOM	3397	CG	GLU	A	416	6.806	34.376	45.061	1.00	18.89	6
ATOM	3398	CD	GLU	A	416	5.452	33.880	44.567	1.00	27.96	6
ATOM	3399	OE1	GLU	A	416	4.652	34.705	44.106	1.00	24.86	8
ATOM	3400	OE2	GLU	A	416	5.116	32.685	44.620	1.00	21.51	8
ATOM	3401	N	GLY	A	417	8.319	38.515	46.930	1.00	20.79	7
ATOM	3402	CA	GLY	A	417	8.275	39.977	46.981	1.00	20.54	6
ATOM	3403	C	GLY	A	417	6.839	40.393	47.208	1.00	22.41	6
ATOM	3404	O	GLY	A	417	5.984	39.541	47.075	1.00	21.28	8
ATOM	3405	N	ASN	A	418	6.550	41.635	47.563	1.00	26.47	7
ATOM	3406	CA	ASN	A	418	5.170	42.093	47.674	1.00	31.49	6
ATOM	3407	C	ASN	A	418	5.114	43.539	47.163	1.00	34.80	6
ATOM	3408	O	ASN	A	418	6.155	44.146	46.924	1.00	34.09	8
ATOM	3409	CB	ASN	A	418	4.540	41.994	49.054	1.00	32.51	6
ATOM	3410	CG	ASN	A	418	5.325	42.721	50.118	1.00	40.02	6
ATOM	3411	OD1	ASN	A	418	6.006	43.724	49.894	1.00	44.94	8
ATOM	3412	ND2	ASN	A	418	5.267	42.210	51.344	1.00	47.27	7
ATOM	3413	N	THR	A	419	3.917	44.100	47.061	1.00	39.20	7
ATOM	3414	CA	THR	A	419	3.754	45.468	46.536	1.00	43.25	6
ATOM	3415	C	THR	A	419	4.284	46.547	47.442	1.00	44.75	6
ATOM	3416	O	THR	A	419	4.880	47.517	46.933	1.00	45.86	8
ATOM	3417	CB	THR	A	419	2.342	45.731	46.006	1.00	54.57	6
ATOM	3418	OG1	THR	A	419	1.353	45.687	47.040	1.00	66.20	8
ATOM	3419	CG2	THR	A	419	2.009	44.626	44.988	1.00	55.68	6
ATOM	3420	N	THR	A	420	4.186	46.410	48.760	1.00	45.25	7
ATOM	3421	CA	THR	A	420	4.927	47.405	49.604	1.00	46.78	6
ATOM	3422	C	THR	A	420	6.370	47.026	49.328	1.00	46.84	6
ATOM	3423	O	THR	A	420	6.524	45.824	48.976	1.00	48.22	8
ATOM	3424	CB	THR	A	420	4.557	47.083	51.063	1.00	54.48	6
ATOM	3425	OG1	THR	A	420	3.747	45.884	51.075	1.00	58.03	8
ATOM	3426	CG2	THR	A	420	3.719	48.205	51.647	1.00	60.68	6

ATOM	3427	N	HIS	A	421	7.468	47.723	49.482	1.00	46.61	7
ATOM	3428	CA	HIS	A	421	8.772	47.088	49.170	1.00	45.15	6
ATOM	3429	C	HIS	A	421	8.861	46.701	47.695	1.00	44.34	6
ATOM	3430	O	HIS	A	421	8.769	45.588	47.177	1.00	44.02	8
ATOM	3431	CB	HIS	A	421	9.116	45.866	50.038	1.00	41.65	6
ATOM	3432	CG	HIS	A	421	8.945	46.140	51.499	1.00	45.00	6
ATOM	3433	ND1	HIS	A	421	7.822	45.690	52.166	1.00	46.28	7
ATOM	3434	CD2	HIS	A	421	9.669	46.858	52.383	1.00	49.53	6
ATOM	3435	CE1	HIS	A	421	7.885	46.115	53.419	1.00	49.03	6
ATOM	3436	NE2	HIS	A	421	8.987	46.828	53.584	1.00	47.10	7
ATOM	3437	N	PRO	A	422	9.168	47.720	46.916	1.00	44.15	7
ATOM	3438	CA	PRO	A	422	9.307	47.609	45.461	1.00	42.61	6
ATOM	3439	C	PRO	A	422	10.670	47.020	45.172	1.00	39.48	6
ATOM	3440	O	PRO	A	422	11.684	47.306	45.824	1.00	39.30	8
ATOM	3441	CB	PRO	A	422	9.095	49.030	44.916	1.00	43.20	6
ATOM	3442	CG	PRO	A	422	9.570	49.868	46.080	1.00	45.14	6
ATOM	3443	CD	PRO	A	422	9.368	49.105	47.365	1.00	44.61	6
ATOM	3444	N	ASN	A	423	10.745	46.110	44.209	1.00	36.22	7
ATOM	3445	CA	ASN	A	423	11.996	45.473	43.830	1.00	32.97	6
ATOM	3446	C	ASN	A	423	12.315	44.285	44.718	1.00	29.70	6
ATOM	3447	O	ASN	A	423	13.340	43.628	44.532	1.00	29.23	8
ATOM	3448	CB	ASN	A	423	13.185	46.447	43.825	1.00	43.57	6
ATOM	3449	CG	ASN	A	423	13.020	47.493	42.717	1.00	52.50	6
ATOM	3450	OD1	ASN	A	423	12.140	47.312	41.857	1.00	53.89	8
ATOM	3451	ND2	ASN	A	423	13.817	48.550	42.776	1.00	51.34	7
ATOM	3452	N	SER	A	424	11.384	43.991	45.601	1.00	27.55	7
ATOM	3453	CA	SER	A	424	11.598	42.917	46.568	1.00	25.84	6
ATOM	3454	C	SER	A	424	11.441	41.558	45.939	1.00	20.78	6
ATOM	3455	O	SER	A	424	10.712	41.423	44.955	1.00	21.97	8
ATOM	3456	CB	SER	A	424	10.709	43.173	47.787	1.00	21.20	6
ATOM	3457	OG	SER	A	424	9.338	42.983	47.528	1.00	26.10	8
ATOM	3458	N	GLY	A	425	12.050	40.537	46.496	1.00	15.88	7
ATOM	3459	CA	GLY	A	425	11.954	39.135	46.045	1.00	11.07	6
ATOM	3460	C	GLY	A	425	13.381	38.628	46.051	1.00	9.56	6
ATOM	3461	O	GLY	A	425	14.252	39.481	45.929	1.00	12.58	8
ATOM	3462	N	LEU	A	426	13.656	37.333	46.160	1.00	9.63	7
ATOM	3463	CA	LEU	A	426	15.049	36.952	46.230	1.00	8.00	6
ATOM	3464	C	LEU	A	426	15.075	35.433	46.125	1.00	6.59	6
ATOM	3465	O	LEU	A	426	14.051	34.830	46.264	1.00	10.84	8
ATOM	3466	CB	LEU	A	426	15.766	37.454	47.493	1.00	12.80	6
ATOM	3467	CG	LEU	A	426	15.217	36.918	48.855	1.00	17.04	6
ATOM	3468	CD1	LEU	A	426	15.485	35.433	49.028	1.00	8.16	6
ATOM	3469	CD2	LEU	A	426	15.896	37.682	50.019	1.00	14.54	6
ATOM	3470	N	ALA	A	427	16.238	34.905	45.878	1.00	8.56	7
ATOM	3471	CA	ALA	A	427	16.470	33.494	45.795	1.00	9.40	6
ATOM	3472	C	ALA	A	427	17.770	33.308	46.632	1.00	11.82	6
ATOM	3473	O	ALA	A	427	18.790	33.846	46.230	1.00	11.64	8
ATOM	3474	CB	ALA	A	427	16.694	32.989	44.389	1.00	12.17	6
ATOM	3475	N	THR	A	428	17.618	32.535	47.755	1.00	12.60	7
ATOM	3476	CA	THR	A	428	18.847	32.242	48.520	1.00	7.12	6
ATOM	3477	C	THR	A	428	19.337	30.874	48.149	1.00	5.21	6
ATOM	3478	O	THR	A	428	18.535	29.938	48.151	1.00	10.00	8
ATOM	3479	CB	THR	A	428	18.458	32.190	50.076	1.00	14.89	6
ATOM	3480	OG1	THR	A	428	18.370	33.536	50.538	1.00	9.37	8
ATOM	3481	CG2	THR	A	428	19.732	31.683	50.770	1.00	7.45	6
ATOM	3482	N	ILE	A	429	20.634	30.609	47.957	1.00	6.52	7
ATOM	3483	CA	ILE	A	429	21.005	29.244	47.625	1.00	6.33	6
ATOM	3484	C	ILE	A	429	22.335	28.967	48.333	1.00	6.38	6
ATOM	3485	O	ILE	A	429	23.192	29.842	48.299	1.00	9.90	8
ATOM	3486	CB	ILE	A	429	21.126	29.049	46.094	1.00	16.71	6
ATOM	3487	CG1	ILE	A	429	21.745	27.675	45.805	1.00	13.81	6
ATOM	3488	CG2	ILE	A	429	22.017	30.132	45.451	1.00	7.87	6
ATOM	3489	CD1	ILE	A	429	21.400	27.207	44.377	1.00	29.66	6
ATOM	3490	N	MET	A	430	22.515	27.739	48.867	1.00	6.66	7
ATOM	3491	CA	MET	A	430	23.803	27.614	49.609	1.00	8.35	6
ATOM	3492	C	MET	A	430	24.210	26.176	49.528	1.00	7.33	6
ATOM	3493	O	MET	A	430	23.320	25.386	49.233	1.00	10.82	8
ATOM	3494	CB	MET	A	430	23.491	28.031	51.114	1.00	12.61	6
ATOM	3495	CG	MET	A	430	22.580	27.071	51.867	1.00	21.63	6
ATOM	3496	SD	MET	A	430	22.237	27.588	53.648	1.00	20.92	16
ATOM	3497	CE	MET	A	430	22.226	29.318	53.467	1.00	5.29	6
ATOM	3498	N	SER	A	431	25.508	25.919	49.763	1.00	9.08	7
ATOM	3499	CA	SER	A	431	25.931	24.524	49.765	1.00	9.29	6
ATOM	3500	C	SER	A	431	26.997	24.353	50.879	1.00	11.18	6

ATOM	3501	O	SER	A	431	27.888	25.180	51.006	1.00	10.71	8
ATOM	3502	CB	SER	A	431	26.737	24.278	48.441	1.00	9.34	6
ATOM	3503	OG	SER	A	431	27.031	22.880	48.398	1.00	10.03	8
ATOM	3504	N	ASP	A	432	27.007	23.193	51.532	1.00	11.88	7
ATOM	3505	CA	ASP	A	432	28.080	23.013	52.509	1.00	17.53	6
ATOM	3506	C	ASP	A	432	29.128	22.106	51.888	1.00	18.48	6
ATOM	3507	O	ASP	A	432	30.059	21.693	52.575	1.00	19.65	8
ATOM	3508	CB	ASP	A	432	27.574	22.500	53.874	1.00	13.62	6
ATOM	3509	CG	ASP	A	432	27.114	21.106	53.762	1.00	20.86	6
ATOM	3510	OD1	ASP	A	432	26.632	20.741	52.631	1.00	25.08	8
ATOM	3511	OD2	ASP	A	432	27.122	20.244	54.643	1.00	21.97	8
ATOM	3512	N	GLY	A	433	28.965	21.728	50.636	1.00	18.06	7
ATOM	3513	CA	GLY	A	433	29.942	20.908	49.901	1.00	17.93	6
ATOM	3514	C	GLY	A	433	30.254	21.615	48.560	1.00	19.65	6
ATOM	3515	O	GLY	A	433	30.256	22.837	48.415	1.00	18.59	8
ATOM	3516	N	PRO	A	434	30.374	20.808	47.531	1.00	20.92	7
ATOM	3517	CA	PRO	A	434	30.671	21.292	46.164	1.00	22.40	6
ATOM	3518	C	PRO	A	434	29.579	22.204	45.633	1.00	19.51	6
ATOM	3519	O	PRO	A	434	28.399	22.111	45.984	1.00	17.28	8
ATOM	3520	CB	PRO	A	434	30.858	20.028	45.287	1.00	23.50	6
ATOM	3521	CG	PRO	A	434	31.162	18.974	46.367	1.00	25.18	6
ATOM	3522	CD	PRO	A	434	30.334	19.331	47.593	1.00	21.90	6
ATOM	3523	N	GLY	A	435	29.977	23.221	44.899	1.00	21.46	7
ATOM	3524	CA	GLY	A	435	29.117	24.193	44.213	1.00	22.25	6
ATOM	3525	C	GLY	A	435	28.199	23.464	43.209	1.00	20.34	6
ATOM	3526	O	GLY	A	435	28.357	22.297	42.932	1.00	18.28	8
ATOM	3527	N	GLY	A	436	27.188	24.182	42.728	1.00	22.42	7
ATOM	3528	CA	GLY	A	436	26.241	23.604	41.777	1.00	19.22	6
ATOM	3529	C	GLY	A	436	25.110	24.613	41.533	1.00	15.97	6
ATOM	3530	O	GLY	A	436	25.232	25.814	41.726	1.00	19.08	8
ATOM	3531	N	GLU	A	437	23.947	24.068	41.202	1.00	15.44	7
ATOM	3532	CA	GLU	A	437	22.879	24.987	40.862	1.00	17.39	6
ATOM	3533	C	GLU	A	437	21.539	24.329	41.094	1.00	16.91	6
ATOM	3534	O	GLU	A	437	21.473	23.132	41.287	1.00	19.16	8
ATOM	3535	CB	GLU	A	437	23.088	25.476	39.401	1.00	37.35	6
ATOM	3536	CG	GLU	A	437	22.561	24.488	38.402	1.00	48.60	6
ATOM	3537	CD	GLU	A	437	23.271	24.417	37.059	1.00	63.89	6
ATOM	3538	OE1	GLU	A	437	24.253	25.163	36.858	1.00	64.25	8
ATOM	3539	OE2	GLU	A	437	22.760	23.611	36.220	1.00	61.31	8
ATOM	3540	N	LYS	A	438	20.513	25.164	41.140	1.00	16.88	7
ATOM	3541	CA	LYS	A	438	19.195	24.652	41.397	1.00	16.71	6
ATOM	3542	C	LYS	A	438	18.197	25.538	40.661	1.00	15.03	6
ATOM	3543	O	LYS	A	438	18.201	26.759	40.615	1.00	14.02	8
ATOM	3544	CB	LYS	A	438	18.822	24.744	42.917	1.00	15.80	6
ATOM	3545	CG	LYS	A	438	17.823	23.612	43.167	1.00	22.46	6
ATOM	3546	CD	LYS	A	438	17.118	23.747	44.517	1.00	27.63	6
ATOM	3547	CE	LYS	A	438	18.087	23.399	45.659	1.00	14.39	6
ATOM	3548	NZ	LYS	A	438	18.332	21.923	45.627	1.00	15.88	7
ATOM	3549	N	TRP	A	439	17.179	24.852	40.212	1.00	17.22	7
ATOM	3550	CA	TRP	A	439	16.073	25.457	39.455	1.00	20.48	6
ATOM	3551	C	TRP	A	439	15.022	25.892	40.475	1.00	19.48	6
ATOM	3552	O	TRP	A	439	14.573	25.008	41.203	1.00	21.32	8
ATOM	3553	CB	TRP	A	439	15.564	24.398	38.458	1.00	40.48	6
ATOM	3554	CG	TRP	A	439	15.732	22.971	38.929	1.00	79.64	6
ATOM	3555	CD1	TRP	A	439	16.851	22.314	39.388	1.00	82.87	6
ATOM	3556	CD2	TRP	A	439	14.689	21.975	38.972	1.00	92.39	6
ATOM	3557	NE1	TRP	A	439	16.577	21.027	39.732	1.00	88.68	7
ATOM	3558	CE2	TRP	A	439	15.250	20.786	39.478	1.00	94.65	6
ATOM	3559	CE3	TRP	A	439	13.328	21.982	38.640	1.00	99.81	6
ATOM	3560	CZ2	TRP	A	439	14.505	19.619	39.647	1.00	99.57	6
ATOM	3561	CZ3	TRP	A	439	12.591	20.827	38.814	1.00	103.16	6
ATOM	3562	CH2	TRP	A	439	13.181	19.657	39.313	1.00	101.89	6
ATOM	3563	N	MET	A	440	14.639	27.147	40.618	1.00	16.39	7
ATOM	3564	CA	MET	A	440	13.662	27.556	41.601	1.00	20.47	6
ATOM	3565	C	MET	A	440	12.726	28.644	41.097	1.00	19.37	6
ATOM	3566	O	MET	A	440	13.133	29.501	40.323	1.00	20.96	8
ATOM	3567	CB	MET	A	440	14.393	28.185	42.862	1.00	14.92	6
ATOM	3568	CG	MET	A	440	15.248	27.194	43.620	1.00	18.19	6
ATOM	3569	SD	MET	A	440	16.016	27.776	45.176	1.00	23.71	16
ATOM	3570	CE	MET	A	440	17.172	28.983	44.595	1.00	23.40	6
ATOM	3571	N	TYR	A	441	11.512	28.662	41.587	1.00	19.17	7
ATOM	3572	CA	TYR	A	441	10.493	29.612	41.193	1.00	17.45	6
ATOM	3573	C	TYR	A	441	10.491	30.925	41.911	1.00	19.37	6
ATOM	3574	O	TYR	A	441	10.306	30.894	43.144	1.00	20.83	8

