(54) Title: NOVEL METALLOPROTEASES

Figure 2 Stereo diagram showing a schematic of the Thermolysin main chain folding (black) and the schematic of PehPro1 (light gray).

(57) **Abstract**: Aspects of the present compositions and methods relate to novel metalloproteases polynucleotides encoding the novel metalloprotease, compositions and methods for use thereof.

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NOVEL METALLOPROTEASES

CROSS REFERENCE TO RELATED APPLICATIONS

This application claims benefit of priority from International patent applications Serial No. PCT/CN2013/076419; Serial No. PCT/CN2013/076387; Serial No. PCT/CN2013/076401; Serial No. PCT/CN2013/076406; Serial No. PCT/CN2013/076414; PCT/CN2013/076384; Serial No. PCT/CN2013/076398; PCT/CN2013/076415; Serial No. PCT/CN2013/076386; Serial No. PCT/CN2013/076390; PCT/CN2013/076383; Serial No. PCT/CN2013/076369, all filed on 29 May 2013, and also claims benefit of priority from U.S. Provisional Application Serial No. 61/874,813 filed on 06 September 2013, the contents of all of which are incorporated herein by reference in their entirety.

FIELD OF THE INVENTION

The present disclosure relates to proteases. Compositions containing the proteases are suitable for use in cleaning, food and feed as well as in a variety of other industrial applications.

Background

Metalloproteases (MPs) are among the hydrolases that mediate nucleophilic attack on peptide bonds using a water molecule coordinated in the active site. Thermolysin-like proteases are found in the M4 family as defined by MEROPS (Rawlings et al., (2012) Nucleic Acids Res 40:D343-D350). They are generally active at elevated temperatures and this stability is attributed to calcium binding. Although proteases have long been known in the art of industrial enzymes, there remains a need for novel proteases that are suitable for particular conditions and uses, such as environments that have calcium chelators that destabilize metalloproteases.

Summary

The present disclosure provides, *inter alia*, metalloproteases comprising modifications in calcium binding regions, novel metalloprotease polypeptides with signature amino acids in the calcium binding regions, nucleic acids encoding the same, and compositions and methods related to the production and use thereof.

In some embodiments, the invention is a metalloprotease polypeptide comprising one or more calcium binding regions. In some embodiments, the polypeptide comprises a modification in at least one amino acid residue in one of the calcium binding regions, Ca1-2, Ca3 and Ca4,

(including residues 55-66, 136, 138, 177-190, and 193-200) of the polypeptide, wherein the amino acid positions of the polypeptide are numbered by correspondence with the amino acid sequence of *Bacillus thermoproteolyticus* metalloprotease set forth in SEQ ID NO: 13. In some embodiments, the polypeptide has a calcium binding region Ca1-2 that binds fewer than two calcium ions. In some embodiments, the polypeptide has a calcium binding region 3 that binds fewer than one calcium ion. In some embodiments, the polypeptide has a calcium binding region 4 that binds fewer than one calcium ion. In some embodiments, the polypeptide is a variant of a parent polypeptide. In some embodiments, the parent polypeptide is an M4 metalloprotease. In some embodiments, the polypeptide has at least 60% sequence identity to any one of SEQ ID NOs: 1-15.

In some embodiments, the invention is a composition comprising at least one variant as listed above. In some embodiments, the invention is a method of cleaning using a cleaning composition as listed above.

Brief Description of the Drawings

Figure 1 provides a schematic showing the arrangement of the two independent molecules of PehPro1 in the asymmetric unit of the crystal unit cell.

Figure 2 provides a stereo showing a schematic of the Thermolysin main chain folding (black) and the schematic of PehPro1 (light gray).

Figure 3 provides a close up view of the 3 residue deletion.

Figure 4 provides a close up view of the 5 residue deletion.

Figure 5 provides a comparison of calcium binding site 1 in PehPro1 and the Ca1-2 calcium binding site in Thermolysin.

Figure 6 provides a schematic comparing Thermolysin (black lines) with PehPro1 (light gray sticks) in the vicinity of the second calcium binding site (Ca4) in PehPro1.

Figure 7 provides a comparison of the structures of Thermolysin (black lines) and PehPro1 (light gray sticks) in the region of calcium binding Ca3 present in Thermolysin.

Figure 8 provides a schematic comparing the main chain folding of PehPro1 (dark gray) and PpoPro2 (light gray).

Figure 9 provides a comparison of the first common calcium binding site between PehPro1 (light gray) and Ppopro2 (dark gray).

Figure 10 provides a comparison of the structure of PehPro1 (light gray) and PpoPro2 (dark gray) at the second common calcium site.

Figure 11 provides a comparison of the third calcium binding site seen in PpoPro2 (dark gray) as compared to PehPro1 (light gray).

Figure 12a-f provides a structure-based alignment of the various metalloproteases Peh1.A (*Paenibacillus ehimensis, protein 1*), PbaPro1 (*Paenibacillus barcinonensis, protein 1*)), PhuPro1 (*Paenibacillus hunanensis, protein 1*), PpoPro2 (*Paenibacillus polymyxa, protein 2*), PpoPro1(*Paenibacillus polymyxa, protein 1*), Thermolysin (*Bacillus thermoproteolyticus, protein 1*), PhuPro2 (*Paenibacillus hunanensis, protein 2*), PspPro2 (*Paenibacillus sp., protein 2*), PspPro3 (*Paenibacillus sp., protein 3*), PpePro1 (*Paenibacillus peoriae, protein 1*), PtePro1 (*Paenibacillus terrae, protein 1*), BbrPro1 (*Brevibacillus brevis, protein 1*), 1KEI.A (*Bacillus thermoproteolyticus, thermolysin*), 1NPC.A (*Bacillus cereus*), Npre_var (*Bacillus subtilis*).

Figure 13 provides a comparison of the calcium binding sites of NprE (gray sticks) with the double calcium site (Ca1,2) of Thermolysin (black lines).

Figure 14 provides a comparison of NprE variant with Thermolysin at the Ca3 site.

Figure 15 provides several proteases contain the double delete and lack of the DxD motif shown in a rectangle.

Figure 16 provides a stereodiagram comparing the overall main chain folding pattern of Thermolysin (black) with the NprE variant structure (gray).

Figure 17 provides a comparison of the structures of the NprE variant and Thermolysin at the Ca4 binding site of Thermolysin. The deletion of three residues in NprE relative to Thermolysin results in the elimination of a calcium binding site.

Detailed Description

        The present invention provides novel variant metalloproteases having modifications at calcium binding regions. The MEROPS database (http://merops.sanger.ac.uk) groups peptidases into families based on sequence homology [Rawlings et al. (2010) Nucleic Acid Res. 38:D227]. A peptidase is classified into a family based on sharing significant similarities in amino acid sequence with the type example or another member of the family. In the current release (Release 9.4) of the MEROPS database, there are a total of 63 metalloprotease families, nine of which include but are not limited to BEMP members. These proteases are distributed among 9 families of metalloproteases because of differences in primary sequences and structural characteristics. So far, all BEMPs are endoproteases that harbor 1 catalytic Zinc ion in their active center. They are synthetized as inactive zymogens with a propeptide and their main function is nutrition of the microorganism. Bacterial extracellular metalloproteases (BEMPs) are a large group of metal-containing proteases secreted by heterotropic bacteria [Wu and Chen (2011) Appl. Biol.

Biotechnol. 92:253]. BEMPs are distributed among the metalloprotease families M4, M5, M9, M10, M12, M13, M23, M30, and M34. The M4 is a large family of metalloproteases, mostly BEMPs. Thermolysin is the prototype of the M4 family.

Thermolysin-like proteases are broad-specificity proteases which contain a catalytic zinc ion in their active sites. The thermostable *Bacillus* neutral metalloproteases bind 4 Ca^{2+} ions. Two Ca^{2+} ions are bound in one double calcium binding site (Ca1-2) and 2 Ca^{2+} ions are bound in single binding sites Ca3 and Ca4 [Stark et al (1992) Eur. J. Biochem. 207:207, Veltman et al (1998) Biochem. 37:5312]. Several studies have shown that these proteases are dependent on calcium binding for their stability [Veltman et al (1997) FEBS 405:241]. The single sites Ca3 and Ca4 are absent in the thermolysin-like proteases considered thermolabile [Eijsink et al (2011) Prot. Sci. 20:1346].

It has also become known that thermolysin-like proteinases can perform well in a number of industrial applications such as a detergent additive for laundry and dish cleaning, potentially as feed additives, fermentation aides, as well as a number of pharmaceutical application such as cell culture and tissue dissociation. Earlier studies have demonstrated the importance of calcium binding in a number of mutational studies. In Eijsink et al 2011, [Eijsink, Matthews and Vriend (2011) Prot Sci 20:1346-1355], mutation of Asp57 or Asp 59 in the Ca3 site were shown to dramatically reduce stability in thermolysin. In the same paper the authors postulate that calcium binding site may have evolved evolutionarily as a means or regulating function but destabilizing structure and hence function in the low calcium environment of the cytosol until secreted into a higher calcium environment outside the cell membrane.

Metalloproteases, for example, M4 clan metalloproteases, have calcium binding regions. Without being bound by theory, these calcium binding regions are thought to contribute to the thermostability of these molecules. In some applications, it is beneficial to reduce the dependence of the metalloproteases on calcium binding. For example, detergent compositions contain metal chelators, such as surfactants, which compete for calcium ions and affects the amount of free calcium available to bind the enzyme [Stoner et al. (2005) Biotechnol Prog. 21(6): 1716-23]. In detergent environments, metalloproteases can be subject to destabilization and autolysis due to this lack of free calcium. Thus, there is a need in the art to discover improved metalloproteases which are stable in environments that compete for free calcium, such as detergent compositions, while allowing for maintained proteolytic activity of the metalloproteases in these environments. As such, it would be beneficial to find variant metalloproteases with modified calcium binding regions.

The invention described here arises in part from the observation of two novel crystal structures of thermolysin-like proteases having fewer calcium binding sites (PehPro1 as shown in Example 2, and PpoPro2, Paenibacillus polymyxa protease in Ruf et al 2013 [Ruf et al (2013) Acta Cryst. D69:24-31). The elimination of calcium binding is attributed to a combination of specific amino acid substitutions and deletion that are found to be common to these and related structures resulting in fewer calcium binding coordination sites. Based on these finding, a means for further reducing the number of calcium bound to only one or none is proposed for thermolysin and other thermolysin-like proteinases.

In some embodiments, the invention is variant metalloproteases having modified calcium binding regions. In some embodiments, these modified calcium binding regions result in reduced calcium binding of the metalloprotease enzyme. In other embodiments, the invention is novel metalloproteases having newly discovered calcium binding regions. In some embodiments, the invention includes compositions comprising at least one of the novel metalloprotease enzymes set forth herein. Some such compositions comprise detergent compositions. The metalloprotease enzymes of the present invention can be combined with other enzymes useful in detergent compositions. The invention also provides methods of cleaning using metalloprotease enzymes of the present invention.

Definitions and Abbreviations

Unless otherwise indicated, the practice of the present invention involves conventional techniques commonly used in molecular biology, protein engineering, microbiology, and recombinant DNA technology, which are within the skill of the art. Such techniques are known to those of skill in the art and are described in numerous texts and reference works well known to those of skill in the art. All patents, patent applications, articles and publications mentioned herein, both *supra* and *infra*, are hereby expressly incorporated herein by reference.

Unless defined otherwise herein, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention pertains. Many technical dictionaries are known to those of skill in the art. Although any methods and materials similar or equivalent to those described herein find use in the practice of the present invention, some suitable methods and materials are described herein. Accordingly, the terms defined immediately below are more fully described by reference to the Specification as a whole. Also, as used herein, the singular "a", "an" and "the" includes the plural reference unless the context clearly indicates otherwise. Unless otherwise indicated, nucleic acids are written left to right in 5' to 3' orientation; amino acid sequences are written left to right in amino

to carboxy orientation, respectively. It is to be understood that this invention is not limited to the particular methodology, protocols, and reagents described, as these may vary, depending upon the context they are used by those of skill in the art.

Furthermore, the headings provided herein are not limitations of the various aspects or embodiments of the invention.

It is intended that every maximum numerical limitation given throughout this specification includes every lower numerical limitation, as if such lower numerical limitations were expressly written herein. Every minimum numerical limitation given throughout this specification will include every higher numerical limitation, as if such higher numerical limitations were expressly written herein. Every numerical range given throughout this specification will include every narrower numerical range that falls within such broader numerical range, as if such narrower numerical ranges were all expressly written herein.

As used herein, the terms "protease" and "proteinase" refer to an enzyme that has the ability to break down proteins and peptides. A protease has the ability to conduct "proteolysis," by hydrolysis of peptide bonds that link amino acids together in a peptide or polypeptide chain forming the protein. This activity of a protease as a protein-digesting enzyme is referred to as "proteolytic activity." Many well known procedures exist for measuring proteolytic activity (*See e.g.*, Kalisz, "Microbial Proteinases," *In*: Fiechter (ed.), <u>Advances in Biochemical Engineering/Biotechnology</u>, (1988)). For example, proteolytic activity may be ascertained by comparative assays which analyze the respective protease's ability to hydrolyze a suitable substrate. Exemplary substrates useful in the analysis of protease or proteolytic activity, include, but are not limited to, di-methyl casein (Sigma C-9801), bovine collagen (Sigma C-9879), bovine elastin (Sigma E-1625), and bovine keratin (ICN Biomedical 902111). Colorimetric assays utilizing these substrates are well known in the art (*See e.g.*, WO 99/34011 and U.S. Pat. No. 6,376,450, both of which are incorporated herein by reference). The pNA peptidyl assay (*See e.g.*, Del Mar *et al.*, Anal. Biochem. 99:316-320 [1979]) also finds use in determining the active enzyme concentration. This assay measures the rate at which p-nitroaniline is released as the enzyme hydrolyzes a soluble synthetic substrate, such as succinyl-alanine-alanine-proline-phenylalanine-p-nitroanilide (suc-AAPF-pNA). The rate of production of yellow color from the hydrolysis reaction is measured at 410 nm on a spectrophotometer and is proportional to the active enzyme concentration. In addition, absorbance measurements at 280 nanometers (nm) can be used to determine the total protein concentration in a sample of purified protein. The activity on substrate/protein concentration gives the enzyme specific activity.

As used herein, the term "variant polypeptide" refers to a polypeptide comprising an amino acid sequence that differs in at least one amino acid residue from the amino acid sequence of a parent or reference polypeptide (including but not limited to wild-type polypeptides).

As used herein, "the genus *Bacillus*" includes all species within the genus "*Bacillus*," as known to those of skill in the art, including but not limited to *B. subtilis*, *B. licheniformis*, *B. lentus*, *B. brevis*, *B. stearothermophilus*, *B.* alkalophilus, *B. amyloliquefaciens*, *B. clausii*, *B. halodurans*, *B. megaterium*, *B. coagulans*, *B. circulans*, *B. lautus*, and *B. thuringiensis*. It is recognized that the genus *Bacillus* continues to undergo taxonomical reorganization. Thus, it is intended that the genus include species that have been reclassified, including but not limited to such organisms as *B. stearothermophilus*, which is now named "*Geobacillus stearothermophilus*." The production of resistant endospores under stressful environmental conditions is considered the defining feature of the genus *Bacillus*, although this characteristic also applies to the recently named *Alicyclobacillus*, *Amphibacillus*, *Aneurinibacillus*, *Anoxybacillus*, *Brevibacillus*, *Filobacillus*, *Gracilibacillus*, *Halobacillus*, *Paenibacillus*, *Salibacillus*, *Thermobacillus*, *Ureibacillus*, and *Virgibacillus*.

As used herein, "calcium binding site" refers to a region within a metalloprotease which can bind a calcium ion in the presence of free calcium. Calcium can act to assist in maintaining the structural integrity of metalloproteases under many conditions. In some embodiments, the amount of free calcium can be related to the water hardness during wash conditions, and can range from soft water, having less than 1.0 Calcium grains per gallon, to slightly hard water, having from about 1.0 to 3.5 Calcium grains per gallon, to moderately hard water, having from about 3.5 to 7.0 Calcium grains per gallon, to hard water, having from about 7.0 to 10.5 or more Calcium grains per gallon. In some embodiments of the present invention, the characteristics of the calcium binding site are modified compared to a parent or reference metalloprotease so as to modify the performance of the metalloprotease. Modification of the calcium binding site may include reducing or increasing the affinity of the site to bind calcium ion. Modifying the performance of the metalloprotease is intended to include modification of the stability (e.g., oxidative or thermal) or the activity (e.g., the rate or efficiency with which the metalloprotease hydrolyzes a protein substrate) of the enzyme in its various applications.

As used herein, "calcium ligand" means an amino acid residue or residues within a metalloprotease enzyme which forms a ligand with calcium ion bound within a calcium binding site.

The terms "polynucleotide" and "nucleic acid," which are used interchangeably herein, refer to a polymer of any length of nucleotide monomers covalently bonded in a chain. DNA

(deoxyribonucleic acid), a polynucleotide comprising deoxyribonucleotides, and RNA (ribonucleic acid), a polymer of ribonucleotides, are examples of polynucleotides or nucleic acids having distinct biological function. Polynucleotides or nucleic acids include, but are not limited to, a single-, double- or triple-stranded DNA, genomic DNA, cDNA, RNA, DNA-RNA hybrid, or a polymer comprising purine and pyrimidine bases, or other natural, chemically, biochemically modified, non-natural or derivatized nucleotide bases. The following are non-limiting examples of polynucleotides: genes, gene fragments, chromosomal fragments, expressed sequence tag(s) (EST(s)), exons, introns, messenger RNA (mRNA), transfer RNA (tRNA), ribosomal RNA (rRNA), ribozymes, complementary DNA (cDNA), recombinant polynucleotides, branched polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes, and primers.

As used herein, the term "modification" refers to changes made to a reference amino acid or nucleic acid sequence. It is intended that the term encompass substitutions, insertions and deletions.

As used herein, the term "vector" refers to a nucleic acid construct used to introduce or transfer nucleic acid(s) into a target cell or tissue. A vector is typically used to introduce foreign DNA into a cell or tissue. Vectors include plasmids, cloning vectors, bacteriophages, viruses (*e.g.*, viral vector), cosmids, expression vectors, shuttle vectors, and the like. A vector typically includes an origin of replication, a multicloning site, and a selectable marker. The process of inserting a vector into a target cell is typically referred to as transformation. The present invention includes, in some embodiments, a vector that comprises a DNA sequence encoding a metalloprotease polypeptide (*e.g.*, precursor or mature metalloprotease polypeptide) that is operably linked to a suitable prosequence (*e.g.*, secretory, signal peptide sequence, etc.) capable of effecting the expression of the DNA sequence in a suitable host, and the folding and translocation of the recombinant polypeptide chain.

As used herein, the term "expression cassette," "expression plasmid" or "expression vector" refers to a nucleic acid construct or vector generated recombinantly or synthetically for the expression of a nucleic acid of interest in a target cell. An expression vector or expression cassette typically comprises a promoter nucleotide sequence that drives expression of the foreign nucleic acid. The expression vector or cassette also typically includes any other specified nucleic acid elements that permit transcription of a particular nucleic acid in a target cell. A recombinant expression cassette can be incorporated into a plasmid, chromosome, mitochondrial DNA, plastid DNA, virus, or nucleic acid fragment. Many prokaryotic and eukaryotic expression vectors are commercially available.

In some embodiments, the ends of the sequence are closed such that the DNA construct forms a closed circle. The nucleic acid sequence of interest, which is incorporated into the DNA construct, using techniques well known in the art, may be a wild-type, mutant, or modified nucleic acid. In some embodiments, the DNA construct comprises one or more nucleic acid sequences homologous to the host cell chromosome. In other embodiments, the DNA construct comprises one or more non-homologous nucleotide sequences. Once the DNA construct is assembled *in vitro*, it may be used, for example, to: 1) insert heterologous sequences into a desired target sequence of a host cell; and/or 2) mutagenize a region of the host cell chromosome (*i.e.*, replace an endogenous sequence with a heterologous sequence); 3) delete target genes; and/or 4) introduce a replicating plasmid into the host. "DNA construct" is used interchangeably herein with "expression cassette."

As used herein, a "plasmid" refers to an extrachromosomal DNA molecule which is capable of replicating independently from the chromosomal DNA. A plasmid is double stranded (ds) and may be circular and is typically used as a cloning vector.

As used herein in the context of introducing a nucleic acid sequence into a cell, the term "introduced" refers to any method suitable for transferring the nucleic acid sequence into the cell. Such methods for introduction include but are not limited to protoplast fusion, transfection, transformation, electroporation, conjugation, and transduction (*See e.g.*, Ferrari *et al.*, "Genetics," in Hardwood *et al.* (eds.), <u>Bacillus</u>, Plenum Publishing Corp., pp. 57-72 [1989]).

Transformation refers to the genetic alteration of a cell which results from the uptake, optional genomic incorporation, and expression of genetic material (*e.g.*, DNA).

As used herein, a nucleic acid is "operably linked" with another nucleic acid sequence when it is placed into a functional relationship with another nucleic acid sequence. For example, a promoter or enhancer is operably linked to a nucleotide coding sequence if the promoter affects the transcription of the coding sequence. A ribosome binding site may be operably linked to a coding sequence if it is positioned so as to facilitate translation of the coding sequence. Typically, "operably linked" DNA sequences are contiguous. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, synthetic oligonucleotide adaptors or linkers may be used in accordance with conventional practice.

As used herein the term "gene" refers to a polynucleotide (*e.g.*, a DNA segment), that encodes a polypeptide and includes regions preceding and following the coding regions as well as intervening sequences (introns) between individual coding segments (exons).

As used herein, "recombinant" when used with reference to a cell typically indicates that the cell has been modified by the introduction of a foreign nucleic acid sequence or that the cell is derived from a cell so modified. For example, a recombinant cell may comprise a gene not found in identical form within the native (non-recombinant) form of the cell, or a recombinant cell may comprise a native gene (found in the native form of the cell) but which has been modified and re-introduced into the cell. A recombinant cell may comprise a nucleic acid endogenous to the cell that has been modified without removing the nucleic acid from the cell; such modifications include those obtained by gene replacement, site-specific mutation, and related techniques known to those of ordinary skill in the art. Recombinant DNA technology includes techniques for the production of recombinant DNA *in vitro,* and transfer of the recombinant DNA into cells where it may be expressed or propagated, thereby producing a recombinant polypeptide. "Recombination," "recombining," and "recombined" of polynucleotides or nucleic acids refer generally to the assembly or combining of two or more nucleic acid or polynucleotide strands or fragments to generate a new polynucleotide or nucleic acid. The recombinant polynucleotide or nucleic acid is sometimes referred to as a chimera. A nucleic acid or polypeptide is "recombinant" when it is artificial or engineered.

A nucleic acid or polynucleotide is said to "encode" a polypeptide if, in its native state or when manipulated by methods known to those of skill in the art, it can be transcribed and/or translated to produce the polypeptide or a fragment thereof. The anti-sense strand of such a nucleic acid is also said to encode the sequence.

"Host strain" or "host cell" refers to a suitable host for an expression vector comprising a DNA sequence of interest.

A "protein" or "polypeptide" comprises a polymeric sequence of amino acid residues. The terms "protein" and "polypeptide" are used interchangeably herein. The single and 3-letter code for amino acids as defined in conformity with the IUPAC-IUB Joint Commission on Biochemical Nomenclature (JCBN) is used through out this disclosure. The single letter X refers to any of the twenty amino acids. It is also understood that a polypeptide may be coded for by more than one nucleotide sequence due to the degeneracy of the genetic code. Mutations can be named by the one letter code for the parent amino acid, followed by a position number and then the one letter code for the variant amino acid. For example, mutating glycine (G) at position 87 to serine (S) is represented as "G087S" or "G87S". Mutations can also be named by using the three letter code for an amino acid followed by its position in the polypeptide chain as counted from the N-terminus; for example, Ala10 for alanine at position 10. Multiple mutations are indicated by inserting a "-," "+," "/," or ";" between the mutations. Mutations at positions 87

and 90 are represented as either "G087S-A090Y" or "G87S-A90Y" or "G87S + A90Y" or "G087S + A090Y". For insertions, one or more inserted amino acids can be listed after a position. For example, "G087GS" describes a serine inserted after the glycine at position 87; as a second example, "G087GSA" describes a serine and alanine inserted after the glycine at position 87. Insertions can be done in combination with substitutions; thus, "G087RS" describes a substitution at position 87 from glycine to arginine, followed by an inserted serine residue. For deletions, either a "Δ" or "del" is used following the position number. Thus, for example, "G087del" describes deletion of the glycine at position 87. When describing modifications, a position followed by amino acids listed in parentheses indicates a list of substitutions at that position by any of the listed amino acids. For example, 6(L,I) means position 6 can be substituted with a leucine or isoleucine.

A "prosequence" or "propetide sequence" refers to an amino acid sequence between the signal peptide sequence and mature protease sequence that is necessary for the proper folding and secretion of the protease; they are sometimes referred to as intramolecular chaperones. Cleavage of the prosequence or propeptide sequence results in a mature active protease. Bacterial metalloproteases are often expressed as pro-enzymes.

The term "signal sequence" or "signal peptide" refers to a sequence of amino acid residues that may participate in the secretion or direct transport of the mature or precursor form of a protein. The signal sequence is typically located N-terminal to the precursor or mature protein sequence. The signal sequence may be endogenous or exogenous. A signal sequence is normally absent from the mature protein. A signal sequence is typically cleaved from the protein by a signal peptidase after the protein is transported.

The term "mature" form of a protein, polypeptide, or peptide refers to the functional form of the protein, polypeptide, or peptide without the signal peptide sequence and propeptide sequence.

The term "precursor" form of a protein or peptide refers to a mature form of the protein having a prosequence operably linked to the amino or carbonyl terminus of the protein. The precursor may also have a "signal" sequence operably linked to the amino terminus of the prosequence. The precursor may also have additional polypeptides that are involved in post-translational activity (*e.g.*, polypeptides cleaved therefrom to leave the mature form of a protein or peptide).

The term "wild-type" in reference to an amino acid sequence or nucleic acid sequence indicates that the amino acid sequence or nucleic acid sequence is native or naturally occurring

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sequence. As used herein, the term "naturally-occurring" refers to anything (*e.g.*, proteins, amino acids, or nucleic acid sequences) that are found in nature.

As used herein, the term "non-naturally occurring" refers to anything that is not found in nature (*e.g.,* recombinant nucleic acids and protein sequences produced in the laboratory), as modification of the wild-type sequence.

As used herein with regard to amino acid residue positions, "corresponding to" or "corresponds to" or "corresponds" refers to an amino acid residue at the enumerated position in a protein or peptide, or an amino acid residue that is analogous, homologous, or equivalent to an enumerated residue in a protein or peptide. As used herein, "corresponding region" generally refers to an analogous position in a related proteins or a reference protein.

The terms "derived from" and "obtained from" refer to not only a protein produced or producible by a strain of the organism in question, but also a protein encoded by a DNA sequence isolated from such strain and produced in a host organism containing such DNA sequence. Additionally, the term refers to a protein which is encoded by a DNA sequence of synthetic and/or cDNA origin and which has the identifying characteristics of the protein in question. To exemplify, "proteases derived from *Bacillus*" refers to those enzymes having proteolytic activity which are naturally produced by *Bacillus*, as well as to metalloproteases like those produced by *Bacillus* sources but which through the use of genetic engineering techniques are produced by non-*Bacillus* organisms transformed with a nucleic acid encoding the serine proteases.

The term "identical" in the context of two nucleic acids or polypeptide sequences refers to the residues in the two sequences that are the same when aligned for maximum correspondence, as measured using one of the following sequence comparison or analysis algorithms.

As used herein, "homologous genes" refers to a pair of genes from different, but usually related species, which correspond to each other and which are identical or very similar to each other. The term encompasses genes that are separated by speciation (i.e., the development of new species) (*e.g.*, orthologous genes), as well as genes that have been separated by genetic duplication (*e.g.*, paralogous genes). As used herein, "homologous proteins" refers to proteins from different, but usually related species, which are very similar to each other.

As used herein, "% identity or percent identity" refers to sequence identity, at the gene or protein level. The output for these calculations are highly dependent on the algorithm used and the parameters selected such as length of compared sequences. Percent identity may be determined using standard techniques known in the art (*See e.g.*, Smith and Waterman, Adv.

Appl. Math. 2:482 [1981]; Needleman and Wunsch, J. Mol. Biol. 48:443 [1970]; Pearson and Lipman, Proc. Natl. Acad. Sci. USA 85:2444 [1988]; software programs such as GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package (Genetics Computer Group, Madison, WI); and Devereux *et al.*, Nucl. Acid Res. 12:387-395 [1984]). One example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pair-wise alignments. It can also plot a tree showing the clustering relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng and Doolittle (*See*, Feng and Doolittle, J. Mol. Evol. 35:351-360 [1987]). The method is similar to that described by Higgins and Sharp (*See*, Higgins and Sharp, CABIOS 5:151-153 [1989]). Useful PILEUP parameters include a default gap weight of 3.00, a default gap length weight of 0.10, and weighted end gaps. Other useful algorithm is the BLAST algorithms described by Altschul *et al.*, (*See*, Altschul *et al.*, J. Mol. Biol. 215:403-410 [1990]; and Karlin and Altschul, Proc. Natl. Acad. Sci. USA 90:5873-5787 [1993]). The BLAST program uses several search parameters, most of which are set to the default values.

The NCBI BLAST algorithm finds the most relevant sequences in terms of biological similarity but is not recommended for query sequences of less than 20 residues (Altschul, SF et al. (1997) Nucleic Acids Res. 25:3389-3402 and Schaffer, AA et al. (2001) Nucleic Acids Res. 29:2994-3005). Example default BLAST parameters for a nucleic acid sequence searches are:

- Neighboring words threshold : 11
- E-value cutoff : 10
- Scoring Matrix : NUC.3.1 (match = 1, mismatch = -3)
- Gap Opening : 5
- Gap Extension : 2

and the following parameters for amino acid sequence searches:

- Word size : 3
- E-value cutoff : 10
- Scoring Matrix : BLOSUM62
- Gap Opening : 11
- Gap extension : 1

A percent (%) amino acid sequence identity value is determined by the number of matching identical residues divided by the total number of residues of the "reference" sequence including any gaps created by the program for optimal/maximum alignment. If a sequence is

90% identical to SEQ ID NO: A, SEQ ID NO: A is is the "reference" sequence. BLAST

algorithms refer the "reference" sequence as "query" sequence.

The CLUSTAL W algorithm is another example of a sequence alignment algorithm. *See*

Thompson *et al.* (1994) *Nucleic Acids Res.* 22:4673-4680. Default parameters for the

CLUSTAL W algorithm are:

Gap opening penalty:	10.0
Gap extension penalty:	0.05
Protein weight matrix:	BLOSUM series
DNA weight matrix:	IUB
Delay divergent sequences %:	40
Gap separation distance:	8
DNA transitions weight:	0.50
List hydrophilic residues:	GPSNDQEKR
Use negative matrix:	OFF
Toggle Residue specific penalties:	ON
Toggle hydrophilic penalties:	ON
Toggle end gap separation penalty	OFF.

In CLUSTAL algorithms, deletions occurring at either terminus are included. For

example, a variant with five amino acid deletion at either terminus (or within the polypeptide) of

a polypeptide of 500 amino acids would have a percent sequence identity of 99% (495/500

identical residues × 100) relative to the "reference" polypeptide. Such a variant would be

encompassed by a variant having "at least 99% sequence identity" to the polypeptide.

A polypeptide of interest may be said to be "substantially identical" to a reference

polypeptide if the polypeptide of interest comprises an amino acid sequence having at least

about 60%, least about 65%, least about 70%, at least about 75%, at least about 80%, at least

about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at

least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%,

at least about 99%, or at least about 99.5% sequence identity to the amino acid sequence of the

reference polypeptide. The percent identity between two such polypeptides can be determined

manually by inspection of the two optimally aligned polypeptide sequences or by using software

programs or algorithms (*e.g.,* BLAST, ALIGN, CLUSTAL) using standard parameters. One

indication that two polypeptides are substantially identical is that the first polypeptide is

immunologically cross-reactive with the second polypeptide. Typically, polypeptides that differ

by conservative amino acid substitutions are immunologically cross-reactive. Thus, a

polypeptide is substantially identical to a second polypeptide, for example, where the two peptides differ only by a conservative amino acid substitution or one or more conservative amino acid substitutions.

A nucleic acid of interest may be said to be "substantially identical" to a reference nucleic acid if the nucleic acid of interest comprises a nucleotide sequence having least about 60%, least about 65%, at least about 70%, at least about 75%, at least about 80%, at least about 85%, at least about 90%, at least about 91%, at least about 92%, at least about 93%, at least about 94%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, at least about 99%, or at least about 99.5% sequence identity to the nucleotide sequence of the reference nucleic acid. The percent identity between two such nucleic acids can be determined manually by inspection of the two optimally aligned nucleic acid sequences or by using software programs or algorithms (*e.g.*, BLAST, ALIGN, CLUSTAL) using standard parameters. One indication that two nucleic acid sequences are substantially identical is that the two nucleic acid molecules hybridize to each other under stringent conditions (*e.g.*, within a range of medium to high stringency).

A nucleic acid or polynucleotide is "isolated" when it is at least partially or completely separated from other components, including but not limited to for example, other proteins, nucleic acids, cells, etc. Similarly, a polypeptide, protein or peptide is "isolated" when it is at least partially or completely separated from other components, including but not limited to for example, other proteins, nucleic acids, cells, etc. On a molar basis, an isolated species is more abundant than are other species in a composition. For example, an isolated species may comprise at least about 60%, about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, or about 100% (on a molar basis) of all macromolecular species present. Preferably, the species of interest is purified to essential homogeneity (*i.e.*, contaminant species cannot be detected in the composition by conventional detection methods). Purity and homogeneity can be determined using a number of techniques well known in the art, such as agarose or polyacrylamide gel electrophoresis of a nucleic acid or a protein sample, respectively, followed by visualization upon staining. If desired, a high-resolution technique, such as high performance liquid chromatography (HPLC) or a similar means can be utilized for purification of the material.

"Hybridization" refers to the process by which one strand of nucleic acid forms a duplex with, *i.e.*, base pairs with, a complementary strand. A nucleic acid sequence is considered to be "selectively hybridizable" to a reference nucleic acid sequence if the two sequences specifically

hybridize to one another under moderate to high stringency hybridization and wash conditions. Hybridization conditions are based on the melting temperature (Tm) of the nucleic acid binding complex or probe. For example, "maximum stringency" typically occurs at about Tm-5°C (5° below the Tm of the probe); "high stringency" at about 5-10°C below the Tm; "intermediate stringency" at about 10-20°C below the Tm of the probe; and "low stringency" at about 20-25°C below the Tm. Functionally, maximum stringency conditions can be used to identify sequences having strict identity or near-strict identity with the hybridization probe; while intermediate or low stringency hybridization can be used to identify or detect polynucleotide sequence homologs.

Moderate and high stringency hybridization conditions are well known in the art. Stringent hybridization conditions are exemplified by hybridization under the following conditions: 65°C and 0.1X SSC (where 1X SSC = 0.15 M NaCl, 0.015 M Na_3 citrate, pH 7.0). Hybridized, duplex nucleic acids are characterized by a melting temperature (T_m), where one half of the hybridized nucleic acids are unpaired with the complementary strand. Mismatched nucleic acids within the duplex lower the T_m. Very stringent hybridization conditions involve 68°C and 0.1X SSC. A nucleic acid encoding a variant metalloprotease can have a T_m reduced by 1°C – 3°C or more compared to a duplex formed between the nucleic acid of SEQ ID NO: 4 and its identical complement.

Another example of high stringency conditions includes hybridization at about 42°C in 50% formamide, 5X SSC, 5X Denhardt's solution, 0.5% SDS and 100 µg/ml denatured carrier DNA followed by washing two times in 2X SSC and 0.5% SDS at room temperature and two additional times in 0.1X SSC and 0.5% SDS at 42°C. An example of moderate stringent conditions include an overnight incubation at 37°C in a solution comprising 20% formamide, 5 x SSC (150mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1x SSC at about 37 - 50°C. Those of skill in the art know how to adjust the temperature, ionic strength, etc. to accommodate factors such as probe length and the like.

The term "purified" as applied to nucleic acids or polypeptides generally denotes a nucleic acid or polypeptide that is essentially free from other components as determined by analytical techniques well known in the art (*e.g.*, a purified polypeptide or polynucleotide forms a discrete band in an electrophoretic gel, chromatographic eluate, and/or a media subjected to density gradient centrifugation). For example, a nucleic acid or polypeptide that gives rise to essentially one band in an electrophoretic gel is "purified." A purified nucleic acid or

polypeptide is at least about 50% pure, usually at least about 60%, about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98%, about 99%, about 99.5%, about 99.6%, about 99.7%, about 99.8% or more pure (*e.g.*, percent by weight on a molar basis). In a related sense, the invention provides methods of enriching compositions for one or more molecules of the invention, such as one or more polypeptides or polynucleotides of the invention. A composition is enriched for a molecule when there is a substantial increase in the concentration of the molecule after application of a purification or enrichment technique. A substantially pure polypeptide or polynucleotide of the invention (*e.g.*, substantially pure metalloprotease polypeptide or polynucleotide encoding a metalloprotease polypeptide of the invention, respectively) will typically comprise at least about 55%, about 60%, about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98, about 99%, about 99.5% or more by weight (on a molar basis) of all macromolecular species in a particular composition.

The term "enriched" refers to a compound, polypeptide, cell, nucleic acid, amino acid, or other specified material or component that is present in a composition at a relative or absolute concentration that is higher than a starting composition.

In a related sense, the invention provides methods of enriching compositions for one or more molecules of the invention, such as one or more polypeptides of the invention (*e.g.*, one or more metalloprotease polypeptides of the invention) or one or more nucleic acids of the invention (*e.g.*, one or more nucleic acids encoding one or more metalloprotease polypeptides of the invention). A composition is enriched for a molecule when there is a substantial increase in the concentration of the molecule after application of a purification or enrichment technique. A substantially pure polypeptide or polynucleotide will typically comprise at least about 55%, about 60%, about 65%, about 70%, about 75%, about 80%, about 85%, about 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about 97%, about 98, about 99%, about 99.5% or more by weight (on a molar basis) of all macromolecular species in a particular composition.

As used herein, the term "functional assay" refers to an assay that provides an indication of a protein's activity. In some embodiments, the term refers to assay systems in which a protein is analyzed for its ability to function in its usual capacity. For example, in the case of a protease, a functional assay involves determining the effectiveness of the protease to hydrolyze a proteinaceous substrate.

The terms "modified nucleic acid sequence" and "modified gene" are used interchangeably herein to refer to a nucleic acid sequence that includes a deletion, insertion or interruption of naturally occurring (*i.e.*, wild-type) nucleic acid sequence. In some embodiments, the expression product of the modified nucleic acid sequence is a truncated protein (*e.g.*, if the modification is a deletion or interruption of the sequence). In some embodiments, the truncated protein retains biological activity. In alternative embodiments, the expression product of the modified nucleic acid sequence is an elongated protein (*e.g.*, modifications comprising an insertion into the nucleic acid sequence). In some embodiments, a nucleotide insertion in the nucleic acid sequence leads to a truncated protein (*e.g.*, when the insertion results in the formation of a stop codon). Thus, an insertion may result in either a truncated protein or an elongated protein as an expression product.

A "mutant" nucleic acid sequence typically refers to a nucleic acid sequence that has an alteration in at least one codon occurring in a host cell's wild-type sequence such that the expression product of the mutant nucleic acid sequence is a protein with an altered amino acid sequence relative to the wild-type protein. The expression product may have an altered functional capacity (*e.g.*, enhanced enzymatic activity).

As used herein, the phrase "alteration in substrate specificity" refers to changes in the substrate specificity of an enzyme. In some embodiments, a change in substrate specificity is defined as a change in k_{cat} and/or K_m for a particular substrate, resulting from mutations of the enzyme or alteration of reaction conditions. The substrate specificity of an enzyme is determined by comparing the catalytic efficiencies it exhibits with different substrates. These determinations find particular use in assessing the efficiency of mutant enzymes, as it is generally desired to produce variant enzymes that exhibit greater ratios of k_{cat}/K_m for substrates of interest. However, it is not intended that the present invention be limited to any particular substrate composition or substrate specificity.

As used herein, "surface property" is used in reference to electrostatic charge, as well as properties such as the hydrophobicity and hydrophilicity exhibited by the surface of a protein.

As used herein, the term "net charge" is defined as the sum of all charges present in a molecule. "Net charge changes" are made to a parent protein molecule to provide a variant that has a net charge that differs from that of the parent molecule (*i.e.*, the variant has a net charge that is not the same as that of the parent molecule). For example, substitution of a neutral amino acid with a negatively charged amino acid or a positively charged amino acid with a neutral amino acid results in net charge of -1 with respect to the parent molecule. Substitution of a positively charged amino acid with a negatively charged amino acid results in a net charge of -2

with respect to the parent. Substitution of a neutral amino acid with a positively charged amino acid or a negatively charged amino acid with a neutral amino acid results in net charge of +1 with respect to the parent. Substitution of a negatively charged amino acid with a positively charged amino acid results in a net charge of +2 with respect to the parent. The net charge of a parent protein can also be altered by deletion and/or insertion of charged amino acids. A net change change applies to changes in charge of a variant versus a parent when measured at the same pH conditions.

The terms "thermally stable" and "thermostable" and "thermostability" refer to proteases that retain a specified amount of enzymatic activity after exposure to identified temperatures over a given period of time under conditions prevailing during the proteolytic, hydrolyzing, cleaning or other process of the invention, while being exposed to altered temperatures. "Altered temperatures" encompass increased or decreased temperatures. In some embodiments, the proteases retain at least about 50%, about 60%, about 70%, about 75%, about 80%, about 85%, about 90%, about 92%, about 95%, about 96%, about 97%, about 98%, or about 99% proteolytic activity after exposure to altered temperatures over a given time period, for example, at least about 60 minutes, about 120 minutes, about 180 minutes, about 240 minutes, about 300 minutes, etc.

The term "enhanced stability" in the context of an oxidation, chelator, thermal, chemical, autolytic and/or pH stable protease refers to a higher retained proteolytic activity over time as compared to other proteases (*e.g.*, thermolysin proteases) and/or wild-type enzymes.

The term "diminished stability" in the context of an oxidation, chelator, thermal and/or pH stable protease refers to a lower retained proteolytic activity over time as compared to other proteases (*e.g.*, thermolysin proteases) and/or wild-type enzymes.

The term "cleaning activity" refers to a cleaning performance achieved by a metalloprotease polypeptide or reference protease under conditions prevailing during the proteolytic, hydrolyzing, cleaning, or other process of the invention. In some embodiments, cleaning performance of a metalloprotease polypeptide or reference protease may be determined by using various assays for cleaning one or more various enzyme sensitive stains on an item or surface (*e.g.*, a stain resulting from food, grass, blood, ink, milk, oil, and/or egg protein). Cleaning performance of a variant or reference protease can be determined by subjecting the stain on the item or surface to standard wash condition(s) and assessing the degree to which the stain is removed by using various chromatographic, spectrophotometric, or other quantitative methodologies. Exemplary cleaning assays and methods are known in the art and include, but are not limited to those described in WO 99/34011 and U.S. Pat. 6,605,458, both of which are

herein incorporated by reference, as well as those cleaning assays and methods included in the Examples provided below.

The term "cleaning effective amount" of a metalloprotease polypeptide or reference protease refers to the amount of protease that achieves a desired level of enzymatic activity in a specific cleaning composition. Such effective amounts are readily ascertained by one of ordinary skill in the art and are based on many factors, such as the particular protease used, the cleaning application, the specific composition of the cleaning composition, and whether a liquid or dry (*e.g.*, granular, tablet, bar) composition is required, etc.

The term "enhanced performance" in the context of cleaning activity refers to an increased or greater cleaning activity by an enzyme with respect to a parent or reference protein as measured on certain enzyme sensitive stains such as egg, milk, grass, ink, oil, and/or blood, as determined by usual evaluation after a standard wash cycle and/or multiple wash cycles.

The term "diminished performance" in the context of cleaning activity refers to a decreased or lesser cleaning activity by an enzyme on certain enzyme sensitive stains such as egg, milk, grass or blood, as determined by usual evaluation after a standard wash cycle and/or multiple wash cycles.

Cleaning compositions and cleaning formulations include any composition that is suited for cleaning, bleaching, disinfecting, and/or sterilizing any object, item, and/or surface. Such compositions and formulations include, but are not limited to for example, liquid and/or solid compositions, including cleaning or detergent compositions (*e.g.*, liquid, tablet, gel, bar, granule, unit dose and/or solid laundry cleaning or detergent compositions and fine fabric detergent compositions; hard surface cleaning compositions and formulations, such as for glass, wood, ceramic and metal counter tops and windows; carpet cleaners; oven cleaners; fabric fresheners; fabric softeners; and textile, laundry booster cleaning or detergent compositions, laundry additive cleaning compositions, and laundry pre-spotter cleaning compositions; dishwashing compositions, including hand or manual dishwash compositions (*e.g.*, "hand" or "manual" dishwashing detergents) and automatic dishwashing compositions (*e.g.,* "automatic dishwashing detergents").

As used herein, the term "bleaching" refers to the treatment of a material (*e.g.*, fabric, laundry, pulp, etc.) or surface for a sufficient length of time and/or under appropriate pH and/or temperature conditions to effect a brightening (*i.e.*, whitening) and/or cleaning of the material. Examples of chemicals suitable for bleaching include, but are not limited to, for example, ClO_2, H_2O_2, peracids, NO_2, etc.

As used herein, "wash performance" of a protease (*e.g.*, a metalloprotease polypeptide of the invention) refers to the contribution of a metalloprotease polypeptide to washing that provides additional cleaning performance to the detergent as compared to the detergent without the addition of the metalloprotease polypeptide to the composition. Wash performance is compared under relevant washing conditions. In some test systems, other relevant factors, such as detergent composition, sud concentration, water hardness, washing mechanics, time, pH, and/or temperature, can be controlled in such a way that condition(s) typical for household application in a certain market segment (*e.g.*, hand or manual dishwashing, automatic dishwashing, dishware cleaning, tableware cleaning, fabric cleaning, etc.) are imitated.

The term "relevant washing conditions" is used herein to indicate the conditions, particularly washing temperature, time, washing mechanics, sud concentration, type of detergent and water hardness, actually used in households in a hand dishwashing, automatic dishwashing, or laundry detergent market segment.

The term "improved wash performance" is used to indicate that a better end result is obtained in stain removal under relevant washing conditions, or that less metalloprotease polypeptide, on weight basis, is needed to obtain the same end result relative to the corresponding wild-type or starting parent protease.

As used herein, the term "disinfecting" refers to the removal of contaminants from the surfaces, as well as the inhibition or killing of microbes on the surfaces of items. It is not intended that the present invention be limited to any particular surface, item, or contaminant(s) or microbes to be removed.

The "compact" form of the cleaning compositions herein is best reflected by density and, in terms of composition, by the amount of inorganic filler salt. Inorganic filler salts are conventional ingredients of detergent compositions in powder form. In conventional detergent compositions, the filler salts are present in substantial amounts, typically about 17 to about 35% by weight of the total composition. In contrast, in compact compositions, the filler salt is present in amounts not exceeding about 15% of the total composition. In some embodiments, the filler salt is present in amounts that do not exceed about 10%, or more preferably, about 5%, by weight of the composition. In some embodiments, the inorganic filler salts are selected from the alkali and alkaline-earth-metal salts of sulfates and chlorides. In some embodiments, the filler salt is sodium sulfate.

As used herein in connection with a numerical value, the term "about" refers to a range of +/- 0.5 of the numerical value, unless the term is otherwise specifically defined in context.

For instance, the phrase a "pH value of about 6" refers to pH values of from 5.5 to 6.5, unless the pH value is specifically defined otherwise.

Oligonucleotide synthesis and purification steps are typically performed according to specifications. Techniques and procedures are generally performed according to conventional methods well known in the art and various general references that are provided throughout this document. Procedures therein are believed to be well known to those of ordinary skill in the art and are provided for the convenience of the reader.

Variant Metalloprotease Polypeptides of the present invention

In some embodiments, the present invention provides novel variant metalloprotease enzyme polypeptides having a modification in a calcium binding region. In some embodiments, the variant is a variant of a parent or reference sequence. The parent or reference sequence can be, for example, any M4 metalloprotease, or a Bacillus derived metalloprotease, such as Bacillus thermoproteolyticus, Bacillus cereus, or Bacillus subtilis (for example, the sequences of SEQ ID NOs: 13-15), or a Paenibacillus derived metalloprotease, such as the sequences of SEQ ID NOs: 1-12.

A residue (amino acid) of a metalloprotease is equivalent to a residue of Thermolysin metalloprotease if it is either homologous (i.e., corresponding in position in either primary or tertiary structure) or analogous to a specific residue or portion of that residue in Thermolysin metalloprotease from *Bacillus thermoproteolyticus* (i.e., having the same or similar functional capacity to react or interact chemically). In order to establish homology to primary structure, the amino acid sequence of a metalloprotease is directly compared to the Thermolysin primary sequence and particularly to a set of residues known to be invariant in diverse M4 metalloproteinases as shown in FIG. 6.1).

After aligning the conserved residues, allowing for necessary insertions and deletions in order to maintain alignment (i.e. avoiding the elimination of conserved residues through arbitrary deletions and insertions) the residues equivalent to particular amino acids in the primary sequence of thermolysin are defined. Suitable methods to produce such modifications include those disclosed herein and an example is shown in Example 6. These conserved residues thus may be used to define the corresponding equivalent amino acid residues of Thermolysin and in other M4 metalloproteinases such as the metalloproteinases from Paenibacillus organisms such as PehPro1. These two particular sequences (Thermolysin (1_KEI) and PehPro1) are aligned in FIG. 6.1 to produce the maximum homology of conserved residues.

As can be seen, there are a number of insertions and deletions in the PehPro1 sequence as compared to Thermolysin.

The position of an amino acid residue in a given amino acid sequence is typically numbered herein using the numbering of the position of the corresponding amino acid residue of the *Bacillus thermoproteolyticus* metalloprotease *Thermolysin* amino acid sequence shown in SEQ ID NO: 13. The *Bacillus thermoproteolyticus* metalloprotease *Thermolysin* amino acid sequence of SEQ ID NO: 13 thus serves as a reference parent sequence. A given amino acid sequence, such as a metalloprotease enzyme amino acid sequence and variants thereof described herein, can be aligned with the *Thermolysin* sequence (SEQ ID NO: 13) using an alignment algorithm as described herein on the primary and/or tertiary structures, and an amino acid residue in the given amino acid sequence that aligns (preferably optimally aligns) with an amino acid residue in the *Thermolysin* sequence can be conveniently numbered by reference to the corresponding amino acid residue in the metalloprotease *Thermolysin* sequence.

The equivalent amino acid of Asp57 in Thermolysin, in PehPro is the particular Serine shown at that aligned position. In FIG. 6.1, the equivalent amino acid at position 57 in PpoPro1 is again Aspartic acid. Thus, these particular residues in PehPro1, and thermolysin may be substituted by a different amino acid to produce a mutant metalloprotease, since they are equivalent in primary structure to Asp 57 in thermolysin. Equivalent amino acids of course are not limited to those for Asp57 but extend to any residue which is equivalent to a residue in Thermolysin, and this is intended as an example of equivalent residues.

Equivalent residues homologous at the level of tertiary structure for a metalloprotease whose tertiary structure has been determined by x-ray crystallography, are defined as those for which the atomic coordinates of 2 or more of the main chain atoms of a particular amino acid residue of the M4 metalloproteinase and Thermolysin (N on N. CA on CA, C on C, and 0 on 0) are within 0.13 nm and preferably 0.1 nm after superposition. Superposition can be accomplished by superimposing the common secondary structure. This can be accomplished using any one of several known algorithms in the art, such as The PyMOL Molecular Graphics System, Version 1.5.0.4 Schrodinger, LLC or *Coot* [Emsley et al. (2010) Acta Crystallogr D Biol Crystallogr. 66(Pt4): 486]. Superposition is achieved after the best model has been oriented and positioned to give the maximum overlap of atomic coordinates of non-hydrogen protein atoms of the metalloprotease in question to the Thermolysin metalloprotease from Bacillus thermoproteolyticus. The best model is the crystallographic model determined at the highest resolution, and if more than one, the one giving the lowest R factor.

Equivalent residues which are functionally analogous to a specific residue of Thermolysin are defined as those amino acids of the metalloproteases which may adopt a conformation such that they either alter, modify or contribute to protein structure, substrate binding or catalysis in a manner defined and attributed to a specific residue of thermolysin as described herein. Further, they are those residues of the metalloproteinase (for which a tertiary structure has been obtained by x-ray crystallography), which occupy an analogous position to the extent that although the main chain atoms of the given residue may not satisfy the criteria of equivalence on the basis of occupying a homologous position, the atomic coordinates of at least two of the side chain atoms of the residue lie with 0.13 nm of the corresponding side chain atoms of Thermolysin. The three dimensional structures would be aligned as outlined above.

Calcium binding region

The structure of the M4 class metalloprotease thermolysin has been found to have four calcium-binding regions. The structural information from Thermolysin and other metalloproteases can be used to determine modifications that can be made to M4 class metalloproteases in order to remove calcium binding.

Based largely on analysis of the three-dimensional structure of thermolysin, it has been discovered that M4 class metalloproteases can have as many as four calcium binding sites. In thermolysin, there is a double cation binding site, herein referred to as Ca1-2, which has a calcium binding region including residues 136, 138 and 177-190 using the numbering of thermolysin from Bacillus thermoproteolyticus found in SEQ ID NO:13. There is also a calcium binding site, herein referred to as Ca3, which has a calcium binding region including residues 55-66, and a fourth binding site referred to as Ca4, which has a calcium binding region including residues 193-200.

In some embodiments, it is desirable to be able to decrease the Ca^{2+} dependency of a metalloprotease. As such, in some embodiments, the invention is a variant of a parent metalloprotease, such as a M4 class metalloprotease or a variant of any one of SEQ ID NOs: 1-15, which exhibits protease activity and which has a decreased Ca^{2+} dependency as compared to the parent metalloprotease. The decreased Ca^{2+} dependency has the functional result that the variant exhibits proteolytic activity in the presence of a lower concentration of calcium ion in the extraneous medium than is necessary for the parent enzyme and, for example, therefore is less sensitive than the parent to calcium ion-depleting conditions such as those obtained in media containing calcium-complexing agents (such as certain detergent builders). In some

embodiments, the variant retains at least 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, 100% or even has greater activity compared to the parent metalloprotease. This can be measured in a proteolytic assay, such as those described in Example 1.

Calcium Binding

A stabilization strategy based around decreased calcium binding can improve enzyme stability in environments with decreased availability of free calcium ions. One of the major industrial uses of subtilisins is in environments containing high concentrations of metal chelators. Additionally, because these calcium binding regions are found in various M4 metalloproteases, it is expected that equivalent mutations for other M4 metalloproteases will likewise eliminate calcium binding and provide for enzymatically active variants. These calcium binding regions can also be found in various metalloproteases that are not categorized as M4 metalloproteases, but share the same properties as an M4 metalloprotease, including the calcium binding regions.

In some embodiments, the invention is a metalloprotease polypeptide comprising a calcium binding region. In some embodiments, the above polypeptide comprises a modification in at least one amino acid residue in one of the calcium binding regions, Ca1-2, Ca3 and Ca4, (including residues 55-66, 136, 138, 177-190, and 193-200) of the polypeptide, wherein the amino acid positions of the polypeptide are numbered by correspondence with the amino acid sequence of *Bacillus thermoproteolyticus* metalloprotease set forth in SEQ ID NO: 13.

In any of the above embodiments and in new embodiments, the variant comprises a modification in at least one amino acid residue in a calcium binding region Ca1-2 of residues 177-190 of a parent M4 metalloprotease. In any of the above embodiments and in new embodiments, the polypeptide at position 184 is a lysine, threonine, alanine, glutamic acid or aspartic acid. In any of the above embodiments and in new embodiments, the polypeptide at position 185 is a residue other than aspartic acid. In some embodiments, the polypeptide at position 185 is a non-negatively charged residue; in other embodiments, the polypeptide at position 185 is a neutrally charged residue; and in yet other embodiments, the polypeptide at position 185 is an asparagine or serine. In any of the above embodiments and in new embodiments, the polypeptide at position 187 is a non-negatively charged residue. In some embodiments, the polypeptide at position 187 is a neutrally charged residue; and in other embodiments, the polypeptide at position 187 is a leucine or methionine; and in yet other embodiments, the polypeptide at position 187 is aspartic acid. In any of the above embodiments and in new embodiments, the polypeptide at position 188 is a leucine, valine, or methionine. In any of the above embodiments and in new embodiments, the polypeptide at position 190 is a

residue other than glutamic acid. In some embodiments, the polypeptide at position 190 is aspartic acid. In sequence alignment of Ca1-2 regions, there are conserved residues glycine at position 173 and tryptophan at position 186 (see Figure 12). In any of the above embodiments and in new embodiments, the polypeptide comprises seven amino acid residues between the glycine residue at position 173 and tryptophan at position 186. In any of the above embodiments and in new embodiments, the polypeptide comprises a deletion of five amino acid residues between the glycine residue at position 173 and tryptophan at position 186. In structural alignment of Ca1-2 regions, there is a known loop structure between residues 176 and 186 (inclusive of amino acids 177 and 185 in the loop). In any of the above embodiments and in new embodiments, the polypeptide comprises a seven amino acid loop sequence between positions 177 to 185 which is replaced by a two amino acid sequence. Without being bound by theory, a polypeptide of the instant invention has improved stability by replacement of the loop structure with a shorter amino acid sequence that can span the region between positions 177 to 185, and in particular, a two amino acid sequence is preferred to span the region between positions 177 to 185. In any of the above embodiments, the two amino acid sequence contains at least one positively charged amino acid, and in some embodiments, the positively charged amino acid is lysine. In any of the above embodiments and in new embodiments, the polypeptide comprises a deletion at amino acid residue positions 179-183. In any of the above embodiments and in new embodiments, the polypeptide at position 177 is a neutrally charged residue or aspartic acid; and in some embodiments, the neutrally charged residue is glutamine. In any of the above embodiments and in new embodiments, the polypeptide at position 178 is a glycine, serine, arginine, alanine, asparagines, and threonine. In any of the above embodiments and in new embodiments, the polypeptide at position 136 is aspartic acid or serine.

In any of the above embodiments and in new embodiments, the invention is a metalloprotease polypeptide having a modification in at least one amino acid residue in a calcium binding region Ca3 of residues 55-66, wherein the amino acid positions of the variant are numbered by correspondence with the amino acid sequence of *Bacillus proteolyticus* metalloprotease set forth in SEQ ID NO: 13. In any of the above embodiments and in new embodiments, the polypeptide at position 55 is a leucine, serine, valine, and methionine. In any of the above embodiments and in new embodiments, the polypeptide at position 56 is a serine, arginine and threonine. In any of the above embodiments and in new embodiments, the polypeptide at position 57 is a serine. In any of the above embodiments and in new embodiments, the polypeptide at position 58 is a serine and threonine. In any of the above embodiments and in new embodiments, the polypeptide at position 59 is a serine, threonine, and

asparagine. In any of the above embodiments and in new embodiments, the polypeptide has a serine at position 57, serine at position 58 and serine or asparagines at position 59. In any of the above embodiments and in new embodiments, the polypeptide at position 60 is a serine. In any of the above embodiments and in new embodiments, the polypeptide at position 61 is an isoleucine, valine, and threonine. In any of the above embodiments and in new embodiments, the polypeptide at position 62 is a tryptophan and phenylalanine. In any of the above embodiments and in new embodiments, the polypeptide at position 63 is a asparagine, glutamic acid, and threonine. In sequence alignment of the Ca3 region, there are conserved residues phenylalanine/tryptophan at position 62 and aspartic acid at position 67 (see Figure 12). In any of the above embodiments and in new embodiments, the polypeptide comprises four amino acid residues between the phenylalanine/tryptophan residue at position 62 and aspartic acid at position 67. In any of the above embodiments and in new embodiments, the polypeptide comprises a deletion of three amino acid residues between the phenylalanine/tryptophan residue at position 62 and aspartic acid at position 67. In structural alignment of the Ca3 region, there is a known loop structure between residues 62 and 67 (inclusive of amino acids 62 and 67 in the loop). In any of the above embodiments and in new embodiments, the polypeptide comprises a four amino acid loop sequence between positions 62 to 67 which is replaced by a one amino acid sequence. Without being bound by theory, a polypeptide of the instant invention has improved stability by replacement of the loop structure with a shorter amino acid sequence that can span the region between positions 62 to 67, and in particular, a one amino acid sequence is preferred to span the region between positions 62 to 67. In any of the above embodiments, the one amino acid sequence is an asparagines, threonine, or glutamic acid. In any of the above embodiments and in new embodiments, the polypeptide comprises a deletion at amino acid residue positions 64-66.

In any of the above embodiments and in new embodiments, the invention is a metalloprotease polypeptide having a modification in at least one amino acid residue in a calcium binding region Ca4 of residues 193-200, wherein the amino acid positions of the variant are numbered by correspondence with the amino acid sequence of *Bacillus proteolyticus* metalloprotease set forth in SEQ ID NO: 13. In any of the above embodiments and in new embodiments, the polypeptide at position 193 is a threonine. In any of the above embodiments and in new embodiments, the polypeptide at position 194 is a isoleucine. In any of the above embodiments and in new embodiments, the polypeptide at position 195 is a serine. In any of the above embodiments and in new embodiments, the polypeptide comprises a deletion at amino acid residue positions 196-198. In any of the above embodiments and in new embodiments, the

polypeptide at position 199 is a glutamine. In any of the above embodiments and in new embodiments, the polypeptide at position 200 is a proline.

In some embodiments of the invention, the calcium binding region Ca1-2 has been modified to bind fewer than two calcium ions. In some embodiments of the invention, the calcium binding region Ca3 has been modified to bind fewer than one calcium ion. In some embodiments of the invention, the calcium binding region Ca4 has been modified to bind fewer than one calcium ion.

In some embodiments, the invention is a variant metalloprotease of a parent metalloprotease polypeptide. In some embodiments, the variant comprises a modification in a calcium binding region of the parent polypeptide. In some embodiments, the variant comprises a modification to any of the amino acids listed above. In some embodiments, the parent polypeptide is an M4 metalloprotease. In some embodiments, the metalloprotease polypeptide of the present invention has at least 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99, or 100% sequence identity to the parent polypeptide. In some embodiments, the metalloprotease polypeptide of the present invention has at least 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99, or 100% sequence identity to any of the sequences found in SEQ ID NOs: 1-15. In some embodiments, the metalloprotease polypeptide of the present invention has at least 60, 65, 70, 75, 80, 85, 90, 95, 96, 97, 98, 99, or 100% sequence identity to SEQ ID NO:13.

In some embodiments, the invention is a variant metalloprotease having immunological cross-reactivity with any of the variant metalloproteases described above. Immunological cross-reactivity can be assayed using an antibody raised against or reactive with at least one epitope of any of the variant metalloproteases listed above. The antibody, which can either be monoclonal or polyclonal, can be produced by methods known in the art. Immunological cross-reactivity can be measured using assays known in the art, such as Western blotting, radial immunodiffusion assay, or enzyme-linked immunosorbant assay (ELISA).

Metalloprotease Polypeptides of the present invention

The present invention provides novel metalloprotease enzyme polypeptides, which may be collectively referred to as "enzymes of the invention" or "polypeptides of the invention." Polypeptides of the invention include isolated, recombinant, substantially pure, or non-naturally occurring polypeptides. In some embodiments, the invention includes variants, as described above, of M4 class metalloproteases. In some embodiments, polypeptides of the invention are useful in cleaning applications and can be incorporated into cleaning compositions that are useful in methods of cleaning an item or a surface in need of cleaning.

In some embodiments, the enzyme of the present invention has 50, 60, 65, 70, 75, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% identity to a M4 class metalloprotease. In some embodiments, the enzyme of the present invention has 50, 60, 65, 70, 75, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% identity to SEQ ID NO: 13. In various embodiments, the enzyme of the present invention has 50, 60, 65, 70, 75, 80, 85, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99 or 100% identity to a metalloprotease enzyme from any of SEQ ID NO:1-15.

In some embodiments, the invention includes an isolated, recombinant, substantially pure, or non-naturally occurring enzyme having protease activity, which polypeptide comprises a polypeptide sequence having at least about 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% sequence identity to a parent enzyme as provided herein.

In some embodiments, the polypeptide of the present invention, is a polypeptide having a specified degree of amino acid sequence homology to the exemplified polypeptides, *e.g.*, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or even at least 99% sequence homology to the amino acid sequence of any of SEQ ID NO: 1-15. Homology can be determined by amino acid sequence alignment, *e.g.*, using a program such as BLAST, ALIGN, or CLUSTAL, as described herein.

Also provided is a polypeptide enzyme of the present invention, having protease activity, said enzyme comprising an amino acid sequence which differs from the amino acid sequence of any of SEQ ID NO:1-15 by no more than 50, no more than 40, no more than 30, no more than 35, no more than 25, no more than 20, no more than 19, no more than 18, no more than 17, no more than 16, no more than 15, no more than 14, no more than 13, no more than 12, no more than 11, no more than 10, no more than 9, no more than 8, no more than 7, no more than 6, no more than 5, no more than 4, no more than 3, no more than 2, or no more than 1 amino acid residue(s), when aligned using any of the previously described alignment methods.

As noted above, the variant enzyme polypeptides of the invention have enzymatic activities (*e.g.*, protease activities) and thus are useful in cleaning applications, including but not limited to, methods for cleaning dishware items, tableware items, fabrics, and items having hard surfaces (*e.g.*, the hard surface of a table, table top, wall, furniture item, floor, ceiling, etc.). Exemplary cleaning compositions comprising one or more variant metalloprotease enzyme polypeptides of the invention are described *infra*. The enzymatic activity (*e.g.*, protease enzyme activity) of an enzyme polypeptide of the invention can be determined readily using procedures well known to those of ordinary skill in the art. The Examples presented *infra* describe methods

for evaluating the enzymatic activity and cleaning performance. The performance of polypeptide enzymes of the invention in removing stains (*e.g.*, a protein stain such as blood/milk/ink or egg yolk), cleaning hard surfaces, or cleaning laundry, dishware or tableware item(s), or cleaning contact lenses can be readily determined using procedures well known in the art and/or by using procedures set forth in the Examples.

The metalloprotease polypeptides of the present invention can have protease activity over a broad range of pH conditions. In some embodiments, the metalloprotease polypeptides have protease activity on azo-casein as a substrate, as demonstrated in Example 3. In some embodiments, the metalloprotease polypeptides have protease activity at a pH of from about 3.0 to about 12.0. In some embodiments, the metalloprotease polypeptides have protease activity at a pH of from about 4.0 to about 11.0.

In some embodiments, the metalloprotease polypeptides of the present invention have protease activity at a temperature range of from about 10°C to about 100°C. In some embodiments, the metalloprotease polypeptides of the present invention have protease activity at a temperature range of from about 20°C to about 90°C.

In some embodiments, the metalloprotease polypeptides of the present invention demonstrate cleaning performance in a cleaning composition. Cleaning compositions often include ingredients harmful to the stability and performance of enzymes, making cleaning compositions a harsh environment for enzymes, e.g. metalloproteases, to retain function. Thus, it is not trivial for an enzyme to be put in a cleaning composition and expect enzymatic function (e.g. metalloprotease activity, such as demonstrated by cleaning performance). In some embodiments, the metalloprotease polypeptides of the present invention demonstrate cleaning performance in automatic dishwashing (ADW) detergent compositions. In some embodiments, the cleaning performance in automatic dishwashing (ADW) detergent compositions includes cleaning of egg yolk stains. In some embodiments, the metalloprotease polypeptides of the present invention demonstrate cleaning performance in laundry detergent compositions. In some embodiments, the cleaning performance in laundry detergent compositions includes cleaning of blood/milk/ink stains. In each of the cleaning compositions, the metalloprotease polypeptides of the present invention demonstrate cleaning performance with or without a bleach component.

A polypeptide of the invention can be subject to various changes, such as one or more amino acid insertions, deletions, and/or substitutions, either conservative or non-conservative, including where such changes do not substantially alter the enzymatic activity of the polypeptide. Similarly, a nucleic acid of the invention can also be subject to various changes,

such as one or more substitutions of one or more nucleotides in one or more codons such that a particular codon encodes the same or a different amino acid, resulting in either a silent variation (*e.g.*, when the encoded amino acid is not altered by the nucleotide mutation) or non-silent variation, one or more deletions of one or more nucleic acids (or codons) in the sequence, one or more additions or insertions of one or more nucleic acids (or codons) in the sequence, and/or cleavage of or one or more truncations of one or more nucleic acids (or codons) in the sequence. Many such changes in the nucleic acid sequence may not substantially alter the enzymatic activity of the resulting encoded polypeptide enzyme compared to the polypeptide enzyme encoded by the original nucleic acid sequence. A nucleic acid sequence of the invention can also be modified to include one or more codons that provide for optimum expression in an expression system (*e.g.*, bacterial expression system), while, if desired, said one or more codons still encode the same amino acid(s).

In some embodiments, the present invention provides a genus of enzyme polypeptides having the desired enzymatic activity (*e.g.*, protease enzyme activity or cleaning performance activity) which comprise sequences having the amino acid substitutions described herein and also which comprise one or more additional amino acid substitutions, such as conservative and non-conservative substitutions, wherein the polypeptide exhibits, maintains, or approximately maintains the desired enzymatic activity (*e.g.*, proteolytic activity, as reflected in the cleaning activity or performance of the polypeptide enzyme of SEQ ID NO: 13). Amino acid substitutions in accordance with the invention may include, but are not limited to, one or more non-conservative substitutions and/or one or more conservative amino acid substitutions. A conservative amino acid residue substitution typically involves exchanging a member within one functional class of amino acid residues for a residue that belongs to the same functional class (conservative amino acid residues are considered functionally homologous or conserved in calculating percent functional homology). A conservative amino acid substitution typically involves the substitution of an amino acid in an amino acid sequence with a functionally similar amino acid. For example, alanine, glycine, serine, and threonine are functionally similar and thus may serve as conservative amino acid substitutions for one another. Aspartic acid and glutamic acid may serve as conservative substitutions for one another. Asparagine and glutamine may serve as conservative substitutions for one another. Arginine, lysine, and histidine may serve as conservative substitutions for one another. Isoleucine, leucine, methionine, and valine may serve as conservative substitutions for one another. Phenylalanine, tyrosine, and tryptophan may serve as conservative substitutions for one another.

Other conservative amino acid substitution groups can be envisioned. For example, amino acids can be grouped by similar function or chemical structure or composition (*e.g.*, acidic, basic, aliphatic, aromatic, sulfur-containing). For instance, an aliphatic grouping may comprise: Glycine (G), Alanine (A), Valine (V), Leucine (L), Isoleucine (I). Other groups containing amino acids that are considered conservative substitutions for one another include: aromatic: Phenylalanine (F), Tyrosine (Y), Tryptophan (W); sulfur-containing: Methionine (M), Cysteine (C); Basic: Arginine (R), Lysine (K), Histidine (H); Acidic: Aspartic acid (D), Glutamic acid (E); non-polar uncharged residues, Cysteine (C), Methionine (M), and Proline (P); hydrophilic uncharged residues: Serine (S), Threonine (T), Asparagine (N), and Glutamine (Q). Additional groupings of amino acids are well-known to those of skill in the art and described in various standard textbooks. Listing of a polypeptide sequence herein, in conjunction with the above substitution groups, provides an express listing of all conservatively substituted polypeptide sequences.

More conservative substitutions exist within the amino acid residue classes described above, which also or alternatively can be suitable. Conservation groups for substitutions that are more conservative include: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, and asparagine-glutamine.

Conservatively substituted variations of a polypeptide sequence of the invention (*e.g.*, variant metalloproteases of the invention) include substitutions of a small percentage, sometimes less than 25%, 20%, 15%, 14%, 13%, 12%, 11%, 10%, 9%, 8%, 7%, or 6% of the amino acids of the polypeptide sequence, or less than 5%, 4%, 3%, 2%, or 1%, or less than 10, 9, 8, 7, 6, 5, 4, 3, 2, or 1 amino acid substitution of the amino acids of the polypeptide sequence, with a conservatively selected amino acid of the same conservative substitution group.

As described elsewhere herein in greater detail and in the Examples provided herein, polypeptides of the invention may have cleaning abilities that may be compared to known proteases, including known metalloproteases.

Nucleic Acids of the Invention

The invention provides isolated, non-naturally occurring, or recombinant nucleic acids which may be collectively referred to as "nucleic acids of the invention" or "polynucleotides of the invention", which encode polypeptides of the invention. Nucleic acids of the invention, including all described below, are useful in recombinant production (e.g., expression) of polypeptides of the invention, typically through expression of a plasmid expression vector comprising a sequence encoding the polypeptide of interest or fragment thereof. As discussed

above, polypeptides include metalloprotease polypeptides having enzymatic activity (e.g., proteolytic activity) which are useful in cleaning applications and cleaning compositions for cleaning an item or a surface (e.g., surface of an item) in need of cleaning.

In some embodiments, the invention provides an isolated, recombinant, substantially pure, or non-naturally occurring nucleic acid comprising a nucleotide sequence encoding any polypeptide (including any fusion protein, etc.) of the invention described above in the section entitled "Polypeptides of the Invention" and elsewhere herein. The invention also provides an isolated, recombinant, substantially pure, or non-naturally-occurring nucleic acid comprising a nucleotide sequence encoding a combination of two or more of any polypeptides of the invention described above and elsewhere herein.

The present invention provides nucleic acids encoding a metalloprotease polypeptide of the present invention, wherein the metalloprotease polypeptide is a mature form having proteolytic activity, wherein the amino acid positions of the thermolysin variant are numbered by correspondence with the amino acid sequence of *Bacillus thermoproteolyticus* metalloprotease polypeptide set forth as SEQ ID NO: 13.

Nucleic acids of the invention can be generated by using any suitable synthesis, manipulation, and/or isolation techniques, or combinations thereof. For example, a polynucleotide of the invention may be produced using standard nucleic acid synthesis techniques, such as solid-phase synthesis techniques that are well-known to those skilled in the art. In such techniques, fragments of up to 50 or more nucleotide bases are typically synthesized, then joined (e.g., by enzymatic or chemical ligation methods) to form essentially any desired continuous nucleic acid sequence. The synthesis of the nucleic acids of the invention can be also facilitated by any suitable method known in the art, including but not limited to chemical synthesis using the classical phosphoramidite method (See e.g., Beaucage et al. Tetrahedron Letters 22:1859-69 [1981]); or the method described by Matthes et al. (See, Matthes et al., EMBO J. 3:801-805 [1984], as is typically practiced in automated synthetic methods. Nucleic acids of the invention also can be produced by using an automatic DNA synthesizer. Customized nucleic acids can be ordered from a variety of commercial sources (e.g., The Midland Certified Reagent Company, the Great American Gene Company, Operon Technologies Inc., and DNA2.0). Other techniques for synthesizing nucleic acids and related principles are known in the art (See e.g., Itakura et al., Ann. Rev. Biochem. 53:323 [1984]; and Itakura et al., Science 198:1056 [1984]).

As indicated above, recombinant DNA techniques useful in modification of nucleic acids are well known in the art. For example, techniques such as restriction endonuclease digestion,

ligation, reverse transcription and cDNA production, and polymerase chain reaction (e.g., PCR) are known and readily employed by those of skill in the art. Nucleotides of the invention may also be obtained by screening cDNA libraries using one or more oligonucleotide probes that can hybridize to or PCR-amplify polynucleotides which encode a metalloprotease polypeptide polypeptide(s) of the invention. Procedures for screening and isolating cDNA clones and PCR amplification procedures are well known to those of skill in the art and described in standard references known to those skilled in the art. Some nucleic acids of the invention can be obtained by altering a naturally occurring polynucleotide backbone (e.g., that encodes an enzyme or parent protease) by, for example, a known mutagenesis procedure (e.g., site-directed mutagenesis, site saturation mutagenesis, and in vitro recombination).

Methods for Making Modified Metalloprotease polypeptides of the Invention

A variety of methods are known in the art that are suitable for generating modified polynucleotides of the invention that encode metalloprotease polypeptides of the invention, including, but not limited to, for example, site-saturation mutagenesis, scanning mutagenesis, insertional mutagenesis, deletion mutagenesis, random mutagenesis, site-directed mutagenesis, and directed-evolution, as well as various other recombinatorial approaches. Methods for making modified polynucleotides and proteins (e.g., metalloprotease polypeptides) include DNA shuffling methodologies, methods based on non-homologous recombination of genes, such as ITCHY (See, Ostermeier et al., 7:2139-44 [1999]), SCRACHY (See, Lutz et al. 98:11248-53 [2001]), SHIPREC (See, Sieber et al., 19:456-60 [2001]), and NRR (See, Bittker et al., 20:1024-9 [2001]; Bittker et al., 101:7011-6 [2004]), and methods that rely on the use of oligonucleotides to insert random and targeted mutations, deletions and/or insertions (See, Ness et al., 20:1251-5 [2002]; Coco et al., 20:1246-50 [2002]; Zha et al., 4:34-9 [2003]; Glaser et al., 149:3903-13 [1992]).

Vectors, Cells, and Methods for Producing Metalloprotease polypeptides of the Invention

The present invention provides vectors comprising at least one metalloprotease polynucleotide of the invention described herein (e.g., a polynucleotide encoding a metalloprotease polypeptide of the invention described herein), expression vectors or expression cassettes comprising at least one nucleic acid or polynucleotide of the invention, isolated, substantially pure, or recombinant DNA constructs comprising at least one nucleic acid or polynucleotide of the invention, isolated or recombinant cells comprising at least one polynucleotide of the invention, and compositions comprising one or more such vectors, nucleic

acids, expression vectors, expression cassettes, DNA constructs, cells, cell cultures, or any combination or mixtures thereof.

In some embodiments, the invention provides recombinant cells comprising at least one vector (e.g., expression vector or DNA construct) of the invention which comprises at least one nucleic acid or polynucleotide of the invention. Some such recombinant cells are transformed or transfected with such at least one vector. Such cells are typically referred to as host cells. Some such cells comprise bacterial cells, including, but are not limited to *Bacillus sp.* cells, such as *B. subtilis* cells. The invention also provides recombinant cells (e.g., recombinant host cells) comprising at least one metalloprotease polypeptide of the invention.

In some embodiments, the invention provides a vector comprising a nucleic acid or polynucleotide of the invention. In some embodiments, the vector is an expression vector or expression cassette in which a polynucleotide sequence of the invention which encodes a metalloprotease polypeptide of the invention is operably linked to one or additional nucleic acid segments required for efficient gene expression (e.g., a promoter operably linked to the polynucleotide of the invention which encodes a metalloprotease polypeptide of the invention). A vector may include a transcription terminator and/or a selection gene, such as an antibiotic resistance gene, that enables continuous cultural maintenance of plasmid-infected host cells by growth in antimicrobial-containing media.

An expression vector may be derived from plasmid or viral DNA, or in alternative embodiments, contains elements of both. Exemplary vectors include, but are not limited to pC194, pJH101, pE194, pHP13 (See, Harwood and Cutting [eds.], Chapter 3, Molecular Biological Methods for Bacillus, John Wiley & Sons [1990]; suitable replicating plasmids for B. subtilis include those listed on p. 92) See also, Perego, Integrational Vectors for Genetic Manipulations in Bacillus subtilis, in Sonenshein et al., [eds.] Bacillus subtilis and Other Gram-Positive Bacteria: Biochemistry, Physiology and Molecular Genetics, American Society for Microbiology, Washington, D.C. [1993], pp. 615-624), and p2JM103BBI.

For expression and production of a protein of interest (e.g., metalloprotease polypeptide) in a cell, at least one expression vector comprising at least one copy of a polynucleotide encoding the metalloprotease polypeptide, and in some instances comprising multiple copies, is transformed into the cell under conditions suitable for expression of the metalloprotease. In some embodiments of the present invention, a polynucleotide sequence encoding the metalloprotease polypeptide (as well as other sequences included in the vector) is integrated into the genome of the host cell, while in other embodiments, a plasmid vector comprising a polynucleotide sequence encoding the metalloprotease polypeptide remains as autonomous

extra-chromosomal element within the cell. The invention provides both extrachromosomal nucleic acid elements as well as incoming nucleotide sequences that are integrated into the host cell genome. The vectors described herein are useful for production of the metalloprotease polypeptides of the invention. In some embodiments, a polynucleotide construct encoding the metalloprotease polypeptide is present on an integrating vector that enables the integration and optionally the amplification of the polynucleotide encoding the metalloprotease polypeptide into the host chromosome. Examples of sites for integration are well known to those skilled in the art. In some embodiments, transcription of a polynucleotide encoding a metalloprotease polypeptide of the invention is effectuated by a promoter that is the wild-type promoter for the selected precursor protease. In some other embodiments, the promoter is heterologous to the precursor protease, but is functional in the host cell. Specifically, examples of suitable promoters for use in bacterial host cells include, but are not limited to, for example, the amyE, amyQ, amyL, pstS, sacB, pSPAC, pAprE, pVeg, pHpaII promoters, the promoter of the B. stearothermophilus maltogenic amylase gene, the B. amyloliquefaciens (BAN) amylase gene, the B. subtilis alkaline protease gene, the B. clausii alkaline protease gene the B. pumilis xylosidase gene, the B. thuringiensis cryIIIA, and the B. licheniformis alpha-amylase gene. Additional promoters include, but are not limited to the A4 promoter, as well as phage Lambda PR or PL promoters, and the *E. coli* lac, trp or tac promoters.

Metalloprotease polypeptides of the present invention can be produced in host cells of any suitable microorganism, including bacteria and fungi. In some embodiments, metalloprotease polypeptides of the present invention can be produced in Gram-positive bacteria. In some embodiments, the host cells are *Bacillus spp., Streptomyces spp., Escherichia spp., Aspergillus spp., Trichoderma spp., Pseudomonas spp., Corynebacterium spp., Saccharomyces spp.,* or *Pichia spp.* In some embodiments, the metalloprotease polypeptides are produced by Bacillus sp. host cells. Examples of *Bacillus sp.* host cells that find use in the production of the metalloprotease polypeptides of the invention include, but are not limited to *B. licheniformis, B. lentus, B. subtilis, B. amyloliquefaciens, B. lentus, B. brevis, B. stearothermophilus, B. alkalophilus, B. coagulans, B. circulans, B. pumilis, B. thuringiensis, B. clausii, and B. megaterium,* as well as other organisms within the genus Bacillus. In some embodiments, B. subtilis host cells are used for production of metalloprotease polypeptides. U.S. Patents 5,264,366 and 4,760,025 (RE 34,606) describe various Bacillus host strains that can be used for producing metalloprotease polypeptide of the invention, although other suitable strains can be used.

Several bacterial strains that can be used to produce metalloprotease polypeptides of the invention include non-recombinant (i.e., wild-type) *Bacillus sp.* strains, as well as variants of naturally-occurring strains and/or recombinant strains. In some embodiments, the host strain is a recombinant strain, wherein a polynucleotide encoding a polypeptide of interest has been introduced into the host. In some embodiments, the host strain is a *B. subtilis* host strain and particularly a recombinant Bacillus subtilis host strain. Numerous *B. subtilis* strains are known, including, but not limited to for example, 1A6 (ATCC 39085), 168 (1A01), SB19, W23, Ts85, B637, PB1753 through PB1758, PB3360, JH642, 1A243 (ATCC 39,087), ATCC 21332, ATCC 6051, MI113, DE100 (ATCC 39,094), GX4931, PBT 110, and PEP 211strain (See e.g., Hoch et al., Genetics 73:215–228 [1973]; See also, U.S. Patent Nos. 4,450,235 and 4,302,544, and EP 0134048, each of which is incorporated by reference in its entirety). The use of *B. subtilis* as an expression host cells is well known in the art (See e.g., Palva et al., Gene 19:81-87 [1982]; Fahnestock and Fischer, J. Bacteriol., 165:796–804 [1986]; and Wang et al., Gene 69:39–47 [1988]).

In some embodiments, the Bacillus host cell is a *Bacillus sp.* that includes a mutation or deletion in at least one of the following genes, degU, degS, degR and degQ. In some embodiments, the mutation is in a degU gene, and in some embodiments the mutation is degU(Hy)32 (See e.g., Msadek et al., J. Bacteriol. 172:824-834 [1990]; and Olmos et al., Mol. Gen. Genet. 253:562–567 [1997]). In some embodiments, the Bacillus host comprises a mutation or deletion in scoC4 (See e.g., Caldwell et al., J. Bacteriol. 183:7329-7340 [2001]); spoIIE (See e.g., Arigoni et al., Mol. Microbiol. 31:1407-1415 [1999]); and/or oppA or other genes of the opp operon (See e.g., Perego et al., Mol. Microbiol. 5:173-185 [1991]). Indeed, it is contemplated that any mutation in the opp operon that causes the same phenotype as a mutation in the oppA gene will find use in some embodiments of the altered Bacillus strain of the invention. In some embodiments, these mutations occur alone, while in other embodiments, combinations of mutations are present. In some embodiments, an altered Bacillus host cell strain that can be used to produce a metalloprotease polypeptide of the invention is a Bacillus host strain that already includes a mutation in one or more of the above-mentioned genes. In addition, Bacillus sp. host cells that comprise mutation(s) and/or deletions of endogenous protease genes find use. In some embodiments, the Bacillus host cell comprises a deletion of the aprE and the nprE genes. In other embodiments, the Bacillus sp. host cell comprises a deletion of 5 protease genes, while in other embodiments, the Bacillus sp. host cell comprises a deletion of 9 protease genes (See e.g., U.S. Pat. Appln. Pub. No. 2005/0202535, incorporated herein by reference).

Host cells are transformed with at least one nucleic acid encoding at least one metalloprotease polypeptide of the invention using any suitable method known in the art. Methods for introducing a nucleic acid (e.g., DNA) into Bacillus cells or *E. coli* cells utilizing plasmid DNA constructs or vectors and transforming such plasmid DNA constructs or vectors into such cells are well known. In some embodiments, the plasmids are subsequently isolated from *E. coli* cells and transformed into Bacillus cells. However, it is not essential to use intervening microorganisms such as *E. coli*, and in some embodiments, a DNA construct or vector is directly introduced into a *Bacillus* host.

Those of skill in the art are well aware of suitable methods for introducing nucleic acid sequences of the invention into Bacillus cells (See e.g., Ferrari et al., "Genetics," in Harwood et al. [eds.], Bacillus, Plenum Publishing Corp. [1989], pp. 57-72; Saunders et al., J. Bacteriol. 157:718-726 [1984]; Hoch et al., J. Bacteriol. 93:1925 -1937 [1967]; Mann et al., Current Microbiol. 13:131-135 [1986]; Holubova, Folia Microbiol. 30:97 [1985]; Chang et al., Mol. Gen. Genet. 168:11-115 [1979]; Vorobjeva et al., FEMS Microbiol. Lett. 7:261-263 [1980]; Smith et al., Appl. Env. Microbiol. 51:634 [1986]; Fisher et al., Arch. Microbiol. 139:213-217 [1981]; and McDonald, J. Gen. Microbiol. 130:203 [1984]). Indeed, such methods as transformation, including protoplast transformation and transfection, transduction, and protoplast fusion are well known and suited for use in the present invention. Methods known in the art to transform Bacillus cells include such methods as plasmid marker rescue transformation, which involves the uptake of a donor plasmid by competent cells carrying a partially homologous resident plasmid (See, Contente et al., Plasmid 2:555-571 [1979]; Haima et al., Mol. Gen. Genet. 223:185-191 [1990]; Weinrauch et al., J. Bacteriol. 154:1077-1087 [1983]; and Weinrauch et al., J. Bacteriol. 169:1205-1211 [1987]). In this method, the incoming donor plasmid recombines with the homologous region of the resident "helper" plasmid in a process that mimics chromosomal transformation.

In addition to commonly used methods, in some embodiments, host cells are directly transformed with a DNA construct or vector comprising a nucleic acid encoding a metalloprotease polypeptide of the invention (i.e., an intermediate cell is not used to amplify, or otherwise process, the DNA construct or vector prior to introduction into the host cell). Introduction of the DNA construct or vector of the invention into the host cell includes those physical and chemical methods known in the art to introduce a nucleic acid sequence (e.g., DNA sequence) into a host cell without insertion into the host genome. Such methods include, but are not limited to calcium chloride precipitation, electroporation, naked DNA, liposomes and the like. In additional embodiments, DNA constructs or vector are co-transformed with a plasmid,

without being inserted into the plasmid. In further embodiments, a selective marker is deleted from the altered *Bacillus* strain by methods known in the art (See, Stahl et al., J. Bacteriol. 158:411-418 [1984]; and Palmeros et al., Gene 247:255 -264 [2000]).

In some embodiments, the transformed cells of the present invention are cultured in conventional nutrient media. The suitable specific culture conditions, such as temperature, pH and the like are known to those skilled in the art and are well described in the scientific literature. In some embodiments, the invention provides a culture (e.g., cell culture) comprising at least one metalloprotease polypeptide or at least one nucleic acid of the invention.

In some embodiments, host cells transformed with at least one polynucleotide sequence encoding at least one metalloprotease polypeptide of the invention are cultured in a suitable nutrient medium under conditions permitting the expression of the present protease, after which the resulting protease is recovered from the culture. In some embodiments, the protease produced by the cells is recovered from the culture medium by conventional procedures, including, but not limited to for example, separating the host cells from the medium by centrifugation or filtration, precipitating the proteinaceous components of the supernatant or filtrate by means of a salt (e.g., ammonium sulfate), chromatographic purification (e.g., ion exchange, gel filtration, affinity, etc.).

In some embodiments, a metalloprotease polypeptide produced by a recombinant host cell is secreted into the culture medium. A nucleic acid sequence that encodes a purification facilitating domain may be used to facilitate purification of proteins. A vector or DNA construct comprising a polynucleotide sequence encoding a metalloprotease polypeptide may further comprise a nucleic acid sequence encoding a purification facilitating domain to facilitate purification of the metalloprotease polypeptide (See e.g., Kroll et al., DNA Cell Biol. 12:441-53 [1993]). Such purification facilitating domains include, but are not limited to, for example, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals (See, Porath, Protein Expr. Purif. 3:263-281 [1992]), protein A domains that allow purification on immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system. The inclusion of a cleavable linker sequence such as Factor XA or enterokinase (e.g., sequences available from Invitrogen, San Diego, CA) between the purification domain and the heterologous protein also find use to facilitate purification.

Assays for detecting and measuring the enzymatic activity of an enzyme, such as a metalloprotease polypeptide of the invention, are well known. Various assays for detecting and measuring activity of proteases (e.g., metalloprotease polypeptides of the invention), are also known to those of ordinary skill in the art. In particular, assays are available for measuring

protease activity that are based on the release of acid-soluble peptides from casein or hemoglobin, measured as absorbance at 280 nm or colorimetrically using the Folin method. Other exemplary assays involve the solubilization of chromogenic substrates (See e.g., Ward, "Proteinases," in Fogarty (ed.)., Microbial Enzymes and Biotechnology, Applied Science, London, [1983], pp. 251-317). Other exemplary assays include, but are not limited to hydrolysis of protein substrates such as casein (azo-casein, dimethyl-casein and other forms), and peptidyl substrates such as succinyl-Ala-Ala-Pro-Phe-para nitroanilide assay (suc-AAPF-pNA) and the 2,4,6-trinitrobenzene sulfonate sodium salt (TNBS). Numerous additional references known to those in the art provide suitable methods (See e.g., Wells et al., Nucleic Acids Res. 11:7911-7925 [1983]; Christianson et al., Anal. Biochem. 223:119 -129 [1994]; and Hsia et al., Anal Biochem. 242:221-227 [1999]).

A variety of methods can be used to determine the level of production of a mature protease (e.g., mature metalloprotease polypeptides of the present invention) in a host cell. Such methods include, but are not limited to, for example, methods that utilize either polyclonal or monoclonal antibodies specific for the protease. Exemplary methods include, but are not limited to enzyme-linked immunosorbent assays (ELISA), radioimmunoassays (RIA), fluorescent immunoassays (FIA), and fluorescent activated cell sorting (FACS). These and other assays are well known in the art (See e.g., Maddox et al., J. Exp. Med. 158:1211 [1983]).

In some other embodiments, the invention provides methods for making or producing a mature metalloprotease polypeptide of the invention. A mature metalloprotease polypeptide does not include a signal peptide or a propeptide sequence. Some methods comprise making or producing a metalloprotease polypeptide of the invention in a recombinant bacterial host cell, such as for example, a Bacillus sp. cell (e.g., a *B. subtilis* cell). In some embodiments, the invention provides a method of producing a metalloprotease polypeptide of the invention, the method comprising cultivating a recombinant host cell comprising a recombinant expression vector comprising a nucleic acid encoding a metalloprotease polypeptide of the invention under conditions conducive to the production of the metalloprotease polypeptide. Some such methods further comprise recovering the metalloprotease polypeptide from the culture.

In some embodiments the invention provides methods of producing a metalloprotease polypeptide of the invention, the methods comprising: (a) introducing a recombinant expression vector comprising a nucleic acid encoding a metalloprotease polypeptide of the invention into a population of cells (e.g., bacterial cells, such as *B. subtilis* cells); and (b) culturing the cells in a culture medium under conditions conducive to produce the metalloprotease polypeptide encoded

by the expression vector. Some such methods further comprise: (c) isolating the metalloprotease polypeptide from the cells or from the culture medium.

<u>Compositions having the metalloprotease polypeptide of the present invention</u>

Unless otherwise noted, all component or composition levels provided herein are made in reference to the active level of that component or composition, and are exclusive of impurities, for example, residual solvents or by-products, which may be present in commercially available sources. Enzyme components weights are based on total active protein. All percentages and ratios are calculated by weight unless otherwise indicated. All percentages and ratios are calculated based on the total composition unless otherwise indicated. Compositions of the invention include cleaning compositions, such as detergent compositions. In the exemplified detergent compositions, the enzymes levels are expressed by pure enzyme by weight of the total composition and unless otherwise specified, the detergent ingredients are expressed by weight of the total compositions.

As indicated herein, in some embodiments, the cleaning compositions of the present invention further comprise adjunct materials including, but not limited to, surfactants, builders, bleaches, bleach activators, bleach catalysts, other enzymes, enzyme stabilizing systems, chelants, optical brighteners, soil release polymers, dye transfer agents, dispersants, suds suppressors, dyes, perfumes, colorants, filler salts, hydrotropes, photoactivators, fluorescers, fabric conditioners, hydrolyzable surfactants, preservatives, anti-oxidants, anti-shrinkage agents, anti-wrinkle agents, germicides, fungicides, color speckles, silvercare, anti-tarnish and/or anti-corrosion agents, alkalinity sources, solubilizing agents, carriers, processing aids, pigments, and pH control agents (See e.g., U.S. Pat. Nos. 6,610,642, 6,605,458, 5,705,464, 5,710,115, 5,698,504, 5,695,679, 5,686,014 and 5,646,101, all of which are incorporated herein by reference). Embodiments of specific cleaning composition materials are exemplified in detail below. In embodiments in which the cleaning adjunct materials are not compatible with the metalloprotease polypeptides of the present invention in the cleaning compositions, then suitable methods of keeping the cleaning adjunct materials and the protease(s) separated (i.e., not in contact with each other) until combination of the two components is appropriate are used. Such separation methods include any suitable method known in the art (e.g., gelcaps, encapsulation, tablets, physical separation, etc.).

The cleaning compositions of the present invention are advantageously employed for example, in laundry applications, hard surface cleaning, dishwashing applications, including automatic dishwashing and hand dishwashing, as well as cosmetic applications such as dentures,

teeth, hair and skin. In addition, due to the unique advantages of increased effectiveness in lower temperature solutions, the enzymes of the present invention are ideally suited for laundry applications. Furthermore, the enzymes of the present invention find use in granular and liquid compositions.

The metalloprotease polypeptides of the present invention also find use in cleaning additive products. In some embodiments, low temperature solution cleaning applications find use. In some embodiments, the present invention provides cleaning additive products including at least one enzyme of the present invention is ideally suited for inclusion in a wash process when additional bleaching effectiveness is desired. Such instances include, but are not limited to low temperature solution cleaning applications. In some embodiments, the additive product is in its simplest form, one or more proteases. In some embodiments, the additive is packaged in dosage form for addition to a cleaning process. In some embodiments, the additive is packaged in dosage form for addition to a cleaning process where a source of peroxygen is employed and increased bleaching effectiveness is desired. Any suitable single dosage unit form finds use with the present invention, including but not limited to pills, tablets, gelcaps, or other single dosage units such as pre-measured powders or liquids. In some embodiments, filler(s) or carrier material(s) are included to increase the volume of such compositions. Suitable filler or carrier materials include, but are not limited to, various salts of sulfate, carbonate and silicate as well as talc, clay and the like. Suitable filler or carrier materials for liquid compositions include, but are not limited to water or low molecular weight primary and secondary alcohols including polyols and diols. Examples of such alcohols include, but are not limited to, methanol, ethanol, propanol and isopropanol. In some embodiments, the compositions contain from about 5% to about 90% of such materials. Acidic fillers find use to reduce pH. Alternatively, in some embodiments, the cleaning additive includes adjunct ingredients, as more fully described below.

The present cleaning compositions and cleaning additives require an effective amount of at least one of the metalloprotease polypeptides provided herein, alone or in combination with other proteases and/or additional enzymes. The required level of enzyme is achieved by the addition of one or more metalloprotease polypeptides of the present invention. Typically the present cleaning compositions comprise at least about 0.0001 weight percent, from about 0.0001 to about 10, from about 0.001 to about 1, or from about 0.01 to about 0.1 weight percent of at least one of the metalloprotease polypeptides of the present invention.

The cleaning compositions herein are typically formulated such that, during use in aqueous cleaning operations, the wash water will have a pH of from about 4.0 to about 11.5 or even from about 5.0 to about 11.5, or even from about 5.0 to about 8.0, or even from about 7.5

to about 10.5. Liquid product formulations are typically formulated to have a pH from about 3.0 to about 9.0 or even from about 3 to about 5. Granular laundry products are typically formulated to have a pH from about 9 to about 11. Techniques for controlling pH at recommended usage levels include the use of buffers, alkalis, acids, etc., and are well known to those skilled in the art.

Suitable "low pH cleaning compositions" typically have a pH of from about 3 to about 5, and are typically free of surfactants that hydrolyze in such a pH environment. Such surfactants include sodium alkyl sulfate surfactants that comprise at least one ethylene oxide moiety or even from about 1 to about 16 moles of ethylene oxide. Such cleaning compositions typically comprise a sufficient amount of a pH modifier, such as sodium hydroxide, monoethanolamine or hydrochloric acid, to provide such cleaning composition with a pH of from about 3 to about 5. Such compositions typically comprise at least one acid stable enzyme. In some embodiments, the compositions are liquids, while in other embodiments, they are solids. The pH of such liquid compositions is typically measured as a neat pH. The pH of such solid compositions is measured as a 10% solids solution of said composition wherein the solvent is distilled water. In these embodiments, all pH measurements are taken at 20°C, unless otherwise indicated.

In some embodiments, when the metalloprotease polypeptide(s) is/are employed in a granular composition or liquid, it is desirable for the metalloprotease polypeptide to be in the form of an encapsulated particle to protect the metalloprotease polypeptide from other components of the granular composition during storage. In addition, encapsulation is also a means of controlling the availability of the metalloprotease polypeptide during the cleaning process. In some embodiments, encapsulation enhances the performance of the metalloprotease polypeptide(s) and/or additional enzymes. In this regard, the metalloprotease polypeptides of the present invention are encapsulated with any suitable encapsulating material known in the art. In some embodiments, the encapsulating material typically encapsulates at least part of the metalloprotease polypeptide(s) of the present invention. Typically, the encapsulating material is water-soluble and/or water-dispersible. In some embodiments, the encapsulating material has a glass transition temperature (Tg) of 0°C or higher. Glass transition temperature is described in more detail in WO 97/11151. The encapsulating material is typically selected from consisting of carbohydrates, natural or synthetic gums, chitin, chitosan, cellulose and cellulose derivatives, silicates, phosphates, borates, polyvinyl alcohol, polyethylene glycol, paraffin waxes, and combinations thereof. When the encapsulating material is a carbohydrate, it is typically selected from monosaccharides, oligosaccharides, polysaccharides, and combinations thereof. In some typical embodiments, the encapsulating material is a starch (See e.g., EP 0 922 499; US

4,977,252; US 5,354,559, and US 5,935,826). In some embodiments, the encapsulating material is a microsphere made from plastic such as thermoplastics, acrylonitrile, methacrylonitrile, polyacrylonitrile, polymethacrylonitrile and mixtures thereof; commercially available microspheres that find use include, but are not limited to those supplied by EXPANCEL® (Stockviksverken, Sweden), and PM 6545, PM 6550, PM 7220, PM 7228, EXTENDOSPHERES®, LUXSIL®, Q-CEL®, and SPHERICEL® (PQ Corp., Valley Forge, PA).

As described herein, the metalloprotease polypeptides of the present invention find particular use in the cleaning industry, including, but not limited to laundry and dish detergents. These applications place enzymes under various environmental stresses. The metalloprotease polypeptides of the present invention provide advantages over many currently used enzymes, due to their stability under various conditions.

Indeed, there are a variety of wash conditions including varying detergent formulations, wash water volumes, wash water temperatures, and lengths of wash time, to which proteases involved in washing are exposed. In addition, detergent formulations used in different geographical areas have different concentrations of their relevant components present in the wash water. For example, European detergents typically have about 4500-5000 ppm of detergent components in the wash water, while Japanese detergents typically have approximately 667 ppm of detergent components in the wash water. In North America, particularly the United States, detergents typically have about 975 ppm of detergent components present in the wash water.

A low detergent concentration system includes detergents where less than about 800 ppm of the detergent components are present in the wash water. Japanese detergents are typically considered low detergent concentration system as they have approximately 667 ppm of detergent components present in the wash water.

A medium detergent concentration includes detergents where between about 800 ppm and about 2000ppm of the detergent components are present in the wash water. North American detergents are generally considered to be medium detergent concentration systems as they have approximately 975 ppm of detergent components present in the wash water. Brazil typically has approximately 1500 ppm of detergent components present in the wash water.

A high detergent concentration system includes detergents where greater than about 2000 ppm of the detergent components are present in the wash water. European detergents are generally considered to be high detergent concentration systems as they have approximately 4500-5000 ppm of detergent components in the wash water.

Latin American detergents are generally high suds phosphate builder detergents and the range of detergents used in Latin America can fall in both the medium and high detergent concentrations as they range from 1500 ppm to 6000 ppm of detergent components in the wash water. As mentioned above, Brazil typically has approximately 1500 ppm of detergent components present in the wash water. However, other high suds phosphate builder detergent geographies, not limited to other Latin American countries, may have high detergent concentration systems up to about 6000 ppm of detergent components present in the wash water.

In light of the foregoing, it is evident that concentrations of detergent compositions in typical wash solutions throughout the world varies from less than about 800 ppm of detergent to about 6000 ppm in high suds phosphate builder geographies.

The concentrations of the typical wash solutions are determined empirically. For example, in the U.S., a typical washing machine holds a volume of about 64.4 L of wash solution. Accordingly, in order to obtain a concentration of about 975 ppm of detergent within the wash solution about 62.79 g of detergent composition must be added to the 64.4 L of wash solution. This amount is the typical amount measured into the wash water by the consumer using the measuring cup provided with the detergent.

As a further example, different geographies use different wash temperatures. The temperature of the wash water in Japan is typically less than that used in Europe. For example, the temperature of the wash water in North America and Japan is typically between about 10 and about 40°C (e.g., about 20°C), whereas the temperature of wash water in Europe is typically between about 30 and about 60°C (e.g., about 40°C). However, in the interest of saving energy, many consumers are switching to using cold water washing. In addition, in some further regions, cold water is typically used for laundry, as well as dish washing applications. In some embodiments, the "cold water washing" of the present invention utilizes "cold water detergent" suitable for washing at temperatures from about 10°C to about 40°C, or from about 20°C to about 30°C, or from about 15°C to about 25°C, as well as all other combinations within the range of about 15°C to about 35°C, and all ranges within 10°C to 40°C.

As a further example, different geographies typically have different water hardness. Water hardness is usually described in terms of the grains per gallon mixed Ca^{2+}/Mg^{2+}. Hardness is a measure of the amount of calcium (Ca^{2+}) and magnesium (Mg^{2+}) in the water. Most water in the United States is hard, but the degree of hardness varies. Moderately hard (60-120 ppm) to hard (121-181 ppm) water has 60 to 181 parts per million (parts per million converted to grains per U.S. gallon is ppm # divided by 17.1 equals grains per gallon) of hardness minerals.

Water	Grains per gallon	Parts per million
Soft	less than 1.0	less than 17
Slightly hard	1.0 to 3.5	17 to 60
Moderately hard	3.5 to 7.0	60 to 120
Hard	7.0 to 10.5	120 to 180
Very hard	greater than 10.5	greater than 180

European water hardness is typically greater than about 10.5 (for example about 10.5 to about 20.0) grains per gallon mixed Ca^{2+}/Mg^{2+} (e.g., about 15 grains per gallon mixed Ca^{2+}/Mg^{2+}). North American water hardness is typically greater than Japanese water hardness, but less than European water hardness. For example, North American water hardness can be between about 3 to about 10 grains, about 3 to about 8 grains or about 6 grains. Japanese water hardness is typically lower than North American water hardness, usually less than about 4, for example about 3 grains per gallon mixed Ca^{2+}/Mg^{2+}.

Accordingly, in some embodiments, the present invention provides metalloprotease polypeptides that show surprising wash performance in at least one set of wash conditions (e.g., water temperature, water hardness, and/or detergent concentration). In some embodiments, the metalloprotease polypeptides of the present invention are comparable in wash performance to other metalloprotease polypeptide proteases. In some embodiments of the present invention, the metalloprotease polypeptides provided herein exhibit enhanced oxidative stability, enhanced thermal stability, enhanced cleaning capabilities under various conditions, and/or enhanced chelator stability. In addition, the metalloprotease polypeptides of the present invention find use in cleaning compositions that do not include detergents, again either alone or in combination with builders and stabilizers.

In some embodiments of the present invention, the cleaning compositions comprise at least one metalloprotease polypeptide of the present invention at a level from about 0.00001 % to about 10% by weight of the composition and the balance (e.g., about 99.999% to about 90.0%) comprising cleaning adjunct materials by weight of composition. In some other embodiments of the present invention, the cleaning compositions of the present invention comprises at least one metalloprotease polypeptide at a level of about 0.0001 % to about 10%, about 0.001% to about 5%, about 0.001% to about 2%, about 0.005% to about 0.5% by weight of the composition and the balance of the cleaning composition (e.g., about 99.9999% to about 90.0%, about 99.999 % to about 98%, about 99.995% to about 99.5% by weight) comprising cleaning adjunct materials.

In some embodiments, the cleaning compositions of the present invention comprise one or more additional detergent enzymes, which provide cleaning performance and/or fabric care and/or dishwashing benefits. Examples of suitable enzymes include, but are not limited to, acyl transferases, alpha-amylases, beta-amylases, alpha-galactosidases, arabinosidases, aryl esterases, beta-galactosidases, carrageenases, catalases, cellobiohydrolases, cellulases, chondroitinases, cutinases, endo-beta-1, 4-glucanases, endo-beta-mannanases, esterases, exo-mannanases, galactanases, glucoamylases, hemicellulases, hyaluronidases, keratinases, laccases, lactases, ligninases, lipases, lipoxygenases, mannanases, oxidases, pectate lyases, pectin acetyl esterases, pectinases, pentosanases, peroxidases, phenoloxidases, phosphatases, phospholipases, phytases, polygalacturonases, proteases, pullulanases, reductases, rhamnogalacturonases, beta-glucanases, tannases, transglutaminases, xylan acetyl-esterases, xylanases, xyloglucanases, and xylosidases, or any combinations or mixtures thereof. In some embodiments, a combination of enzymes is used (i.e., a "cocktail") comprising conventional applicable enzymes like protease, lipase, cutinase and/or cellulase in conjunction with amylase is used.

In addition to the metalloprotease polypeptides provided herein, any other suitable protease finds use in the compositions of the present invention. Suitable proteases include those of animal, vegetable or microbial origin. In some embodiments, microbial proteases are used. In some embodiments, chemically or genetically modified mutants are included. In some embodiments, the protease is a serine protease, preferably an alkaline microbial protease or a trypsin-like protease. Examples of alkaline proteases include subtilisins, especially those derived from Bacillus (e.g., subtilisin, lentus, amyloliquefaciens, subtilisin Carlsberg, subtilisin 309, subtilisin 147 and subtilisin 168). Additional examples include those mutant proteases described in U.S. Pat. Nos. RE 34,606, 5,955,340, 5,700,676, 6,312,936, and 6,482,628, all of which are incorporated herein by reference. Additional protease examples include, but are not limited to trypsin (e.g., of porcine or bovine origin), and the Fusarium protease described in WO 89/06270. In some embodiments, commercially available protease enzymes that find use in the present invention include, but are not limited to MAXATASE®, MAXACAL™, MAXAPEM™, OPTICLEAN®, OPTIMASE®, PROPERASE®, PURAFECT®, PURAFECT® OXP, PURAMAX™, EXCELLASE™, and PURAFAST™ (Genencor); ALCALASE®, SAVINASE®, PRIMASE®, DURAZYM™, POLARZYME®, OVOZYME®, KANNASE®, LIQUANASE®, NEUTRASE®, RELASE® and ESPERASE® (Novozymes); BLAP™ and BLAP™ variants (Henkel Kommanditgesellschaft auf Aktien, Duesseldorf, Germany), and KAP (B. alkalophilus subtilisin; Kao Corp., Tokyo, Japan). Various proteases are described in WO95/23221, WO 92/21760, WO 09/149200, WO 09/149144, WO 09/149145,

WO 11/072099, WO 10/056640, WO 10/056653, WO 11/140364, WO 12/151534, U.S. Pat. Publ. No. 2008/0090747, and U.S. Pat. Nos. 5,801,039, 5,340,735, 5,500,364, 5,855,625, US RE 34,606, 5,955,340, 5,700,676, 6,312,936, and 6,482,628, and various other patents. In some further embodiments, metalloproteases find use in the present invention, including but not limited to the neutral metalloprotease described in WO 07/044993.

In addition, any suitable lipase finds use in the present invention. Suitable lipases include, but are not limited to those of bacterial or fungal origin. Chemically or genetically modified mutants are encompassed by the present invention. Examples of useful lipases include Humicola lanuginosa lipase (See e.g., EP 258 068, and EP 305 216), Rhizomucor miehei lipase (See e.g., EP 238 023), Candida lipase, such as C. antarctica lipase (e.g., the C. antarctica lipase A or B; See e.g., EP 214 761), Pseudomonas lipases such as P. alcaligenes lipase and P. pseudoalcaligenes lipase (See e.g., EP 218 272), P. cepacia lipase (See e.g., EP 331 376), P. stutzeri lipase (See e.g., GB 1,372,034), P. fluorescens lipase, Bacillus lipase (e.g., B. subtilis lipase [Dartois et al., Biochem. Biophys. Acta 1131:253-260 [1993]); B. stearothermophilus lipase [See e.g., JP 64/744992]; and B. pumilus lipase [See e.g., WO 91/16422]).

Furthermore, a number of cloned lipases find use in some embodiments of the present invention, including but not limited to Penicillium camembertii lipase (See, Yamaguchi et al., Gene 103:61-67 [1991]), Geotricum candidum lipase (See, Schimada et al., J. Biochem., 106:383-388 [1989]), and various Rhizopus lipases such as R. delemar lipase (See, Hass et al., Gene 109:117-113 [1991]), a R. niveus lipase (Kugimiya et al., Biosci. Biotech. Biochem. 56:716-719 [1992]) and R. oryzae lipase.

Other types of lipase polypeptide enzymes such as cutinases also find use in some embodiments of the present invention, including but not limited to the cutinase derived from Pseudomonas mendocina (See, WO 88/09367), and the cutinase derived from Fusarium solani pisi (See, WO 90/09446).

Additional suitable lipases include commercially available lipases such as M1 LIPASE™, LUMA FAST™, and LIPOMAX™ (Genencor); LIPEX®, LIPOLASE® and LIPOLASE® ULTRA (Novozymes); and LIPASE P™ "Amano" (Amano Pharmaceutical Co. Ltd., Japan). Various lipases are described in WO2010065455, WO2010107560, WO2011084412, WO2011084417, WO2011084599, WO2011078949, WO2011150157, WO2012137147, WO2013033318, WO2013096653, and US Patent Application No. 61/713436.

In some embodiments of the present invention, the cleaning compositions of the present invention further comprise lipases at a level from about 0.00001 % to about 10% of additional lipase by weight of the composition and the balance of cleaning adjunct materials by weight of

composition. In some other embodiments of the present invention, the cleaning compositions of the present invention also comprise lipases at a level of about 0.0001 % to about 10%, about 0.001% to about 5%, about 0.001% to about 2%, about 0.005% to about 0.5% lipase by weight of the composition.

In some embodiments of the present invention, any suitable amylase finds use in the present invention. In some embodiments, any amylase (e.g., alpha and/or beta) suitable for use in alkaline solutions also find use. Suitable amylases include, but are not limited to those of bacterial or fungal origin. Chemically or genetically modified mutants are included in some embodiments. Amylases that find use in the present invention, include, but are not limited to α-amylases obtained from B. licheniformis (See e.g., GB 1,296,839). Additional suitable amylases include those found in WO9510603, WO9526397, WO9623874, WO9623873, WO9741213, WO9919467, WO0060060, WO0029560, WO9923211, WO9946399, WO0060058, WO0060059, WO9942567, WO0114532, WO02092797, WO0166712, WO0188107, WO0196537, WO0210355, WO9402597, WO0231124, WO9943793, WO9943794, WO2004113551, WO2005001064, WO2005003311, WO0164852, WO2006063594, WO2006066594, WO2006066596, WO2006012899, WO2008092919, WO2008000825, WO2005018336, WO2005066338, WO2009140504, WO2005019443, WO2010091221, WO2010088447, WO0134784, WO2006012902, WO2006031554, WO2006136161, WO2008101894, WO2010059413, WO2011098531, WO2011080352, WO2011080353, WO2011080354, WO2011082425, WO2011082429, WO2011076123, WO2011087836, WO2011076897, WO94183314, WO9535382, WO9909183, WO9826078, WO9902702, WO9743424, WO9929876, WO9100353, WO9605295, WO9630481, WO9710342, WO2008088493, WO2009149419, WO2009061381, WO2009100102, WO2010104675, WO2010117511, and WO2010115021. Commercially available amylases that find use in the present invention include, but are not limited to DURAMYL®, TERMAMYL®, FUNGAMYL®, STAINZYME®, STAINZYME PLUS®, STAINZYME ULTRA®, and BAN™ (Novozymes), as well as POWERASE™, RAPIDASE® and MAXAMYL® P (Genencor).

In some embodiments of the present invention, the cleaning compositions of the present invention further comprise amylases at a level from about 0.00001 % to about 10% of additional amylase by weight of the composition and the balance of cleaning adjunct materials by weight of composition. In some other embodiments of the present invention, the cleaning compositions of the present invention also comprise amylases at a level of about 0.0001 % to about 10%,

about 0.001% to about 5%, about 0.001% to about 2%, about 0.005% to about 0.5% amylase by weight of the composition.

In some further embodiments, any suitable cellulase finds used in the cleaning compositions of the present invention. Suitable cellulases include, but are not limited to those of bacterial or fungal origin. Chemically or genetically modified mutants are included in some embodiments. Suitable cellulases include, but are not limited to Humicola insolens cellulases (See e.g., U.S. Pat. No. 4,435,307). Especially suitable cellulases are the cellulases having color care benefits (See e.g., EP 0 495 257). Commercially available cellulases that find use in the present include, but are not limited to CELLUZYME®, CAREZYME® (Novozymes), and KAC-500(B)™ (Kao Corporation). In some embodiments, cellulases are incorporated as portions or fragments of mature wild-type or variant cellulases, wherein a portion of the N-terminus is deleted (See e.g., U.S. Pat. No. 5,874,276). Additional suitable cellulases include those found in WO2005054475, WO2005056787, U.S. Pat. No. 7,449,318, and U.S. Pat. No. 7,833,773. In some embodiments, the cleaning compositions of the present invention further comprise cellulases at a level from about 0.00001 % to about 10% of additional cellulase by weight of the composition and the balance of cleaning adjunct materials by weight of composition. In some other embodiments of the present invention, the cleaning compositions of the present invention also comprise cellulases at a level of about 0.0001 % to about 10%, about 0.001% to about 5%, about 0.001% to about 2%, about 0.005% to about 0.5% cellulase by weight of the composition.

Any mannanase suitable for use in detergent compositions also finds use in the present invention. Suitable mannanases include, but are not limited to those of bacterial or fungal origin. Chemically or genetically modified mutants are included in some embodiments. Various mannanases are known which find use in the present invention (See e.g., U.S. Pat. No. 6,566,114, U.S. Pat. No.6,602,842, and US Patent No. 6,440,991, all of which are incorporated herein by reference). Commercially available mannanases that find use in the present invention include, but are not limited to MANNASTAR®, PURABRITE™, and MANNAWAY®. In some embodiments, the cleaning compositions of the present invention further comprise mannanases at a level from about 0.00001 % to about 10% of additional mannanase by weight of the composition and the balance of cleaning adjunct materials by weight of composition. In some embodiments of the present invention, the cleaning compositions of the present invention also comprise mannanases at a level of about 0.0001 % to about 10%, about 0.001% to about 5%, about 0.001% to about 2%, about 0.005% to about 0.5% mannanase by weight of the composition.

In some embodiments, peroxidases are used in combination with hydrogen peroxide or a source thereof (e.g., a percarbonate, perborate or persulfate) in the compositions of the present invention. In some alternative embodiments, oxidases are used in combination with oxygen. Both types of enzymes are used for "solution bleaching" (i.e., to prevent transfer of a textile dye from a dyed fabric to another fabric when the fabrics are washed together in a wash liquor), preferably together with an enhancing agent (See e.g., WO 94/12621 and WO 95/01426). Suitable peroxidases/oxidases include, but are not limited to those of plant, bacterial or fungal origin. Chemically or genetically modified mutants are included in some embodiments. In some embodiments, the cleaning compositions of the present invention further comprise peroxidase and/or oxidase enzymes at a level from about 0.00001 % to about 10% of additional peroxidase and/or oxidase by weight of the composition and the balance of cleaning adjunct materials by weight of composition. In some other embodiments of the present invention, the cleaning compositions of the present invention also comprise, peroxidase and/or oxidase enzymes at a level of about 0.0001 % to about 10%, about 0.001% to about 5%, about 0.001% to about 2%, about 0.005% to about 0.5% peroxidase and/or oxidase enzymes by weight of the composition.

In some embodiments, additional enzymes find use, including but not limited to perhydrolases (See e.g., WO 05/056782). In addition, in some embodiments, mixtures of the above mentioned enzymes are encompassed herein, in particular one or more additional protease, amylase, lipase, mannanase, and/or at least one cellulase. Indeed, it is contemplated that various mixtures of these enzymes will find use in the present invention.   It is also contemplated that the varying levels of the metalloprotease polypeptide (s) and one or more additional enzymes may both independently range to about 10%, the balance of the cleaning composition being cleaning adjunct materials. The specific selection of cleaning adjunct materials are readily made by considering the surface, item, or fabric to be cleaned, and the desired form of the composition for the cleaning conditions during use (e.g., through the wash detergent use).

Examples of suitable cleaning adjunct materials include, but are not limited to, surfactants, builders, bleaches, bleach activators, bleach catalysts, other enzymes, enzyme stabilizing systems, chelants, optical brighteners, soil release polymers, dye transfer agents, dye transfer inhibiting agents, catalytic materials, hydrogen peroxide, sources of hydrogen peroxide, preformed peracids, polymeric dispersing agents, clay soil removal agents, structure elasticizing agents, dispersants, suds suppressors, dyes, perfumes, colorants, filler salts, hydrotropes, photoactivators, fluorescers, fabric conditioners, fabric softeners, carriers, hydrotropes, processing aids, solvents, pigments, hydrolyzable surfactants, preservatives, anti-oxidants, anti-

shrinkage agents, anti-wrinkle agents, germicides, fungicides, color speckles, silvercare, anti-tarnish and/or anti-corrosion agents, alkalinity sources, solubilizing agents, carriers, processing aids, pigments, and pH control agents (See e.g., U.S. Pat. Nos. 6,610,642, 6,605,458, 5,705,464, 5,710,115, 5,698,504, 5,695,679, 5,686,014 and 5,646,101, all of which are incorporated herein by reference). Embodiments of specific cleaning composition materials are exemplified in detail below. In embodiments in which the cleaning adjunct materials are not compatible with the metalloprotease polypeptides of the present invention in the cleaning compositions, then suitable methods of keeping the cleaning adjunct materials and the protease(s) separated (i.e., not in contact with each other) until combination of the two components is appropriate are used. Such separation methods include any suitable method known in the art (e.g., gelcaps, encapsulation, tablets, physical separation, etc.).

In some embodiments, an effective amount of one or more metalloprotease polypeptide (s) provided herein is included in compositions useful for cleaning a variety of surfaces in need of proteinaceous stain removal. Such cleaning compositions include cleaning compositions for such applications as cleaning hard surfaces, fabrics, and dishes. Indeed, in some embodiments, the present invention provides fabric cleaning compositions, while in other embodiments, the present invention provides non-fabric cleaning compositions. Notably, the present invention also provides cleaning compositions suitable for personal care, including oral care (including dentrifices, toothpastes, mouthwashes, etc., as well as denture cleaning compositions), skin, and hair cleaning compositions. It is intended that the present invention encompass detergent compositions in any form (i.e., liquid, granular, bar, semi-solid, gels, emulsions, tablets, capsules, etc.).

By way of example, several cleaning compositions wherein the metalloprotease polypeptides of the present invention find use are described in greater detail below. In some embodiments in which the cleaning compositions of the present invention are formulated as compositions suitable for use in laundry machine washing method(s), the compositions of the present invention preferably contain at least one surfactant and at least one builder compound, as well as one or more cleaning adjunct materials preferably selected from organic polymeric compounds, bleaching agents, additional enzymes, suds suppressors, dispersants, lime-soap dispersants, soil suspension and anti-redeposition agents and corrosion inhibitors. In some embodiments, laundry compositions also contain softening agents (i.e., as additional cleaning adjunct materials). The compositions of the present invention also find use in detergent additive products in solid or liquid form. Such additive products are intended to supplement and/or boost the performance of conventional detergent compositions and can be added at any stage of the

cleaning process. In some embodiments, the density of the laundry detergent compositions herein ranges from about 400 to about 1200 g/liter, while in other embodiments, it ranges from about 500 to about 950 g/liter of composition measured at 20°C.

In embodiments formulated as compositions for use in manual dishwashing methods, the compositions of the invention preferably contain at least one surfactant and preferably at least one additional cleaning adjunct material selected from organic polymeric compounds, suds enhancing agents, group II metal ions, solvents, hydrotropes and additional enzymes.

In some embodiments, various cleaning compositions such as those provided in U.S, Pat. No. 6,605,458, find use with the metalloprotease polypeptides of the present invention. Thus, in some embodiments, the compositions comprising at least one metalloprotease polypeptide of the present invention is a compact granular fabric cleaning composition, while in other embodiments, the composition is a granular fabric cleaning composition useful in the laundering of colored fabrics, in further embodiments, the composition is a granular fabric cleaning composition which provides softening through the wash capacity, in additional embodiments, the composition is a heavy duty liquid fabric cleaning composition. In some embodiments, the compositions comprising at least one metalloprotease polypeptide of the present invention are fabric cleaning compositions such as those described in U.S. Pat. Nos. 6,610,642 and 6,376,450. In addition, the metalloprotease polypeptides of the present invention find use in granular laundry detergent compositions of particular utility under European or Japanese washing conditions (See e.g., U.S. Pat. No. 6,610,642).

In some alternative embodiments, the present invention provides hard surface cleaning compositions comprising at least one metalloprotease polypeptide provided herein. Thus, in some embodiments, the compositions comprising at least one metalloprotease polypeptide of the present invention is a hard surface cleaning composition such as those described in U.S. Pat. Nos. 6,610,642, 6,376,450, and 6,376,450.

In yet further embodiments, the present invention provides dishwashing compositions comprising at least one metalloprotease polypeptide provided herein. Thus, in some embodiments, the compositions comprising at least one metalloprotease polypeptide of the present invention is a hard surface cleaning composition such as those in U.S. Pat. Nos. 6,610,642 and 6,376,450. In some still further embodiments, the present invention provides dishwashing compositions comprising at least one metalloprotease polypeptide provided herein. In some further embodiments, the compositions comprising at least one metalloprotease polypeptide of the present invention comprise oral care compositions such as those in U.S. Pat. No. 6,376,450, and 6,376,450. The formulations and descriptions of the compounds and

cleaning adjunct materials contained in the aforementioned US Pat. Nos. 6,376,450, 6,605,458, 6,605,458, and 6,610,642, find use with the metalloprotease polypeptides provided herein.

The cleaning compositions of the present invention are formulated into any suitable form and prepared by any process chosen by the formulator, non-limiting examples of which are described in U.S. Pat. Nos. 5,879,584, 5,691,297, 5,574,005, 5,569,645, 5,565,422, 5,516,448, 5,489,392, and 5,486,303, all of which are incorporated herein by reference. When a low pH cleaning composition is desired, the pH of such composition is adjusted via the addition of a material such as monoethanolamine or an acidic material such as HCl.

In some embodiments, the cleaning compositions of the present invention can be formulated to have an alkaline pH under wash conditions, such as a pH of from about 8.0 to about 12.0, or from about 8.5 to about 11.0, or from about 9.0 to about 11.0. In some embodiments, the cleaning compositions of the present invention can be formulated to have a neutral pH under wash conditions, such as a pH of from about 5.0 to about 8.0, or from about 5.5 to about 8.0, or from about 6.0 to about 8.0, or from about 6.0 to about 7.5. In some embodiments, the neutral pH conditions can be measured when the cleaning composition is dissolved 1:100 (wt:wt) in de-ionised water at 20°C., measured using a conventional pH meter.

While not essential for the purposes of the present invention, the non-limiting list of adjuncts illustrated hereinafter are suitable for use in the instant cleaning compositions. In some embodiments, these adjuncts are incorporated for example, to assist or enhance cleaning performance, for treatment of the substrate to be cleaned, or to modify the aesthetics of the cleaning composition as is the case with perfumes, colorants, dyes or the like. It is understood that such adjuncts are in addition to the metalloprotease polypeptides of the present invention. The precise nature of these additional components, and levels of incorporation thereof, will depend on the physical form of the composition and the nature of the cleaning operation for which it is to be used. Suitable adjunct materials include, but are not limited to, surfactants, builders, chelating agents, dye transfer inhibiting agents, deposition aids, dispersants, additional enzymes, and enzyme stabilizers, catalytic materials, bleach activators, bleach boosters, hydrogen peroxide, sources of hydrogen peroxide, preformed peracids, polymeric dispersing agents, clay soil removal/anti-redeposition agents, brighteners, suds suppressors, dyes, perfumes, structure elasticizing agents, fabric softeners, carriers, hydrotropes, processing aids and/or pigments. In addition to the disclosure below, suitable examples of such other adjuncts and levels of use are found in U.S. Patent Nos. 5,576,282, 6,306,812, and 6,326,348, incorporated by reference. The aforementioned adjunct ingredients may constitute the balance of the cleaning compositions of the present invention.

In some embodiments, the cleaning compositions according to the present invention comprise an acidifying particle or an amino carboxylic builder. Examples of an amino carboxylic builder include aminocarboxylic acids, salts and derivatives thereof. In some embodiment, the amino carboxylic builder is an aminopolycarboxylic builder, such as glycine-N,N-diacetic acid or derivative of general formula $MOOC\text{-}CHR\text{-}N\ (CH_2COOM)_2$ where R is C_{1-12} alkyl and M is alkali metal. In some embodiments, the amino carboxylic builder can be methylglycine diacetic acid (MGDA), GLDA (glutamic-N,N-diacetic acid), iminodisuccinic acid (IDS), carboxymethyl inulin and salts and derivatives thereof, aspartic acid-N-monoacetic acid (ASMA), aspartic acid-N,N-diacetic acid (ASDA), aspartic acid-N-monopropionic acid (ASMP), iminodisuccinic acid (IDA), N-(2-sulfomethyl) aspartic acid (SMAS), N-(2-sulfoethyl)aspartic acid (SEAS), N-(2-sulfomethyl)glutamic acid (SMGL), N-(2-sulfoethyl) glutamic acid (SEGL), IDS (iminodiacetic acid) and salts and derivatives thereof such as N-methyliminodiacetic acid (MIDA) , alpha-alanine-N,N-diacetic acid (alpha-ALDA) , serine-N,N-diacetic acid (SEDA), isoserine-N,Ndiacetic acid (ISDA) , phenylalanine-N,N-diacetic acid (PHDA), anthranilic acid-N,N-diacetic acid (ANDA), sulfanilic acid-N,N-diacetic acid (SLDA), taurine-N,N-diacetic acid (TUDA) and sulfomethyl-N,N-diacetic acid (SMDA) and alkali metal salts and derivative thereof. In some embodiments, the acidifying particle has a weight geometric mean particle size of from about 400 µ to about 1200 µ and a bulk density of at least 550 g/L. In some embodiments, the acidifying particle comprises at least about 5% of the builder.

In some embodiments, the acidifying particle can comprise any acid, including organic acids and mineral acids. Organic acids can have one or two carboxyls and in some instances up to 15 carbons, especially up to 10 carbons, such as formic, acetic, propionic, capric, oxalic, succinic, adipic, maleic, fumaric, sebacic, malic, lactic, glycolic, tartaric and glyoxylic acids. In some embodiments, the acid is citric acid. Mineral acids include hydrochloric and sulphuric acid. In some instances, the acidifying particle of the invention is a highly active particle comprising a high level of amino carboxylic builder. Sulphuric acid has been found to further contribute to the stability of the final particle.

In some embodiments, the cleaning compositions according to the present invention comprise at least one surfactant and/or a surfactant system wherein the surfactant is selected from nonionic surfactants, anionic surfactants, cationic surfactants, ampholytic surfactants, zwitterionic surfactants, semi-polar nonionic surfactants and mixtures thereof. In some low pH cleaning composition embodiments (e.g., compositions having a neat pH of from about 3 to about 5), the composition typically does not contain alkyl ethoxylated sulfate, as it is believed

that such surfactant may be hydrolyzed by such compositions the acidic contents. In some embodiments, the surfactant is present at a level of from about 0.1% to about 60%, while in alternative embodiments the level is from about 1% to about 50%, while in still further embodiments the level is from about 5% to about 40%, by weight of the cleaning composition.

In some embodiments, the cleaning compositions of the present invention comprise one or more detergent builders or builder systems. In some embodiments incorporating at least one builder, the cleaning compositions comprise at least about 1%, from about 3% to about 60% or even from about 5% to about 40% builder by weight of the cleaning composition. Builders include, but are not limited to, the alkali metal, ammonium and alkanolammonium salts of polyphosphates, alkali metal silicates, alkaline earth and alkali metal carbonates, aluminosilicates, polycarboxylate compounds, ether hydroxypolycarboxylates, copolymers of maleic anhydride with ethylene or vinyl methyl ether, 1, 3, 5-trihydroxy benzene-2, 4, 6-trisulphonic acid, and carboxymethyloxysuccinic acid, the various alkali metal, ammonium and substituted ammonium salts of polyacetic acids such as ethylenediamine tetraacetic acid and nitrilotriacetic acid, as well as polycarboxylates such as mellitic acid, succinic acid, citric acid, oxydisuccinic acid, polymaleic acid, benzene 1,3,5-tricarboxylic acid, carboxymethyloxysuccinic acid, and soluble salts thereof. Indeed, it is contemplated that any suitable builder will find use in various embodiments of the present invention.

In some embodiments, the builders form water-soluble hardness ion complexes (e.g., sequestering builders), such as citrates and polyphosphates (e.g., sodium tripolyphosphate and sodium tripolyphospate hexahydrate, potassium tripolyphosphate, and mixed sodium and potassium tripolyphosphate, etc.). It is contemplated that any suitable builder will find use in the present invention, including those known in the art (See e.g., EP 2 100 949).

In some embodiments, builders for use herein include phosphate builders and non-phosphate builders. In some embodiments, the builder is a phosphate builder. In some embodiments, the builder is a non-phosphate builder. If present, builders are used in a level of from 0.1% to 80%, or from 5 to 60%, or from 10 to 50% by weight of the composition. In some embodiments the product comprises a mixture of phosphate and non-phosphate builders. Suitable phosphate builders include mono-phosphates, di-phosphates, tri-polyphosphates or oligomeric-poylphosphates, including the alkali metal salts of these compounds, including the sodium salts. In some embodiments, a builder can be sodium tripolyphosphate (STPP). Additionally, the composition can comprise carbonate and/or citrate, preferably citrate that helps to achieve a neutral pH composition of the invention. Other suitable non-phosphate builders include homopolymers and copolymers of polycarboxylic acids and their partially or completely

neutralized salts, monomeric polycarboxylic acids and hydroxycarboxylic acids and their salts. In some embodiments, salts of the above mentioned compounds include the ammonium and/or alkali metal salts, i.e. the lithium, sodium, and potassium salts, including sodium salts. Suitable polycarboxylic acids include acyclic, alicyclic, hetero-cyclic and aromatic carboxylic acids, wherein in some embodiments, they can contain at least two carboxyl groups which are in each case separated from one another by, in some instances, no more than two carbon atoms.

In some embodiments, the cleaning compositions of the present invention contain at least one chelating agent. Suitable chelating agents include, but are not limited to copper, iron and/or manganese chelating agents and mixtures thereof. In embodiments in which at least one chelating agent is used, the cleaning compositions of the present invention comprise from about 0.1% to about 15% or even from about 3.0% to about 10% chelating agent by weight of the subject cleaning composition.

In some still further embodiments, the cleaning compositions provided herein contain at least one deposition aid. Suitable deposition aids include, but are not limited to, polyethylene glycol, polypropylene glycol, polycarboxylate, soil release polymers such as polytelephthalic acid, clays such as kaolinite, montmorillonite, atapulgite, illite, bentonite, halloysite, and mixtures thereof.

As indicated herein, in some embodiments, anti-redeposition agents find use in some embodiments of the present invention. In some embodiments, non-ionic surfactants find use. For example, in automatic dishwashing embodiments, non-ionic surfactants find use for surface modification purposes, in particular for sheeting, to avoid filming and spotting and to improve shine. These non-ionic surfactants also find use in preventing the re-deposition of soils. In some embodiments, the anti-redeposition agent is a non-ionic surfactant as known in the art (See e.g., EP 2 100 949). In some embodiments, the non-ionic surfactant can be ethoxylated nonionic surfactants, epoxy-capped poly(oxyalkylated) alcohols and amine oxides surfactants.

In some embodiments, the cleaning compositions of the present invention include one or more dye transfer inhibiting agents. Suitable polymeric dye transfer inhibiting agents include, but are not limited to, polyvinylpyrrolidone polymers, polyamine N-oxide polymers, copolymers of N-vinylpyrrolidone and N-vinylimidazole, polyvinyloxazolidones and polyvinylimidazoles or mixtures thereof. In embodiments in which at least one dye transfer inhibiting agent is used, the cleaning compositions of the present invention comprise from about 0.0001% to about 10%, from about 0.01% to about 5%, or even from about 0.1% to about 3% by weight of the cleaning composition.

In some embodiments, silicates are included within the compositions of the present invention. In some such embodiments, sodium silicates (e.g., sodium disilicate, sodium metasilicate, and crystalline phyllosilicates) find use. In some embodiments, silicates are present at a level of from about 1% to about 20%. In some embodiments, silicates are present at a level of from about 5% to about 15% by weight of the composition.

In some still additional embodiments, the cleaning compositions of the present invention also contain dispersants. Suitable water-soluble organic materials include, but are not limited to the homo- or co-polymeric acids or their salts, in which the polycarboxylic acid comprises at least two carboxyl radicals separated from each other by not more than two carbon atoms.

In some further embodiments, the enzymes used in the cleaning compositions are stabilized by any suitable technique. In some embodiments, the enzymes employed herein are stabilized by the presence of water-soluble sources of calcium and/or magnesium ions in the finished compositions that provide such ions to the enzymes. In some embodiments, the enzyme stabilizers include oligosaccharides, polysaccharides, and inorganic divalent metal salts, including alkaline earth metals, such as calcium salts, such as calcium formate. It is contemplated that various techniques for enzyme stabilization will find use in the present invention. For example, in some embodiments, the enzymes employed herein are stabilized by the presence of water-soluble sources of zinc (II), calcium (II) and/or magnesium (II) ions in the finished compositions that provide such ions to the enzymes, as well as other metal ions (e.g., barium (II), scandium (II), iron (II), manganese (II), aluminum (III), Tin (II), cobalt (II), copper (II), nickel (II), and oxovanadium (IV). Chlorides and sulfates also find use in some embodiments of the present invention. Examples of suitable oligosaccharides and polysaccharides (e.g., dextrins) are known in the art (See e.g., WO 07/145964). In some embodiments, reversible protease inhibitors also find use, such as boron-containing compounds (e.g., borate, 4-formyl phenyl boronic acid) and/or a tripeptide aldehyde find use to further improve stability, as desired.

In some embodiments, bleaches, bleach activators and/or bleach catalysts are present in the compositions of the present invention. In some embodiments, the cleaning compositions of the present invention comprise inorganic and/or organic bleaching compound(s). Inorganic bleaches include, but are not limited to perhydrate salts (e.g., perborate, percarbonate, perphosphate, persulfate, and persilicate salts). In some embodiments, inorganic perhydrate salts are alkali metal salts. In some embodiments, inorganic perhydrate salts are included as the crystalline solid, without additional protection, although in some other embodiments, the salt is

coated. Any suitable salt known in the art finds use in the present invention (See e.g., EP 2 100 949).

In some embodiments, bleach activators are used in the compositions of the present invention. Bleach activators are typically organic peracid precursors that enhance the bleaching action in the course of cleaning at temperatures of 60°C and below. Bleach activators suitable for use herein include compounds which, under perhydrolysis conditions, give aliphatic peroxoycarboxylic acids having preferably from about 1 to about 10 carbon atoms, in particular from about 2 to about 4 carbon atoms, and/or optionally substituted perbenzoic acid. Additional bleach activators are known in the art and find use in the present invention (See e.g., EP 2 100 949).

In addition, in some embodiments and as further described herein, the cleaning compositions of the present invention further comprise at least one bleach catalyst. In some embodiments, the manganese triazacyclononane and related complexes find use, as well as cobalt, copper, manganese, and iron complexes. Additional bleach catalysts find use in the present invention (See e.g., US 4,246,612, 5,227,084, 4,810410, WO 99/06521, and EP 2 100 949).

In some embodiments, the cleaning compositions of the present invention contain one or more catalytic metal complexes. In some embodiments, a metal-containing bleach catalyst finds use. In some embodiments, the metal bleach catalyst comprises a catalyst system comprising a transition metal cation of defined bleach catalytic activity, (e.g., copper, iron, titanium, ruthenium, tungsten, molybdenum, or manganese cations), an auxiliary metal cation having little or no bleach catalytic activity (e.g., zinc or aluminum cations), and a sequestrate having defined stability constants for the catalytic and auxiliary metal cations, particularly ethylenediaminetetraacetic acid, ethylenediaminetetra (methylenephosphonic acid) and water-soluble salts thereof are used (See e.g., US Patent No. 4,430,243). In some embodiments, the cleaning compositions of the present invention are catalyzed by means of a manganese compound. Such compounds and levels of use are well known in the art (See e.g., US Patent No. 5,576,282). In additional embodiments, cobalt bleach catalysts find use in the cleaning compositions of the present invention. Various cobalt bleach catalysts are known in the art (See e.g., US Patent Nos. 5,597,936 and 5,595,967) and are readily prepared by known procedures.

In some additional embodiments, the cleaning compositions of the present invention include a transition metal complex of a macropolycyclic rigid ligand (MRL). As a practical matter, and not by way of limitation, in some embodiments, the compositions and cleaning processes provided by the present invention are adjusted to provide on the order of at least one

part per hundred million of the active MRL species in the aqueous washing medium, and in some embodiments, provide from about 0.005 ppm to about 25 ppm, more preferably from about 0.05 ppm to about 10 ppm, and most preferably from about 0.1 ppm to about 5 ppm, of the MRL in the wash liquor.

In some embodiments, transition-metals in the instant transition-metal bleach catalyst include, but are not limited to manganese, iron and chromium. MRLs also include, but are not limited to special ultra-rigid ligands that are cross-bridged (e.g., 5,12-diethyl-1,5,8,12-tetraazabicyclo[6.6.2]hexadecane). Suitable transition metal MRLs are readily prepared by known procedures (See e.g., WO 2000/32601, and US Patent No. 6,225,464).

In some embodiments, the cleaning compositions of the present invention comprise metal care agents. Metal care agents find use in preventing and/or reducing the tarnishing, corrosion, and/or oxidation of metals, including aluminum, stainless steel, and non-ferrous metals (e.g., silver and copper). Suitable metal care agents include those described in EP 2 100 949, WO 9426860 and WO 94/26859). In some embodiments, the metal care agent is a zinc salt. In some further embodiments, the cleaning compositions of the present invention comprise from about 0.1% to about 5% by weight of one or more metal care agent.