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ATOM   3575  CB  TYR A 441       9.158  28.882  41.392  1.00 18.76   6
ATOM   3576  CG  TYR A 441       7.946  29.700  41.019  1.00 23.90   6
ATOM   3577  CD1 TYR A 441       7.714  30.003  39.663  1.00 24.83   6
ATOM   3578  CD2 TYR A 441       7.035  30.174  41.929  1.00 26.10   6
ATOM   3579  CE1 TYR A 441       6.622  30.734  39.268  1.00 22.74   6
ATOM   3580  CE2 TYR A 441       5.936  30.926  41.560  1.00 26.92   6
ATOM   3581  CZ  TYR A 441       5.735  31.181  40.213  1.00 26.49   6
ATOM   3582  OH  TYR A 441       4.644  31.921  39.817  1.00 27.24   8
ATOM   3583  N   VAL A 442      10.551  32.102  41.275  1.00 17.33   7
ATOM   3584  CA  VAL A 442      10.503  33.378  41.934  1.00 17.24   6
ATOM   3585  C   VAL A 442       9.215  34.147  41.685  1.00 19.14   6
ATOM   3586  O   VAL A 442       8.989  35.223  42.261  1.00 18.47   8
ATOM   3587  CB  VAL A 442      11.711  34.267  41.631  1.00 21.08   6
ATOM   3588  CG1 VAL A 442      12.950  33.529  42.117  1.00 12.81   6
ATOM   3589  CG2 VAL A 442      11.819  34.555  40.118  1.00 17.82   6
ATOM   3590  N   GLY A 443       8.355  33.583  40.824  1.00 19.01   7
ATOM   3591  CA  GLY A 443       7.106  34.258  40.520  1.00 20.35   6
ATOM   3592  C   GLY A 443       7.037  34.695  39.040  1.00 22.26   6
ATOM   3593  O   GLY A 443       7.945  35.338  38.527  1.00 22.27   8
ATOM   3594  N   GLN A 444       5.910  34.362  38.422  1.00 24.17   7
ATOM   3595  CA  GLN A 444       5.600  34.665  37.021  1.00 24.96   6
ATOM   3596  C   GLN A 444       5.765  36.122  36.660  1.00 23.35   6
ATOM   3597  O   GLN A 444       6.399  36.407  35.636  1.00 27.45   8
ATOM   3598  CB  GLN A 444       4.162  34.299  36.663  1.00 29.53   6
ATOM   3599  CG  GLN A 444       3.900  32.806  36.803  1.00 46.12   6
ATOM   3600  CD  GLN A 444       2.592  32.427  36.120  1.00 62.67   6
ATOM   3601  OE1 GLN A 444       1.849  33.279  35.625  1.00 63.63   8
ATOM   3602  NE2 GLN A 444       2.355  31.119  36.112  1.00 71.09   7
ATOM   3603  N   ASN A 445       5.375  37.067  37.464  1.00 21.45   7
ATOM   3604  CA  ASN A 445       5.605  38.469  37.254  1.00 21.23   6
ATOM   3605  C   ASN A 445       7.054  38.890  37.261  1.00 21.93   6
ATOM   3606  O   ASN A 445       7.246  40.099  37.088  1.00 25.78   8
ATOM   3607  CB  ASN A 445       4.839  39.358  38.236  1.00 30.03   6
ATOM   3608  CG  ASN A 445       5.320  39.194  39.679  1.00 45.80   6
ATOM   3609  OD1 ASN A 445       5.987  38.202  40.013  1.00 42.55   8
ATOM   3610  ND2 ASN A 445       4.998  40.136  40.574  1.00 36.92   7
ATOM   3611  N   LYS A 446       8.078  38.064  37.438  1.00 21.07   7
ATOM   3612  CA  LYS A 446       9.449  38.580  37.424  1.00 18.80   6
ATOM   3613  C   LYS A 446      10.117  38.163  36.087  1.00 16.42   6
ATOM   3614  O   LYS A 446      11.325  38.297  35.908  1.00 14.00   8
ATOM   3615  CB  LYS A 446      10.274  38.016  38.607  1.00 22.87   6
ATOM   3616  CG  LYS A 446       9.714  38.055  40.045  1.00 20.43   6
ATOM   3617  CD  LYS A 446       9.144  39.421  40.333  1.00 19.39   6
ATOM   3618  CE  LYS A 446       8.549  39.569  41.735  1.00 33.48   6
ATOM   3619  NZ  LYS A 446       9.619  39.947  42.686  1.00 20.28   7
ATOM   3620  N   ALA A 447       9.313  37.561  35.214  1.00 18.69   7
ATOM   3621  CA  ALA A 447       9.807  37.132  33.863  1.00 18.64   6
ATOM   3622  C   ALA A 447      10.638  38.198  33.169  1.00 16.44   6
ATOM   3623  O   ALA A 447      10.212  39.357  33.172  1.00 16.52   8
ATOM   3624  CB  ALA A 447       8.615  36.834  32.962  1.00 12.08   6
ATOM   3625  N   GLY A 448      11.828  37.822  32.725  1.00 18.95   7
ATOM   3626  CA  GLY A 448      12.714  38.717  32.003  1.00 21.86   6
ATOM   3627  C   GLY A 448      13.580  39.636  32.844  1.00 25.00   6
ATOM   3628  O   GLY A 448      14.406  40.334  32.251  1.00 22.21   8
ATOM   3629  N   GLN A 449      13.460  39.625  34.209  1.00 23.94   7
ATOM   3630  CA  GLN A 449      14.356  40.485  35.002  1.00 20.19   6
ATOM   3631  C   GLN A 449      15.726  39.824  35.110  1.00 19.28   6
ATOM   3632  O   GLN A 449      15.911  38.609  34.932  1.00 18.29   8
ATOM   3633  CB  GLN A 449      13.798  40.688  36.402  1.00 22.06   6
ATOM   3634  CG  GLN A 449      12.373  41.221  36.448  1.00 19.83   6
ATOM   3635  CD  GLN A 449      11.966  41.512  37.899  1.00 33.19   6
ATOM   3636  OE1 GLN A 449      10.960  42.166  38.157  1.00 27.87   8
ATOM   3637  NE2 GLN A 449      12.776  41.029  38.836  1.00 18.13   7
ATOM   3638  N   VAL A 450      16.697  40.709  35.289  1.00 18.52   7
ATOM   3639  CA  VAL A 450      18.074  40.243  35.369  1.00 22.23   6
ATOM   3640  C   VAL A 450      18.481  40.412  36.875  1.00 21.59   6
ATOM   3641  O   VAL A 450      18.406  41.522  37.392  1.00 19.00   8
ATOM   3642  CB  VAL A 450      19.009  41.180  34.587  1.00 21.38   6
ATOM   3643  CG1 VAL A 450      20.465  40.804  34.829  1.00 18.85   6
ATOM   3644  CG2 VAL A 450      18.645  41.095  33.101  1.00 25.37   6
ATOM   3645  N   TRP A 451      18.919  39.327  37.462  1.00 21.95   7
ATOM   3646  CA  TRP A 451      19.269  39.345  38.893  1.00 22.78   6
ATOM   3647  C   TRP A 451      20.737  39.173  39.144  1.00 22.81   6
ATOM   3648  O   TRP A 451      21.421  38.496  38.371  1.00 24.18   8
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ATOM	3649	CB	TRP	A	451	18.473	38.191	39.545	1.00	18.72	6
ATOM	3650	CG	TRP	A	451	17.006	38.481	39.743	1.00	15.12	6
ATOM	3651	CD1	TRP	A	451	16.210	39.359	39.083	1.00	19.62	6
ATOM	3652	CD2	TRP	A	451	16.154	37.891	40.730	1.00	25.22	6
ATOM	3653	NE1	TRP	A	451	14.920	39.350	39.542	1.00	22.83	7
ATOM	3654	CE2	TRP	A	451	14.873	38.437	40.575	1.00	24.01	6
ATOM	3655	CE3	TRP	A	451	16.375	36.957	41.768	1.00	20.26	6
ATOM	3656	CZ2	TRP	A	451	13.808	38.095	41.406	1.00	15.77	6
ATOM	3657	CZ3	TRP	A	451	15.302	36.589	42.552	1.00	16.21	6
ATOM	3658	CH2	TRP	A	451	14.060	37.165	42.384	1.00	11.49	6
ATOM	3659	N	HIS	A	452	21.241	39.675	40.274	1.00	22.72	7
ATOM	3660	CA	HIS	A	452	22.651	39.425	40.598	1.00	21.61	6
ATOM	3661	C	HIS	A	452	22.806	39.006	42.086	1.00	22.69	6
ATOM	3662	O	HIS	A	452	21.833	38.928	42.854	1.00	22.08	8
ATOM	3663	CB	HIS	A	452	23.469	40.648	40.251	1.00	19.24	6
ATOM	3664	CG	HIS	A	452	23.193	41.764	41.225	1.00	37.38	6
ATOM	3665	ND1	HIS	A	452	24.209	42.528	41.757	1.00	43.93	7
ATOM	3666	CD2	HIS	A	452	22.043	42.190	41.808	1.00	41.64	6
ATOM	3667	CE1	HIS	A	452	23.693	43.404	42.597	1.00	41.75	6
ATOM	3668	NE2	HIS	A	452	22.392	43.222	42.646	1.00	38.20	7
ATOM	3669	N	ASP	A	453	24.007	38.542	42.389	1.00	21.14	7
ATOM	3670	CA	ASP	A	453	24.298	37.985	43.727	1.00	21.43	6
ATOM	3671	C	ASP	A	453	24.675	39.145	44.647	1.00	20.48	6
ATOM	3672	O	ASP	A	453	25.785	39.620	44.557	1.00	19.57	8
ATOM	3673	CB	ASP	A	453	25.361	36.906	43.679	1.00	16.37	6
ATOM	3674	CG	ASP	A	453	25.748	36.255	45.020	1.00	30.12	6
ATOM	3675	OD1	ASP	A	453	25.197	36.660	46.082	1.00	17.12	8
ATOM	3676	OD2	ASP	A	453	26.600	35.324	45.079	1.00	13.59	8
ATOM	3677	N	ILE	A	454	23.768	39.576	45.504	1.00	21.42	7
ATOM	3678	CA	ILE	A	454	24.030	40.669	46.453	1.00	21.19	6
ATOM	3679	C	ILE	A	454	25.184	40.396	47.398	1.00	21.47	6
ATOM	3680	O	ILE	A	454	25.822	41.366	47.838	1.00	22.17	8
ATOM	3681	CB	ILE	A	454	22.786	41.083	47.230	1.00	21.21	6
ATOM	3682	CG1	ILE	A	454	22.867	42.506	47.792	1.00	27.82	6
ATOM	3683	CG2	ILE	A	454	22.392	40.067	48.293	1.00	12.48	6
ATOM	3684	CD1	ILE	A	454	21.525	42.918	48.415	1.00	22.75	6
ATOM	3685	N	THR	A	455	25.652	39.166	47.580	1.00	21.33	7
ATOM	3686	CA	THR	A	455	26.806	38.928	48.418	1.00	24.19	6
ATOM	3687	C	THR	A	455	28.094	39.164	47.634	1.00	28.00	6
ATOM	3688	O	THR	A	455	29.175	39.281	48.243	1.00	25.46	8
ATOM	3689	CB	THR	A	455	26.869	37.516	48.996	1.00	20.94	6
ATOM	3690	OG1	THR	A	455	27.101	36.595	47.918	1.00	13.03	8
ATOM	3691	CG2	THR	A	455	25.576	37.131	49.723	1.00	11.73	6
ATOM	3692	N	GLY	A	456	27.936	39.109	46.284	1.00	26.42	7
ATOM	3693	CA	GLY	A	456	29.126	39.237	45.452	1.00	26.72	6
ATOM	3694	C	GLY	A	456	29.929	37.951	45.434	1.00	27.50	6
ATOM	3695	O	GLY	A	456	31.055	37.929	44.936	1.00	28.81	8
ATOM	3696	N	ASN	A	457	29.429	36.834	45.956	1.00	27.72	7
ATOM	3697	CA	ASN	A	457	30.161	35.582	45.935	1.00	28.88	6
ATOM	3698	C	ASN	A	457	30.186	35.037	44.505	1.00	30.88	6
ATOM	3699	O	ASN	A	457	31.208	34.478	44.116	1.00	32.05	8
ATOM	3700	CB	ASN	A	457	29.597	34.558	46.931	1.00	29.41	6
ATOM	3701	CG	ASN	A	457	29.776	34.897	48.411	1.00	35.69	6
ATOM	3702	OD1	ASN	A	457	28.943	34.630	49.300	1.00	34.46	8
ATOM	3703	ND2	ASN	A	457	30.905	35.518	48.721	1.00	20.50	7
ATOM	3704	N	LYS	A	458	29.078	35.062	43.779	1.00	31.28	7
ATOM	3705	CA	LYS	A	458	28.936	34.566	42.402	1.00	32.10	6
ATOM	3706	C	LYS	A	458	28.835	35.765	41.467	1.00	32.39	6
ATOM	3707	O	LYS	A	458	27.916	36.597	41.513	1.00	31.80	8
ATOM	3708	CB	LYS	A	458	27.586	33.853	42.246	1.00	30.51	6
ATOM	3709	CG	LYS	A	458	27.661	32.358	42.238	1.00	28.44	6
ATOM	3710	CD	LYS	A	458	28.557	31.874	41.120	1.00	30.75	6
ATOM	3711	CE	LYS	A	458	28.709	30.366	41.267	1.00	38.53	6
ATOM	3712	NZ	LYS	A	458	29.127	29.819	39.947	1.00	46.81	7
ATOM	3713	N	PRO	A	459	29.801	35.912	40.582	1.00	35.18	7
ATOM	3714	CA	PRO	A	459	29.929	37.091	39.739	1.00	35.47	6
ATOM	3715	C	PRO	A	459	28.953	37.258	38.602	1.00	37.23	6
ATOM	3716	O	PRO	A	459	28.746	38.445	38.202	1.00	40.65	8
ATOM	3717	CB	PRO	A	459	31.403	37.168	39.320	1.00	35.59	6
ATOM	3718	CG	PRO	A	459	31.844	35.739	39.467	1.00	35.76	6
ATOM	3719	CD	PRO	A	459	30.946	35.014	40.452	1.00	35.97	6
ATOM	3720	N	GLY	A	460	28.241	36.255	38.096	1.00	35.36	7
ATOM	3721	CA	GLY	A	460	27.370	36.618	36.959	1.00	33.99	6
ATOM	3722	C	GLY	A	460	26.079	37.355	37.124	1.00	31.39	6