In some embodiments, the cleaning composition is a high density liquid (HDL) composition having a variant metalloprotease polypeptide protease. The HDL liquid laundry detergent can comprise a detersive surfactant (10%-40%) comprising anionic detersive surfactant (selected from a group of linear or branched or random chain, substituted or unsubstituted alkyl sulphates, alkyl sulphonates, alkyl alkoxylated sulphate, alkyl phosphates, alkyl phosphonates, alkyl carboxylates, and/or mixtures thereof); and optionally non-ionic surfactant (selected from a group of linear or branched or random chain, substituted or unsubstituted alkyl alkoxylated alcohol, for example a C_8-C_{18} alkyl ethoxylated alcohol and/or C_6-C_{12} alkyl phenol alkoxylates), optionally wherein the weight ratio of anionic detersive surfactant (with a hydrophilic index (HIc) of from 6.0 to 9) to non-ionic detersive surfactant is greater than 1: 1.

The composition can comprise optionally, a surfactancy boosting polymer consisting of amphiphilic alkoxylated grease cleaning polymers (selected from a group of alkoxylated polymers having branched hydrophilic and hydrophobic properties, such as alkoxylated polyalkylenimines in the range of 0.05wt%-10wt%) and/or random graft polymers (typically comprising of hydrophilic backbone comprising monomers selected from the group consisting of: unsaturated C_1-C_6 carboxylic acids, ethers, alcohols, aldehydes, ketones, esters, sugar units, alkoxy units, maleic anhydride, saturated polyalcohols such as glycerol, and mixtures thereof;

and hydrophobic side chain(s) selected from the group consisting of: C_4-C_{25} alkyl group, polypropylene, polybutylene, vinyl ester of a saturated C-C_6 mono-carboxylic acid, C_1-C_6 alkyl ester of acrylic or methacrylic acid, and mixtures thereof.

The composition can comprise additional polymers such as soil release polymers (include anionically end-capped polyesters, for example SRP1, polymers comprising at least one monomer unit selected from saccharide, dicarboxylic acid, polyol and combinations thereof, in random or block configuration, ethylene terephthalate-based polymers and co-polymers thereof in random or block configuration, for example Repel-o-tex SF, SF-2 and SRP6, Texcare SRA100, SRA300, SRN100, SRN170, SRN240, SRN300 and SRN325, Marloquest SL), anti-redeposition polymers (0.1 wt% to 10wt%, include carboxylate polymers, such as polymers comprising at least one monomer selected from acrylic acid, maleic acid (or maleic anhydride), fumaric acid, itaconic acid, aconitic acid, mesaconic acid, citraconic acid, methylenemalonic acid, and any mixture thereof, vinylpyrrolidone homopolymer, and/or polyethylene glycol, molecular weight in the range of from 500 to 100,000 Da); cellulosic polymer (including those selected from alkyl cellulose, alkyl alkoxyalkyl cellulose, carboxyalkyl cellulose, alkyl carboxyalkyl cellulose examples of which include carboxymethyl cellulose, methyl cellulose, methyl hydroxyethyl cellulose, methyl carboxymethyl cellulose, and mixures thereof) and polymeric carboxylate (such as maleate/acrylate random copolymer or polyacrylate homopolymer).

The composition can further comprise saturated or unsaturated fatty acid, preferably saturated or unsaturated C_{12}-C_{24} fatty acid (0 wt% to 10 wt%); deposition aids (examples for which include polysaccharides, preferably cellulosic polymers, poly diallyl dimethyl ammonium halides (DADMAC), and co-polymers of DAD MAC with vinyl pyrrolidone, acrylamides, imidazoles, imidazolinium halides, and mixtures thereof, in random or block configuration, cationic guar gum, cationic cellulose such as cationic hydoxyethyl cellulose, cationic starch, cationic polyacylamides, and mixtures thereof.

The composition can further comprise dye transfer inhibiting agents examples of which include manganese phthalocyanine, peroxidases, polyvinylpyrrolidone polymers, polyamine N-oxide polymers, copolymers of N-vinylpyrrolidone and N-vinylimidazole, polyvinyloxazolidones and polyvinylimidazoles and/or mixtures thereof; chelating agents examples of which include ethylene-diamine-tetraacetic acid (EDTA); diethylene triamine penta methylene phosphonic acid (DTPMP); hydroxy-ethane diphosphonic acid (HEDP); ethylenediamine N,N'-disuccinic acid (EDDS); methyl glycine diacetic acid (MGDA);

diethylene triamine penta acetic acid (DTPA); propylene diamine tetracetic acid (PDT A); 2-hydroxypyridine-N-oxide (HPNO); or methyl glycine diacetic acid (MGDA); glutamic acid N,N-diacetic acid (N,N-dicarboxymethyl glutamic acid tetrasodium salt (GLDA); nitrilotriacetic acid (NTA); 4,5-dihydroxy-m-benzenedisulfonic acid; citric acid and any salts thereof; N-hydroxyethylethylenediaminetri-acetic acid (HEDTA), triethylenetetraaminehexaacetic acid (TTHA), N-hydroxyethyliminodiacetic acid (HEIDA), dihydroxyethylglycine (DHEG), ethylenediaminetetrapropionic acid (EDTP) and derivatives thereof.

The composition can further comprise enzymes (0.01 wt% active enzyme to 0.03wt% active enzyme) selected from a group of acyl transferases, alpha-amylases, beta-amylases, alpha-galactosidases, arabinosidases, aryl esterases, beta-galactosidases, carrageenases, catalases, cellobiohydrolases, cellulases, chondroitinases, cutinases, endo-beta-1, 4-glucanases, endo-beta-mannanases, esterases, exo-mannanases, galactanases, glucoamylases, hemicellulases, hyaluronidases, keratinases, laccases, lactases, ligninases, lipases, lipoxygenases, mannanases, oxidases, pectate lyases, pectin acetyl esterases, pectinases, pentosanases, peroxidases, phenoloxidases, phosphatases, phospholipases, phytases, polygalacturonases, proteases, pullulanases, reductases, rhamnogalacturonases, beta-glucanases, tannases, transglutaminases, xylan acetyl-esterases, xylanases, xyloglucanases, and xylosidases, and any mixture thereof. The composition may comprise an enzyme stabilizer (examples of which include polyols such as propylene glycol or glycerol, sugar or sugar alcohol, lactic acid, reversible protease inhibitor, boric acid, or a boric acid derivative, e.g., an aromatic borate ester, or a phenyl boronic acid derivative such as 4-formylphenyl boronic acid).

The composition can further comprise silicone or fatty-acid based suds suppressors; heuing dyes, calcium and magnesium cations, visual signaling ingredients, anti-foam (0.001 wt% to about 4.0wt%), and/or structurant/thickener (0.01 wt% to 5wt%, selected from the group consisting of diglycerides and triglycerides, ethylene glycol distearate, microcrystalline cellulose, cellulose based materials, microfiber cellulose, biopolymers, xanthan gum, gellan gum, and mixtures thereof).

Suitable detersive surfactants also include cationic detersive surfactants (selected from a group of alkyl pyridinium compounds, alkyl quarternary ammonium compounds, alkyl quarternary phosphonium compounds, alkyl ternary sulphonium compounds, and/or mixtures thereof); zwitterionic and/or amphoteric detersive surfactants (selected from a group of alkanolamine sulpho-betaines); ampholytic surfactants; semi-polar non-ionic surfactants and mixtures thereof.

The composition can be any liquid form, for example a liquid or gel form, or any combination thereof. The composition may be in any unit dose form, for example a pouch.

In some embodiments, the cleaning composition is a high density powder (HDD) composition having a variant metalloprotease polypeptide protease. The HDD powder laundry detergent can comprise a detersive surfactant including anionic detersive surfactants (selected from a group of linear or branched or random chain, substituted or unsubstituted alkyl sulphates, alkyl sulphonates, alkyl alkoxylated sulphate, alkyl phosphates, alkyl phosphonates, alkyl carboxylates and/or mixtures thereof), non-ionic detersive surfactant (selected from a group of linear or branched or random chain, substituted or unsubstituted C_8-C_{18} alkyl ethoxylates, and/or C_6-C_{12} alkyl phenol alkoxylates), cationic detersive surfactants (selected from a group of alkyl pyridinium compounds, alkyl quaternary ammonium compounds, alkyl quaternary phosphonium compounds, alkyl ternary sulphonium compounds, and mixtures thereof), zwitterionic and/or amphoteric detersive surfactants (selected from a group of alkanolamine sulpho-betaines); ampholytic surfactants; semi-polar non-ionic surfactants and mixtures thereof; builders (phosphate free builders [for example zeolite builders examples of which include zeolite A, zeolite X, zeolite P and zeolite MAP in the range of 0wt% to less than 10wt%]; phosphate builders [examples of which include sodium tri-polyphosphate in the range of 0wt% to less than 10wt%]; citric acid, citrate salts and nitrilotriacetic acid or salt thereof in the range of less than 15 wt%); silicate salt (sodium or potassium silicate or sodium meta-silicate in the range of 0wt% to less than 10wt%, or layered silicate (SKS-6)); carbonate salt (sodium carbonate and/or sodium bicarbonate in the range of 0 wt% to less than 10 wt%); and bleaching agents (photobleaches, examples of which include sulfonated zinc phthalocyanines, sulfonated aluminum phthalocyanines, xanthenes dyes, and mixtures thereof; hydrophobic or hydrophilic bleach activators (examples of which include dodecanoyl oxybenzene sulfonate, decanoyl oxybenzene sulfonate, decanoyl oxybenzoic acid or salts thereof, 3,5,5-trimethy hexanoyl oxybenzene sulfonate, tetraacetyl ethylene diamine-TAED, and nonanoyloxybenzene sulfonate-NOBS, nitrile quats, and mixtures thereof; hydrogen peroxide; sources of hydrogen peroxide (inorganic perhydrate salts examples of which include mono or tetra hydrate sodium salt of perborate, percarbonate, persulfate, perphosphate, or persilicate); preformed hydrophilic and/or hydrophobic peracids (selected from a group consisting of percarboxylic acids and salts, percarbonic acids and salts, perimidic acids and salts, peroxymonosulfuric acids and salts) & mixtures thereof and/or bleach catalyst (such as imine bleach boosters examples of which include iminium cations and polyions; iminium zwitterions; modified amines; modified amine oxides; N-sulphonyl imines; N-phosphonyl imines; N-acyl imines; thiadiazole dioxides;

perfluoroimines; cyclic sugar ketones and mixtures thereof; metal-containing bleach catalyst for example copper, iron, titanium, ruthenium, tungsten, molybdenum, or manganese cations along with an auxiliary metal cations such as zinc or aluminum and a sequestrate such as ethylenediaminetetraacetic acid, ethylenediaminetetra(methylenephos¬phonic acid) and water-soluble salts thereof).

The composition can further comprise enzymes selected from a group of acyl transferases, alpha-amylases, beta-amylases, alpha-galactosidases, arabinosidases, aryl esterases, beta-galactosidases, carrageenases, catalases, cellobiohydrolases, cellulases, chondroitinases, cutinases, endo-beta-1, 4-glucanases, endo-beta-mannanases, esterases, exo-mannanases, galactanases, glucoamylases, glucose oxidases, hemicellulases, hyaluronidases, keratinases, laccases, lactases, ligninases, lipases, lipoxygenases, mannanases, oxidases, pectate lyases, pectin acetyl esterases, pectinases, pentosanases, perhydrolases, peroxidases, phenoloxidases, phosphatases, phospholipases, phytases, polygalacturonases, proteases, pullulanases, reductases, rhamnogalacturonases, beta-glucanases, tannases, transglutaminases, xylan acetyl-esterases, xylanases, xyloglucanases, and xylosidases and any mixture thereof.

The composition can further comprise additional detergent ingredients including perfume microcapsules, starch encapsulated perfume accord, hueing agents, additional polymers including fabric integrity and cationic polymers, dye lock ingredients, fabric-softening agents, brighteners (for example C.I. Fluorescent brighteners), flocculating agents, chelating agents, alkoxylated polyamines, fabric deposition aids, and/or cyclodextrin.

In some embodiments, the cleaning composition is an automatic dishwashing (ADW) detergent composition having a metalloprotease of the present invention. The ADW detergent composition can comprise two or more non-ionic surfactants selected from a group of ethoxylated non-ionic surfactants, alcohol alkoxylated surfactants, epoxy-capped poly(oxyalkylated) alcohols, or amine oxide surfactants present in amounts from 0 to 10% by weight; builders in the range of 5-60% comprising either phosphate (mono-phosphates, di-phosphates, tri-polyphosphates or oligomeric-poylphosphates, preferred sodium tripolyphosphate-STPP or phosphate-free builders [amino acid based compounds, examples of which include MGDA (methyl-glycine-diacetic acid), and salts and derivatives thereof, GLDA (glutamic-N,Ndiacetic acid) and salts and derivatives thereof, IDS (iminodisuccinic acid) and salts and derivatives thereof, carboxy methyl inulin and salts and derivatives thereof and mixtures thereof, nitrilotriacetic acid (NTA), diethylene triamine penta acetic acid (DTPA), B-alaninediacetic acid (B-ADA) and their salts], homopolymers and copolymers of poly-carboxylic acids and their partially or completely neutralized salts, monomeric polycarboxylic

acids and hydroxycarboxylic acids and their salts in the range of 0.5% to 50% by weight;
sulfonated/carboxylated polymers (provide dimensional stability to the product) in the range of
about 0.1 % to about 50% by weight; drying aids in the range of about 0.1 % to about 10% by
weight (selected from polyesters, especially anionic polyesters optionally together with further
monomers with 3 to 6 functionalities which are conducive to polycondensation, specifically
acid, alcohol or ester functionalities, polycarbonate-, polyurethane- and/or polyurea-
polyorganosiloxane compounds or precursor compounds thereof of the reactive cyclic carbonate
and urea type); silicates in the range from about 1 % to about 20% by weight (sodium or
potassium silicates for example sodium disilicate, sodium meta-silicate and crystalline
phyllosilicates); bleach-inorganic (for example perhydrate salts such as perborate, percarbonate,
perphosphate, persulfate and persilicate salts) and organic (for example organic peroxyacids
including diacyl and tetraacylperoxides, especially diperoxydodecanedioc acid,
diperoxytetradecanedioc acid, and diperoxyhexadecanedioc acid); bleach activators- organic
peracid precursors in the range from about 0.1 % to about 10% by weight; bleach catalysts
(selected from manganese triazacyclononane and related complexes, Co, Cu, Mn and Fe
bispyridylamine and related complexes, and pentamine acetate cobalt(III) and related
complexes); metal care agents in the range from about 0.1% to 5% by weight (selected from
benzatriazoles, metal salts and complexes, and/or silicates); enzymes in the range from about
0.01 to 5.0mg of active enzyme per gram of automatic dishwashing detergent composition (acyl
transferases, alpha-amylases, beta-amylases, alpha-galactosidases, arabinosidases, aryl esterases,
beta-galactosidases, carrageenases, catalases, cellobiohydrolases, cellulases, chondroitinases,
cutinases, endo-beta-1, 4-glucanases, endo-beta-mannanases, esterases, exo-mannanases,
galactanases, glucoamylases, hemicellulases, hyaluronidases, keratinases, laccases, lactases,
ligninases, lipases, lipoxygenases, mannanases, oxidases, pectate lyases, pectin acetyl esterases,
pectinases, pentosanases, peroxidases, phenoloxidases, phosphatases, phospholipases, phytases,
polygalacturonases, proteases, pullulanases, reductases, rhamnogalacturonases, beta-glucanases,
tannases, transglutaminases, xylan acetyl-esterases, xylanases, xyloglucanases, and xylosidases,
and any mixture thereof); and enzyme stabilizer components (selected from oligosaccharides,
polysaccharides and inorganic divalent metal salts).

Representative detergent formulations that beneficially include a metalloprotease
polypeptide of the present invention include the detergent formulations found in
WO2013063460, pages 78-152, and in particular the tables of pages 94 to 152 are hereby
incorporated by reference. The metalloproteases are normally incorporated into the detergent
composition at a level of from 0.000001 % to 5% of enzyme protein by weight of the

composition, or from 0.00001 % to 2 %, or from 0.0001% to 1%, or from 0.001 % to 0.75% of enzyme protein by weight of the composition.

Metalloprotease polypeptides of the present invention for use in Animal Feed

In a further aspect of the invention, the metalloprotease polypeptides of the present invention can be used as a compontent of an animal feed composition, animal feed additive and/or pet food comprising a metalloprotease and variants thereof. The present invention further relates to a method for preparing such an animal feed composition, animal feed additive composition and/or pet food comprising mixing the metalloprotease polypeptide with one or more animal feed ingredients and/or animal feed additive ingredients and/or pet food ingredients. Furthermore, the present invention relates to the use of the metalloprotease polypeptide in the preparation of an animal feed composition and/or animal feed additive composition and/or pet food.

The term "animal" includes all non-ruminant and ruminant animals. In a particular embodiment, the animal is a non-ruminant animal, such as a horse and a mono-gastric animal. Examples of mono-gastric animals include, but are not limited to, pigs and swine, such as piglets, growing pigs, sows; poultry such as turkeys, ducks, chicken, broiler chicks, layers; fish such as salmon, trout, tilapia, catfish and carps; and crustaceans such as shrimps and prawns. In a further embodiment the animal is a ruminant animal including, but not limited to, cattle, young calves, goats, sheep, giraffes, bison, moose, elk, yaks, water buffalo, deer, camels, alpacas, llamas, antelope, pronghorn and nilgai.

In the present context, it is intended that the term "pet food" is understood to mean a food for a household animal such as, but not limited to, dogs, cats, gerbils, hamsters, chinchillas, fancy rats, guinea pigs; avian pets, such as canaries, parakeets, and parrots; reptile pets, such as turtles, lizards and snakes; and aquatic pets, such as tropical fish and frogs.

The terms "animal feed composition," "feedstuff" and "fodder" are used interchangeably and can comprise one or more feed materials selected from the group comprising a) cereals, such as small grains (e.g., wheat, barley, rye, oats and combinations thereof) and/or large grains such as maize or sorghum; b) by products from cereals, such as corn gluten meal, Distillers Dried Grain Solubles (DDGS) (particularly corn based Distillers Dried Grain Solubles (cDDGS), wheat bran, wheat middlings, wheat shorts, rice bran, rice hulls, oat hulls, palm kernel, and citrus pulp; c) protein obtained from sources such as soya, sunflower, peanut, lupin, peas, fava beans, cotton, canola, fish meal, dried plasma protein, meat and bone meal, potato

protein, whey, copra, sesame; d) oils and fats obtained from vegetable and animal sources; e) minerals and vitamins.

Metalloprotease polypeptides of the present invention for use in Textile Desizing

Also contemplated are compositions and methods of treating fabrics (*e.g.*, to desize a textile) using a metalloprotease polypeptide of the present invention. Fabric-treating methods are well known in the art (*see, e.g.*, U.S. Patent No. 6,077,316). For example, the feel and appearance of a fabric can be improved by a method comprising contacting the fabric with a metalloprotease in a solution. The fabric can be treated with the solution under pressure.

A metalloprotease of the present invention can be applied during or after the weaving of a textile, or during the desizing stage, or one or more additional fabric processing steps. During the weaving of textiles, the threads are exposed to considerable mechanical strain. Prior to weaving on mechanical looms, warp yarns are often coated with sizing starch or starch derivatives to increase their tensile strength and to prevent breaking. A metalloprotease of the present invention can be applied during or after the weaving to remove these sizing starch or starch derivatives. After weaving, the metalloprotease can be used to remove the size coating before further processing the fabric to ensure a homogeneous and wash-proof result.

A metalloprotease of the present invention can be used alone or with other desizing chemical reagents and/or desizing enzymes to desize fabrics, including cotton-containing fabrics, as detergent additives, *e.g.*, in aqueous compositions. An amylase also can be used in compositions and methods for producing a stonewashed look on indigo-dyed denim fabric and garments. For the manufacture of clothes, the fabric can be cut and sewn into clothes or garments, which are afterwards finished. In particular, for the manufacture of denim jeans, different enzymatic finishing methods have been developed. The finishing of denim garment normally is initiated with an enzymatic desizing step, during which garments are subjected to the action of proteolytic enzymes to provide softness to the fabric and make the cotton more accessible to the subsequent enzymatic finishing steps. The metalloprotease can be used in methods of finishing denim garments (*e.g.*, a "bio-stoning process"), enzymatic desizing and providing softness to fabrics, and/or finishing process.

Metalloprotease polypeptides of the present invention for use in Paper Pulp Bleaching

The metalloprotease polypeptides described herein find further use in the enzyme aided bleaching of paper pulps such as chemical pulps, semi-chemical pulps, kraft pulps, mechanical pulps or pulps prepared by the sulfite method. In general terms, paper pulps are

incubated with a metalloprotease polypeptide of the present invention under conditions suitable for bleaching the paper pulp.

In some embodiments, the pulps are chlorine free pulps bleached with oxygen, ozone, peroxide or peroxyacids. In some embodiments, the metalloprotease polypeptides are used in enzyme aided bleaching of pulps produced by modified or continuous pulping methods that exhibit low lignin contents. In some other embodiments, the metalloprotease polypeptides are applied alone or preferably in combination with xylanase and/or endoglucanase and/or alpha-galactosidase and/or cellobiohydrolase enzymes.

Metalloprotease polypeptides of the present invention for use in Protein degradation

The metalloprotease polypeptides described herein find further use in the enzyme aided removal of proteins from animals and their subsequent degradation or disposal, such as feathers, skin, hair, hide, and the like. In some instances, immersion of the animal carcass in a solution comprising a metalloprotease polypeptide of the present invention can act to protect the skin from damage in comparison to the traditional immersion in scalding water or the defeathering process. In one embodiment, feathers can be sprayed with an isolated metalloprotase polypeptide of the present invention under conditions suitable for digesting or initiating degradation of the plumage. In some embodiments, a metalloprotease of the present invention can be used, as above, in combination with an oxidizing agent.

In some embodiments, removal of the oil or fat associated with raw feathers is assisted by using a metalloprotease polypeptide of the present invention. In some embodiments, the metalloprotease polypeptides are used in compositions for cleaning the feathers as well as to sanitize and partially dehydrate the fibers. In some other embodiments, the metalloprotease polypeptides are applied in a wash solution in combination with 95% ethanol or other polar organic solvent with or without a surfactant at about 0.5% (v/v).

In yet other embodiments, the disclosed metalloprotease polypeptides find use in recovering protein from plumage. In some embodiments, the recovered protein can be subsequently used in animal or fish feed.

Metalloprotease polypeptides of the present invention for use in Tissue Debridement

The metalloprotease polypeptides described herein find further use in the enzyme aided debridement of tissue. This involves the removal of dead or damaged tissue, for example, removal from wounds to aid in healing.

Metalloprotease polypeptides of the present invention for use in tissue culture

The metalloprotease polypeptides described herein find further use in tissue culture. In particular, metalloproteases of the present invention can be used to suspend or resuspend cells adherent to a cell culture wall, such as during the process of harvesting cells. Metalloproteases of the present invention can be used to cleave protein bonds between cultured cells and the dish, allowing cells to become suspended in solution.

Metalloprotease polypeptides of the present invention for use in leather processing

The metalloprotease polypeptides described herein find further use in leather processing by removing hair from animal hides, soaking, degreasing, or bating, which is a process involving degradation of non-structural proteins during leather making.

EXPERIMENTAL

The claimed invention is described in further detail in the following examples which are not in any way intended to limit the scope of the invention as claimed.

EXAMPLE 1

Crystallization and structure determination of PehPro1 metalloprotease

The metalloprotease PehPro1, encoded by a *Paenibacillus ehimensis* strain was crystallized using the hanging drop method from a solution of protein stock at a concentration of 27.9 mg/mL in 20mM Tris pH 8.5 + 0.10M Sodium chloride + 1mM Calcium chloride. Aliquots of 2 μL of the protein stock and 2 μL of the crystallization solution were mixed on a plastic coverslip and inverted and sealed on a chamber containing 15-25% Polyethylene Glycol 8000 + 50mM Potassium phosphate monobasic + 0.10M HEPES pH 7.5 in a Linbro 6 X 4 culture plate.

Crystals grew in the space group C 2 2 2_1 with unit cell dimensions; a=58.814 Å, b=194.346 Å, and c=138.355 Å. Data were collected on native crystal to 2.79 Å resolution and the structure of PehPro1 was determined by molecular replacement using a related protein (pdb ID 1ESP) as the phasing model. The statistics of data collected are presented in Table 1.1.

Table 1.1: Statistics of PehPro1 Data collection	
Wavelength	1.54 Å
Space group	C222
Molecules in asymmetric unit	2
Unit cell dimensions	a=58.81 Å, b=194.35 Å and c=138.36 Å
Resolution	32.6 - 2.79 Å
Unique reflections	19103
Multiplicity	17 (11*)
Completeness	99.33% (92%*)
R_{merge}	0.08 (0.30*)
I/σ_I	17 (8*)

*Value in parenthesis is that of the outermost shell of data

The model was fitted in the resulting electron density using the program COOT (Emsley, P et al Acta Cryst. D66 486-501 (2010)). After fitting and refitting adjustments, the coordinates were refined using the REFMAC program with standard defaults in the CCP4 software suite. The statistics of the current model are presented in Table 1.2.

Table 1.2: Statistics of the refined model	
R work	0.19
R free	0.25
No. protein residues	304
No. atoms	4742
rmsd Bond lengths	0.013Å
rmsd bond angles	1.6°

EXAMPLE 2

PehPro1 crystal structure details

The structure of PehPro1 consists of a dimer of two equivalent molecules.   Electron density was available for residues 1-304 of each monomer. Each model was fitted to contiguous density. The overall dimer arrangement is presented in Figure 1. The residues forming the active site regions include the catalytic residues; His135, Glu136, His139 and Glu159 (numbering based on PehPro1 mature sequence) forming the characteristic zinc metal binding site, along with other residues forming the substrate binding pocket are conserved between the

PehPro1 and Thermolysin structures (Matthews, B.W., Weaver, L.H., Kester, W.R., The

Conformation of Thermolysin, (1974) J.Biol.Chem. 249: 8030; Dahlquist, F.W., Long, J.W.,

Bigbee, W.L., Role of Calcium in the Thermal Stability of Thermolysin, (1976) *Biochemistry*

15: 1103).

The coordinates for this molecule are listed below.

```
ATOM      1   N    ALA A   1    -17.159 -64.455  -9.260  1.00 39.68      A   N
ATOM      2   CA   ALA A   1    -18.338 -64.728 -10.130  1.00 33.72      A   C
ATOM      3   CB   ALA A   1    -19.640 -64.092  -9.687  1.00 32.16      A   C
ATOM      4   C    ALA A   1    -17.839 -63.991 -11.323  1.00 30.98      A   C
ATOM      5   O    ALA A   1    -17.083 -63.038 -11.132  1.00 31.11      A   O
ATOM      6   N    THR A   2    -18.230 -64.375 -12.537  1.00 27.24      A   N
ATOM      7   CA   THR A   2    -17.655 -63.718 -13.709  1.00 23.73      A   C
ATOM      8   CB   THR A   2    -16.933 -64.722 -14.609  1.00 23.24      A   C
ATOM      9   OG1  THR A   2    -16.035 -65.475 -13.800  1.00 23.09      A   O
ATOM     10   CG2  THR A   2    -16.117 -64.026 -15.659  1.00 22.84      A   C
ATOM     11   C    THR A   2    -18.690 -62.894 -14.454  1.00 22.06      A   C
ATOM     12   O    THR A   2    -19.503 -63.421 -15.169  1.00 22.29      A   O
ATOM     13   N    GLY A   3    -18.652 -61.581 -14.259  1.00 21.36      A   N
ATOM     14   CA   GLY A   3    -19.512 -60.660 -14.981  1.00 20.30      A   C
ATOM     15   C    GLY A   3    -18.962 -60.326 -16.364  1.00 20.22      A   C
ATOM     16   O    GLY A   3    -17.744 -60.439 -16.667  1.00 18.32      A   O
ATOM     17   N    THR A   4    -19.885 -59.870 -17.199  1.00 20.55      A   N
ATOM     18   CA   THR A   4    -19.612 -59.576 -18.593  1.00 20.58      A   C
ATOM     19   CB   THR A   4    -19.948 -60.825 -19.426  1.00 20.39      A   C
ATOM     20   OG1  THR A   4    -19.095 -60.904 -20.570  1.00 21.45      A   O
ATOM     21   CG2  THR A   4    -21.404 -60.866 -19.797  1.00 20.52      A   C
ATOM     22   C    THR A   4    -20.371 -58.290 -18.979  1.00 20.82      A   C
ATOM     23   O    THR A   4    -21.362 -57.946 -18.344  1.00 20.84      A   O
ATOM     24   N    GLY A   5    -19.870 -57.532 -19.955  1.00 22.14      A   N
ATOM     25   CA   GLY A   5    -20.474 -56.214 -20.307  1.00 21.26      A   C
ATOM     26   C    GLY A   5    -19.683 -55.446 -21.353  1.00 21.65      A   C
ATOM     27   O    GLY A   5    -18.525 -55.770 -21.629  1.00 21.95      A   O
ATOM     28   N    LYS A   6    -20.293 -54.433 -21.958  1.00 23.22      A   N
ATOM     29   CA   LYS A   6    -19.599 -53.661 -22.999  1.00 23.98      A   C
ATOM     30   CB   LYS A   6    -20.501 -53.316 -24.191  1.00 26.75      A   C
ATOM     31   CG   LYS A   6    -21.062 -54.545 -24.928  1.00 31.43      A   C
ATOM     32   CD   LYS A   6    -21.426 -54.362 -26.429  1.00 34.80      A   C
ATOM     33   CE   LYS A   6    -22.314 -53.151 -26.767  1.00 37.30      A   C
ATOM     34   NZ   LYS A   6    -23.750 -53.306 -26.350  1.00 38.51      A   N
ATOM     35   C    LYS A   6    -19.019 -52.412 -22.379  1.00 21.52      A   C
ATOM     36   O    LYS A   6    -19.655 -51.799 -21.527  1.00 21.20      A   O
ATOM     37   N    GLY A   7    -17.806 -52.049 -22.801  1.00 19.41      A   N
ATOM     38   CA   GLY A   7    -17.124 -50.843 -22.311  1.00 17.91      A   C
ATOM     39   C    GLY A   7    -17.709 -49.607 -22.918  1.00 17.02      A   C
ATOM     40   O    GLY A   7    -18.733 -49.657 -23.599  1.00 17.62      A   O
ATOM     41   N    VAL A   8    -17.062 -48.481 -22.697  1.00 16.27      A   N
ATOM     42   CA   VAL A   8    -17.536 -47.207 -23.273  1.00 15.98      A   C
ATOM     43   CB   VAL A   8    -16.608 -46.061 -22.849  1.00 16.24      A   C
ATOM     44   CG1  VAL A   8    -16.843 -44.785 -23.665  1.00 15.97      A   C
ATOM     45   CG2  VAL A   8    -16.770 -45.827 -21.354  1.00 16.69      A   C
ATOM     46   C    VAL A   8    -17.580 -47.271 -24.800  1.00 15.88      A   C
ATOM     47   O    VAL A   8    -18.502 -46.760 -25.430  1.00 14.79      A   O
ATOM     48   N    LEU A   9    -16.564 -47.928 -25.366  1.00 15.93      A   N
ATOM     49   CA   LEU A   9    -16.361 -48.015 -26.814  1.00 15.86      A   C
ATOM     50   CB   LEU A   9    -14.852 -48.093 -27.086  1.00 15.92      A   C
ATOM     51   CG   LEU A   9    -14.126 -46.852 -27.579  1.00 15.70      A   C
ATOM     52   CD1  LEU A   9    -14.696 -45.602 -26.965  1.00 15.39      A   C
ATOM     53   CD2  LEU A   9    -12.636 -46.998 -27.283  1.00 15.95      A   C
ATOM     54   C    LEU A   9    -17.023 -49.217 -27.493  1.00 15.36      A   C
ATOM     55   O    LEU A   9    -16.577 -49.596 -28.592  1.00 15.14      A   O
ATOM     56   N    GLY A  10    -18.010 -49.842 -26.831  1.00 14.23      A   N
ATOM     57   CA   GLY A  10    -18.771 -50.970 -27.404  1.00 13.71      A   C
ATOM     58   C    GLY A  10    -18.144 -52.351 -27.326  1.00 13.72      A   C
ATOM     59   O    GLY A  10    -18.738 -53.341 -27.753  1.00 13.58      A   O
ATOM     60   N    ASP A  11    -16.945 -52.433 -26.768  1.00 13.97      A   N
ATOM     61   CA   ASP A  11    -16.223 -53.677 -26.721  1.00 14.03      A   C
ATOM     62   CB   ASP A  11    -14.715 -53.447 -26.716  1.00 14.10      A   C
ATOM     63   CG   ASP A  11    -14.243 -52.431 -25.655  1.00 14.65      A   C
ATOM     64   OD1  ASP A  11    -14.971 -51.470 -25.307  1.00 14.45      A   O
ATOM     65   OD2  ASP A  11    -13.091 -52.593 -25.195  1.00 15.19      A   O
ATOM     66   C    ASP A  11    -16.647 -54.501 -25.529  1.00 14.72      A   C
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ATOM	67	O	ASP	A	11	-16.756	-53.984	-24.433	1.00	14.88	A	O
ATOM	68	N	THR	A	12	-16.844	-55.802	-25.763	1.00	15.81	A	N
ATOM	69	CA	THR	A	12	-17.317	-56.754	-24.758	1.00	15.88	A	C
ATOM	70	CB	THR	A	12	-17.962	-57.966	-25.452	1.00	15.68	A	C
ATOM	71	OG1	THR	A	12	-19.275	-57.606	-25.914	1.00	15.63	A	O
ATOM	72	CG2	THR	A	12	-18.054	-59.155	-24.518	1.00	15.69	A	C
ATOM	73	C	THR	A	12	-16.171	-57.235	-23.884	1.00	16.48	A	C
ATOM	74	O	THR	A	12	-15.136	-57.569	-24.392	1.00	16.69	A	O
ATOM	75	N	LYS	A	13	-16.380	-57.296	-22.572	1.00	17.65	A	N
ATOM	76	CA	LYS	A	13	-15.333	-57.703	-21.603	1.00	18.19	A	C
ATOM	77	CB	LYS	A	13	-14.788	-56.474	-20.861	1.00	19.32	A	C
ATOM	78	CG	LYS	A	13	-13.717	-55.737	-21.568	1.00	20.03	A	C
ATOM	79	CD	LYS	A	13	-13.757	-54.265	-21.245	1.00	20.24	A	C
ATOM	80	CE	LYS	A	13	-12.730	-53.620	-22.168	1.00	21.08	A	C
ATOM	81	NZ	LYS	A	13	-13.089	-52.212	-22.399	1.00	21.72	A	N
ATOM	82	C	LYS	A	13	-15.855	-58.583	-20.482	1.00	17.16	A	C
ATOM	83	O	LYS	A	13	-17.047	-58.515	-20.130	1.00	15.92	A	O
ATOM	84	N	SER	A	14	-14.904	-59.286	-19.864	1.00	16.11	A	N
ATOM	85	CA	SER	A	14	-15.114	-60.029	-18.621	1.00	16.16	A	C
ATOM	86	CB	SER	A	14	-14.659	-61.492	-18.751	1.00	15.77	A	C
ATOM	87	OG	SER	A	14	-15.523	-62.202	-19.587	1.00	15.69	A	O
ATOM	88	C	SER	A	14	-14.324	-59.439	-17.460	1.00	15.77	A	C
ATOM	89	O	SER	A	14	-13.254	-58.842	-17.641	1.00	16.38	A	O
ATOM	90	N	PHE	A	15	-14.833	-59.712	-16.263	1.00	14.76	A	N
ATOM	91	CA	PHE	A	15	-14.281	-59.224	-15.009	1.00	13.44	A	C
ATOM	92	CB	PHE	A	15	-14.562	-57.741	-14.855	1.00	12.78	A	C
ATOM	93	CG	PHE	A	15	-15.901	-57.329	-15.375	1.00	12.44	A	C
ATOM	94	CD1	PHE	A	15	-17.004	-57.402	-14.588	1.00	12.46	A	C
ATOM	95	CE1	PHE	A	15	-18.248	-57.033	-15.066	1.00	12.45	A	C
ATOM	96	CZ	PHE	A	15	-18.398	-56.582	-16.350	1.00	12.34	A	C
ATOM	97	CE2	PHE	A	15	-17.288	-56.491	-17.148	1.00	12.82	A	C
ATOM	98	CD2	PHE	A	15	-16.046	-56.868	-16.655	1.00	12.74	A	C
ATOM	99	C	PHE	A	15	-14.946	-59.973	-13.852	1.00	13.24	A	C
ATOM	100	O	PHE	A	15	-15.970	-60.647	-14.005	1.00	12.99	A	O
ATOM	101	N	THR	A	16	-14.373	-59.798	-12.679	1.00	12.90	A	N
ATOM	102	CA	THR	A	16	-14.843	-60.461	-11.492	1.00	12.27	A	C
ATOM	103	CB	THR	A	16	-13.661	-60.746	-10.602	1.00	11.79	A	C
ATOM	104	OG1	THR	A	16	-12.628	-61.323	-11.424	1.00	11.21	A	O
ATOM	105	CG2	THR	A	16	-14.056	-61.662	-9.465	1.00	11.43	A	C
ATOM	106	C	THR	A	16	-15.862	-59.593	-10.771	1.00	12.41	A	C
ATOM	107	O	THR	A	16	-15.728	-58.359	-10.686	1.00	12.07	A	O
ATOM	108	N	THR	A	17	-16.914	-60.252	-10.303	1.00	12.28	A	N
ATOM	109	CA	THR	A	17	-17.952	-59.582	-9.540	1.00	12.14	A	C
ATOM	110	CB	THR	A	17	-19.202	-59.303	-10.396	1.00	11.78	A	C
ATOM	111	OG1	THR	A	17	-19.721	-60.532	-10.919	1.00	11.36	A	O
ATOM	112	CG2	THR	A	17	-18.838	-58.371	-11.537	1.00	11.82	A	C
ATOM	113	C	THR	A	17	-18.321	-60.453	-8.367	1.00	12.21	A	C
ATOM	114	O	THR	A	17	-17.882	-61.580	-8.242	1.00	10.79	A	O
ATOM	115	N	THR	A	18	-19.156	-59.908	-7.515	1.00	13.29	A	N
ATOM	116	CA	THR	A	18	-19.482	-60.584	-6.301	1.00	14.74	A	C
ATOM	117	CB	THR	A	18	-18.921	-59.785	-5.103	1.00	14.74	A	C
ATOM	118	OG1	THR	A	18	-17.470	-59.893	-5.058	1.00	14.74	A	O
ATOM	119	CG2	THR	A	18	-19.524	-60.310	-3.835	1.00	15.11	A	C
ATOM	120	C	THR	A	18	-21.010	-60.819	-6.232	1.00	15.79	A	C
ATOM	121	O	THR	A	18	-21.779	-59.898	-6.354	1.00	14.67	A	O
ATOM	122	N	GLN	A	19	-21.424	-62.076	-6.075	1.00	17.88	A	N
ATOM	123	CA	GLN	A	19	-22.843	-62.418	-5.943	1.00	19.54	A	C
ATOM	124	CB	GLN	A	19	-23.100	-63.901	-6.252	1.00	21.61	A	C
ATOM	125	CG	GLN	A	19	-24.527	-64.361	-5.945	1.00	22.69	A	C
ATOM	126	CD	GLN	A	19	-24.762	-65.830	-6.230	1.00	22.70	A	C
ATOM	127	OE1	GLN	A	19	-23.902	-66.679	-6.031	1.00	22.41	A	O
ATOM	128	NE2	GLN	A	19	-25.944	-66.128	-6.686	1.00	23.42	A	N
ATOM	129	C	GLN	A	19	-23.281	-62.147	-4.541	1.00	19.39	A	C
ATOM	130	O	GLN	A	19	-22.680	-62.642	-3.603	1.00	19.37	A	O
ATOM	131	N	SER	A	20	-24.364	-61.405	-4.416	1.00	20.36	A	N
ATOM	132	CA	SER	A	20	-24.805	-60.864	-3.142	1.00	21.93	A	C
ATOM	133	CB	SER	A	20	-24.242	-59.446	-2.917	1.00	20.94	A	C
ATOM	134	OG	SER	A	20	-24.848	-58.804	-1.798	1.00	20.47	A	O
ATOM	135	C	SER	A	20	-26.316	-60.793	-3.153	1.00	24.09	A	C
ATOM	136	O	SER	A	20	-26.900	-59.913	-3.817	1.00	24.70	A	O
ATOM	137	N	GLY	A	21	-26.941	-61.719	-2.431	1.00	25.06	A	N
ATOM	138	CA	GLY	A	21	-28.389	-61.717	-2.286	1.00	25.86	A	C
ATOM	139	C	GLY	A	21	-29.009	-62.180	-3.585	1.00	26.74	A	C
ATOM	140	O	GLY	A	21	-28.612	-63.233	-4.137	1.00	26.33	A	O
ATOM	141	N	SER	A	22	-29.973	-61.376	-4.055	1.00	26.86	A	N
ATOM	142	CA	SER	A	22	-30.620	-61.522	-5.374	1.00	26.16	A	C
ATOM	143	CB	SER	A	22	-31.916	-60.704	-5.410	1.00	25.69	A	C
ATOM	144	OG	SER	A	22	-32.699	-60.973	-4.264	1.00	25.00	A	O
ATOM	145	C	SER	A	22	-29.765	-61.040	-6.537	1.00	25.41	A	C

ATOM	146	O	SER	A	22	-30.092	-61.342	-7.678	1.00	28.42	A	O
ATOM	147	N	THR	A	23	-28.692	-60.295	-6.259	1.00	24.03	A	N
ATOM	148	CA	THR	A	23	-27.894	-59.630	-7.305	1.00	23.15	A	C
ATOM	149	CB	THR	A	23	-27.851	-58.107	-7.116	1.00	22.84	A	C
ATOM	150	OG1	THR	A	23	-28.241	-57.818	-5.783	1.00	23.29	A	O
ATOM	151	CG2	THR	A	23	-28.727	-57.393	-8.116	1.00	23.29	A	C
ATOM	152	C	THR	A	23	-26.442	-59.995	-7.328	1.00	21.31	A	C
ATOM	153	O	THR	A	23	-26.004	-60.983	-6.747	1.00	20.69	A	O
ATOM	154	N	TYR	A	24	-25.721	-59.153	-8.058	1.00	20.03	A	N
ATOM	155	CA	TYR	A	24	-24.288	-59.137	-8.090	1.00	19.44	A	C
ATOM	156	CB	TYR	A	24	-23.808	-59.724	-9.415	1.00	20.32	A	C
ATOM	157	CG	TYR	A	24	-24.253	-61.153	-9.647	1.00	20.98	A	C
ATOM	158	CD1	TYR	A	24	-25.577	-61.463	-10.012	1.00	22.25	A	C
ATOM	159	CE1	TYR	A	24	-25.973	-62.786	-10.223	1.00	22.82	A	C
ATOM	160	CZ	TYR	A	24	-25.027	-63.803	-10.075	1.00	22.98	A	C
ATOM	161	OH	TYR	A	24	-25.333	-65.114	-10.258	1.00	22.47	A	O
ATOM	162	CE2	TYR	A	24	-23.725	-63.508	-9.714	1.00	22.86	A	C
ATOM	163	CD2	TYR	A	24	-23.353	-62.193	-9.502	1.00	21.74	A	C
ATOM	164	C	TYR	A	24	-23.790	-57.707	-7.944	1.00	18.03	A	C
ATOM	165	O	TYR	A	24	-24.420	-56.776	-8.398	1.00	18.83	A	O
ATOM	166	N	GLN	A	25	-22.646	-57.554	-7.304	1.00	16.91	A	N
ATOM	167	CA	GLN	A	25	-22.035	-56.282	-7.074	1.00	16.05	A	C
ATOM	168	CB	GLN	A	25	-21.610	-56.204	-5.617	1.00	17.12	A	C
ATOM	169	CG	GLN	A	25	-22.750	-56.234	-4.604	1.00	18.02	A	C
ATOM	170	CD	GLN	A	25	-22.238	-56.131	-3.157	1.00	18.84	A	C
ATOM	171	OE1	GLN	A	25	-21.652	-57.073	-2.611	1.00	18.68	A	O
ATOM	172	NE2	GLN	A	25	-22.436	-54.961	-2.547	1.00	19.37	A	N
ATOM	173	C	GLN	A	25	-20.804	-56.174	-7.940	1.00	14.92	A	C
ATOM	174	O	GLN	A	25	-20.054	-57.139	-8.082	1.00	13.71	A	O
ATOM	175	N	LEU	A	26	-20.586	-54.991	-8.507	1.00	14.84	A	N
ATOM	176	CA	LEU	A	26	-19.323	-54.675	-9.200	1.00	14.71	A	C
ATOM	177	CB	LEU	A	26	-19.445	-53.347	-9.978	1.00	14.61	A	C
ATOM	178	CG	LEU	A	26	-19.423	-53.351	-11.519	1.00	14.51	A	C
ATOM	179	CD1	LEU	A	26	-19.059	-51.976	-12.079	1.00	14.06	A	C
ATOM	180	CD2	LEU	A	26	-18.478	-54.406	-12.088	1.00	14.65	A	C
ATOM	181	C	LEU	A	26	-18.128	-54.605	-8.242	1.00	14.74	A	C
ATOM	182	O	LEU	A	26	-17.595	-53.535	-8.002	1.00	15.14	A	O
ATOM	183	N	LYS	A	27	-17.714	-55.748	-7.703	1.00	15.19	A	N
ATOM	184	CA	LYS	A	27	-16.706	-55.808	-6.643	1.00	15.66	A	C
ATOM	185	CB	LYS	A	27	-17.364	-55.826	-5.267	1.00	17.97	A	C
ATOM	186	CG	LYS	A	27	-16.461	-55.674	-4.013	1.00	20.16	A	C
ATOM	187	CD	LYS	A	27	-17.235	-56.135	-2.756	1.00	22.07	A	C
ATOM	188	CE	LYS	A	27	-16.523	-55.982	-1.402	1.00	23.86	A	C
ATOM	189	NZ	LYS	A	27	-16.851	-54.674	-0.719	1.00	24.48	A	N
ATOM	190	C	LYS	A	27	-15.913	-57.057	-6.827	1.00	14.55	A	C
ATOM	191	O	LYS	A	27	-16.489	-58.120	-6.996	1.00	14.47	A	O
ATOM	192	N	ASP	A	28	-14.587	-56.917	-6.825	1.00	13.97	A	N
ATOM	193	CA	ASP	A	28	-13.659	-58.031	-7.050	1.00	13.42	A	C
ATOM	194	CB	ASP	A	28	-12.763	-57.725	-8.266	1.00	13.08	A	C
ATOM	195	CG	ASP	A	28	-11.674	-58.771	-8.521	1.00	13.48	A	C
ATOM	196	OD1	ASP	A	28	-11.473	-59.690	-7.689	1.00	14.37	A	O
ATOM	197	OD2	ASP	A	28	-11.005	-58.691	-9.587	1.00	12.98	A	O
ATOM	198	C	ASP	A	28	-12.893	-58.207	-5.739	1.00	13.01	A	C
ATOM	199	O	ASP	A	28	-12.178	-57.368	-5.343	1.00	12.32	A	O
ATOM	200	N	THR	A	29	-13.117	-59.315	-5.068	1.00	13.89	A	N
ATOM	201	CA	THR	A	29	-12.519	-59.651	-3.769	1.00	14.71	A	C
ATOM	202	CB	THR	A	29	-13.399	-60.741	-3.052	1.00	15.35	A	C
ATOM	203	OG1	THR	A	29	-14.777	-60.336	-3.027	1.00	15.18	A	O
ATOM	204	CG2	THR	A	29	-12.900	-61.030	-1.614	1.00	16.17	A	C
ATOM	205	C	THR	A	29	-11.158	-60.301	-3.937	1.00	14.50	A	C
ATOM	206	O	THR	A	29	-10.416	-60.477	-2.966	1.00	14.03	A	O
ATOM	207	N	THR	A	30	-10.858	-60.707	-5.166	1.00	14.01	A	N
ATOM	208	CA	THR	A	30	-9.723	-61.573	-5.413	1.00	13.87	A	C
ATOM	209	CB	THR	A	30	-9.932	-62.391	-6.680	1.00	13.93	A	C
ATOM	210	OG1	THR	A	30	-9.673	-61.570	-7.827	1.00	14.25	A	O
ATOM	211	CG2	THR	A	30	-11.361	-62.916	-6.702	1.00	13.81	A	C
ATOM	212	C	THR	A	30	-8.429	-60.802	-5.518	1.00	13.58	A	C
ATOM	213	O	THR	A	30	-7.359	-61.401	-5.502	1.00	12.36	A	O
ATOM	214	N	ARG	A	31	-8.521	-59.476	-5.615	1.00	14.16	A	N
ATOM	215	CA	ARG	A	31	-7.297	-58.698	-5.580	1.00	15.08	A	C
ATOM	216	CB	ARG	A	31	-6.770	-58.358	-6.990	1.00	15.55	A	C
ATOM	217	CG	ARG	A	31	-7.598	-57.511	-7.921	1.00	16.02	A	C
ATOM	218	CD	ARG	A	31	-8.195	-58.329	-9.061	1.00	16.47	A	C
ATOM	219	NE	ARG	A	31	-7.390	-58.608	-10.270	1.00	15.99	A	N
ATOM	220	CZ	ARG	A	31	-7.738	-59.539	-11.181	1.00	15.52	A	C
ATOM	221	NH1	ARG	A	31	-8.823	-60.305	-11.035	1.00	15.13	A	N
ATOM	222	NH2	ARG	A	31	-6.991	-59.741	-12.238	1.00	15.37	A	N
ATOM	223	C	ARG	A	31	-7.235	-57.525	-4.589	1.00	14.78	A	C
ATOM	224	O	ARG	A	31	-8.080	-56.638	-4.583	1.00	14.51	A	O

ATOM	225	N	GLY	A	32	-6.182	-57.584	-3.753	1.00	14.67	A	N
ATOM	226	CA	GLY	A	32	-6.087	-56.875	-2.471	1.00	14.18	A	C
ATOM	227	C	GLY	A	32	-7.325	-56.959	-1.608	1.00	13.91	A	C
ATOM	228	O	GLY	A	32	-8.032	-57.952	-1.604	1.00	13.27	A	O
ATOM	229	N	GLN	A	33	-7.608	-55.897	-0.875	1.00	14.47	A	N
ATOM	230	CA	GLN	A	33	-8.876	-55.840	-0.160	1.00	15.13	A	C
ATOM	231	CB	GLN	A	33	-8.834	-54.815	0.957	1.00	16.42	A	C
ATOM	232	CG	GLN	A	33	-7.964	-55.204	2.146	1.00	17.07	A	C
ATOM	233	CD	GLN	A	33	-7.000	-54.094	2.468	1.00	18.22	A	C
ATOM	234	OE1	GLN	A	33	-5.796	-54.344	2.529	1.00	18.93	A	O
ATOM	235	NE2	GLN	A	33	-7.516	-52.821	2.619	1.00	18.12	A	N
ATOM	236	C	GLN	A	33	-10.024	-55.539	-1.099	1.00	14.63	A	C
ATOM	237	O	GLN	A	33	-11.164	-55.372	-0.671	1.00	14.46	A	O
ATOM	238	N	GLY	A	34	-9.727	-55.477	-2.386	1.00	14.20	A	N
ATOM	239	CA	GLY	A	34	-10.766	-55.551	-3.369	1.00	13.93	A	C
ATOM	240	C	GLY	A	34	-10.802	-54.379	-4.303	1.00	13.69	A	C
ATOM	241	O	GLY	A	34	-10.151	-53.360	-4.073	1.00	14.83	A	O
ATOM	242	N	ILE	A	35	-11.563	-54.533	-5.371	1.00	12.80	A	N
ATOM	243	CA	ILE	A	35	-11.706	-53.495	-6.353	1.00	12.48	A	C
ATOM	244	CB	ILE	A	35	-11.136	-53.951	-7.695	1.00	12.26	A	C
ATOM	245	CG1	ILE	A	35	-9.639	-54.116	-7.554	1.00	12.72	A	C
ATOM	246	CD1	ILE	A	35	-8.906	-54.294	-8.876	1.00	13.19	A	C
ATOM	247	CG2	ILE	A	35	-11.468	-52.976	-8.798	1.00	12.20	A	C
ATOM	248	C	ILE	A	35	-13.193	-53.286	-6.417	1.00	12.31	A	C
ATOM	249	O	ILE	A	35	-13.938	-54.242	-6.575	1.00	12.03	A	O
ATOM	250	N	VAL	A	36	-13.625	-52.043	-6.257	1.00	12.28	A	N
ATOM	251	CA	VAL	A	36	-15.051	-51.755	-6.160	1.00	12.25	A	C
ATOM	252	CB	VAL	A	36	-15.459	-51.351	-4.737	1.00	12.50	A	C
ATOM	253	CG1	VAL	A	36	-16.968	-51.376	-4.631	1.00	12.79	A	C
ATOM	254	CG2	VAL	A	36	-14.829	-52.271	-3.691	1.00	12.49	A	C
ATOM	255	C	VAL	A	36	-15.378	-50.600	-7.042	1.00	11.79	A	C
ATOM	256	O	VAL	A	36	-14.656	-49.627	-7.068	1.00	11.66	A	O
ATOM	257	N	THR	A	37	-16.480	-50.693	-7.752	1.00	11.73	A	N
ATOM	258	CA	THR	A	37	-16.821	-49.656	-8.699	1.00	11.95	A	C
ATOM	259	CB	THR	A	37	-16.651	-50.214	-10.125	1.00	12.12	A	C
ATOM	260	OG1	THR	A	37	-15.306	-50.678	-10.323	1.00	11.60	A	O
ATOM	261	CG2	THR	A	37	-16.978	-49.158	-11.163	1.00	12.41	A	C
ATOM	262	C	THR	A	37	-18.242	-49.064	-8.450	1.00	12.02	A	C
ATOM	263	O	THR	A	37	-19.220	-49.806	-8.348	1.00	11.27	A	O
ATOM	264	N	TYR	A	38	-18.310	-47.727	-8.348	1.00	12.30	A	N
ATOM	265	CA	TYR	A	38	-19.531	-46.984	-8.027	1.00	12.80	A	C
ATOM	266	CB	TYR	A	38	-19.301	-46.102	-6.793	1.00	13.01	A	C
ATOM	267	CG	TYR	A	38	-18.714	-46.788	-5.592	1.00	13.05	A	C
ATOM	268	CD1	TYR	A	38	-17.349	-47.059	-5.500	1.00	12.97	A	C
ATOM	269	CE1	TYR	A	38	-16.826	-47.706	-4.387	1.00	12.85	A	C
ATOM	270	CZ	TYR	A	38	-17.664	-48.041	-3.345	1.00	12.79	A	C
ATOM	271	OH	TYR	A	38	-17.222	-48.655	-2.229	1.00	13.25	A	O
ATOM	272	CE2	TYR	A	38	-18.991	-47.767	-3.402	1.00	13.05	A	C
ATOM	273	CD2	TYR	A	38	-19.519	-47.145	-4.523	1.00	13.15	A	C
ATOM	274	C	TYR	A	38	-19.921	-46.001	-9.123	1.00	13.22	A	C
ATOM	275	O	TYR	A	38	-19.061	-45.563	-9.886	1.00	13.13	A	O
ATOM	276	N	SER	A	39	-21.196	-45.588	-9.132	1.00	13.71	A	N
ATOM	277	CA	SER	A	39	-21.668	-44.417	-9.919	1.00	14.12	A	C
ATOM	278	CB	SER	A	39	-22.854	-44.784	-10.823	1.00	13.74	A	C
ATOM	279	OG	SER	A	39	-23.634	-43.628	-11.165	1.00	13.56	A	O
ATOM	280	C	SER	A	39	-22.052	-43.226	-9.009	1.00	14.90	A	C
ATOM	281	O	SER	A	39	-22.651	-43.409	-7.942	1.00	15.79	A	O
ATOM	282	N	ALA	A	40	-21.697	-42.011	-9.422	1.00	15.34	A	N
ATOM	283	CA	ALA	A	40	-22.070	-40.810	-8.672	1.00	15.65	A	C
ATOM	284	CB	ALA	A	40	-21.026	-39.738	-8.857	1.00	15.26	A	C
ATOM	285	C	ALA	A	40	-23.444	-40.255	-9.080	1.00	16.51	A	C
ATOM	286	O	ALA	A	40	-23.871	-39.252	-8.542	1.00	16.26	A	O
ATOM	287	N	GLY	A	41	-24.125	-40.884	-10.037	1.00	17.11	A	N
ATOM	288	CA	GLY	A	41	-25.400	-40.386	-10.509	1.00	17.44	A	C
ATOM	289	C	GLY	A	41	-25.335	-38.944	-10.945	1.00	18.31	A	C
ATOM	290	O	GLY	A	41	-26.259	-38.156	-10.687	1.00	18.80	A	O
ATOM	291	N	ASN	A	42	-24.230	-38.586	-11.583	1.00	18.86	A	N
ATOM	292	CA	ASN	A	42	-24.007	-37.213	-12.060	1.00	19.31	A	C
ATOM	293	CB	ASN	A	42	-24.917	-36.897	-13.253	1.00	18.59	A	C
ATOM	294	CG	ASN	A	42	-24.664	-37.831	-14.428	1.00	18.02	A	C
ATOM	295	OD1	ASN	A	42	-25.567	-38.474	-14.893	1.00	18.09	A	O
ATOM	296	ND2	ASN	A	42	-23.419	-37.928	-14.879	1.00	17.76	A	N
ATOM	297	C	ASN	A	42	-24.075	-36.119	-11.010	1.00	20.65	A	C
ATOM	298	O	ASN	A	42	-24.293	-34.976	-11.332	1.00	20.22	A	O
ATOM	299	N	ARG	A	43	-23.827	-36.470	-9.761	1.00	23.59	A	N
ATOM	300	CA	ARG	A	43	-23.646	-35.496	-8.707	1.00	26.15	A	C
ATOM	301	CB	ARG	A	43	-24.688	-35.719	-7.618	1.00	30.73	A	C
ATOM	302	CG	ARG	A	43	-26.103	-35.379	-8.056	1.00	35.36	A	C
ATOM	303	CD	ARG	A	43	-27.117	-36.068	-7.163	1.00	42.30	A	C

ATOM	304	NE	ARG	A	43	-28.483	-35.870	-7.661	1.00	51.16	A	N
ATOM	305	CZ	ARG	A	43	-29.263	-36.813	-8.216	1.00	54.64	A	C
ATOM	306	NH1	ARG	A	43	-28.842	-38.082	-8.366	1.00	55.48	A	N
ATOM	307	NH2	ARG	A	43	-30.493	-36.474	-8.620	1.00	51.20	A	N
ATOM	308	C	ARG	A	43	-22.227	-35.710	-8.203	1.00	25.25	A	C
ATOM	309	O	ARG	A	43	-21.465	-36.443	-8.850	1.00	25.16	A	O
ATOM	310	N	SER	A	44	-21.856	-35.091	-7.080	1.00	23.65	A	N
ATOM	311	CA	SER	A	44	-20.469	-35.117	-6.638	1.00	23.20	A	C
ATOM	312	CB	SER	A	44	-19.913	-33.725	-6.728	1.00	23.30	A	C
ATOM	313	OG	SER	A	44	-20.575	-32.930	-5.806	1.00	24.80	A	O
ATOM	314	C	SER	A	44	-20.254	-35.685	-5.235	1.00	22.60	A	C
ATOM	315	O	SER	A	44	-19.168	-35.591	-4.637	1.00	23.35	A	O
ATOM	316	N	SER	A	45	-21.291	-36.310	-4.728	1.00	21.47	A	N
ATOM	317	CA	SER	A	45	-21.198	-37.091	-3.516	1.00	20.72	A	C
ATOM	318	CB	SER	A	45	-22.604	-37.567	-3.142	1.00	20.80	A	C
ATOM	319	OG	SER	A	45	-22.968	-37.078	-1.894	1.00	21.92	A	O
ATOM	320	C	SER	A	45	-20.325	-38.324	-3.784	1.00	19.65	A	C
ATOM	321	O	SER	A	45	-20.563	-39.037	-4.775	1.00	19.28	A	O
ATOM	322	N	LEU	A	46	-19.357	-38.602	-2.901	1.00	17.76	A	N
ATOM	323	CA	LEU	A	46	-18.494	-39.787	-3.055	1.00	16.26	A	C
ATOM	324	CB	LEU	A	46	-17.059	-39.358	-3.308	1.00	15.57	A	C
ATOM	325	CG	LEU	A	46	-16.799	-38.486	-4.528	1.00	15.28	A	C
ATOM	326	CD1	LEU	A	46	-15.336	-38.131	-4.537	1.00	15.11	A	C
ATOM	327	CD2	LEU	A	46	-17.173	-39.184	-5.834	1.00	15.38	A	C
ATOM	328	C	LEU	A	46	-18.528	-40.707	-1.854	1.00	15.97	A	C
ATOM	329	O	LEU	A	46	-18.512	-40.255	-0.740	1.00	15.97	A	O
ATOM	330	N	PRO	A	47	-18.450	-42.021	-2.068	1.00	16.23	A	N
ATOM	331	CA	PRO	A	47	-18.098	-42.713	-3.302	1.00	16.33	A	C
ATOM	332	CB	PRO	A	47	-17.593	-44.069	-2.806	1.00	16.02	A	C
ATOM	333	CG	PRO	A	47	-17.843	-44.110	-1.340	1.00	15.83	A	C
ATOM	334	CD	PRO	A	47	-18.710	-42.968	-0.980	1.00	15.87	A	C
ATOM	335	C	PRO	A	47	-19.271	-42.898	-4.262	1.00	16.88	A	C
ATOM	336	O	PRO	A	47	-19.062	-43.188	-5.448	1.00	16.98	A	O
ATOM	337	N	GLY	A	48	-20.496	-42.741	-3.752	1.00	16.89	A	N
ATOM	338	CA	GLY	A	48	-21.680	-42.866	-4.577	1.00	15.71	A	C
ATOM	339	C	GLY	A	48	-22.281	-44.214	-4.323	1.00	14.63	A	C
ATOM	340	O	GLY	A	48	-21.984	-44.833	-3.317	1.00	13.70	A	O
ATOM	341	N	THR	A	49	-23.111	-44.644	-5.262	1.00	14.42	A	N
ATOM	342	CA	THR	A	49	-23.844	-45.889	-5.184	1.00	15.14	A	C
ATOM	343	CB	THR	A	49	-25.186	-45.825	-5.997	1.00	15.13	A	C
ATOM	344	OG1	THR	A	49	-25.981	-44.687	-5.619	1.00	14.36	A	O
ATOM	345	CG2	THR	A	49	-25.983	-47.129	-5.846	1.00	14.54	A	C
ATOM	346	C	THR	A	49	-23.005	-46.995	-5.821	1.00	15.82	A	C
ATOM	347	O	THR	A	49	-22.654	-46.911	-7.008	1.00	15.76	A	O
ATOM	348	N	LEU	A	50	-22.696	-48.036	-5.055	1.00	16.29	A	N
ATOM	349	CA	LEU	A	50	-21.971	-49.177	-5.612	1.00	16.67	A	C
ATOM	350	CB	LEU	A	50	-21.402	-50.030	-4.494	1.00	16.62	A	C
ATOM	351	CG	LEU	A	50	-21.206	-51.532	-4.619	1.00	17.18	A	C
ATOM	352	CD1	LEU	A	50	-20.505	-51.964	-5.905	1.00	17.48	A	C
ATOM	353	CD2	LEU	A	50	-20.430	-51.992	-3.379	1.00	17.09	A	C
ATOM	354	C	LEU	A	50	-22.908	-49.955	-6.527	1.00	16.87	A	C
ATOM	355	O	LEU	A	50	-24.039	-50.225	-6.155	1.00	18.03	A	O
ATOM	356	N	LEU	A	51	-22.438	-50.289	-7.724	1.00	16.66	A	N
ATOM	357	CA	LEU	A	51	-23.304	-50.807	-8.767	1.00	16.90	A	C
ATOM	358	CB	LEU	A	51	-22.702	-50.580	-10.165	1.00	17.78	A	C
ATOM	359	CG	LEU	A	51	-22.995	-49.231	-10.854	1.00	18.55	A	C
ATOM	360	CD1	LEU	A	51	-21.780	-48.321	-10.737	1.00	18.87	A	C
ATOM	361	CD2	LEU	A	51	-23.352	-49.435	-12.335	1.00	19.37	A	C
ATOM	362	C	LEU	A	51	-23.664	-52.270	-8.629	1.00	16.37	A	C
ATOM	363	O	LEU	A	51	-22.888	-53.090	-8.130	1.00	16.35	A	O
ATOM	364	N	THR	A	52	-24.843	-52.591	-9.151	1.00	16.12	A	N
ATOM	365	CA	THR	A	52	-25.398	-53.941	-9.097	1.00	15.93	A	C
ATOM	366	CB	THR	A	52	-26.453	-54.014	-7.998	1.00	15.10	A	C
ATOM	367	OG1	THR	A	52	-27.129	-52.773	-7.961	1.00	14.51	A	O
ATOM	368	CG2	THR	A	52	-25.826	-54.189	-6.670	1.00	15.28	A	C
ATOM	369	C	THR	A	52	-26.087	-54.312	-10.398	1.00	16.34	A	C
ATOM	370	O	THR	A	52	-26.640	-53.474	-11.070	1.00	16.38	A	O
ATOM	371	N	SER	A	53	-26.044	-55.575	-10.764	1.00	17.42	A	N
ATOM	372	CA	SER	A	53	-26.900	-56.061	-11.829	1.00	18.54	A	C
ATOM	373	CB	SER	A	53	-26.179	-56.074	-13.170	1.00	19.26	A	C
ATOM	374	OG	SER	A	53	-26.656	-57.168	-13.945	1.00	19.86	A	O
ATOM	375	C	SER	A	53	-27.334	-57.468	-11.510	1.00	18.55	A	C
ATOM	376	O	SER	A	53	-26.473	-58.367	-11.355	1.00	17.72	A	O
ATOM	377	N	SER	A	54	-28.651	-57.665	-11.445	1.00	18.20	A	N
ATOM	378	CA	SER	A	54	-29.183	-58.969	-11.039	1.00	19.04	A	C
ATOM	379	CB	SER	A	54	-30.671	-58.894	-10.731	1.00	19.67	A	C
ATOM	380	OG	SER	A	54	-31.362	-58.586	-11.907	1.00	21.03	A	O
ATOM	381	C	SER	A	54	-28.905	-60.070	-12.047	1.00	17.88	A	C
ATOM	382	O	SER	A	54	-28.803	-61.243	-11.644	1.00	18.22	A	O

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ATOM	383	N	SER	A	55	-28.737	-59.695	-13.324	1.00	16.80	A	N
ATOM	384	CA	SER	A	55	-28.274	-60.644	-14.363	1.00	16.20	A	C
ATOM	385	CB	SER	A	55	-28.701	-60.186	-15.757	1.00	15.87	A	C
ATOM	386	OG	SER	A	55	-28.447	-58.827	-15.969	1.00	15.88	A	O
ATOM	387	C	SER	A	55	-26.775	-60.983	-14.384	1.00	15.91	A	C
ATOM	388	O	SER	A	55	-26.388	-61.948	-15.025	1.00	15.99	A	O
ATOM	389	N	ASN	A	56	-25.947	-60.220	-13.671	1.00	16.14	A	N
ATOM	390	CA	ASN	A	56	-24.472	-60.215	-13.852	1.00	15.95	A	C
ATOM	391	CB	ASN	A	56	-23.805	-61.536	-13.382	1.00	15.78	A	C
ATOM	392	CG	ASN	A	56	-22.360	-61.358	-12.860	1.00	15.19	A	C
ATOM	393	OD1	ASN	A	56	-21.554	-62.306	-12.853	1.00	14.47	A	O
ATOM	394	ND2	ASN	A	56	-22.041	-60.169	-12.400	1.00	14.98	A	N
ATOM	395	C	ASN	A	56	-24.092	-59.885	-15.296	1.00	16.66	A	C
ATOM	396	O	ASN	A	56	-23.018	-60.280	-15.756	1.00	16.28	A	O
ATOM	397	N	ILE	A	57	-24.984	-59.161	-15.989	1.00	17.56	A	N
ATOM	398	CA	ILE	A	57	-24.682	-58.525	-17.259	1.00	18.93	A	C
ATOM	399	CB	ILE	A	57	-25.650	-58.958	-18.366	1.00	20.60	A	C
ATOM	400	CG1	ILE	A	57	-25.606	-60.475	-18.578	1.00	21.60	A	C
ATOM	401	CD1	ILE	A	57	-26.715	-60.933	-19.510	1.00	21.99	A	C
ATOM	402	CG2	ILE	A	57	-25.300	-58.247	-19.673	1.00	20.37	A	C
ATOM	403	C	ILE	A	57	-24.827	-57.017	-17.089	1.00	18.81	A	C
ATOM	404	O	ILE	A	57	-25.830	-56.572	-16.550	1.00	18.38	A	O
ATOM	405	N	TRP	A	58	-23.869	-56.241	-17.603	1.00	18.79	A	N
ATOM	406	CA	TRP	A	58	-23.663	-54.869	-17.151	1.00	19.08	A	C
ATOM	407	CB	TRP	A	58	-22.285	-54.753	-16.467	1.00	18.65	A	C
ATOM	408	CG	TRP	A	58	-22.126	-55.653	-15.263	1.00	17.04	A	C
ATOM	409	CD1	TRP	A	58	-21.699	-56.943	-15.248	1.00	16.33	A	C
ATOM	410	NE1	TRP	A	58	-21.716	-57.436	-13.972	1.00	15.66	A	N
ATOM	411	CE2	TRP	A	58	-22.166	-56.454	-13.135	1.00	15.87	A	C
ATOM	412	CD2	TRP	A	58	-22.431	-55.318	-13.921	1.00	15.82	A	C
ATOM	413	CE3	TRP	A	58	-22.930	-54.178	-13.310	1.00	15.17	A	C
ATOM	414	CZ3	TRP	A	58	-23.119	-54.190	-11.949	1.00	15.35	A	C
ATOM	415	CH2	TRP	A	58	-22.833	-55.320	-11.181	1.00	15.47	A	C
ATOM	416	CZ2	TRP	A	58	-22.357	-56.465	-11.757	1.00	15.91	A	C
ATOM	417	C	TRP	A	58	-23.743	-53.866	-18.273	1.00	21.25	A	C
ATOM	418	O	TRP	A	58	-22.885	-53.847	-19.163	1.00	21.87	A	O
ATOM	419	N	ASN	A	59	-24.748	-52.994	-18.211	1.00	23.98	A	N
ATOM	420	CA	ASN	A	59	-25.040	-52.065	-19.306	1.00	24.38	A	C
ATOM	421	CB	ASN	A	59	-26.548	-51.940	-19.490	1.00	26.43	A	C
ATOM	422	CG	ASN	A	59	-27.209	-51.187	-18.334	1.00	29.93	A	C
ATOM	423	OD1	ASN	A	59	-26.529	-50.504	-17.551	1.00	31.64	A	O
ATOM	424	ND2	ASN	A	59	-28.536	-51.308	-18.213	1.00	32.05	A	N
ATOM	425	C	ASN	A	59	-24.455	-50.672	-19.083	1.00	23.75	A	C
ATOM	426	O	ASN	A	59	-24.810	-49.744	-19.806	1.00	27.95	A	O
ATOM	427	N	ASP	A	60	-23.589	-50.499	-18.093	1.00	20.98	A	N
ATOM	428	CA	ASP	A	60	-22.892	-49.230	-17.924	1.00	19.55	A	C
ATOM	429	CB	ASP	A	60	-22.924	-48.781	-16.477	1.00	19.97	A	C
ATOM	430	CG	ASP	A	60	-22.413	-47.377	-16.304	1.00	21.08	A	C
ATOM	431	OD1	ASP	A	60	-21.574	-46.928	-17.121	1.00	22.86	A	O
ATOM	432	OD2	ASP	A	60	-22.856	-46.703	-15.354	1.00	22.23	A	O
ATOM	433	C	ASP	A	60	-21.437	-49.304	-18.376	1.00	18.14	A	C
ATOM	434	O	ASP	A	60	-20.592	-49.914	-17.694	1.00	17.59	A	O
ATOM	435	N	GLY	A	61	-21.133	-48.599	-19.466	1.00	16.48	A	N
ATOM	436	CA	GLY	A	61	-19.822	-48.709	-20.138	1.00	15.68	A	C
ATOM	437	C	GLY	A	61	-18.639	-48.102	-19.392	1.00	14.75	A	C
ATOM	438	O	GLY	A	61	-17.577	-48.719	-19.298	1.00	14.18	A	O
ATOM	439	N	ALA	A	62	-18.826	-46.885	-18.896	1.00	13.68	A	N
ATOM	440	CA	ALA	A	62	-17.870	-46.232	-18.027	1.00	13.21	A	C
ATOM	441	CB	ALA	A	62	-18.383	-44.874	-17.598	1.00	13.34	A	C
ATOM	442	C	ALA	A	62	-17.597	-47.074	-16.805	1.00	12.94	A	C
ATOM	443	O	ALA	A	62	-16.441	-47.297	-16.457	1.00	12.77	A	O
ATOM	444	N	ALA	A	63	-18.646	-47.569	-16.161	1.00	12.70	A	N
ATOM	445	CA	ALA	A	63	-18.434	-48.493	-15.027	1.00	12.59	A	C
ATOM	446	CB	ALA	A	63	-19.759	-48.903	-14.401	1.00	12.74	A	C
ATOM	447	C	ALA	A	63	-17.626	-49.732	-15.433	1.00	11.84	A	C
ATOM	448	O	ALA	A	63	-16.674	-50.096	-14.771	1.00	11.48	A	O
ATOM	449	N	VAL	A	64	-18.007	-50.362	-16.530	1.00	11.59	A	N
ATOM	450	CA	VAL	A	64	-17.296	-51.555	-17.001	1.00	11.64	A	C
ATOM	451	CB	VAL	A	64	-17.946	-52.163	-18.282	1.00	11.76	A	C
ATOM	452	CG1	VAL	A	64	-16.973	-53.097	-18.988	1.00	11.89	A	C
ATOM	453	CG2	VAL	A	64	-19.239	-52.927	-17.954	1.00	11.63	A	C
ATOM	454	C	VAL	A	64	-15.811	-51.314	-17.274	1.00	11.25	A	C
ATOM	455	O	VAL	A	64	-14.967	-52.092	-16.889	1.00	10.71	A	O
ATOM	456	N	ASP	A	65	-15.499	-50.244	-17.972	1.00	11.62	A	N
ATOM	457	CA	ASP	A	65	-14.103	-49.937	-18.299	1.00	11.62	A	C
ATOM	458	CB	ASP	A	65	-13.988	-48.750	-19.282	1.00	11.58	A	C
ATOM	459	CG	ASP	A	65	-14.272	-49.144	-20.735	1.00	11.39	A	C
ATOM	460	OD1	ASP	A	65	-14.119	-50.315	-21.053	1.00	11.29	A	O
ATOM	461	OD2	ASP	A	65	-14.647	-48.294	-21.563	1.00	11.28	A	O

ATOM	462	C	ASP	A	65	-13.343	-49.657	-17.011	1.00	11.68	A	C
ATOM	463	O	ASP	A	65	-12.287	-50.237	-16.795	1.00	12.17	A	O
ATOM	464	N	ALA	A	66	-13.881	-48.805	-16.142	1.00	11.22	A	N
ATOM	465	CA	ALA	A	66	-13.206	-48.530	-14.877	1.00	11.26	A	C
ATOM	466	CB	ALA	A	66	-14.002	-47.545	-14.038	1.00	11.11	A	C
ATOM	467	C	ALA	A	66	-12.942	-49.816	-14.076	1.00	11.77	A	C
ATOM	468	O	ALA	A	66	-11.835	-50.016	-13.538	1.00	11.80	A	O
ATOM	469	N	HIS	A	67	-13.944	-50.690	-13.995	1.00	11.93	A	N
ATOM	470	CA	HIS	A	67	-13.758	-51.933	-13.275	1.00	12.20	A	C
ATOM	471	CB	HIS	A	67	-15.047	-52.745	-13.195	1.00	12.39	A	C
ATOM	472	CG	HIS	A	67	-15.079	-53.722	-12.053	1.00	12.80	A	C
ATOM	473	ND1	HIS	A	67	-15.102	-53.327	-10.736	1.00	13.19	A	N
ATOM	474	CE1	HIS	A	67	-15.143	-54.396	-9.955	1.00	13.25	A	C
ATOM	475	NE2	HIS	A	67	-15.176	-55.469	-10.719	1.00	12.96	A	N
ATOM	476	CD2	HIS	A	67	-15.137	-55.075	-12.033	1.00	13.09	A	C
ATOM	477	C	HIS	A	67	-12.649	-52.740	-13.934	1.00	12.01	A	C
ATOM	478	O	HIS	A	67	-11.651	-53.041	-13.316	1.00	12.49	A	O
ATOM	479	N	ALA	A	68	-12.809	-53.051	-15.205	1.00	11.74	A	N
ATOM	480	CA	ALA	A	68	-11.876	-53.929	-15.905	1.00	11.42	A	C
ATOM	481	CB	ALA	A	68	-12.395	-54.188	-17.313	1.00	11.62	A	C
ATOM	482	C	ALA	A	68	-10.449	-53.368	-15.986	1.00	10.67	A	C
ATOM	483	O	ALA	A	68	-9.451	-54.078	-15.807	1.00	10.44	A	O
ATOM	484	N	TYR	A	69	-10.368	-52.089	-16.267	1.00	10.14	A	N
ATOM	485	CA	TYR	A	69	-9.083	-51.445	-16.372	1.00	9.92	A	C
ATOM	486	CB	TYR	A	69	-9.211	-50.127	-17.137	1.00	9.77	A	C
ATOM	487	CG	TYR	A	69	-9.568	-50.343	-18.608	1.00	9.70	A	C
ATOM	488	CD1	TYR	A	69	-9.263	-51.544	-19.258	1.00	9.60	A	C
ATOM	489	CE1	TYR	A	69	-9.588	-51.750	-20.584	1.00	9.57	A	C
ATOM	490	CZ	TYR	A	69	-10.204	-50.755	-21.307	1.00	9.49	A	C
ATOM	491	OH	TYR	A	69	-10.500	-50.982	-22.645	1.00	8.99	A	O
ATOM	492	CE2	TYR	A	69	-10.509	-49.549	-20.685	1.00	9.61	A	C
ATOM	493	CD2	TYR	A	69	-10.201	-49.356	-19.341	1.00	9.63	A	C
ATOM	494	C	TYR	A	69	-8.366	-51.278	-15.053	1.00	9.69	A	C
ATOM	495	O	TYR	A	69	-7.129	-51.268	-15.022	1.00	9.58	A	O
ATOM	496	N	THR	A	70	-9.129	-51.193	-13.965	1.00	9.51	A	N
ATOM	497	CA	THR	A	70	-8.532	-51.019	-12.645	1.00	9.27	A	C
ATOM	498	CB	THR	A	70	-9.549	-50.438	-11.620	1.00	9.02	A	C
ATOM	499	OG1	THR	A	70	-9.925	-49.095	-11.972	1.00	8.65	A	O
ATOM	500	CG2	THR	A	70	-8.960	-50.394	-10.262	1.00	8.99	A	C
ATOM	501	C	THR	A	70	-7.970	-52.395	-12.257	1.00	9.35	A	C
ATOM	502	O	THR	A	70	-6.910	-52.516	-11.659	1.00	9.65	A	O
ATOM	503	N	ALA	A	71	-8.655	-53.452	-12.651	1.00	9.39	A	N
ATOM	504	CA	ALA	A	71	-8.127	-54.785	-12.428	1.00	9.42	A	C
ATOM	505	CB	ALA	A	71	-9.190	-55.834	-12.721	1.00	9.15	A	C
ATOM	506	C	ALA	A	71	-6.854	-54.985	-13.284	1.00	9.65	A	C
ATOM	507	O	ALA	A	71	-5.878	-55.594	-12.835	1.00	9.53	A	O
ATOM	508	N	LYS	A	72	-6.842	-54.432	-14.491	1.00	10.10	A	N
ATOM	509	CA	LYS	A	72	-5.638	-54.469	-15.315	1.00	10.84	A	C
ATOM	510	CB	LYS	A	72	-5.945	-53.814	-16.635	1.00	11.60	A	C
ATOM	511	CG	LYS	A	72	-5.034	-54.225	-17.764	1.00	12.60	A	C
ATOM	512	CD	LYS	A	72	-5.285	-53.298	-18.948	1.00	13.78	A	C
ATOM	513	CE	LYS	A	72	-4.237	-53.477	-20.052	1.00	14.79	A	C
ATOM	514	NZ	LYS	A	72	-4.525	-54.698	-20.852	1.00	15.32	A	N
ATOM	515	C	LYS	A	72	-4.428	-53.773	-14.648	1.00	10.95	A	C
ATOM	516	O	LYS	A	72	-3.320	-54.296	-14.566	1.00	10.53	A	O
ATOM	517	N	VAL	A	73	-4.666	-52.580	-14.143	1.00	11.11	A	N
ATOM	518	CA	VAL	A	73	-3.613	-51.873	-13.539	1.00	11.29	A	C
ATOM	519	CB	VAL	A	73	-4.052	-50.456	-13.206	1.00	11.29	A	C
ATOM	520	CG1	VAL	A	73	-2.976	-49.773	-12.375	1.00	11.51	A	C
ATOM	521	CG2	VAL	A	73	-4.297	-49.674	-14.477	1.00	11.25	A	C
ATOM	522	C	VAL	A	73	-3.179	-52.631	-12.286	1.00	11.79	A	C
ATOM	523	O	VAL	A	73	-1.973	-52.775	-12.023	1.00	12.54	A	O
ATOM	524	N	TYR	A	74	-4.146	-53.094	-11.488	1.00	11.69	A	N
ATOM	525	CA	TYR	A	74	-3.803	-53.789	-10.253	1.00	11.38	A	C
ATOM	526	CB	TYR	A	74	-5.052	-54.356	-9.512	1.00	10.72	A	C
ATOM	527	CG	TYR	A	74	-4.642	-55.235	-8.341	1.00	9.87	A	C
ATOM	528	CD1	TYR	A	74	-4.236	-56.541	-8.538	1.00	9.52	A	C
ATOM	529	CE1	TYR	A	74	-3.798	-57.334	-7.492	1.00	9.27	A	C
ATOM	530	CZ	TYR	A	74	-3.767	-56.822	-6.235	1.00	9.43	A	C
ATOM	531	OH	TYR	A	74	-3.319	-57.598	-5.195	1.00	9.43	A	O
ATOM	532	CE2	TYR	A	74	-4.152	-55.514	-6.010	1.00	9.49	A	C
ATOM	533	CD2	TYR	A	74	-4.577	-54.729	-7.062	1.00	9.59	A	C
ATOM	534	C	TYR	A	74	-2.797	-54.923	-10.602	1.00	12.02	A	C
ATOM	535	O	TYR	A	74	-1.816	-55.093	-9.905	1.00	11.97	A	O
ATOM	536	N	ASP	A	75	-3.062	-55.670	-11.683	1.00	12.59	A	N
ATOM	537	CA	ASP	A	75	-2.225	-56.802	-12.099	1.00	13.15	A	C
ATOM	538	CB	ASP	A	75	-2.863	-57.577	-13.258	1.00	12.65	A	C
ATOM	539	CG	ASP	A	75	-4.140	-58.272	-12.887	1.00	12.28	A	C
ATOM	540	OD1	ASP	A	75	-4.408	-58.613	-11.704	1.00	11.68	A	O

ATOM	541	OD2	ASP	A	75	-4.889	-58.488	-13.848	1.00	12.29	A	O
ATOM	542	C	ASP	A	75	-0.884	-56.370	-12.652	1.00	13.93	A	C
ATOM	543	O	ASP	A	75	0.029	-57.189	-12.744	1.00	14.31	A	O
ATOM	544	N	TYR	A	76	-0.790	-55.129	-13.108	1.00	14.12	A	N
ATOM	545	CA	TYR	A	76	0.435	-54.684	-13.703	1.00	15.01	A	C
ATOM	546	CB	TYR	A	76	0.232	-53.411	-14.549	1.00	14.93	A	C
ATOM	547	CG	TYR	A	76	1.483	-52.846	-15.181	1.00	14.82	A	C
ATOM	548	CD1	TYR	A	76	2.257	-51.907	-14.523	1.00	15.03	A	C
ATOM	549	CE1	TYR	A	76	3.409	-51.387	-15.107	1.00	15.40	A	C
ATOM	550	CZ	TYR	A	76	3.787	-51.815	-16.375	1.00	15.55	A	C
ATOM	551	OH	TYR	A	76	4.929	-51.315	-16.990	1.00	15.74	A	O
ATOM	552	CE2	TYR	A	76	3.022	-52.753	-17.036	1.00	15.06	A	C
ATOM	553	CD2	TYR	A	76	1.880	-53.248	-16.444	1.00	15.02	A	C
ATOM	554	C	TYR	A	76	1.381	-54.465	-12.538	1.00	15.85	A	C
ATOM	555	O	TYR	A	76	2.541	-54.932	-12.545	1.00	16.76	A	O
ATOM	556	N	TYR	A	77	0.898	-53.779	-11.522	1.00	16.19	A	N
ATOM	557	CA	TYR	A	77	1.796	-53.445	-10.429	1.00	17.84	A	C
ATOM	558	CB	TYR	A	77	1.163	-52.449	-9.451	1.00	16.53	A	C
ATOM	559	CG	TYR	A	77	1.341	-50.967	-9.805	1.00	15.02	A	C
ATOM	560	CD1	TYR	A	77	2.441	-50.267	-9.364	1.00	14.53	A	C
ATOM	561	CE1	TYR	A	77	2.587	-48.923	-9.613	1.00	14.07	A	C
ATOM	562	CZ	TYR	A	77	1.622	-48.263	-10.311	1.00	13.99	A	C
ATOM	563	OH	TYR	A	77	1.805	-46.916	-10.568	1.00	14.22	A	O
ATOM	564	CE2	TYR	A	77	0.492	-48.927	-10.740	1.00	13.72	A	C
ATOM	565	CD2	TYR	A	77	0.360	-50.266	-10.487	1.00	14.12	A	C
ATOM	566	C	TYR	A	77	2.211	-54.723	-9.712	1.00	19.97	A	C
ATOM	567	O	TYR	A	77	3.325	-54.819	-9.174	1.00	21.51	A	O
ATOM	568	N	LYS	A	78	1.315	-55.704	-9.730	1.00	22.11	A	N
ATOM	569	CA	LYS	A	78	1.556	-56.962	-9.075	1.00	23.87	A	C
ATOM	570	CB	LYS	A	78	0.239	-57.743	-8.908	1.00	25.91	A	C
ATOM	571	CG	LYS	A	78	0.347	-59.104	-8.221	1.00	28.58	A	C
ATOM	572	CD	LYS	A	78	1.136	-59.006	-6.918	1.00	33.48	A	C
ATOM	573	CE	LYS	A	78	0.619	-59.934	-5.815	1.00	37.52	A	C
ATOM	574	NZ	LYS	A	78	-0.673	-59.444	-5.218	1.00	39.88	A	N
ATOM	575	C	LYS	A	78	2.622	-57.747	-9.855	1.00	22.86	A	C
ATOM	576	O	LYS	A	78	3.600	-58.188	-9.247	1.00	22.16	A	O
ATOM	577	N	ASN	A	79	2.471	-57.888	-11.173	1.00	21.47	A	N
ATOM	578	CA	ASN	A	79	3.422	-58.714	-11.919	1.00	22.64	A	C
ATOM	579	CB	ASN	A	79	2.899	-59.148	-13.278	1.00	23.04	A	C
ATOM	580	CG	ASN	A	79	1.578	-59.888	-13.188	1.00	24.12	A	C
ATOM	581	OD1	ASN	A	79	0.759	-59.783	-14.094	1.00	24.68	A	O
ATOM	582	ND2	ASN	A	79	1.348	-60.617	-12.087	1.00	24.13	A	N
ATOM	583	C	ASN	A	79	4.769	-58.059	-12.103	1.00	23.13	A	C
ATOM	584	O	ASN	A	79	5.794	-58.714	-11.909	1.00	23.42	A	O
ATOM	585	N	LYS	A	80	4.776	-56.780	-12.460	1.00	23.09	A	N
ATOM	586	CA	LYS	A	80	6.024	-56.117	-12.778	1.00	24.20	A	C
ATOM	587	CB	LYS	A	80	5.783	-54.871	-13.631	1.00	27.00	A	C
ATOM	588	CG	LYS	A	80	5.314	-55.181	-15.037	1.00	30.36	A	C
ATOM	589	CD	LYS	A	80	6.423	-55.858	-15.854	1.00	33.94	A	C
ATOM	590	CE	LYS	A	80	5.916	-57.048	-16.688	1.00	36.49	A	C
ATOM	591	NZ	LYS	A	80	5.336	-56.639	-17.999	1.00	37.18	A	N
ATOM	592	C	LYS	A	80	6.841	-55.741	-11.554	1.00	22.72	A	C
ATOM	593	O	LYS	A	80	8.080	-55.784	-11.599	1.00	24.14	A	O
ATOM	594	N	PHE	A	81	6.173	-55.352	-10.472	1.00	20.24	A	N
ATOM	595	CA	PHE	A	81	6.876	-54.813	-9.318	1.00	18.15	A	C
ATOM	596	CB	PHE	A	81	6.447	-53.380	-9.064	1.00	18.87	A	C
ATOM	597	CG	PHE	A	81	6.461	-52.505	-10.289	1.00	18.61	A	C
ATOM	598	CD1	PHE	A	81	7.599	-52.404	-11.065	1.00	18.00	A	C
ATOM	599	CE1	PHE	A	81	7.632	-51.587	-12.184	1.00	18.22	A	C
ATOM	600	CZ	PHE	A	81	6.510	-50.862	-12.542	1.00	18.35	A	C
ATOM	601	CE2	PHE	A	81	5.354	-50.955	-11.759	1.00	18.91	A	C
ATOM	602	CD2	PHE	A	81	5.335	-51.770	-10.643	1.00	18.40	A	C
ATOM	603	C	PHE	A	81	6.655	-55.584	-8.054	1.00	16.49	A	C
ATOM	604	O	PHE	A	81	7.232	-55.247	-7.031	1.00	15.88	A	O
ATOM	605	N	GLY	A	82	5.840	-56.626	-8.098	1.00	15.73	A	N
ATOM	606	CA	GLY	A	82	5.448	-57.296	-6.856	1.00	15.78	A	C
ATOM	607	C	GLY	A	82	4.790	-56.346	-5.834	1.00	15.32	A	C
ATOM	608	O	GLY	A	82	4.948	-56.516	-4.643	1.00	15.40	A	O
ATOM	609	N	ARG	A	83	4.057	-55.343	-6.311	1.00	14.39	A	N
ATOM	610	CA	ARG	A	83	3.366	-54.424	-5.447	1.00	13.68	A	C
ATOM	611	CB	ARG	A	83	3.555	-52.995	-5.912	1.00	13.45	A	C
ATOM	612	CG	ARG	A	83	3.011	-52.011	-4.904	1.00	13.06	A	C
ATOM	613	CD	ARG	A	83	2.913	-50.629	-5.479	1.00	13.28	A	C
ATOM	614	NE	ARG	A	83	2.721	-49.736	-4.358	1.00	13.46	A	N
ATOM	615	CZ	ARG	A	83	3.697	-49.171	-3.662	1.00	13.30	A	C
ATOM	616	NH1	ARG	A	83	4.971	-49.321	-3.998	1.00	13.23	A	N
ATOM	617	NH2	ARG	A	83	3.375	-48.419	-2.631	1.00	13.54	A	N
ATOM	618	C	ARG	A	83	1.871	-54.704	-5.384	1.00	13.51	A	C
ATOM	619	O	ARG	A	83	1.183	-54.725	-6.390	1.00	13.70	A	O

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ATOM	620	N	ASN A	84	1.390	-54.879	-4.167	1.00	13.56	A	N
ATOM	621	CA	ASN A	84	0.009	-55.148	-3.893	1.00	13.51	A	C
ATOM	622	CB	ASN A	84	-0.088	-56.018	-2.658	1.00	13.59	A	C
ATOM	623	CG	ASN A	84	-1.491	-56.487	-2.384	1.00	14.02	A	C
ATOM	624	OD1	ASN A	84	-1.725	-57.145	-1.381	1.00	15.08	A	O
ATOM	625	ND2	ASN A	84	-2.428	-56.165	-3.261	1.00	13.79	A	N
ATOM	626	C	ASN A	84	-0.760	-53.864	-3.630	1.00	13.38	A	C
ATOM	627	O	ASN A	84	-0.857	-53.447	-2.476	1.00	13.02	A	O
ATOM	628	N	SER A	85	-1.301	-53.271	-4.707	1.00	12.63	A	N
ATOM	629	CA	SER A	85	-2.121	-52.055	-4.669	1.00	11.89	A	C
ATOM	630	CB	SER A	85	-3.343	-52.185	-3.746	1.00	11.20	A	C
ATOM	631	OG	SER A	85	-4.254	-51.134	-3.980	1.00	10.14	A	O
ATOM	632	C	SER A	85	-1.291	-50.867	-4.273	1.00	12.38	A	C
ATOM	633	O	SER A	85	-0.066	-50.944	-4.210	1.00	12.63	A	O
ATOM	634	N	ILE A	86	-1.990	-49.773	-3.990	1.00	12.96	A	N
ATOM	635	CA	ILE A	86	-1.396	-48.453	-3.822	1.00	13.20	A	C
ATOM	636	CB	ILE A	86	-2.512	-47.385	-3.647	1.00	13.89	A	C
ATOM	637	CG1	ILE A	86	-3.144	-47.100	-5.011	1.00	13.93	A	C
ATOM	638	CD1	ILE A	86	-4.318	-46.147	-4.967	1.00	14.24	A	C
ATOM	639	CG2	ILE A	86	-1.996	-46.082	-3.034	1.00	14.48	A	C
ATOM	640	C	ILE A	86	-0.431	-48.423	-2.663	1.00	13.17	A	C
ATOM	641	O	ILE A	86	0.620	-47.786	-2.759	1.00	13.10	A	O
ATOM	642	N	ASP A	87	-0.767	-49.114	-1.569	1.00	12.99	A	N
ATOM	643	CA	ASP A	87	0.130	-49.095	-0.380	1.00	12.59	A	C
ATOM	644	CB	ASP A	87	-0.644	-48.780	0.920	1.00	12.29	A	C
ATOM	645	CG	ASP A	87	-1.666	-49.810	1.265	1.00	11.98	A	C
ATOM	646	OD1	ASP A	87	-1.658	-50.921	0.683	1.00	12.11	A	O
ATOM	647	OD2	ASP A	87	-2.496	-49.479	2.115	1.00	11.43	A	O
ATOM	648	C	ASP A	87	1.028	-50.320	-0.225	1.00	12.13	A	C
ATOM	649	O	ASP A	87	1.692	-50.494	0.782	1.00	11.57	A	O
ATOM	650	N	GLY A	88	1.067	-51.168	-1.236	1.00	12.40	A	N
ATOM	651	CA	GLY A	88	1.807	-52.407	-1.092	1.00	12.89	A	C
ATOM	652	C	GLY A	88	1.201	-53.421	-0.146	1.00	13.24	A	C
ATOM	653	O	GLY A	88	1.699	-54.542	-0.132	1.00	14.52	A	O
ATOM	654	N	ASN A	89	0.115	-53.051	0.567	1.00	12.96	A	N
ATOM	655	CA	ASN A	89	-0.658	-53.912	1.473	1.00	12.96	A	C
ATOM	656	CB	ASN A	89	-0.669	-53.249	2.844	1.00	13.56	A	C
ATOM	657	CG	ASN A	89	0.641	-53.362	3.537	1.00	13.79	A	C
ATOM	658	OD1	ASN A	89	1.205	-54.457	3.631	1.00	14.84	A	O
ATOM	659	ND2	ASN A	89	1.149	-52.242	4.029	1.00	13.75	A	N
ATOM	660	C	ASN A	89	-2.147	-54.210	1.165	1.00	12.88	A	C
ATOM	661	O	ASN A	89	-2.907	-54.462	2.095	1.00	12.88	A	O
ATOM	662	N	GLY A	90	-2.574	-54.175	-0.097	1.00	12.86	A	N
ATOM	663	CA	GLY A	90	-3.958	-54.471	-0.469	1.00	12.39	A	C
ATOM	664	C	GLY A	90	-4.961	-53.302	-0.474	1.00	12.26	A	C
ATOM	665	O	GLY A	90	-6.137	-53.514	-0.791	1.00	12.36	A	O
ATOM	666	N	PHE A	91	-4.527	-52.091	-0.118	1.00	11.47	A	N
ATOM	667	CA	PHE A	91	-5.390	-50.906	-0.131	1.00	11.28	A	C
ATOM	668	CB	PHE A	91	-4.545	-49.680	-0.502	1.00	11.72	A	C
ATOM	669	CG	PHE A	91	-5.262	-48.333	-0.429	1.00	11.82	A	C
ATOM	670	CD1	PHE A	91	-6.027	-47.869	-1.503	1.00	11.80	A	C
ATOM	671	CE1	PHE A	91	-6.634	-46.609	-1.454	1.00	11.78	A	C
ATOM	672	CZ	PHE A	91	-6.457	-45.791	-0.341	1.00	11.56	A	C
ATOM	673	CE2	PHE A	91	-5.647	-46.217	0.706	1.00	11.63	A	C
ATOM	674	CD2	PHE A	91	-5.053	-47.470	0.663	1.00	11.62	A	C
ATOM	675	C	PHE A	91	-6.509	-51.027	-1.132	1.00	10.82	A	C
ATOM	676	O	PHE A	91	-6.262	-50.984	-2.306	1.00	11.40	A	O
ATOM	677	N	GLN A	92	-7.739	-51.128	-0.659	1.00	10.46	A	N
ATOM	678	CA	GLN A	92	-8.903	-51.300	-1.520	1.00	10.16	A	C
ATOM	679	CB	GLN A	92	-10.190	-51.348	-0.665	1.00	9.81	A	C
ATOM	680	CG	GLN A	92	-11.435	-51.789	-1.424	1.00	9.40	A	C
ATOM	681	CD	GLN A	92	-12.658	-51.830	-0.560	1.00	9.00	A	C
ATOM	682	OE1	GLN A	92	-13.251	-50.800	-0.244	1.00	8.91	A	O
ATOM	683	NE2	GLN A	92	-13.056	-53.023	-0.179	1.00	8.85	A	N
ATOM	684	C	GLN A	92	-9.020	-50.172	-2.547	1.00	10.41	A	C
ATOM	685	O	GLN A	92	-8.852	-49.014	-2.220	1.00	10.73	A	O
ATOM	686	N	LEU A	93	-9.372	-50.531	-3.774	1.00	10.45	A	N
ATOM	687	CA	LEU A	93	-9.461	-49.608	-4.873	1.00	10.53	A	C
ATOM	688	CB	LEU A	93	-8.795	-50.248	-6.088	1.00	10.43	A	C
ATOM	689	CG	LEU A	93	-7.325	-50.530	-5.783	1.00	10.45	A	C
ATOM	690	CD1	LEU A	93	-6.629	-51.095	-6.991	1.00	10.58	A	C
ATOM	691	CD2	LEU A	93	-6.606	-49.286	-5.321	1.00	10.42	A	C
ATOM	692	C	LEU A	93	-10.894	-49.254	-5.222	1.00	10.87	A	C
ATOM	693	O	LEU A	93	-11.686	-50.097	-5.637	1.00	10.94	A	O
ATOM	694	N	LYS A	94	-11.228	-47.996	-5.085	1.00	11.36	A	N
ATOM	695	CA	LYS A	94	-12.557	-47.606	-5.384	1.00	12.41	A	C
ATOM	696	CB	LYS A	94	-13.181	-46.937	-4.197	1.00	13.22	A	C
ATOM	697	CG	LYS A	94	-13.478	-47.903	-3.087	1.00	13.81	A	C
ATOM	698	CD	LYS A	94	-14.287	-47.225	-1.995	1.00	14.67	A	C

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ATOM	699	CE	LYS A	94	-13.694	-47.606	-0.647	1.00	15.89	A	C
ATOM	700	NZ	LYS A	94	-14.804	-47.787	0.313	1.00	16.73	A	N
ATOM	701	C	LYS A	94	-12.553	-46.638	-6.490	1.00	12.80	A	C
ATOM	702	O	LYS A	94	-11.826	-45.662	-6.437	1.00	14.03	A	O
ATOM	703	N	SER A	95	-13.419	-46.878	-7.462	1.00	12.71	A	N
ATOM	704	CA	SER A	95	-13.544	-46.022	-8.613	1.00	12.55	A	C
ATOM	705	CB	SER A	95	-13.161	-46.813	-9.861	1.00	12.73	A	C
ATOM	706	OG	SER A	95	-11.804	-47.234	-9.800	1.00	12.59	A	O
ATOM	707	C	SER A	95	-14.974	-45.525	-8.688	1.00	12.34	A	C
ATOM	708	O	SER A	95	-15.918	-46.275	-8.456	1.00	12.56	A	O
ATOM	709	N	THR A	96	-15.138	-44.241	-8.962	1.00	12.35	A	N
ATOM	710	CA	THR A	96	-16.466	-43.667	-9.154	1.00	12.18	A	C
ATOM	711	CB	THR A	96	-16.765	-42.598	-8.118	1.00	12.24	A	C
ATOM	712	OG1	THR A	96	-16.552	-43.158	-6.828	1.00	12.21	A	O
ATOM	713	CG2	THR A	96	-18.231	-42.087	-8.247	1.00	12.24	A	C
ATOM	714	C	THR A	96	-16.560	-42.995	-10.490	1.00	12.02	A	C
ATOM	715	O	THR A	96	-15.804	-42.073	-10.768	1.00	11.98	A	O
ATOM	716	N	VAL A	97	-17.512	-43.453	-11.286	1.00	12.10	A	N
ATOM	717	CA	VAL A	97	-17.796	-42.903	-12.610	1.00	12.29	A	C
ATOM	718	CB	VAL A	97	-18.031	-44.046	-13.614	1.00	11.84	A	C
ATOM	719	CG1	VAL A	97	-16.842	-44.997	-13.607	1.00	11.85	A	C
ATOM	720	CG2	VAL A	97	-19.294	-44.816	-13.291	1.00	11.48	A	C
ATOM	721	C	VAL A	97	-19.043	-41.989	-12.574	1.00	12.50	A	C
ATOM	722	O	VAL A	97	-19.760	-41.922	-11.573	1.00	12.20	A	O
ATOM	723	N	HIS A	98	-19.307	-41.321	-13.693	1.00	12.79	A	N
ATOM	724	CA	HIS A	98	-20.400	-40.338	-13.803	1.00	12.70	A	C
ATOM	725	CB	HIS A	98	-21.764	-40.997	-13.788	1.00	12.30	A	C
ATOM	726	CG	HIS A	98	-21.870	-42.180	-14.687	1.00	11.98	A	C
ATOM	727	ND1	HIS A	98	-21.648	-42.103	-16.040	1.00	11.73	A	N
ATOM	728	CE1	HIS A	98	-21.815	-43.295	-16.574	1.00	11.81	A	C
ATOM	729	NE2	HIS A	98	-22.147	-44.138	-15.617	1.00	11.79	A	N
ATOM	730	CD2	HIS A	98	-22.206	-43.463	-14.429	1.00	11.79	A	C
ATOM	731	C	HIS A	98	-20.334	-39.328	-12.685	1.00	13.21	A	C
ATOM	732	O	HIS A	98	-21.348	-38.988	-12.091	1.00	13.62	A	O
ATOM	733	N	TYR A	99	-19.117	-38.883	-12.389	1.00	13.68	A	N
ATOM	734	CA	TYR A	99	-18.894	-37.826	-11.446	1.00	13.61	A	C
ATOM	735	CB	TYR A	99	-17.410	-37.665	-11.086	1.00	13.46	A	C
ATOM	736	CG	TYR A	99	-17.177	-36.565	-10.042	1.00	13.94	A	C
ATOM	737	CD1	TYR A	99	-17.426	-36.805	-8.691	1.00	14.10	A	C
ATOM	738	CE1	TYR A	99	-17.213	-35.826	-7.731	1.00	13.91	A	C
ATOM	739	CZ	TYR A	99	-16.774	-34.579	-8.108	1.00	13.62	A	C
ATOM	740	OH	TYR A	99	-16.605	-33.644	-7.112	1.00	12.97	A	O
ATOM	741	CE2	TYR A	99	-16.553	-34.292	-9.445	1.00	13.47	A	C
ATOM	742	CD2	TYR A	99	-16.756	-35.278	-10.400	1.00	13.78	A	C
ATOM	743	C	TYR A	99	-19.384	-36.564	-12.086	1.00	13.49	A	C
ATOM	744	O	TYR A	99	-18.870	-36.163	-13.106	1.00	12.90	A	O
ATOM	745	N	SER A	100	-20.399	-35.974	-11.471	1.00	14.43	A	N
ATOM	746	CA	SER A	100	-20.823	-34.601	-11.733	1.00	15.24	A	C
ATOM	747	CB	SER A	100	-19.639	-33.661	-11.530	1.00	15.55	A	C
ATOM	748	OG	SER A	100	-20.037	-32.309	-11.482	1.00	15.70	A	O
ATOM	749	C	SER A	100	-21.440	-34.469	-13.114	1.00	16.08	A	C
ATOM	750	O	SER A	100	-21.916	-35.443	-13.679	1.00	16.02	A	O
ATOM	751	N	SER A	101	-21.448	-33.271	-13.668	1.00	18.00	A	N
ATOM	752	CA	SER A	101	-22.109	-33.064	-14.954	1.00	20.04	A	C
ATOM	753	CB	SER A	101	-23.285	-32.117	-14.785	1.00	20.79	A	C
ATOM	754	OG	SER A	101	-24.125	-32.255	-15.909	1.00	22.68	A	O
ATOM	755	C	SER A	101	-21.172	-32.557	-16.074	1.00	20.29	A	C
ATOM	756	O	SER A	101	-20.448	-31.590	-15.909	1.00	18.68	A	O
ATOM	757	N	ARG A	102	-21.210	-33.275	-17.212	1.00	21.31	A	N
ATOM	758	CA	ARG A	102	-20.354	-32.962	-18.351	1.00	22.92	A	C
ATOM	759	CB	ARG A	102	-20.973	-31.842	-19.222	1.00	25.54	A	C
ATOM	760	CG	ARG A	102	-22.375	-32.170	-19.771	1.00	29.36	A	C
ATOM	761	CD	ARG A	102	-22.597	-31.658	-21.202	1.00	32.59	A	C
ATOM	762	NE	ARG A	102	-22.425	-30.196	-21.266	1.00	35.58	A	N
ATOM	763	CZ	ARG A	102	-21.863	-29.501	-22.268	1.00	38.08	A	C
ATOM	764	NH1	ARG A	102	-21.371	-30.080	-23.375	1.00	37.26	A	N
ATOM	765	NH2	ARG A	102	-21.785	-28.183	-22.160	1.00	40.05	A	N
ATOM	766	C	ARG A	102	-18.972	-32.558	-17.854	1.00	21.22	A	C
ATOM	767	O	ARG A	102	-18.499	-31.478	-18.155	1.00	22.96	A	O
ATOM	768	N	TYR A	103	-18.337	-33.431	-17.088	1.00	19.27	A	N
ATOM	769	CA	TYR A	103	-17.131	-33.068	-16.304	1.00	18.16	A	C
ATOM	770	CB	TYR A	103	-17.246	-33.653	-14.876	1.00	17.43	A	C
ATOM	771	CG	TYR A	103	-16.076	-33.397	-14.001	1.00	17.19	A	C
ATOM	772	CD1	TYR A	103	-15.957	-32.216	-13.283	1.00	18.00	A	C
ATOM	773	CE1	TYR A	103	-14.860	-31.991	-12.450	1.00	18.06	A	C
ATOM	774	CZ	TYR A	103	-13.875	-32.964	-12.348	1.00	17.35	A	C
ATOM	775	OH	TYR A	103	-12.774	-32.784	-11.574	1.00	17.41	A	O
ATOM	776	CE2	TYR A	103	-13.985	-34.135	-13.042	1.00	17.27	A	C
ATOM	777	CD2	TYR A	103	-15.078	-34.345	-13.864	1.00	17.58	A	C

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ATOM	778	C	TYR	A	103	-15.854	-33.534	-17.030	1.00	16.89	A	C
ATOM	779	O	TYR	A	103	-15.682	-34.721	-17.328	1.00	16.93	A	O
ATOM	780	N	ASN	A	104	-14.967	-32.600	-17.341	1.00	15.51	A	N
ATOM	781	CA	ASN	A	104	-13.893	-32.910	-18.257	1.00	14.63	A	C
ATOM	782	CB	ASN	A	104	-13.665	-31.743	-19.205	1.00	14.81	A	C
ATOM	783	CG	ASN	A	104	-14.612	-31.750	-20.400	1.00	15.08	A	C
ATOM	784	OD1	ASN	A	104	-15.024	-32.796	-20.896	1.00	15.19	A	O
ATOM	785	ND2	ASN	A	104	-14.920	-30.571	-20.894	1.00	14.99	A	N
ATOM	786	C	ASN	A	104	-12.614	-33.257	-17.504	1.00	13.94	A	C
ATOM	787	O	ASN	A	104	-11.578	-32.636	-17.730	1.00	13.92	A	O
ATOM	788	N	ASN	A	105	-12.697	-34.257	-16.616	1.00	12.63	A	N
ATOM	789	CA	ASN	A	105	-11.555	-34.707	-15.844	1.00	11.74	A	C
ATOM	790	CB	ASN	A	105	-11.145	-33.649	-14.826	1.00	11.60	A	C
ATOM	791	CG	ASN	A	105	-9.690	-33.277	-14.949	1.00	11.53	A	C
ATOM	792	OD1	ASN	A	105	-8.832	-34.125	-15.116	1.00	11.68	A	O
ATOM	793	ND2	ASN	A	105	-9.410	-32.009	-14.887	1.00	11.47	A	N
ATOM	794	C	ASN	A	105	-11.738	-36.035	-15.116	1.00	11.37	A	C
ATOM	795	O	ASN	A	105	-12.840	-36.575	-15.031	1.00	11.26	A	O
ATOM	796	N	ALA	A	106	-10.614	-36.562	-14.637	1.00	11.03	A	N
ATOM	797	CA	ALA	A	106	-10.579	-37.638	-13.650	1.00	10.62	A	C
ATOM	798	CB	ALA	A	106	-10.233	-38.958	-14.290	1.00	10.51	A	C
ATOM	799	C	ALA	A	106	-9.512	-37.269	-12.681	1.00	10.35	A	C
ATOM	800	O	ALA	A	106	-8.663	-36.428	-12.992	1.00	10.10	A	O
ATOM	801	N	PHE	A	107	-9.522	-37.920	-11.525	1.00	10.44	A	N
ATOM	802	CA	PHE	A	107	-8.637	-37.527	-10.431	1.00	10.55	A	C
ATOM	803	CB	PHE	A	107	-8.983	-36.124	-9.903	1.00	10.32	A	C
ATOM	804	CG	PHE	A	107	-10.352	-36.015	-9.323	1.00	10.51	A	C
ATOM	805	CD2	PHE	A	107	-11.421	-35.620	-10.104	1.00	10.75	A	C
ATOM	806	CE2	PHE	A	107	-12.694	-35.504	-9.561	1.00	10.83	A	C
ATOM	807	CZ	PHE	A	107	-12.905	-35.812	-8.233	1.00	10.89	A	C