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ATOM   3723  O   GLY A 460      25.723  38.162  37.987  1.00 31.32   8
ATOM   3724  N   THR A 461      25.172  37.089  36.168  1.00 28.63   7
ATOM   3725  CA  THR A 461      23.820  37.591  36.201  1.00 26.63   6
ATOM   3726  C   THR A 461      22.977  36.365  35.857  1.00 26.19   6
ATOM   3727  O   THR A 461      23.509  35.368  35.372  1.00 25.69   8
ATOM   3728  CB  THR A 461      23.406  38.714  35.253  1.00 34.32   6
ATOM   3729  OG1 THR A 461      23.582  38.196  33.940  1.00 39.98   8
ATOM   3730  CG2 THR A 461      24.197  39.984  35.459  1.00 36.81   6
ATOM   3731  N   VAL A 462      21.682  36.479  36.097  1.00 24.35   7
ATOM   3732  CA  VAL A 462      20.801  35.342  35.840  1.00 24.97   6
ATOM   3733  C   VAL A 462      19.525  36.061  35.394  1.00 25.20   6
ATOM   3734  O   VAL A 462      19.129  37.029  36.059  1.00 26.38   8
ATOM   3735  CB  VAL A 462      20.574  34.535  37.138  1.00 26.35   6
ATOM   3736  CG1 VAL A 462      19.170  34.009  37.299  1.00 27.37   6
ATOM   3737  CG2 VAL A 462      21.533  33.362  37.172  1.00 37.60   6
ATOM   3738  N   THR A 463      18.932  35.524  34.343  1.00 24.53   7
ATOM   3739  CA  THR A 463      17.720  36.194  33.827  1.00 22.54   6
ATOM   3740  C   THR A 463      16.530  35.314  34.144  1.00 19.39   6
ATOM   3741  O   THR A 463      16.687  34.104  33.936  1.00 18.11   8
ATOM   3742  CB  THR A 463      17.799  36.326  32.270  1.00 27.00   6
ATOM   3743  OG1 THR A 463      18.933  37.127  31.946  1.00 25.69   8
ATOM   3744  CG2 THR A 463      16.563  37.080  31.786  1.00 21.84   6
ATOM   3745  N   ILE A 464      15.443  35.905  34.620  1.00 18.98   7
ATOM   3746  CA  ILE A 464      14.318  35.002  34.950  1.00 19.00   6
ATOM   3747  C   ILE A 464      13.588  34.598  33.646  1.00 23.41   6
ATOM   3748  O   ILE A 464      13.346  35.458  32.794  1.00 22.97   8
ATOM   3749  CB  ILE A 464      13.345  35.759  35.871  1.00 23.33   6
ATOM   3750  CG1 ILE A 464      14.049  36.430  37.059  1.00 19.89   6
ATOM   3751  CG2 ILE A 464      12.261  34.806  36.345  1.00 23.29   6
ATOM   3752  CD1 ILE A 464      15.140  35.555  37.656  1.00 14.03   6
ATOM   3753  N   ASN A 465      13.178  33.347  33.558  1.00 21.94   7
ATOM   3754  CA  ASN A 465      12.516  32.846  32.387  1.00 22.42   6
ATOM   3755  C   ASN A 465      11.097  33.333  32.280  1.00 23.26   6
ATOM   3756  O   ASN A 465      10.512  33.991  33.139  1.00 23.81   8
ATOM   3757  CB  ASN A 465      12.731  31.359  32.224  1.00 13.06   6
ATOM   3758  CG  ASN A 465      11.672  30.476  32.848  1.00 24.11   6
ATOM   3759  OD1 ASN A 465      10.653  30.845  33.442  1.00 27.47   8
ATOM   3760  ND2 ASN A 465      11.913  29.185  32.652  1.00 26.50   7
ATOM   3761  N   ALA A 466      10.436  32.919  31.184  1.00 22.42   7
ATOM   3762  CA  ALA A 466       9.107  33.388  30.855  1.00 20.19   6
ATOM   3763  C   ALA A 466       8.060  32.877  31.815  1.00 20.86   6
ATOM   3764  O   ALA A 466       7.005  33.519  31.862  1.00 19.65   8
ATOM   3765  CB  ALA A 466       8.720  32.927  29.440  1.00 27.57   6
ATOM   3766  N   ASP A 467       8.339  31.758  32.472  1.00 20.43   7
ATOM   3767  CA  ASP A 467       7.375  31.236  33.432  1.00 25.15   6
ATOM   3768  C   ASP A 467       7.714  31.622  34.898  1.00 26.69   6
ATOM   3769  O   ASP A 467       6.988  31.198  35.814  1.00 27.50   8
ATOM   3770  CB  ASP A 467       7.280  29.718  33.419  1.00 35.94   6
ATOM   3771  CG  ASP A 467       7.447  28.991  32.113  1.00 57.11   6
ATOM   3772  OD1 ASP A 467       6.618  29.149  31.191  1.00 55.73   8
ATOM   3773  OD2 ASP A 467       8.416  28.211  31.968  1.00 68.22   8
ATOM   3774  N   GLY A 468       8.787  32.333  35.124  1.00 25.27   7
ATOM   3775  CA  GLY A 468       9.169  32.772  36.449  1.00 25.94   6
ATOM   3776  C   GLY A 468      10.173  31.846  37.129  1.00 26.60   6
ATOM   3777  O   GLY A 468      10.379  31.937  38.329  1.00 23.74   8
ATOM   3778  N   TRP A 469      10.857  30.984  36.384  1.00 26.03   7
ATOM   3779  CA  TRP A 469      11.866  30.075  36.864  1.00 24.07   6
ATOM   3780  C   TRP A 469      13.252  30.507  36.421  1.00 24.59   6
ATOM   3781  O   TRP A 469      13.360  31.256  35.447  1.00 24.16   8
ATOM   3782  CB  TRP A 469      11.711  28.639  36.344  1.00 24.41   6
ATOM   3783  CG  TRP A 469      10.483  28.028  36.943  1.00 29.23   6
ATOM   3784  CD1 TRP A 469       9.187  28.305  36.618  1.00 34.11   6
ATOM   3785  CD2 TRP A 469      10.454  27.060  37.998  1.00 29.54   6
ATOM   3786  NE1 TRP A 469       8.336  27.562  37.415  1.00 33.70   7
ATOM   3787  CE2 TRP A 469       9.095  26.767  38.250  1.00 31.92   6
ATOM   3788  CE3 TRP A 469      11.426  26.377  38.726  1.00 30.77   6
ATOM   3789  CZ2 TRP A 469       8.709  25.856  39.233  1.00 35.82   6
ATOM   3790  CZ3 TRP A 469      11.040  25.474  39.697  1.00 30.23   6
ATOM   3791  CH2 TRP A 469       9.688  25.235  39.954  1.00 30.75   6
ATOM   3792  N   ALA A 470      14.261  30.045  37.151  1.00 22.85   7
ATOM   3793  CA  ALA A 470      15.628  30.383  36.788  1.00 21.53   6
ATOM   3794  C   ALA A 470      16.546  29.352  37.431  1.00 23.57   6
ATOM   3795  O   ALA A 470      16.167  28.716  38.421  1.00 23.74   8
ATOM   3796  CB  ALA A 470      16.026  31.769  37.199  1.00 21.25   6
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ATOM	3797	N	ASN	A	471	17.685	29.139	36.815	1.00	20.45	7
ATOM	3798	CA	ASN	A	471	18.653	28.210	37.305	1.00	22.12	6
ATOM	3799	C	ASN	A	471	19.645	29.034	38.152	1.00	22.93	6
ATOM	3800	O	ASN	A	471	20.502	29.705	37.574	1.00	23.29	8
ATOM	3801	CB	ASN	A	471	19.444	27.600	36.160	1.00	35.69	6
ATOM	3802	CG	ASN	A	471	19.698	26.130	36.384	1.00	47.51	6
ATOM	3803	OD1	ASN	A	471	20.841	25.728	36.333	1.00	50.34	8
ATOM	3804	ND2	ASN	A	471	18.684	25.322	36.598	1.00	59.19	7
ATOM	3805	N	PHE	A	472	19.494	28.961	39.468	1.00	19.79	7
ATOM	3806	CA	PHE	A	472	20.419	29.796	40.310	1.00	16.18	6
ATOM	3807	C	PHE	A	472	21.655	29.058	40.663	1.00	12.19	6
ATOM	3808	O	PHE	A	472	21.623	27.815	40.786	1.00	17.32	8
ATOM	3809	CB	PHE	A	472	19.541	30.196	41.489	1.00	13.15	6
ATOM	3810	CG	PHE	A	472	18.432	31.150	41.246	1.00	6.63	6
ATOM	3811	CD1	PHE	A	472	18.667	32.489	41.067	1.00	13.56	6
ATOM	3812	CD2	PHE	A	472	17.122	30.703	41.236	1.00	7.40	6
ATOM	3813	CE1	PHE	A	472	17.639	33.393	40.825	1.00	13.16	6
ATOM	3814	CE2	PHE	A	472	16.099	31.585	40.959	1.00	12.05	6
ATOM	3815	CZ	PHE	A	472	16.345	32.935	40.759	1.00	14.01	6
ATOM	3816	N	SER	A	473	22.870	29.595	40.786	1.00	13.50	7
ATOM	3817	CA	SER	A	473	23.961	28.697	41.169	1.00	14.11	6
ATOM	3818	C	SER	A	473	24.726	29.176	42.424	1.00	12.54	6
ATOM	3819	O	SER	A	473	24.490	30.293	42.846	1.00	13.13	8
ATOM	3820	CB	SER	A	473	24.999	28.680	39.999	1.00	18.25	6
ATOM	3821	OG	SER	A	473	25.372	30.054	39.899	1.00	20.56	8
ATOM	3822	N	VAL	A	474	25.705	28.401	42.881	1.00	13.61	7
ATOM	3823	CA	VAL	A	474	26.412	28.909	44.097	1.00	16.44	6
ATOM	3824	C	VAL	A	474	27.764	28.251	44.127	1.00	15.20	6
ATOM	3825	O	VAL	A	474	27.856	27.095	43.703	1.00	18.90	8
ATOM	3826	CB	VAL	A	474	25.539	28.505	45.332	1.00	12.07	6
ATOM	3827	CG1	VAL	A	474	25.307	26.998	45.341	1.00	4.17	6
ATOM	3828	CG2	VAL	A	474	26.120	28.842	46.690	1.00	19.53	6
ATOM	3829	N	ASN	A	475	28.761	28.905	44.681	1.00	16.23	7
ATOM	3830	CA	ASN	A	475	30.069	28.301	44.876	1.00	17.52	6
ATOM	3831	C	ASN	A	475	30.050	27.213	45.938	1.00	20.97	6
ATOM	3832	O	ASN	A	475	29.049	27.130	46.676	1.00	20.95	8
ATOM	3833	CB	ASN	A	475	31.046	29.414	45.253	1.00	21.99	6
ATOM	3834	CG	ASN	A	475	31.374	30.221	43.978	1.00	30.21	6
ATOM	3835	OD1	ASN	A	475	31.377	29.592	42.917	1.00	29.36	8
ATOM	3836	ND2	ASN	A	475	31.631	31.510	44.084	1.00	26.76	7
ATOM	3837	N	GLY	A	476	31.106	26.400	46.029	1.00	20.35	7
ATOM	3838	CA	GLY	A	476	31.140	25.343	47.050	1.00	19.93	6
ATOM	3839	C	GLY	A	476	31.348	25.970	48.453	1.00	19.53	6
ATOM	3840	O	GLY	A	476	31.977	27.014	48.576	1.00	14.05	8
ATOM	3841	N	GLY	A	477	30.658	25.410	49.493	1.00	19.68	7
ATOM	3842	CA	GLY	A	477	30.888	25.911	50.867	1.00	17.22	6
ATOM	3843	C	GLY	A	477	30.567	27.376	50.985	1.00	17.16	6
ATOM	3844	O	GLY	A	477	31.300	28.184	51.538	1.00	16.37	8
ATOM	3845	N	SER	A	478	29.413	27.756	50.402	1.00	15.45	7
ATOM	3846	CA	SER	A	478	29.132	29.190	50.345	1.00	13.71	6
ATOM	3847	C	SER	A	478	27.644	29.438	50.244	1.00	11.85	6
ATOM	3848	O	SER	A	478	26.866	28.524	50.190	1.00	14.63	8
ATOM	3849	CB	SER	A	478	29.720	29.555	48.930	1.00	14.86	6
ATOM	3850	OG	SER	A	478	29.794	30.947	48.838	1.00	20.40	8
ATOM	3851	N	VAL	A	479	27.275	30.697	50.221	1.00	11.60	7
ATOM	3852	CA	VAL	A	479	25.905	31.087	49.998	1.00	12.55	6
ATOM	3853	C	VAL	A	479	25.880	32.212	48.924	1.00	11.49	6
ATOM	3854	O	VAL	A	479	26.741	33.083	48.864	1.00	11.55	8
ATOM	3855	CB	VAL	A	479	25.273	31.623	51.311	1.00	12.79	6
ATOM	3856	CG1	VAL	A	479	26.115	32.797	51.835	1.00	9.12	6
ATOM	3857	CG2	VAL	A	479	23.817	32.055	51.166	1.00	4.71	6
ATOM	3858	N	SER	A	480	24.780	32.237	48.166	1.00	13.81	7
ATOM	3859	CA	SER	A	480	24.597	33.365	47.238	1.00	11.93	6
ATOM	3860	C	SER	A	480	23.180	33.821	47.451	1.00	8.76	6
ATOM	3861	O	SER	A	480	22.252	33.053	47.650	1.00	11.76	8
ATOM	3862	CB	SER	A	480	24.856	32.914	45.765	1.00	20.36	6
ATOM	3863	OG	SER	A	480	26.221	33.103	45.402	1.00	13.39	8
ATOM	3864	N	ILE	A	481	22.897	35.104	47.407	1.00	11.45	7
ATOM	3865	CA	ILE	A	481	21.517	35.554	47.543	1.00	13.32	6
ATOM	3866	C	ILE	A	481	21.173	36.380	46.268	1.00	14.81	6
ATOM	3867	O	ILE	A	481	21.643	37.490	46.094	1.00	13.00	8
ATOM	3868	CB	ILE	A	481	21.369	36.401	48.839	1.00	12.79	6
ATOM	3869	CG1	ILE	A	481	21.711	35.500	50.091	1.00	16.67	6
ATOM	3870	CG2	ILE	A	481	19.939	36.934	48.878	1.00	6.58	6

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ATOM   3871  CD1 ILE A 481      21.809  36.366  51.349  1.00 14.77   6
ATOM   3872  N   TRP A 482      20.266  35.842  45.450  1.00 16.67   7
ATOM   3873  CA  TRP A 482      19.996  36.529  44.159  1.00 16.84   6
ATOM   3874  C   TRP A 482      18.854  37.489  44.220  1.00 15.36   6
ATOM   3875  O   TRP A 482      17.773  37.074  44.690  1.00 16.15   8
ATOM   3876  CB  TRP A 482      19.791  35.479  43.055  1.00 11.32   6
ATOM   3877  CG  TRP A 482      20.966  34.610  42.832  1.00 13.31   6
ATOM   3878  CD1 TRP A 482      21.210  33.414  43.426  1.00 13.12   6
ATOM   3879  CD2 TRP A 482      22.055  34.820  41.906  1.00 20.71   6
ATOM   3880  NE1 TRP A 482      22.395  32.886  42.975  1.00 13.99   7
ATOM   3881  CE2 TRP A 482      22.923  33.727  42.033  1.00 17.34   6
ATOM   3882  CE3 TRP A 482      22.349  35.834  40.969  1.00 24.46   6
ATOM   3883  CZ2 TRP A 482      24.100  33.594  41.281  1.00 23.61   6
ATOM   3884  CZ3 TRP A 482      23.527  35.734  40.237  1.00 15.44   6
ATOM   3885  CH2 TRP A 482      24.375  34.608  40.391  1.00 15.55   6
ATOM   3886  N   VAL A 483      19.077  38.750  43.833  1.00 15.53   7
ATOM   3887  CA  VAL A 483      18.002  39.734  43.801  1.00 18.71   6
ATOM   3888  C   VAL A 483      18.016  40.540  42.454  1.00 18.89   6
ATOM   3889  O   VAL A 483      19.077  40.622  41.835  1.00 18.73   8
ATOM   3890  CB  VAL A 483      18.094  40.853  44.884  1.00 19.44   6
ATOM   3891  CG1 VAL A 483      18.117  40.240  46.286  1.00 24.26   6
ATOM   3892  CG2 VAL A 483      19.315  41.744  44.705  1.00 15.59   6
ATOM   3893  N   LYS A 484      16.913  41.189  42.139  1.00 19.32   7
ATOM   3894  CA  LYS A 484      16.841  42.076  40.980  1.00 21.09   6
ATOM   3895  C   LYS A 484      17.961  43.100  40.983  1.00 24.00   6
ATOM   3896  O   LYS A 484      18.192  43.826  41.973  1.00 23.05   8
ATOM   3897  CB  LYS A 484      15.530  42.867  40.958  1.00 28.12   6
ATOM   3898  CG  LYS A 484      15.350  43.773  39.739  1.00 32.20   6
ATOM   3899  CD  LYS A 484      14.045  44.535  39.852  1.00 44.02   6
ATOM   3900  CE  LYS A 484      13.718  45.239  38.534  1.00 55.99   6
ATOM   3901  NZ  LYS A 484      12.396  45.944  38.628  1.00 59.77   7
ATOM   3902  N   ARG A 485      18.719  43.105  39.867  1.00 24.97   7
ATOM   3903  CA  ARG A 485      19.804  44.080  39.768  1.00 29.19   6
ATOM   3904  C   ARG A 485      19.283  45.475  39.450  1.00 30.80   6
ATOM   3905  O   ARG A 485      19.850  46.446  39.999  1.00 33.55   8
ATOM   3906  CB  ARG A 485      20.903  43.779  38.748  1.00 40.45   6
ATOM   3907  CG  ARG A 485      22.106  44.686  39.037  1.00 59.45   6
ATOM   3908  CD  ARG A 485      23.403  43.990  38.638  1.00 78.70   6
ATOM   3909  NE  ARG A 485      23.356  43.672  37.209  1.00 93.35   7
ATOM   3910  CZ  ARG A 485      23.460  44.555  36.221  1.00 97.50   6
ATOM   3911  NH1 ARG A 485      23.646  45.839  36.505  1.00 99.91   7
ATOM   3912  NH2 ARG A 485      23.381  44.130  34.965  1.00 98.10   7
ATOM   3913  OT  ARG A 485      18.315  45.575  38.684  1.00 36.53   8
ATOM   3914 CA   IUM A 486      16.403  28.839  91.080  1.00 13.38  20
ATOM   3915 CA   IUM A 487      11.326  27.396  97.560  1.00 14.89  20
ATOM   3916 CA   IUM A 488      12.079  41.438  41.820  1.00 65.35  20
ATOM   3917 CA   IUM A 489      26.215  18.079  53.059  1.00 20.01  20
ATOM   3918 NA   IUM A 490      14.404  28.621  94.442  1.00 13.98  11
ATOM   3919  OW0 WAT W   1      15.331  30.924  91.968  1.00  8.40   8
ATOM   3920  OW0 WAT W   2      20.672  29.374  91.814  1.00  9.95   8
ATOM   3921  OW0 WAT W   3      10.621  27.443 100.167  1.00 10.46   8
ATOM   3922  OW0 WAT W   4      28.869  20.050  56.659  1.00 11.85   8
ATOM   3923  OW0 WAT W   5      14.586  33.181  61.484  1.00 12.59   8
ATOM   3924  OW0 WAT W   6      18.392  34.544  86.249  1.00 13.31   8
ATOM   3925  OW0 WAT W   7      12.636  28.973  91.117  1.00 13.68   8
ATOM   3926  OW0 WAT W   8      15.634  35.829  85.277  1.00 13.76   8
ATOM   3927  OW0 WAT W   9      18.872  29.499  66.652  1.00 14.41   8
ATOM   3928  OW0 WAT W  10      15.541  28.877  74.819  1.00 14.80   8
ATOM   3929  OW0 WAT W  11      17.655  22.379  93.167  1.00 15.02   8
ATOM   3930  OW0 WAT W  12      10.694  30.117  84.366  1.00 15.45   8
ATOM   3931  OW0 WAT W  13      18.071  28.115  81.035  1.00 15.55   8
ATOM   3932  OW0 WAT W  14      26.048  15.607  52.885  1.00 15.91   8
ATOM   3933  OW0 WAT W  15      29.348  31.173  86.751  1.00 16.00   8
ATOM   3934  OW0 WAT W  16      10.192  22.022  80.509  1.00 16.03   8
ATOM   3935  OW0 WAT W  17      27.199  31.182 100.558  1.00 16.19   8
ATOM   3936  OW0 WAT W  18      29.018  45.155  85.220  1.00 16.88   8
ATOM   3937  OW0 WAT W  19       5.482  31.285  76.403  1.00 16.88   8
ATOM   3938  OW0 WAT W  20      26.381  45.012  84.704  1.00 17.27   8
ATOM   3939  OW0 WAT W  21      25.881  32.894  83.269  1.00 17.32   8
ATOM   3940  OW0 WAT W  22      25.409  35.676  97.523  1.00 17.35   8
ATOM   3941  OW0 WAT W  23       7.309  25.461  94.547  1.00 17.78   8
ATOM   3942  OW0 WAT W  24      20.157  53.017  89.490  1.00 18.71   8
ATOM   3943  OW0 WAT W  25      18.501  20.523  81.617  1.00 18.85   8
ATOM   3944  OW0 WAT W  26      30.763  42.059  78.813  1.00 18.95   8
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ATOM	3945	OW0	WAT	W	27	23.018	30.980	81.026	1.00	19.13	8
ATOM	3946	OW0	WAT	W	28	18.707	38.961	91.110	1.00	19.60	8
ATOM	3947	OW0	WAT	W	29	31.590	37.922	84.751	1.00	19.76	8
ATOM	3948	OW0	WAT	W	30	28.452	29.435	92.663	1.00	19.87	8
ATOM	3949	OW0	WAT	W	31	21.360	29.012	81.691	1.00	19.98	8
ATOM	3950	OW0	WAT	W	32	25.513	33.621	80.784	1.00	20.06	8
ATOM	3951	OW0	WAT	W	33	9.572	35.390	68.425	1.00	20.13	8
ATOM	3952	OW0	WAT	W	34	6.621	38.273	73.833	1.00	20.26	8
ATOM	3953	OW0	WAT	W	35	5.165	26.241	88.156	1.00	20.30	8
ATOM	3954	OW0	WAT	W	36	23.265	33.446	79.934	1.00	20.36	8
ATOM	3955	OW0	WAT	W	37	28.248	31.837	82.126	1.00	20.40	8
ATOM	3956	OW0	WAT	W	38	23.025	15.287	58.844	1.00	20.72	8
ATOM	3957	OW0	WAT	W	39	20.923	33.873	72.690	1.00	20.85	8
ATOM	3958	OW0	WAT	W	40	12.290	35.963	59.757	1.00	20.91	8
ATOM	3959	OW0	WAT	W	41	20.845	33.669	75.672	1.00	20.97	8
ATOM	3960	OW0	WAT	W	42	22.075	21.682	81.126	1.00	21.31	8
ATOM	3961	OW0	WAT	W	43	14.396	41.282	43.561	1.00	21.67	8
ATOM	3962	OW0	WAT	W	44	26.359	38.541	40.833	1.00	21.93	8
ATOM	3963	OW0	WAT	W	45	29.566	32.232	79.652	1.00	21.98	8
ATOM	3964	OW0	WAT	W	46	23.283	35.309	65.908	1.00	22.07	8
ATOM	3965	OW0	WAT	W	47	23.194	24.642	81.389	1.00	22.19	8
ATOM	3966	OW0	WAT	W	48	31.442	30.641	53.232	1.00	22.24	8
ATOM	3967	OW0	WAT	W	49	16.139	44.310	95.813	1.00	22.31	8
ATOM	3968	OW0	WAT	W	50	29.098	45.750	88.021	1.00	22.46	8
ATOM	3969	OW0	WAT	W	51	29.561	30.748	84.019	1.00	22.47	8
ATOM	3970	OW0	WAT	W	52	27.980	37.414	52.564	1.00	22.67	8
ATOM	3971	OW0	WAT	W	53	15.060	20.624	57.494	1.00	22.69	8
ATOM	3972	OW0	WAT	W	54	35.494	34.127	73.318	1.00	23.02	8
ATOM	3973	OW0	WAT	W	55	21.252	26.982	82.323	1.00	23.16	8
ATOM	3974	OW0	WAT	W	56	8.169	23.595	96.531	1.00	23.42	8
ATOM	3975	OW0	WAT	W	57	28.306	31.271	46.286	1.00	23.97	8
ATOM	3976	OW0	WAT	W	58	4.904	32.005	52.469	1.00	24.08	8
ATOM	3977	OW0	WAT	W	59	34.680	17.452	59.617	1.00	24.12	8
ATOM	3978	OW0	WAT	W	60	33.674	21.421	58.909	1.00	24.14	8
ATOM	3979	OW0	WAT	W	61	26.569	31.013	97.686	1.00	24.18	8
ATOM	3980	OW0	WAT	W	62	20.007	44.821	80.894	1.00	24.42	8
ATOM	3981	OW0	WAT	W	63	11.817	37.503	56.024	1.00	24.64	8
ATOM	3982	OW0	WAT	W	64	29.823	54.365	78.471	1.00	24.84	8
ATOM	3983	OW0	WAT	W	65	31.313	24.657	101.086	1.00	24.86	8
ATOM	3984	OW0	WAT	W	66	21.188	24.062	81.773	1.00	25.00	8
ATOM	3985	OW0	WAT	W	67	27.530	23.190	74.325	1.00	25.05	8
ATOM	3986	OW0	WAT	W	68	24.237	27.662	82.417	1.00	25.21	8
ATOM	3987	OW0	WAT	W	69	13.220	20.441	98.339	1.00	25.29	8
ATOM	3988	OW0	WAT	W	70	9.835	20.463	84.092	1.00	25.33	8
ATOM	3989	OW0	WAT	W	71	24.649	23.948	89.723	1.00	25.58	8
ATOM	3990	OW0	WAT	W	72	5.014	36.356	89.453	1.00	25.65	8
ATOM	3991	OW0	WAT	W	73	10.492	20.729	64.885	1.00	25.70	8
ATOM	3992	OW0	WAT	W	74	32.733	31.987	63.454	1.00	25.93	8
ATOM	3993	OW0	WAT	W	75	28.377	16.603	97.373	1.00	26.22	8
ATOM	3994	OW0	WAT	W	76	26.237	18.558	98.847	1.00	26.31	8
ATOM	3995	OW0	WAT	W	77	18.836	44.197	94.602	1.00	26.32	8
ATOM	3996	OW0	WAT	W	78	30.554	38.651	99.023	1.00	26.53	8
ATOM	3997	OW0	WAT	W	79	34.139	42.534	70.785	1.00	26.66	8
ATOM	3998	OW0	WAT	W	80	19.699	41.304	95.115	1.00	26.70	8
ATOM	3999	OW0	WAT	W	81	11.380	18.430	92.339	1.00	26.75	8
ATOM	4000	OW0	WAT	W	82	33.445	25.595	69.634	1.00	26.97	8
ATOM	4001	OW0	WAT	W	83	24.662	13.696	54.197	1.00	27.11	8
ATOM	4002	OW0	WAT	W	84	28.266	31.003	94.890	1.00	27.29	8
ATOM	4003	OW0	WAT	W	85	20.725	40.832	92.186	1.00	27.45	8
ATOM	4004	OW0	WAT	W	86	25.146	50.544	83.841	1.00	27.48	8
ATOM	4005	OW0	WAT	W	87	15.057	18.749	69.240	1.00	27.74	8
ATOM	4006	OW0	WAT	W	88	13.048	28.893	58.627	1.00	27.83	8
ATOM	4007	OW0	WAT	W	89	13.377	28.399	53.950	1.00	27.90	8
ATOM	4008	OW0	WAT	W	90	5.299	31.836	93.231	1.00	27.96	8
ATOM	4009	OW0	WAT	W	91	3.937	37.319	47.632	1.00	28.09	8
ATOM	4010	OW0	WAT	W	92	23.639	21.750	78.833	1.00	28.09	8
ATOM	4011	OW0	WAT	W	93	37.239	40.159	72.537	1.00	28.14	8
ATOM	4012	OW0	WAT	W	94	23.345	33.695	85.122	1.00	28.24	8
ATOM	4013	OW0	WAT	W	95	27.712	33.751	84.311	1.00	28.35	8
ATOM	4014	OW0	WAT	W	96	29.746	32.309	51.898	1.00	28.37	8
ATOM	4015	OW0	WAT	W	97	24.950	23.431	86.718	1.00	28.90	8
ATOM	4016	OW0	WAT	W	98	30.172	32.741	97.140	1.00	28.98	8
ATOM	4017	OW0	WAT	W	99	28.686	34.680	86.651	1.00	29.30	8
ATOM	4018	OW0	WAT	W	100	29.828	22.276	104.713	1.00	29.31	8

ATOM	4019	OW0	WAT	W	101	14.236	21.944	103.773	1.00	29.36	8
ATOM	4020	OW0	WAT	W	102	23.731	32.676	83.036	1.00	30.10	8
ATOM	4021	OW0	WAT	W	103	29.261	29.122	89.584	1.00	30.19	8
ATOM	4022	OW0	WAT	W	104	27.892	34.046	96.695	1.00	30.42	8
ATOM	4023	OW0	WAT	W	105	31.548	31.196	93.135	1.00	30.52	8
ATOM	4024	OW0	WAT	W	106	29.180	35.694	97.563	1.00	30.65	8
ATOM	4025	OW0	WAT	W	107	36.148	32.510	77.016	1.00	30.87	8
ATOM	4026	OW0	WAT	W	108	19.500	19.810	67.860	1.00	30.97	8
ATOM	4027	OW0	WAT	W	109	12.234	17.699	57.066	1.00	31.02	8
ATOM	4028	OW0	WAT	W	110	30.140	30.959	90.861	1.00	31.02	8
ATOM	4029	OW0	WAT	W	111	29.245	29.005	87.140	1.00	31.20	8
ATOM	4030	OW0	WAT	W	112	8.712	44.931	98.058	1.00	31.25	8
ATOM	4031	OW0	WAT	W	113	6.559	35.891	71.686	1.00	31.48	8
ATOM	4032	OW0	WAT	W	114	16.096	46.682	97.419	1.00	31.49	8
ATOM	4033	OW0	WAT	W	115	28.702	37.358	84.954	1.00	31.52	8
ATOM	4034	OW0	WAT	W	116	23.269	36.298	69.635	1.00	31.73	8
ATOM	4035	OW0	WAT	W	117	19.112	14.848	51.560	1.00	32.26	8
ATOM	4036	OW0	WAT	W	118	34.859	46.381	91.799	1.00	32.30	8
ATOM	4037	OW0	WAT	W	119	33.356	24.877	66.359	1.00	32.33	8
ATOM	4038	OW0	WAT	W	120	36.212	28.332	58.979	1.00	32.66	8
ATOM	4039	OW0	WAT	W	121	32.357	32.702	89.962	1.00	32.67	8
ATOM	4040	OW0	WAT	W	122	15.791	18.309	98.565	1.00	32.94	8
ATOM	4041	OW0	WAT	W	123	10.728	37.304	43.329	1.00	33.06	8
ATOM	4042	OW0	WAT	W	124	9.424	44.511	70.118	1.00	33.07	8
ATOM	4043	OW0	WAT	W	125	7.444	40.322	33.258	1.00	33.08	8
ATOM	4044	OW0	WAT	W	126	26.139	24.623	81.599	1.00	33.35	8
ATOM	4045	OW0	WAT	W	127	29.976	39.216	50.980	1.00	33.37	8
ATOM	4046	OW0	WAT	W	128	12.352	20.468	101.408	1.00	33.41	8
ATOM	4047	OW0	WAT	W	129	14.605	43.579	93.366	1.00	33.46	8
ATOM	4048	OW0	WAT	W	130	14.568	25.226	100.442	1.00	33.95	8
ATOM	4049	OW0	WAT	W	131	29.845	36.606	88.663	1.00	33.96	8
ATOM	4050	OW0	WAT	W	132	29.315	35.203	52.245	1.00	34.39	8
ATOM	4051	OW0	WAT	W	133	25.213	28.912	81.291	1.00	34.73	8
ATOM	4052	OW0	WAT	W	134	4.056	25.026	86.078	1.00	34.75	8
ATOM	4053	OW0	WAT	W	135	35.592	22.208	66.460	1.00	34.79	8
ATOM	4054	OW0	WAT	W	136	30.056	32.499	94.980	1.00	35.03	8
ATOM	4055	OW0	WAT	W	137	31.642	34.050	97.446	1.00	35.16	8
ATOM	4056	OW0	WAT	W	138	6.399	39.252	53.656	1.00	35.16	8
ATOM	4057	OW0	WAT	W	139	24.631	22.787	80.787	1.00	35.70	8
ATOM	4058	OW0	WAT	W	140	17.164	40.603	93.345	1.00	35.88	8
ATOM	4059	OW0	WAT	W	141	32.517	48.802	78.888	1.00	35.91	8
ATOM	4060	OW0	WAT	W	142	12.605	47.246	48.871	1.00	36.06	8
ATOM	4061	OW0	WAT	W	143	11.936	19.902	81.296	1.00	36.07	8
ATOM	4062	OW0	WAT	W	144	14.511	30.434	59.331	1.00	36.46	8
ATOM	4063	OW0	WAT	W	145	24.904	20.322	90.078	1.00	36.46	8
ATOM	4064	OW0	WAT	W	146	11.636	21.530	50.698	1.00	36.73	8
ATOM	4065	OW0	WAT	W	147	19.239	17.437	61.534	1.00	36.95	8
ATOM	4066	OW0	WAT	W	148	16.418	12.433	100.613	1.00	37.57	8
ATOM	4067	OW0	WAT	W	149	36.156	29.107	62.733	1.00	37.66	8
ATOM	4068	OW0	WAT	W	150	6.477	18.289	83.974	1.00	38.23	8
ATOM	4069	OW0	WAT	W	151	26.962	19.421	46.014	1.00	38.28	8
ATOM	4070	OW0	WAT	W	152	29.388	47.864	98.637	1.00	38.32	8
ATOM	4071	OW0	WAT	W	153	26.646	55.807	96.596	1.00	38.49	8
ATOM	4072	OW0	WAT	W	154	28.646	13.763	51.700	1.00	38.50	8
ATOM	4073	OW0	WAT	W	155	8.410	25.455	43.443	1.00	38.68	8
ATOM	4074	OW0	WAT	W	156	25.347	58.866	86.231	1.00	38.79	8
ATOM	4075	OW0	WAT	W	157	31.258	40.850	95.798	1.00	38.83	8
ATOM	4076	OW0	WAT	W	158	7.378	49.910	91.085	1.00	39.20	8
ATOM	4077	OW0	WAT	W	159	9.042	38.586	56.053	1.00	39.25	8
ATOM	4078	OW0	WAT	W	160	22.671	18.146	64.655	1.00	39.33	8
ATOM	4079	OW0	WAT	W	161	26.367	57.488	76.515	1.00	39.61	8
ATOM	4080	OW0	WAT	W	162	13.588	22.645	41.622	1.00	39.65	8
ATOM	4081	OW0	WAT	W	163	22.142	20.782	77.722	1.00	39.83	8
ATOM	4082	OW0	WAT	W	164	19.678	14.382	85.326	1.00	40.14	8
ATOM	4083	OW0	WAT	W	165	0.073	38.203	87.061	1.00	40.22	8
ATOM	4084	OW0	WAT	W	166	12.125	44.320	65.523	1.00	40.42	8
ATOM	4085	OW0	WAT	W	167	33.005	23.458	44.185	1.00	40.49	8
ATOM	4086	OW0	WAT	W	168	13.676	35.688	29.856	1.00	40.58	8
ATOM	4087	OW0	WAT	W	169	7.713	34.066	62.308	1.00	41.00	8
ATOM	4088	OW0	WAT	W	170	33.626	28.969	81.496	1.00	41.00	8
ATOM	4089	OW0	WAT	W	171	34.640	39.088	81.088	1.00	41.27	8
ATOM	4090	OW0	WAT	W	172	7.508	25.738	50.220	1.00	41.32	8
ATOM	4091	OW0	WAT	W	173	27.507	32.995	78.641	1.00	41.44	8
ATOM	4092	OW0	WAT	W	174	24.673	18.334	69.762	1.00	41.47	8

ATOM	4093	OW0	WAT	W	175	23.738	57.783	66.442	1.00	41.59	8
ATOM	4094	OW0	WAT	W	176	19.624	22.721	38.089	1.00	41.60	8
ATOM	4095	OW0	WAT	W	177	27.605	34.431	110.231	1.00	41.68	8
ATOM	4096	OW0	WAT	W	178	21.996	49.909	104.001	1.00	41.90	8
ATOM	4097	OW0	WAT	W	179	39.172	40.763	66.149	1.00	41.90	8
ATOM	4098	OW0	WAT	W	180	38.537	22.909	101.858	1.00	41.95	8
ATOM	4099	OW0	WAT	W	181	23.698	34.735	111.561	1.00	42.12	8
ATOM	4100	OW0	WAT	W	182	17.645	48.828	100.481	1.00	42.16	8
ATOM	4101	OW0	WAT	W	183	30.615	32.188	88.694	1.00	42.29	8
ATOM	4102	OW0	WAT	W	184	17.123	23.998	35.527	1.00	42.30	8
ATOM	4103	OW0	WAT	W	185	2.539	26.609	84.787	1.00	42.40	8
ATOM	4104	OW0	WAT	W	186	24.033	19.860	84.650	1.00	42.65	8
ATOM	4105	OW0	WAT	W	187	31.887	40.293	98.414	1.00	42.89	8
ATOM	4106	OW0	WAT	W	188	33.506	18.210	98.947	1.00	42.96	8
ATOM	4107	OW0	WAT	W	189	2.974	18.178	83.400	1.00	43.15	8
ATOM	4108	OW0	WAT	W	190	33.171	54.574	88.941	1.00	43.20	8
ATOM	4109	OW0	WAT	W	191	3.299	33.009	41.931	1.00	43.24	8
ATOM	4110	OW0	WAT	W	192	35.304	24.551	60.466	1.00	43.36	8
ATOM	4111	OW0	WAT	W	193	34.043	42.579	58.374	1.00	43.48	8
ATOM	4112	OW0	WAT	W	194	10.996	27.113	59.197	1.00	43.50	8
ATOM	4113	OW0	WAT	W	195	15.166	18.417	80.762	1.00	43.54	8
ATOM	4114	OW0	WAT	W	196	37.193	39.072	80.259	1.00	43.54	8
ATOM	4115	OW0	WAT	W	197	12.438	18.505	96.190	1.00	43.72	8
ATOM	4116	OW0	WAT	W	198	17.695	44.501	36.700	1.00	43.76	8
ATOM	4117	OW0	WAT	W	199	24.143	20.985	40.867	1.00	44.18	8
ATOM	4118	OW0	WAT	W	200	15.460	20.954	43.611	1.00	44.25	8
ATOM	4119	OW0	WAT	W	201	4.001	35.301	72.707	1.00	44.35	8
ATOM	4120	OW0	WAT	W	202	10.808	47.706	96.612	1.00	44.60	8
ATOM	4121	OW0	WAT	W	203	2.700	27.115	67.478	1.00	44.62	8
ATOM	4122	OW0	WAT	W	204	20.270	21.380	43.441	1.00	44.66	8
ATOM	4123	OW0	WAT	W	205	34.265	41.303	81.840	1.00	44.75	8
ATOM	4124	OW0	WAT	W	206	20.804	19.886	76.193	1.00	44.76	8
ATOM	4125	OW0	WAT	W	207	-1.913	32.845	78.176	1.00	44.88	8
ATOM	4126	OW0	WAT	W	208	3.571	20.702	86.366	1.00	44.94	8
ATOM	4127	OW0	WAT	W	209	21.880	36.365	32.858	1.00	44.94	8
ATOM	4128	OW0	WAT	W	210	31.952	36.977	98.567	1.00	45.02	8
ATOM	4129	OW0	WAT	W	211	33.791	22.964	69.030	1.00	45.06	8
ATOM	4130	OW0	WAT	W	212	7.729	42.702	98.969	1.00	45.07	8
ATOM	4131	OW0	WAT	W	213	37.694	42.784	73.625	1.00	45.22	8
ATOM	4132	OW0	WAT	W	214	4.724	28.533	29.235	1.00	45.25	8
ATOM	4133	OW0	WAT	W	215	21.892	60.975	73.720	1.00	45.41	8
ATOM	4134	OW0	WAT	W	216	27.561	61.645	85.916	1.00	45.58	8
ATOM	4135	OW0	WAT	W	217	3.363	20.188	78.686	1.00	45.61	8
ATOM	4136	OW0	WAT	W	218	6.061	28.087	58.848	1.00	45.69	8
ATOM	4137	OW0	WAT	W	219	28.536	22.771	93.894	1.00	45.79	8
ATOM	4138	OW0	WAT	W	220	20.591	18.347	79.227	1.00	45.81	8
ATOM	4139	OW0	WAT	W	221	30.557	17.389	50.458	1.00	45.89	8
ATOM	4140	OW0	WAT	W	222	23.413	19.795	75.273	1.00	45.93	8
ATOM	4141	OW0	WAT	W	223	15.330	26.238	35.832	1.00	46.01	8
ATOM	4142	OW0	WAT	W	224	35.298	21.980	95.583	1.00	46.08	8
ATOM	4143	OW0	WAT	W	225	-0.227	45.804	77.922	1.00	46.08	8
ATOM	4144	OW0	WAT	W	226	20.449	45.041	43.691	1.00	46.16	8
ATOM	4145	OW0	WAT	W	227	36.625	44.442	71.826	1.00	46.29	8
ATOM	4146	OW0	WAT	W	228	-0.564	35.140	82.998	1.00	46.42	8
ATOM	4147	OW0	WAT	W	229	30.786	30.184	87.592	1.00	46.52	8
ATOM	4148	OW0	WAT	W	230	18.209	37.127	109.332	1.00	46.61	8
ATOM	4149	OW0	WAT	W	231	5.290	35.674	32.713	1.00	46.73	8
ATOM	4150	OW0	WAT	W	232	5.154	17.424	79.518	1.00	46.77	8
ATOM	4151	OW0	WAT	W	233	32.476	32.647	94.155	1.00	46.78	8
ATOM	4152	OW0	WAT	W	234	7.852	42.603	68.371	1.00	46.78	8
ATOM	4153	OW0	WAT	W	235	25.458	20.989	77.688	1.00	46.83	8
ATOM	4154	OW0	WAT	W	236	10.154	43.709	40.698	1.00	46.83	8
ATOM	4155	OW0	WAT	W	237	17.064	27.389	108.176	1.00	47.00	8
ATOM	4156	OW0	WAT	W	238	12.045	33.710	108.176	1.00	47.00	8
ATOM	4157	OW0	WAT	W	239	21.079	35.817	70.824	1.00	47.00	8
ATOM	4158	OW0	WAT	W	240	4.062	33.751	91.030	1.00	47.05	8
ATOM	4159	OW0	WAT	W	241	12.236	21.901	56.733	1.00	47.06	8
ATOM	4160	OW0	WAT	W	242	8.504	42.719	43.711	1.00	47.30	8
ATOM	4161	OW0	WAT	W	243	16.036	14.646	61.411	1.00	47.31	8
ATOM	4162	OW0	WAT	W	244	11.756	59.123	67.674	1.00	47.35	8
ATOM	4163	OW0	WAT	W	245	13.009	42.732	103.719	1.00	47.60	8
ATOM	4164	OW0	WAT	W	246	4.038	19.904	75.633	1.00	47.63	8
ATOM	4165	OW0	WAT	W	247	18.647	28.978	110.196	1.00	47.69	8
ATOM	4166	OW0	WAT	W	248	11.570	17.428	62.551	1.00	47.71	8