ATOM	808	CE1	PHE	A	107	-11.841	-36.197	-7.445	1.00	10.78	A	C
ATOM	809	CD1	PHE	A	107	-10.575	-36.280	-7.994	1.00	10.79	A	C
ATOM	810	C	PHE	A	107	-8.568	-38.494	-9.258	1.00	10.67	A	C
ATOM	811	O	PHE	A	107	-9.372	-39.418	-9.136	1.00	10.36	A	O
ATOM	812	N	TRP	A	108	-7.575	-38.222	-8.404	1.00	11.14	A	N
ATOM	813	CA	TRP	A	108	-7.276	-38.991	-7.221	1.00	11.55	A	C
ATOM	814	CB	TRP	A	108	-5.895	-39.634	-7.328	1.00	11.58	A	C
ATOM	815	CG	TRP	A	108	-5.269	-39.991	-6.019	1.00	11.70	A	C
ATOM	816	CD1	TRP	A	108	-4.276	-39.320	-5.372	1.00	11.59	A	C
ATOM	817	NE1	TRP	A	108	-3.967	-39.954	-4.192	1.00	11.77	A	N
ATOM	818	CE2	TRP	A	108	-4.765	-41.058	-4.059	1.00	11.81	A	C
ATOM	819	CD2	TRP	A	108	-5.600	-41.113	-5.189	1.00	12.15	A	C
ATOM	820	CE3	TRP	A	108	-6.526	-42.169	-5.295	1.00	12.29	A	C
ATOM	821	CZ3	TRP	A	108	-6.583	-43.109	-4.277	1.00	11.79	A	C
ATOM	822	CH2	TRP	A	108	-5.736	-43.017	-3.178	1.00	11.69	A	C
ATOM	823	CZ2	TRP	A	108	-4.827	-42.005	-3.049	1.00	11.78	A	C
ATOM	824	C	TRP	A	108	-7.301	-38.046	-6.058	1.00	11.89	A	C
ATOM	825	O	TRP	A	108	-6.541	-37.070	-6.011	1.00	12.66	A	O
ATOM	826	N	ASN	A	109	-8.146	-38.361	-5.086	1.00	12.02	A	N
ATOM	827	CA	ASN	A	109	-8.413	-37.441	-3.998	1.00	11.55	A	C
ATOM	828	CB	ASN	A	109	-9.910	-37.250	-3.866	1.00	10.98	A	C
ATOM	829	CG	ASN	A	109	-10.615	-38.456	-3.291	1.00	10.78	A	C
ATOM	830	OD1	ASN	A	109	-10.027	-39.428	-2.857	1.00	9.78	A	O
ATOM	831	ND2	ASN	A	109	-11.918	-38.378	-3.297	1.00	11.23	A	N
ATOM	832	C	ASN	A	109	-7.821	-37.800	-2.637	1.00	11.83	A	C
ATOM	833	O	ASN	A	109	-8.205	-37.180	-1.653	1.00	12.98	A	O
ATOM	834	N	GLY	A	110	-6.911	-38.767	-2.566	1.00	11.58	A	N
ATOM	835	CA	GLY	A	110	-6.353	-39.211	-1.286	1.00	11.33	A	C
ATOM	836	C	GLY	A	110	-6.978	-40.526	-0.825	1.00	11.37	A	C
ATOM	837	O	GLY	A	110	-6.430	-41.220	0.014	1.00	12.11	A	O
ATOM	838	N	VAL	A	111	-8.105	-40.898	-1.404	1.00	11.10	A	N
ATOM	839	CA	VAL	A	111	-8.926	-42.006	-0.912	1.00	10.97	A	C
ATOM	840	CB	VAL	A	111	-10.193	-41.411	-0.186	1.00	11.34	A	C
ATOM	841	CG1	VAL	A	111	-11.387	-42.362	-0.056	1.00	11.21	A	C
ATOM	842	CG2	VAL	A	111	-9.789	-40.889	1.181	1.00	11.73	A	C
ATOM	843	C	VAL	A	111	-9.306	-42.918	-2.065	1.00	10.59	A	C
ATOM	844	O	VAL	A	111	-9.366	-44.119	-1.902	1.00	10.53	A	O
ATOM	845	N	GLN	A	112	-9.574	-42.345	-3.227	1.00	10.74	A	N
ATOM	846	CA	GLN	A	112	-10.166	-43.079	-4.322	1.00	10.93	A	C
ATOM	847	CB	GLN	A	112	-11.652	-43.280	-4.029	1.00	10.80	A	C
ATOM	848	CG	GLN	A	112	-12.502	-42.023	-4.050	1.00	10.59	A	C
ATOM	849	CD	GLN	A	112	-13.930	-42.371	-4.436	1.00	10.69	A	C
ATOM	850	OE1	GLN	A	112	-14.867	-42.252	-3.631	1.00	10.62	A	O
ATOM	851	NE2	GLN	A	112	-14.092	-42.878	-5.659	1.00	10.64	A	N
ATOM	852	C	GLN	A	112	-10.020	-42.410	-5.681	1.00	11.08	A	C
ATOM	853	O	GLN	A	112	-9.555	-41.283	-5.792	1.00	10.83	A	O
ATOM	854	N	MET	A	113	-10.449	-43.117	-6.713	1.00	11.57	A	N
ATOM	855	CA	MET	A	113	-10.386	-42.607	-8.068	1.00	12.22	A	C
ATOM	856	CB	MET	A	113	-9.770	-43.655	-9.012	1.00	12.75	A	C

ATOM	857	CG	MET	A	113	-8.248	-43.793	-8.921	1.00	12.88	A	C
ATOM	858	SD	MET	A	113	-7.704	-44.724	-7.465	1.00	13.61	A	S
ATOM	859	CE	MET	A	113	-8.484	-46.336	-7.684	1.00	12.88	A	C
ATOM	860	C	MET	A	113	-11.779	-42.229	-8.566	1.00	12.30	A	C
ATOM	861	O	MET	A	113	-12.777	-42.930	-8.298	1.00	11.89	A	O
ATOM	862	N	VAL	A	114	-11.813	-41.138	-9.338	1.00	12.45	A	N
ATOM	863	CA	VAL	A	114	-13.060	-40.524	-9.829	1.00	12.39	A	C
ATOM	864	CB	VAL	A	114	-13.312	-39.200	-9.108	1.00	12.60	A	C
ATOM	865	CG1	VAL	A	114	-14.735	-38.756	-9.269	1.00	12.58	A	C
ATOM	866	CG2	VAL	A	114	-13.006	-39.354	-7.641	1.00	13.14	A	C
ATOM	867	C	VAL	A	114	-12.892	-40.165	-11.291	1.00	11.82	A	C
ATOM	868	O	VAL	A	114	-11.824	-39.682	-11.672	1.00	11.70	A	O
ATOM	869	N	TYR	A	115	-13.943	-40.368	-12.085	1.00	11.01	A	N
ATOM	870	CA	TYR	A	115	-13.868	-40.205	-13.517	1.00	10.70	A	C
ATOM	871	CB	TYR	A	115	-13.724	-41.578	-14.192	1.00	10.58	A	C
ATOM	872	CG	TYR	A	115	-12.538	-42.408	-13.680	1.00	10.64	A	C
ATOM	873	CD1	TYR	A	115	-11.258	-42.218	-14.179	1.00	10.65	A	C
ATOM	874	CE1	TYR	A	115	-10.189	-42.936	-13.703	1.00	10.73	A	C
ATOM	875	CZ	TYR	A	115	-10.376	-43.877	-12.724	1.00	11.06	A	C
ATOM	876	OH	TYR	A	115	-9.298	-44.623	-12.258	1.00	11.31	A	O
ATOM	877	CE2	TYR	A	115	-11.637	-44.098	-12.219	1.00	10.82	A	C
ATOM	878	CD2	TYR	A	115	-12.698	-43.351	-12.682	1.00	10.64	A	C
ATOM	879	C	TYR	A	115	-15.103	-39.493	-14.016	1.00	10.93	A	C
ATOM	880	O	TYR	A	115	-16.210	-40.015	-13.945	1.00	11.10	A	O
ATOM	881	N	GLY	A	116	-14.917	-38.278	-14.505	1.00	11.20	A	N
ATOM	882	CA	GLY	A	116	-15.952	-37.601	-15.247	1.00	11.38	A	C
ATOM	883	C	GLY	A	116	-16.368	-38.324	-16.522	1.00	11.63	A	C
ATOM	884	O	GLY	A	116	-15.747	-39.265	-16.955	1.00	10.90	A	O
ATOM	885	N	ASP	A	117	-17.456	-37.839	-17.105	1.00	12.56	A	N
ATOM	886	CA	ASP	A	117	-18.020	-38.340	-18.365	1.00	12.79	A	C
ATOM	887	CB	ASP	A	117	-19.545	-38.204	-18.392	1.00	12.28	A	C
ATOM	888	CG	ASP	A	117	-20.245	-39.348	-17.701	1.00	12.14	A	C
ATOM	889	OD1	ASP	A	117	-19.932	-40.511	-17.976	1.00	11.76	A	O
ATOM	890	OD2	ASP	A	117	-21.149	-39.081	-16.895	1.00	12.59	A	O
ATOM	891	C	ASP	A	117	-17.509	-37.570	-19.541	1.00	13.10	A	C
ATOM	892	O	ASP	A	117	-17.586	-38.054	-20.648	1.00	13.73	A	O
ATOM	893	N	GLY	A	118	-17.039	-36.356	-19.301	1.00	13.57	A	N
ATOM	894	CA	GLY	A	118	-16.573	-35.481	-20.364	1.00	13.80	A	C
ATOM	895	C	GLY	A	118	-17.762	-34.764	-20.948	1.00	14.14	A	C
ATOM	896	O	GLY	A	118	-18.900	-35.121	-20.631	1.00	14.07	A	O
ATOM	897	N	ASP	A	119	-17.507	-33.780	-21.812	1.00	14.55	A	N
ATOM	898	CA	ASP	A	119	-18.589	-32.932	-22.323	1.00	15.19	A	C
ATOM	899	CB	ASP	A	119	-18.176	-31.444	-22.475	1.00	14.84	A	C
ATOM	900	CG	ASP	A	119	-17.010	-31.211	-23.418	1.00	14.26	A	C
ATOM	901	OD1	ASP	A	119	-16.861	-31.947	-24.414	1.00	14.21	A	O
ATOM	902	OD2	ASP	A	119	-16.275	-30.231	-23.168	1.00	13.01	A	O
ATOM	903	C	ASP	A	119	-19.192	-33.458	-23.599	1.00	16.45	A	C
ATOM	904	O	ASP	A	119	-20.148	-32.880	-24.119	1.00	16.55	A	O
ATOM	905	N	GLY	A	120	-18.645	-34.573	-24.091	1.00	18.15	A	N
ATOM	906	CA	GLY	A	120	-19.134	-35.212	-25.316	1.00	18.51	A	C
ATOM	907	C	GLY	A	120	-18.466	-34.701	-26.573	1.00	19.67	A	C
ATOM	908	O	GLY	A	120	-18.547	-35.358	-27.603	1.00	21.88	A	O
ATOM	909	N	VAL	A	121	-17.798	-33.549	-26.504	1.00	19.75	A	N
ATOM	910	CA	VAL	A	121	-17.223	-32.918	-27.683	1.00	20.14	A	C
ATOM	911	CB	VAL	A	121	-17.736	-31.456	-27.839	1.00	20.88	A	C
ATOM	912	CG1	VAL	A	121	-16.946	-30.680	-28.902	1.00	21.41	A	C
ATOM	913	CG2	VAL	A	121	-19.228	-31.416	-28.157	1.00	20.58	A	C
ATOM	914	C	VAL	A	121	-15.679	-32.991	-27.596	1.00	20.30	A	C
ATOM	915	O	VAL	A	121	-15.035	-33.586	-28.457	1.00	19.79	A	O
ATOM	916	N	THR	A	122	-15.090	-32.404	-26.555	1.00	20.14	A	N
ATOM	917	CA	THR	A	122	-13.635	-32.494	-26.351	1.00	19.96	A	C
ATOM	918	CB	THR	A	122	-13.061	-31.238	-25.637	1.00	21.45	A	C
ATOM	919	OG1	THR	A	122	-13.999	-30.796	-24.662	1.00	24.36	A	O
ATOM	920	CG2	THR	A	122	-12.845	-30.074	-26.636	1.00	21.78	A	C
ATOM	921	C	THR	A	122	-13.191	-33.764	-25.610	1.00	17.15	A	C
ATOM	922	O	THR	A	122	-12.032	-34.113	-25.706	1.00	15.97	A	O
ATOM	923	N	PHE	A	123	-14.103	-34.428	-24.892	1.00	15.54	A	N
ATOM	924	CA	PHE	A	123	-13.837	-35.724	-24.212	1.00	14.59	A	C
ATOM	925	CB	PHE	A	123	-13.458	-35.540	-22.736	1.00	14.75	A	C
ATOM	926	CG	PHE	A	123	-12.146	-34.912	-22.502	1.00	14.63	A	C
ATOM	927	CD1	PHE	A	123	-11.007	-35.663	-22.517	1.00	15.07	A	C
ATOM	928	CE1	PHE	A	123	-9.772	-35.088	-22.268	1.00	15.58	A	C
ATOM	929	CZ	PHE	A	123	-9.678	-33.744	-21.996	1.00	15.40	A	C
ATOM	930	CE2	PHE	A	123	-10.830	-32.989	-21.968	1.00	15.55	A	C
ATOM	931	CD2	PHE	A	123	-12.056	-33.583	-22.207	1.00	15.01	A	C
ATOM	932	C	PHE	A	123	-15.054	-36.631	-24.117	1.00	13.43	A	C
ATOM	933	O	PHE	A	123	-16.159	-36.177	-24.004	1.00	13.18	A	O
ATOM	934	N	ILE	A	124	-14.808	-37.916	-24.031	1.00	13.11	A	N
ATOM	935	CA	ILE	A	124	-15.829	-38.898	-23.717	1.00	12.99	A	C

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ATOM    936   CB    ILE A 124   -15.856 -40.029 -24.779  1.00 13.41      A   C
ATOM    937   CG1   ILE A 124   -14.577 -40.925 -24.768  1.00 13.15      A   C
ATOM    938   CD1   ILE A 124   -14.749 -42.242 -25.530  1.00 12.52      A   C
ATOM    939   CG2   ILE A 124   -16.078 -39.429 -26.161  1.00 13.31      A   C
ATOM    940   C     ILE A 124   -15.517 -39.451 -22.339  1.00 12.74      A   C
ATOM    941   O     ILE A 124   -14.551 -39.000 -21.705  1.00 13.23      A   O
ATOM    942   N     PRO A 125   -16.331 -40.396 -21.844  1.00 12.24      A   N
ATOM    943   CA    PRO A 125   -16.094 -40.854 -20.471  1.00 12.10      A   C
ATOM    944   CB    PRO A 125   -17.132 -41.978 -20.285  1.00 12.45      A   C
ATOM    945   CG    PRO A 125   -18.265 -41.554 -21.152  1.00 12.47      A   C
ATOM    946   CD    PRO A 125   -17.607 -40.918 -22.360  1.00 12.48      A   C
ATOM    947   C     PRO A 125   -14.674 -41.348 -20.232  1.00 11.45      A   C
ATOM    948   O     PRO A 125   -14.164 -42.208 -20.969  1.00 10.89      A   O
ATOM    949   N     PHE A 126   -14.071 -40.769 -19.199  1.00 10.85      A   N
ATOM    950   CA    PHE A 126   -12.645 -40.875 -18.936  1.00 10.71      A   C
ATOM    951   CB    PHE A 126   -12.247 -39.967 -17.783  1.00 10.54      A   C
ATOM    952   CG    PHE A 126   -12.017 -38.547 -18.201  1.00 10.47      A   C
ATOM    953   CD1   PHE A 126   -13.050 -37.780 -18.712  1.00 10.57      A   C
ATOM    954   CE1   PHE A 126   -12.828 -36.463 -19.123  1.00 10.33      A   C
ATOM    955   CZ    PHE A 126   -11.574 -35.925 -19.018  1.00 10.16      A   C
ATOM    956   CE2   PHE A 126   -10.544 -36.690 -18.518  1.00 10.11      A   C
ATOM    957   CD2   PHE A 126   -10.760 -37.981 -18.116  1.00 10.22      A   C
ATOM    958   C     PHE A 126   -12.090 -42.276 -18.691  1.00 10.71      A   C
ATOM    959   O     PHE A 126   -10.893 -42.501 -18.969  1.00 10.90      A   O
ATOM    960   N     SER A 127   -12.930 -43.220 -18.246  1.00 10.31      A   N
ATOM    961   CA    SER A 127   -12.456 -44.588 -18.018  1.00 10.08      A   C
ATOM    962   CB    SER A 127   -13.430 -45.374 -17.180  1.00 10.12      A   C
ATOM    963   OG    SER A 127   -14.738 -45.075 -17.550  1.00 10.16      A   O
ATOM    964   C     SER A 127   -12.147 -45.358 -19.281  1.00  9.98      A   C
ATOM    965   O     SER A 127   -11.453 -46.356 -19.242  1.00 10.28      A   O
ATOM    966   N     ALA A 128   -12.598 -44.864 -20.412  1.00 10.04      A   N
ATOM    967   CA    ALA A 128   -12.371 -45.532 -21.693  1.00 10.10      A   C
ATOM    968   CB    ALA A 128   -13.180 -44.831 -22.782  1.00 10.16      A   C
ATOM    969   C     ALA A 128   -10.899 -45.715 -22.144  1.00 10.16      A   C
ATOM    970   O     ALA A 128   -10.633 -46.559 -23.017  1.00 10.10      A   O
ATOM    971   N     ASP A 129    -9.957 -44.956 -21.580  1.00 10.09      A   N
ATOM    972   CA    ASP A 129    -8.545 -45.186 -21.882  1.00 10.27      A   C
ATOM    973   CB    ASP A 129    -7.842 -43.893 -22.314  1.00 10.08      A   C
ATOM    974   CG    ASP A 129    -6.541 -44.156 -23.060  1.00 10.15      A   C
ATOM    975   OD1   ASP A 129    -5.845 -45.112 -22.681  1.00 10.22      A   O
ATOM    976   OD2   ASP A 129    -6.191 -43.422 -24.030  1.00 10.06      A   O
ATOM    977   C     ASP A 129    -7.836 -45.809 -20.686  1.00 10.67      A   C
ATOM    978   O     ASP A 129    -7.789 -45.228 -19.607  1.00 11.36      A   O
ATOM    979   N     PRO A 130    -7.247 -46.992 -20.866  1.00 11.05      A   N
ATOM    980   CA    PRO A 130    -6.480 -47.543 -19.758  1.00 11.13      A   C
ATOM    981   CB    PRO A 130    -5.810 -48.755 -20.375  1.00 11.09      A   C
ATOM    982   CG    PRO A 130    -6.739 -49.200 -21.455  1.00 11.13      A   C
ATOM    983   CD    PRO A 130    -7.447 -47.969 -21.952  1.00 11.07      A   C
ATOM    984   C     PRO A 130    -5.425 -46.594 -19.201  1.00 11.90      A   C
ATOM    985   O     PRO A 130    -5.090 -46.672 -18.021  1.00 11.81      A   O
ATOM    986   N     ASP A 131    -4.871 -45.691 -20.012  1.00 12.81      A   N
ATOM    987   CA    ASP A 131    -3.767 -44.936 -19.473  1.00 13.21      A   C
ATOM    988   CB    ASP A 131    -2.861 -44.298 -20.538  1.00 12.98      A   C
ATOM    989   CG    ASP A 131    -3.566 -43.310 -21.446  1.00 13.07      A   C
ATOM    990   OD1   ASP A 131    -4.133 -42.275 -21.008  1.00 13.36      A   O
ATOM    991   OD2   ASP A 131    -3.468 -43.524 -22.667  1.00 13.50      A   O
ATOM    992   C     ASP A 131    -4.291 -43.959 -18.422  1.00 14.31      A   C
ATOM    993   O     ASP A 131    -3.505 -43.461 -17.584  1.00 14.98      A   O
ATOM    994   N     VAL A 132    -5.607 -43.685 -18.438  1.00 14.33      A   N
ATOM    995   CA    VAL A 132    -6.153 -42.702 -17.498  1.00 14.09      A   C
ATOM    996   CB    VAL A 132    -7.528 -42.180 -17.937  1.00 14.79      A   C
ATOM    997   CG1   VAL A 132    -8.084 -41.168 -16.922  1.00 14.72      A   C
ATOM    998   CG2   VAL A 132    -7.420 -41.532 -19.314  1.00 15.01      A   C
ATOM    999   C     VAL A 132    -6.253 -43.352 -16.140  1.00 13.25      A   C
ATOM   1000   O     VAL A 132    -5.903 -42.755 -15.150  1.00 12.79      A   O
ATOM   1001   N     ILE A 133    -6.691 -44.603 -16.121  1.00 12.74      A   N
ATOM   1002   CA    ILE A 133    -6.835 -45.351 -14.883  1.00 12.12      A   C
ATOM   1003   CB    ILE A 133    -7.565 -46.703 -15.122  1.00 12.05      A   C
ATOM   1004   CG1   ILE A 133    -9.069 -46.437 -15.301  1.00 12.13      A   C
ATOM   1005   CD1   ILE A 133    -9.507 -46.212 -16.734  1.00 12.16      A   C
ATOM   1006   CG2   ILE A 133    -7.403 -47.665 -13.948  1.00 12.02      A   C
ATOM   1007   C     ILE A 133    -5.476 -45.527 -14.246  1.00 11.61      A   C
ATOM   1008   O     ILE A 133    -5.292 -45.217 -13.067  1.00 11.61      A   O
ATOM   1009   N     GLY A 134    -4.515 -45.989 -15.029  1.00 11.10      A   N
ATOM   1010   CA    GLY A 134    -3.132 -46.092 -14.555  1.00 10.85      A   C
ATOM   1011   C     GLY A 134    -2.611 -44.784 -13.982  1.00 10.75      A   C
ATOM   1012   O     GLY A 134    -1.919 -44.773 -12.946  1.00 11.06      A   O
ATOM   1013   N     HIS A 135    -2.962 -43.675 -14.631  1.00 10.39      A   N
ATOM   1014   CA    HIS A 135    -2.510 -42.340 -14.219  1.00 10.07      A   C
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ATOM   1015  CB  HIS A 135      -2.987 -41.329 -15.262  1.00  9.93      A  C
ATOM   1016  CG  HIS A 135      -2.513 -39.933 -15.049  1.00  9.63      A  C
ATOM   1017  ND1 HIS A 135      -1.472 -39.389 -15.765  1.00  9.67      A  N
ATOM   1018  CE1 HIS A 135      -1.291 -38.133 -15.392  1.00  9.59      A  C
ATOM   1019  NE2 HIS A 135      -2.181 -37.845 -14.459  1.00  9.71      A  N
ATOM   1020  CD2 HIS A 135      -2.964 -38.953 -14.237  1.00  9.62      A  C
ATOM   1021  C   HIS A 135      -3.024 -41.996 -12.813  1.00 10.10      A  C
ATOM   1022  O   HIS A 135      -2.251 -41.630 -11.902  1.00 10.09      A  O
ATOM   1023  N   GLU A 136      -4.326 -42.136 -12.624  1.00 10.10      A  N
ATOM   1024  CA  GLU A 136      -4.951 -41.752 -11.347  1.00 10.17      A  C
ATOM   1025  CB  GLU A 136      -6.475 -41.654 -11.514  1.00 10.47      A  C
ATOM   1026  CG  GLU A 136      -6.894 -40.641 -12.554  1.00 10.55      A  C
ATOM   1027  CD  GLU A 136      -6.148 -39.345 -12.359  1.00 11.18      A  C
ATOM   1028  OE1 GLU A 136      -5.972 -38.931 -11.195  1.00 11.67      A  O
ATOM   1029  OE2 GLU A 136      -5.723 -38.736 -13.351  1.00 11.52      A  O
ATOM   1030  C   GLU A 136      -4.592 -42.714 -10.224  1.00  9.84      A  C
ATOM   1031  O   GLU A 136      -4.247 -42.287  -9.155  1.00  9.75      A  O
ATOM   1032  N   LEU A 137      -4.638 -44.006 -10.482  1.00  9.71      A  N
ATOM   1033  CA  LEU A 137      -4.113 -44.998  -9.549  1.00 10.13      A  C
ATOM   1034  CB  LEU A 137      -4.199 -46.328 -10.278  1.00 10.76      A  C
ATOM   1035  CG  LEU A 137      -4.003 -47.670  -9.581  1.00 11.56      A  C
ATOM   1036  CD1 LEU A 137      -2.714 -47.741  -8.743  1.00 11.82      A  C
ATOM   1037  CD2 LEU A 137      -5.230 -48.010  -8.760  1.00 11.81      A  C
ATOM   1038  C   LEU A 137      -2.644 -44.669  -9.113  1.00  9.92      A  C
ATOM   1039  O   LEU A 137      -2.286 -44.625  -7.953  1.00  9.14      A  O
ATOM   1040  N   THR A 138      -1.796 -44.397 -10.086  1.00 10.20      A  N
ATOM   1041  CA  THR A 138      -0.425 -44.011  -9.817  1.00 10.26      A  C
ATOM   1042  CB  THR A 138       0.361 -43.954 -11.146  1.00 10.02      A  C
ATOM   1043  OG1 THR A 138       0.355 -45.258 -11.754  1.00  9.32      A  O
ATOM   1044  CG2 THR A 138       1.785 -43.463 -10.929  1.00  9.83      A  C
ATOM   1045  C   THR A 138      -0.303 -42.695  -8.973  1.00 10.57      A  C
ATOM   1046  O   THR A 138       0.662 -42.538  -8.183  1.00 10.60      A  O
ATOM   1047  N   HIS A 139      -1.263 -41.771  -9.095  1.00 10.54      A  N
ATOM   1048  CA  HIS A 139      -1.272 -40.620  -8.177  1.00 10.42      A  C
ATOM   1049  CB  HIS A 139      -2.468 -39.695  -8.370  1.00 10.27      A  C
ATOM   1050  CG  HIS A 139      -2.317 -38.717  -9.486  1.00 10.44      A  C
ATOM   1051  ND1 HIS A 139      -1.094 -38.259  -9.918  1.00 10.59      A  N
ATOM   1052  CE1 HIS A 139      -1.265 -37.406 -10.914  1.00 10.87      A  C
ATOM   1053  NE2 HIS A 139      -2.563 -37.285 -11.142  1.00 11.18      A  N
ATOM   1054  CD2 HIS A 139      -3.241 -38.089 -10.249  1.00 10.94      A  C
ATOM   1055  C   HIS A 139      -1.245 -41.129  -6.747  1.00 10.73      A  C
ATOM   1056  O   HIS A 139      -0.491 -40.621  -5.920  1.00 10.94      A  O
ATOM   1057  N   GLY A 140      -2.052 -42.151  -6.466  1.00 11.04      A  N
ATOM   1058  CA  GLY A 140      -2.056 -42.807  -5.160  1.00 10.90      A  C
ATOM   1059  C   GLY A 140      -0.692 -43.407  -4.803  1.00 10.98      A  C
ATOM   1060  O   GLY A 140      -0.171 -43.198  -3.693  1.00 11.37      A  O
ATOM   1061  N   VAL A 141      -0.086 -44.150  -5.726  1.00 10.36      A  N
ATOM   1062  CA  VAL A 141       1.177 -44.811  -5.416  1.00  9.75      A  C
ATOM   1063  CB  VAL A 141       1.682 -45.578  -6.619  1.00  9.53      A  C
ATOM   1064  CG1 VAL A 141       3.058 -46.151  -6.348  1.00  9.58      A  C
ATOM   1065  CG2 VAL A 141       0.705 -46.676  -6.968  1.00  9.43      A  C
ATOM   1066  C   VAL A 141       2.215 -43.784  -5.013  1.00  9.84      A  C
ATOM   1067  O   VAL A 141       2.931 -43.938  -4.031  1.00  9.44      A  O
ATOM   1068  N   THR A 142       2.255 -42.703  -5.779  1.00 10.29      A  N
ATOM   1069  CA  THR A 142       3.151 -41.590  -5.513  1.00 10.26      A  C
ATOM   1070  CB  THR A 142       3.000 -40.503  -6.577  1.00 10.08      A  C
ATOM   1071  OG1 THR A 142       3.358 -41.026  -7.880  1.00  9.80      A  O
ATOM   1072  CG2 THR A 142       3.871 -39.305  -6.210  1.00 10.03      A  C
ATOM   1073  C   THR A 142       2.904 -40.965  -4.158  1.00 10.52      A  C
ATOM   1074  O   THR A 142       3.843 -40.718  -3.399  1.00 10.56      A  O
ATOM   1075  N   GLU A 143       1.650 -40.695  -3.841  1.00 10.94      A  N
ATOM   1076  CA  GLU A 143       1.352 -40.031  -2.570  1.00 11.25      A  C
ATOM   1077  CB  GLU A 143      -0.118 -39.677  -2.462  1.00 11.65      A  C
ATOM   1078  CG  GLU A 143      -0.691 -39.862  -1.082  1.00 12.22      A  C
ATOM   1079  CD  GLU A 143      -1.934 -39.052  -0.832  1.00 12.99      A  C
ATOM   1080  OE1 GLU A 143      -2.020 -38.543   0.317  1.00 12.86      A  O
ATOM   1081  OE2 GLU A 143      -2.804 -38.922  -1.764  1.00 13.79      A  O
ATOM   1082  C   GLU A 143       1.782 -40.903  -1.415  1.00 11.45      A  C
ATOM   1083  O   GLU A 143       2.210 -40.390  -0.398  1.00 11.64      A  O
ATOM   1084  N   HIS A 144       1.680 -42.218  -1.589  1.00 11.88      A  N
ATOM   1085  CA  HIS A 144       2.095 -43.209  -0.589  1.00 12.29      A  C
ATOM   1086  CB  HIS A 144       1.247 -44.484  -0.746  1.00 13.27      A  C
ATOM   1087  CG  HIS A 144      -0.045 -44.440  -0.009  1.00 14.23      A  C
ATOM   1088  ND1 HIS A 144      -1.080 -43.600  -0.368  1.00 15.20      A  N
ATOM   1089  CE1 HIS A 144      -2.097 -43.770   0.457  1.00 15.20      A  C
ATOM   1090  NE2 HIS A 144      -1.749 -44.684   1.343  1.00 15.38      A  N
ATOM   1091  CD2 HIS A 144      -0.467 -45.116   1.079  1.00 14.62      A  C
ATOM   1092  C   HIS A 144       3.586 -43.619  -0.631  1.00 11.95      A  C
ATOM   1093  O   HIS A 144       4.007 -44.456   0.135  1.00 11.54      A  O
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ATOM   1094  N    THR A 145      4.383  -43.055  -1.532  1.00  11.84      A    N
ATOM   1095  CA   THR A 145      5.798  -43.407  -1.620  1.00  11.38      A    C
ATOM   1096  CB   THR A 145      6.062  -44.234  -2.900  1.00  11.59      A    C
ATOM   1097  OG1  THR A 145      5.547  -43.557  -4.068  1.00  11.59      A    O
ATOM   1098  CG2  THR A 145      5.398  -45.593  -2.785  1.00  11.38      A    C
ATOM   1099  C    THR A 145      6.655  -42.135  -1.532  1.00  11.05      A    C
ATOM   1100  O    THR A 145      6.939  -41.644  -0.443  1.00  11.35      A    O
ATOM   1101  N    ALA A 146      7.038  -41.572  -2.667  1.00  10.67      A    N
ATOM   1102  CA   ALA A 146      7.849  -40.366  -2.692  1.00  10.41      A    C
ATOM   1103  CB   ALA A 146      8.226  -40.046  -4.120  1.00  10.53      A    C
ATOM   1104  C    ALA A 146      7.137  -39.167  -2.080  1.00  10.31      A    C
ATOM   1105  O    ALA A 146      7.769  -38.361  -1.394  1.00   9.96      A    O
ATOM   1106  N    GLY A 147      5.827  -39.051  -2.349  1.00  10.33      A    N
ATOM   1107  CA   GLY A 147      5.001  -37.925  -1.877  1.00  10.08      A    C
ATOM   1108  C    GLY A 147      5.238  -36.619  -2.623  1.00  10.00      A    C
ATOM   1109  O    GLY A 147      4.962  -35.549  -2.107  1.00   9.60      A    O
ATOM   1110  N    LEU A 148      5.745  -36.706  -3.848  1.00  10.31      A    N
ATOM   1111  CA   LEU A 148      5.933  -35.528  -4.707  1.00  10.49      A    C
ATOM   1112  CB   LEU A 148      6.018  -35.939  -6.165  1.00  10.25      A    C
ATOM   1113  CG   LEU A 148      7.210  -36.812  -6.508  1.00  10.29      A    C
ATOM   1114  CD1  LEU A 148      6.994  -37.473  -7.848  1.00  10.47      A    C
ATOM   1115  CD2  LEU A 148      8.476  -36.004  -6.551  1.00  10.32      A    C
ATOM   1116  C    LEU A 148      4.772  -34.565  -4.557  1.00  10.94      A    C
ATOM   1117  O    LEU A 148      3.636  -34.881  -4.915  1.00  10.71      A    O
ATOM   1118  N    GLU A 149      5.066  -33.387  -4.026  1.00  11.38      A    N
ATOM   1119  CA   GLU A 149      4.042  -32.384  -3.824  1.00  11.72      A    C
ATOM   1120  CB   GLU A 149      4.614  -31.224  -3.046  1.00  12.01      A    C
ATOM   1121  CG   GLU A 149      4.981  -31.624  -1.637  1.00  12.44      A    C
ATOM   1122  CD   GLU A 149      5.857  -30.602  -0.954  1.00  12.98      A    C
ATOM   1123  OE1  GLU A 149      6.421  -29.712  -1.679  1.00  13.15      A    O
ATOM   1124  OE2  GLU A 149      5.975  -30.714   0.305  1.00  12.81      A    O
ATOM   1125  C    GLU A 149      3.503  -31.865  -5.139  1.00  11.83      A    C
ATOM   1126  O    GLU A 149      4.282  -31.557  -6.060  1.00  11.79      A    O
ATOM   1127  N    TYR A 150      2.178  -31.724  -5.199  1.00  11.76      A    N
ATOM   1128  CA   TYR A 150      1.503  -31.382  -6.438  1.00  11.73      A    C
ATOM   1129  CB   TYR A 150      0.047  -31.854  -6.381  1.00  11.48      A    C
ATOM   1130  CG   TYR A 150     -0.495  -32.275  -7.722  1.00  11.34      A    C
ATOM   1131  CD1  TYR A 150     -0.009  -33.409  -8.366  1.00  11.48      A    C
ATOM   1132  CE1  TYR A 150     -0.488  -33.787  -9.606  1.00  11.42      A    C
ATOM   1133  CZ   TYR A 150     -1.466  -33.024 -10.215  1.00  11.47      A    C
ATOM   1134  OH   TYR A 150     -1.983  -33.385 -11.434  1.00  11.35      A    O
ATOM   1135  CE2  TYR A 150     -1.948  -31.898  -9.591  1.00  11.34      A    C
ATOM   1136  CD2  TYR A 150     -1.465  -31.540  -8.353  1.00  11.15      A    C
ATOM   1137  C    TYR A 150      1.594  -29.893  -6.778  1.00  12.17      A    C
ATOM   1138  O    TYR A 150      0.579  -29.194  -6.852  1.00  11.75      A    O
ATOM   1139  N    TYR A 151      2.820  -29.409  -7.010  1.00  13.06      A    N
ATOM   1140  CA   TYR A 151      3.052  -27.998  -7.425  1.00  13.68      A    C
ATOM   1141  CB   TYR A 151      2.853  -27.019  -6.258  1.00  14.30      A    C
ATOM   1142  CG   TYR A 151      2.377  -25.641  -6.701  1.00  15.46      A    C
ATOM   1143  CD1  TYR A 151      3.284  -24.631  -7.111  1.00  16.45      A    C
ATOM   1144  CE1  TYR A 151      2.838  -23.378  -7.544  1.00  16.21      A    C
ATOM   1145  CZ   TYR A 151      1.480  -23.114  -7.542  1.00  16.63      A    C
ATOM   1146  OH   TYR A 151      0.955  -21.884  -7.943  1.00  17.27      A    O
ATOM   1147  CE2  TYR A 151      0.586  -24.098  -7.141  1.00  16.39      A    C
ATOM   1148  CD2  TYR A 151      1.036  -25.341  -6.732  1.00  15.76      A    C
ATOM   1149  C    TYR A 151      4.455  -27.817  -7.980  1.00  13.62      A    C
ATOM   1150  O    TYR A 151      5.397  -28.390  -7.467  1.00  14.39      A    O
ATOM   1151  N    GLY A 152      4.614  -27.011  -9.019  1.00  13.51      A    N
ATOM   1152  CA   GLY A 152      5.939  -26.701  -9.531  1.00  13.34      A    C
ATOM   1153  C    GLY A 152      6.653  -27.917 -10.097  1.00  13.83      A    C
ATOM   1154  O    GLY A 152      6.032  -28.807 -10.695  1.00  14.49      A    O
ATOM   1155  N    GLU A 153      7.966  -27.961  -9.916  1.00  13.72      A    N
ATOM   1156  CA   GLU A 153      8.749  -29.047 -10.468  1.00  13.56      A    C
ATOM   1157  CB   GLU A 153     10.238  -28.725 -10.362  1.00  13.75      A    C
ATOM   1158  CG   GLU A 153     10.664  -27.555 -11.240  1.00  13.88      A    C
ATOM   1159  CD   GLU A 153     12.180  -27.399 -11.424  1.00  14.09      A    C
ATOM   1160  OE1  GLU A 153     12.942  -28.380 -11.352  1.00  14.77      A    O
ATOM   1161  OE2  GLU A 153     12.626  -26.283 -11.700  1.00  13.79      A    O
ATOM   1162  C    GLU A 153      8.392  -30.427  -9.867  1.00  13.23      A    C
ATOM   1163  O    GLU A 153      8.317  -31.407 -10.607  1.00  13.02      A    O
ATOM   1164  N    SER A 154      8.152  -30.502  -8.556  1.00  13.06      A    N
ATOM   1165  CA   SER A 154      7.720  -31.766  -7.919  1.00  12.61      A    C
ATOM   1166  CB   SER A 154      7.509  -31.629  -6.409  1.00  12.60      A    C
ATOM   1167  OG   SER A 154      6.935  -30.397  -6.002  1.00  12.59      A    O
ATOM   1168  C    SER A 154      6.438  -32.211  -8.546  1.00  12.47      A    C
ATOM   1169  O    SER A 154      6.205  -33.388  -8.804  1.00  12.67      A    O
ATOM   1170  N    GLY A 155      5.586  -31.245  -8.817  1.00  12.56      A    N
ATOM   1171  CA   GLY A 155      4.310  -31.540  -9.447  1.00  12.03      A    C
ATOM   1172  C    GLY A 155      4.443  -32.051 -10.869  1.00  11.39      A    C
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ATOM   1173  O   GLY A 155       3.646 -32.860 -11.295  1.00 11.89           A    O
ATOM   1174  N   ALA A 156       5.413 -31.568 -11.633  1.00 10.56           A    N
ATOM   1175  CA  ALA A 156       5.536 -32.047 -13.008  1.00  9.90           A    C
ATOM   1176  CB  ALA A 156       6.481 -31.175 -13.804  1.00  9.92           A    C
ATOM   1177  C   ALA A 156       6.015 -33.501 -13.004  1.00  9.25           A    C
ATOM   1178  O   ALA A 156       5.502 -34.330 -13.728  1.00  9.03           A    O
ATOM   1179  N   LEU A 157       7.020 -33.773 -12.184  1.00  8.76           A    N
ATOM   1180  CA  LEU A 157       7.532 -35.104 -11.970  1.00  8.36           A    C
ATOM   1181  CB  LEU A 157       8.540 -35.070 -10.837  1.00  8.37           A    C
ATOM   1182  CG  LEU A 157      10.041 -35.045 -11.062  1.00  8.61           A    C
ATOM   1183  CD1 LEU A 157      10.463 -34.666 -12.454  1.00  8.77           A    C
ATOM   1184  CD2 LEU A 157      10.705 -34.119 -10.052  1.00  8.91           A    C
ATOM   1185  C   LEU A 157       6.376 -36.025 -11.596  1.00  8.07           A    C
ATOM   1186  O   LEU A 157       6.255 -37.135 -12.142  1.00  7.77           A    O
ATOM   1187  N   ASN A 158       5.538 -35.544 -10.669  1.00  7.73           A    N
ATOM   1188  CA  ASN A 158       4.376 -36.292 -10.195  1.00  7.65           A    C
ATOM   1189  CB  ASN A 158       3.618 -35.443  -9.175  1.00  7.60           A    C
ATOM   1190  CG  ASN A 158       2.454 -36.174  -8.544  1.00  7.45           A    C
ATOM   1191  OD1 ASN A 158       2.219 -36.081  -7.338  1.00  7.24           A    O
ATOM   1192  ND2 ASN A 158       1.713 -36.889  -9.354  1.00  7.41           A    N
ATOM   1193  C   ASN A 158       3.454 -36.711 -11.351  1.00  7.65           A    C
ATOM   1194  O   ASN A 158       3.092 -37.888 -11.501  1.00  7.48           A    O
ATOM   1195  N   GLU A 159       3.108 -35.731 -12.180  1.00  7.81           A    N
ATOM   1196  CA  GLU A 159       2.317 -35.962 -13.381  1.00  7.91           A    C
ATOM   1197  CB  GLU A 159       1.910 -34.630 -14.000  1.00  7.94           A    C
ATOM   1198  CG  GLU A 159       0.601 -34.083 -13.429  1.00  8.02           A    C
ATOM   1199  CD  GLU A 159      -0.576 -34.968 -13.795  1.00  8.26           A    C
ATOM   1200  OE1 GLU A 159      -0.653 -35.249 -15.012  1.00  8.90           A    O
ATOM   1201  OE2 GLU A 159      -1.397 -35.417 -12.935  1.00  8.04           A    O
ATOM   1202  C   GLU A 159       3.072 -36.857 -14.356  1.00  8.02           A    C
ATOM   1203  O   GLU A 159       2.509 -37.755 -14.950  1.00  8.32           A    O
ATOM   1204  N   SER A 160       4.373 -36.676 -14.460  1.00  8.05           A    N
ATOM   1205  CA  SER A 160       5.141 -37.443 -15.423  1.00  7.94           A    C
ATOM   1206  CB  SER A 160       6.597 -36.950 -15.477  1.00  7.76           A    C
ATOM   1207  OG  SER A 160       7.318 -37.607 -16.500  1.00  7.64           A    O
ATOM   1208  C   SER A 160       5.060 -38.907 -15.036  1.00  8.03           A    C
ATOM   1209  O   SER A 160       4.736 -39.785 -15.860  1.00  7.90           A    O
ATOM   1210  N   ILE A 161       5.343 -39.165 -13.767  1.00  8.08           A    N
ATOM   1211  CA  ILE A 161       5.358 -40.532 -13.276  1.00  8.23           A    C
ATOM   1212  CB  ILE A 161       5.615 -40.592 -11.763  1.00  8.23           A    C
ATOM   1213  CG1 ILE A 161       7.021 -40.033 -11.446  1.00  8.35           A    C
ATOM   1214  CD1 ILE A 161       8.170 -41.019 -11.674  1.00  8.40           A    C
ATOM   1215  CG2 ILE A 161       5.459 -42.016 -11.243  1.00  8.11           A    C
ATOM   1216  C   ILE A 161       4.017 -41.190 -13.593  1.00  8.64           A    C
ATOM   1217  O   ILE A 161       3.995 -42.329 -14.107  1.00  8.86           A    O
ATOM   1218  N   SER A 162       2.903 -40.468 -13.327  1.00  8.55           A    N
ATOM   1219  CA  SER A 162       1.563 -41.009 -13.583  1.00  8.24           A    C
ATOM   1220  CB  SER A 162       0.470 -40.063 -13.041  1.00  8.36           A    C
ATOM   1221  OG  SER A 162       0.268 -40.222 -11.610  1.00  8.36           A    O
ATOM   1222  C   SER A 162       1.401 -41.315 -15.066  1.00  7.96           A    C
ATOM   1223  O   SER A 162       0.870 -42.360 -15.452  1.00  7.78           A    O
ATOM   1224  N   ASP A 163       1.900 -40.410 -15.891  1.00  7.89           A    N
ATOM   1225  CA  ASP A 163       1.939 -40.609 -17.346  1.00  8.00           A    C
ATOM   1226  CB  ASP A 163       2.451 -39.323 -18.029  1.00  7.81           A    C
ATOM   1227  CG  ASP A 163       1.371 -38.310 -18.242  1.00  7.61           A    C
ATOM   1228  OD1 ASP A 163       0.228 -38.669 -17.919  1.00  7.69           A    O
ATOM   1229  OD2 ASP A 163       1.637 -37.194 -18.750  1.00  7.24           A    O
ATOM   1230  C   ASP A 163       2.842 -41.791 -17.764  1.00  8.39           A    C
ATOM   1231  O   ASP A 163       2.464 -42.654 -18.573  1.00  8.14           A    O
ATOM   1232  N   ILE A 164       4.058 -41.823 -17.223  1.00  8.75           A    N
ATOM   1233  CA  ILE A 164       4.955 -42.900 -17.590  1.00  9.10           A    C
ATOM   1234  CB  ILE A 164       6.308 -42.744 -16.902  1.00  8.62           A    C
ATOM   1235  CG1 ILE A 164       7.058 -41.631 -17.541  1.00  8.29           A    C
ATOM   1236  CD1 ILE A 164       7.945 -40.950 -16.552  1.00  8.37           A    C
ATOM   1237  CG2 ILE A 164       7.109 -44.018 -17.007  1.00  8.59           A    C
ATOM   1238  C   ILE A 164       4.326 -44.280 -17.276  1.00  9.63           A    C
ATOM   1239  O   ILE A 164       4.408 -45.188 -18.076  1.00  9.83           A    O
ATOM   1240  N   ILE A 165       3.688 -44.427 -16.125  1.00 10.31           A    N
ATOM   1241  CA  ILE A 165       3.113 -45.730 -15.759  1.00 11.09           A    C
ATOM   1242  CB  ILE A 165       3.142 -45.965 -14.238  1.00 11.45           A    C
ATOM   1243  CG1 ILE A 165       4.583 -46.312 -13.859  1.00 11.73           A    C
ATOM   1244  CD1 ILE A 165       4.846 -46.351 -12.376  1.00 12.06           A    C
ATOM   1245  CG2 ILE A 165       2.257 -47.137 -13.843  1.00 11.71           A    C
ATOM   1246  C   ILE A 165       1.743 -45.953 -16.396  1.00 11.24           A    C
ATOM   1247  O   ILE A 165       1.519 -46.993 -16.983  1.00 10.71           A    O
ATOM   1248  N   GLY A 166       0.866 -44.956 -16.352  1.00 11.84           A    N
ATOM   1249  CA  GLY A 166      -0.347 -44.989 -17.161  1.00 12.20           A    C
ATOM   1250  C   GLY A 166      -0.114 -45.522 -18.568  1.00 12.55           A    C
ATOM   1251  O   GLY A 166      -0.856 -46.371 -19.055  1.00 13.27           A    O
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ATOM	1252	N	ASN	A	167	0.936	-45.042	-19.219	1.00	13.01	A	N
ATOM	1253	CA	ASN	A	167	1.211	-45.411	-20.617	1.00	13.46	A	C
ATOM	1254	CB	ASN	A	167	2.130	-44.379	-21.255	1.00	13.54	A	C
ATOM	1255	CG	ASN	A	167	2.598	-44.799	-22.620	1.00	13.80	A	C
ATOM	1256	OD1	ASN	A	167	3.650	-45.428	-22.768	1.00	13.76	A	O
ATOM	1257	ND2	ASN	A	167	1.794	-44.495	-23.630	1.00	13.97	A	N
ATOM	1258	C	ASN	A	167	1.831	-46.800	-20.769	1.00	13.70	A	C
ATOM	1259	O	ASN	A	167	1.633	-47.497	-21.769	1.00	13.68	A	O
ATOM	1260	N	ALA	A	168	2.607	-47.179	-19.767	1.00	14.07	A	N
ATOM	1261	CA	ALA	A	168	3.260	-48.453	-19.765	1.00	13.94	A	C
ATOM	1262	CB	ALA	A	168	4.247	-48.531	-18.618	1.00	13.53	A	C
ATOM	1263	C	ALA	A	168	2.231	-49.547	-19.667	1.00	14.33	A	C
ATOM	1264	O	ALA	A	168	2.429	-50.581	-20.227	1.00	13.98	A	O
ATOM	1265	N	ILE	A	169	1.131	-49.324	-18.960	1.00	15.94	A	N
ATOM	1266	CA	ILE	A	169	0.218	-50.428	-18.655	1.00	18.10	A	C
ATOM	1267	CB	ILE	A	169	-0.969	-50.037	-17.743	1.00	18.79	A	C
ATOM	1268	CG1	ILE	A	169	-0.561	-50.080	-16.280	1.00	19.73	A	C
ATOM	1269	CD1	ILE	A	169	-0.048	-48.784	-15.730	1.00	20.46	A	C
ATOM	1270	CG2	ILE	A	169	-2.130	-51.016	-17.942	1.00	18.64	A	C
ATOM	1271	C	ILE	A	169	-0.394	-50.822	-19.949	1.00	19.50	A	C
ATOM	1272	O	ILE	A	169	-0.420	-51.982	-20.301	1.00	17.56	A	O
ATOM	1273	N	ASP	A	170	-0.941	-49.782	-20.581	1.00	22.96	A	N
ATOM	1274	CA	ASP	A	170	-1.495	-49.783	-21.922	1.00	25.80	A	C
ATOM	1275	CB	ASP	A	170	-1.761	-48.290	-22.319	1.00	28.80	A	C
ATOM	1276	CG	ASP	A	170	-3.056	-48.077	-23.198	1.00	31.65	A	C
ATOM	1277	OD1	ASP	A	170	-3.727	-49.094	-23.585	1.00	32.68	A	O
ATOM	1278	OD2	ASP	A	170	-3.385	-46.874	-23.485	1.00	27.68	A	O
ATOM	1279	C	ASP	A	170	-0.556	-50.556	-22.895	1.00	25.17	A	C
ATOM	1280	O	ASP	A	170	-0.916	-51.613	-23.330	1.00	26.97	A	O
ATOM	1281	N	GLY	A	171	0.654	-50.077	-23.186	1.00	25.32	A	N
ATOM	1282	CA	GLY	A	171	1.589	-50.813	-24.048	1.00	25.14	A	C
ATOM	1283	C	GLY	A	171	1.799	-50.195	-25.428	1.00	26.60	A	C
ATOM	1284	O	GLY	A	171	2.914	-50.233	-25.976	1.00	26.53	A	O
ATOM	1285	N	LYS	A	172	0.759	-49.524	-25.930	1.00	26.94	A	N
ATOM	1286	CA	LYS	A	172	0.444	-49.463	-27.366	1.00	26.88	A	C
ATOM	1287	CB	LYS	A	172	-1.051	-49.132	-27.537	1.00	30.72	A	C
ATOM	1288	CG	LYS	A	172	-2.071	-50.219	-27.134	1.00	33.65	A	C
ATOM	1289	CD	LYS	A	172	-3.392	-50.025	-27.922	1.00	36.81	A	C
ATOM	1290	CE	LYS	A	172	-4.669	-50.070	-27.073	1.00	38.06	A	C
ATOM	1291	NZ	LYS	A	172	-5.038	-48.814	-26.339	1.00	36.90	A	N
ATOM	1292	C	LYS	A	172	1.213	-48.471	-28.238	1.00	23.70	A	C
ATOM	1293	O	LYS	A	172	1.584	-48.768	-29.365	1.00	23.20	A	O
ATOM	1294	N	ASN	A	173	1.390	-47.273	-27.716	1.00	20.08	A	N
ATOM	1295	CA	ASN	A	173	1.898	-46.146	-28.467	1.00	17.00	A	C
ATOM	1296	CB	ASN	A	173	0.736	-45.383	-29.125	1.00	16.90	A	C
ATOM	1297	CG	ASN	A	173	-0.422	-45.079	-28.148	1.00	16.63	A	C
ATOM	1298	OD1	ASN	A	173	-0.260	-44.495	-27.064	1.00	15.50	A	O
ATOM	1299	ND2	ASN	A	173	-1.602	-45.470	-28.552	1.00	16.78	A	N
ATOM	1300	C	ASN	A	173	2.538	-45.275	-27.429	1.00	14.76	A	C
ATOM	1301	O	ASN	A	173	2.573	-45.681	-26.284	1.00	15.23	A	O
ATOM	1302	N	TRP	A	174	2.986	-44.078	-27.784	1.00	12.57	A	N
ATOM	1303	CA	TRP	A	174	3.504	-43.159	-26.790	1.00	11.39	A	C
ATOM	1304	CB	TRP	A	174	4.895	-42.700	-27.180	1.00	11.51	A	C
ATOM	1305	CG	TRP	A	174	5.894	-43.735	-27.116	1.00	11.10	A	C
ATOM	1306	CD1	TRP	A	174	6.445	-44.349	-28.137	1.00	10.94	A	C
ATOM	1307	NE1	TRP	A	174	7.375	-45.235	-27.722	1.00	11.20	A	N
ATOM	1308	CE2	TRP	A	174	7.431	-45.189	-26.362	1.00	11.59	A	C
ATOM	1309	CD2	TRP	A	174	6.499	-44.247	-25.953	1.00	11.43	A	C
ATOM	1310	CE3	TRP	A	174	6.344	-44.000	-24.584	1.00	11.96	A	C
ATOM	1311	CZ3	TRP	A	174	7.125	-44.722	-23.675	1.00	11.80	A	C
ATOM	1312	CH2	TRP	A	174	8.045	-45.657	-24.122	1.00	11.84	A	C
ATOM	1313	CZ2	TRP	A	174	8.216	-45.910	-25.461	1.00	11.89	A	C
ATOM	1314	C	TRP	A	174	2.619	-41.936	-26.558	1.00	10.44	A	C
ATOM	1315	O	TRP	A	174	3.119	-40.869	-26.219	1.00	9.94	A	O
ATOM	1316	N	LEU	A	175	1.309	-42.121	-26.673	1.00	9.73	A	N
ATOM	1317	CA	LEU	A	175	0.346	-41.082	-26.370	1.00	9.50	A	C
ATOM	1318	CB	LEU	A	175	-0.739	-41.054	-27.450	1.00	9.31	A	C
ATOM	1319	CG	LEU	A	175	-0.164	-41.226	-28.865	1.00	9.05	A	C
ATOM	1320	CD1	LEU	A	175	-1.260	-41.361	-29.880	1.00	8.82	A	C
ATOM	1321	CD2	LEU	A	175	0.776	-40.096	-29.223	1.00	8.97	A	C
ATOM	1322	C	LEU	A	175	-0.308	-41.248	-24.998	1.00	9.46	A	C
ATOM	1323	O	LEU	A	175	-0.256	-42.298	-24.395	1.00	9.36	A	O
ATOM	1324	N	ILE	A	176	-0.927	-40.172	-24.528	1.00	9.67	A	N
ATOM	1325	CA	ILE	A	176	-1.810	-40.190	-23.373	1.00	9.57	A	C
ATOM	1326	CB	ILE	A	176	-1.257	-39.265	-22.274	1.00	9.83	A	C
ATOM	1327	CG1	ILE	A	176	0.182	-39.690	-21.898	1.00	10.01	A	C
ATOM	1328	CD1	ILE	A	176	0.280	-41.016	-21.150	1.00	9.93	A	C
ATOM	1329	CG2	ILE	A	176	-2.184	-39.218	-21.049	1.00	9.82	A	C
ATOM	1330	C	ILE	A	176	-3.206	-39.704	-23.778	1.00	9.56	A	C

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ATOM   1331  O    ILE A 176     -3.349 -38.639 -24.428  1.00  8.84      A   O
ATOM   1332  N    GLY A 177     -4.220 -40.486 -23.367  1.00  9.68      A   N
ATOM   1333  CA   GLY A 177     -5.622 -40.131 -23.517  1.00  9.79      A   C
ATOM   1334  C    GLY A 177     -6.120 -40.170 -24.946  1.00 10.29      A   C
ATOM   1335  O    GLY A 177     -7.167 -39.604 -25.249  1.00 10.78      A   O
ATOM   1336  N    ASP A 178     -5.381 -40.826 -25.840  1.00 10.68      A   N
ATOM   1337  CA   ASP A 178     -5.808 -40.998 -27.226  1.00 10.63      A   C
ATOM   1338  CB   ASP A 178     -4.848 -41.873 -28.063  1.00 10.79      A   C
ATOM   1339  CG   ASP A 178     -4.414 -43.165 -27.352  1.00 11.25      A   C
ATOM   1340  OD1  ASP A 178     -4.028 -43.125 -26.137  1.00 11.72      A   O
ATOM   1341  OD2  ASP A 178     -4.445 -44.230 -28.017  1.00 11.08      A   O
ATOM   1342  C    ASP A 178     -7.221 -41.536 -27.336  1.00 10.59      A   C
ATOM   1343  O    ASP A 178     -7.904 -41.156 -28.272  1.00 11.28      A   O
ATOM   1344  N    LEU A 179     -7.671 -42.364 -26.395  1.00 10.20      A   N
ATOM   1345  CA   LEU A 179     -8.985 -43.023 -26.512  1.00 10.39      A   C
ATOM   1346  CB   LEU A 179     -8.959 -44.429 -25.884  1.00 10.21      A   C
ATOM   1347  CG   LEU A 179     -8.140 -45.483 -26.620  1.00 10.17      A   C
ATOM   1348  CD1  LEU A 179     -8.127 -46.713 -25.763  1.00 10.31      A   C
ATOM   1349  CD2  LEU A 179     -8.653 -45.828 -28.003  1.00  9.96      A   C
ATOM   1350  C    LEU A 179    -10.171 -42.272 -25.891  1.00 10.69      A   C
ATOM   1351  O    LEU A 179    -11.324 -42.757 -25.993  1.00 10.57      A   O
ATOM   1352  N    ILE A 180     -9.884 -41.142 -25.240  1.00 10.58      A   N
ATOM   1353  CA   ILE A 180    -10.901 -40.329 -24.611  1.00 10.92      A   C
ATOM   1354  CB   ILE A 180    -10.662 -40.171 -23.101  1.00 11.08      A   C
ATOM   1355  CG1  ILE A 180     -9.227 -39.759 -22.788  1.00 10.99      A   C
ATOM   1356  CD1  ILE A 180     -9.107 -39.174 -21.404  1.00 11.00      A   C
ATOM   1357  CG2  ILE A 180    -10.988 -41.455 -22.355  1.00 11.54      A   C
ATOM   1358  C    ILE A 180    -11.031 -38.915 -25.192  1.00 11.35      A   C
ATOM   1359  O    ILE A 180    -12.085 -38.286 -25.012  1.00 11.56      A   O
ATOM   1360  N    TYR A 181     -9.969 -38.421 -25.844  1.00 11.08      A   N
ATOM   1361  CA   TYR A 181     -9.888 -37.060 -26.366  1.00 11.01      A   C
ATOM   1362  CB   TYR A 181     -8.420 -36.640 -26.406  1.00 10.90      A   C
ATOM   1363  CG   TYR A 181     -8.183 -35.157 -26.669  1.00 10.79      A   C
ATOM   1364  CD1  TYR A 181     -8.717 -34.181 -25.830  1.00 10.58      A   C
ATOM   1365  CE1  TYR A 181     -8.480 -32.830 -26.058  1.00 10.73      A   C
ATOM   1366  CZ   TYR A 181     -7.665 -32.423 -27.122  1.00 10.52      A   C
ATOM   1367  OH   TYR A 181     -7.417 -31.084 -27.349  1.00  9.91      A   O
ATOM   1368  CE2  TYR A 181     -7.122 -33.375 -27.956  1.00 10.67      A   C
ATOM   1369  CD2  TYR A 181     -7.377 -34.734 -27.723  1.00 10.92      A   C
ATOM   1370  C    TYR A 181    -10.429 -36.894 -27.772  1.00 11.14      A   C
ATOM   1371  O    TYR A 181    -10.050 -37.616 -28.648  1.00 11.55      A   O
ATOM   1372  N    THR A 182    -11.277 -35.901 -28.001  1.00 12.04      A   N
ATOM   1373  CA   THR A 182    -11.754 -35.522 -29.366  1.00 12.29      A   C
ATOM   1374  CB   THR A 182    -10.647 -34.772 -30.147  1.00 12.04      A   C
ATOM   1375  OG1  THR A 182     -9.549 -35.675 -30.435  1.00 11.78      A   O
ATOM   1376  CG2  THR A 182    -10.182 -33.532 -29.383  1.00 11.44      A   C
ATOM   1377  C    THR A 182    -12.249 -36.731 -30.203  1.00 12.70      A   C
ATOM   1378  O    THR A 182    -11.491 -37.287 -31.039  1.00 12.48      A   O
ATOM   1379  N    PRO A 183    -13.497 -37.159 -29.955  1.00 13.03      A   N
ATOM   1380  CA   PRO A 183    -14.066 -38.320 -30.627  1.00 13.57      A   C
ATOM   1381  CB   PRO A 183    -15.451 -38.487 -29.993  1.00 13.44      A   C
ATOM   1382  CG   PRO A 183    -15.611 -37.419 -28.985  1.00 13.35      A   C
ATOM   1383  CD   PRO A 183    -14.320 -36.699 -28.831  1.00 13.41      A   C
ATOM   1384  C    PRO A 183    -14.199 -38.181 -32.135  1.00 13.75      A   C
ATOM   1385  O    PRO A 183    -14.230 -39.180 -32.839  1.00 13.12      A   O
ATOM   1386  N    ASN A 184    -14.285 -36.955 -32.616  1.00 14.63      A   N
ATOM   1387  CA   ASN A 184    -14.499 -36.726 -34.034  1.00 15.68      A   C
ATOM   1388  CB   ASN A 184    -15.679 -35.797 -34.216  1.00 16.64      A   C
ATOM   1389  CG   ASN A 184    -16.978 -36.426 -33.740  1.00 17.82      A   C
ATOM   1390  OD1  ASN A 184    -17.165 -37.653 -33.767  1.00 18.50      A   O
ATOM   1391  ND2  ASN A 184    -17.878 -35.586 -33.293  1.00 18.75      A   N
ATOM   1392  C    ASN A 184    -13.291 -36.194 -34.751  1.00 15.70      A   C
ATOM   1393  O    ASN A 184    -13.363 -35.865 -35.931  1.00 15.92      A   O
ATOM   1394  N    THR A 185    -12.182 -36.102 -34.027  1.00 15.51      A   N
ATOM   1395  CA   THR A 185    -10.898 -35.823 -34.620  1.00 14.77      A   C
ATOM   1396  CB   THR A 185    -10.251 -34.603 -33.976  1.00 14.28      A   C
ATOM   1397  OG1  THR A 185    -11.137 -33.476 -34.101  1.00 13.52      A   O
ATOM   1398  CG2  THR A 185     -8.912 -34.341 -34.633  1.00 13.98      A   C
ATOM   1399  C    THR A 185    -10.039 -37.035 -34.382  1.00 14.98      A   C
ATOM   1400  O    THR A 185     -9.666 -37.310 -33.243  1.00 16.15      A   O
ATOM   1401  N    PRO A 186     -9.769 -37.814 -35.435  1.00 14.99      A   N
ATOM   1402  CA   PRO A 186     -8.988 -39.026 -35.190  1.00 14.73      A   C
ATOM   1403  CB   PRO A 186     -9.308 -39.914 -36.399  1.00 14.75      A   C
ATOM   1404  CG   PRO A 186     -9.666 -38.966 -37.480  1.00 14.83      A   C
ATOM   1405  CD   PRO A 186    -10.245 -37.732 -36.828  1.00 14.83      A   C
ATOM   1406  C    PRO A 186     -7.510 -38.741 -35.136  1.00 14.30      A   C
ATOM   1407  O    PRO A 186     -7.056 -37.670 -35.509  1.00 14.74      A   O
ATOM   1408  N    GLY A 187     -6.778 -39.711 -34.630  1.00 14.35      A   N
ATOM   1409  CA   GLY A 187     -5.330 -39.677 -34.597  1.00 14.24      A   C
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ATOM	1410	C	GLY A 187	-4.707 -38.787 -33.543	1.00 14.00	A	C
ATOM	1411	O	GLY A 187	-3.502 -38.880 -33.301	1.00 13.60	A	O
ATOM	1412	N	ASP A 188	-5.504 -37.925 -32.907	1.00 13.79	A	N
ATOM	1413	CA	ASP A 188	-4.957 -37.050 -31.879	1.00 13.64	A	C
ATOM	1414	CB	ASP A 188	-5.532 -35.633 -32.008	1.00 13.33	A	C
ATOM	1415	CG	ASP A 188	-6.943 -35.496 -31.502	1.00 13.39	A	C
ATOM	1416	OD1	ASP A 188	-7.707 -36.462 -31.383	1.00 13.27	A	O
ATOM	1417	OD2	ASP A 188	-7.318 -34.350 -31.215	1.00 14.35	A	O
ATOM	1418	C	ASP A 188	-5.070 -37.612 -30.452	1.00 13.88	A	C
ATOM	1419	O	ASP A 188	-5.619 -38.712 -30.208	1.00 14.39	A	O
ATOM	1420	N	ALA A 189	-4.540 -36.842 -29.515	1.00 13.78	A	N
ATOM	1421	CA	ALA A 189	-4.466 -37.257 -28.144	1.00 13.80	A	C
ATOM	1422	CB	ALA A 189	-3.329 -38.259 -27.955	1.00 13.78	A	C
ATOM	1423	C	ALA A 189	-4.288 -36.053 -27.242	1.00 13.69	A	C
ATOM	1424	O	ALA A 189	-4.183 -34.937 -27.707	1.00 13.66	A	O
ATOM	1425	N	LEU A 190	-4.260 -36.310 -25.941	1.00 14.07	A	N
ATOM	1426	CA	LEU A 190	-4.173 -35.276 -24.926	1.00 14.36	A	C
ATOM	1427	CB	LEU A 190	-4.778 -35.797 -23.621	1.00 14.90	A	C
ATOM	1428	CG	LEU A 190	-4.925 -34.762 -22.530	1.00 15.37	A	C
ATOM	1429	CD1	LEU A 190	-5.581 -33.503 -23.056	1.00 15.75	A	C
ATOM	1430	CD2	LEU A 190	-5.757 -35.349 -21.418	1.00 15.87	A	C
ATOM	1431	C	LEU A 190	-2.730 -34.822 -24.710	1.00 13.65	A	C
ATOM	1432	O	LEU A 190	-2.470 -33.616 -24.670	1.00 14.14	A	O
ATOM	1433	N	ARG A 191	-1.808 -35.785 -24.610	1.00 12.55	A	N
ATOM	1434	CA	ARG A 191	-0.373 -35.501 -24.585	1.00 11.67	A	C
ATOM	1435	CB	ARG A 191	0.172 -35.511 -23.158	1.00 11.66	A	C
ATOM	1436	CG	ARG A 191	-0.511 -34.557 -22.197	1.00 11.40	A	C
ATOM	1437	CD	ARG A 191	0.195 -34.508 -20.853	1.00 11.14	A	C
ATOM	1438	NE	ARG A 191	-0.205 -35.582 -19.945	1.00 10.68	A	N
ATOM	1439	CZ	ARG A 191	-1.333 -35.589 -19.264	1.00 10.70	A	C
ATOM	1440	NH1	ARG A 191	-2.205 -34.590 -19.381	1.00 11.00	A	N
ATOM	1441	NH2	ARG A 191	-1.598 -36.590 -18.450	1.00 10.72	A	N
ATOM	1442	C	ARG A 191	0.398 -36.543 -25.332	1.00 11.21	A	C
ATOM	1443	O	ARG A 191	-0.009 -37.712 -25.424	1.00 10.54	A	O
ATOM	1444	N	SER A 192	1.555 -36.128 -25.807	1.00 11.04	A	N
ATOM	1445	CA	SER A 192	2.431 -37.032 -26.528	1.00 11.41	A	C
ATOM	1446	CB	SER A 192	2.631 -36.558 -27.971	1.00 11.37	A	C
ATOM	1447	OG	SER A 192	3.803 -37.111 -28.558	1.00 11.38	A	O
ATOM	1448	C	SER A 192	3.765 -37.098 -25.819	1.00 11.56	A	C
ATOM	1449	O	SER A 192	4.463 -36.094 -25.698	1.00 11.58	A	O
ATOM	1450	N	MET A 193	4.127 -38.289 -25.384	1.00 11.67	A	N
ATOM	1451	CA	MET A 193	5.411 -38.483 -24.767	1.00 12.16	A	C
ATOM	1452	CB	MET A 193	5.413 -39.767 -23.944	1.00 12.44	A	C
ATOM	1453	CG	MET A 193	4.355 -39.828 -22.870	1.00 12.51	A	C
ATOM	1454	SD	MET A 193	4.455 -41.399 -22.016	1.00 12.70	A	S
ATOM	1455	CE	MET A 193	6.110 -41.322 -21.326	1.00 13.02	A	C
ATOM	1456	C	MET A 193	6.562 -38.560 -25.776	1.00 12.02	A	C
ATOM	1457	O	MET A 193	7.719 -38.425 -25.398	1.00 11.80	A	O
ATOM	1458	N	GLU A 194	6.292 -38.847 -27.033	1.00 12.27	A	N
ATOM	1459	CA	GLU A 194	7.421 -38.982 -27.980	1.00 12.83	A	C
ATOM	1460	CB	GLU A 194	7.081 -39.968 -29.077	1.00 13.09	A	C
ATOM	1461	CG	GLU A 194	5.903 -39.511 -29.951	1.00 13.52	A	C
ATOM	1462	CD	GLU A 194	5.281 -40.631 -30.743	1.00 13.63	A	C
ATOM	1463	OE1	GLU A 194	5.799 -41.773 -30.651	1.00 14.89	A	O
ATOM	1464	OE2	GLU A 194	4.296 -40.372 -31.447	1.00 12.72	A	O
ATOM	1465	C	GLU A 194	7.764 -37.621 -28.572	1.00 13.17	A	C
ATOM	1466	O	GLU A 194	8.872 -37.403 -28.987	1.00 13.22	A	O
ATOM	1467	N	ASN A 195	6.788 -36.712 -28.558	1.00 13.78	A	N
ATOM	1468	CA	ASN A 195	6.905 -35.373 -29.097	1.00 14.09	A	C
ATOM	1469	CB	ASN A 195	6.568 -35.428 -30.580	1.00 13.89	A	C
ATOM	1470	CG	ASN A 195	6.721 -34.074 -31.267	1.00 13.72	A	C
ATOM	1471	OD1	ASN A 195	7.627 -33.311 -30.972	1.00 13.41	A	O
ATOM	1472	ND2	ASN A 195	5.834 -33.786 -32.198	1.00 13.75	A	N
ATOM	1473	C	ASN A 195	5.967 -34.375 -28.387	1.00 14.61	A	C
ATOM	1474	O	ASN A 195	4.898 -34.055 -28.885	1.00 15.66	A	O
ATOM	1475	N	PRO A 196	6.347 -33.900 -27.209	1.00 14.75	A	N
ATOM	1476	CA	PRO A 196	5.418 -33.102 -26.381	1.00 14.82	A	C
ATOM	1477	CB	PRO A 196	6.265 -32.773 -25.157	1.00 14.80	A	C
ATOM	1478	CG	PRO A 196	7.180 -33.963 -25.022	1.00 15.30	A	C
ATOM	1479	CD	PRO A 196	7.505 -34.382 -26.437	1.00 15.18	A	C
ATOM	1480	C	PRO A 196	4.894 -31.812 -27.012	1.00 14.89	A	C
ATOM	1481	O	PRO A 196	3.743 -31.393 -26.764	1.00 14.12	A	O
ATOM	1482	N	LYS A 197	5.751 -31.193 -27.816	1.00 15.78	A	N
ATOM	1483	CA	LYS A 197	5.454 -29.918 -28.464	1.00 16.20	A	C
ATOM	1484	CB	LYS A 197	6.607 -29.476 -29.345	1.00 17.65	A	C
ATOM	1485	CG	LYS A 197	7.392 -28.274 -28.883	1.00 19.35	A	C
ATOM	1486	CD	LYS A 197	8.470 -28.028 -29.955	1.00 21.72	A	C
ATOM	1487	CE	LYS A 197	9.427 -26.872 -29.652	1.00 22.98	A	C
ATOM	1488	NZ	LYS A 197	8.975 -25.622 -30.336	1.00 23.87	A	N

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ATOM   1489  C    LYS A 197      4.219 -30.061 -29.310  1.00 14.95      A    C