ATOM	4167	OW0	WAT	W	249	28.148	15.319	92.300	1.00	47.72	8
ATOM	4168	OW0	WAT	W	250	30.840	41.602	100.804	1.00	47.72	8
ATOM	4169	OW0	WAT	W	251	14.520	13.079	91.654	1.00	47.75	8
ATOM	4170	OW0	WAT	W	252	33.257	35.871	106.556	1.00	47.84	8
ATOM	4171	OW0	WAT	W	253	1.506	20.542	67.428	1.00	48.00	8
ATOM	4172	OW0	WAT	W	254	9.536	23.702	53.845	1.00	48.00	8
ATOM	4173	OW0	WAT	W	255	28.105	14.221	96.049	1.00	48.00	8
ATOM	4174	OW0	WAT	W	256	31.668	37.095	50.965	1.00	48.05	8
ATOM	4175	OW0	WAT	W	257	31.136	23.241	93.584	1.00	48.09	8
ATOM	4176	OW0	WAT	W	258	34.162	27.890	52.268	1.00	48.19	8
ATOM	4177	OW0	WAT	W	259	28.257	59.913	83.794	1.00	48.22	8
ATOM	4178	OW0	WAT	W	260	11.231	34.132	85.631	1.00	48.26	8
ATOM	4179	OW0	WAT	W	261	28.468	26.940	40.649	1.00	48.28	8
ATOM	4180	OW0	WAT	W	262	4.668	30.175	32.084	1.00	48.29	8
ATOM	4181	OW0	WAT	W	263	33.486	33.217	55.794	1.00	48.30	8
ATOM	4182	OW0	WAT	W	264	6.053	46.878	74.207	1.00	48.41	8
ATOM	4183	OW0	WAT	W	265	16.402	26.298	33.796	1.00	48.49	8
ATOM	4184	OW0	WAT	W	266	26.202	21.497	83.893	1.00	48.51	8
ATOM	4185	OW0	WAT	W	267	20.785	36.028	111.236	1.00	48.54	8
ATOM	4186	OW0	WAT	W	268	30.461	53.163	68.296	1.00	48.60	8
ATOM	4187	OW0	WAT	W	269	0.696	21.394	79.805	1.00	48.82	8
ATOM	4188	OW0	WAT	W	270	5.982	32.107	60.137	1.00	48.90	8
ATOM	4189	OW0	WAT	W	271	13.998	16.761	78.562	1.00	48.92	8
ATOM	4190	OW0	WAT	W	272	37.139	25.809	58.211	1.00	49.00	8
ATOM	4191	OW0	WAT	W	273	24.090	56.359	101.385	1.00	49.00	8
ATOM	4192	OW0	WAT	W	274	18.068	43.717	58.211	1.00	49.00	8
ATOM	4193	OW0	WAT	W	275	5.008	30.008	59.014	1.00	49.03	8
ATOM	4194	OW0	WAT	W	276	24.231	58.496	93.637	1.00	49.04	8
ATOM	4195	OW0	WAT	W	277	25.516	55.866	63.971	1.00	49.05	8
ATOM	4196	OW0	WAT	W	278	8.821	24.366	46.833	1.00	49.06	8
ATOM	4197	OW0	WAT	W	279	18.557	30.050	34.351	1.00	49.07	8
ATOM	4198	OW0	WAT	W	280	7.575	44.935	72.565	1.00	49.07	8
ATOM	4199	OW0	WAT	W	281	32.725	15.893	52.239	1.00	49.18	8
ATOM	4200	OW0	WAT	W	282	21.693	17.319	68.259	1.00	49.19	8
ATOM	4201	OW0	WAT	W	283	31.079	23.166	75.579	1.00	49.30	8
ATOM	4202	OW0	WAT	W	284	21.228	20.750	39.179	1.00	49.34	8
ATOM	4203	OW0	WAT	W	285	19.380	17.588	77.097	1.00	49.37	8
ATOM	4204	OW0	WAT	W	286	33.523	39.507	89.817	1.00	49.38	8
ATOM	4205	OW0	WAT	W	287	15.676	43.664	35.502	1.00	49.41	8
ATOM	4206	OW0	WAT	W	288	30.624	48.924	69.928	1.00	49.44	8
ATOM	4207	OW0	WAT	W	289	20.158	44.944	34.473	1.00	49.44	8
ATOM	4208	OW0	WAT	W	290	13.755	18.014	54.141	1.00	49.53	8
ATOM	4209	OW0	WAT	W	291	22.712	56.885	98.458	1.00	49.55	8
ATOM	4210	OW0	WAT	W	292	9.421	40.612	61.458	1.00	49.63	8
ATOM	4211	OW0	WAT	W	293	10.544	38.205	62.017	1.00	49.65	8
ATOM	4212	OW0	WAT	W	294	13.256	61.174	66.843	1.00	49.66	8
ATOM	4213	OW0	WAT	W	295	7.047	28.393	101.031	1.00	49.76	8
ATOM	4214	OW0	WAT	W	296	9.174	30.089	101.877	1.00	49.84	8
ATOM	4215	OW0	WAT	W	297	23.631	10.416	92.206	1.00	49.86	8
ATOM	4216	OW0	WAT	W	298	14.646	57.631	84.015	1.00	50.00	8
ATOM	4217	OW0	WAT	W	299	13.679	27.889	30.169	1.00	50.03	8
ATOM	4218	OW0	WAT	W	300	30.079	44.318	52.674	1.00	50.09	8
ATOM	4219	OW0	WAT	W	301	36.058	24.067	95.389	1.00	50.27	8
ATOM	4220	OW0	WAT	W	302	27.531	61.533	81.274	1.00	50.33	8
ATOM	4221	OW0	WAT	W	303	2.018	19.978	73.415	1.00	50.40	8
ATOM	4222	OW0	WAT	W	304	25.416	18.871	43.049	1.00	50.40	8
ATOM	4223	OW0	WAT	W	305	24.002	61.548	72.183	1.00	50.45	8
ATOM	4224	OW0	WAT	W	306	26.674	27.842	84.339	1.00	50.53	8
ATOM	4225	OW0	WAT	W	307	10.414	26.991	32.858	1.00	50.68	8
ATOM	4226	OW0	WAT	W	308	8.984	49.959	66.547	1.00	50.84	8
ATOM	4227	OW0	WAT	W	309	31.052	26.170	92.925	1.00	50.84	8
ATOM	4228	OW0	WAT	W	310	31.650	14.800	103.619	1.00	50.96	8
ATOM	4229	OW0	WAT	W	311	4.552	44.172	94.195	1.00	51.18	8
ATOM	4230	OW0	WAT	W	312	19.321	32.742	33.306	1.00	51.19	8
ATOM	4231	OW0	WAT	W	313	39.664	44.974	80.079	1.00	51.34	8
ATOM	4232	OW0	WAT	W	314	11.111	50.044	94.730	1.00	51.60	8
ATOM	4233	OW0	WAT	W	315	41.633	35.268	62.507	1.00	51.64	8
ATOM	4234	OW0	WAT	W	316	16.161	15.675	50.606	1.00	51.69	8
ATOM	4235	OW0	WAT	W	317	17.076	13.663	54.383	1.00	52.35	8
ATOM	4236	OW0	WAT	W	318	-0.485	20.371	75.337	1.00	52.37	8
ATOM	4237	OW0	WAT	W	319	-1.074	32.905	75.009	1.00	52.93	8
ATOM	4238	OW0	WAT	W	320	30.884	26.827	41.173	1.00	53.46	8
ATOM	4239	OW0	WAT	W	321	34.249	25.468	77.767	1.00	54.80	8
ATOM	4240	OW0	WAT	W	322	16.235	59.585	76.936	1.00	55.11	8

CLAIMS

1. A variant of a parent Termamyl-like alpha-amylase, comprising an alteration at one or more positions selected from the group of:
R28, R118, N174; R181, G182, D183, G184, G186, W189, N195, M202, Y298, N299, K302, S303, N306, R310, N314; R320, H324, E345, Y396, R400, W439, R444, N445, K446, Q449, R458, N471, N484,
wherein
(a) the alteration(s) are independently
(i) an insertion of an amino acid downstream of the amino acid which occupies the position,
(ii) a deletion of the amino acid which occupies the position, or
(iii) a substitution of the amino acid which occupies the position with a different amino acid,
(b) the variant has alpha-amylase activity and (c) each position corresponds to a position of the amino acid sequence of the parent Termamyl-like alpha-amylase having the amino acid sequence of AA560 shown in SEQ ID NO: 12.

2. The variant of claim 1, which variant has one or more of the following mutations:
Delta G184; Delta (R181-G182); Delta (D183-G184);
R28N,K; S94K; R118K; N125A,R,K; N174D; R181Q,E,K; G186R; W189R,K; N195F; M202L; Y298H,F; N299A; K302R, S303Q, N306G,D,R,K; R310A,K,Q,E,H,D,N; N314D; R320K; H324K; E345R,D,K,N; Y396F; R400T,K; W439R; R444K; N445K,Q; K446N; Q449E; R458K; N471E; N484Q.

3. The variant of claim 1-2, wherein the variant further comprises a mutation in M202, in particular M202L,T.

4. The variant of claim 1-3, wherein the variant further comprises a mutation in N195, inparticular N195F.

5. The variant of claim 1-4, wherein the variant further

comprises a mutation in G186, in particular G186R.

6. The variant of claim 1-5, wherein the variant further comprises a mutation in R181, in particular R181Q.

7. The variant of any of claims 1-6, wherein the parent Termamyl-like alpha-amylase is derived from a strain of *B. licheniformis, B. amyloliquefaciens, B. stearothermophilus, Bacillus* sp. NCIB 12289, NCIB 12512, NCIB 12513 or DSM 9375, or DSMZ no. 12649, KSM AP1378, or KSM K36 or KSM K38.

8. The variant of claims 1-7, wherein the parent Termamyl-like alpha-amylase is any of the alpha-amylases selected from the group depicted in SEQ ID NOS: 2, 4, 6, 8, 10, 12, and 13.

9. The variant according to any of claims 1-8, wherein the parent Termamyl-like alpha-amylase has an amino acid sequence which has a degree of identity to SEQ ID NO: 4 of at least 60%, preferably 70%, more preferably at least 80%, even more preferably at least about 90%, even more preferably at least 95%, even more preferably at least 97%, and even more preferably at least 99%.

10. The variant of any of claims 1-9, wherein the parent Termamyl-like alpha-amylase is encoded by a nucleic acid sequence, which hydridizes under low, preferably medium, preferred high stringency conditions, with the nucleic acid sequence of SEQ ID NO: 11.

11. The variant of claims 1-10, which variant has altered solubility, preferably increased solubility, in particular under washing, dish washing or hard surface cleaning conditions.

12. A DNA construct comprising a DNA sequence encoding an alpha-amylase variant according to any one of claims 1 to 11.

13. A recombinant expression vector which carries a DNA con-

struct according to claim 12.

14. A cell which is transformed with a DNA construct according to claim 9 or a vector according to claim 10.

15. A cell according to claim 14, which is a microorganism, preferably a bacterium or a fungus, in particular a gram-positive bacterium, such as *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus lentus*, *Bacillus brevis*, *Bacillus stearothermophilus*, *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus coagulans*, *Bacillus circulans*, *Bacillus lautus* or *Bacillus thuringiensis*.

16. A composition comprising an alpha-amylase variant of claims 1-11.

17. A detergent additive comprising an alpha-amylase variant according to any one of claims 1 to 11, optionally in the form of a non-dusting granulate, stabilised liquid or protected enzyme.

18. A detergent additive according to claim 17, which contains 0.02-200 mg of enzyme protein/g of the additive.

19. A detergent additive according to claims 17 or 18, which additionally comprises another enzyme such as a protease, a lipase, a peroxidase, mannanase, maltogenic amylase, CGTase, amylase or another amylolytic enzyme, such as glucoamylase, and/or a cellulase.

20. A detergent composition comprising an alpha-amylase variant according to any of claims 1 to 11.

21. A detergent composition according to claim 20, which additionally comprises another enzyme such as a protease, a lipase, a peroxidase, mannanase, maltogenic amylase, CGTase, another amylolytic enzyme and/or a cellulase.

22. A manual or automatic dishwashing detergent composition comprising an alpha-amylase variant according to any of claims 1 to 11.

23. A dishwashing detergent composition according to claim 22, which additionally comprises another enzyme such as a protease, a lipase, a peroxidase, mannanase, maltogenic amylase, CGTase, amylase or another amylolytic enzyme, such as glucoamylase, and/or a cellulase.

24. A manual or automatic laundry washing composition comprising an alpha-amylase variant according to any of claims 1 to 11.

25. A laundry washing composition according to claim 24, which additionally comprises another enzyme such as a protease, a lipase, a peroxidase, mannanase, maltogenic amylase, CGTase, an amylase and/or another an amylolytic enzyme, such as glucoamylase and/or a cellulase.

26. Use of an alpha-amylase variant according to any one of claims 1 to 11 or a composition according to claims 16 to 25 for washing and/or dishwashing.

27. Use of an alpha-amylase variant according to any one of claims 1 to 11 or a composition according to claims 16 to 25 for textile desizing.

28. Use of an alpha-amylase variant according to any of claims 1 to 11 or a composition according to claims 16 to 25 for starch liquefaction.

29. A method of producing a variant of a parent alpha-amylase having an altered property relative to the parent, wherein the parent alpha-amylase has the sequence of SEQ ID Nos: 2, 4, 6, 8, 10, 12 or 13, or has a sequence at least 60 % identity to said sequence, said method comprising

(a) modelling the parent alpha-amylase on the three-

dimensional structure of SEQ ID NO:4 depicted in the Appendix 1 to produce a three-dimensional structure of the parent alpha-amylase;

(b) identifying in the three-dimensional structure obtained in step (a) at least one structural part of the parent wherein an alteration in said structural part is predicted to result in said altered property;

(c) modifying the sequence of a nucleic acid encoding the parent alpha-amylase to produce a nucleic acid encoding a deletion, insertion, or substitution of one or more amino acids at a position corresponding to said structural part; and

(d) expressing the modified nucleic acid in a host cell to produce the variant alpha-amylase,

wherein the variant has alpha-amylase enzymatic activity and has at least one altered property relative to the parent.

30. The method of claim 29, wherein the altered property is selected from the group consisting of substrate specificity, substrate binding, substrate cleavage pattern, temperature stability, pH dependence of enzymatic activity, pH dependence of stability, stability towards oxidation, Ca^{2+}-dependency, specific activity or altered solubility, preferably increased solubility.

31. A method of constructing a variant of a parent alpha-amylase having an altered property relative to the parent, wherein the parent alpha-amylase has the sequence of SEQ ID Nos: 2, 4, 6, 8, 10, 12 or 13 or has a sequence at least 60 % identity to said sequence, said method comprising

(a) modelling the parent alpha-amylase on the three-dimensional structure of SEQ ID NO: 4 depicted in the Appendix 1 to produce a three-dimensional structure of the parent alpha-amylase;

(b) comparing the three-dimensional structure obtained in step (a) with a three-dimensional structure of an unrelated alpha-amylase, wherein the unrelated alpha-amylase differs from the parent alpha-amylase in said property;

(c) identifying a structural part of the three-dimensional structure obtained in step (a) which is different from the three-dimensional structure of the unrelated alpha-amylase and which is predicted to be relevant to said property,

(d) modifying the sequence of a nucleic acid encoding the parent alpha-amylase to produce a nucleic acid encoding a deletion, insertion, or substitution of one or more amino acids at a position corresponding to said structural part; and

(e) expressing the modified nucleic acid in a host cell to produce the variant alpha-amylase,

wherein the variant has alpha-amylase activity and has one or more altered properties as compared to the parent alpha-amylase.

32. The method of claim 31, wherein, in step (d), the modification is a deletion, substitution, or insertion of one or more amino acid residues in the parent alpha-amylase so that the structural part in the variant corresponds to the structural part in the unrelated alpha-amylase.

33. A method of increasing the solubility of polypeptide crystals, in particular enzyme crystals, wherein one or more amino acid residue(s),

1) located within a distance of 6.0 Å of a neighbouring enzyme molecule in the tertiary crystal structure, and

2) interacting with said neighbouring enzyme molecule,

are mutated.

34. The method of claim 33, wherein the amino acid residues to be mutated are located with 3.5 Å of a neighbouring enzyme.

35. The method of claim 33 or 34, wherein the enzyme has protease, amylase, CGTase, mannanase, maltogenic amylase, glucoamylase carbohydrase, transferase, lyase, oxidoreductase, lipase, activity.

36. The method of claim 32, wherein the amylase is an alpha-amylase, such as Termamyl-like amylase.

37. The method of claims 33-36, wherein the polypeptide is a protein having biological activity

38. The method of claims 33-37, wherein the polypeptide has antimicrobial activity.

39. The method of claim 3-38, wherein the polypeptide is selected from the group comprising: insulin, growth hormone, EPO, TPO, factor VII, Factor VIII.

40. A method of increasing the solubility of Termamyl-like alpha-amylase crystals, wherein one or more amino acid residue(s),

1) located within a distance of 6.0 Å of a neighbouring Termamyl-like alpha-amylase molecule in the tertiary crystal structure, and

2) interacting with said neighbouring Termamyl-like alpha-amylase molecule,

are mutated.

41. The method of claim 40, wherein the amino acid residues to be mutated are located with 3.5 Å of a neighbouring Termamyl-like alpha-amylase.

42. The method of claims 40 or 41, wherein the crystal structure of SP722 depicted in APPENDIX 1 is used as a reference for determining the distance between neighbouring alpha-amylases.

43. The method of claims 40-42, wherein the crystal structure is a structure modelled in accordance with any of claims 26-29 from of SP722 depicted in APPENDIX 1 is used as a reference for determining the distance between neighbouring alpha-amylases

44. The method of claims 40-43, wherein the Termamyl-like alpha-amylase include amylases selected from the group of alpha-amylase derived from a strain of *B. licheniformis, B. amyloliquefaciens, B. stearothermophilus, Bacillus* sp. NCIB 12289, NCIB 12512, NCIB 12513 or DSM 9375, or DSMZ no. 12649, KSM AP1378, K38, K36.

45. The method of claim 44, wherein the Termamyl-like alpha-amylase is any of the alpha-amylases selected from the group depicted in SEQ ID NOS: 2, 4, 6, 8, 10, 12, and 13.

46. The methof of any of claims 40-45, wherein the Termamyl-like alpha-amylase has an amino acid sequence which has a degree of identity to SEQ ID NO: 4 of at least 60%, preferably 70%, more preferably at least 80%, even more preferably at least about 90%, even more preferably at least 95%, even more preferably at least 97%, and even more preferably at least 99%.

47. The method of any of claims 40-46, wherein the Termamyl-like alpha-amylase is encoded by a nucleic acid sequence, which hydridizes under low, preferably medium, preferred high stringency conditions, with the nucleic acid sequence of SEQ ID NO: 11.

48. The method of claims 40-47, wherein the Termamyl-like alpha-amylase amino acid residues being less than 6.0 Å from the nearest neighbouring amylase molecule are the following (using the SP722 numbering):
19, 20, 21, 22, 25, 28, 29, 53, 76, 84, 87, 90, 93, 94, 124, 125, 126, 128, 142, 144, 156, 157, 158, 159, 160, 161, 170, 171, 172, 173, 174, 175, 183, 184, 185, 186, 187, 188, 189,

190, 193, 195, 196, 197, 209, 212, 226, 229, 256, 257, 258, 259, 280, 281, 298, 299, 300, 302, 303, 304, 305, 306, 310, 311, 314, 319, 320, 321, 322, 341, 345, 405, 406, 408, 444, 447, 448, 449, 463, 464, 465, 466, 467.

49. The method of claims 40-47, wherein the Termamyl-like alpha-amylase amino acid residues being less than 3.5 Å from the nearest neighbouring amylase molecule are the following (using the SP722 numbering):