ATOM   1490  O    LYS A 197      3.513 -29.114 -29.515  1.00 13.94      A    O
ATOM   1491  N    LEU A 198      3.956 -31.257 -29.791  1.00 14.64      A    N
ATOM   1492  CA   LEU A 198      2.770 -31.476 -30.581  1.00 15.36      A    C
ATOM   1493  CB   LEU A 198      2.576 -32.969 -30.863  1.00 15.67      A    C
ATOM   1494  CG   LEU A 198      1.296 -33.521 -31.533  1.00 15.57      A    C
ATOM   1495  CD1  LEU A 198      0.973 -32.894 -32.886  1.00 15.47      A    C
ATOM   1496  CD2  LEU A 198      1.415 -35.038 -31.654  1.00 15.06      A    C
ATOM   1497  C    LEU A 198      1.554 -30.888 -29.906  1.00 15.80      A    C
ATOM   1498  O    LEU A 198      0.812 -30.175 -30.537  1.00 17.11      A    O
ATOM   1499  N    TYR A 199      1.347 -31.155 -28.628  1.00 16.25      A    N
ATOM   1500  CA   TYR A 199      0.175 -30.598 -27.921  1.00 16.26      A    C
ATOM   1501  CB   TYR A 199     -0.650 -31.738 -27.300  1.00 15.53      A    C
ATOM   1502  CG   TYR A 199     -1.040 -32.822 -28.279  1.00 14.71      A    C
ATOM   1503  CD1  TYR A 199     -1.966 -32.579 -29.279  1.00 14.13      A    C
ATOM   1504  CE1  TYR A 199     -2.340 -33.559 -30.171  1.00 13.70      A    C
ATOM   1505  CZ   TYR A 199     -1.790 -34.803 -30.078  1.00 14.03      A    C
ATOM   1506  OH   TYR A 199     -2.164 -35.782 -30.956  1.00 14.59      A    O
ATOM   1507  CE2  TYR A 199     -0.875 -35.098 -29.085  1.00 14.38      A    C
ATOM   1508  CD2  TYR A 199     -0.492 -34.098 -28.198  1.00 14.66      A    C
ATOM   1509  C    TYR A 199      0.572 -29.551 -26.857  1.00 17.22      A    C
ATOM   1510  O    TYR A 199      0.113 -29.585 -25.712  1.00 17.25      A    O
ATOM   1511  N    ASN A 200      1.441 -28.624 -27.242  1.00 18.43      A    N
ATOM   1512  CA   ASN A 200      1.827 -27.479 -26.386  1.00 18.86      A    C
ATOM   1513  CB   ASN A 200      0.631 -26.532 -26.215  1.00 21.02      A    C
ATOM   1514  CG   ASN A 200      0.375 -25.721 -27.468  1.00 23.20      A    C
ATOM   1515  OD1  ASN A 200      1.312 -25.396 -28.219  1.00 26.27      A    O
ATOM   1516  ND2  ASN A 200     -0.876 -25.382 -27.704  1.00 24.08      A    N
ATOM   1517  C    ASN A 200      2.439 -27.802 -25.035  1.00 17.25      A    C
ATOM   1518  O    ASN A 200      2.142 -27.171 -24.036  1.00 16.12      A    O
ATOM   1519  N    GLN A 201      3.287 -28.816 -25.018  1.00 16.59      A    N
ATOM   1520  CA   GLN A 201      4.176 -29.045 -23.898  1.00 15.78      A    C
ATOM   1521  CB   GLN A 201      4.079 -30.469 -23.387  1.00 15.50      A    C
ATOM   1522  CG   GLN A 201      2.816 -30.765 -22.619  1.00 15.69      A    C
ATOM   1523  CD   GLN A 201      2.783 -32.192 -22.089  1.00 16.07      A    C
ATOM   1524  OE1  GLN A 201      2.975 -33.164 -22.829  1.00 15.13      A    O
ATOM   1525  NE2  GLN A 201      2.540 -32.322 -20.790  1.00 16.64      A    N
ATOM   1526  C    GLN A 201      5.602 -28.747 -24.336  1.00 15.44      A    C
ATOM   1527  O    GLN A 201      6.000 -29.038 -25.453  1.00 14.82      A    O
ATOM   1528  N    PRO A 202      6.365 -28.113 -23.463  1.00 16.00      A    N
ATOM   1529  CA   PRO A 202      7.760 -27.900 -23.754  1.00 16.63      A    C
ATOM   1530  CB   PRO A 202      8.227 -27.048 -22.586  1.00 16.94      A    C
ATOM   1531  CG   PRO A 202      7.226 -27.316 -21.507  1.00 17.12      A    C
ATOM   1532  CD   PRO A 202      5.949 -27.401 -22.249  1.00 16.49      A    C
ATOM   1533  C    PRO A 202      8.482 -29.203 -23.734  1.00 16.91      A    C
ATOM   1534  O    PRO A 202      8.043 -30.115 -23.030  1.00 17.59      A    O
ATOM   1535  N    ASP A 203      9.563 -29.286 -24.497  1.00 16.60      A    N
ATOM   1536  CA   ASP A 203     10.369 -30.469 -24.532  1.00 17.19      A    C
ATOM   1537  CB   ASP A 203     10.337 -31.157 -25.911  1.00 17.40      A    C
ATOM   1538  CG   ASP A 203     10.885 -30.299 -27.056  1.00 17.15      A    C
ATOM   1539  OD1  ASP A 203     11.307 -29.124 -26.880  1.00 16.43      A    O
ATOM   1540  OD2  ASP A 203     10.849 -30.843 -28.180  1.00 16.95      A    O
ATOM   1541  C    ASP A 203     11.791 -30.209 -24.112  1.00 18.70      A    C
ATOM   1542  O    ASP A 203     12.676 -31.022 -24.429  1.00 19.51      A    O
ATOM   1543  N    ARG A 204     12.020 -29.116 -23.381  1.00 19.82      A    N
ATOM   1544  CA   ARG A 204     13.245 -28.985 -22.593  1.00 20.95      A    C
ATOM   1545  CB   ARG A 204     14.421 -28.585 -23.458  1.00 23.56      A    C
ATOM   1546  CG   ARG A 204     14.337 -27.186 -24.020  1.00 27.12      A    C
ATOM   1547  CD   ARG A 204     15.383 -27.032 -25.090  1.00 30.35      A    C
ATOM   1548  NE   ARG A 204     14.974 -26.129 -26.152  1.00 34.09      A    N
ATOM   1549  CZ   ARG A 204     15.738 -25.158 -26.639  1.00 37.57      A    C
ATOM   1550  NH1  ARG A 204     16.955 -24.947 -26.119  1.00 38.53      A    N
ATOM   1551  NH2  ARG A 204     15.277 -24.384 -27.633  1.00 37.08      A    N
ATOM   1552  C    ARG A 204     13.103 -27.993 -21.473  1.00 19.87      A    C
ATOM   1553  O    ARG A 204     12.316 -27.060 -21.576  1.00 18.88      A    O
ATOM   1554  N    TYR A 205     13.886 -28.202 -20.417  1.00 19.61      A    N
ATOM   1555  CA   TYR A 205     13.838 -27.375 -19.190  1.00 20.53      A    C
ATOM   1556  CB   TYR A 205     15.060 -27.682 -18.280  1.00 20.73      A    C
ATOM   1557  CG   TYR A 205     14.926 -27.129 -16.882  1.00 20.80      A    C
ATOM   1558  CD1  TYR A 205     13.810 -27.430 -16.109  1.00 21.37      A    C
ATOM   1559  CE1  TYR A 205     13.660 -26.932 -14.832  1.00 21.21      A    C
ATOM   1560  CZ   TYR A 205     14.641 -26.148 -14.306  1.00 20.82      A    C
ATOM   1561  OH   TYR A 205     14.447 -25.681 -13.053  1.00 20.22      A    O
ATOM   1562  CE2  TYR A 205     15.776 -25.857 -15.025  1.00 20.57      A    C
ATOM   1563  CD2  TYR A 205     15.908 -26.336 -16.317  1.00 20.84      A    C
ATOM   1564  C    TYR A 205     13.749 -25.859 -19.440  1.00 20.17      A    C
ATOM   1565  O    TYR A 205     12.904 -25.167 -18.875  1.00 18.72      A    O
ATOM   1566  N    GLN A 206     14.603 -25.377 -20.335  1.00 21.34      A    N
ATOM   1567  CA   GLN A 206     14.715 -23.948 -20.671  1.00 22.58      A    C
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ATOM	1568	CB	GLN A 206	15.767	-23.764	-21.757	1.00	24.80	A	C
ATOM	1569	CG	GLN A 206	17.129	-24.352	-21.385	1.00	28.21	A	C
ATOM	1570	CD	GLN A 206	17.413	-25.682	-22.073	1.00	31.20	A	C
ATOM	1571	OE1	GLN A 206	16.776	-26.702	-21.784	1.00	33.57	A	O
ATOM	1572	NE2	GLN A 206	18.366	-25.673	-23.013	1.00	34.48	A	N
ATOM	1573	C	GLN A 206	13.413	-23.257	-21.115	1.00	21.39	A	C
ATOM	1574	O	GLN A 206	13.335	-22.012	-21.080	1.00	21.09	A	O
ATOM	1575	N	ASP A 207	12.419	-24.061	-21.530	1.00	19.47	A	N
ATOM	1576	CA	ASP A 207	11.158	-23.578	-22.108	1.00	17.35	A	C
ATOM	1577	CB	ASP A 207	10.898	-24.207	-23.492	1.00	17.00	A	C
ATOM	1578	CG	ASP A 207	11.998	-23.917	-24.494	1.00	16.98	A	C
ATOM	1579	OD1	ASP A 207	12.681	-22.892	-24.342	1.00	17.05	A	O
ATOM	1580	OD2	ASP A 207	12.192	-24.713	-25.433	1.00	16.83	A	O
ATOM	1581	C	ASP A 207	10.007	-23.911	-21.198	1.00	15.93	A	C
ATOM	1582	O	ASP A 207	8.858	-23.867	-21.605	1.00	15.49	A	O
ATOM	1583	N	ARG A 208	10.299	-24.246	-19.960	1.00	14.96	A	N
ATOM	1584	CA	ARG A 208	9.222	-24.567	-19.046	1.00	14.60	A	C
ATOM	1585	CB	ARG A 208	9.746	-25.100	-17.708	1.00	14.67	A	C
ATOM	1586	CG	ARG A 208	10.371	-24.035	-16.833	1.00	14.67	A	C
ATOM	1587	CD	ARG A 208	11.284	-24.671	-15.819	1.00	14.86	A	C
ATOM	1588	NE	ARG A 208	12.055	-23.638	-15.162	1.00	15.29	A	N
ATOM	1589	CZ	ARG A 208	13.206	-23.171	-15.614	1.00	16.10	A	C
ATOM	1590	NH1	ARG A 208	13.731	-23.649	-16.721	1.00	17.73	A	N
ATOM	1591	NH2	ARG A 208	13.845	-22.226	-14.964	1.00	16.00	A	N
ATOM	1592	C	ARG A 208	8.373	-23.358	-18.777	1.00	13.74	A	C
ATOM	1593	O	ARG A 208	8.860	-22.278	-18.641	1.00	12.69	A	O
ATOM	1594	N	TYR A 209	7.081	-23.595	-18.688	1.00	14.32	A	N
ATOM	1595	CA	TYR A 209	6.136	-22.639	-18.140	1.00	14.70	A	C
ATOM	1596	CB	TYR A 209	4.711	-23.201	-18.179	1.00	14.05	A	C
ATOM	1597	CG	TYR A 209	3.623	-22.377	-17.503	1.00	13.32	A	C
ATOM	1598	CD1	TYR A 209	3.136	-21.228	-18.076	1.00	13.15	A	C
ATOM	1599	CE1	TYR A 209	2.097	-20.516	-17.498	1.00	12.94	A	C
ATOM	1600	CZ	TYR A 209	1.528	-20.944	-16.330	1.00	13.00	A	C
ATOM	1601	OH	TYR A 209	0.493	-20.212	-15.726	1.00	12.90	A	O
ATOM	1602	CE2	TYR A 209	2.012	-22.088	-15.741	1.00	12.96	A	C
ATOM	1603	CD2	TYR A 209	3.043	-22.796	-16.334	1.00	12.99	A	C
ATOM	1604	C	TYR A 209	6.513	-22.419	-16.714	1.00	15.33	A	C
ATOM	1605	O	TYR A 209	6.889	-23.363	-16.023	1.00	15.11	A	O
ATOM	1606	N	THR A 210	6.359	-21.175	-16.286	1.00	16.15	A	N
ATOM	1607	CA	THR A 210	6.796	-20.737	-14.986	1.00	17.20	A	C
ATOM	1608	CB	THR A 210	8.162	-19.996	-15.135	1.00	18.44	A	C
ATOM	1609	OG1	THR A 210	8.620	-19.652	-13.838	1.00	22.63	A	O
ATOM	1610	CG2	THR A 210	8.092	-18.692	-15.962	1.00	18.69	A	C
ATOM	1611	C	THR A 210	5.720	-19.937	-14.186	1.00	16.04	A	C
ATOM	1612	O	THR A 210	5.983	-19.437	-13.110	1.00	15.79	A	O
ATOM	1613	N	GLY A 211	4.497	-19.885	-14.697	1.00	16.00	A	N
ATOM	1614	CA	GLY A 211	3.389	-19.131	-14.079	1.00	16.15	A	C
ATOM	1615	C	GLY A 211	2.576	-19.933	-13.066	1.00	16.36	A	C
ATOM	1616	O	GLY A 211	2.959	-21.048	-12.712	1.00	17.38	A	O
ATOM	1617	N	PRO A 212	1.458	-19.375	-12.575	1.00	15.90	A	N
ATOM	1618	CA	PRO A 212	0.825	-19.956	-11.405	1.00	15.80	A	C
ATOM	1619	CB	PRO A 212	0.200	-18.756	-10.716	1.00	15.94	A	C
ATOM	1620	CG	PRO A 212	-0.123	-17.809	-11.817	1.00	16.11	A	C
ATOM	1621	CD	PRO A 212	0.825	-18.103	-12.955	1.00	16.30	A	C
ATOM	1622	C	PRO A 212	-0.258	-20.921	-11.730	1.00	16.41	A	C
ATOM	1623	O	PRO A 212	-0.656	-21.692	-10.857	1.00	16.72	A	O
ATOM	1624	N	SER A 213	-0.724	-20.898	-12.973	1.00	16.53	A	N
ATOM	1625	CA	SER A 213	-1.837	-21.716	-13.358	1.00	16.75	A	C
ATOM	1626	CB	SER A 213	-2.284	-21.316	-14.748	1.00	17.51	A	C
ATOM	1627	OG	SER A 213	-3.661	-21.579	-14.853	1.00	18.94	A	O
ATOM	1628	C	SER A 213	-1.481	-23.209	-13.345	1.00	17.13	A	C
ATOM	1629	O	SER A 213	-0.285	-23.588	-13.469	1.00	17.29	A	O
ATOM	1630	N	ASP A 214	-2.513	-24.059	-13.209	1.00	16.27	A	N
ATOM	1631	CA	ASP A 214	-2.329	-25.508	-13.237	1.00	15.08	A	C
ATOM	1632	CB	ASP A 214	-1.851	-25.926	-14.630	1.00	15.42	A	C
ATOM	1633	CG	ASP A 214	-1.721	-27.430	-14.796	1.00	15.51	A	C
ATOM	1634	OD1	ASP A 214	-2.543	-28.180	-14.216	1.00	16.01	A	O
ATOM	1635	OD2	ASP A 214	-0.798	-27.862	-15.528	1.00	14.86	A	O
ATOM	1636	C	ASP A 214	-1.305	-25.901	-12.213	1.00	14.27	A	C
ATOM	1637	O	ASP A 214	-0.375	-26.606	-12.522	1.00	13.66	A	O
ATOM	1638	N	ASN A 215	-1.466	-25.409	-10.995	1.00	14.22	A	N
ATOM	1639	CA	ASN A 215	-0.507	-25.653	-9.924	1.00	14.30	A	C
ATOM	1640	CB	ASN A 215	-0.702	-27.060	-9.334	1.00	13.77	A	C
ATOM	1641	CG	ASN A 215	-1.959	-27.172	-8.472	1.00	13.33	A	C
ATOM	1642	OD1	ASN A 215	-2.241	-26.309	-7.648	1.00	13.58	A	O
ATOM	1643	ND2	ASN A 215	-2.705	-28.225	-8.658	1.00	12.58	A	N
ATOM	1644	C	ASN A 215	0.944	-25.479	-10.367	1.00	15.43	A	C
ATOM	1645	O	ASN A 215	1.768	-26.360	-10.129	1.00	17.15	A	O
ATOM	1646	N	GLY A 216	1.267	-24.372	-11.033	1.00	15.63	A	N

ATOM	1647	CA	GLY	A	216	2.641	-24.132	-11.479	1.00	15.35	A	C
ATOM	1648	C	GLY	A	216	3.070	-24.980	-12.666	1.00	15.58	A	C
ATOM	1649	O	GLY	A	216	4.219	-25.467	-12.737	1.00	16.25	A	O
ATOM	1650	N	GLY	A	217	2.158	-25.181	-13.611	1.00	15.34	A	N
ATOM	1651	CA	GLY	A	217	2.524	-25.840	-14.884	1.00	14.91	A	C
ATOM	1652	C	GLY	A	217	2.633	-27.352	-14.829	1.00	14.14	A	C
ATOM	1653	O	GLY	A	217	3.387	-27.969	-15.596	1.00	14.67	A	O
ATOM	1654	N	VAL	A	218	1.829	-27.949	-13.972	1.00	12.95	A	N
ATOM	1655	CA	VAL	A	218	2.024	-29.338	-13.605	1.00	12.93	A	C
ATOM	1656	CB	VAL	A	218	1.198	-29.641	-12.327	1.00	12.94	A	C
ATOM	1657	CG1	VAL	A	218	0.249	-30.815	-12.469	1.00	12.92	A	C
ATOM	1658	CG2	VAL	A	218	2.142	-29.767	-11.133	1.00	12.90	A	C
ATOM	1659	C	VAL	A	218	1.825	-30.284	-14.785	1.00	12.86	A	C
ATOM	1660	O	VAL	A	218	2.681	-31.110	-15.074	1.00	13.09	A	O
ATOM	1661	N	HIS	A	219	0.733	-30.092	-15.512	1.00	12.63	A	N
ATOM	1662	CA	HIS	A	219	0.478	-30.819	-16.744	1.00	12.21	A	C
ATOM	1663	CB	HIS	A	219	-1.019	-30.845	-17.028	1.00	12.29	A	C
ATOM	1664	CG	HIS	A	219	-1.812	-31.473	-15.932	1.00	12.04	A	C
ATOM	1665	ND1	HIS	A	219	-2.339	-30.747	-14.895	1.00	11.93	A	N
ATOM	1666	CE1	HIS	A	219	-2.961	-31.562	-14.064	1.00	12.18	A	C
ATOM	1667	NE2	HIS	A	219	-2.828	-32.794	-14.514	1.00	12.05	A	N
ATOM	1668	CD2	HIS	A	219	-2.113	-32.765	-15.682	1.00	11.89	A	C
ATOM	1669	C	HIS	A	219	1.167	-30.213	-17.943	1.00	11.95	A	C
ATOM	1670	O	HIS	A	219	1.170	-30.826	-19.008	1.00	11.86	A	O
ATOM	1671	N	ILE	A	220	1.725	-29.015	-17.805	1.00	11.44	A	N
ATOM	1672	CA	ILE	A	220	2.414	-28.443	-18.914	1.00	11.45	A	C
ATOM	1673	CB	ILE	A	220	2.384	-26.927	-18.838	1.00	11.68	A	C
ATOM	1674	CG1	ILE	A	220	0.951	-26.446	-19.053	1.00	12.04	A	C
ATOM	1675	CD1	ILE	A	220	0.737	-24.988	-18.653	1.00	12.23	A	C
ATOM	1676	CG2	ILE	A	220	3.293	-26.302	-19.894	1.00	11.57	A	C
ATOM	1677	C	ILE	A	220	3.841	-28.999	-18.991	1.00	11.72	A	C
ATOM	1678	O	ILE	A	220	4.228	-29.616	-20.020	1.00	11.22	A	O
ATOM	1679	N	ASN	A	221	4.601	-28.809	-17.897	1.00	11.49	A	N
ATOM	1680	CA	ASN	A	221	6.051	-29.113	-17.882	1.00	11.39	A	C
ATOM	1681	CB	ASN	A	221	6.761	-28.288	-16.820	1.00	11.36	A	C
ATOM	1682	CG	ASN	A	221	6.457	-26.809	-16.934	1.00	11.22	A	C
ATOM	1683	OD1	ASN	A	221	6.580	-26.185	-17.993	1.00	11.34	A	O
ATOM	1684	ND2	ASN	A	221	6.032	-26.250	-15.851	1.00	11.20	A	N
ATOM	1685	C	ASN	A	221	6.413	-30.581	-17.667	1.00	11.36	A	C
ATOM	1686	O	ASN	A	221	7.587	-30.933	-17.639	1.00	11.44	A	O
ATOM	1687	N	SER	A	222	5.403	-31.442	-17.547	1.00	11.25	A	N
ATOM	1688	CA	SER	A	222	5.638	-32.877	-17.417	1.00	10.81	A	C
ATOM	1689	CB	SER	A	222	4.345	-33.617	-17.026	1.00	10.68	A	C
ATOM	1690	OG	SER	A	222	3.340	-33.460	-17.996	1.00	10.76	A	O
ATOM	1691	C	SER	A	222	6.217	-33.444	-18.689	1.00	10.49	A	C
ATOM	1692	O	SER	A	222	6.888	-34.485	-18.652	1.00	10.48	A	O
ATOM	1693	N	GLY	A	223	5.946	-32.771	-19.810	1.00	10.19	A	N
ATOM	1694	CA	GLY	A	223	6.413	-33.226	-21.107	1.00	10.08	A	C
ATOM	1695	C	GLY	A	223	7.927	-33.301	-21.164	1.00	10.06	A	C
ATOM	1696	O	GLY	A	223	8.491	-34.143	-21.859	1.00	9.81	A	O
ATOM	1697	N	ILE	A	224	8.578	-32.431	-20.398	1.00	10.10	A	N
ATOM	1698	CA	ILE	A	224	10.020	-32.426	-20.317	1.00	10.23	A	C
ATOM	1699	CB	ILE	A	224	10.519	-31.272	-19.422	1.00	10.49	A	C
ATOM	1700	CG1	ILE	A	224	10.159	-29.913	-20.031	1.00	10.32	A	C
ATOM	1701	CD1	ILE	A	224	9.939	-28.841	-18.985	1.00	10.40	A	C
ATOM	1702	CG2	ILE	A	224	12.037	-31.376	-19.189	1.00	10.68	A	C
ATOM	1703	C	ILE	A	224	10.505	-33.749	-19.756	1.00	10.23	A	C
ATOM	1704	O	ILE	A	224	11.364	-34.386	-20.336	1.00	9.86	A	O
ATOM	1705	N	ASN	A	225	9.949	-34.164	-18.625	1.00	10.63	A	N
ATOM	1706	CA	ASN	A	225	10.323	-35.454	-18.082	1.00	11.23	A	C
ATOM	1707	CB	ASN	A	225	9.905	-35.631	-16.640	1.00	11.81	A	C
ATOM	1708	CG	ASN	A	225	10.579	-36.830	-15.998	1.00	12.52	A	C
ATOM	1709	OD1	ASN	A	225	9.945	-37.827	-15.680	1.00	13.05	A	O
ATOM	1710	ND2	ASN	A	225	11.883	-36.753	-15.847	1.00	12.97	A	N
ATOM	1711	C	ASN	A	225	9.780	-36.617	-18.879	1.00	11.45	A	C
ATOM	1712	O	ASN	A	225	10.456	-37.629	-18.972	1.00	11.51	A	O
ATOM	1713	N	ASN	A	226	8.575	-36.500	-19.457	1.00	11.45	A	N
ATOM	1714	CA	ASN	A	226	8.081	-37.559	-20.356	1.00	11.23	A	C
ATOM	1715	CB	ASN	A	226	6.650	-37.267	-20.854	1.00	11.25	A	C
ATOM	1716	CG	ASN	A	226	5.584	-37.417	-19.761	1.00	11.15	A	C
ATOM	1717	OD1	ASN	A	226	5.901	-37.722	-18.614	1.00	10.97	A	O
ATOM	1718	ND2	ASN	A	226	4.313	-37.165	-20.112	1.00	11.00	A	N
ATOM	1719	C	ASN	A	226	9.039	-37.761	-21.539	1.00	11.16	A	C
ATOM	1720	O	ASN	A	226	9.376	-38.871	-21.901	1.00	10.70	A	O
ATOM	1721	N	LYS	A	227	9.501	-36.669	-22.125	1.00	11.75	A	N
ATOM	1722	CA	LYS	A	227	10.371	-36.759	-23.271	1.00	12.42	A	C
ATOM	1723	CB	LYS	A	227	10.731	-35.370	-23.764	1.00	12.84	A	C
ATOM	1724	CG	LYS	A	227	11.611	-35.359	-24.990	1.00	13.61	A	C
ATOM	1725	CD	LYS	A	227	10.945	-35.898	-26.266	1.00	14.22	A	C

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ATOM   1726   CE    LYS A 227     12.014 -36.340 -27.269   1.00 15.09        A    C
ATOM   1727   NZ    LYS A 227     11.580 -36.298 -28.698   1.00 15.81        A    N
ATOM   1728   C     LYS A 227     11.612 -37.562 -22.904   1.00 12.89        A    C
ATOM   1729   O     LYS A 227     12.015 -38.460 -23.641   1.00 13.47        A    O
ATOM   1730   N     ALA A 228     12.193 -37.269 -21.740   1.00 12.98        A    N
ATOM   1731   CA    ALA A 228     13.335 -38.036 -21.243   1.00 12.64        A    C
ATOM   1732   CB    ALA A 228     13.813 -37.442 -19.926   1.00 12.73        A    C
ATOM   1733   C     ALA A 228     13.068 -39.558 -21.096   1.00 12.18        A    C
ATOM   1734   O     ALA A 228     13.905 -40.380 -21.471   1.00 12.38        A    O
ATOM   1735   N     PHE A 229     11.914 -39.929 -20.545   1.00 11.74        A    N
ATOM   1736   CA    PHE A 229     11.555 -41.334 -20.434   1.00 11.22        A    C
ATOM   1737   CB    PHE A 229     10.240 -41.554 -19.676   1.00 10.83        A    C
ATOM   1738   CG    PHE A 229      9.932 -42.999 -19.513   1.00 10.75        A    C
ATOM   1739   CD1   PHE A 229     10.570 -43.735 -18.552   1.00 10.84        A    C
ATOM   1740   CE1   PHE A 229     10.358 -45.093 -18.457   1.00 11.22        A    C
ATOM   1741   CZ    PHE A 229      9.505 -45.741 -19.351   1.00 10.84        A    C
ATOM   1742   CE2   PHE A 229      8.890 -45.023 -20.333   1.00 10.64        A    C
ATOM   1743   CD2   PHE A 229      9.104 -43.659 -20.409   1.00 10.89        A    C
ATOM   1744   C     PHE A 229     11.470 -41.957 -21.827   1.00 11.34        A    C
ATOM   1745   O     PHE A 229     11.985 -43.054 -22.072   1.00 11.16        A    O
ATOM   1746   N     TYR A 230     10.831 -41.248 -22.750   1.00 11.53        A    N
ATOM   1747   CA    TYR A 230     10.803 -41.695 -24.136   1.00 11.74        A    C
ATOM   1748   CB    TYR A 230     10.119 -40.669 -25.062   1.00 11.82        A    C
ATOM   1749   CG    TYR A 230     10.185 -41.060 -26.522   1.00 11.70        A    C
ATOM   1750   CD1   TYR A 230      9.407 -42.076 -27.041   1.00 11.41        A    C
ATOM   1751   CE1   TYR A 230      9.497 -42.427 -28.377   1.00 11.72        A    C
ATOM   1752   CZ    TYR A 230     10.387 -41.744 -29.222   1.00 12.00        A    C
ATOM   1753   OH    TYR A 230     10.553 -41.983 -30.564   1.00 11.37        A    O
ATOM   1754   CE2   TYR A 230     11.161 -40.741 -28.709   1.00 12.22        A    C
ATOM   1755   CD2   TYR A 230     11.058 -40.409 -27.367   1.00 12.28        A    C
ATOM   1756   C     TYR A 230     12.200 -42.005 -24.645   1.00 11.45        A    C
ATOM   1757   O     TYR A 230     12.438 -43.097 -25.119   1.00 11.78        A    O
ATOM   1758   N     LEU A 231     13.114 -41.058 -24.519   1.00 11.40        A    N
ATOM   1759   CA    LEU A 231     14.473 -41.254 -24.997   1.00 11.79        A    C
ATOM   1760   CB    LEU A 231     15.288 -39.996 -24.808   1.00 11.69        A    C
ATOM   1761   CG    LEU A 231     14.814 -38.855 -25.698   1.00 11.76        A    C
ATOM   1762   CD1   LEU A 231     15.341 -37.549 -25.148   1.00 11.92        A    C
ATOM   1763   CD2   LEU A 231     15.246 -39.049 -27.144   1.00 11.76        A    C
ATOM   1764   C     LEU A 231     15.190 -42.435 -24.338   1.00 12.58        A    C
ATOM   1765   O     LEU A 231     15.881 -43.196 -25.035   1.00 12.49        A    O
ATOM   1766   N     ILE A 232     15.003 -42.611 -23.021   1.00 13.10        A    N
ATOM   1767   CA    ILE A 232     15.600 -43.750 -22.306   1.00 13.31        A    C
ATOM   1768   CB    ILE A 232     15.493 -43.616 -20.781   1.00 13.13        A    C
ATOM   1769   CG1   ILE A 232     16.478 -42.569 -20.316   1.00 13.85        A    C
ATOM   1770   CD1   ILE A 232     16.013 -41.724 -19.150   1.00 14.38        A    C
ATOM   1771   CG2   ILE A 232     15.890 -44.889 -20.075   1.00 12.88        A    C
ATOM   1772   C     ILE A 232     15.048 -45.077 -22.764   1.00 14.10        A    C
ATOM   1773   O     ILE A 232     15.825 -46.032 -22.986   1.00 14.59        A    O
ATOM   1774   N     ALA A 233     13.727 -45.158 -22.924   1.00 15.20        A    N
ATOM   1775   CA    ALA A 233     13.080 -46.436 -23.335   1.00 15.74        A    C
ATOM   1776   CB    ALA A 233     11.598 -46.388 -23.053   1.00 15.72        A    C
ATOM   1777   C     ALA A 233     13.306 -46.738 -24.814   1.00 16.24        A    C
ATOM   1778   O     ALA A 233     13.765 -47.824 -25.156   1.00 16.87        A    O
ATOM   1779   N     GLN A 234     13.030 -45.743 -25.661   1.00 15.67        A    N
ATOM   1780   CA    GLN A 234     12.883 -45.933 -27.091   1.00 15.40        A    C
ATOM   1781   CB    GLN A 234     11.714 -45.074 -27.555   1.00 14.97        A    C
ATOM   1782   CG    GLN A 234     11.303 -45.270 -28.993   1.00 14.65        A    C
ATOM   1783   CD    GLN A 234     10.815 -46.672 -29.269   1.00 14.44        A    C
ATOM   1784   OE1   GLN A 234      9.965 -47.219 -28.560   1.00 14.43        A    O
ATOM   1785   NE2   GLN A 234     11.323 -47.247 -30.327   1.00 14.09        A    N
ATOM   1786   C     GLN A 234     14.139 -45.538 -27.894   1.00 15.79        A    C
ATOM   1787   O     GLN A 234     14.349 -46.002 -29.017   1.00 14.62        A    O
ATOM   1788   N     GLY A 235     14.970 -44.664 -27.344   1.00 16.03        A    N
ATOM   1789   CA    GLY A 235     16.065 -44.118 -28.151   1.00 16.48        A    C
ATOM   1790   C     GLY A 235     15.602 -43.077 -29.169   1.00 16.81        A    C
ATOM   1791   O     GLY A 235     14.511 -43.182 -29.751   1.00 17.76        A    O
ATOM   1792   N     GLY A 236     16.422 -42.048 -29.351   1.00 16.10        A    N
ATOM   1793   CA    GLY A 236     16.220 -41.069 -30.403   1.00 15.98        A    C
ATOM   1794   C     GLY A 236     17.318 -40.016 -30.319   1.00 16.20        A    C
ATOM   1795   O     GLY A 236     18.156 -40.076 -29.432   1.00 17.05        A    O
ATOM   1796   N     THR A 237     17.335 -39.061 -31.239   1.00 15.70        A    N
ATOM   1797   CA    THR A 237     18.164 -37.893 -31.078   1.00 15.66        A    C
ATOM   1798   CB    THR A 237     19.028 -37.680 -32.316   1.00 15.65        A    C
ATOM   1799   OG1   THR A 237     20.044 -38.688 -32.371   1.00 15.12        A    O
ATOM   1800   CG2   THR A 237     19.671 -36.339 -32.258   1.00 15.82        A    C
ATOM   1801   C     THR A 237     17.280 -36.671 -30.870   1.00 16.10        A    C
ATOM   1802   O     THR A 237     16.260 -36.549 -31.531   1.00 17.31        A    O
ATOM   1803   N     HIS A 238     17.707 -35.747 -30.000   1.00 16.14        A    N
ATOM   1804   CA    HIS A 238     16.896 -34.631 -29.507   1.00 15.59        A    C
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ATOM	1805	CB	HIS	A	238	16.100	-35.136	-28.320	1.00	15.65	A	C
ATOM	1806	CG	HIS	A	238	15.015	-34.220	-27.870	1.00	15.62	A	C
ATOM	1807	ND1	HIS	A	238	15.038	-33.597	-26.642	1.00	15.28	A	N
ATOM	1808	CE1	HIS	A	238	13.957	-32.857	-26.511	1.00	15.61	A	C
ATOM	1809	NE2	HIS	A	238	13.239	-32.969	-27.616	1.00	15.96	A	N
ATOM	1810	CD2	HIS	A	238	13.874	-33.828	-28.478	1.00	15.56	A	C
ATOM	1811	C	HIS	A	238	17.811	-33.486	-29.054	1.00	16.36	A	C
ATOM	1812	O	HIS	A	238	18.767	-33.708	-28.308	1.00	16.31	A	O
ATOM	1813	N	TYR	A	239	17.509	-32.261	-29.481	1.00	17.28	A	N
ATOM	1814	CA	TYR	A	239	18.437	-31.129	-29.358	1.00	18.38	A	C
ATOM	1815	CB	TYR	A	239	18.194	-30.334	-28.055	1.00	18.88	A	C
ATOM	1816	CG	TYR	A	239	16.844	-29.703	-28.089	1.00	19.54	A	C
ATOM	1817	CD1	TYR	A	239	16.565	-28.661	-28.966	1.00	19.99	A	C
ATOM	1818	CE1	TYR	A	239	15.286	-28.100	-29.034	1.00	21.13	A	C
ATOM	1819	CZ	TYR	A	239	14.263	-28.596	-28.214	1.00	21.56	A	C
ATOM	1820	OH	TYR	A	239	12.986	-28.064	-28.260	1.00	23.19	A	O
ATOM	1821	CE2	TYR	A	239	14.530	-29.623	-27.329	1.00	20.93	A	C
ATOM	1822	CD2	TYR	A	239	15.809	-30.183	-27.281	1.00	20.58	A	C
ATOM	1823	C	TYR	A	239	19.906	-31.552	-29.542	1.00	18.22	A	C
ATOM	1824	O	TYR	A	239	20.776	-31.289	-28.713	1.00	18.56	A	O
ATOM	1825	N	GLY	A	240	20.155	-32.254	-30.633	1.00	18.16	A	N
ATOM	1826	CA	GLY	A	240	21.496	-32.645	-30.989	1.00	17.75	A	C
ATOM	1827	C	GLY	A	240	22.090	-33.814	-30.251	1.00	17.52	A	C
ATOM	1828	O	GLY	A	240	23.170	-34.223	-30.605	1.00	19.02	A	O
ATOM	1829	N	VAL	A	241	21.407	-34.384	-29.263	1.00	17.08	A	N
ATOM	1830	CA	VAL	A	241	22.001	-35.435	-28.424	1.00	16.66	A	C
ATOM	1831	CB	VAL	A	241	21.800	-35.134	-26.929	1.00	16.31	A	C
ATOM	1832	CG1	VAL	A	241	22.300	-36.290	-26.063	1.00	15.93	A	C
ATOM	1833	CG2	VAL	A	241	22.477	-33.828	-26.550	1.00	16.07	A	C
ATOM	1834	C	VAL	A	241	21.381	-36.786	-28.715	1.00	17.12	A	C
ATOM	1835	O	VAL	A	241	20.177	-36.895	-28.798	1.00	17.62	A	O
ATOM	1836	N	THR	A	242	22.204	-37.820	-28.817	1.00	17.43	A	N
ATOM	1837	CA	THR	A	242	21.744	-39.121	-29.280	1.00	18.51	A	C
ATOM	1838	CB	THR	A	242	22.672	-39.649	-30.391	1.00	18.77	A	C
ATOM	1839	OG1	THR	A	242	22.716	-38.675	-31.456	1.00	20.65	A	O
ATOM	1840	CG2	THR	A	242	22.198	-40.996	-30.941	1.00	17.75	A	C
ATOM	1841	C	THR	A	242	21.696	-40.102	-28.124	1.00	19.15	A	C
ATOM	1842	O	THR	A	242	22.645	-40.197	-27.349	1.00	20.63	A	O
ATOM	1843	N	VAL	A	243	20.597	-40.841	-28.008	1.00	18.62	A	N
ATOM	1844	CA	VAL	A	243	20.381	-41.700	-26.852	1.00	17.91	A	C
ATOM	1845	CB	VAL	A	243	19.219	-41.203	-25.937	1.00	17.53	A	C
ATOM	1846	CG1	VAL	A	243	18.882	-42.211	-24.866	1.00	17.59	A	C
ATOM	1847	CG2	VAL	A	243	19.540	-39.887	-25.267	1.00	17.36	A	C
ATOM	1848	C	VAL	A	243	20.045	-43.047	-27.402	1.00	17.83	A	C
ATOM	1849	O	VAL	A	243	19.182	-43.165	-28.255	1.00	17.31	A	O
ATOM	1850	N	ASN	A	244	20.728	-44.064	-26.896	1.00	18.98	A	N
ATOM	1851	CA	ASN	A	244	20.444	-45.429	-27.283	1.00	19.14	A	C
ATOM	1852	CB	ASN	A	244	21.743	-46.233	-27.435	1.00	20.07	A	C
ATOM	1853	CG	ASN	A	244	22.687	-45.637	-28.492	1.00	22.13	A	C
ATOM	1854	OD1	ASN	A	244	23.898	-45.673	-28.328	1.00	25.76	A	O
ATOM	1855	ND2	ASN	A	244	22.139	-45.076	-29.571	1.00	22.37	A	N
ATOM	1856	C	ASN	A	244	19.487	-46.073	-26.293	1.00	17.74	A	C
ATOM	1857	O	ASN	A	244	19.867	-46.368	-25.167	1.00	17.39	A	O
ATOM	1858	N	GLY	A	245	18.250	-46.288	-26.756	1.00	16.76	A	N
ATOM	1859	CA	GLY	A	245	17.168	-46.961	-26.003	1.00	15.81	A	C
ATOM	1860	C	GLY	A	245	17.533	-48.262	-25.293	1.00	14.82	A	C
ATOM	1861	O	GLY	A	245	18.329	-49.031	-25.768	1.00	13.85	A	O
ATOM	1862	N	ILE	A	246	16.931	-48.493	-24.137	1.00	14.54	A	N
ATOM	1863	CA	ILE	A	246	17.202	-49.690	-23.331	1.00	14.23	A	C
ATOM	1864	CB	ILE	A	246	17.692	-49.293	-21.907	1.00	14.22	A	C
ATOM	1865	CG1	ILE	A	246	16.529	-48.766	-21.060	1.00	13.97	A	C
ATOM	1866	CD1	ILE	A	246	16.857	-48.508	-19.623	1.00	14.08	A	C
ATOM	1867	CG2	ILE	A	246	18.784	-48.218	-22.012	1.00	14.32	A	C
ATOM	1868	C	ILE	A	246	15.965	-50.552	-23.209	1.00	13.73	A	C
ATOM	1869	O	ILE	A	246	15.987	-51.557	-22.540	1.00	12.83	A	O
ATOM	1870	N	GLY	A	247	14.880	-50.097	-23.820	1.00	14.78	A	N
ATOM	1871	CA	GLY	A	247	13.606	-50.812	-23.849	1.00	15.96	A	C
ATOM	1872	C	GLY	A	247	12.624	-50.351	-22.790	1.00	17.03	A	C
ATOM	1873	O	GLY	A	247	12.999	-49.794	-21.732	1.00	17.49	A	O
ATOM	1874	N	ARG	A	248	11.349	-50.581	-23.066	1.00	17.34	A	N
ATOM	1875	CA	ARG	A	248	10.309	-50.188	-22.118	1.00	17.10	A	C
ATOM	1876	CB	ARG	A	248	8.940	-50.518	-22.669	1.00	16.58	A	C
ATOM	1877	CG	ARG	A	248	8.433	-49.504	-23.662	1.00	16.47	A	C
ATOM	1878	CD	ARG	A	248	7.050	-49.883	-24.118	1.00	16.25	A	C
ATOM	1879	NE	ARG	A	248	6.539	-48.977	-25.139	1.00	17.32	A	N
ATOM	1880	CZ	ARG	A	248	5.613	-48.024	-24.967	1.00	18.41	A	C
ATOM	1881	NH1	ARG	A	248	5.058	-47.761	-23.787	1.00	18.84	A	N
ATOM	1882	NH2	ARG	A	248	5.232	-47.308	-26.009	1.00	18.99	A	N
ATOM	1883	C	ARG	A	248	10.493	-50.875	-20.763	1.00	17.84	A	C

ATOM	1884	O	ARG	A	248	10.415	-50.214	-19.716	1.00	18.39	A	O
ATOM	1885	N	ASP	A	249	10.747	-52.182	-20.760	1.00	17.69	A	N
ATOM	1886	CA	ASP	A	249	10.706	-52.918	-19.487	1.00	17.91	A	C
ATOM	1887	CB	ASP	A	249	10.937	-54.421	-19.668	1.00	19.68	A	C
ATOM	1888	CG	ASP	A	249	9.848	-55.096	-20.488	1.00	21.62	A	C
ATOM	1889	OD1	ASP	A	249	8.623	-54.884	-20.223	1.00	23.50	A	O
ATOM	1890	OD2	ASP	A	249	10.246	-55.848	-21.401	1.00	22.32	A	O
ATOM	1891	C	ASP	A	249	11.718	-52.389	-18.500	1.00	15.89	A	C
ATOM	1892	O	ASP	A	249	11.395	-52.143	-17.365	1.00	15.97	A	O
ATOM	1893	N	ALA	A	250	12.943	-52.202	-18.940	1.00	14.48	A	N
ATOM	1894	CA	ALA	A	250	13.986	-51.761	-18.044	1.00	13.79	A	C
ATOM	1895	CB	ALA	A	250	15.331	-51.950	-18.717	1.00	13.75	A	C
ATOM	1896	C	ALA	A	250	13.806	-50.299	-17.587	1.00	13.38	A	C
ATOM	1897	O	ALA	A	250	14.111	-49.946	-16.455	1.00	12.91	A	O
ATOM	1898	N	ALA	A	251	13.325	-49.444	-18.474	1.00	13.31	A	N
ATOM	1899	CA	ALA	A	251	13.146	-48.054	-18.117	1.00	13.55	A	C
ATOM	1900	CB	ALA	A	251	12.906	-47.192	-19.342	1.00	13.75	A	C
ATOM	1901	C	ALA	A	251	12.032	-47.853	-17.090	1.00	13.33	A	C
ATOM	1902	O	ALA	A	251	12.242	-47.100	-16.146	1.00	13.54	A	O
ATOM	1903	N	VAL	A	252	10.872	-48.499	-17.238	1.00	13.18	A	N
ATOM	1904	CA	VAL	A	252	9.833	-48.337	-16.191	1.00	13.49	A	C
ATOM	1905	CB	VAL	A	252	8.454	-49.008	-16.461	1.00	13.62	A	C
ATOM	1906	CG2	VAL	A	252	8.450	-50.435	-15.961	1.00	14.26	A	C
ATOM	1907	CG1	VAL	A	252	8.094	-49.017	-17.928	1.00	13.79	A	C
ATOM	1908	C	VAL	A	252	10.377	-48.832	-14.850	1.00	13.05	A	C
ATOM	1909	O	VAL	A	252	10.070	-48.244	-13.836	1.00	12.86	A	O
ATOM	1910	N	GLN	A	253	11.193	-49.886	-14.855	1.00	13.17	A	N
ATOM	1911	CA	GLN	A	253	11.744	-50.453	-13.619	1.00	13.59	A	C
ATOM	1912	CB	GLN	A	253	12.576	-51.689	-13.924	1.00	14.23	A	C
ATOM	1913	CG	GLN	A	253	12.479	-52.726	-12.823	1.00	15.43	A	C
ATOM	1914	CD	GLN	A	253	11.152	-53.484	-12.862	1.00	16.19	A	C
ATOM	1915	OE1	GLN	A	253	10.488	-53.660	-11.849	1.00	16.30	A	O
ATOM	1916	NE2	GLN	A	253	10.760	-53.921	-14.052	1.00	16.56	A	N
ATOM	1917	C	GLN	A	253	12.614	-49.427	-12.890	1.00	13.62	A	C
ATOM	1918	O	GLN	A	253	12.418	-49.127	-11.705	1.00	13.49	A	O
ATOM	1919	N	ILE	A	254	13.559	-48.862	-13.633	1.00	13.32	A	N
ATOM	1920	CA	ILE	A	254	14.372	-47.776	-13.145	1.00	13.03	A	C
ATOM	1921	CB	ILE	A	254	15.269	-47.254	-14.264	1.00	13.19	A	C
ATOM	1922	CG1	ILE	A	254	16.277	-48.338	-14.647	1.00	13.74	A	C
ATOM	1923	CD1	ILE	A	254	17.007	-48.092	-15.967	1.00	13.85	A	C
ATOM	1924	CG2	ILE	A	254	15.985	-45.984	-13.832	1.00	13.13	A	C
ATOM	1925	C	ILE	A	254	13.521	-46.622	-12.589	1.00	12.90	A	C
ATOM	1926	O	ILE	A	254	13.843	-46.043	-11.541	1.00	12.83	A	O
ATOM	1927	N	PHE	A	255	12.453	-46.249	-13.273	1.00	12.49	A	N
ATOM	1928	CA	PHE	A	255	11.664	-45.128	-12.753	1.00	12.76	A	C
ATOM	1929	CB	PHE	A	255	10.822	-44.475	-13.840	1.00	12.83	A	C
ATOM	1930	CG	PHE	A	255	11.582	-43.498	-14.655	1.00	12.70	A	C
ATOM	1931	CD1	PHE	A	255	12.530	-43.932	-15.557	1.00	12.83	A	C
ATOM	1932	CE1	PHE	A	255	13.259	-43.028	-16.307	1.00	12.62	A	C
ATOM	1933	CZ	PHE	A	255	13.044	-41.683	-16.153	1.00	12.29	A	C
ATOM	1934	CE2	PHE	A	255	12.105	-41.249	-15.251	1.00	12.48	A	C
ATOM	1935	CD2	PHE	A	255	11.384	-42.153	-14.498	1.00	12.59	A	C
ATOM	1936	C	PHE	A	255	10.813	-45.495	-11.534	1.00	12.72	A	C
ATOM	1937	O	PHE	A	255	10.656	-44.670	-10.623	1.00	12.55	A	O
ATOM	1938	N	TYR	A	256	10.308	-46.730	-11.494	1.00	12.65	A	N
ATOM	1939	CA	TYR	A	256	9.621	-47.217	-10.288	1.00	12.85	A	C
ATOM	1940	CB	TYR	A	256	8.944	-48.575	-10.520	1.00	12.32	A	C
ATOM	1941	CG	TYR	A	256	8.231	-49.150	-9.321	1.00	12.10	A	C
ATOM	1942	CD1	TYR	A	256	6.940	-48.766	-8.987	1.00	11.97	A	C
ATOM	1943	CE1	TYR	A	256	6.291	-49.324	-7.886	1.00	12.35	A	C
ATOM	1944	CZ	TYR	A	256	6.958	-50.305	-7.087	1.00	12.71	A	C
ATOM	1945	OH	TYR	A	256	6.407	-50.893	-5.963	1.00	11.74	A	O
ATOM	1946	CE2	TYR	A	256	8.240	-50.693	-7.431	1.00	12.63	A	C
ATOM	1947	CD2	TYR	A	256	8.857	-50.119	-8.537	1.00	12.42	A	C
ATOM	1948	C	TYR	A	256	10.606	-47.259	-9.105	1.00	13.23	A	C
ATOM	1949	O	TYR	A	256	10.259	-46.767	-8.003	1.00	13.67	A	O
ATOM	1950	N	ASP	A	257	11.821	-47.782	-9.328	1.00	12.80	A	N
ATOM	1951	CA	ASP	A	257	12.798	-47.841	-8.248	1.00	12.91	A	C
ATOM	1952	CB	ASP	A	257	14.042	-48.604	-8.654	1.00	13.70	A	C
ATOM	1953	CG	ASP	A	257	13.783	-50.108	-8.772	1.00	14.87	A	C
ATOM	1954	OD1	ASP	A	257	12.705	-50.623	-8.313	1.00	14.92	A	O
ATOM	1955	OD2	ASP	A	257	14.671	-50.780	-9.354	1.00	16.53	A	O
ATOM	1956	C	ASP	A	257	13.162	-46.462	-7.742	1.00	12.44	A	C
ATOM	1957	O	ASP	A	257	13.202	-46.234	-6.512	1.00	11.99	A	O
ATOM	1958	N	ALA	A	258	13.393	-45.540	-8.675	1.00	11.72	A	N
ATOM	1959	CA	ALA	A	258	13.632	-44.133	-8.324	1.00	11.33	A	C
ATOM	1960	CB	ALA	A	258	13.821	-43.289	-9.581	1.00	11.03	A	C
ATOM	1961	C	ALA	A	258	12.476	-43.580	-7.512	1.00	11.08	A	C
ATOM	1962	O	ALA	A	258	12.650	-42.782	-6.597	1.00	10.58	A	O

ATOM	1963	N	LEU	A	259	11.274	-43.985	-7.885	1.00	11.33	A	N
ATOM	1964	CA	LEU	A	259	10.070	-43.427	-7.265	1.00	11.50	A	C
ATOM	1965	CB	LEU	A	259	8.813	-43.839	-8.048	1.00	11.12	A	C
ATOM	1966	CG	LEU	A	259	7.498	-43.498	-7.383	1.00	11.01	A	C
ATOM	1967	CD1	LEU	A	259	7.281	-41.998	-7.298	1.00	11.10	A	C
ATOM	1968	CD2	LEU	A	259	6.381	-44.152	-8.163	1.00	11.25	A	C
ATOM	1969	C	LEU	A	259	9.974	-43.858	-5.809	1.00	11.65	A	C
ATOM	1970	O	LEU	A	259	9.729	-43.042	-4.933	1.00	11.15	A	O
ATOM	1971	N	ILE	A	260	10.190	-45.143	-5.559	1.00	12.27	A	N
ATOM	1972	CA	ILE	A	260	9.993	-45.655	-4.222	1.00	13.14	A	C
ATOM	1973	CB	ILE	A	260	9.454	-47.117	-4.241	1.00	13.43	A	C
ATOM	1974	CG1	ILE	A	260	10.522	-48.112	-4.719	1.00	13.50	A	C
ATOM	1975	CD1	ILE	A	260	10.234	-49.531	-4.306	1.00	13.29	A	C
ATOM	1976	CG2	ILE	A	260	8.188	-47.221	-5.092	1.00	13.46	A	C
ATOM	1977	C	ILE	A	260	11.215	-45.571	-3.302	1.00	13.39	A	C
ATOM	1978	O	ILE	A	260	11.093	-45.924	-2.160	1.00	14.38	A	O
ATOM	1979	N	ASN	A	261	12.376	-45.141	-3.776	1.00	13.69	A	N
ATOM	1980	CA	ASN	A	261	13.594	-45.072	-2.958	1.00	13.71	A	C
ATOM	1981	CB	ASN	A	261	14.671	-46.031	-3.498	1.00	13.86	A	C
ATOM	1982	CG	ASN	A	261	14.287	-47.512	-3.332	1.00	14.28	A	C
ATOM	1983	OD1	ASN	A	261	13.711	-47.912	-2.344	1.00	14.95	A	O
ATOM	1984	ND2	ASN	A	261	14.606	-48.317	-4.304	1.00	14.25	A	N
ATOM	1985	C	ASN	A	261	14.149	-43.646	-2.898	1.00	14.22	A	C
ATOM	1986	O	ASN	A	261	14.355	-43.085	-1.825	1.00	14.32	A	O
ATOM	1987	N	TYR	A	262	14.379	-43.034	-4.044	1.00	14.90	A	N
ATOM	1988	CA	TYR	A	262	15.196	-41.827	-4.071	1.00	15.53	A	C
ATOM	1989	CB	TYR	A	262	16.323	-41.998	-5.092	1.00	15.60	A	C
ATOM	1990	CG	TYR	A	262	17.157	-43.252	-4.863	1.00	15.76	A	C
ATOM	1991	CD1	TYR	A	262	17.756	-43.490	-3.638	1.00	15.71	A	C
ATOM	1992	CE1	TYR	A	262	18.511	-44.630	-3.413	1.00	15.96	A	C
ATOM	1993	CZ	TYR	A	262	18.692	-45.572	-4.420	1.00	15.60	A	C
ATOM	1994	OH	TYR	A	262	19.453	-46.702	-4.174	1.00	13.73	A	O
ATOM	1995	CE2	TYR	A	262	18.097	-45.353	-5.655	1.00	16.02	A	C
ATOM	1996	CD2	TYR	A	262	17.341	-44.199	-5.872	1.00	15.99	A	C
ATOM	1997	C	TYR	A	262	14.422	-40.520	-4.293	1.00	15.92	A	C
ATOM	1998	O	TYR	A	262	14.850	-39.469	-3.830	1.00	17.27	A	O
ATOM	1999	N	LEU	A	263	13.284	-40.543	-4.957	1.00	15.38	A	N
ATOM	2000	CA	LEU	A	263	12.508	-39.307	-5.019	1.00	15.76	A	C
ATOM	2001	CB	LEU	A	263	11.362	-39.431	-6.036	1.00	16.59	A	C
ATOM	2002	CG	LEU	A	263	11.562	-38.897	-7.463	1.00	16.71	A	C
ATOM	2003	CD1	LEU	A	263	13.023	-38.786	-7.862	1.00	16.41	A	C
ATOM	2004	CD2	LEU	A	263	10.766	-39.742	-8.454	1.00	16.56	A	C
ATOM	2005	C	LEU	A	263	11.949	-38.939	-3.637	1.00	15.00	A	C
ATOM	2006	O	LEU	A	263	11.773	-39.803	-2.785	1.00	15.82	A	O
ATOM	2007	N	THR	A	264	11.680	-37.654	-3.439	1.00	14.04	A	N
ATOM	2008	CA	THR	A	264	11.150	-37.105	-2.182	1.00	13.18	A	C
ATOM	2009	CB	THR	A	264	12.254	-36.395	-1.347	1.00	12.53	A	C
ATOM	2010	OG1	THR	A	264	12.519	-35.080	-1.876	1.00	12.08	A	O
ATOM	2011	CG2	THR	A	264	13.522	-37.213	-1.294	1.00	12.33	A	C
ATOM	2012	C	THR	A	264	10.061	-36.059	-2.490	1.00	13.48	A	C
ATOM	2013	O	THR	A	264	9.862	-35.671	-3.655	1.00	13.25	A	O
ATOM	2014	N	PRO	A	265	9.396	-35.535	-1.446	1.00	13.46	A	N
ATOM	2015	CA	PRO	A	265	8.244	-34.703	-1.688	1.00	13.44	A	C
ATOM	2016	CB	PRO	A	265	7.713	-34.453	-0.278	1.00	13.36	A	C
ATOM	2017	CG	PRO	A	265	8.105	-35.667	0.469	1.00	13.47	A	C
ATOM	2018	CD	PRO	A	265	9.514	-35.838	-0.014	1.00	13.66	A	C
ATOM	2019	C	PRO	A	265	8.584	-33.392	-2.320	1.00	13.55	A	C
ATOM	2020	O	PRO	A	265	7.713	-32.600	-2.615	1.00	14.25	A	O
ATOM	2021	N	THR	A	266	9.862	-33.187	-2.529	1.00	13.50	A	N
ATOM	2022	CA	THR	A	266	10.439	-31.881	-2.743	1.00	12.66	A	C
ATOM	2023	CB	THR	A	266	11.222	-31.577	-1.437	1.00	12.59	A	C
ATOM	2024	OG1	THR	A	266	10.606	-30.478	-0.813	1.00	12.07	A	O
ATOM	2025	CG2	THR	A	266	12.736	-31.331	-1.610	1.00	12.62	A	C
ATOM	2026	C	THR	A	266	11.320	-31.926	-3.951	1.00	12.14	A	C
ATOM	2027	O	THR	A	266	11.955	-30.972	-4.264	1.00	12.11	A	O
ATOM	2028	N	SER	A	267	11.378	-33.074	-4.611	1.00	12.40	A	N
ATOM	2029	CA	SER	A	267	12.317	-33.305	-5.672	1.00	12.42	A	C
ATOM	2030	CB	SER	A	267	12.291	-34.755	-6.099	1.00	12.13	A	C
ATOM	2031	OG	SER	A	267	12.643	-35.580	-5.035	1.00	11.99	A	O
ATOM	2032	C	SER	A	267	11.968	-32.465	-6.859	1.00	13.24	A	C
ATOM	2033	O	SER	A	267	10.812	-32.409	-7.303	1.00	13.97	A	O
ATOM	2034	N	ASN	A	268	12.978	-31.795	-7.366	1.00	13.85	A	N
ATOM	2035	CA	ASN	A	268	12.878	-31.150	-8.667	1.00	14.49	A	C
ATOM	2036	CB	ASN	A	268	13.528	-29.763	-8.601	1.00	14.22	A	C
ATOM	2037	CG	ASN	A	268	15.016	-29.822	-8.253	1.00	13.98	A	C
ATOM	2038	OD1	ASN	A	268	15.707	-30.838	-8.451	1.00	13.99	A	O
ATOM	2039	ND2	ASN	A	268	15.511	-28.726	-7.730	1.00	13.52	A	N
ATOM	2040	C	ASN	A	268	13.532	-31.987	-9.787	1.00	15.25	A	C
ATOM	2041	O	ASN	A	268	14.066	-33.113	-9.552	1.00	14.36	A	O

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ATOM   2042  N    PHE A 269      13.499 -31.408 -10.994  1.00 15.91           A  N
ATOM   2043  CA   PHE A 269      13.978 -32.076 -12.198  1.00 16.68           A  C
ATOM   2044  CB   PHE A 269      13.906 -31.122 -13.401  1.00 16.90           A  C
ATOM   2045  CG   PHE A 269      12.562 -31.075 -14.062  1.00 16.51           A  C
ATOM   2046  CD2  PHE A 269      11.620 -30.146 -13.683  1.00 16.34           A  C
ATOM   2047  CE2  PHE A 269      10.379 -30.116 -14.305  1.00 16.36           A  C
ATOM   2048  CZ   PHE A 269      10.067 -31.015 -15.318  1.00 15.85           A  C
ATOM   2049  CE1  PHE A 269      10.985 -31.944 -15.704  1.00 15.68           A  C
ATOM   2050  CD1  PHE A 269      12.236 -31.971 -15.078  1.00 16.47           A  C
ATOM   2051  C    PHE A 269      15.412 -32.571 -12.004  1.00 16.65           A  C
ATOM   2052  O    PHE A 269      15.734 -33.714 -12.297  1.00 16.47           A  O
ATOM   2053  N    SER A 270      16.261 -31.703 -11.487  1.00 17.12           A  N
ATOM   2054  CA   SER A 270      17.660 -32.075 -11.211  1.00 17.53           A  C
ATOM   2055  CB   SER A 270      18.420 -30.901 -10.589  1.00 17.92           A  C
ATOM   2056  OG   SER A 270      19.771 -31.074 -10.914  1.00 19.56           A  O
ATOM   2057  C    SER A 270      17.776 -33.298 -10.309  1.00 16.25           A  C
ATOM   2058  O    SER A 270      18.521 -34.249 -10.592  1.00 16.12           A  O
ATOM   2059  N    ALA A 271      17.014 -33.274  -9.226  1.00 15.54           A  N
ATOM   2060  CA   ALA A 271      16.898 -34.441  -8.354  1.00 14.92           A  C
ATOM   2061  CB   ALA A 271      16.098 -34.060  -7.101  1.00 15.08           A  C
ATOM   2062  C    ALA A 271      16.276 -35.679  -9.083  1.00 13.85           A  C
ATOM   2063  O    ALA A 271      16.669 -36.848  -8.852  1.00 12.80           A  O
ATOM   2064  N    MET A 272      15.314 -35.433  -9.965  1.00 13.07           A  N
ATOM   2065  CA   MET A 272      14.781 -36.544 -10.730  1.00 13.25           A  C
ATOM   2066  CB   MET A 272      13.622 -36.100 -11.628  1.00 13.09           A  C
ATOM   2067  CG   MET A 272      13.165 -37.128 -12.682  1.00 12.47           A  C
ATOM   2068  SD   MET A 272      12.018 -38.351 -12.062  1.00 11.85           A  S
ATOM   2069  CE   MET A 272      12.986 -39.846 -11.892  1.00 11.70           A  C
ATOM   2070  C    MET A 272      15.882 -37.220 -11.555  1.00 13.54           A  C
ATOM   2071  O    MET A 272      15.903 -38.452 -11.661  1.00 13.35           A  O
ATOM   2072  N    ARG A 273      16.773 -36.405 -12.127  1.00 13.96           A  N
ATOM   2073  CA   ARG A 273      17.927 -36.880 -12.896  1.00 14.72           A  C
ATOM   2074  CB   ARG A 273      18.732 -35.678 -13.439  1.00 16.09           A  C
ATOM   2075  CG   ARG A 273      19.897 -36.062 -14.351  1.00 17.57           A  C
ATOM   2076  CD   ARG A 273      20.932 -34.937 -14.559  1.00 19.14           A  C
ATOM   2077  NE   ARG A 273      22.199 -35.555 -15.019  1.00 20.49           A  N
ATOM   2078  CZ   ARG A 273      22.627 -35.627 -16.282  1.00 19.97           A  C
ATOM   2079  NH1  ARG A 273      21.946 -35.082 -17.277  1.00 21.14           A  N
ATOM   2080  NH2  ARG A 273      23.746 -36.263 -16.557  1.00 19.78           A  N
ATOM   2081  C    ARG A 273      18.832 -37.792 -12.058  1.00 14.15           A  C
ATOM   2082  O    ARG A 273      19.154 -38.934 -12.442  1.00 13.74           A  O
ATOM   2083  N    ALA A 274      19.233 -37.270 -10.904  1.00 13.53           A  N
ATOM   2084  CA   ALA A 274      20.050 -38.025  -9.967  1.00 12.90           A  C
ATOM   2085  CB   ALA A 274      20.334 -37.174  -8.741  1.00 12.64           A  C
ATOM   2086  C    ALA A 274      19.346 -39.314  -9.574  1.00 12.59           A  C
ATOM   2087  O    ALA A 274      19.946 -40.390  -9.501  1.00 12.04           A  O
ATOM   2088  N    ALA A 275      18.060 -39.202  -9.309  1.00 12.71           A  N
ATOM   2089  CA   ALA A 275      17.357 -40.339  -8.776  1.00 13.34           A  C
ATOM   2090  CB   ALA A 275      15.961 -39.931  -8.356  1.00 13.53           A  C
ATOM   2091  C    ALA A 275      17.318 -41.459  -9.804  1.00 13.49           A  C
ATOM   2092  O    ALA A 275      17.594 -42.638  -9.496  1.00 13.79           A  O
ATOM   2093  N    ALA A 276      16.987 -41.086 -11.036  1.00 13.40           A  N
ATOM   2094  CA   ALA A 276      16.968 -42.041 -12.114  1.00 13.48           A  C
ATOM   2095  CB   ALA A 276      16.478 -41.373 -13.387  1.00 13.69           A  C
ATOM   2096  C    ALA A 276      18.370 -42.622 -12.286  1.00 13.41           A  C
ATOM   2097  O    ALA A 276      18.531 -43.833 -12.411  1.00 12.81           A  O
ATOM   2098  N    ILE A 277      19.390 -41.767 -12.244  1.00 13.47           A  N
ATOM   2099  CA   ILE A 277      20.744 -42.282 -12.313  1.00 13.96           A  C
ATOM   2100  CB   ILE A 277      21.797 -41.190 -12.261  1.00 14.04           A  C
ATOM   2101  CG1  ILE A 277      21.814 -40.438 -13.581  1.00 14.13           A  C
ATOM   2102  CD1  ILE A 277      22.709 -39.232 -13.583  1.00 14.32           A  C
ATOM   2103  CG2  ILE A 277      23.163 -41.829 -12.023  1.00 14.29           A  C
ATOM   2104  C    ILE A 277      21.066 -43.276 -11.210  1.00 14.15           A  C
ATOM   2105  O    ILE A 277      21.596 -44.354 -11.478  1.00 14.38           A  O
ATOM   2106  N    GLN A 278      20.762 -42.921  -9.973  1.00 14.64           A  N
ATOM   2107  CA   GLN A 278      21.044 -43.832  -8.881  1.00 15.29           A  C
ATOM   2108  CB   GLN A 278      20.665 -43.220  -7.546  1.00 15.95           A  C
ATOM   2109  CG   GLN A 278      21.138 -44.034  -6.336  1.00 16.69           A  C
ATOM   2110  CD   GLN A 278      22.656 -44.231  -6.267  1.00 16.71           A  C
ATOM   2111  OE1  GLN A 278      23.418 -43.326  -5.935  1.00 16.42           A  O
ATOM   2112  NE2  GLN A 278      23.084 -45.437  -6.552  1.00 17.15           A  N
ATOM   2113  C    GLN A 278      20.343 -45.163  -9.067  1.00 15.22           A  C
ATOM   2114  O    GLN A 278      20.930 -46.204  -8.832  1.00 15.46           A  O
ATOM   2115  N    ALA A 279      19.100 -45.141  -9.522  1.00 15.50           A  N
ATOM   2116  CA   ALA A 279      18.344 -46.381  -9.668  1.00 15.59           A  C
ATOM   2117  CB   ALA A 279      16.872 -46.074  -9.868  1.00 15.79           A  C
ATOM   2118  C    ALA A 279      18.870 -47.272 -10.789  1.00 15.64           A  C
ATOM   2119  O    ALA A 279      18.837 -48.496 -10.692  1.00 16.17           A  O
ATOM   2120  N    ALA A 280      19.357 -46.670 -11.858  1.00 15.94           A  N
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ATOM	2121	CA	ALA	A	280	19.950	-47.456	-12.910	1.00	16.38	A	C
ATOM	2122	CB	ALA	A	280	20.116	-46.649	-14.174	1.00	16.73	A	C
ATOM	2123	C	ALA	A	280	21.286	-47.972	-12.446	1.00	16.78	A	C
ATOM	2124	O	ALA	A	280	21.616	-49.113	-12.734	1.00	17.18	A	O
ATOM	2125	N	THR	A	281	22.054	-47.145	-11.732	1.00	17.16	A	N
ATOM	2126	CA	THR	A	281	23.322	-47.592	-11.185	1.00	17.22	A	C
ATOM	2127	CB	THR	A	281	23.996	-46.539	-10.315	1.00	17.66	A	C
ATOM	2128	OG1	THR	A	281	24.434	-45.442	-11.137	1.00	17.89	A	O
ATOM	2129	CG2	THR	A	281	25.202	-47.154	-9.572	1.00	17.44	A	C
ATOM	2130	C	THR	A	281	23.074	-48.819	-10.355	1.00	17.79	A	C
ATOM	2131	O	THR	A	281	23.709	-49.845	-10.578	1.00	18.78	A	O
ATOM	2132	N	ASP	A	282	22.119	-48.745	-9.432	1.00	18.24	A	N
ATOM	2133	CA	ASP	A	282	21.722	-49.930	-8.616	1.00	18.73	A	C
ATOM	2134	CB	ASP	A	282	20.399	-49.683	-7.892	1.00	17.78	A	C
ATOM	2135	CG	ASP	A	282	20.513	-48.689	-6.767	1.00	17.00	A	C
ATOM	2136	OD1	ASP	A	282	21.661	-48.244	-6.447	1.00	15.10	A	O
ATOM	2137	OD2	ASP	A	282	19.413	-48.384	-6.218	1.00	16.44	A	O
ATOM	2138	C	ASP	A	282	21.538	-51.236	-9.375	1.00	19.72	A	C
ATOM	2139	O	ASP	A	282	21.845	-52.281	-8.873	1.00	19.64	A	O
ATOM	2140	N	LEU	A	283	20.992	-51.163	-10.575	1.00	22.83	A	N
ATOM	2141	CA	LEU	A	283	20.581	-52.346	-11.323	1.00	23.96	A	C
ATOM	2142	CB	LEU	A	283	19.265	-52.043	-12.036	1.00	24.88	A	C
ATOM	2143	CG	LEU	A	283	18.029	-51.915	-11.148	1.00	25.50	A	C
ATOM	2144	CD1	LEU	A	283	16.958	-51.126	-11.898	1.00	26.24	A	C
ATOM	2145	CD2	LEU	A	283	17.524	-53.299	-10.763	1.00	25.11	A	C
ATOM	2146	C	LEU	A	283	21.554	-52.812	-12.388	1.00	23.80	A	C
ATOM	2147	O	LEU	A	283	21.489	-53.966	-12.790	1.00	23.32	A	O
ATOM	2148	N	TYR	A	284	22.385	-51.915	-12.904	1.00	24.03	A	N
ATOM	2149	CA	TYR	A	284	23.184	-52.237	-14.085	1.00	25.72	A	C
ATOM	2150	CB	TYR	A	284	22.597	-51.570	-15.350	1.00	25.41	A	C
ATOM	2151	CG	TYR	A	284	21.211	-52.073	-15.711	1.00	25.02	A	C
ATOM	2152	CD1	TYR	A	284	21.037	-53.340	-16.265	1.00	24.40	A	C
ATOM	2153	CE1	TYR	A	284	19.766	-53.811	-16.579	1.00	25.54	A	C
ATOM	2154	CZ	TYR	A	284	18.630	-53.007	-16.344	1.00	24.69	A	C
ATOM	2155	OH	TYR	A	284	17.349	-53.493	-16.656	1.00	23.49	A	O
ATOM	2156	CE2	TYR	A	284	18.801	-51.748	-15.782	1.00	23.41	A	C
ATOM	2157	CD2	TYR	A	284	20.071	-51.292	-15.469	1.00	23.48	A	C
ATOM	2158	C	TYR	A	284	24.632	-51.848	-13.937	1.00	27.83	A	C
ATOM	2159	O	TYR	A	284	25.428	-52.120	-14.841	1.00	29.91	A	O
ATOM	2160	N	GLY	A	285	24.982	-51.213	-12.822	1.00	27.88	A	N
ATOM	2161	CA	GLY	A	285	26.361	-50.831	-12.567	1.00	29.33	A	C
ATOM	2162	C	GLY	A	285	26.614	-49.435	-13.076	1.00	32.33	A	C
ATOM	2163	O	GLY	A	285	26.058	-49.040	-14.098	1.00	36.64	A	O
ATOM	2164	N	ALA	A	286	27.481	-48.698	-12.392	1.00	32.78	A	N
ATOM	2165	CA	ALA	A	286	27.576	-47.250	-12.579	1.00	33.56	A	C
ATOM	2166	CB	ALA	A	286	28.379	-46.627	-11.440	1.00	34.16	A	C
ATOM	2167	C	ALA	A	286	28.143	-46.799	-13.923	1.00	33.26	A	C
ATOM	2168	O	ALA	A	286	28.010	-45.618	-14.292	1.00	34.56	A	O
ATOM	2169	N	ASN	A	287	28.772	-47.707	-14.656	1.00	31.09	A	N
ATOM	2170	CA	ASN	A	287	29.308	-47.430	-15.949	1.00	29.96	A	C
ATOM	2171	CB	ASN	A	287	30.821	-47.577	-15.965	1.00	30.24	A	C
ATOM	2172	CG	ASN	A	287	31.522	-46.889	-17.130	1.00	30.47	A	C
ATOM	2173	OD1	ASN	A	287	31.112	-45.823	-17.601	1.00	26.91	A	O
ATOM	2174	ND2	ASN	A	287	32.576	-47.529	-17.626	1.00	31.27	A	N
ATOM	2175	C	ASN	A	287	28.568	-48.065	-17.076	1.00	27.79	A	C
ATOM	2176	O	ASN	A	287	29.058	-48.213	-18.185	1.00	26.46	A	O
ATOM	2177	N	SER	A	288	27.350	-48.482	-16.802	1.00	27.08	A	N
ATOM	2178	CA	SER	A	288	26.584	-49.237	-17.781	1.00	26.73	A	C
ATOM	2179	CB	SER	A	288	25.406	-49.971	-17.108	1.00	27.43	A	C
ATOM	2180	OG	SER	A	288	24.598	-49.085	-16.318	1.00	28.18	A	O
ATOM	2181	C	SER	A	288	26.070	-48.333	-18.879	1.00	24.80	A	C
ATOM	2182	O	SER	A	288	26.043	-47.106	-18.746	1.00	23.67	A	O
ATOM	2183	N	SER	A	289	25.657	-48.976	-19.963	1.00	24.24	A	N
ATOM	2184	CA	SER	A	289	24.931	-48.317	-21.052	1.00	24.51	A	C
ATOM	2185	CB	SER	A	289	24.697	-49.308	-22.203	1.00	23.11	A	C
ATOM	2186	OG	SER	A	289	24.340	-50.588	-21.729	1.00	21.73	A	O
ATOM	2187	C	SER	A	289	23.576	-47.698	-20.591	1.00	25.23	A	C
ATOM	2188	O	SER	A	289	23.156	-46.616	-21.073	1.00	27.12	A	O
ATOM	2189	N	GLN	A	290	22.919	-48.376	-19.656	1.00	23.65	A	N
ATOM	2190	CA	GLN	A	290	21.640	-47.929	-19.149	1.00	23.31	A	C
ATOM	2191	CB	GLN	A	290	21.030	-48.994	-18.253	1.00	22.58	A	C
ATOM	2192	CG	GLN	A	290	20.519	-50.209	-19.023	1.00	22.68	A	C
ATOM	2193	CD	GLN	A	290	21.505	-51.364	-19.101	1.00	22.39	A	C
ATOM	2194	OE1	GLN	A	290	22.711	-51.186	-19.035	1.00	23.40	A	O
ATOM	2195	NE2	GLN	A	290	20.980	-52.561	-19.222	1.00	22.20	A	N
ATOM	2196	C	GLN	A	290	21.855	-46.649	-18.386	1.00	24.05	A	C
ATOM	2197	O	GLN	A	290	21.177	-45.636	-18.626	1.00	23.70	A	O
ATOM	2198	N	VAL	A	291	22.836	-46.672	-17.493	1.00	24.02	A	N
ATOM	2199	CA	VAL	A	291	23.154	-45.475	-16.754	1.00	23.78	A	C

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ATOM   2200  CB   VAL A 291      24.348 -45.668 -15.809  1.00 24.04      A    C
ATOM   2201  CG1  VAL A 291      24.995 -44.332 -15.456  1.00 23.39      A    C
ATOM   2202  CG2  VAL A 291      23.882 -46.376 -14.555  1.00 24.62      A    C
ATOM   2203  C    VAL A 291      23.475 -44.407 -17.748  1.00 24.05      A    C
ATOM   2204  O    VAL A 291      23.070 -43.242 -17.593  1.00 22.27      A    O
ATOM   2205  N    ASN A 292      24.215 -44.790 -18.781  1.00 25.34      A    N
ATOM   2206  CA   ASN A 292      24.673 -43.762 -19.676  1.00 26.69      A    C
ATOM   2207  CB   ASN A 292      25.884 -44.205 -20.478  1.00 30.49      A    C
ATOM   2208  CG   ASN A 292      26.820 -43.042 -20.731  1.00 35.02      A    C
ATOM   2209  OD1  ASN A 292      27.508 -42.596 -19.808  1.00 39.60      A    O
ATOM   2210  ND2  ASN A 292      26.793 -42.487 -21.952  1.00 35.12      A    N