22, 25, 28, 76, 94, 125, 128, 158, 160, 171, 173, 174, 184, 189, 209, 226, 229, 298, 299, 302, 306, 310, 314, 320, 345, 405, 447, 466.

```
     1                                                                 50
1    HHNGTNGTMM QYFEWHLPND GNHWNRLRDD ASNLRNRGIT AIWIPPAWKG
2    HHNGTNGTMM QYFEWYLPND GNHWNRLRDD AANLKSKGIT AVWIPPAWKG
3    ....VNGTLM QYFEWYTPND GQHWKRLQND AEHLSDIGIT AVWIPPAYKG
4    ..ANLNGTLM QYFEWYMPND GQHWRRLQND SAYLAEHGIT AVWIPPAYKG
5    .AAPFNGTMM QYFEWYLPDD GTLWTKVANE ANNLSSLGIT ALWLPPAYKG

     51                                                               100
1    TSQNDVGYGA YDLYDLGEFN QKGTVRTKYG TRSQLESAIH ALKNNGVQVY
2    TSQNDVGYGA YDLYDLGEFN QKGTVRTKYG TRNQLQAAVT SLKNNGIQVY
3    LSQSDNGYGP YDLYDLGEFQ QKGTVRTKYG TKSELQDAIG SLHSRNVQVY
4    TSQADVGYGA YDLYDLGEFH QKGTVRTKYG TKGELQSAIK SLHSRDINVY
5    TSRSDVGYGV YDLYDLGEFN QKGTVRTKYG TKAQYLQAIQ AAHAAGMQVY

     101                                                              150
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2    GDVVMNHKGG ADGTEIVNAV EVNRSNRNQE TSGEYAIEAW TKFDFPGRGN
3    GDVVLNHKAG ADATEDVTAV EVNPANRNQE TSEEYQIKAW TDFRFPGRGN
4    GDVVINHKGG ADATEDVTAV EVDPADRNRV ISGEHLIKAW THFHFPGRGS
5    ADVVFDHKGG ADGTEWVDAV EVNPSDRNQE ISGTYQIQAW TKFDFPGRGN

     151                                                              200
1    TYSDFKWRWY HFDGVDWDQS RQFQNRIYKF RGDGKAWDWE VDSENGNYDY
2    NHSSFKWRWY HFDGTDWDQS RQLQNKIYKF RGTGKAWDWE VDTENGNYDY
3    TYSDFKWHWY HFDGADWDES RKI.SRIFKF RGEGKAWDWE VSSENGNYDY
4    TYSDFKWHWY HFDGTDWDES RKL.NRIYKF ..QGKAWDWE VSNENGNYDY
5    TYSSFKWRWY HFDGVDWDES RKL.SRIYKF RGIGKAWDWE VDTENGNYDY
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Fig. 1

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2   LMYADVDMDH PEVIHELRNW GVWYTNTLNL DGFRIDAVKH IKYSFTRDWL
3   LMYADVDYDH PDVVAETKKW GIWYANELSL DGFRIDAAKH IKFSFLRDWV
4   LMYADIDYDH PDVAAEIKRW GTWYANELQL DGFRLDAVKH IKFSFLRDWV
5   LMYADLDMDH PEVVTELKNW GKWYVNTTNI DGFRLDAVKH IKFSFFPDWL

    251                                                        300
1   THVRNATGKE MFAVAEFWKN DLGALENYLN KTNWNHSVFD VPLHYNLYNA
2   THVRNTTGKP MFAVAEFWKN DLGAIENYLN KTSWNHSAFD VPLHYNLYNA
3   QAVRQATGKE MFTVAEYWQN NAGKLENYLN KTSFNQSVFD VPLHFNLQAA
4   NHVREKTGKE MFTVAEYWQN DLGALENYLN KTNFNHSVFD VPLHYQFHAA
5   SYVRSQTGKP LFTVGEYWSY DINKLHNYIT KTDGTMSLFD APLHNKFYTA

    301                                                        350
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2   SNSGGYYDMR NILNGSVVQK HPTHAVTFVD NHDSQPGEAL ESFVQQWFKP
3   SSQGGGYDMR RLLDGTVVSR HPEKAVTFVE NHDTQPGQSL ESTVQTWFKP
4   STQGGGYDMR KLLNGTVVSK HPLKSVTFVD NHDTQPGQSL ESTVQTWFKP
5   SKSGGAFDMR TLMTNTLMKD QPTLAVTFVD NHDTEPGQAL QSWVDPWFKP

    351                                                        400
1   LAYALILTRE QGYPSVFYGD YYGIPTHS.. .VPAMKAKID PILEARQNFA
2   LAYALVLTRE QGYPSVFYGD YYGIPTHG.. .VPAMKSKID PLLQARQTFA
3   LAYAFILTRE SGYPQVFYGD MYGTKGTSPK EIPSLKDNIE PILKARKEYA
4   LAYAFILTRE SGYPQVFYGD MYGTKGDSQR EIPALKHKIE PILKARKQYA
5   LAYAFILTRQ EGYPCVFYGD YYGIPQYN.. .IPSLKSKID PLLIARRDYA

    401                                                        450
1   YGTQHDYFDH HNIIGWTREG NTTHPNSGLA TIMSDGPGGE KWMYVGQNKA
2   YGTQHDYFDH HDIIGWTREG NSSHPNSGLA TIMSDGPGGN KWMYVGKNKA
3   YGPQHDYIDH PDVIGWTREG DSSAAKSGLA ALITDGPGGS KRMYAGLKNA
4   YGAQHDYFDH HDIVGWTREG DSSVANSGLA ALITDGPGGA KRMYVGRQNA
5   YGTQHDYLDH SDIIGWTREG GTEKPGSGLA ALITDGPGGS KWMYVGKQHA
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Fig. 1 (continued)

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    451                                                        500
1   GQVWHDITGN KPGTVTINAD GWANFSVNGG SVSIWVKR.. ..........
2   GQVWRDITGN RTGTVTINAD GWGNFSVNGG SVSVWVKQ.. ..........
3   GETWYDITGN RSDTVKIGSD GWGEFHVNDG SVSIYVQ... ..........
4   GETWHDITGN RSEPVVINSE GWGEFHVNGG SVSIYVQR.. ..........
5   GKVFYDLTGN RSDTVTINSD GWGEFKVNGG SVSVWVPRKT TVSTIARPIT

    501                 519
1   .......... .........
2   .......... .........
3   .......... .........
4   .......... .........
5   TRPWTGEFVR WTEPRLVAW
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Fig. 1 (continued)

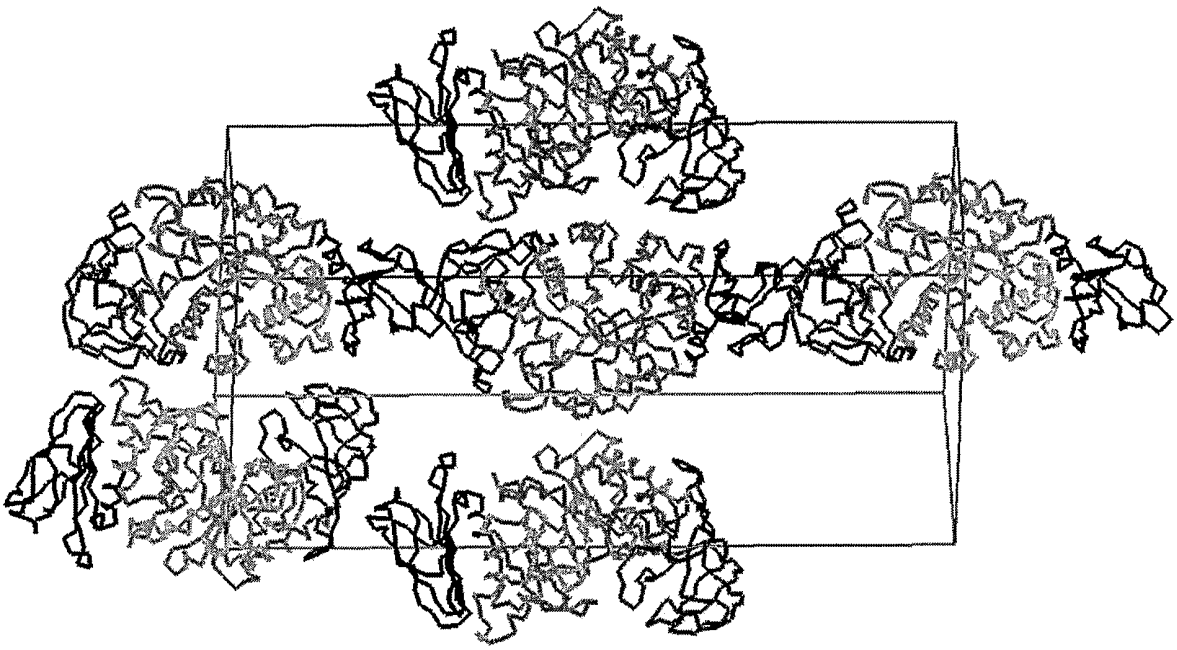


Fig. 2

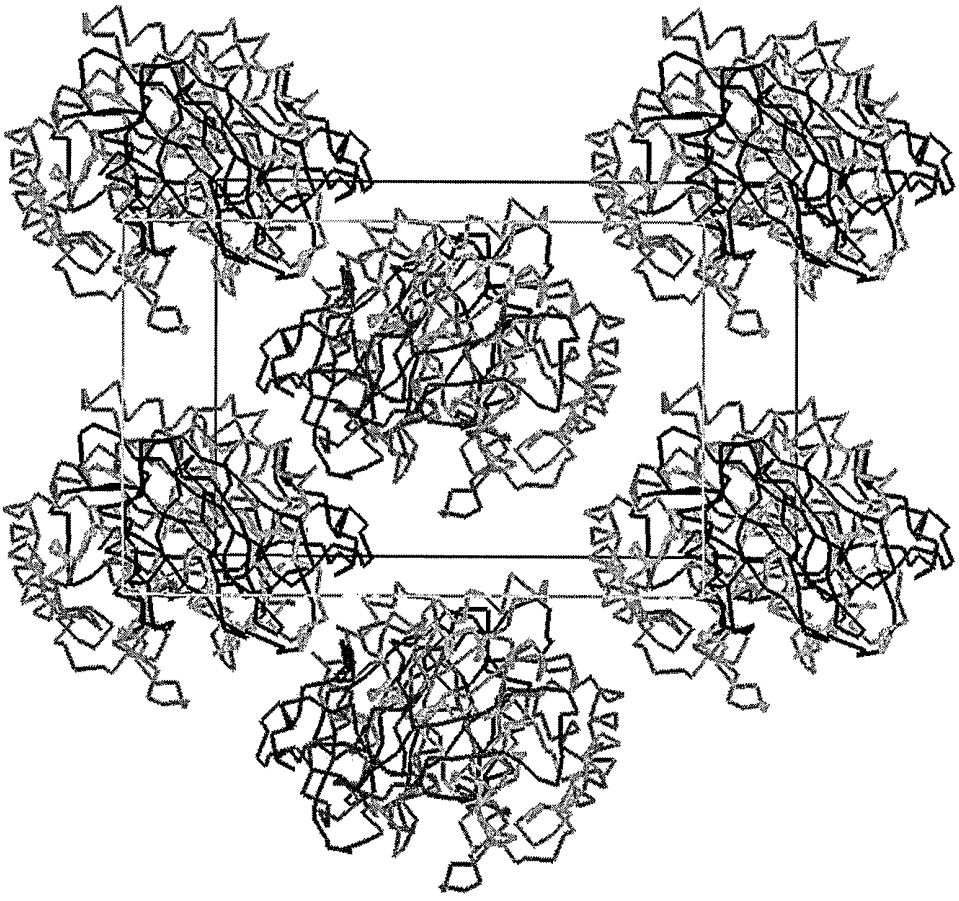


Fig. 3

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Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Asp Asp Ala Ala
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aac tta aag agt aaa ggg ata aca gct gta tgg atc cca cct gca tgg   144
Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
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aag ggg act tcc cag aat gat gta ggt tat gga gcc tat gat tta tat   192
Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
      50                  55                  60

gat ctt gga gag ttt aac cag aag ggg acg gtt cgt aca aaa tat gga   240
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                 85                  90                  95

att cag gta tat ggt gat gtc gtc atg aat cat aaa ggt gga gca gat   336
Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
            100                 105                 110

ggt acg gaa att gta aat gcg gta gaa gtg aat cgg agc aac cga aac   384
Gly Thr Glu Ile Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn
        115                 120                 125

cag gaa acc tca gga gag tat gca ata gaa gcg tgg aca aag ttt gat   432
Gln Glu Thr Ser Gly Glu Tyr Ala Ile Glu Ala Trp Thr Lys Phe Asp
    130                 135                 140

ttt cct gga aga gga aat aac cat tcc agc ttt aag tgg cgc tgg tat   480
Phe Pro Gly Arg Gly Asn Asn His Ser Ser Phe Lys Trp Arg Trp Tyr
145                 150                 155                 160

cat ttt gat ggg aca gat tgg gat cag tca cgc cag ctt caa aac aaa   528
His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys
                165                 170                 175

ata tat aaa ttc agg gga aca ggc aag gcc tgg gac tgg gaa gtc gat   576
Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp
            180                 185                 190

aca gag aat ggc aac tat gac tat ctt atg tat gca gac gtg gat atg   624
Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
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     225                 230                 235                 240
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     ata aaa tat agc ttt acg aga gat tgg ctt aca cat gtg cgt aac acc   768
     Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr
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     Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
25       290                 295                 300

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     Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys
     305                 310                 315                 320
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                     325                 330                 335

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45       370                 375                 380

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     Lys Ile Asp Pro Leu Leu Gln Ala Arg Gln Thr Phe Ala Tyr Gly Thr
     385                 390                 395                 400
50
     cag cat gat tac ttt gat cat cat gat att atc ggt tgg aca aga gag  1248
     Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu
                     405                 410                 415

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             20                  25                  30

Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
          35                  40                  45

Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
      50                  55                  60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
 65                  70                  75                  80

Thr Arg Asn Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly
                 85                  90                  95

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
            100                 105                 110

Gly Thr Glu Ile Val Asn Ala Val Glu Val Asn Arg Ser Asn Arg Asn
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Gln Glu Thr Ser Gly Glu Tyr Ala Ile Glu Ala Trp Thr Lys Phe Asp
    130                 135                 140

Phe Pro Gly Arg Gly Asn Asn His Ser Ser Phe Lys Trp Arg Trp Tyr
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His Phe Asp Gly Thr Asp Trp Asp Gln Ser Arg Gln Leu Gln Asn Lys
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Ile Tyr Lys Phe Arg Gly Thr Gly Lys Ala Trp Asp Trp Glu Val Asp
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Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
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Asp His Pro Glu Val Ile His Glu Leu Arg Asn Trp Gly Val Trp Tyr
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Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
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Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Thr
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Thr Gly Lys Pro Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
            260                 265                 270

Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Ser Trp Asn His Ser Val
        275                 280                 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Asn Ser Gly
    290                 295                 300

Gly Tyr Tyr Asp Met Arg Asn Ile Leu Asn Gly Ser Val Val Gln Lys
305                 310                 315                 320

His Pro Thr His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
                325                 330                 335

Gly Glu Ala Leu Glu Ser Phe Val Gln Gln Trp Phe Lys Pro Leu Ala
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     Gln His Asp Tyr Phe Asp His His Asp Ile Ile Gly Trp Thr Arg Glu
10                   405                 410                 415

     Gly Asn Ser Ser His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
                 420                 425                 430

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             435                 440                 445

     Gln Val Trp Arg Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile
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     ttg cct aat gat ggg aat cac tgg aat aga tta aga gat gat gct agt   96
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                  20                  25                  30

     aat cta aga aat aga ggt ata acc gct att tgg att ccg cct gcc tgg   144
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50              35                  40                  45

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     Lys Gly Thr Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
          50                  55                  60
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                     85                  90                  95

     gtt caa gtt tat ggg gat gta gtg atg aac cat aaa gga gga gct gat   336
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                 100                 105                 110

     gct aca gaa aac gtt ctt gct gtc gag gtg aat cca aat aac cgg aat   384
     Ala Thr Glu Asn Val Leu Ala Val Glu Val Asn Pro Asn Asn Arg Asn
70               115                 120                 125

     caa gaa ata tct ggg gac tac aca att gag gct tgg act aag ttt gat   432
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His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Gln Phe Gln Asn Arg
                165                 170                 175

atc tac aaa ttc cga ggt gat ggt aag gca tgg gat tgg gaa gta gat   576
Ile Tyr Lys Phe Arg Gly Asp Gly Lys Ala Trp Asp Trp Glu Val Asp
            180                 185                 190

tcg gaa aat gga aat tat gat tat tta atg tat gca gat gta gat atg   624
Ser Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
        195                 200                 205

gat cat ccg gag gta gta aat gag ctt aga aga tgg gga gaa tgg tat   672
Asp His Pro Glu Val Val Asn Glu Leu Arg Arg Trp Gly Glu Trp Tyr
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Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Ala
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    370                 375                 380

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385                 390                 395                 400

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Thr Arg Ser Gln Leu Glu Ser Ala Ile His Ala Leu Lys Asn Asn Gly
                85                  90                  95

Val Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
            100                 105                 110

Ala Thr Glu Asn Val Leu Ala Val Glu Val Asn Pro Asn Asn Arg Asn
        115                 120                 125

Gln Glu Ile Ser Gly Asp Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp
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Ile Tyr Lys Phe Arg Gly Asp Gly Lys Ala Trp Asp Trp Glu Val Asp
            180                 185                 190

Ser Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met
        195                 200                 205

Asp His Pro Glu Val Val Asn Glu Leu Arg Arg Trp Gly Glu Trp Tyr
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Thr Asn Thr Leu Asn Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
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Ile Lys Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Ala
                245                 250                 255

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Gly Ala Leu Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val
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  1               5                  10                  15

ccg gat gat ggc acg tta tgg acc aaa gtg gcc aat gaa gcc aac aac   96
Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala Asn Asn
              20                  25                  30

tta tcc agc ctt ggc atc acc gct ctt tgg ctg ccg ccc gct tac aaa   144
Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala Tyr Lys
          35                  40                  45

gga aca agc cgc agc gac gta ggg tac gga gta tac gac ttg tat gac   192
Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp
      50                  55                  60

ctc ggc gaa ttc aat caa aaa ggg acc gtc cgc aca aaa tac gga aca   240
Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr
  65                  70                  75                  80
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aaa gct caa tat ctt caa gcc att caa gcc gcc cac gcc gct gga atg   288
Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala Gly Met
                85                  90                  95

caa gtg tac gcc gat gtc gtg ttc gac cat aaa ggc ggc gct gac ggc   336
Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala Asp Gly
            100                 105                 110

acg gaa tgg gtg gac gcc gtc gaa gtc aat ccg tcc gac cgc aac caa   384
Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg Asn Gln
        115                 120                 125

gaa atc tcg ggc acc tat caa atc caa gca tgg acg aaa ttt gat ttt   432
Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe
    130                 135                 140

ccc ggg cgg ggc aac acc tac tcc agc ttt aag tgg cgc tgg tac cat   480
Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr His
145                 150                 155                 160

ttt gac ggc gtt gat tgg gac gaa agc cga aaa ttg agc cgc att tac   528
Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg Ile Tyr
                165                 170                 175

aaa ttc cgc ggc atc ggc aaa gcg tgg gat tgg gaa gta gac acg gaa   576
Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu
            180                 185                 190

aac gga aac tat gac tac tta atg tat gcc gac ctt gat atg gat cat   624
Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met Asp His
        195                 200                 205

ccc gaa gtc gtg acc gag ctg aaa aac tgg ggg aaa tgg tat gtc aac   672
Pro Glu Val Val Thr Glu Leu Lys Asn Trp Gly Lys Trp Tyr Val Asn
    210                 215                 220

aca acg aac att gat ggg ttc cgg ctt gat gcc gtc aag cat att aag   720
Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys
225                 230                 235                 240

ttc agt ttt ttt cct gat tgg ttg tcg tat gtg cgt tct cag act ggc   768
Phe Ser Phe Phe Pro Asp Trp Leu Ser Tyr Val Arg Ser Gln Thr Gly
                245                 250                 255

aag ccg cta ttt acc gtc ggg gaa tat tgg agc tat gac atc aac aag   816
Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile Asn Lys
            260                 265                 270

ttg cac aat tac att acg aaa aca gac gga acg atg tct ttg ttt gat   864
Leu His Asn Tyr Ile Thr Lys Thr Asp Gly Thr Met Ser Leu Phe Asp
        275                 280                 285

gcc ccg tta cac aac aaa ttt tat acc gct tcc aaa tca ggg ggc gca   912
Ala Pro Leu His Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly Gly Ala
    290                 295                 300

ttt gat atg cgc acg tta atg acc aat act ctc atg aaa gat caa ccg   960
Phe Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp Gln Pro
305                 310                 315                 320

aca ttg gcc gtc acc ttc gtt gat aat cat gac acc gaa ccc ggc caa  1008
Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro Gly Gln
                325                 330                 335

gcg ctg cag tca tgg gtc gac cca tgg ttc aaa ccg ttg gct tac gcc  1056
Ala Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala Tyr Ala
            340                 345                 350

ttt att cta act cgg cag gaa gga tac ccg tgc gtc ttt tat ggt gac  1104
Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp
        355                 360                 365

tat tat ggc att cca caa tat aac att cct tcg ctg aaa agc aaa atc  1152
Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser Lys Ile
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        370                 375                 380

    gat ccg ctc ctc atc gcg cgc agg gat tat gct tac gga acg caa cat   1200
    Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln His
5   385                 390                 395                 400

    gat tat ctt gat cac tcc gac atc atc ggg tgg aca agg gaa ggg ggc   1248
    Asp Tyr Leu Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu Gly Gly
                    405                 410                 415
10
    act gaa aaa cca gga tcc gga ctg gcc gca ctg atc acc gat ggg ccg   1296
    Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
                420                 425                 430

15  gga gga agc aaa tgg atg tac gtt ggc aaa caa cac gct gga aaa gtg   1344
    Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly Lys Val
            435                 440                 445

    ttc tat gac ctt acc ggc aac cgg agt gac acc gtc acc atc aac agt   1392
20  Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ser
        450                 455                 460

    gat gga tgg ggg gaa ttc aaa gtc aat ggc ggt tcg gtt tcg gtt tgg   1440
    Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Val Trp
25  465                 470                 475                 480

    gtt cct aga aaa acg acc gtt tct acc atc gct cgg ccg atc aca acc   1488
    Val Pro Arg Lys Thr Thr Val Ser Thr Ile Ala Arg Pro Ile Thr Thr
                    485                 490                 495
30
    cga ccg tgg act ggt gaa ttc gtc cgt tgg acc gaa cca cgg ttg gtg   1536
    Arg Pro Trp Thr Gly Glu Phe Val Arg Trp Thr Glu Pro Arg Leu Val
                500                 505                 510

35  gca tgg cct tga                                                 1548
    Ala Trp Pro
            515


40  <210> 6
    <211> 515
    <212> PRT
    <213> Bacillus stearothermophilus

45  <400> 6
    Ala Ala Pro Phe Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr Leu
      1               5                  10                  15

    Pro Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala Asn Asn
50                 20                  25                  30

    Leu Ser Ser Leu Gly Ile Thr Ala Leu Trp Leu Pro Pro Ala Tyr Lys
             35                  40                  45

55  Gly Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp
         50                  55                  60

    Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr
     65                  70                  75                  80
60
    Lys Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala Gly Met
                    85                  90                  95

    Gln Val Tyr Ala Asp Val Val Phe Asp His Lys Gly Gly Ala Asp Gly
65              100                 105                 110

    Thr Glu Trp Val Asp Ala Val Glu Val Asn Pro Ser Asp Arg Asn Gln
            115                 120                 125

70  Glu Ile Ser Gly Thr Tyr Gln Ile Gln Ala Trp Thr Lys Phe Asp Phe
        130                 135                 140

    Pro Gly Arg Gly Asn Thr Tyr Ser Ser Phe Lys Trp Arg Trp Tyr His
    145                 150                 155                 160
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Phe Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg Ile Tyr
                165                 170                 175

Lys Phe Arg Gly Ile Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu
            180                 185                 190

Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Leu Asp Met Asp His
        195                 200                 205

Pro Glu Val Val Thr Glu Leu Lys Asn Trp Gly Lys Trp Tyr Val Asn
    210                 215                 220

Thr Thr Asn Ile Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys
225                 230                 235                 240

Phe Ser Phe Phe Pro Asp Trp Leu Ser Tyr Val Arg Ser Gln Thr Gly
                245                 250                 255

Lys Pro Leu Phe Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile Asn Lys
            260                 265                 270

Leu His Asn Tyr Ile Thr Lys Thr Asp Gly Thr Met Ser Leu Phe Asp
        275                 280                 285

Ala Pro Leu His Asn Lys Phe Tyr Thr Ala Ser Lys Ser Gly Gly Ala
    290                 295                 300

Phe Asp Met Arg Thr Leu Met Thr Asn Thr Leu Met Lys Asp Gln Pro
305                 310                 315                 320

Thr Leu Ala Val Thr Phe Val Asp Asn His Asp Thr Glu Pro Gly Gln
                325                 330                 335

Ala Leu Gln Ser Trp Val Asp Pro Trp Phe Lys Pro Leu Ala Tyr Ala
            340                 345                 350

Phe Ile Leu Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp
        355                 360                 365

Tyr Tyr Gly Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser Lys Ile
    370                 375                 380

Asp Pro Leu Leu Ile Ala Arg Arg Asp Tyr Ala Tyr Gly Thr Gln His
385                 390                 395                 400

Asp Tyr Leu Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu Gly Gly
                405                 410                 415

Thr Glu Lys Pro Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
            420                 425                 430

Gly Gly Ser Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly Lys Val
        435                 440                 445

Phe Tyr Asp Leu Thr Gly Asn Arg Ser Asp Thr Val Thr Ile Asn Ser
    450                 455                 460

Asp Gly Trp Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Val Trp
465                 470                 475                 480

Val Pro Arg Lys Thr Thr Val Ser Thr Ile Ala Arg Pro Ile Thr Thr
                485                 490                 495

Arg Pro Trp Thr Gly Glu Phe Val Arg Trp Thr Glu Pro Arg Leu Val
            500                 505                 510

Ala Trp Pro
        515
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<210> 7
<211> 1920

<212> DNA
<213> Bacillus licheniformis

<220>
<221> CDS
<222> (421)..(1872)
<223> Termamyl

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gagacggaaa aatcgtctta atgcacgata tttatgcaac gttcgcagat gctgctgaag 120

agattattaa aaagctgaaa gcaaaaggct atcaattggt aactgtatct cagcttgaag 180

aagtgaagaa gcagagaggc tattgaataa atgagtagaa gcgccatatc ggcgcttttc 240

ttttggaaga aaatataggg aaaatggtac ttgttaaaaa ttcggaatat ttatacaaca 300

tcatatgttt cacattgaaa ggggaggaga atcatgaaac aacaaaaacg gctttacgcc 360

cgattgctga cgctgttatt tgcgctcatc ttcttgctgc ctcattctgc agcagcggcg 420

gca aat ctt aat ggg acg ctg atg cag tat ttt gaa tgg tac atg ccc 468
Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
1 5 10 15

aat gac ggc caa cat tgg agg cgt ttg caa aac gac tcg gca tat ttg 516
Asn Asp Gly Gln His Trp Arg Arg Leu Gln Asn Asp Ser Ala Tyr Leu
20 25 30

gct gaa cac ggt att act gcc gtc tgg att ccc ccg gca tat aag gga 564
Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
35 40 45

acg agc caa gcg gat gtg ggc tac ggt gct tac gac ctt tat gat tta 612
Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
50 55 60

ggg gag ttt cat caa aaa ggg acg gtt cgg aca aag tac ggc aca aaa 660
Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65 70 75 80

gga gag ctg caa tct gcg atc aaa agt ctt cat tcc cgc gac att aac 708
Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn
85 90 95

gtt tac ggg gat gtg gtc atc aac cac aaa ggc ggc gct gat gcg acc 756
Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr
100 105 110

gaa gat gta acc gcg gtt gaa gtc gat ccc gct gac cgc aac cgc gta 804
Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val
115 120 125

att tca gga gaa cac cta att aaa gcc tgg aca cat ttt cat ttt ccg 852
Ile Ser Gly Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro
130 135 140

ggg cgc ggc agc aca tac agc gat ttt aaa tgg cat tgg tac cat ttt 900
Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
145 150 155 160

gac gga acc gat tgg gac gag tcc cga aag ctg aac cgc atc tat aag 948
Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys
165 170 175

ttt caa gga aag gct tgg gat tgg gaa gtt tcc aat gaa aac ggc aac 996
Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn
180 185 190

tat gat tat ttg atg tat gcc gac atc gat tat gac cat cct gat gtc 1044
Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val
195 200 205

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gca gca gaa att aag aga tgg ggc act tgg tat gcc aat gaa ctg caa   1092
Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln
    210                 215                 220

ttg gac ggt ttc cgt ctt gat gct gtc aaa cac att aaa ttt tct ttt   1140
Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe
225                 230                 235                 240

ttg cgg gat tgg gtt aat cat gtc agg gaa aaa acg ggg aag gaa atg   1188
Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met
                245                 250                 255

ttt acg gta gct gaa tat tgg cag aat gac ttg ggc gcg ctg gaa aac   1236
Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn
            260                 265                 270

tat ttg aac aaa aca aat ttt aat cat tca gtg ttt gac gtg ccg ctt   1284
Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu
        275                 280                 285

cat tat cag ttc cat gct gca tcg aca cag gga ggc ggc tat gat atg   1332
His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met
    290                 295                 300

agg aaa ttg ctg aac ggt acg gtc gtt tcc aag cat ccg ttg aaa tcg   1380
Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser
305                 310                 315                 320

gtt aca ttt gtc gat aac cat gat aca cag ccg ggg caa tcg ctt gag   1428
Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
                325                 330                 335

tcg act gtc caa aca tgg ttt aag ccg ctt gct tac gct ttt att ctc   1476
Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
            340                 345                 350

aca agg gaa tct gga tac cct cag gtt ttc tac ggg gat atg tac ggg   1524
Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
        355                 360                 365

acg aaa gga gac tcc cag cgc gaa att cct gcc ttg aaa cac aaa att   1572
Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile
    370                 375                 380

gaa ccg atc tta aaa gcg aga aaa cag tat gcg tac gga gca cag cat   1620
Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
385                 390                 395                 400

gat tat ttc gac cac cat gac att gtc ggc tgg aca agg gaa ggc gac   1668
Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp
                405                 410                 415

agc tcg gtt gca aat tca ggt ttg gcg gca tta ata aca gac gga ccc   1716
Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
            420                 425                 430

ggt ggg gca aag cga atg tat gtc ggc cgg caa aac gcc ggt gag aca   1764
Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
        435                 440                 445

tgg cat gac att acc gga aac cgt tcg gag ccg gtt gtc atc aat tcg   1812
Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
    450                 455                 460

gaa ggc tgg gga gag ttt cac gta aac ggc ggg tcg gtt tca att tat   1860
Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
465                 470                 475                 480

gtt caa aga tag aagagcagag aggacggatt tcctgaagga aatccgtttt       1912
Val Gln Arg

tttatttt                                                          1920
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<210> 8
<211> 483
<212> PRT
<213> Bacillus licheniformis

<400> 8
Ala Asn Leu Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Met Pro
1 5 10 15

Asn Asp Gly Gln His Trp Arg Arg Leu Gln Asn Asp Ser Ala Tyr Leu
20 25 30

Ala Glu His Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly
35 40 45

Thr Ser Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu
50 55 60

Gly Glu Phe His Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys
65 70 75 80

Gly Glu Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn
85 90 95

Val Tyr Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr
100 105 110

Glu Asp Val Thr Ala Val Glu Val Asp Pro Ala Asp Arg Asn Arg Val
115 120 125

Ile Ser Gly Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro
130 135 140

Gly Arg Gly Ser Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe
145 150 155 160

Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys
165 170 175

Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn
180 185 190

Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Tyr Asp His Pro Asp Val
195 200 205

Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln
210 215 220

Leu Asp Gly Phe Arg Leu Asp Ala Val Lys His Ile Lys Phe Ser Phe
225 230 235 240

Leu Arg Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met
245 250 255

Phe Thr Val Ala Glu Tyr Trp Gln Asn Asp Leu Gly Ala Leu Glu Asn
260 265 270

Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu
275 280 285

His Tyr Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met
290 295 300

Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser
305 310 315 320

Val Thr Phe Val Asp Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
325 330 335

Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
340 345 350

Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly

355 360 365

Thr Lys Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile
370 375 380

Glu Pro Ile Leu Lys Ala Arg Lys Gln Tyr Ala Tyr Gly Ala Gln His
385 390 395 400

Asp Tyr Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp
405 410 415

Ser Ser Val Ala Asn Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
420 425 430

Gly Gly Ala Lys Arg Met Tyr Val Gly Arg Gln Asn Ala Gly Glu Thr
435 440 445

Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
450 455 460

Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
465 470 475 480

Val Gln Arg

<210> 9
<211> 2084
<212> DNA
<213> Bacillus amyloliquefaciens

<220>
<221> CDS
<222> (343)..(1794)
<223> BAN

<400> 9
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ctgaagaagt ggatcgattg tttgagaaaa gaagaagacc ataaaaatac cttgtctgtc 120

atcagacagg gtatttttta tgctgtccag actgtccgct gtgtaaaaat aaggaataaa 180

ggggggttgt tattatttta ctgatatgta aaatataatt tgtataagaa aatgagaggg 240

agaggaaaca tgattcaaaa acgaaagcgg acagtttcgt tcagacttgt gcttatgtgc 300

acgctgttat ttgtcagttt gccgattaca aaaacatcag cc gta aat ggc acg 354
Val Asn Gly Thr
1

ctg atg cag tat ttt gaa tgg tat acg ccg aac gac ggc cag cat tgg 402
Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp Gly Gln His Trp
5 10 15 20

aaa cga ttg cag aat gat gcg gaa cat tta tcg gat atc gga atc act 450
Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp Ile Gly Ile Thr
25 30 35

gcc gtc tgg att cct ccc gca tac aaa gga ttg agc caa tcc gat aac 498
Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser Gln Ser Asp Asn
40 45 50

gga tac gga cct tat gat ttg tat gat tta gga gaa ttc cag caa aaa 546
Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu Phe Gln Gln Lys
55 60 65

ggg acg gtc aga acg aaa tac ggc aca aaa tca gag ctt caa gat gcg 594
Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu Leu Gln Asp Ala
70 75 80

atc ggc tca ctg cat tcc cgg aac gtc caa gta tac gga gat gtg gtt 642
Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr Gly Asp Val Val

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 85                  90                  95                  100

    ttg aat cat aag gct ggt gct gat gca aca gaa gat gta act gcc gtc   690
    Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp Val Thr Ala Val
5                   105                 110                 115

    gaa gtc aat ccg gcc aat aga aat cag gaa act tcg gag gaa tat caa   738
    Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser Glu Glu Tyr Gln
                120                 125                 130
10
    atc aaa gcg tgg acg gat ttt cgt ttt ccg ggc cgt gga aac acg tac   786
    Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg Gly Asn Thr Tyr
            135                 140                 145

15  agt gat ttt aaa tgg cat tgg tat cat ttc gac gga gcg gac tgg gat   834
    Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly Ala Asp Trp Asp
        150                 155                 160

    gaa tcc cgg aag atc agc cgc atc ttt aag ttt cgt ggg gaa gga aaa   882
20  Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg Gly Glu Gly Lys
    165                 170                 175                 180

    gcg tgg gat tgg gaa gta tca agt gaa aac ggc aac tat gac tat tta   930
    Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn Tyr Asp Tyr Leu
25                  185                 190                 195

    atg tat gct gat gtt gac tac gac cac cct gat gtc gtg gca gag aca   978
    Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val Val Ala Glu Thr
                200                 205                 210
30
    aaa aaa tgg ggt atc tgg tat gcg aat gaa ctg tca tta gac ggc ttc   1026
    Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser Leu Asp Gly Phe
            215                 220                 225

35  cgt att gat gcc gcc aaa cat att aaa ttt tca ttt ctg cgt gat tgg   1074
    Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe Leu Arg Asp Trp
        230                 235                 240

    gtt cag gcg gtc aga cag gcg acg gga aaa gaa atg ttt acg gtt gcg   1122
40  Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met Phe Thr Val Ala
    245                 250                 255                 260

    gag tat tgg cag aat aat gcc ggg aaa ctc gaa aac tac ttg aat aaa   1170
    Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn Tyr Leu Asn Lys
45                  265                 270                 275

    aca agc ttt aat caa tcc gtg ttt gat gtt ccg ctt cat ttc aat tta   1218
    Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu His Phe Asn Leu
                280                 285                 290
50
    cag gcg gct tcc tca caa gga ggc gga tat gat atg agg cgt ttg ctg   1266
    Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp Met Arg Arg Leu Leu
            295                 300                 305

55  gac ggt acc gtt gtg tcc agg cat ccg gaa aag gcg gtt aca ttt gtt   1314
    Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala Val Thr Phe Val
        310                 315                 320

    gaa aat cat gac aca cag ccg gga cag tca ttg gaa tcg aca gtc caa   1362
60  Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu Ser Thr Val Gln
    325                 330                 335                 340

    act tgg ttt aaa ccg ctt gca tac gcc ttt att ttg aca aga gaa tcc   1410
    Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu Thr Arg Glu Ser
65                  345                 350                 355

    ggt tat cct cag gtg ttc tat ggg gat atg tac ggg aca aaa ggg aca   1458
    Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys Gly Thr
                360                 365                 370
70
    tcg cca aag gaa att ccc tca ctg aaa gat aat ata gag ccg att tta   1506
    Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile Glu Pro Ile Leu
            375                 380                 385
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aaa gcg cgt aag gag tac gca tac ggg ccc cag cac gat tat att gac   1554
Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His Asp Tyr Ile Asp
    390                 395                 400

cac ccg gat gtg atc gga tgg acg agg gaa ggt gac agc tcc gcc gcc   1602
His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp Ser Ser Ala Ala
405                 410                 415                 420

aaa tca ggt ttg gcc gct tta atc acg gac gga ccc ggc gga tca aag   1650
Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly Ser Lys
                425                 430                 435

cgg atg tat gcc ggc ctg aaa aat gcc ggc gag aca tgg tat gac ata   1698
Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr Trp Tyr Asp Ile
            440                 445                 450

acg ggc aac cgt tca gat act gta aaa atc gga tct gac ggc tgg gga   1746
Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser Asp Gly Trp Gly
        455                 460                 465

gag ttt cat gta aac gat ggg tcc gtc tcc att tat gtt cag aaa taa   1794
Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr Val Gln Lys
    470                 475                 480

ggtaataaaa aaacacctcc aagctgagtg cgggtatcag cttggaggtg cgtttatttt 1854

ttcagccgta tgacaaggtc ggcatcaggt gtgacaaata cggtatgctg gctgtcatag 1914

gtgacaaatc cgggttttgc gccgtttggc tttttcacat gtctgatttt tgtataatca 1974

acaggcacgg agccggaatc tttcgccttg gaaaaataag cggcgatcgt agctgcttcc 2034

aatatggatt gttcatcggg atcgctgctt ttaatcacaa cgtgggatcc            2084
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<210> 10
<211> 483
<212> PRT
<213> Bacillus amyloliquefaciens

<400> 10

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Val Asn Gly Thr Leu Met Gln Tyr Phe Glu Trp Tyr Thr Pro Asn Asp
  1               5                  10                  15

Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
             20                  25                  30

Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
         35                  40                  45

Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
     50                  55                  60

Phe Gln Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly Thr Lys Ser Glu
 65                  70                  75                  80

Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
                 85                  90                  95

Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
            100                 105                 110

Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser
        115                 120                 125

Glu Glu Tyr Gln Ile Lys Ala Trp Thr Asp Phe Arg Phe Pro Gly Arg
    130                 135                 140

Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
145                 150                 155                 160

Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg
                165                 170                 175
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Gly Glu Gly Lys Ala Trp Asp Trp Glu Val Ser Ser Glu Asn Gly Asn
180 185 190

Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Tyr Asp His Pro Asp Val
195 200 205

Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser
210 215 220

Leu Asp Gly Phe Arg Ile Asp Ala Ala Lys His Ile Lys Phe Ser Phe
225 230 235 240

Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met
245 250 255

Phe Thr Val Ala Glu Tyr Trp Gln Asn Asn Ala Gly Lys Leu Glu Asn
260 265 270

Tyr Leu Asn Lys Thr Ser Phe Asn Gln Ser Val Phe Asp Val Pro Leu
275 280 285

His Phe Asn Leu Gln Ala Ala Ser Ser Gln Gly Gly Gly Tyr Asp Met
290 295 300

Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala
305 310 315 320

Val Thr Phe Val Glu Asn His Asp Thr Gln Pro Gly Gln Ser Leu Glu
325 330 335

Ser Thr Val Gln Thr Trp Phe Lys Pro Leu Ala Tyr Ala Phe Ile Leu
340 345 350

Thr Arg Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly
355 360 365

Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile
370 375 380

Glu Pro Ile Leu Lys Ala Arg Lys Glu Tyr Ala Tyr Gly Pro Gln His
385 390 395 400

Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp
405 410 415

Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
420 425 430

Gly Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr
435 440 445

Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser
450 455 460

Asp Gly Trp Gly Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr
465 470 475 480

Val Gln Lys

<210> 11
<211> 1458
<212> DNA
<213> Bacillus sp.

<220>
<221> CDS
<222> (1)..(1458)
<223> AA560

<400> 11
cac cat aat ggt acg aac ggc aca atg atg cag tac ttt gaa tgg tat 48
His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr

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  1               5                  10                  15

cta cca aat gac gga aac cat tgg aat aga tta agg tct gat gca agt   96
Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Ser Asp Ala Ser
            20                  25                  30

aac cta aaa gat aaa ggg atc tca gcg gtt tgg att cct cct gca tgg   144
Asn Leu Lys Asp Lys Gly Ile Ser Ala Val Trp Ile Pro Pro Ala Trp
        35                  40                  45

aag ggt gcc tct caa aat gat gtg ggg tat ggt gct tat gat ctg tat   192
Lys Gly Ala Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
    50                  55                  60

gat tta gga gaa ttc aat caa aaa gga acc att cgt aca aaa tat gga   240
Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Ile Arg Thr Lys Tyr Gly
65                  70                  75                  80

acg cgc aat cag tta caa gct gca gtt aac gcc ttg aaa agt aat gga   288
Thr Arg Asn Gln Leu Gln Ala Ala Val Asn Ala Leu Lys Ser Asn Gly
                85                  90                  95

att caa gtg tat ggc gat gtt gta atg aat cat aaa ggg gga gca gac   336
Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
            100                 105                 110

gct acc gaa atg gtt agg gca gtt gaa gta aac ccg aat aat aga aat   384
Ala Thr Glu Met Val Arg Ala Val Glu Val Asn Pro Asn Asn Arg Asn
        115                 120                 125

caa gaa gtg tcc ggt gaa tat aca att gag gct tgg aca aag ttt gac   432
Gln Glu Val Ser Gly Glu Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp
    130                 135                 140

ttt cca gga cga ggt aat act cat tca aac ttc aaa tgg aga tgg tat   480
Phe Pro Gly Arg Gly Asn Thr His Ser Asn Phe Lys Trp Arg Trp Tyr
145                 150                 155                 160

cac ttt gat gga gta gat tgg gat cag tca cgt aag ctg aac aat cga   528
His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Lys Leu Asn Asn Arg
                165                 170                 175

att tat aaa ttt aga ggt gat gga aaa ggg tgg gat tgg gaa gtc gat   576
Ile Tyr Lys Phe Arg Gly Asp Gly Lys Gly Trp Asp Trp Glu Val Asp
            180                 185                 190

aca gaa aac ggt aac tat gat tac cta atg tat gca gat att gac atg   624
Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Met
        195                 200                 205

gat cac cca gag gta gtg aat gag cta aga aat tgg ggt gtt tgg tat   672
Asp His Pro Glu Val Val Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr
    210                 215                 220

acg aat aca tta ggc ctt gat ggt ttt aga ata gat gca gta aaa cat   720
Thr Asn Thr Leu Gly Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
225                 230                 235                 240

ata aaa tac agc ttt act cgt gat tgg att aat cat gtt aga agt gca   768
Ile Lys Tyr Ser Phe Thr Arg Asp Trp Ile Asn His Val Arg Ser Ala
                245                 250                 255

act ggc aaa aat atg ttt gcg gtt gcg gaa ttt tgg aaa aat gat tta   816
Thr Gly Lys Asn Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
            260                 265                 270

ggt gct att gaa aac tat tta aac aaa aca aac tgg aac cat tca gtc   864
Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val
        275                 280                 285

ttt gat gtt ccg ctg cac tat aac ctc tat aat gct tca aaa agc gga   912
Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Lys Ser Gly
    290                 295                 300
```

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ggg aat tat gat atg agg caa ata ttt aat ggt aca gtc gtg caa aga   960
Gly Asn Tyr Asp Met Arg Gln Ile Phe Asn Gly Thr Val Val Gln Arg
305                 310                 315                 320

cat cca atg cat gct gtt aca ttt gtt gat aat cat gat tcg caa cct   1008
His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
                325                 330                 335

gaa gaa gct tta gag tct ttt gtt gaa gaa tgg ttc aaa cca tta gcg   1056
Glu Glu Ala Leu Glu Ser Phe Val Glu Glu Trp Phe Lys Pro Leu Ala
            340                 345                 350

tat gct ttg aca tta aca cgt gaa caa ggc tac cct tct gta ttt tat   1104
Tyr Ala Leu Thr Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
        355                 360                 365

gga gat tat tat ggc att cca acg cat ggt gta cca gcg atg aaa tcg   1152
Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser
    370                 375                 380

aaa att gac ccg att cta gaa gcg cgt caa aag tat gca tat gga aga   1200
Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Lys Tyr Ala Tyr Gly Arg
385                 390                 395                 400

caa aat gac tac tta gac cat cat aat atc atc ggt tgg aca cgt gaa   1248
Gln Asn Asp Tyr Leu Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
                405                 410                 415

ggg aat aca gca cac ccc aac tcc ggt tta gct act atc atg tcc gat   1296
Gly Asn Thr Ala His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
            420                 425                 430

ggg gca gga gga aat aag tgg atg ttt gtt ggg cgt aat aaa gct ggt   1344
Gly Ala Gly Gly Asn Lys Trp Met Phe Val Gly Arg Asn Lys Ala Gly
        435                 440                 445

caa gtt tgg acc gat atc act gga aat cgt gca ggt act gtt acg att   1392
Gln Val Trp Thr Asp Ile Thr Gly Asn Arg Ala Gly Thr Val Thr Ile
    450                 455                 460

aat gct gat gga tgg ggt aat ttt tct gta aat gga gga tca gtt tct   1440
Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
465                 470                 475                 480

att tgg gta aac aaa taa                                          1458
Ile Trp Val Asn Lys
                485
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<210> 12
<211> 485
<212> PRT
<213> Bacillus sp.

<400> 12

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His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
  1               5                  10                  15

Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Arg Ser Asp Ala Ser
            20                  25                  30

Asn Leu Lys Asp Lys Gly Ile Ser Ala Val Trp Ile Pro Pro Ala Trp
        35                  40                  45

Lys Gly Ala Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
    50                  55                  60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Ile Arg Thr Lys Tyr Gly
65                  70                  75                  80

Thr Arg Asn Gln Leu Gln Ala Ala Val Asn Ala Leu Lys Ser Asn Gly
                85                  90                  95

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
```

100 105 110

Ala Thr Glu Met Val Arg Ala Val Glu Val Asn Pro Asn Asn Arg Asn
115 120 125

Gln Glu Val Ser Gly Glu Tyr Thr Ile Glu Ala Trp Thr Lys Phe Asp
130 135 140

Phe Pro Gly Arg Gly Asn Thr His Ser Asn Phe Lys Trp Arg Trp Tyr
145 150 155 160

His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Lys Leu Asn Asn Arg
165 170 175

Ile Tyr Lys Phe Arg Gly Asp Gly Lys Gly Trp Asp Trp Glu Val Asp
180 185 190

Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Met
195 200 205

Asp His Pro Glu Val Val Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr
210 215 220

Thr Asn Thr Leu Gly Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
225 230 235 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Ile Asn His Val Arg Ser Ala
245 250 255

Thr Gly Lys Asn Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
260 265 270

Gly Ala Ile Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val
275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Lys Ser Gly
290 295 300

Gly Asn Tyr Asp Met Arg Gln Ile Phe Asn Gly Thr Val Val Gln Arg
305 310 315 320

His Pro Met His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
325 330 335

Glu Glu Ala Leu Glu Ser Phe Val Glu Glu Trp Phe Lys Pro Leu Ala
340 345 350

Tyr Ala Leu Thr Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Lys Ser
370 375 380

Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Lys Tyr Ala Tyr Gly Arg
385 390 395 400

Gln Asn Asp Tyr Leu Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
405 410 415

Gly Asn Thr Ala His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
420 425 430

Gly Ala Gly Gly Asn Lys Trp Met Phe Val Gly Arg Asn Lys Ala Gly
435 440 445

Gln Val Trp Thr Asp Ile Thr Gly Asn Arg Ala Gly Thr Val Thr Ile
450 455 460

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
465 470 475 480

Ile Trp Val Asn Lys
485

<210> 13
<211> 485
<212> PRT
<213> Bacillus sp. 707

<400> 13
His His Asn Gly Thr Asn Gly Thr Met Met Gln Tyr Phe Glu Trp Tyr
1 5 10 15

Leu Pro Asn Asp Gly Asn His Trp Asn Arg Leu Asn Ser Asp Ala Ser
20 25 30

Asn Leu Lys Ser Lys Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Trp
35 40 45

Lys Gly Ala Ser Gln Asn Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr
50 55 60

Asp Leu Gly Glu Phe Asn Gln Lys Gly Thr Val Arg Thr Lys Tyr Gly
65 70 75 80

Thr Arg Ser Gln Leu Gln Ala Ala Val Thr Ser Leu Lys Asn Asn Gly
85 90 95

Ile Gln Val Tyr Gly Asp Val Val Met Asn His Lys Gly Gly Ala Asp
100 105 110

Ala Thr Glu Met Val Arg Ala Val Glu Val Asn Pro Asn Asn Arg Asn
115 120 125

Gln Glu Val Thr Gly Glu Tyr Thr Ile Glu Ala Trp Thr Arg Phe Asp
130 135 140

Phe Pro Gly Arg Gly Asn Thr His Ser Ser Phe Lys Trp Arg Trp Tyr
145 150 155 160

His Phe Asp Gly Val Asp Trp Asp Gln Ser Arg Arg Leu Asn Asn Arg
165 170 175

Ile Tyr Lys Phe Arg Gly His Gly Lys Ala Trp Asp Trp Glu Val Asp
180 185 190

Thr Glu Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Ile Asp Met
195 200 205

Asp His Pro Glu Val Val Asn Glu Leu Arg Asn Trp Gly Val Trp Tyr
210 215 220

Thr Asn Thr Leu Gly Leu Asp Gly Phe Arg Ile Asp Ala Val Lys His
225 230 235 240

Ile Lys Tyr Ser Phe Thr Arg Asp Trp Ile Asn His Val Arg Ser Ala
245 250 255

Thr Gly Lys Asn Met Phe Ala Val Ala Glu Phe Trp Lys Asn Asp Leu
260 265 270

Gly Ala Ile Glu Asn Tyr Leu Gln Lys Thr Asn Trp Asn His Ser Val
275 280 285

Phe Asp Val Pro Leu His Tyr Asn Leu Tyr Asn Ala Ser Lys Ser Gly
290 295 300

Gly Asn Tyr Asp Met Arg Asn Ile Phe Asn Gly Thr Val Val Gln Arg
305 310 315 320

His Pro Ser His Ala Val Thr Phe Val Asp Asn His Asp Ser Gln Pro
325 330 335

Glu Glu Ala Leu Glu Ser Phe Val Glu Glu Trp Phe Lys Pro Leu Ala
340 345 350

Tyr Ala Leu Thr Leu Thr Arg Glu Gln Gly Tyr Pro Ser Val Phe Tyr
355 360 365

Gly Asp Tyr Tyr Gly Ile Pro Thr His Gly Val Pro Ala Met Arg Ser
370 375 380

Lys Ile Asp Pro Ile Leu Glu Ala Arg Gln Lys Tyr Ala Tyr Gly Lys
385 390 395 400

Gln Asn Asp Tyr Leu Asp His His Asn Ile Ile Gly Trp Thr Arg Glu
405 410 415

Gly Asn Thr Ala His Pro Asn Ser Gly Leu Ala Thr Ile Met Ser Asp
420 425 430

Gly Ala Gly Gly Ser Lys Trp Met Phe Val Gly Arg Asn Lys Ala Gly
435 440 445

Gln Val Trp Ser Asp Ile Thr Gly Asn Arg Thr Gly Thr Val Thr Ile
450 455 460

Asn Ala Asp Gly Trp Gly Asn Phe Ser Val Asn Gly Gly Ser Val Ser
465 470 475 480

Ile Trp Val Asn Lys
485

<210> 14

<211> 60

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> ()..()

<223> Primer FSA

<400> 14
caaaatcgta tctacaaatt cmrkrsyarg dvktgggatt sggaagtaga ttcggaaaat 60

<210> 15

<211> 21

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> ()..()

<223> Primer RSA

<400> 15
gaatttgtag atacgatttt g 21

<210> 16

<211> 24

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> ()..()

<223> Primer B1

<400> 16
cgattgctga cgctgttatt tgcg 24

<210> 17

<211> 24

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> ()..()

<223> Primer Y2

<400> 17
cttgttccct tgtcagaacc aatg 24

<210> 18

<211> 30

<212> DNA

<213> Artificial/Unknown

<220>

<221> misc_feature

<222> ()..()

<223> Primer 101458

<400> 18
gtcatagttg ccgaaatctg tatcgacttc 30