ATOM   2211  C    ASN A 292      23.553 -43.174 -20.551  1.00 23.23      A    C
ATOM   2212  O    ASN A 292      23.547 -41.978 -20.829  1.00 21.51      A    O
ATOM   2213  N    ALA A 293      22.594 -44.013 -20.932  1.00 20.89      A    N
ATOM   2214  CA   ALA A 293      21.432 -43.577 -21.719  1.00 19.66      A    C
ATOM   2215  CB   ALA A 293      20.559 -44.780 -22.043  1.00 20.04      A    C
ATOM   2216  C    ALA A 293      20.614 -42.573 -20.957  1.00 18.76      A    C
ATOM   2217  O    ALA A 293      20.105 -41.606 -21.499  1.00 17.05      A    O
ATOM   2218  N    VAL A 294      20.461 -42.866 -19.669  1.00 18.81      A    N
ATOM   2219  CA   VAL A 294      19.729 -42.016 -18.771  1.00 17.38      A    C
ATOM   2220  CB   VAL A 294      19.646 -42.671 -17.382  1.00 16.37      A    C
ATOM   2221  CG1  VAL A 294      19.185 -41.672 -16.324  1.00 16.38      A    C
ATOM   2222  CG2  VAL A 294      18.736 -43.875 -17.422  1.00 15.72      A    C
ATOM   2223  C    VAL A 294      20.396 -40.645 -18.748  1.00 17.76      A    C
ATOM   2224  O    VAL A 294      19.713 -39.640 -18.840  1.00 17.49      A    O
ATOM   2225  N    LYS A 295      21.727 -40.613 -18.654  1.00 18.95      A    N
ATOM   2226  CA   LYS A 295      22.461 -39.349 -18.560  1.00 19.76      A    C
ATOM   2227  CB   LYS A 295      23.964 -39.577 -18.381  1.00 21.38      A    C
ATOM   2228  CG   LYS A 295      24.399 -39.923 -16.961  1.00 22.34      A    C
ATOM   2229  CD   LYS A 295      25.900 -40.268 -16.887  1.00 23.25      A    C
ATOM   2230  CE   LYS A 295      26.277 -40.738 -15.476  1.00 23.34      A    C
ATOM   2231  NZ   LYS A 295      27.731 -40.846 -15.162  1.00 22.84      A    N
ATOM   2232  C    LYS A 295      22.239 -38.480 -19.774  1.00 19.36      A    C
ATOM   2233  O    LYS A 295      21.916 -37.284 -19.655  1.00 18.79      A    O
ATOM   2234  N    LYS A 296      22.394 -39.073 -20.944  1.00 19.79      A    N
ATOM   2235  CA   LYS A 296      22.200 -38.316 -22.176  1.00 21.18      A    C
ATOM   2236  CB   LYS A 296      22.618 -39.143 -23.379  1.00 23.67      A    C
ATOM   2237  CG   LYS A 296      24.126 -39.307 -23.392  1.00 27.94      A    C
ATOM   2238  CD   LYS A 296      24.657 -39.899 -24.691  1.00 32.89      A    C
ATOM   2239  CE   LYS A 296      26.166 -39.650 -24.836  1.00 37.16      A    C
ATOM   2240  NZ   LYS A 296      26.520 -38.247 -25.268  1.00 38.34      A    N
ATOM   2241  C    LYS A 296      20.785 -37.754 -22.325  1.00 19.72      A    C
ATOM   2242  O    LYS A 296      20.603 -36.553 -22.615  1.00 18.85      A    O
ATOM   2243  N    ALA A 297      19.804 -38.618 -22.087  1.00 18.65      A    N
ATOM   2244  CA   ALA A 297      18.395 -38.236 -22.059  1.00 18.30      A    C
ATOM   2245  CB   ALA A 297      17.544 -39.389 -21.570  1.00 19.00      A    C
ATOM   2246  C    ALA A 297      18.141 -37.014 -21.207  1.00 18.02      A    C
ATOM   2247  O    ALA A 297      17.575 -36.041 -21.683  1.00 18.61      A    O
ATOM   2248  N    TYR A 298      18.578 -37.016 -19.960  1.00 17.55      A    N
ATOM   2249  CA   TYR A 298      18.361 -35.808 -19.165  1.00 17.98      A    C
ATOM   2250  CB   TYR A 298      18.595 -36.043 -17.662  1.00 17.98      A    C
ATOM   2251  CG   TYR A 298      17.361 -36.698 -17.049  1.00 17.27      A    C
ATOM   2252  CD1  TYR A 298      16.272 -35.926 -16.677  1.00 16.76      A    C
ATOM   2253  CE1  TYR A 298      15.140 -36.498 -16.150  1.00 16.52      A    C
ATOM   2254  CZ   TYR A 298      15.057 -37.866 -16.011  1.00 16.59      A    C
ATOM   2255  OH   TYR A 298      13.898 -38.414 -15.489  1.00 15.41      A    O
ATOM   2256  CE2  TYR A 298      16.135 -38.665 -16.381  1.00 16.79      A    C
ATOM   2257  CD2  TYR A 298      17.268 -38.079 -16.910  1.00 16.48      A    C
ATOM   2258  C    TYR A 298      19.123 -34.601 -19.686  1.00 17.99      A    C
ATOM   2259  O    TYR A 298      18.623 -33.470 -19.572  1.00 19.07      A    O
ATOM   2260  N    THR A 299      20.307 -34.828 -20.255  1.00 17.65      A    N
ATOM   2261  CA   THR A 299      21.056 -33.746 -20.902  1.00 17.98      A    C
ATOM   2262  CB   THR A 299      22.472 -34.217 -21.368  1.00 17.57      A    C
ATOM   2263  OG1  THR A 299      23.235 -34.706 -20.250  1.00 16.90      A    O
ATOM   2264  CG2  THR A 299      23.217 -33.076 -22.047  1.00 16.53      A    C
ATOM   2265  C    THR A 299      20.231 -33.206 -22.118  1.00 18.22      A    C
ATOM   2266  O    THR A 299      20.019 -31.985 -22.289  1.00 16.64      A    O
ATOM   2267  N    ALA A 300      19.744 -34.132 -22.938  1.00 18.02      A    N
ATOM   2268  CA   ALA A 300      18.960 -33.751 -24.087  1.00 18.32      A    C
ATOM   2269  CB   ALA A 300      18.408 -34.982 -24.786  1.00 18.60      A    C
ATOM   2270  C    ALA A 300      17.840 -32.798 -23.701  1.00 18.60      A    C
ATOM   2271  O    ALA A 300      17.659 -31.798 -24.366  1.00 20.19      A    O
ATOM   2272  N    VAL A 301      17.101 -33.074 -22.630  1.00 18.61      A    N
ATOM   2273  CA   VAL A 301      15.996 -32.189 -22.240  1.00 18.71      A    C
ATOM   2274  CB   VAL A 301      14.856 -32.940 -21.538  1.00 19.41      A    C
ATOM   2275  CG1  VAL A 301      14.404 -34.146 -22.338  1.00 19.54      A    C
ATOM   2276  CG2  VAL A 301      15.298 -33.395 -20.170  1.00 20.37      A    C
ATOM   2277  C    VAL A 301      16.457 -31.043 -21.350  1.00 18.65      A    C
ATOM   2278  O    VAL A 301      15.646 -30.314 -20.777  1.00 18.51      A    O
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ATOM	2279	N	GLY	A	302	17.758	-30.871	-21.231	1.00	19.01	A	N
ATOM	2280	CA	GLY	A	302	18.282	-29.621	-20.718	1.00	19.86	A	C
ATOM	2281	C	GLY	A	302	18.370	-29.640	-19.219	1.00	21.35	A	C
ATOM	2282	O	GLY	A	302	18.411	-28.580	-18.581	1.00	20.19	A	O
ATOM	2283	N	VAL	A	303	18.392	-30.858	-18.659	1.00	23.47	A	N
ATOM	2284	CA	VAL	A	303	18.503	-31.054	-17.208	1.00	23.96	A	C
ATOM	2285	CB	VAL	A	303	17.367	-31.958	-16.677	1.00	23.91	A	C
ATOM	2286	CG1	VAL	A	303	17.488	-32.161	-15.169	1.00	24.18	A	C
ATOM	2287	CG2	VAL	A	303	16.027	-31.330	-16.985	1.00	24.04	A	C
ATOM	2288	C	VAL	A	303	19.868	-31.647	-16.845	1.00	23.68	A	C
ATOM	2289	O	VAL	A	303	20.199	-32.752	-17.266	1.00	22.79	A	O
ATOM	2290	N	ASN	A	304	20.630	-30.924	-16.033	1.00	24.44	A	N
ATOM	2291	CA	ASN	A	304	21.971	-31.369	-15.668	1.00	27.13	A	C
ATOM	2292	CB	ASN	A	304	22.976	-30.333	-16.137	1.00	27.63	A	C
ATOM	2293	CG	ASN	A	304	22.782	-29.969	-17.602	1.00	28.08	A	C
ATOM	2294	OD1	ASN	A	304	22.758	-30.844	-18.497	1.00	26.81	A	O
ATOM	2295	ND2	ASN	A	304	22.632	-28.666	-17.855	1.00	27.74	A	N
ATOM	2296	C	ASN	A	304	22.203	-31.666	-14.188	1.00	27.90	A	C
ATOM	2297	O	ASN	A	304	21.646	-31.075	-13.248	1.00	28.54	A	O
ATOM	2298	OXT	ASN	A	304	23.015	-32.544	-13.941	1.00	27.35	A	O
ATOM	2299	N	ALA	B	1	-27.118	-11.588	16.141	1.00	36.52	B	N
ATOM	2300	CA	ALA	B	1	-26.133	-11.218	17.198	1.00	37.78	B	C
ATOM	2301	CB	ALA	B	1	-25.839	-12.399	18.109	1.00	36.98	B	C
ATOM	2302	C	ALA	B	1	-24.878	-10.774	16.492	1.00	39.27	B	C
ATOM	2303	O	ALA	B	1	-24.736	-11.016	15.302	1.00	43.37	B	O
ATOM	2304	N	THR	B	2	-23.958	-10.156	17.220	1.00	39.24	B	N
ATOM	2305	CA	THR	B	2	-22.776	-9.556	16.609	1.00	38.21	B	C
ATOM	2306	CB	THR	B	2	-22.792	-8.015	16.742	1.00	38.56	B	C
ATOM	2307	OG1	THR	B	2	-23.817	-7.475	15.901	1.00	37.57	B	O
ATOM	2308	CG2	THR	B	2	-21.445	-7.408	16.322	1.00	39.78	B	C
ATOM	2309	C	THR	B	2	-21.477	-10.140	17.183	1.00	37.53	B	C
ATOM	2310	O	THR	B	2	-21.027	-9.766	18.266	1.00	32.77	B	O
ATOM	2311	N	GLY	B	3	-20.864	-11.037	16.413	1.00	38.90	B	N
ATOM	2312	CA	GLY	B	3	-19.625	-11.693	16.822	1.00	39.37	B	C
ATOM	2313	C	GLY	B	3	-18.385	-10.922	16.439	1.00	37.66	B	C
ATOM	2314	O	GLY	B	3	-18.379	-10.180	15.475	1.00	38.38	B	O
ATOM	2315	N	THR	B	4	-17.325	-11.116	17.193	1.00	37.26	B	N
ATOM	2316	CA	THR	B	4	-16.066	-10.493	16.873	1.00	39.03	B	C
ATOM	2317	CB	THR	B	4	-15.631	-9.497	17.978	1.00	38.57	B	C
ATOM	2318	OG1	THR	B	4	-14.242	-9.154	17.811	1.00	38.10	B	O
ATOM	2319	CG2	THR	B	4	-15.829	-10.089	19.342	1.00	36.87	B	C
ATOM	2320	C	THR	B	4	-14.993	-11.568	16.642	1.00	39.28	B	C
ATOM	2321	O	THR	B	4	-15.018	-12.622	17.277	1.00	37.20	B	O
ATOM	2322	N	GLY	B	5	-14.064	-11.284	15.725	1.00	38.89	B	N
ATOM	2323	CA	GLY	B	5	-12.864	-12.101	15.541	1.00	37.29	B	C
ATOM	2324	C	GLY	B	5	-11.851	-11.559	14.531	1.00	35.59	B	C
ATOM	2325	O	GLY	B	5	-12.190	-10.789	13.611	1.00	34.39	B	O
ATOM	2326	N	LYS	B	6	-10.601	-11.982	14.704	1.00	32.33	B	N
ATOM	2327	CA	LYS	B	6	-9.501	-11.572	13.834	1.00	30.16	B	C
ATOM	2328	CB	LYS	B	6	-8.164	-11.793	14.523	1.00	28.67	B	C
ATOM	2329	CG	LYS	B	6	-8.056	-11.021	15.798	1.00	29.42	B	C
ATOM	2330	CD	LYS	B	6	-6.667	-11.050	16.395	1.00	31.17	B	C
ATOM	2331	CE	LYS	B	6	-6.396	-9.726	17.100	1.00	31.96	B	C
ATOM	2332	NZ	LYS	B	6	-5.427	-9.958	18.189	1.00	33.82	B	N
ATOM	2333	C	LYS	B	6	-9.528	-12.360	12.547	1.00	28.68	B	C
ATOM	2334	O	LYS	B	6	-9.889	-13.529	12.555	1.00	29.96	B	O
ATOM	2335	N	GLY	B	7	-9.141	-11.718	11.447	1.00	26.88	B	N
ATOM	2336	CA	GLY	B	7	-9.082	-12.374	10.150	1.00	24.95	B	C
ATOM	2337	C	GLY	B	7	-7.727	-13.011	10.017	1.00	23.60	B	C
ATOM	2338	O	GLY	B	7	-6.884	-12.864	10.883	1.00	23.09	B	O
ATOM	2339	N	VAL	B	8	-7.515	-13.700	8.912	1.00	22.56	B	N
ATOM	2340	CA	VAL	B	8	-6.255	-14.375	8.641	1.00	22.38	B	C
ATOM	2341	CB	VAL	B	8	-6.215	-14.891	7.197	1.00	22.59	B	C
ATOM	2342	CG1	VAL	B	8	-4.869	-15.545	6.892	1.00	22.83	B	C
ATOM	2343	CG2	VAL	B	8	-7.357	-15.870	6.940	1.00	22.50	B	C
ATOM	2344	C	VAL	B	8	-5.041	-13.479	8.847	1.00	22.68	B	C
ATOM	2345	O	VAL	B	8	-4.003	-13.935	9.296	1.00	21.46	B	O
ATOM	2346	N	LEU	B	9	-5.173	-12.201	8.498	1.00	24.54	B	N
ATOM	2347	CA	LEU	B	9	-4.063	-11.242	8.600	1.00	24.12	B	C
ATOM	2348	CB	LEU	B	9	-4.135	-10.261	7.432	1.00	23.12	B	C
ATOM	2349	CG	LEU	B	9	-3.359	-10.564	6.154	1.00	21.95	B	C
ATOM	2350	CD1	LEU	B	9	-3.041	-12.036	6.027	1.00	20.77	B	C
ATOM	2351	CD2	LEU	B	9	-4.141	-9.999	4.961	1.00	21.42	B	C
ATOM	2352	C	LEU	B	9	-4.046	-10.456	9.890	1.00	25.26	B	C
ATOM	2353	O	LEU	B	9	-3.442	-9.408	9.933	1.00	28.39	B	O
ATOM	2354	N	GLY	B	10	-4.723	-10.932	10.930	1.00	26.73	B	N
ATOM	2355	CA	GLY	B	10	-4.586	-10.358	12.279	1.00	26.45	B	C
ATOM	2356	C	GLY	B	10	-5.481	-9.174	12.586	1.00	26.20	B	C
ATOM	2357	O	GLY	B	10	-5.297	-8.504	13.614	1.00	24.13	B	O

ATOM	2358	N	ASP	B	11	-6.481	-8.966	11.727	1.00	26.26	B	N
ATOM	2359	CA	ASP	B	11	-7.342	-7.781	11.761	1.00	26.23	B	C
ATOM	2360	CB	ASP	B	11	-7.410	-7.155	10.356	1.00	24.59	B	C
ATOM	2361	CG	ASP	B	11	-7.968	-8.109	9.295	1.00	24.79	B	C
ATOM	2362	OD1	ASP	B	11	-7.465	-9.238	9.139	1.00	25.46	B	O
ATOM	2363	OD2	ASP	B	11	-8.922	-7.739	8.596	1.00	23.52	B	O
ATOM	2364	C	ASP	B	11	-8.767	-8.052	12.313	1.00	28.01	B	C
ATOM	2365	O	ASP	B	11	-9.541	-8.838	11.737	1.00	29.86	B	O
ATOM	2366	N	THR	B	12	-9.127	-7.357	13.397	1.00	28.40	B	N
ATOM	2367	CA	THR	B	12	-10.417	-7.555	14.073	1.00	27.68	B	C
ATOM	2368	CB	THR	B	12	-10.402	-6.914	15.465	1.00	25.99	B	C
ATOM	2369	OG1	THR	B	12	-9.232	-7.350	16.173	1.00	25.66	B	O
ATOM	2370	CG2	THR	B	12	-11.645	-7.298	16.258	1.00	24.54	B	C
ATOM	2371	C	THR	B	12	-11.633	-7.041	13.285	1.00	29.85	B	C
ATOM	2372	O	THR	B	12	-11.677	-5.875	12.875	1.00	32.91	B	O
ATOM	2373	N	LYS	B	13	-12.618	-7.922	13.090	1.00	30.70	B	N
ATOM	2374	CA	LYS	B	13	-13.867	-7.580	12.402	1.00	31.16	B	C
ATOM	2375	CB	LYS	B	13	-14.036	-8.339	11.087	1.00	31.49	B	C
ATOM	2376	CG	LYS	B	13	-12.756	-8.854	10.458	1.00	32.70	B	C
ATOM	2377	CD	LYS	B	13	-13.037	-9.300	9.041	1.00	32.47	B	C
ATOM	2378	CE	LYS	B	13	-11.763	-9.658	8.315	1.00	32.16	B	C
ATOM	2379	NZ	LYS	B	13	-10.786	-8.555	8.175	1.00	31.87	B	N
ATOM	2380	C	LYS	B	13	-15.052	-7.967	13.238	1.00	33.23	B	C
ATOM	2381	O	LYS	B	13	-14.940	-8.784	14.157	1.00	39.07	B	O
ATOM	2382	N	SER	B	14	-16.196	-7.403	12.866	1.00	31.47	B	N
ATOM	2383	CA	SER	B	14	-17.474	-7.714	13.446	1.00	29.93	B	C
ATOM	2384	CB	SER	B	14	-18.225	-6.440	13.792	1.00	31.68	B	C
ATOM	2385	OG	SER	B	14	-17.421	-5.631	14.618	1.00	34.18	B	O
ATOM	2386	C	SER	B	14	-18.244	-8.385	12.377	1.00	28.96	B	C
ATOM	2387	O	SER	B	14	-17.989	-8.156	11.196	1.00	27.52	B	O
ATOM	2388	N	PHE	B	15	-19.225	-9.178	12.773	1.00	28.58	B	N
ATOM	2389	CA	PHE	B	15	-20.097	-9.822	11.797	1.00	28.92	B	C
ATOM	2390	CB	PHE	B	15	-19.330	-10.903	11.010	1.00	27.95	B	C
ATOM	2391	CG	PHE	B	15	-18.345	-11.675	11.853	1.00	26.41	B	C
ATOM	2392	CD1	PHE	B	15	-18.751	-12.766	12.586	1.00	24.71	B	C
ATOM	2393	CE1	PHE	B	15	-17.861	-13.459	13.368	1.00	24.48	B	C
ATOM	2394	CZ	PHE	B	15	-16.548	-13.067	13.437	1.00	25.51	B	C
ATOM	2395	CE2	PHE	B	15	-16.130	-11.967	12.722	1.00	26.27	B	C
ATOM	2396	CD2	PHE	B	15	-17.028	-11.281	11.934	1.00	26.09	B	C
ATOM	2397	C	PHE	B	15	-21.283	-10.421	12.515	1.00	30.15	B	C
ATOM	2398	O	PHE	B	15	-21.231	-10.661	13.735	1.00	28.64	B	O
ATOM	2399	N	THR	B	16	-22.350	-10.643	11.756	1.00	32.13	B	N
ATOM	2400	CA	THR	B	16	-23.564	-11.231	12.297	1.00	35.95	B	C
ATOM	2401	CB	THR	B	16	-24.775	-10.980	11.371	1.00	35.50	B	C
ATOM	2402	OG1	THR	B	16	-25.103	-9.584	11.373	1.00	34.31	B	O
ATOM	2403	CG2	THR	B	16	-26.013	-11.807	11.799	1.00	35.19	B	C
ATOM	2404	C	THR	B	16	-23.380	-12.745	12.499	1.00	40.78	B	C
ATOM	2405	O	THR	B	16	-23.020	-13.467	11.556	1.00	41.40	B	O
ATOM	2406	N	THR	B	17	-23.627	-13.198	13.732	1.00	42.02	B	N
ATOM	2407	CA	THR	B	17	-23.766	-14.616	14.057	1.00	43.39	B	C
ATOM	2408	CB	THR	B	17	-22.819	-14.986	15.206	1.00	42.77	B	C
ATOM	2409	OG1	THR	B	17	-23.194	-14.299	16.410	1.00	40.33	B	O
ATOM	2410	CG2	THR	B	17	-21.392	-14.597	14.826	1.00	42.32	B	C
ATOM	2411	C	THR	B	17	-25.237	-14.905	14.412	1.00	47.94	B	C
ATOM	2412	O	THR	B	17	-26.098	-14.036	14.216	1.00	53.17	B	O
ATOM	2413	N	THR	B	18	-25.536	-16.119	14.880	1.00	48.55	B	N
ATOM	2414	CA	THR	B	18	-26.883	-16.470	15.372	1.00	47.03	B	C
ATOM	2415	CB	THR	B	18	-27.715	-17.260	14.322	1.00	46.64	B	C
ATOM	2416	OG1	THR	B	18	-27.903	-16.465	13.143	1.00	47.35	B	O
ATOM	2417	CG2	THR	B	18	-29.098	-17.635	14.867	1.00	47.20	B	C
ATOM	2418	C	THR	B	18	-26.781	-17.247	16.695	1.00	49.03	B	C
ATOM	2419	O	THR	B	18	-25.845	-18.027	16.910	1.00	45.35	B	O
ATOM	2420	N	GLN	B	19	-27.735	-16.996	17.592	1.00	54.36	B	N
ATOM	2421	CA	GLN	B	19	-27.790	-17.676	18.879	1.00	54.96	B	C
ATOM	2422	CB	GLN	B	19	-28.436	-16.770	19.934	1.00	58.37	B	C
ATOM	2423	CG	GLN	B	19	-27.996	-17.086	21.361	1.00	62.57	B	C
ATOM	2424	CD	GLN	B	19	-28.459	-16.067	22.402	1.00	63.05	B	C
ATOM	2425	OE1	GLN	B	19	-27.896	-14.971	22.517	1.00	60.83	B	O
ATOM	2426	NE2	GLN	B	19	-29.472	-16.437	23.185	1.00	62.16	B	N
ATOM	2427	C	GLN	B	19	-28.597	-18.953	18.685	1.00	53.79	B	C
ATOM	2428	O	GLN	B	19	-29.711	-18.899	18.167	1.00	53.84	B	O
ATOM	2429	N	SER	B	20	-28.016	-20.097	19.046	1.00	54.80	B	N
ATOM	2430	CA	SER	B	20	-28.744	-21.381	19.062	1.00	54.29	B	C
ATOM	2431	CB	SER	B	20	-28.141	-22.387	18.081	1.00	53.79	B	C
ATOM	2432	OG	SER	B	20	-29.021	-23.476	17.888	1.00	49.78	B	O
ATOM	2433	C	SER	B	20	-28.687	-21.918	20.481	1.00	53.51	B	C
ATOM	2434	O	SER	B	20	-27.696	-22.552	20.883	1.00	51.94	B	O
ATOM	2435	N	GLY	B	21	-29.746	-21.617	21.235	1.00	52.98	B	N
ATOM	2436	CA	GLY	B	21	-29.787	-21.842	22.675	1.00	53.72	B	C

ATOM	2437	C	GLY	B	21	-28.455	-21.571	23.358	1.00	53.77	B	C
ATOM	2438	O	GLY	B	21	-28.115	-20.417	23.666	1.00	50.85	B	O
ATOM	2439	N	SER	B	22	-27.690	-22.641	23.549	1.00	53.12	B	N
ATOM	2440	CA	SER	B	22	-26.521	-22.621	24.419	1.00	59.41	B	C
ATOM	2441	CB	SER	B	22	-26.174	-24.057	24.820	1.00	59.03	B	C
ATOM	2442	OG	SER	B	22	-25.106	-24.053	25.747	1.00	61.97	B	O
ATOM	2443	C	SER	B	22	-25.272	-21.930	23.824	1.00	61.98	B	C
ATOM	2444	O	SER	B	22	-24.452	-21.348	24.563	1.00	61.14	B	O
ATOM	2445	N	THR	B	23	-25.134	-21.998	22.501	1.00	57.12	B	N
ATOM	2446	CA	THR	B	23	-23.930	-21.532	21.828	1.00	55.19	B	C
ATOM	2447	CB	THR	B	23	-23.101	-22.755	21.366	1.00	52.30	B	C
ATOM	2448	OG1	THR	B	23	-21.696	-22.470	21.419	1.00	49.29	B	O
ATOM	2449	CG2	THR	B	23	-23.522	-23.221	19.960	1.00	51.82	B	C
ATOM	2450	C	THR	B	23	-24.344	-20.627	20.655	1.00	55.21	B	C
ATOM	2451	O	THR	B	23	-25.542	-20.492	20.358	1.00	54.01	B	O
ATOM	2452	N	TYR	B	24	-23.365	-19.996	20.010	1.00	52.08	B	N
ATOM	2453	CA	TYR	B	24	-23.622	-19.217	18.798	1.00	50.27	B	C
ATOM	2454	CB	TYR	B	24	-23.019	-17.812	18.884	1.00	52.10	B	C
ATOM	2455	CG	TYR	B	24	-23.470	-16.931	20.029	1.00	51.06	B	C
ATOM	2456	CD1	TYR	B	24	-24.563	-16.095	19.888	1.00	49.59	B	C
ATOM	2457	CE1	TYR	B	24	-24.967	-15.278	20.923	1.00	52.70	B	C
ATOM	2458	CZ	TYR	B	24	-24.268	-15.276	22.121	1.00	52.07	B	C
ATOM	2459	OH	TYR	B	24	-24.689	-14.454	23.153	1.00	52.35	B	O
ATOM	2460	CE2	TYR	B	24	-23.160	-16.085	22.277	1.00	50.76	B	C
ATOM	2461	CD2	TYR	B	24	-22.764	-16.903	21.235	1.00	50.70	B	C
ATOM	2462	C	TYR	B	24	-22.990	-19.902	17.600	1.00	50.42	B	C
ATOM	2463	O	TYR	B	24	-21.978	-20.595	17.725	1.00	50.73	B	O
ATOM	2464	N	GLN	B	25	-23.547	-19.640	16.425	1.00	49.79	B	N
ATOM	2465	CA	GLN	B	25	-23.089	-20.217	15.193	1.00	51.16	B	C
ATOM	2466	CB	GLN	B	25	-24.083	-21.380	14.804	1.00	52.14	B	C
ATOM	2467	CG	GLN	B	25	-25.550	-20.946	14.773	1.00	51.47	B	C
ATOM	2468	CD	GLN	B	25	-26.509	-22.069	14.400	1.00	49.02	B	C
ATOM	2469	OE1	GLN	B	25	-26.386	-23.186	14.879	1.00	43.29	B	O
ATOM	2470	NE2	GLN	B	25	-27.483	-21.759	13.549	1.00	49.61	B	N
ATOM	2471	C	GLN	B	25	-22.919	-19.219	14.064	1.00	52.10	B	C
ATOM	2472	O	GLN	B	25	-23.666	-18.240	14.038	1.00	54.65	B	O
ATOM	2473	N	LEU	B	26	-21.940	-19.406	13.158	1.00	49.06	B	N
ATOM	2474	CA	LEU	B	26	-21.703	-18.464	12.035	1.00	45.19	B	C
ATOM	2475	CB	LEU	B	26	-20.376	-18.751	11.315	1.00	46.15	B	C
ATOM	2476	CG	LEU	B	26	-19.037	-18.374	11.951	1.00	45.52	B	C
ATOM	2477	CD1	LEU	B	26	-17.937	-18.472	10.912	1.00	46.14	B	C
ATOM	2478	CD2	LEU	B	26	-19.057	-16.972	12.511	1.00	44.30	B	C
ATOM	2479	C	LEU	B	26	-22.827	-18.489	11.006	1.00	44.22	B	C
ATOM	2480	O	LEU	B	26	-22.671	-19.012	9.903	1.00	45.46	B	O
ATOM	2481	N	LYS	B	27	-23.955	-17.902	11.377	1.00	44.24	B	N
ATOM	2482	CA	LYS	B	27	-25.140	-17.854	10.539	1.00	44.91	B	C
ATOM	2483	CB	LYS	B	27	-26.279	-18.702	11.154	1.00	47.98	B	C
ATOM	2484	CG	LYS	B	27	-26.908	-19.739	10.222	1.00	50.64	B	C
ATOM	2485	CD	LYS	B	27	-28.321	-20.163	10.639	1.00	51.72	B	C
ATOM	2486	CE	LYS	B	27	-28.667	-21.578	10.160	1.00	50.07	B	C
ATOM	2487	NZ	LYS	B	27	-30.130	-21.767	9.974	1.00	48.98	B	N
ATOM	2488	C	LYS	B	27	-25.533	-16.389	10.501	1.00	43.09	B	C
ATOM	2489	O	LYS	B	27	-25.380	-15.676	11.500	1.00	42.47	B	O
ATOM	2490	N	ASP	B	28	-26.028	-15.939	9.357	1.00	40.93	B	N
ATOM	2491	CA	ASP	B	28	-26.461	-14.555	9.190	1.00	40.17	B	C
ATOM	2492	CB	ASP	B	28	-25.400	-13.747	8.407	1.00	40.04	B	C
ATOM	2493	CG	ASP	B	28	-25.757	-12.248	8.223	1.00	39.03	B	C
ATOM	2494	OD1	ASP	B	28	-26.943	-11.879	7.999	1.00	39.21	B	O
ATOM	2495	OD2	ASP	B	28	-24.807	-11.438	8.258	1.00	34.92	B	O
ATOM	2496	C	ASP	B	28	-27.793	-14.620	8.472	1.00	39.30	B	C
ATOM	2497	O	ASP	B	28	-27.863	-14.812	7.260	1.00	37.02	B	O
ATOM	2498	N	THR	B	29	-28.863	-14.460	9.234	1.00	41.34	B	N
ATOM	2499	CA	THR	B	29	-30.206	-14.595	8.673	1.00	42.38	B	C
ATOM	2500	CB	THR	B	29	-31.217	-15.019	9.771	1.00	42.14	B	C
ATOM	2501	OG1	THR	B	29	-31.801	-13.865	10.404	1.00	41.11	B	O
ATOM	2502	CG2	THR	B	29	-30.511	-15.907	10.837	1.00	41.47	B	C
ATOM	2503	C	THR	B	29	-30.610	-13.293	7.942	1.00	42.90	B	C
ATOM	2504	O	THR	B	29	-31.536	-13.303	7.113	1.00	41.57	B	O
ATOM	2505	N	THR	B	30	-29.862	-12.208	8.209	1.00	42.18	B	N
ATOM	2506	CA	THR	B	30	-30.243	-10.849	7.803	1.00	42.26	B	C
ATOM	2507	CB	THR	B	30	-29.460	-9.772	8.569	1.00	41.59	B	C
ATOM	2508	OG1	THR	B	30	-28.125	-9.732	8.078	1.00	44.54	B	O
ATOM	2509	CG2	THR	B	30	-29.427	-10.041	10.071	1.00	41.22	B	C
ATOM	2510	C	THR	B	30	-30.012	-10.576	6.324	1.00	43.07	B	C
ATOM	2511	O	THR	B	30	-30.569	-9.628	5.790	1.00	43.49	B	O
ATOM	2512	N	ARG	B	31	-29.170	-11.381	5.676	1.00	43.41	B	N
ATOM	2513	CA	ARG	B	31	-28.950	-11.270	4.234	1.00	42.73	B	C
ATOM	2514	CB	ARG	B	31	-27.457	-11.104	3.947	1.00	41.54	B	C
ATOM	2515	CG	ARG	B	31	-26.880	-9.779	4.412	1.00	40.12	B	C

ATOM	2516	CD	ARG	B	31	-25.358	-9.694	4.271	1.00	40.81	B	C
ATOM	2517	NE	ARG	B	31	-24.850	-8.404	4.746	1.00	39.64	B	N
ATOM	2518	CZ	ARG	B	31	-24.620	-8.104	6.025	1.00	37.51	B	C
ATOM	2519	NH1	ARG	B	31	-24.818	-9.001	6.977	1.00	40.18	B	N
ATOM	2520	NH2	ARG	B	31	-24.184	-6.906	6.361	1.00	34.41	B	N
ATOM	2521	C	ARG	B	31	-29.492	-12.510	3.521	1.00	42.99	B	C
ATOM	2522	O	ARG	B	31	-29.076	-13.639	3.813	1.00	41.18	B	O
ATOM	2523	N	GLY	B	32	-30.421	-12.288	2.595	1.00	44.05	B	N
ATOM	2524	CA	GLY	B	32	-31.026	-13.364	1.795	1.00	47.95	B	C
ATOM	2525	C	GLY	B	32	-31.677	-14.463	2.618	1.00	49.75	B	C
ATOM	2526	O	GLY	B	32	-32.181	-14.216	3.717	1.00	52.02	B	O
ATOM	2527	N	GLN	B	33	-31.633	-15.689	2.101	1.00	49.78	B	N
ATOM	2528	CA	GLN	B	33	-32.066	-16.860	2.865	1.00	48.09	B	C
ATOM	2529	CB	GLN	B	33	-32.511	-17.987	1.926	1.00	49.40	B	C
ATOM	2530	CG	GLN	B	33	-33.652	-17.599	0.979	1.00	51.77	B	C
ATOM	2531	CD	GLN	B	33	-33.573	-18.279	-0.391	1.00	52.73	B	C
ATOM	2532	OE1	GLN	B	33	-33.197	-19.442	-0.508	1.00	50.83	B	O
ATOM	2533	NE2	GLN	B	33	-33.944	-17.546	-1.436	1.00	56.68	B	N
ATOM	2534	C	GLN	B	33	-30.966	-17.360	3.803	1.00	45.74	B	C
ATOM	2535	O	GLN	B	33	-31.055	-18.473	4.292	1.00	48.18	B	O
ATOM	2536	N	GLY	B	34	-29.933	-16.551	4.048	1.00	44.06	B	N
ATOM	2537	CA	GLY	B	34	-28.862	-16.901	4.998	1.00	40.43	B	C
ATOM	2538	C	GLY	B	34	-27.446	-16.828	4.428	1.00	37.82	B	C
ATOM	2539	O	GLY	B	34	-27.265	-16.890	3.210	1.00	35.60	B	O
ATOM	2540	N	ILE	B	35	-26.453	-16.679	5.320	1.00	34.43	B	N
ATOM	2541	CA	ILE	B	35	-25.030	-16.796	4.984	1.00	33.25	B	C
ATOM	2542	CB	ILE	B	35	-24.312	-15.420	4.930	1.00	37.23	B	C
ATOM	2543	CG1	ILE	B	35	-24.686	-14.664	3.653	1.00	38.63	B	C
ATOM	2544	CD1	ILE	B	35	-24.189	-13.226	3.623	1.00	39.64	B	C
ATOM	2545	CG2	ILE	B	35	-22.779	-15.561	4.974	1.00	37.29	B	C
ATOM	2546	C	ILE	B	35	-24.372	-17.650	6.052	1.00	31.28	B	C
ATOM	2547	O	ILE	B	35	-24.379	-17.291	7.239	1.00	29.76	B	O
ATOM	2548	N	VAL	B	36	-23.779	-18.768	5.629	1.00	30.21	B	N
ATOM	2549	CA	VAL	B	36	-23.278	-19.763	6.577	1.00	29.18	B	C
ATOM	2550	CB	VAL	B	36	-24.183	-21.024	6.652	1.00	29.87	B	C
ATOM	2551	CG1	VAL	B	36	-24.401	-21.390	8.107	1.00	31.50	B	C
ATOM	2552	CG2	VAL	B	36	-25.537	-20.825	5.979	1.00	29.38	B	C
ATOM	2553	C	VAL	B	36	-21.869	-20.237	6.267	1.00	27.11	B	C
ATOM	2554	O	VAL	B	36	-21.508	-20.504	5.123	1.00	26.29	B	O
ATOM	2555	N	THR	B	37	-21.101	-20.409	7.319	1.00	26.36	B	N
ATOM	2556	CA	THR	B	37	-19.716	-20.767	7.182	1.00	27.97	B	C
ATOM	2557	CB	THR	B	37	-18.851	-19.545	7.550	1.00	29.05	B	C
ATOM	2558	OG1	THR	B	37	-19.158	-18.474	6.637	1.00	30.25	B	O
ATOM	2559	CG2	THR	B	37	-17.335	-19.865	7.538	1.00	28.48	B	C
ATOM	2560	C	THR	B	37	-19.367	-22.015	8.026	1.00	28.89	B	C
ATOM	2561	O	THR	B	37	-19.527	-22.015	9.258	1.00	26.39	B	O
ATOM	2562	N	TYR	B	38	-18.894	-23.055	7.321	1.00	30.58	B	N
ATOM	2563	CA	TYR	B	38	-18.515	-24.352	7.890	1.00	33.15	B	C
ATOM	2564	CB	TYR	B	38	-19.122	-25.498	7.067	1.00	33.68	B	C
ATOM	2565	CG	TYR	B	38	-20.602	-25.408	6.810	1.00	34.72	B	C
ATOM	2566	CD1	TYR	B	38	-21.101	-24.645	5.751	1.00	33.58	B	C
ATOM	2567	CE1	TYR	B	38	-22.459	-24.560	5.503	1.00	33.35	B	C
ATOM	2568	CZ	TYR	B	38	-23.338	-25.250	6.307	1.00	33.94	B	C
ATOM	2569	OH	TYR	B	38	-24.675	-25.190	6.053	1.00	32.94	B	O
ATOM	2570	CE2	TYR	B	38	-22.875	-26.007	7.369	1.00	36.31	B	C
ATOM	2571	CD2	TYR	B	38	-21.509	-26.091	7.610	1.00	36.06	B	C
ATOM	2572	C	TYR	B	38	-17.006	-24.557	7.858	1.00	33.86	B	C
ATOM	2573	O	TYR	B	38	-16.284	-23.768	7.244	1.00	35.29	B	O
ATOM	2574	N	SER	B	39	-16.555	-25.648	8.483	1.00	32.45	B	N
ATOM	2575	CA	SER	B	39	-15.151	-26.094	8.447	1.00	31.81	B	C
ATOM	2576	CB	SER	B	39	-14.480	-25.943	9.826	1.00	30.22	B	C
ATOM	2577	OG	SER	B	39	-13.271	-26.688	9.939	1.00	28.69	B	O
ATOM	2578	C	SER	B	39	-15.130	-27.560	8.023	1.00	32.86	B	C
ATOM	2579	O	SER	B	39	-15.972	-28.338	8.481	1.00	32.92	B	O
ATOM	2580	N	ALA	B	40	-14.171	-27.940	7.169	1.00	31.62	B	N
ATOM	2581	CA	ALA	B	40	-14.112	-29.305	6.650	1.00	30.64	B	C
ATOM	2582	CB	ALA	B	40	-13.763	-29.298	5.174	1.00	29.75	B	C
ATOM	2583	C	ALA	B	40	-13.130	-30.173	7.436	1.00	31.48	B	C
ATOM	2584	O	ALA	B	40	-12.928	-31.349	7.097	1.00	29.96	B	O
ATOM	2585	N	GLY	B	41	-12.535	-29.603	8.487	1.00	31.27	B	N
ATOM	2586	CA	GLY	B	41	-11.567	-30.329	9.308	1.00	32.58	B	C
ATOM	2587	C	GLY	B	41	-10.464	-30.911	8.448	1.00	34.88	B	C
ATOM	2588	O	GLY	B	41	-10.005	-32.016	8.681	1.00	41.21	B	O
ATOM	2589	N	ASN	B	42	-10.055	-30.164	7.432	1.00	35.41	B	N
ATOM	2590	CA	ASN	B	42	-8.963	-30.556	6.542	1.00	35.57	B	C
ATOM	2591	CB	ASN	B	42	-7.626	-30.565	7.290	1.00	35.12	B	C
ATOM	2592	CG	ASN	B	42	-7.341	-29.234	7.988	1.00	35.46	B	C
ATOM	2593	OD1	ASN	B	42	-6.975	-29.225	9.143	1.00	37.01	B	O
ATOM	2594	ND2	ASN	B	42	-7.508	-28.109	7.281	1.00	35.13	B	N

ATOM	2595	C	ASN B	42	-9.235	-31.851	5.820	1.00	35.04	B	C
ATOM	2596	O	ASN B	42	-8.323	-32.620	5.567	1.00	31.81	B	O
ATOM	2597	N	ARG B	43	-10.501	-32.017	5.426	1.00	39.05	B	N
ATOM	2598	CA	ARG B	43	-11.015	-33.222	4.776	1.00	43.00	B	C
ATOM	2599	CB	ARG B	43	-11.892	-33.984	5.775	1.00	48.73	B	C
ATOM	2600	CG	ARG B	43	-11.097	-34.876	6.718	1.00	53.88	B	C
ATOM	2601	CD	ARG B	43	-10.656	-36.140	6.001	1.00	59.88	B	C
ATOM	2602	NE	ARG B	43	-10.497	-37.266	6.925	1.00	71.15	B	N
ATOM	2603	CZ	ARG B	43	-11.497	-37.925	7.523	1.00	72.97	B	C
ATOM	2604	NH1	ARG B	43	-12.772	-37.577	7.324	1.00	70.94	B	N
ATOM	2605	NH2	ARG B	43	-11.216	-38.937	8.346	1.00	74.66	B	N
ATOM	2606	C	ARG B	43	-11.806	-32.894	3.521	1.00	40.05	B	C
ATOM	2607	O	ARG B	43	-11.901	-31.731	3.132	1.00	42.57	B	O
ATOM	2608	N	SER B	44	-12.381	-33.915	2.894	1.00	38.32	B	N
ATOM	2609	CA	SER B	44	-12.999	-33.759	1.574	1.00	39.47	B	C
ATOM	2610	CB	SER B	44	-12.712	-34.982	0.695	1.00	40.23	B	C
ATOM	2611	OG	SER B	44	-11.445	-34.869	0.078	1.00	42.89	B	O
ATOM	2612	C	SER B	44	-14.501	-33.503	1.554	1.00	37.25	B	C
ATOM	2613	O	SER B	44	-15.006	-32.835	0.655	1.00	36.44	B	O
ATOM	2614	N	SER B	45	-15.244	-34.065	2.486	1.00	36.28	B	N
ATOM	2615	CA	SER B	45	-16.688	-34.005	2.324	1.00	36.90	B	C
ATOM	2616	CB	SER B	45	-17.413	-35.089	3.144	1.00	36.36	B	C
ATOM	2617	OG	SER B	45	-17.285	-34.843	4.525	1.00	36.97	B	O
ATOM	2618	C	SER B	45	-17.190	-32.595	2.645	1.00	36.54	B	C
ATOM	2619	O	SER B	45	-16.577	-31.857	3.420	1.00	33.48	B	O
ATOM	2620	N	LEU B	46	-18.304	-32.246	2.012	1.00	37.13	B	N
ATOM	2621	CA	LEU B	46	-18.929	-30.944	2.147	1.00	39.27	B	C
ATOM	2622	CB	LEU B	46	-18.853	-30.188	0.811	1.00	38.08	B	C
ATOM	2623	CG	LEU B	46	-17.468	-30.074	0.156	1.00	36.84	B	C
ATOM	2624	CD1	LEU B	46	-17.606	-29.703	-1.326	1.00	35.76	B	C
ATOM	2625	CD2	LEU B	46	-16.578	-29.092	0.925	1.00	35.95	B	C
ATOM	2626	C	LEU B	46	-20.399	-31.131	2.546	1.00	41.41	B	C
ATOM	2627	O	LEU B	46	-20.968	-32.200	2.316	1.00	44.36	B	O
ATOM	2628	N	PRO B	47	-21.020	-30.093	3.130	1.00	39.28	B	N
ATOM	2629	CA	PRO B	47	-20.411	-28.820	3.520	1.00	37.84	B	C
ATOM	2630	CB	PRO B	47	-21.611	-28.006	4.011	1.00	40.67	B	C
ATOM	2631	CG	PRO B	47	-22.644	-29.037	4.374	1.00	40.15	B	C
ATOM	2632	CD	PRO B	47	-22.479	-30.061	3.306	1.00	38.74	B	C
ATOM	2633	C	PRO B	47	-19.403	-28.941	4.649	1.00	35.08	B	C
ATOM	2634	O	PRO B	47	-18.610	-28.044	4.831	1.00	32.64	B	O
ATOM	2635	N	GLY B	48	-19.438	-30.045	5.390	1.00	33.92	B	N
ATOM	2636	CA	GLY B	48	-18.651	-30.180	6.603	1.00	32.39	B	C
ATOM	2637	C	GLY B	48	-19.466	-29.671	7.770	1.00	33.27	B	C
ATOM	2638	O	GLY B	48	-20.677	-29.476	7.644	1.00	33.45	B	O
ATOM	2639	N	THR B	49	-18.790	-29.432	8.892	1.00	34.94	B	N
ATOM	2640	CA	THR B	49	-19.414	-28.958	10.130	1.00	38.98	B	C
ATOM	2641	CB	THR B	49	-18.513	-29.273	11.339	1.00	39.73	B	C
ATOM	2642	OG1	THR B	49	-18.099	-30.641	11.273	1.00	40.95	B	O
ATOM	2643	CG2	THR B	49	-19.242	-29.015	12.663	1.00	39.97	B	C
ATOM	2644	C	THR B	49	-19.720	-27.444	10.184	1.00	42.89	B	C
ATOM	2645	O	THR B	49	-18.880	-26.602	9.868	1.00	40.45	B	O
ATOM	2646	N	LEU B	50	-20.933	-27.114	10.623	1.00	48.49	B	N
ATOM	2647	CA	LEU B	50	-21.292	-25.732	10.920	1.00	48.73	B	C
ATOM	2648	CB	LEU B	50	-22.795	-25.610	11.146	1.00	49.85	B	C
ATOM	2649	CG	LEU B	50	-23.368	-24.241	11.494	1.00	51.48	B	C
ATOM	2650	CD1	LEU B	50	-22.680	-23.122	10.722	1.00	52.59	B	C
ATOM	2651	CD2	LEU B	50	-24.875	-24.227	11.229	1.00	52.22	B	C
ATOM	2652	C	LEU B	50	-20.518	-25.298	12.157	1.00	47.59	B	C
ATOM	2653	O	LEU B	50	-20.480	-26.016	13.158	1.00	49.60	B	O
ATOM	2654	N	LEU B	51	-19.877	-24.138	12.057	1.00	46.71	B	N
ATOM	2655	CA	LEU B	51	-18.968	-23.635	13.080	1.00	43.84	B	C
ATOM	2656	CB	LEU B	51	-17.950	-22.670	12.451	1.00	45.70	B	C
ATOM	2657	CG	LEU B	51	-16.529	-23.222	12.293	1.00	46.99	B	C
ATOM	2658	CD1	LEU B	51	-15.996	-22.783	10.946	1.00	47.24	B	C
ATOM	2659	CD2	LEU B	51	-15.613	-22.792	13.454	1.00	46.81	B	C
ATOM	2660	C	LEU B	51	-19.690	-22.965	14.244	1.00	41.22	B	C
ATOM	2661	O	LEU B	51	-20.753	-22.352	14.083	1.00	37.73	B	O
ATOM	2662	N	THR B	52	-19.043	-23.038	15.403	1.00	40.19	B	N
ATOM	2663	CA	THR B	52	-19.694	-22.874	16.699	1.00	38.68	B	C
ATOM	2664	CB	THR B	52	-20.030	-24.303	17.224	1.00	37.51	B	C
ATOM	2665	OG1	THR B	52	-21.182	-24.776	16.532	1.00	34.76	B	O
ATOM	2666	CG2	THR B	52	-20.290	-24.379	18.732	1.00	37.73	B	C
ATOM	2667	C	THR B	52	-18.788	-22.103	17.672	1.00	37.74	B	C
ATOM	2668	O	THR B	52	-17.577	-22.245	17.639	1.00	39.97	B	O
ATOM	2669	N	SER B	53	-19.371	-21.279	18.529	1.00	39.22	B	N
ATOM	2670	CA	SER B	53	-18.636	-20.722	19.673	1.00	41.33	B	C
ATOM	2671	CB	SER B	53	-17.766	-19.518	19.263	1.00	40.16	B	C
ATOM	2672	OG	SER B	53	-17.139	-18.905	20.382	1.00	37.49	B	O
ATOM	2673	C	SER B	53	-19.643	-20.307	20.739	1.00	45.00	B	C

ATOM	2674	O	SER B	53	-20.589	-19.556	20.450	1.00	46.25	B	O
ATOM	2675	N	SER B	54	-19.461	-20.823	21.955	1.00	46.91	B	N
ATOM	2676	CA	SER B	54	-20.263	-20.398	23.104	1.00	47.89	B	C
ATOM	2677	CB	SER B	54	-20.046	-21.350	24.292	1.00	47.12	B	C
ATOM	2678	OG	SER B	54	-18.666	-21.531	24.586	1.00	46.27	B	O
ATOM	2679	C	SER B	54	-19.953	-18.928	23.478	1.00	48.96	B	C
ATOM	2680	O	SER B	54	-20.833	-18.202	23.926	1.00	49.21	B	O
ATOM	2681	N	SER B	55	-18.718	-18.493	23.219	1.00	47.87	B	N
ATOM	2682	CA	SER B	55	-18.222	-17.161	23.587	1.00	44.68	B	C
ATOM	2683	CB	SER B	55	-16.685	-17.209	23.560	1.00	44.59	B	C
ATOM	2684	OG	SER B	55	-16.106	-16.112	24.240	1.00	44.52	B	O
ATOM	2685	C	SER B	55	-18.707	-15.986	22.695	1.00	44.27	B	C
ATOM	2686	O	SER B	55	-18.553	-14.809	23.068	1.00	44.09	B	O
ATOM	2687	N	ASN B	56	-19.279	-16.300	21.526	1.00	42.16	B	N
ATOM	2688	CA	ASN B	56	-19.411	-15.344	20.385	1.00	38.46	B	C
ATOM	2689	CB	ASN B	56	-20.558	-14.340	20.601	1.00	35.65	B	C
ATOM	2690	CG	ASN B	56	-21.226	-13.902	19.290	1.00	34.01	B	C
ATOM	2691	OD1	ASN B	56	-21.996	-12.952	19.283	1.00	36.17	B	O
ATOM	2692	ND2	ASN B	56	-20.947	-14.590	18.194	1.00	30.20	B	N
ATOM	2693	C	ASN B	56	-18.101	-14.601	19.985	1.00	38.13	B	C
ATOM	2694	O	ASN B	56	-18.137	-13.659	19.202	1.00	35.54	B	O
ATOM	2695	N	ILE B	57	-16.967	-15.032	20.536	1.00	38.44	B	N
ATOM	2696	CA	ILE B	57	-15.654	-14.668	20.039	1.00	42.11	B	C
ATOM	2697	CB	ILE B	57	-14.683	-14.350	21.189	1.00	42.20	B	C
ATOM	2698	CG1	ILE B	57	-15.350	-13.491	22.273	1.00	44.11	B	C
ATOM	2699	CD1	ILE B	57	-15.809	-12.115	21.839	1.00	44.60	B	C
ATOM	2700	CG2	ILE B	57	-13.437	-13.665	20.654	1.00	41.76	B	C
ATOM	2701	C	ILE B	57	-15.113	-15.873	19.234	1.00	46.06	B	C
ATOM	2702	O	ILE B	57	-15.270	-17.026	19.669	1.00	50.20	B	O
ATOM	2703	N	TRP B	58	-14.475	-15.607	18.085	1.00	43.11	B	N
ATOM	2704	CA	TRP B	58	-14.066	-16.648	17.136	1.00	40.89	B	C
ATOM	2705	CB	TRP B	58	-14.801	-16.457	15.834	1.00	40.59	B	C
ATOM	2706	CG	TRP B	58	-16.245	-16.402	16.008	1.00	40.53	B	C
ATOM	2707	CD1	TRP B	58	-16.962	-15.345	16.414	1.00	40.30	B	C
ATOM	2708	NE1	TRP B	58	-18.288	-15.660	16.467	1.00	40.67	B	N
ATOM	2709	CE2	TRP B	58	-18.449	-16.960	16.090	1.00	41.82	B	C
ATOM	2710	CD2	TRP B	58	-17.168	-17.463	15.793	1.00	43.03	B	C
ATOM	2711	CE3	TRP B	58	-17.038	-18.798	15.378	1.00	44.52	B	C
ATOM	2712	CZ3	TRP B	58	-18.194	-19.573	15.257	1.00	46.89	B	C
ATOM	2713	CH2	TRP B	58	-19.466	-19.033	15.563	1.00	46.00	B	C
ATOM	2714	CZ2	TRP B	58	-19.608	-17.734	15.987	1.00	43.73	B	C
ATOM	2715	C	TRP B	58	-12.583	-16.598	16.838	1.00	43.33	B	C
ATOM	2716	O	TRP B	58	-12.073	-15.572	16.390	1.00	41.28	B	O
ATOM	2717	N	ASN B	59	-11.893	-17.720	17.041	1.00	46.24	B	N
ATOM	2718	CA	ASN B	59	-10.441	-17.752	16.912	1.00	45.70	B	C
ATOM	2719	CB	ASN B	59	-9.830	-18.319	18.178	1.00	49.90	B	C
ATOM	2720	CG	ASN B	59	-9.910	-17.334	19.326	1.00	57.71	B	C
ATOM	2721	OD1	ASN B	59	-9.071	-16.430	19.449	1.00	61.14	B	O
ATOM	2722	ND2	ASN B	59	-10.934	-17.481	20.165	1.00	62.09	B	N
ATOM	2723	C	ASN B	59	-9.972	-18.509	15.696	1.00	42.04	B	C
ATOM	2724	O	ASN B	59	-8.950	-19.169	15.726	1.00	45.30	B	O
ATOM	2725	N	ASP B	60	-10.707	-18.369	14.609	1.00	37.51	B	N
ATOM	2726	CA	ASP B	60	-10.363	-19.023	13.371	1.00	36.63	B	C
ATOM	2727	CB	ASP B	60	-11.337	-20.170	13.119	1.00	37.97	B	C
ATOM	2728	CG	ASP B	60	-11.017	-20.941	11.861	1.00	36.97	B	C
ATOM	2729	OD1	ASP B	60	-9.899	-20.784	11.310	1.00	35.18	B	O
ATOM	2730	OD2	ASP B	60	-11.902	-21.710	11.429	1.00	37.14	B	O
ATOM	2731	C	ASP B	60	-10.381	-18.016	12.211	1.00	35.22	B	C
ATOM	2732	O	ASP B	60	-11.461	-17.568	11.745	1.00	33.57	B	O
ATOM	2733	N	GLY B	61	-9.172	-17.694	11.746	1.00	31.50	B	N
ATOM	2734	CA	GLY B	61	-8.947	-16.600	10.815	1.00	29.00	B	C
ATOM	2735	C	GLY B	61	-9.628	-16.829	9.495	1.00	28.50	B	C
ATOM	2736	O	GLY B	61	-10.389	-15.978	9.025	1.00	29.45	B	O
ATOM	2737	N	ALA B	62	-9.380	-17.980	8.886	1.00	27.01	B	N
ATOM	2738	CA	ALA B	62	-9.980	-18.248	7.581	1.00	26.15	B	C
ATOM	2739	CB	ALA B	62	-9.484	-19.558	7.008	1.00	27.22	B	C
ATOM	2740	C	ALA B	62	-11.494	-18.232	7.642	1.00	25.10	B	C
ATOM	2741	O	ALA B	62	-12.121	-17.707	6.755	1.00	25.58	B	O
ATOM	2742	N	ALA B	63	-12.090	-18.777	8.695	1.00	25.77	B	N
ATOM	2743	CA	ALA B	63	-13.560	-18.757	8.810	1.00	27.21	B	C
ATOM	2744	CB	ALA B	63	-14.029	-19.602	9.998	1.00	27.02	B	C
ATOM	2745	C	ALA B	63	-14.118	-17.325	8.934	1.00	27.71	B	C
ATOM	2746	O	ALA B	63	-15.165	-17.007	8.343	1.00	27.87	B	O
ATOM	2747	N	VAL B	64	-13.417	-16.488	9.712	1.00	26.10	B	N
ATOM	2748	CA	VAL B	64	-13.806	-15.112	9.932	1.00	24.19	B	C
ATOM	2749	CB	VAL B	64	-12.831	-14.437	10.882	1.00	24.11	B	C
ATOM	2750	CG1	VAL B	64	-13.003	-12.926	10.833	1.00	24.36	B	C
ATOM	2751	CG2	VAL B	64	-13.047	-14.965	12.292	1.00	24.69	B	C
ATOM	2752	C	VAL B	64	-13.819	-14.352	8.619	1.00	24.48	B	C

ATOM	2753	O	VAL	B	64	-14.837	-13.747	8.233	1.00	23.08	B	O
ATOM	2754	N	ASP	B	65	-12.687	-14.386	7.924	1.00	24.36	B	N
ATOM	2755	CA	ASP	B	65	-12.597	-13.691	6.657	1.00	24.27	B	C
ATOM	2756	CB	ASP	B	65	-11.194	-13.785	6.053	1.00	24.29	B	C
ATOM	2757	CG	ASP	B	65	-10.179	-12.899	6.778	1.00	24.48	B	C
ATOM	2758	OD1	ASP	B	65	-10.541	-11.803	7.209	1.00	23.48	B	O
ATOM	2759	OD2	ASP	B	65	-9.004	-13.284	6.922	1.00	25.28	B	O
ATOM	2760	C	ASP	B	65	-13.650	-14.266	5.731	1.00	24.81	B	C
ATOM	2761	O	ASP	B	65	-14.431	-13.507	5.130	1.00	24.32	B	O
ATOM	2762	N	ALA	B	66	-13.720	-15.597	5.660	1.00	24.42	B	N
ATOM	2763	CA	ALA	B	66	-14.745	-16.245	4.827	1.00	26.00	B	C
ATOM	2764	CB	ALA	B	66	-14.748	-17.751	5.038	1.00	26.76	B	C
ATOM	2765	C	ALA	B	66	-16.143	-15.693	5.096	1.00	25.63	B	C
ATOM	2766	O	ALA	B	66	-16.880	-15.319	4.181	1.00	22.75	B	O
ATOM	2767	N	HIS	B	67	-16.480	-15.650	6.375	1.00	27.71	B	N
ATOM	2768	CA	HIS	B	67	-17.789	-15.198	6.817	1.00	30.45	B	C
ATOM	2769	CB	HIS	B	67	-17.945	-15.490	8.305	1.00	32.99	B	C
ATOM	2770	CG	HIS	B	67	-19.353	-15.419	8.779	1.00	34.84	B	C
ATOM	2771	ND1	HIS	B	67	-20.373	-16.117	8.170	1.00	36.52	B	N
ATOM	2772	CE1	HIS	B	67	-21.509	-15.850	8.785	1.00	37.20	B	C
ATOM	2773	NE2	HIS	B	67	-21.257	-15.016	9.778	1.00	36.99	B	N
ATOM	2774	CD2	HIS	B	67	-19.916	-14.729	9.794	1.00	34.94	B	C
ATOM	2775	C	HIS	B	67	-18.026	-13.710	6.536	1.00	29.77	B	C
ATOM	2776	O	HIS	B	67	-18.971	-13.350	5.823	1.00	28.30	B	O
ATOM	2777	N	ALA	B	68	-17.159	-12.853	7.076	1.00	29.76	B	N
ATOM	2778	CA	ALA	B	68	-17.281	-11.398	6.850	1.00	30.76	B	C
ATOM	2779	CB	ALA	B	68	-16.138	-10.632	7.523	1.00	30.67	B	C
ATOM	2780	C	ALA	B	68	-17.320	-11.067	5.362	1.00	29.91	B	C
ATOM	2781	O	ALA	B	68	-18.336	-10.605	4.842	1.00	29.77	B	O
ATOM	2782	N	TYR	B	69	-16.217	-11.347	4.676	1.00	27.97	B	N
ATOM	2783	CA	TYR	B	69	-16.103	-10.975	3.281	1.00	26.15	B	C
ATOM	2784	CB	TYR	B	69	-14.755	-11.400	2.656	1.00	25.06	B	C
ATOM	2785	CG	TYR	B	69	-13.523	-10.767	3.264	1.00	23.20	B	C
ATOM	2786	CD1	TYR	B	69	-13.542	-9.468	3.784	1.00	22.72	B	C
ATOM	2787	CE1	TYR	B	69	-12.406	-8.906	4.356	1.00	21.86	B	C
ATOM	2788	CZ	TYR	B	69	-11.242	-9.635	4.396	1.00	21.61	B	C
ATOM	2789	OH	TYR	B	69	-10.096	-9.115	4.939	1.00	20.56	B	O
ATOM	2790	CE2	TYR	B	69	-11.214	-10.921	3.894	1.00	21.81	B	C
ATOM	2791	CD2	TYR	B	69	-12.343	-11.472	3.329	1.00	22.03	B	C
ATOM	2792	C	TYR	B	69	-17.240	-11.529	2.460	1.00	25.31	B	C
ATOM	2793	O	TYR	B	69	-17.527	-11.003	1.400	1.00	25.46	B	O
ATOM	2794	N	THR	B	70	-17.899	-12.582	2.916	1.00	27.08	B	N
ATOM	2795	CA	THR	B	70	-19.056	-13.065	2.145	1.00	28.79	B	C
ATOM	2796	CB	THR	B	70	-19.421	-14.549	2.426	1.00	29.13	B	C
ATOM	2797	OG1	THR	B	70	-18.350	-15.412	2.011	1.00	28.17	B	O
ATOM	2798	CG2	THR	B	70	-20.666	-14.947	1.640	1.00	30.19	B	C
ATOM	2799	C	THR	B	70	-20.236	-12.077	2.332	1.00	28.56	B	C
ATOM	2800	O	THR	B	70	-20.896	-11.713	1.345	1.00	26.58	B	O
ATOM	2801	N	ALA	B	71	-20.457	-11.607	3.569	1.00	28.13	B	N
ATOM	2802	CA	ALA	B	71	-21.405	-10.506	3.805	1.00	27.78	B	C
ATOM	2803	CB	ALA	B	71	-21.412	-10.101	5.261	1.00	26.69	B	C
ATOM	2804	C	ALA	B	71	-21.075	-9.293	2.922	1.00	28.42	B	C
ATOM	2805	O	ALA	B	71	-21.969	-8.680	2.317	1.00	27.67	B	O
ATOM	2806	N	LYS	B	72	-19.789	-8.964	2.840	1.00	29.66	B	N
ATOM	2807	CA	LYS	B	72	-19.346	-7.772	2.133	1.00	31.07	B	C
ATOM	2808	CB	LYS	B	72	-17.842	-7.590	2.277	1.00	32.79	B	C
ATOM	2809	CG	LYS	B	72	-17.258	-6.408	1.512	1.00	35.11	B	C
ATOM	2810	CD	LYS	B	72	-15.747	-6.289	1.716	1.00	36.65	B	C
ATOM	2811	CE	LYS	B	72	-15.242	-4.933	1.257	1.00	38.51	B	C
ATOM	2812	NZ	LYS	B	72	-13.761	-4.866	1.344	1.00	40.21	B	N
ATOM	2813	C	LYS	B	72	-19.717	-7.872	0.677	1.00	32.30	B	C
ATOM	2814	O	LYS	B	72	-20.162	-6.889	0.079	1.00	35.50	B	O
ATOM	2815	N	VAL	B	73	-19.546	-9.066	0.112	1.00	32.14	B	N
ATOM	2816	CA	VAL	B	73	-19.814	-9.304	-1.320	1.00	30.81	B	C
ATOM	2817	CB	VAL	B	73	-19.131	-10.611	-1.824	1.00	29.58	B	C
ATOM	2818	CG1	VAL	B	73	-19.415	-10.861	-3.297	1.00	27.79	B	C
ATOM	2819	CG2	VAL	B	73	-17.620	-10.558	-1.574	1.00	30.18	B	C
ATOM	2820	C	VAL	B	73	-21.312	-9.362	-1.576	1.00	30.15	B	C
ATOM	2821	O	VAL	B	73	-21.756	-9.011	-2.646	1.00	28.69	B	O
ATOM	2822	N	TYR	B	74	-22.075	-9.825	-0.587	1.00	32.57	B	N
ATOM	2823	CA	TYR	B	74	-23.525	-9.800	-0.654	1.00	34.78	B	C
ATOM	2824	CB	TYR	B	74	-24.141	-10.527	0.543	1.00	38.44	B	C
ATOM	2825	CG	TYR	B	74	-25.653	-10.515	0.518	1.00	42.42	B	C
ATOM	2826	CD1	TYR	B	74	-26.367	-9.478	1.108	1.00	45.08	B	C
ATOM	2827	CE1	TYR	B	74	-27.747	-9.452	1.072	1.00	46.85	B	C
ATOM	2828	CZ	TYR	B	74	-28.423	-10.461	0.432	1.00	46.58	B	C
ATOM	2829	OH	TYR	B	74	-29.792	-10.430	0.400	1.00	48.77	B	O
ATOM	2830	CE2	TYR	B	74	-27.740	-11.498	-0.165	1.00	44.52	B	C
ATOM	2831	CD2	TYR	B	74	-26.363	-11.521	-0.118	1.00	42.52	B	C

ATOM	2832	C	TYR	B	74	-23.990	-8.348	-0.685	1.00	34.57	B	C
ATOM	2833	O	TYR	B	74	-24.756	-7.962	-1.585	1.00	34.24	B	O
ATOM	2834	N	ASP	B	75	-23.517	-7.558	0.289	1.00	32.83	B	N
ATOM	2835	CA	ASP	B	75	-23.765	-6.110	0.313	1.00	32.00	B	C
ATOM	2836	CB	ASP	B	75	-22.966	-5.400	1.423	1.00	30.80	B	C
ATOM	2837	CG	ASP	B	75	-23.468	-5.736	2.823	1.00	29.68	B	C
ATOM	2838	OD1	ASP	B	75	-24.558	-6.343	2.956	1.00	26.51	B	O
ATOM	2839	OD2	ASP	B	75	-22.742	-5.406	3.791	1.00	27.80	B	O
ATOM	2840	C	ASP	B	75	-23.456	-5.451	-1.030	1.00	32.02	B	C
ATOM	2841	O	ASP	B	75	-24.321	-4.795	-1.602	1.00	34.17	B	O
ATOM	2842	N	TYR	B	76	-22.241	-5.632	-1.540	1.00	31.51	B	N
ATOM	2843	CA	TYR	B	76	-21.849	-5.008	-2.805	1.00	30.68	B	C
ATOM	2844	CB	TYR	B	76	-20.422	-5.408	-3.183	1.00	31.50	B	C
ATOM	2845	CG	TYR	B	76	-19.954	-4.945	-4.549	1.00	32.80	B	C
ATOM	2846	CD1	TYR	B	76	-20.312	-5.644	-5.677	1.00	33.28	B	C
ATOM	2847	CE1	TYR	B	76	-19.893	-5.247	-6.928	1.00	33.91	B	C
ATOM	2848	CZ	TYR	B	76	-19.094	-4.147	-7.077	1.00	34.08	B	C
ATOM	2849	OH	TYR	B	76	-18.735	-3.832	-8.366	1.00	36.34	B	O
ATOM	2850	CE2	TYR	B	76	-18.696	-3.416	-5.974	1.00	33.35	B	C
ATOM	2851	CD2	TYR	B	76	-19.119	-3.825	-4.710	1.00	34.22	B	C
ATOM	2852	C	TYR	B	76	-22.847	-5.352	-3.904	1.00	31.30	B	C
ATOM	2853	O	TYR	B	76	-23.356	-4.456	-4.550	1.00	33.09	B	O
ATOM	2854	N	TYR	B	77	-23.154	-6.633	-4.100	1.00	31.67	B	N
ATOM	2855	CA	TYR	B	77	-24.106	-7.030	-5.143	1.00	33.09	B	C
ATOM	2856	CB	TYR	B	77	-24.288	-8.571	-5.236	1.00	34.51	B	C
ATOM	2857	CG	TYR	B	77	-23.373	-9.296	-6.237	1.00	32.63	B	C
ATOM	2858	CD1	TYR	B	77	-22.119	-9.767	-5.856	1.00	32.93	B	C
ATOM	2859	CE1	TYR	B	77	-21.279	-10.412	-6.756	1.00	32.14	B	C
ATOM	2860	CZ	TYR	B	77	-21.695	-10.624	-8.049	1.00	32.06	B	C
ATOM	2861	OH	TYR	B	77	-20.861	-11.295	-8.923	1.00	32.13	B	O
ATOM	2862	CE2	TYR	B	77	-22.936	-10.168	-8.450	1.00	31.38	B	C
ATOM	2863	CD2	TYR	B	77	-23.766	-9.512	-7.544	1.00	31.01	B	C
ATOM	2864	C	TYR	B	77	-25.460	-6.358	-4.924	1.00	33.60	B	C
ATOM	2865	O	TYR	B	77	-26.025	-5.791	-5.864	1.00	31.95	B	O
ATOM	2866	N	LYS	B	78	-25.968	-6.428	-3.693	1.00	35.21	B	N
ATOM	2867	CA	LYS	B	78	-27.226	-5.743	-3.305	1.00	38.16	B	C
ATOM	2868	CB	LYS	B	78	-27.499	-5.943	-1.798	1.00	41.05	B	C
ATOM	2869	CG	LYS	B	78	-28.442	-4.930	-1.143	1.00	44.48	B	C
ATOM	2870	CD	LYS	B	78	-29.548	-5.574	-0.305	1.00	46.27	B	C
ATOM	2871	CE	LYS	B	78	-30.629	-6.155	-1.224	1.00	49.31	B	C
ATOM	2872	NZ	LYS	B	78	-31.826	-6.666	-0.496	1.00	50.68	B	N
ATOM	2873	C	LYS	B	78	-27.214	-4.242	-3.666	1.00	38.50	B	C
ATOM	2874	O	LYS	B	78	-28.116	-3.739	-4.348	1.00	37.83	B	O
ATOM	2875	N	ASN	B	79	-26.163	-3.552	-3.237	1.00	36.81	B	N
ATOM	2876	CA	ASN	B	79	-26.072	-2.119	-3.390	1.00	35.01	B	C
ATOM	2877	CB	ASN	B	79	-25.037	-1.568	-2.428	1.00	34.32	B	C
ATOM	2878	CG	ASN	B	79	-25.446	-1.750	-0.968	1.00	34.68	B	C
ATOM	2879	OD1	ASN	B	79	-26.640	-1.847	-0.631	1.00	31.67	B	O
ATOM	2880	ND2	ASN	B	79	-24.451	-1.805	-0.090	1.00	35.09	B	N
ATOM	2881	C	ASN	B	79	-25.783	-1.659	-4.800	1.00	36.29	B	C
ATOM	2882	O	ASN	B	79	-26.446	-0.757	-5.290	1.00	36.69	B	O
ATOM	2883	N	LYS	B	80	-24.821	-2.271	-5.472	1.00	39.00	B	N
ATOM	2884	CA	LYS	B	80	-24.394	-1.768	-6.782	1.00	41.10	B	C
ATOM	2885	CB	LYS	B	80	-22.927	-2.094	-7.036	1.00	45.28	B	C
ATOM	2886	CG	LYS	B	80	-21.982	-1.547	-5.982	1.00	51.45	B	C
ATOM	2887	CD	LYS	B	80	-21.444	-0.164	-6.329	1.00	56.78	B	C
ATOM	2888	CE	LYS	B	80	-20.650	0.395	-5.153	1.00	60.79	B	C
ATOM	2889	NZ	LYS	B	80	-21.524	0.661	-3.966	1.00	62.58	B	N
ATOM	2890	C	LYS	B	80	-25.202	-2.277	-7.965	1.00	41.13	B	C
ATOM	2891	O	LYS	B	80	-25.033	-1.754	-9.072	1.00	40.54	B	O
ATOM	2892	N	PHE	B	81	-26.046	-3.296	-7.764	1.00	40.60	B	N
ATOM	2893	CA	PHE	B	81	-26.746	-3.941	-8.892	1.00	40.39	B	C
ATOM	2894	CB	PHE	B	81	-26.047	-5.257	-9.274	1.00	42.38	B	C
ATOM	2895	CG	PHE	B	81	-24.628	-5.111	-9.754	1.00	43.89	B	C
ATOM	2896	CD1	PHE	B	81	-24.300	-4.227	-10.770	1.00	45.90	B	C
ATOM	2897	CE1	PHE	B	81	-22.990	-4.112	-11.214	1.00	47.25	B	C
ATOM	2898	CZ	PHE	B	81	-22.000	-4.911	-10.664	1.00	47.90	B	C
ATOM	2899	CE2	PHE	B	81	-22.319	-5.821	-9.672	1.00	46.56	B	C
ATOM	2900	CD2	PHE	B	81	-23.626	-5.921	-9.226	1.00	45.90	B	C
ATOM	2901	C	PHE	B	81	-28.217	-4.290	-8.659	1.00	40.16	B	C
ATOM	2902	O	PHE	B	81	-28.880	-4.759	-9.574	1.00	39.11	B	O
ATOM	2903	N	GLY	B	82	-28.720	-4.127	-7.443	1.00	40.78	B	N
ATOM	2904	CA	GLY	B	82	-30.054	-4.617	-7.106	1.00	42.16	B	C
ATOM	2905	C	GLY	B	82	-30.193	-6.135	-7.065	1.00	44.48	B	C
ATOM	2906	O	GLY	B	82	-31.308	-6.662	-7.002	1.00	46.91	B	O
ATOM	2907	N	ARG	B	83	-29.071	-6.853	-7.065	1.00	44.64	B	N
ATOM	2908	CA	ARG	B	83	-29.108	-8.311	-7.112	1.00	42.54	B	C
ATOM	2909	CB	ARG	B	83	-27.970	-8.851	-7.980	1.00	43.50	B	C
ATOM	2910	CG	ARG	B	83	-27.861	-10.374	-7.915	1.00	44.21	B	C

ATOM	2911	CD	ARG	B	83	-26.887	-10.972	-8.920	1.00	42.64	B	C
ATOM	2912	NE	ARG	B	83	-27.330	-12.309	-9.284	1.00	41.71	B	N
ATOM	2913	CZ	ARG	B	83	-28.056	-12.605	-10.359	1.00	41.59	B	C
ATOM	2914	NH1	ARG	B	83	-28.397	-11.672	-11.239	1.00	38.71	B	N
ATOM	2915	NH2	ARG	B	83	-28.427	-13.862	-10.570	1.00	44.02	B	N
ATOM	2916	C	ARG	B	83	-29.078	-8.955	-5.722	1.00	39.03	B	C
ATOM	2917	O	ARG	B	83	-28.308	-8.560	-4.851	1.00	36.63	B	O
ATOM	2918	N	ASN	B	84	-29.910	-9.979	-5.559	1.00	37.19	B	N
ATOM	2919	CA	ASN	B	84	-30.100	-10.669	-4.277	1.00	35.57	B	C
ATOM	2920	CB	ASN	B	84	-31.602	-10.752	-3.969	1.00	32.60	B	C
ATOM	2921	CG	ASN	B	84	-31.912	-11.200	-2.559	1.00	30.63	B	C
ATOM	2922	OD1	ASN	B	84	-33.073	-11.419	-2.241	1.00	30.00	B	O
ATOM	2923	ND2	ASN	B	84	-30.903	-11.321	-1.709	1.00	29.72	B	N
ATOM	2924	C	ASN	B	84	-29.493	-12.069	-4.355	1.00	35.30	B	C
ATOM	2925	O	ASN	B	84	-30.018	-12.925	-5.050	1.00	35.02	B	O
ATOM	2926	N	SER	B	85	-28.379	-12.275	-3.648	1.00	37.34	B	N
ATOM	2927	CA	SER	B	85	-27.523	-13.490	-3.757	1.00	37.67	B	C
ATOM	2928	CB	SER	B	85	-28.072	-14.642	-2.910	1.00	37.87	B	C
ATOM	2929	OG	SER	B	85	-27.019	-15.470	-2.452	1.00	36.06	B	O
ATOM	2930	C	SER	B	85	-27.271	-13.918	-5.209	1.00	36.47	B	C
ATOM	2931	O	SER	B	85	-27.404	-13.093	-6.117	1.00	38.17	B	O
ATOM	2932	N	ILE	B	86	-26.911	-15.177	-5.445	1.00	35.78	B	N
ATOM	2933	CA	ILE	B	86	-26.422	-15.556	-6.788	1.00	38.90	B	C
ATOM	2934	CB	ILE	B	86	-25.482	-16.789	-6.767	1.00	40.34	B	C
ATOM	2935	CG1	ILE	B	86	-26.280	-18.073	-6.741	1.00	43.61	B	C
ATOM	2936	CD1	ILE	B	86	-25.397	-19.286	-6.631	1.00	47.20	B	C
ATOM	2937	CG2	ILE	B	86	-24.540	-16.770	-5.564	1.00	40.32	B	C
ATOM	2938	C	ILE	B	86	-27.543	-15.744	-7.829	1.00	38.42	B	C
ATOM	2939	O	ILE	B	86	-27.374	-15.397	-8.994	1.00	36.18	B	O
ATOM	2940	N	ASP	B	87	-28.672	-16.290	-7.387	1.00	41.14	B	N
ATOM	2941	CA	ASP	B	87	-29.843	-16.563	-8.233	1.00	41.69	B	C
ATOM	2942	CB	ASP	B	87	-30.586	-17.806	-7.714	1.00	41.60	B	C
ATOM	2943	CG	ASP	B	87	-31.249	-17.572	-6.344	1.00	41.11	B	C
ATOM	2944	OD1	ASP	B	87	-30.790	-16.683	-5.603	1.00	38.26	B	O
ATOM	2945	OD2	ASP	B	87	-32.205	-18.286	-5.983	1.00	40.33	B	O
ATOM	2946	C	ASP	B	87	-30.862	-15.420	-8.293	1.00	43.82	B	C
ATOM	2947	O	ASP	B	87	-31.952	-15.624	-8.833	1.00	45.59	B	O
ATOM	2948	N	GLY	B	88	-30.554	-14.254	-7.714	1.00	42.79	B	N
ATOM	2949	CA	GLY	B	88	-31.467	-13.107	-7.774	1.00	42.83	B	C
ATOM	2950	C	GLY	B	88	-32.580	-13.102	-6.734	1.00	43.95	B	C
ATOM	2951	O	GLY	B	88	-33.034	-12.041	-6.334	1.00	41.75	B	O
ATOM	2952	N	ASN	B	89	-33.061	-14.284	-6.346	1.00	49.48	B	N
ATOM	2953	CA	ASN	B	89	-33.806	-14.473	-5.085	1.00	52.34	B	C
ATOM	2954	CB	ASN	B	89	-34.804	-15.628	-5.189	1.00	56.66	B	C
ATOM	2955	CG	ASN	B	89	-35.843	-15.406	-6.287	1.00	62.28	B	C
ATOM	2956	OD1	ASN	B	89	-35.693	-14.522	-7.145	1.00	63.04	B	O
ATOM	2957	ND2	ASN	B	89	-36.909	-16.202	-6.259	1.00	63.74	B	N
ATOM	2958	C	ASN	B	89	-32.735	-14.793	-4.086	1.00	49.08	B	C
ATOM	2959	O	ASN	B	89	-31.630	-15.116	-4.486	1.00	57.39	B	O
ATOM	2960	N	GLY	B	90	-33.003	-14.724	-2.798	1.00	44.73	B	N
ATOM	2961	CA	GLY	B	90	-31.880	-14.648	-1.838	1.00	42.09	B	C
ATOM	2962	C	GLY	B	90	-31.136	-15.934	-1.533	1.00	40.51	B	C
ATOM	2963	O	GLY	B	90	-30.983	-16.274	-0.367	1.00	38.47	B	O
ATOM	2964	N	PHE	B	91	-30.654	-16.623	-2.577	1.00	40.34	B	N
ATOM	2965	CA	PHE	B	91	-30.044	-17.961	-2.471	1.00	41.32	B	C
ATOM	2966	CB	PHE	B	91	-29.339	-18.344	-3.801	1.00	45.43	B	C
ATOM	2967	CG	PHE	B	91	-28.680	-19.715	-3.800	1.00	49.29	B	C
ATOM	2968	CD1	PHE	B	91	-29.447	-20.880	-3.899	1.00	48.89	B	C
ATOM	2969	CE1	PHE	B	91	-28.837	-22.121	-3.886	1.00	50.44	B	C
ATOM	2970	CZ	PHE	B	91	-27.450	-22.219	-3.792	1.00	49.76	B	C
ATOM	2971	CE2	PHE	B	91	-26.679	-21.081	-3.708	1.00	47.44	B	C
ATOM	2972	CD2	PHE	B	91	-27.288	-19.837	-3.719	1.00	49.23	B	C
ATOM	2973	C	PHE	B	91	-29.071	-18.048	-1.308	1.00	38.84	B	C
ATOM	2974	O	PHE	B	91	-28.177	-17.219	-1.185	1.00	41.42	B	O
ATOM	2975	N	GLN	B	92	-29.259	-19.038	-0.440	1.00	38.23	B	N
ATOM	2976	CA	GLN	B	92	-28.398	-19.195	0.738	1.00	37.91	B	C
ATOM	2977	CB	GLN	B	92	-28.943	-20.290	1.660	1.00	38.21	B	C
ATOM	2978	CG	GLN	B	92	-28.030	-20.632	2.834	1.00	41.26	B	C
ATOM	2979	CD	GLN	B	92	-28.635	-21.661	3.787	1.00	41.52	B	C
ATOM	2980	OE1	GLN	B	92	-29.230	-22.645	3.356	1.00	44.14	B	O
ATOM	2981	NE2	GLN	B	92	-28.453	-21.451	5.079	1.00	40.35	B	N
ATOM	2982	C	GLN	B	92	-26.930	-19.456	0.322	1.00	36.58	B	C
ATOM	2983	O	GLN	B	92	-26.652	-20.169	-0.649	1.00	38.61	B	O
ATOM	2984	N	LEU	B	93	-26.003	-18.857	1.055	1.00	35.02	B	N
ATOM	2985	CA	LEU	B	93	-24.599	-18.840	0.670	1.00	35.33	B	C
ATOM	2986	CB	LEU	B	93	-24.106	-17.398	0.619	1.00	35.64	B	C
ATOM	2987	CG	LEU	B	93	-24.765	-16.482	-0.435	1.00	36.84	B	C
ATOM	2988	CD1	LEU	B	93	-24.304	-15.036	-0.267	1.00	36.03	B	C
ATOM	2989	CD2	LEU	B	93	-24.506	-16.983	-1.859	1.00	37.70	B	C

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ATOM   2990  C    LEU B  93     -23.745 -19.658   1.632  1.00 36.40      B   C
ATOM   2991  O    LEU B  93     -23.507 -19.249   2.770  1.00 36.65      B   O
ATOM   2992  N    LYS B  94     -23.292 -20.820   1.173  1.00 37.02      B   N
ATOM   2993  CA   LYS B  94     -22.555 -21.738   2.041  1.00 40.31      B   C
ATOM   2994  CB   LYS B  94     -23.009 -23.211   1.813  1.00 43.72      B   C
ATOM   2995  CG   LYS B  94     -24.379 -23.603   2.386  1.00 44.25      B   C
ATOM   2996  CD   LYS B  94     -25.058 -24.748   1.617  1.00 46.62      B   C
ATOM   2997  CE   LYS B  94     -26.527 -24.981   2.021  1.00 46.67      B   C
ATOM   2998  NZ   LYS B  94     -26.707 -25.189   3.493  1.00 44.46      B   N
ATOM   2999  C    LYS B  94     -21.059 -21.562   1.748  1.00 38.21      B   C
ATOM   3000  O    LYS B  94     -20.677 -21.435   0.599  1.00 36.56      B   O
ATOM   3001  N    SER B  95     -20.226 -21.552   2.784  1.00 35.66      B   N
ATOM   3002  CA   SER B  95     -18.801 -21.364   2.615  1.00 35.30      B   C
ATOM   3003  CB   SER B  95     -18.393 -19.953   3.037  1.00 37.34      B   C
ATOM   3004  OG   SER B  95     -19.004 -18.966   2.224  1.00 40.01      B   O
ATOM   3005  C    SER B  95     -18.084 -22.335   3.508  1.00 35.67      B   C
ATOM   3006  O    SER B  95     -18.331 -22.355   4.712  1.00 35.97      B   O
ATOM   3007  N    THR B  96     -17.186 -23.139   2.952  1.00 34.75      B   N
ATOM   3008  CA   THR B  96     -16.447 -24.087   3.788  1.00 34.33      B   C
ATOM   3009  CB   THR B  96     -16.594 -25.545   3.289  1.00 33.88      B   C
ATOM   3010  OG1  THR B  96     -17.978 -25.859   3.076  1.00 34.75      B   O
ATOM   3011  CG2  THR B  96     -16.021 -26.523   4.291  1.00 33.52      B   C
ATOM   3012  C    THR B  96     -14.983 -23.703   3.791  1.00 33.72      B   C
ATOM   3013  O    THR B  96     -14.398 -23.508   2.729  1.00 33.99      B   O
ATOM   3014  N    VAL B  97     -14.397 -23.586   4.978  1.00 33.07      B   N
ATOM   3015  CA   VAL B  97     -12.952 -23.374   5.093  1.00 34.16      B   C
ATOM   3016  CB   VAL B  97     -12.592 -22.282   6.128  1.00 34.28      B   C
ATOM   3017  CG1  VAL B  97     -13.159 -20.957   5.683  1.00 35.98      B   C
ATOM   3018  CG2  VAL B  97     -13.100 -22.619   7.515  1.00 35.36      B   C
ATOM   3019  C    VAL B  97     -12.224 -24.672   5.432  1.00 34.05      B   C
ATOM   3020  O    VAL B  97     -12.849 -25.727   5.565  1.00 34.39      B   O
ATOM   3021  N    HIS B  98     -10.898 -24.575   5.543  1.00 33.56      B   N
ATOM   3022  CA   HIS B  98     -10.042 -25.695   5.882  1.00 32.14      B   C
ATOM   3023  CB   HIS B  98     -10.257 -26.060   7.328  1.00 33.55      B   C
ATOM   3024  CG   HIS B  98     -10.063 -24.924   8.258  1.00 34.25      B   C
ATOM   3025  ND1  HIS B  98      -8.841 -24.315   8.436  1.00 35.12      B   N
ATOM   3026  CE1  HIS B  98      -8.961 -23.356   9.332  1.00 36.99      B   C
ATOM   3027  NE2  HIS B  98     -10.220 -23.320   9.733  1.00 37.68      B   N
ATOM   3028  CD2  HIS B  98     -10.927 -24.299   9.084  1.00 34.92      B   C
ATOM   3029  C    HIS B  98     -10.337 -26.911   5.043  1.00 31.42      B   C
ATOM   3030  O    HIS B  98     -10.422 -28.024   5.578  1.00 30.39      B   O
ATOM   3031  N    TYR B  99     -10.524 -26.701   3.738  1.00 29.84      B   N
ATOM   3032  CA   TYR B  99     -10.814 -27.799   2.820  1.00 28.03      B   C
ATOM   3033  CB   TYR B  99     -11.373 -27.284   1.524  1.00 27.78      B   C
ATOM   3034  CG   TYR B  99     -11.713 -28.379   0.558  1.00 28.82      B   C
ATOM   3035  CD1  TYR B  99     -12.884 -29.113   0.710  1.00 30.01      B   C
ATOM   3036  CE1  TYR B  99     -13.234 -30.098  -0.193  1.00 29.32      B   C
ATOM   3037  CZ   TYR B  99     -12.406 -30.367  -1.259  1.00 28.91      B   C
ATOM   3038  OH   TYR B  99     -12.778 -31.345  -2.132  1.00 27.23      B   O
ATOM   3039  CE2  TYR B  99     -11.227 -29.664  -1.436  1.00 28.87      B   C
ATOM   3040  CD2  TYR B  99     -10.888 -28.671  -0.526  1.00 29.25      B   C
ATOM   3041  C    TYR B  99      -9.568 -28.584   2.503  1.00 26.15      B   C
ATOM   3042  O    TYR B  99      -8.635 -28.055   1.878  1.00 24.18      B   O
ATOM   3043  N    SER B 100      -9.576 -29.839   2.942  1.00 24.97      B   N
ATOM   3044  CA   SER B 100      -8.515 -30.805   2.656  1.00 25.57      B   C
ATOM   3045  CB   SER B 100      -8.519 -31.186   1.174  1.00 23.87      B   C
ATOM   3046  OG   SER B 100      -7.308 -31.791   0.828  1.00 22.41      B   O
ATOM   3047  C    SER B 100      -7.140 -30.320   3.143  1.00 26.93      B   C
ATOM   3048  O    SER B 100      -7.067 -29.280   3.782  1.00 28.15      B   O
ATOM   3049  N    SER B 101      -6.074 -31.083   2.875  1.00 27.99      B   N
ATOM   3050  CA   SER B 101      -4.750 -30.814   3.463  1.00 28.45      B   C
ATOM   3051  CB   SER B 101      -4.040 -32.123   3.845  1.00 28.72      B   C
ATOM   3052  OG   SER B 101      -2.682 -32.138   3.419  1.00 29.51      B   O
ATOM   3053  C    SER B 101      -3.884 -29.984   2.519  1.00 29.04      B   C
ATOM   3054  O    SER B 101      -3.783 -30.299   1.331  1.00 27.72      B   O
ATOM   3055  N    ARG B 102      -3.289 -28.919   3.069  1.00 30.50      B   N
ATOM   3056  CA   ARG B 102      -2.401 -27.999   2.354  1.00 30.50      B   C
ATOM   3057  CB   ARG B 102      -0.949 -28.479   2.461  1.00 33.61      B   C
ATOM   3058  CG   ARG B 102      -0.281 -28.133   3.800  1.00 37.70      B   C
ATOM   3059  CD   ARG B 102       1.209 -28.482   3.815  1.00 40.99      B   C
ATOM   3060  NE   ARG B 102       1.410 -29.932   3.662  1.00 45.77      B   N
ATOM   3061  CZ   ARG B 102       2.389 -30.528   2.961  1.00 47.99      B   C
ATOM   3062  NH1  ARG B 102       3.304 -29.804   2.311  1.00 50.01      B   N
ATOM   3063  NH2  ARG B 102       2.460 -31.870   2.914  1.00 44.90      B   N
ATOM   3064  C    ARG B 102      -2.840 -27.800   0.900  1.00 28.31      B   C
ATOM   3065  O    ARG B 102      -2.069 -27.986  -0.020  1.00 27.45      B   O
ATOM   3066  N    TYR B 103      -4.098 -27.396   0.740  1.00 26.02      B   N
ATOM   3067  CA   TYR B 103      -4.787 -27.284  -0.548  1.00 23.64      B   C
ATOM   3068  CB   TYR B 103      -6.247 -27.678  -0.330  1.00 23.86      B   C
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ATOM	3069	CG	TYR	B	103	-7.039	-27.730	-1.575	1.00	24.13	B	C
ATOM	3070	CD1	TYR	B	103	-6.841	-28.754	-2.479	1.00	25.33	B	C
ATOM	3071	CE1	TYR	B	103	-7.554	-28.825	-3.652	1.00	25.32	B	C
ATOM	3072	CZ	TYR	B	103	-8.476	-27.862	-3.928	1.00	26.06	B	C
ATOM	3073	OH	TYR	B	103	-9.167	-27.961	-5.104	1.00	27.97	B	O
ATOM	3074	CE2	TYR	B	103	-8.707	-26.819	-3.041	1.00	24.94	B	C
ATOM	3075	CD2	TYR	B	103	-7.979	-26.763	-1.869	1.00	24.27	B	C
ATOM	3076	C	TYR	B	103	-4.718	-25.851	-1.153	1.00	21.60	B	C
ATOM	3077	O	TYR	B	103	-5.217	-24.885	-0.546	1.00	19.52	B	O
ATOM	3078	N	ASN	B	104	-4.110	-25.743	-2.349	1.00	19.76	B	N
ATOM	3079	CA	ASN	B	104	-3.842	-24.452	-3.015	1.00	18.78	B	C
ATOM	3080	CB	ASN	B	104	-2.521	-24.503	-3.810	1.00	18.63	B	C
ATOM	3081	CG	ASN	B	104	-1.267	-24.521	-2.930	1.00	18.22	B	C
ATOM	3082	OD1	ASN	B	104	-1.220	-23.993	-1.815	1.00	18.11	B	O
ATOM	3083	ND2	ASN	B	104	-0.230	-25.118	-3.461	1.00	17.67	B	N
ATOM	3084	C	ASN	B	104	-4.969	-23.980	-3.962	1.00	17.89	B	C
ATOM	3085	O	ASN	B	104	-4.729	-23.661	-5.119	1.00	16.38	B	O
ATOM	3086	N	ASN	B	105	-6.195	-23.906	-3.463	1.00	17.58	B	N
ATOM	3087	CA	ASN	B	105	-7.247	-23.368	-4.261	1.00	18.17	B	C
ATOM	3088	CB	ASN	B	105	-7.549	-24.310	-5.395	1.00	17.95	B	C
ATOM	3089	CG	ASN	B	105	-7.575	-23.611	-6.739	1.00	18.43	B	C
ATOM	3090	OD1	ASN	B	105	-7.983	-22.445	-6.890	1.00	18.76	B	O
ATOM	3091	ND2	ASN	B	105	-7.147	-24.340	-7.740	1.00	19.03	B	N
ATOM	3092	C	ASN	B	105	-8.558	-23.035	-3.544	1.00	20.12	B	C
ATOM	3093	O	ASN	B	105	-8.807	-23.426	-2.391	1.00	22.03	B	O
ATOM	3094	N	ALA	B	106	-9.386	-22.274	-4.247	1.00	19.79	B	N
ATOM	3095	CA	ALA	B	106	-10.718	-22.010	-3.819	1.00	19.99	B	C
ATOM	3096	CB	ALA	B	106	-10.897	-20.520	-3.551	1.00	20.22	B	C
ATOM	3097	C	ALA	B	106	-11.540	-22.440	-4.990	1.00	20.21	B	C
ATOM	3098	O	ALA	B	106	-11.021	-22.459	-6.098	1.00	19.79	B	O
ATOM	3099	N	PHE	B	107	-12.813	-22.758	-4.768	1.00	21.28	B	N
ATOM	3100	CA	PHE	B	107	-13.684	-23.129	-5.883	1.00	22.81	B	C
ATOM	3101	CB	PHE	B	107	-13.343	-24.553	-6.408	1.00	24.23	B	C
ATOM	3102	CG	PHE	B	107	-13.461	-25.660	-5.365	1.00	25.42	B	C
ATOM	3103	CD1	PHE	B	107	-12.387	-25.980	-4.532	1.00	26.00	B	C
ATOM	3104	CE1	PHE	B	107	-12.496	-26.993	-3.590	1.00	26.52	B	C
ATOM	3105	CZ	PHE	B	107	-13.686	-27.714	-3.479	1.00	26.55	B	C
ATOM	3106	CE2	PHE	B	107	-14.754	-27.427	-4.310	1.00	25.62	B	C
ATOM	3107	CD2	PHE	B	107	-14.640	-26.408	-5.247	1.00	25.85	B	C
ATOM	3108	C	PHE	B	107	-15.174	-23.011	-5.576	1.00	22.11	B	C
ATOM	3109	O	PHE	B	107	-15.581	-22.879	-4.422	1.00	21.96	B	O
ATOM	3110	N	TRP	B	108	-15.962	-23.035	-6.644	1.00	21.93	B	N
ATOM	3111	CA	TRP	B	108	-17.418	-23.093	-6.576	1.00	22.59	B	C
ATOM	3112	CB	TRP	B	108	-18.045	-21.893	-7.330	1.00	21.95	B	C
ATOM	3113	CG	TRP	B	108	-19.427	-22.087	-7.888	1.00	20.54	B	C
ATOM	3114	CD1	TRP	B	108	-19.743	-22.448	-9.159	1.00	20.50	B	C
ATOM	3115	NE1	TRP	B	108	-21.102	-22.522	-9.318	1.00	20.10	B	N
ATOM	3116	CE2	TRP	B	108	-21.701	-22.176	-8.143	1.00	20.03	B	C
ATOM	3117	CD2	TRP	B	108	-20.666	-21.888	-7.213	1.00	20.47	B	C
ATOM	3118	CE3	TRP	B	108	-21.012	-21.496	-5.918	1.00	20.91	B	C
ATOM	3119	CZ3	TRP	B	108	-22.392	-21.423	-5.591	1.00	21.48	B	C
ATOM	3120	CH2	TRP	B	108	-23.393	-21.729	-6.552	1.00	20.23	B	C
ATOM	3121	CZ2	TRP	B	108	-23.064	-22.094	-7.824	1.00	19.90	B	C
ATOM	3122	C	TRP	B	108	-17.813	-24.400	-7.210	1.00	24.22	B	C
ATOM	3123	O	TRP	B	108	-17.449	-24.649	-8.357	1.00	24.63	B	O
ATOM	3124	N	ASN	B	109	-18.555	-25.233	-6.479	1.00	26.95	B	N
ATOM	3125	CA	ASN	B	109	-18.965	-26.547	-6.990	1.00	27.50	B	C
ATOM	3126	CB	ASN	B	109	-18.725	-27.619	-5.921	1.00	27.76	B	C
ATOM	3127	CG	ASN	B	109	-19.755	-27.595	-4.793	1.00	28.70	B	C
ATOM	3128	OD1	ASN	B	109	-20.754	-26.849	-4.814	1.00	27.27	B	O
ATOM	3129	ND2	ASN	B	109	-19.510	-28.443	-3.785	1.00	29.61	B	N
ATOM	3130	C	ASN	B	109	-20.405	-26.611	-7.505	1.00	28.31	B	C
ATOM	3131	O	ASN	B	109	-21.001	-27.658	-7.523	1.00	28.32	B	O
ATOM	3132	N	GLY	B	110	-20.971	-25.490	-7.919	1.00	31.03	B	N
ATOM	3133	CA	GLY	B	110	-22.345	-25.465	-8.439	1.00	32.29	B	C
ATOM	3134	C	GLY	B	110	-23.355	-25.216	-7.333	1.00	33.16	B	C
ATOM	3135	O	GLY	B	110	-24.504	-24.822	-7.595	1.00	33.81	B	O
ATOM	3136	N	VAL	B	111	-22.913	-25.405	-6.095	1.00	33.45	B	N
ATOM	3137	CA	VAL	B	111	-23.799	-25.336	-4.942	1.00	35.17	B	C
ATOM	3138	CB	VAL	B	111	-24.201	-26.785	-4.535	1.00	34.30	B	C
ATOM	3139	CG1	VAL	B	111	-23.952	-27.096	-3.048	1.00	33.42	B	C
ATOM	3140	CG2	VAL	B	111	-25.649	-27.041	-4.959	1.00	34.43	B	C
ATOM	3141	C	VAL	B	111	-23.244	-24.503	-3.758	1.00	36.29	B	C
ATOM	3142	O	VAL	B	111	-24.018	-23.960	-2.969	1.00	37.98	B	O
ATOM	3143	N	GLN	B	112	-21.923	-24.398	-3.625	1.00	35.91	B	N
ATOM	3144	CA	GLN	B	112	-21.327	-23.587	-2.558	1.00	35.06	B	C
ATOM	3145	CB	GLN	B	112	-21.404	-24.355	-1.234	1.00	35.50	B	C
ATOM	3146	CG	GLN	B	112	-20.563	-25.625	-1.199	1.00	34.97	B	C
ATOM	3147	CD	GLN	B	112	-20.178	-26.032	0.207	1.00	33.92	B	C

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ATOM   3148  OE1 GLN B 112     -20.655 -27.036   0.715  1.00 34.45      B    O
ATOM   3149  NE2 GLN B 112     -19.318 -25.250   0.843  1.00 33.47      B    N
ATOM   3150  C   GLN B 112     -19.861 -23.172  -2.833  1.00 33.71      B    C
ATOM   3151  O   GLN B 112     -19.261 -23.555  -3.847  1.00 34.36      B    O
ATOM   3152  N   MET B 113     -19.295 -22.404  -1.907  1.00 30.68      B    N
ATOM   3153  CA  MET B 113     -17.933 -21.911  -2.017  1.00 28.51      B    C
ATOM   3154  CB  MET B 113     -17.849 -20.424  -1.641  1.00 29.34      B    C
ATOM   3155  CG  MET B 113     -18.299 -19.432  -2.709  1.00 29.87      B    C
ATOM   3156  SD  MET B 113     -20.078 -19.409  -2.981  1.00 29.78      B    S
ATOM   3157  CE  MET B 113     -20.613 -18.711  -1.419  1.00 30.48      B    C
ATOM   3158  C   MET B 113     -17.070 -22.692  -1.060  1.00 27.82      B    C
ATOM   3159  O   MET B 113     -17.493 -23.039   0.062  1.00 26.31      B    O
ATOM   3160  N   VAL B 114     -15.833 -22.914  -1.497  1.00 27.54      B    N
ATOM   3161  CA  VAL B 114     -14.882 -23.775  -0.794  1.00 26.67      B    C
ATOM   3162  CB  VAL B 114     -14.799 -25.172  -1.472  1.00 27.48      B    C
ATOM   3163  CG1 VAL B 114     -13.869 -26.096  -0.697  1.00 27.84      B    C
ATOM   3164  CG2 VAL B 114     -16.183 -25.792  -1.594  1.00 27.90      B    C
ATOM   3165  C   VAL B 114     -13.510 -23.112  -0.845  1.00 23.88      B    C
ATOM   3166  O   VAL B 114     -13.093 -22.652  -1.913  1.00 22.42      B    O
ATOM   3167  N   TYR B 115     -12.822 -23.087   0.291  1.00 21.58      B    N
ATOM   3168  CA  TYR B 115     -11.557 -22.383   0.411  1.00 21.93      B    C
ATOM   3169  CB  TYR B 115     -11.718 -21.092   1.229  1.00 21.40      B    C
ATOM   3170  CG  TYR B 115     -12.731 -20.164   0.665  1.00 21.37      B    C
ATOM   3171  CD1 TYR B 115     -12.421 -19.308  -0.358  1.00 21.96      B    C
ATOM   3172  CE1 TYR B 115     -13.389 -18.468  -0.910  1.00 22.81      B    C
ATOM   3173  CZ  TYR B 115     -14.677 -18.480  -0.422  1.00 22.74      B    C
ATOM   3174  OH  TYR B 115     -15.665 -17.644  -0.940  1.00 22.96      B    O
ATOM   3175  CE2 TYR B 115     -14.992 -19.339   0.605  1.00 22.43      B    C
ATOM   3176  CD2 TYR B 115     -14.028 -20.175   1.130  1.00 22.02      B    C
ATOM   3177  C   TYR B 115     -10.500 -23.244   1.092  1.00 22.23      B    C
ATOM   3178  O   TYR B 115     -10.611 -23.520   2.287  1.00 21.55      B    O
ATOM   3179  N   GLY B 116      -9.458 -23.609   0.341  1.00 21.40      B    N
ATOM   3180  CA  GLY B 116      -8.302 -24.273   0.901  1.00 21.51      B    C
ATOM   3181  C   GLY B 116      -7.513 -23.366   1.821  1.00 21.86      B    C
ATOM   3182  O   GLY B 116      -7.773 -22.181   1.900  1.00 22.60      B    O
ATOM   3183  N   ASP B 117      -6.549 -23.936   2.523  1.00 22.59      B    N
ATOM   3184  CA  ASP B 117      -5.689 -23.176   3.412  1.00 23.66      B    C
ATOM   3185  CB  ASP B 117      -5.446 -23.933   4.723  1.00 24.06      B    C
ATOM   3186  CG  ASP B 117      -6.583 -23.800   5.710  1.00 24.67      B    C
ATOM   3187  OD1 ASP B 117      -7.346 -22.803   5.728  1.00 25.59      B    O
ATOM   3188  OD2 ASP B 117      -6.695 -24.723   6.502  1.00 25.80      B    O
ATOM   3189  C   ASP B 117      -4.346 -22.926   2.766  1.00 23.69      B    C
ATOM   3190  O   ASP B 117      -3.480 -22.273   3.347  1.00 23.57      B    O
ATOM   3191  N   GLY B 118      -4.152 -23.465   1.575  1.00 24.06      B    N
ATOM   3192  CA  GLY B 118      -2.868 -23.321   0.912  1.00 24.13      B    C
ATOM   3193  C   GLY B 118      -1.737 -24.045   1.622  1.00 22.97      B    C
ATOM   3194  O   GLY B 118      -1.779 -24.292   2.834  1.00 22.31      B    O
ATOM   3195  N   ASP B 119      -0.709 -24.364   0.847  1.00 22.43      B    N
ATOM   3196  CA  ASP B 119       0.478 -25.039   1.368  1.00 21.83      B    C
ATOM   3197  CB  ASP B 119       1.323 -25.608   0.197  1.00 20.08      B    C
ATOM   3198  CG  ASP B 119       2.036 -24.543  -0.596  1.00 19.22      B    C
ATOM   3199  OD1 ASP B 119       2.324 -23.446  -0.078  1.00 19.73      B    O
ATOM   3200  OD2 ASP B 119       2.347 -24.810  -1.752  1.00 17.52      B    O
ATOM   3201  C   ASP B 119       1.321 -24.187   2.353  1.00 21.78      B    C
ATOM   3202  O   ASP B 119       2.321 -24.651   2.875  1.00 21.12      B    O
ATOM   3203  N   GLY B 120       0.916 -22.943   2.587  1.00 23.30      B    N
ATOM   3204  CA  GLY B 120       1.636 -22.047   3.486  1.00 23.87      B    C
ATOM   3205  C   GLY B 120       2.932 -21.462   2.957  1.00 24.49      B    C
ATOM   3206  O   GLY B 120       3.629 -20.779   3.676  1.00 24.47      B    O
ATOM   3207  N   VAL B 121       3.284 -21.718   1.711  1.00 26.95      B    N
ATOM   3208  CA  VAL B 121       4.523 -21.143   1.163  1.00 29.85      B    C
ATOM   3209  CB  VAL B 121       5.613 -22.221   0.856  1.00 29.49      B    C
ATOM   3210  CG1 VAL B 121       6.777 -21.618   0.072  1.00 28.64      B    C
ATOM   3211  CG2 VAL B 121       6.142 -22.843   2.140  1.00 28.93      B    C
ATOM   3212  C   VAL B 121       4.211 -20.346  -0.094  1.00 31.76      B    C
ATOM   3213  O   VAL B 121       4.770 -19.262  -0.314  1.00 36.09      B    O
ATOM   3214  N   THR B 122       3.333 -20.892  -0.924  1.00 30.83      B    N
ATOM   3215  CA  THR B 122       2.924 -20.223  -2.139  1.00 29.94      B    C
ATOM   3216  CB  THR B 122       2.957 -21.220  -3.312  1.00 32.47      B    C
ATOM   3217  OG1 THR B 122       2.621 -22.519  -2.826  1.00 33.51      B    O
ATOM   3218  CG2 THR B 122       4.399 -21.336  -3.879  1.00 35.40      B    C
ATOM   3219  C   THR B 122       1.562 -19.555  -1.934  1.00 26.62      B    C
ATOM   3220  O   THR B 122       1.221 -18.626  -2.642  1.00 26.32      B    O
ATOM   3221  N   PHE B 123       0.790 -20.010  -0.955  1.00 23.60      B    N
ATOM   3222  CA  PHE B 123      -0.483 -19.367  -0.627  1.00 21.85      B    C
ATOM   3223  CB  PHE B 123      -1.700 -20.064  -1.261  1.00 21.42      B    C
ATOM   3224  CG  PHE B 123      -1.758 -19.968  -2.752  1.00 20.41      B    C
ATOM   3225  CD2 PHE B 123      -2.454 -18.948  -3.362  1.00 20.18      B    C
ATOM   3226  CE2 PHE B 123      -2.516 -18.853  -4.741  1.00 20.20      B    C
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ATOM	3227	CZ	PHE	B	123	-1.865	-19.781	-5.527	1.00	20.04	B	C
ATOM	3228	CE1	PHE	B	123	-1.156	-20.809	-4.928	1.00	20.65	B	C
ATOM	3229	CD1	PHE	B	123	-1.120	-20.906	-3.544	1.00	20.63	B	C
ATOM	3230	C	PHE	B	123	-0.669	-19.445	0.854	1.00	21.39	B	C
ATOM	3231	O	PHE	B	123	-0.128	-20.345	1.499	1.00	23.40	B	O
ATOM	3232	N	ILE	B	124	-1.434	-18.499	1.383	1.00	20.17	B	N
ATOM	3233	CA	ILE	B	124	-1.961	-18.572	2.736	1.00	18.39	B	C
ATOM	3234	CB	ILE	B	124	-1.640	-17.310	3.541	1.00	17.54	B	C
ATOM	3235	CG1	ILE	B	124	-2.396	-16.082	3.033	1.00	16.90	B	C
ATOM	3236	CD1	ILE	B	124	-2.386	-14.964	4.038	1.00	16.17	B	C
ATOM	3237	CG2	ILE	B	124	-0.147	-17.048	3.498	1.00	17.65	B	C
ATOM	3238	C	ILE	B	124	-3.444	-18.826	2.549	1.00	18.58	B	C
ATOM	3239	O	ILE	B	124	-3.891	-18.998	1.407	1.00	18.36	B	O
ATOM	3240	N	PRO	B	125	-4.203	-18.918	3.649	1.00	18.87	B	N
ATOM	3241	CA	PRO	B	125	-5.577	-19.377	3.443	1.00	19.02	B	C
ATOM	3242	CB	PRO	B	125	-6.169	-19.403	4.854	1.00	19.23	B	C
ATOM	3243	CG	PRO	B	125	-4.980	-19.587	5.754	1.00	19.46	B	C
ATOM	3244	CD	PRO	B	125	-3.825	-18.905	5.077	1.00	19.29	B	C
ATOM	3245	C	PRO	B	125	-6.356	-18.467	2.510	1.00	19.07	B	C
ATOM	3246	O	PRO	B	125	-6.278	-17.247	2.613	1.00	18.93	B	O
ATOM	3247	N	PHE	B	126	-7.105	-19.080	1.604	1.00	18.81	B	N
ATOM	3248	CA	PHE	B	126	-7.614	-18.381	0.437	1.00	18.56	B	C
ATOM	3249	CB	PHE	B	126	-8.131	-19.385	-0.604	1.00	18.49	B	C
ATOM	3250	CG	PHE	B	126	-7.064	-19.911	-1.508	1.00	18.66	B	C
ATOM	3251	CD1	PHE	B	126	-6.020	-20.664	-1.006	1.00	19.04	B	C
ATOM	3252	CE1	PHE	B	126	-5.020	-21.148	-1.831	1.00	18.97	B	C
ATOM	3253	CZ	PHE	B	126	-5.055	-20.874	-3.176	1.00	19.04	B	C
ATOM	3254	CE2	PHE	B	126	-6.100	-20.132	-3.692	1.00	18.90	B	C
ATOM	3255	CD2	PHE	B	126	-7.098	-19.653	-2.860	1.00	18.72	B	C
ATOM	3256	C	PHE	B	126	-8.703	-17.362	0.755	1.00	18.62	B	C
ATOM	3257	O	PHE	B	126	-9.003	-16.516	-0.081	1.00	19.38	B	O
ATOM	3258	N	SER	B	127	-9.292	-17.422	1.945	1.00	17.97	B	N
ATOM	3259	CA	SER	B	127	-10.348	-16.474	2.291	1.00	17.25	B	C
ATOM	3260	CB	SER	B	127	-11.203	-17.006	3.427	1.00	17.21	B	C
ATOM	3261	OG	SER	B	127	-10.384	-17.220	4.554	1.00	17.32	B	O
ATOM	3262	C	SER	B	127	-9.808	-15.133	2.712	1.00	16.62	B	C
ATOM	3263	O	SER	B	127	-10.606	-14.248	2.963	1.00	16.39	B	O
ATOM	3264	N	ALA	B	128	-8.481	-14.984	2.782	1.00	16.07	B	N
ATOM	3265	CA	ALA	B	128	-7.847	-13.752	3.257	1.00	15.85	B	C
ATOM	3266	CB	ALA	B	128	-6.407	-14.027	3.600	1.00	15.64	B	C
ATOM	3267	C	ALA	B	128	-7.920	-12.530	2.315	1.00	16.85	B	C
ATOM	3268	O	ALA	B	128	-7.759	-11.373	2.775	1.00	17.34	B	O
ATOM	3269	N	ASP	B	129	-8.144	-12.759	1.019	1.00	17.61	B	N
ATOM	3270	CA	ASP	B	129	-8.243	-11.666	0.041	1.00	17.88	B	C
ATOM	3271	CB	ASP	B	129	-7.283	-11.861	-1.165	1.00	18.05	B	C
ATOM	3272	CG	ASP	B	129	-7.173	-10.596	-2.055	1.00	19.36	B	C
ATOM	3273	OD1	ASP	B	129	-8.206	-9.927	-2.291	1.00	19.57	B	O
ATOM	3274	OD2	ASP	B	129	-6.063	-10.247	-2.541	1.00	20.33	B	O
ATOM	3275	C	ASP	B	129	-9.681	-11.618	-0.426	1.00	17.31	B	C
ATOM	3276	O	ASP	B	129	-10.152	-12.569	-1.029	1.00	17.85	B	O
ATOM	3277	N	PRO	B	130	-10.371	-10.493	-0.196	1.00	17.22	B	N
ATOM	3278	CA	PRO	B	130	-11.786	-10.369	-0.601	1.00	17.02	B	C
ATOM	3279	CB	PRO	B	130	-12.140	-8.911	-0.243	1.00	16.73	B	C
ATOM	3280	CG	PRO	B	130	-11.099	-8.456	0.723	1.00	16.71	B	C
ATOM	3281	CD	PRO	B	130	-9.855	-9.235	0.392	1.00	17.19	B	C
ATOM	3282	C	PRO	B	130	-12.074	-10.631	-2.085	1.00	16.62	B	C
ATOM	3283	O	PRO	B	130	-13.211	-10.958	-2.436	1.00	15.51	B	O
ATOM	3284	N	ASP	B	131	-11.072	-10.485	-2.948	1.00	16.98	B	N
ATOM	3285	CA	ASP	B	131	-11.310	-10.688	-4.384	1.00	18.29	B	C
ATOM	3286	CB	ASP	B	131	-10.235	-9.999	-5.283	1.00	19.03	B	C
ATOM	3287	CG	ASP	B	131	-8.835	-10.602	-5.142	1.00	19.39	B	C
ATOM	3288	OD1	ASP	B	131	-8.691	-11.825	-5.259	1.00	19.96	B	O
ATOM	3289	OD2	ASP	B	131	-7.859	-9.851	-4.923	1.00	20.07	B	O
ATOM	3290	C	ASP	B	131	-11.495	-12.171	-4.702	1.00	19.01	B	C
ATOM	3291	O	ASP	B	131	-12.097	-12.542	-5.721	1.00	17.48	B	O
ATOM	3292	N	VAL	B	132	-10.995	-13.028	-3.804	1.00	19.89	B	N
ATOM	3293	CA	VAL	B	132	-11.221	-14.456	-3.922	1.00	21.16	B	C
ATOM	3294	CB	VAL	B	132	-10.333	-15.232	-2.948	1.00	22.10	B	C
ATOM	3295	CG1	VAL	B	132	-10.779	-16.695	-2.865	1.00	22.23	B	C
ATOM	3296	CG2	VAL	B	132	-8.867	-15.110	-3.357	1.00	22.87	B	C
ATOM	3297	C	VAL	B	132	-12.683	-14.825	-3.651	1.00	21.46	B	C
ATOM	3298	O	VAL	B	132	-13.300	-15.590	-4.402	1.00	20.31	B	O
ATOM	3299	N	ILE	B	133	-13.220	-14.282	-2.562	1.00	21.93	B	N
ATOM	3300	CA	ILE	B	133	-14.609	-14.519	-2.215	1.00	21.56	B	C
ATOM	3301	CB	ILE	B	133	-15.025	-13.773	-0.956	1.00	21.14	B	C
ATOM	3302	CG1	ILE	B	133	-14.046	-14.023	0.199	1.00	22.31	B	C
ATOM	3303	CD1	ILE	B	133	-13.855	-15.454	0.620	1.00	22.87	B	C
ATOM	3304	CG2	ILE	B	133	-16.455	-14.105	-0.599	1.00	20.64	B	C
ATOM	3305	C	ILE	B	133	-15.465	-13.987	-3.346	1.00	22.51	B	C

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ATOM   3306  O   ILE B 133     -16.421 -14.642  -3.763  1.00 24.23      B  O
ATOM   3307  N   GLY B 134     -15.108 -12.798  -3.844  1.00 22.08      B  N
ATOM   3308  CA  GLY B 134     -15.828 -12.177  -4.929  1.00 21.41      B  C
ATOM   3309  C   GLY B 134     -15.719 -13.033  -6.162  1.00 22.33      B  C
ATOM   3310  O   GLY B 134     -16.690 -13.223  -6.891  1.00 23.18      B  O
ATOM   3311  N   HIS B 135     -14.528 -13.569  -6.390  1.00 23.11      B  N
ATOM   3312  CA  HIS B 135     -14.280 -14.385  -7.573  1.00 23.08      B  C
ATOM   3313  CB  HIS B 135     -12.829 -14.804  -7.601  1.00 21.45      B  C
ATOM   3314  CG  HIS B 135     -12.442 -15.596  -8.804  1.00 20.35      B  C
ATOM   3315  ND1 HIS B 135     -12.056 -15.007  -9.982  1.00 19.67      B  N
ATOM   3316  CE1 HIS B 135     -11.717 -15.942 -10.847  1.00 19.76      B  C
ATOM   3317  NE2 HIS B 135     -11.876 -17.120 -10.274  1.00 19.91      B  N
ATOM   3318  CD2 HIS B 135     -12.317 -16.930  -8.991  1.00 20.18      B  C
ATOM   3319  C   HIS B 135     -15.164 -15.628  -7.593  1.00 25.10      B  C
ATOM   3320  O   HIS B 135     -15.726 -15.994  -8.651  1.00 27.12      B  O
ATOM   3321  N   GLU B 136     -15.295 -16.272  -6.436  1.00 25.03      B  N
ATOM   3322  CA  GLU B 136     -16.004 -17.549  -6.379  1.00 25.06      B  C
ATOM   3323  CB  GLU B 136     -15.518 -18.377  -5.191  1.00 24.35      B  C
ATOM   3324  CG  GLU B 136     -14.098 -18.882  -5.369  1.00 24.50      B  C
ATOM   3325  CD  GLU B 136     -13.846 -19.503  -6.744  1.00 25.78      B  C
ATOM   3326  OE1 GLU B 136     -12.713 -19.404  -7.229  1.00 29.10      B  O
ATOM   3327  OE2 GLU B 136     -14.753 -20.096  -7.371  1.00 25.51      B  O
ATOM   3328  C   GLU B 136     -17.519 -17.378  -6.375  1.00 25.55      B  C
ATOM   3329  O   GLU B 136     -18.227 -18.100  -7.086  1.00 23.74      B  O
ATOM   3330  N   LEU B 137     -17.993 -16.404  -5.594  1.00 26.39      B  N
ATOM   3331  CA  LEU B 137     -19.406 -16.077  -5.519  1.00 26.59      B  C
ATOM   3332  CB  LEU B 137     -19.572 -14.815  -4.694  1.00 27.82      B  C
ATOM   3333  CG  LEU B 137     -20.822 -14.488  -3.869  1.00 29.11      B  C
ATOM   3334  CD1 LEU B 137     -22.031 -14.318  -4.757  1.00 30.30      B  C
ATOM   3335  CD2 LEU B 137     -21.094 -15.501  -2.771  1.00 30.20      B  C
ATOM   3336  C   LEU B 137     -19.893 -15.841  -6.930  1.00 28.03      B  C
ATOM   3337  O   LEU B 137     -20.952 -16.353  -7.334  1.00 29.88      B  O
ATOM   3338  N   THR B 138     -19.098 -15.068  -7.677  1.00 28.04      B  N
ATOM   3339  CA  THR B 138     -19.400 -14.703  -9.054  1.00 27.52      B  C
ATOM   3340  CB  THR B 138     -18.403 -13.654  -9.578  1.00 27.58      B  C
ATOM   3341  OG1 THR B 138     -18.419 -12.512  -8.720  1.00 25.48      B  O
ATOM   3342  CG2 THR B 138     -18.744 -13.228 -11.013  1.00 27.35      B  C
ATOM   3343  C   THR B 138     -19.371 -15.928  -9.967  1.00 28.01      B  C
ATOM   3344  O   THR B 138     -20.163 -16.016 -10.896  1.00 29.23      B  O
ATOM   3345  N   HIS B 139     -18.472 -16.881  -9.715  1.00 28.67      B  N
ATOM   3346  CA  HIS B 139     -18.529 -18.184 -10.421  1.00 27.39      B  C
ATOM   3347  CB  HIS B 139     -17.532 -19.196  -9.824  1.00 26.16      B  C
ATOM   3348  CG  HIS B 139     -16.138 -19.145 -10.411  1.00 25.53      B  C
ATOM   3349  ND1 HIS B 139     -15.900 -19.058 -11.764  1.00 25.15      B  N
ATOM   3350  CE1 HIS B 139     -14.595 -19.065 -11.988  1.00 24.31      B  C
ATOM   3351  NE2 HIS B 139     -13.974 -19.181 -10.830  1.00 24.44      B  N
ATOM   3352  CD2 HIS B 139     -14.915 -19.249  -9.829  1.00 24.67      B  C
ATOM   3353  C   HIS B 139     -19.987 -18.721 -10.357  1.00 28.40      B  C
ATOM   3354  O   HIS B 139     -20.511 -19.275 -11.337  1.00 27.07      B  O
ATOM   3355  N   GLY B 140     -20.640 -18.506  -9.209  1.00 29.45      B  N
ATOM   3356  CA  GLY B 140     -22.074 -18.781  -9.033  1.00 30.38      B  C
ATOM   3357  C   GLY B 140     -23.047 -17.934  -9.872  1.00 31.74      B  C
ATOM   3358  O   GLY B 140     -23.870 -18.491 -10.622  1.00 32.56      B  O
ATOM   3359  N   VAL B 141     -22.982 -16.605  -9.742  1.00 30.73      B  N
ATOM   3360  CA  VAL B 141     -23.765 -15.712 -10.609  1.00 30.84      B  C
ATOM   3361  CB  VAL B 141     -23.302 -14.229 -10.488  1.00 30.98      B  C
ATOM   3362  CG1 VAL B 141     -24.079 -13.307 -11.417  1.00 30.38      B  C
ATOM   3363  CG2 VAL B 141     -23.418 -13.731  -9.059  1.00 33.19      B  C
ATOM   3364  C   VAL B 141     -23.653 -16.184 -12.087  1.00 32.64      B  C
ATOM   3365  O   VAL B 141     -24.680 -16.395 -12.764  1.00 34.17      B  O
ATOM   3366  N   THR B 142     -22.425 -16.371 -12.584  1.00 30.57      B  N
ATOM   3367  CA  THR B 142     -22.238 -16.711 -13.978  1.00 30.33      B  C
ATOM   3368  CB  THR B 142     -20.747 -16.814 -14.342  1.00 28.78      B  C
ATOM   3369  OG1 THR B 142     -20.107 -15.548 -14.169  1.00 28.27      B  O
ATOM   3370  CG2 THR B 142     -20.562 -17.241 -15.778  1.00 28.27      B  C
ATOM   3371  C   THR B 142     -23.018 -18.012 -14.321  1.00 34.44      B  C
ATOM   3372  O   THR B 142     -23.756 -18.043 -15.311  1.00 31.77      B  O
ATOM   3373  N   GLU B 143     -22.891 -19.058 -13.496  1.00 39.28      B  N
ATOM   3374  CA  GLU B 143     -23.609 -20.331 -13.746  1.00 44.10      B  C
ATOM   3375  CB  GLU B 143     -23.199 -21.447 -12.749  1.00 46.26      B  C
ATOM   3376  CG  GLU B 143     -23.758 -22.829 -13.098  1.00 46.77      B  C
ATOM   3377  CD  GLU B 143     -23.520 -23.911 -12.036  1.00 50.51      B  C
ATOM   3378  OE1 GLU B 143     -24.476 -24.652 -11.712  1.00 52.85      B  O
ATOM   3379  OE2 GLU B 143     -22.388 -24.056 -11.531  1.00 51.61      B  O
ATOM   3380  C   GLU B 143     -25.141 -20.147 -13.737  1.00 43.41      B  C
ATOM   3381  O   GLU B 143     -25.837 -20.722 -14.579  1.00 42.45      B  O
ATOM   3382  N   HIS B 144     -25.657 -19.350 -12.803  1.00 41.46      B  N
ATOM   3383  CA  HIS B 144     -27.095 -19.050 -12.768  1.00 42.89      B  C
ATOM   3384  CB  HIS B 144     -27.500 -18.615 -11.363  1.00 43.93      B  C
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ATOM	3385	CG	HIS	B	144	-27.711	-19.748	-10.415	1.00	48.17	B	C
ATOM	3386	ND1	HIS	B	144	-26.683	-20.562	-9.985	1.00	53.25	B	N
ATOM	3387	CE1	HIS	B	144	-27.156	-21.457	-9.134	1.00	53.12	B	C
ATOM	3388	NE2	HIS	B	144	-28.453	-21.245	-8.991	1.00	52.99	B	N
ATOM	3389	CD2	HIS	B	144	-28.827	-20.187	-9.787	1.00	49.42	B	C
ATOM	3390	C	HIS	B	144	-27.596	-17.985	-13.790	1.00	41.27	B	C
ATOM	3391	O	HIS	B	144	-28.773	-17.664	-13.803	1.00	41.71	B	O
ATOM	3392	N	THR	B	145	-26.729	-17.451	-14.646	1.00	39.46	B	N
ATOM	3393	CA	THR	B	145	-27.124	-16.412	-15.614	1.00	37.58	B	C
ATOM	3394	CB	THR	B	145	-26.559	-15.013	-15.211	1.00	39.34	B	C
ATOM	3395	OG1	THR	B	145	-25.127	-15.071	-15.027	1.00	36.83	B	O
ATOM	3396	CG2	THR	B	145	-27.213	-14.517	-13.918	1.00	39.08	B	C
ATOM	3397	C	THR	B	145	-26.685	-16.769	-17.042	1.00	34.70	B	C
ATOM	3398	O	THR	B	145	-27.380	-17.459	-17.750	1.00	36.43	B	O
ATOM	3399	N	ALA	B	146	-25.523	-16.305	-17.455	1.00	33.64	B	N
ATOM	3400	CA	ALA	B	146	-25.006	-16.605	-18.769	1.00	33.70	B	C
ATOM	3401	CB	ALA	B	146	-23.739	-15.803	-19.000	1.00	33.49	B	C
ATOM	3402	C	ALA	B	146	-24.709	-18.100	-18.948	1.00	34.85	B	C
ATOM	3403	O	ALA	B	146	-24.835	-18.639	-20.052	1.00	36.76	B	O
ATOM	3404	N	GLY	B	147	-24.277	-18.752	-17.873	1.00	33.97	B	N
ATOM	3405	CA	GLY	B	147	-23.841	-20.144	-17.930	1.00	32.43	B	C
ATOM	3406	C	GLY	B	147	-22.627	-20.388	-18.804	1.00	31.88	B	C
ATOM	3407	O	GLY	B	147	-22.585	-21.373	-19.541	1.00	32.47	B	O
ATOM	3408	N	LEU	B	148	-21.632	-19.506	-18.744	1.00	32.61	B	N
ATOM	3409	CA	LEU	B	148	-20.451	-19.658	-19.605	1.00	33.79	B	C
ATOM	3410	CB	LEU	B	148	-19.475	-18.492	-19.444	1.00	35.60	B	C
ATOM	3411	CG	LEU	B	148	-19.982	-17.190	-20.083	1.00	38.31	B	C
ATOM	3412	CD1	LEU	B	148	-19.402	-15.964	-19.399	1.00	37.11	B	C
ATOM	3413	CD2	LEU	B	148	-19.694	-17.157	-21.585	1.00	40.39	B	C
ATOM	3414	C	LEU	B	148	-19.783	-20.967	-19.246	1.00	32.02	B	C
ATOM	3415	O	LEU	B	148	-19.587	-21.241	-18.078	1.00	29.10	B	O
ATOM	3416	N	GLU	B	149	-19.474	-21.789	-20.246	1.00	31.33	B	N
ATOM	3417	CA	GLU	B	149	-18.940	-23.146	-19.978	1.00	29.16	B	C
ATOM	3418	CB	GLU	B	149	-19.192	-24.108	-21.161	1.00	27.96	B	C
ATOM	3419	CG	GLU	B	149	-20.666	-24.425	-21.298	1.00	26.85	B	C
ATOM	3420	CD	GLU	B	149	-21.026	-25.095	-22.589	1.00	24.90	B	C
ATOM	3421	OE1	GLU	B	149	-22.188	-25.536	-22.681	1.00	23.70	B	O
ATOM	3422	OE2	GLU	B	149	-20.181	-25.161	-23.493	1.00	23.35	B	O
ATOM	3423	C	GLU	B	149	-17.471	-23.082	-19.639	1.00	25.48	B	C
ATOM	3424	O	GLU	B	149	-16.708	-22.371	-20.273	1.00	24.06	B	O
ATOM	3425	N	TYR	B	150	-17.091	-23.848	-18.640	1.00	23.26	B	N
ATOM	3426	CA	TYR	B	150	-15.795	-23.690	-18.059	1.00	23.09	B	C
ATOM	3427	CB	TYR	B	150	-15.847	-24.115	-16.606	1.00	22.13	B	C
ATOM	3428	CG	TYR	B	150	-14.796	-23.476	-15.770	1.00	22.41	B	C
ATOM	3429	CD1	TYR	B	150	-14.899	-22.133	-15.406	1.00	22.39	B	C
ATOM	3430	CE1	TYR	B	150	-13.920	-21.529	-14.620	1.00	22.34	B	C
ATOM	3431	CZ	TYR	B	150	-12.828	-22.277	-14.176	1.00	22.55	B	C
ATOM	3432	OH	TYR	B	150	-11.884	-21.671	-13.406	1.00	21.97	B	O
ATOM	3433	CE2	TYR	B	150	-12.697	-23.623	-14.518	1.00	22.68	B	C
ATOM	3434	CD2	TYR	B	150	-13.676	-24.213	-15.319	1.00	22.78	B	C
ATOM	3435	C	TYR	B	150	-14.760	-24.462	-18.871	1.00	23.03	B	C
ATOM	3436	O	TYR	B	150	-14.194	-25.466	-18.425	1.00	25.23	B	O
ATOM	3437	N	TYR	B	151	-14.522	-23.970	-20.075	1.00	21.89	B	N
ATOM	3438	CA	TYR	B	151	-13.540	-24.533	-20.963	1.00	22.19	B	C
ATOM	3439	CB	TYR	B	151	-14.012	-25.873	-21.514	1.00	22.84	B	C
ATOM	3440	CG	TYR	B	151	-12.869	-26.737	-21.992	1.00	24.39	B	C
ATOM	3441	CD1	TYR	B	151	-12.365	-26.643	-23.293	1.00	24.16	B	C
ATOM	3442	CE1	TYR	B	151	-11.298	-27.439	-23.704	1.00	23.84	B	C
ATOM	3443	CZ	TYR	B	151	-10.738	-28.326	-22.820	1.00	24.46	B	C
ATOM	3444	OH	TYR	B	151	-9.695	-29.143	-23.159	1.00	26.46	B	O
ATOM	3445	CE2	TYR	B	151	-11.214	-28.432	-21.538	1.00	25.25	B	C
ATOM	3446	CD2	TYR	B	151	-12.263	-27.640	-21.125	1.00	25.13	B	C
ATOM	3447	C	TYR	B	151	-13.325	-23.580	-22.124	1.00	22.44	B	C
ATOM	3448	O	TYR	B	151	-14.227	-22.838	-22.485	1.00	22.50	B	O
ATOM	3449	N	GLY	B	152	-12.139	-23.613	-22.717	1.00	23.25	B	N
ATOM	3450	CA	GLY	B	152	-11.812	-22.762	-23.866	1.00	24.07	B	C
ATOM	3451	C	GLY	B	152	-12.135	-21.280	-23.685	1.00	24.84	B	C
ATOM	3452	O	GLY	B	152	-12.043	-20.733	-22.564	1.00	25.07	B	O
ATOM	3453	N	GLU	B	153	-12.539	-20.635	-24.787	1.00	25.04	B	N
ATOM	3454	CA	GLU	B	153	-12.871	-19.202	-24.766	1.00	24.00	B	C
ATOM	3455	CB	GLU	B	153	-13.149	-18.678	-26.183	1.00	23.71	B	C
ATOM	3456	CG	GLU	B	153	-11.936	-18.864	-27.107	1.00	23.71	B	C
ATOM	3457	CD	GLU	B	153	-11.913	-17.978	-28.361	1.00	24.91	B	C
ATOM	3458	OE1	GLU	B	153	-12.587	-16.903	-28.423	1.00	24.29	B	O
ATOM	3459	OE2	GLU	B	153	-11.174	-18.362	-29.304	1.00	24.99	B	O
ATOM	3460	C	GLU	B	153	-14.005	-18.909	-23.771	1.00	23.93	B	C
ATOM	3461	O	GLU	B	153	-13.861	-18.016	-22.931	1.00	23.19	B	O
ATOM	3462	N	SER	B	154	-15.085	-19.689	-23.812	1.00	23.68	B	N
ATOM	3463	CA	SER	B	154	-16.128	-19.584	-22.790	1.00	24.55	B	C

ATOM	3464	CB	SER	B	154	-16.967	-20.848	-22.696	1.00	25.82	B	C
ATOM	3465	OG	SER	B	154	-18.170	-20.690	-23.396	1.00	29.35	B	O
ATOM	3466	C	SER	B	154	-15.567	-19.381	-21.419	1.00	24.67	B	C
ATOM	3467	O	SER	B	154	-15.952	-18.454	-20.715	1.00	26.62	B	O
ATOM	3468	N	GLY	B	155	-14.688	-20.288	-21.023	1.00	24.28	B	N
ATOM	3469	CA	GLY	B	155	-14.237	-20.370	-19.635	1.00	24.21	B	C
ATOM	3470	C	GLY	B	155	-13.255	-19.268	-19.266	1.00	24.50	B	C
ATOM	3471	O	GLY	B	155	-13.162	-18.878	-18.081	1.00	24.34	B	O
ATOM	3472	N	ALA	B	156	-12.518	-18.776	-20.272	1.00	22.74	B	N
ATOM	3473	CA	ALA	B	156	-11.638	-17.640	-20.087	1.00	21.34	B	C
ATOM	3474	CB	ALA	B	156	-10.756	-17.444	-21.302	1.00	21.61	B	C
ATOM	3475	C	ALA	B	156	-12.447	-16.379	-19.758	1.00	20.58	B	C
ATOM	3476	O	ALA	B	156	-12.066	-15.588	-18.881	1.00	19.77	B	O
ATOM	3477	N	LEU	B	157	-13.573	-16.213	-20.435	1.00	20.76	B	N
ATOM	3478	CA	LEU	B	157	-14.554	-15.186	-20.067	1.00	21.15	B	C
ATOM	3479	CB	LEU	B	157	-15.696	-15.131	-21.091	1.00	22.03	B	C
ATOM	3480	CG	LEU	B	157	-15.537	-14.290	-22.373	1.00	23.05	B	C
ATOM	3481	CD1	LEU	B	157	-14.127	-14.275	-22.957	1.00	23.70	B	C
ATOM	3482	CD2	LEU	B	157	-16.520	-14.776	-23.429	1.00	23.26	B	C
ATOM	3483	C	LEU	B	157	-15.124	-15.451	-18.670	1.00	20.38	B	C
ATOM	3484	O	LEU	B	157	-15.166	-14.576	-17.837	1.00	20.58	B	O
ATOM	3485	N	ASN	B	158	-15.558	-16.669	-18.414	1.00	20.57	B	N
ATOM	3486	CA	ASN	B	158	-16.143	-17.009	-17.122	1.00	20.45	B	C
ATOM	3487	CB	ASN	B	158	-16.434	-18.523	-17.105	1.00	19.60	B	C
ATOM	3488	CG	ASN	B	158	-16.948	-19.017	-15.773	1.00	18.40	B	C
ATOM	3489	OD1	ASN	B	158	-17.952	-19.699	-15.705	1.00	17.09	B	O
ATOM	3490	ND2	ASN	B	158	-16.260	-18.667	-14.711	1.00	18.42	B	N
ATOM	3491	C	ASN	B	158	-15.205	-16.580	-15.964	1.00	21.47	B	C
ATOM	3492	O	ASN	B	158	-15.643	-15.988	-14.948	1.00	21.75	B	O
ATOM	3493	N	GLU	B	159	-13.923	-16.919	-16.124	1.00	21.70	B	N
ATOM	3494	CA	GLU	B	159	-12.856	-16.482	-15.213	1.00	21.57	B	C
ATOM	3495	CB	GLU	B	159	-11.542	-17.158	-15.612	1.00	20.39	B	C
ATOM	3496	CG	GLU	B	159	-11.355	-18.493	-14.966	1.00	20.39	B	C
ATOM	3497	CD	GLU	B	159	-11.302	-18.353	-13.467	1.00	21.79	B	C
ATOM	3498	OE1	GLU	B	159	-10.430	-17.542	-13.054	1.00	25.14	B	O
ATOM	3499	OE2	GLU	B	159	-12.105	-18.981	-12.712	1.00	20.07	B	O
ATOM	3500	C	GLU	B	159	-12.692	-14.940	-15.195	1.00	23.60	B	C
ATOM	3501	O	GLU	B	159	-12.857	-14.289	-14.147	1.00	22.28	B	O
ATOM	3502	N	SER	B	160	-12.393	-14.354	-16.360	1.00	25.08	B	N
ATOM	3503	CA	SER	B	160	-12.228	-12.906	-16.432	1.00	26.35	B	C
ATOM	3504	CB	SER	B	160	-12.121	-12.385	-17.864	1.00	26.83	B	C
ATOM	3505	OG	SER	B	160	-11.919	-10.970	-17.841	1.00	27.65	B	O
ATOM	3506	C	SER	B	160	-13.362	-12.181	-15.740	1.00	26.39	B	C
ATOM	3507	O	SER	B	160	-13.108	-11.202	-15.049	1.00	27.56	B	O
ATOM	3508	N	ILE	B	161	-14.602	-12.640	-15.906	1.00	25.59	B	N
ATOM	3509	CA	ILE	B	161	-15.716	-11.934	-15.265	1.00	25.62	B	C
ATOM	3510	CB	ILE	B	161	-17.102	-12.304	-15.858	1.00	25.50	B	C
ATOM	3511	CG1	ILE	B	161	-17.410	-11.343	-17.010	1.00	26.10	B	C
ATOM	3512	CD1	ILE	B	161	-18.251	-11.934	-18.118	1.00	26.54	B	C
ATOM	3513	CG2	ILE	B	161	-18.232	-12.168	-14.845	1.00	25.32	B	C
ATOM	3514	C	ILE	B	161	-15.633	-12.060	-13.752	1.00	24.63	B	C
ATOM	3515	O	ILE	B	161	-15.751	-11.057	-13.032	1.00	25.26	B	O
ATOM	3516	N	SER	B	162	-15.393	-13.268	-13.277	1.00	22.63	B	N
ATOM	3517	CA	SER	B	162	-15.191	-13.452	-11.859	1.00	22.29	B	C
ATOM	3518	CB	SER	B	162	-14.971	-14.944	-11.505	1.00	22.14	B	C
ATOM	3519	OG	SER	B	162	-16.160	-15.704	-11.695	1.00	22.68	B	O
ATOM	3520	C	SER	B	162	-14.026	-12.561	-11.365	1.00	21.42	B	C
ATOM	3521	O	SER	B	162	-14.094	-12.053	-10.261	1.00	22.43	B	O
ATOM	3522	N	ASP	B	163	-12.974	-12.365	-12.159	1.00	20.02	B	N
ATOM	3523	CA	ASP	B	163	-11.870	-11.480	-11.757	1.00	20.14	B	C
ATOM	3524	CB	ASP	B	163	-10.676	-11.584	-12.721	1.00	19.49	B	C
ATOM	3525	CG	ASP	B	163	-9.815	-12.793	-12.467	1.00	18.52	B	C
ATOM	3526	OD1	ASP	B	163	-10.121	-13.559	-11.555	1.00	18.96	B	O
ATOM	3527	OD2	ASP	B	163	-8.819	-12.979	-13.170	1.00	17.18	B	O
ATOM	3528	C	ASP	B	163	-12.306	-10.011	-11.726	1.00	21.75	B	C
ATOM	3529	O	ASP	B	163	-11.987	-9.257	-10.797	1.00	22.65	B	O
ATOM	3530	N	ILE	B	164	-13.027	-9.594	-12.758	1.00	22.58	B	N
ATOM	3531	CA	ILE	B	164	-13.462	-8.207	-12.857	1.00	22.48	B	C
ATOM	3532	CB	ILE	B	164	-14.299	-7.988	-14.114	1.00	22.54	B	C
ATOM	3533	CG1	ILE	B	164	-13.386	-8.005	-15.345	1.00	23.45	B	C
ATOM	3534	CD1	ILE	B	164	-14.066	-8.416	-16.632	1.00	23.65	B	C
ATOM	3535	CG2	ILE	B	164	-15.030	-6.663	-14.047	1.00	21.95	B	C
ATOM	3536	C	ILE	B	164	-14.258	-7.827	-11.634	1.00	22.72	B	C
ATOM	3537	O	ILE	B	164	-14.064	-6.750	-11.049	1.00	23.59	B	O
ATOM	3538	N	ILE	B	165	-15.145	-8.718	-11.229	1.00	23.05	B	N
ATOM	3539	CA	ILE	B	165	-16.010	-8.405	-10.127	1.00	23.88	B	C
ATOM	3540	CB	ILE	B	165	-17.296	-9.240	-10.153	1.00	25.46	B	C
ATOM	3541	CG1	ILE	B	165	-18.236	-8.725	-11.258	1.00	25.84	B	C
ATOM	3542	CD1	ILE	B	165	-19.692	-9.093	-11.047	1.00	25.86	B	C

ATOM	3543	CG2	ILE	B	165	-17.987	-9.179	-8.793	1.00	26.66	B	C
ATOM	3544	C	ILE	B	165	-15.281	-8.569	-8.814	1.00	23.03	B	C
ATOM	3545	O	ILE	B	165	-15.446	-7.770	-7.914	1.00	23.61	B	O
ATOM	3546	N	GLY	B	166	-14.475	-9.601	-8.693	1.00	22.77	B	N
ATOM	3547	CA	GLY	B	166	-13.811	-9.838	-7.437	1.00	23.61	B	C
ATOM	3548	C	GLY	B	166	-12.910	-8.666	-7.100	1.00	24.48	B	C
ATOM	3549	O	GLY	B	166	-12.834	-8.213	-5.949	1.00	24.77	B	O
ATOM	3550	N	ASN	B	167	-12.218	-8.185	-8.122	1.00	24.92	B	N
ATOM	3551	CA	ASN	B	167	-11.332	-7.061	-7.974	1.00	25.37	B	C
ATOM	3552	CB	ASN	B	167	-10.538	-6.834	-9.250	1.00	25.09	B	C
ATOM	3553	CG	ASN	B	167	-9.722	-5.578	-9.179	1.00	24.84	B	C
ATOM	3554	OD1	ASN	B	167	-8.663	-5.557	-8.554	1.00	24.32	B	O
ATOM	3555	ND2	ASN	B	167	-10.223	-4.509	-9.792	1.00	25.27	B	N
ATOM	3556	C	ASN	B	167	-12.098	-5.789	-7.648	1.00	25.52	B	C
ATOM	3557	O	ASN	B	167	-11.629	-4.960	-6.876	1.00	27.09	B	O
ATOM	3558	N	ALA	B	168	-13.262	-5.636	-8.258	1.00	25.33	B	N
ATOM	3559	CA	ALA	B	168	-14.077	-4.456	-8.054	1.00	26.46	B	C
ATOM	3560	CB	ALA	B	168	-15.209	-4.423	-9.078	1.00	26.58	B	C
ATOM	3561	C	ALA	B	168	-14.627	-4.372	-6.633	1.00	27.05	B	C
ATOM	3562	O	ALA	B	168	-14.769	-3.305	-6.099	1.00	25.94	B	O
ATOM	3563	N	ILE	B	169	-14.948	-5.496	-6.021	1.00	30.59	B	N
ATOM	3564	CA	ILE	B	169	-15.426	-5.488	-4.640	1.00	34.83	B	C
ATOM	3565	CB	ILE	B	169	-15.783	-6.925	-4.196	1.00	37.29	B	C
ATOM	3566	CG1	ILE	B	169	-17.197	-7.244	-4.697	1.00	40.64	B	C
ATOM	3567	CD1	ILE	B	169	-17.388	-8.660	-5.177	1.00	41.49	B	C
ATOM	3568	CG2	ILE	B	169	-15.710	-7.094	-2.681	1.00	36.37	B	C
ATOM	3569	C	ILE	B	169	-14.388	-4.882	-3.715	1.00	36.99	B	C
ATOM	3570	O	ILE	B	169	-14.662	-3.984	-2.918	1.00	33.86	B	O
ATOM	3571	N	ASP	B	170	-13.186	-5.413	-3.841	1.00	43.53	B	N
ATOM	3572	CA	ASP	B	170	-12.072	-5.011	-3.016	1.00	48.08	B	C
ATOM	3573	CB	ASP	B	170	-10.814	-5.803	-3.463	1.00	51.67	B	C
ATOM	3574	CG	ASP	B	170	-9.755	-5.980	-2.344	1.00	52.92	B	C
ATOM	3575	OD1	ASP	B	170	-9.729	-5.192	-1.351	1.00	50.54	B	O
ATOM	3576	OD2	ASP	B	170	-8.931	-6.919	-2.499	1.00	50.26	B	O
ATOM	3577	C	ASP	B	170	-11.919	-3.483	-3.142	1.00	44.26	B	C
ATOM	3578	O	ASP	B	170	-12.078	-2.785	-2.164	1.00	43.51	B	O
ATOM	3579	N	GLY	B	171	-11.672	-2.990	-4.358	1.00	43.91	B	N
ATOM	3580	CA	GLY	B	171	-11.467	-1.557	-4.634	1.00	44.24	B	C
ATOM	3581	C	GLY	B	171	-10.003	-1.160	-4.820	1.00	44.95	B	C
ATOM	3582	O	GLY	B	171	-9.634	-0.569	-5.831	1.00	43.83	B	O
ATOM	3583	N	LYS	B	172	-9.194	-1.498	-3.815	1.00	46.20	B	N
ATOM	3584	CA	LYS	B	172	-7.749	-1.197	-3.709	1.00	46.62	B	C
ATOM	3585	CB	LYS	B	172	-7.096	-2.285	-2.836	1.00	52.15	B	C
ATOM	3586	CG	LYS	B	172	-7.272	-2.161	-1.319	1.00	57.60	B	C
ATOM	3587	CD	LYS	B	172	-6.481	-3.256	-0.557	1.00	62.15	B	C
ATOM	3588	CE	LYS	B	172	-4.946	-3.091	-0.575	1.00	60.28	B	C
ATOM	3589	NZ	LYS	B	172	-4.444	-1.991	0.304	1.00	61.46	B	N
ATOM	3590	C	LYS	B	172	-6.850	-1.027	-4.980	1.00	42.61	B	C
ATOM	3591	O	LYS	B	172	-6.188	-0.001	-5.125	1.00	42.17	B	O
ATOM	3592	N	ASN	B	173	-6.769	-2.039	-5.854	1.00	36.61	B	N
ATOM	3593	CA	ASN	B	173	-5.709	-2.089	-6.899	1.00	30.24	B	C
ATOM	3594	CB	ASN	B	173	-4.433	-2.744	-6.350	1.00	28.81	B	C
ATOM	3595	CG	ASN	B	173	-4.692	-4.072	-5.650	1.00	29.12	B	C
ATOM	3596	OD1	ASN	B	173	-5.413	-4.949	-6.145	1.00	30.32	B	O
ATOM	3597	ND2	ASN	B	173	-4.092	-4.228	-4.481	1.00	28.75	B	N
ATOM	3598	C	ASN	B	173	-6.168	-2.796	-8.164	1.00	26.96	B	C
ATOM	3599	O	ASN	B	173	-7.342	-3.036	-8.324	1.00	24.81	B	O
ATOM	3600	N	TRP	B	174	-5.241	-3.078	-9.070	1.00	25.49	B	N
ATOM	3601	CA	TRP	B	174	-5.513	-3.837	-10.283	1.00	25.26	B	C
ATOM	3602	CB	TRP	B	174	-4.795	-3.193	-11.470	1.00	25.93	B	C
ATOM	3603	CG	TRP	B	174	-5.293	-1.836	-11.778	1.00	26.89	B	C
ATOM	3604	CD1	TRP	B	174	-4.593	-0.665	-11.679	1.00	26.32	B	C
ATOM	3605	NE1	TRP	B	174	-5.397	0.382	-12.017	1.00	26.11	B	N
ATOM	3606	CE2	TRP	B	174	-6.637	-0.087	-12.361	1.00	26.19	B	C
ATOM	3607	CD2	TRP	B	174	-6.607	-1.487	-12.217	1.00	26.18	B	C
ATOM	3608	CE3	TRP	B	174	-7.761	-2.215	-12.487	1.00	26.75	B	C
ATOM	3609	CZ3	TRP	B	174	-8.904	-1.520	-12.907	1.00	28.43	B	C
ATOM	3610	CH2	TRP	B	174	-8.895	-0.122	-13.051	1.00	26.84	B	C
ATOM	3611	CZ2	TRP	B	174	-7.777	0.606	-12.787	1.00	26.52	B	C
ATOM	3612	C	TRP	B	174	-5.052	-5.296	-10.209	1.00	24.68	B	C
ATOM	3613	O	TRP	B	174	-4.843	-5.937	-11.257	1.00	24.26	B	O
ATOM	3614	N	LEU	B	175	-4.878	-5.827	-9.001	1.00	22.75	B	N
ATOM	3615	CA	LEU	B	175	-4.318	-7.160	-8.859	1.00	21.88	B	C
ATOM	3616	CB	LEU	B	175	-3.150	-7.131	-7.894	1.00	20.46	B	C
ATOM	3617	CG	LEU	B	175	-2.144	-5.994	-8.090	1.00	19.93	B	C
ATOM	3618	CD1	LEU	B	175	-1.194	-5.955	-6.916	1.00	20.20	B	C
ATOM	3619	CD2	LEU	B	175	-1.336	-6.095	-9.364	1.00	19.56	B	C
ATOM	3620	C	LEU	B	175	-5.389	-8.154	-8.417	1.00	22.98	B	C
ATOM	3621	O	LEU	B	175	-6.489	-7.765	-8.000	1.00	23.17	B	O

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ATOM   3622  N   ILE B 176      -5.065  -9.439  -8.541  1.00 24.28           B   N
ATOM   3623  CA  ILE B 176      -5.893 -10.524  -7.968  1.00 24.99           B   C
ATOM   3624  CB  ILE B 176      -6.531 -11.412  -9.059  1.00 26.10           B   C
ATOM   3625  CG1 ILE B 176      -7.357 -10.570 -10.055  1.00 26.43           B   C
ATOM   3626  CD1 ILE B 176      -8.802 -10.335  -9.660  1.00 26.54           B   C
ATOM   3627  CG2 ILE B 176      -7.375 -12.507  -8.413  1.00 26.92           B   C
ATOM   3628  C   ILE B 176      -5.044 -11.412  -7.040  1.00 23.20           B   C
ATOM   3629  O   ILE B 176      -3.889 -11.741  -7.341  1.00 21.47           B   O
ATOM   3630  N   GLY B 177      -5.620 -11.773  -5.902  1.00 22.18           B   N
ATOM   3631  CA  GLY B 177      -4.925 -12.603  -4.925  1.00 21.76           B   C
ATOM   3632  C   GLY B 177      -3.641 -11.978  -4.396  1.00 20.91           B   C
ATOM   3633  O   GLY B 177      -2.768 -12.680  -3.908  1.00 19.00           B   O
ATOM   3634  N   ASP B 178      -3.528 -10.652  -4.488  1.00 21.50           B   N
ATOM   3635  CA  ASP B 178      -2.352  -9.928  -3.952  1.00 20.88           B   C
ATOM   3636  CB  ASP B 178      -2.447  -8.386  -4.153  1.00 20.48           B   C
ATOM   3637  CG  ASP B 178      -3.764  -7.757  -3.622  1.00 20.78           B   C
ATOM   3638  OD1 ASP B 178      -4.882  -8.233  -3.951  1.00 21.09           B   O
ATOM   3639  OD2 ASP B 178      -3.680  -6.747  -2.891  1.00 20.74           B   O
ATOM   3640  C   ASP B 178      -2.109 -10.303  -2.482  1.00 20.38           B   C
ATOM   3641  O   ASP B 178      -0.951 -10.556  -2.090  1.00 21.24           B   O
ATOM   3642  N   LEU B 179      -3.198 -10.400  -1.711  1.00 18.74           B   N
ATOM   3643  CA  LEU B 179      -3.130 -10.728  -0.287  1.00 18.78           B   C
ATOM   3644  CB  LEU B 179      -4.449 -10.345   0.395  1.00 18.48           B   C
ATOM   3645  CG  LEU B 179      -4.697  -8.834   0.495  1.00 18.11           B   C
ATOM   3646  CD1 LEU B 179      -5.946  -8.555   1.305  1.00 17.54           B   C
ATOM   3647  CD2 LEU B 179      -3.488  -8.118   1.091  1.00 17.78           B   C
ATOM   3648  C   LEU B 179      -2.776 -12.178   0.103  1.00 18.56           B   C
ATOM   3649  O   LEU B 179      -2.211 -12.399   1.176  1.00 20.52           B   O
ATOM   3650  N   ILE B 180      -3.101 -13.155  -0.735  1.00 17.63           B   N
ATOM   3651  CA  ILE B 180      -2.873 -14.586  -0.399  1.00 17.04           B   C
ATOM   3652  CB  ILE B 180      -4.068 -15.475  -0.767  1.00 15.77           B   C
ATOM   3653  CG1 ILE B 180      -4.340 -15.399  -2.264  1.00 15.25           B   C
ATOM   3654  CD1 ILE B 180      -5.519 -16.216  -2.719  1.00 15.28           B   C
ATOM   3655  CG2 ILE B 180      -5.267 -15.102   0.092  1.00 15.84           B   C
ATOM   3656  C   ILE B 180      -1.628 -15.229  -1.033  1.00 17.27           B   C
ATOM   3657  O   ILE B 180      -1.215 -16.305  -0.630  1.00 16.09           B   O
ATOM   3658  N   TYR B 181      -1.032 -14.546  -1.996  1.00 17.64           B   N
ATOM   3659  CA  TYR B 181      -0.004 -15.128  -2.796  1.00 18.26           B   C
ATOM   3660  CB  TYR B 181      -0.095 -14.544  -4.179  1.00 17.80           B   C
ATOM   3661  CG  TYR B 181       0.789 -15.211  -5.177  1.00 17.24           B   C
ATOM   3662  CD1 TYR B 181       0.678 -16.565  -5.429  1.00 16.90           B   C
ATOM   3663  CE1 TYR B 181       1.461 -17.182  -6.364  1.00 16.27           B   C
ATOM   3664  CZ  TYR B 181       2.349 -16.457  -7.064  1.00 16.18           B   C
ATOM   3665  OH  TYR B 181       3.129 -17.077  -7.986  1.00 16.18           B   O
ATOM   3666  CE2 TYR B 181       2.477 -15.117  -6.853  1.00 16.98           B   C
ATOM   3667  CD2 TYR B 181       1.693 -14.495  -5.905  1.00 16.99           B   C
ATOM   3668  C   TYR B 181       1.357 -14.831  -2.207  1.00 20.02           B   C
ATOM   3669  O   TYR B 181       1.564 -13.757  -1.650  1.00 20.40           B   O
ATOM   3670  N   THR B 182       2.255 -15.812  -2.327  1.00 22.26           B   N
ATOM   3671  CA  THR B 182       3.651 -15.730  -1.896  1.00 25.08           B   C
ATOM   3672  CB  THR B 182       4.512 -15.160  -3.027  1.00 24.99           B   C
ATOM   3673  OG1 THR B 182       3.846 -14.005  -3.582  1.00 24.72           B   O
ATOM   3674  CG2 THR B 182       4.758 -16.227  -4.105  1.00 24.58           B   C
ATOM   3675  C   THR B 182       3.832 -14.850  -0.671  1.00 28.60           B   C
ATOM   3676  O   THR B 182       4.283 -13.693  -0.784  1.00 30.04           B   O
ATOM   3677  N   PRO B 183       3.456 -15.368   0.504  1.00 31.17           B   N
ATOM   3678  CA  PRO B 183       3.595 -14.570   1.747  1.00 31.48           B   C
ATOM   3679  CB  PRO B 183       3.080 -15.521   2.843  1.00 30.90           B   C
ATOM   3680  CG  PRO B 183       3.126 -16.903   2.223  1.00 31.55           B   C
ATOM   3681  CD  PRO B 183       2.875 -16.701   0.756  1.00 31.17           B   C
ATOM   3682  C   PRO B 183       5.033 -14.084   2.022  1.00 29.96           B   C
ATOM   3683  O   PRO B 183       5.213 -13.051   2.626  1.00 28.64           B   O
ATOM   3684  N   ASN B 184       6.034 -14.795   1.531  1.00 31.82           B   N
ATOM   3685  CA  ASN B 184       7.418 -14.330   1.641  1.00 34.54           B   C
ATOM   3686  CB  ASN B 184       8.349 -15.531   1.782  1.00 37.59           B   C
ATOM   3687  CG  ASN B 184       8.493 -15.958   3.219  1.00 40.66           B   C
ATOM   3688  OD1 ASN B 184       7.511 -16.023   3.964  1.00 43.19           B   O
ATOM   3689  ND2 ASN B 184       9.726 -16.202   3.637  1.00 43.92           B   N
ATOM   3690  C   ASN B 184       7.932 -13.407   0.529  1.00 33.21           B   C
ATOM   3691  O   ASN B 184       9.088 -13.008   0.557  1.00 31.64           B   O
ATOM   3692  N   THR B 185       7.072 -13.065  -0.431  1.00 32.76           B   N
ATOM   3693  CA  THR B 185       7.391 -12.095  -1.489  1.00 29.86           B   C
ATOM   3694  CB  THR B 185       7.364 -12.773  -2.865  1.00 28.78           B   C
ATOM   3695  OG1 THR B 185       8.096 -14.008  -2.838  1.00 26.37           B   O
ATOM   3696  CG2 THR B 185       7.922 -11.871  -3.926  1.00 28.45           B   C
ATOM   3697  C   THR B 185       6.331 -10.995  -1.522  1.00 30.62           B   C
ATOM   3698  O   THR B 185       5.205 -11.248  -1.957  1.00 29.21           B   O
ATOM   3699  N   PRO B 186       6.666  -9.783  -1.033  1.00 33.29           B   N
ATOM   3700  CA  PRO B 186       5.722  -8.657  -1.130  1.00 32.23           B   C
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ATOM	3701	CB	PRO	B	186	6.304	-7.611	-0.161	1.00	33.18	B	C
ATOM	3702	CG	PRO	B	186	7.766	-7.921	-0.084	1.00	32.85	B	C
ATOM	3703	CD	PRO	B	186	7.839	-9.429	-0.197	1.00	34.69	B	C
ATOM	3704	C	PRO	B	186	5.660	-8.066	-2.522	1.00	30.17	B	C
ATOM	3705	O	PRO	B	186	6.550	-8.322	-3.337	1.00	28.22	B	O
ATOM	3706	N	GLY	B	187	4.596	-7.298	-2.778	1.00	28.51	B	N
ATOM	3707	CA	GLY	B	187	4.409	-6.578	-4.045	1.00	27.51	B	C
ATOM	3708	C	GLY	B	187	3.834	-7.367	-5.220	1.00	26.61	B	C
ATOM	3709	O	GLY	B	187	3.282	-6.772	-6.151	1.00	24.33	B	O
ATOM	3710	N	ASP	B	188	3.956	-8.702	-5.198	1.00	25.58	B	N
ATOM	3711	CA	ASP	B	188	3.484	-9.510	-6.321	1.00	23.74	B	C
ATOM	3712	CB	ASP	B	188	4.340	-10.765	-6.539	1.00	23.72	B	C
ATOM	3713	CG	ASP	B	188	4.212	-11.774	-5.429	1.00	24.47	B	C
ATOM	3714	OD1	ASP	B	188	3.517	-11.480	-4.436	1.00	26.68	B	O
ATOM	3715	OD2	ASP	B	188	4.805	-12.876	-5.549	1.00	23.28	B	O
ATOM	3716	C	ASP	B	188	2.006	-9.823	-6.175	1.00	22.61	B	C
ATOM	3717	O	ASP	B	188	1.335	-9.343	-5.259	1.00	22.22	B	O
ATOM	3718	N	ALA	B	189	1.502	-10.584	-7.135	1.00	22.07	B	N
ATOM	3719	CA	ALA	B	189	0.119	-10.970	-7.179	1.00	21.72	B	C
ATOM	3720	CB	ALA	B	189	-0.686	-9.866	-7.814	1.00	21.95	B	C
ATOM	3721	C	ALA	B	189	-0.063	-12.285	-7.949	1.00	21.99	B	C
ATOM	3722	O	ALA	B	189	0.894	-12.860	-8.477	1.00	21.72	B	O
ATOM	3723	N	LEU	B	190	-1.299	-12.772	-7.982	1.00	22.12	B	N
ATOM	3724	CA	LEU	B	190	-1.603	-14.002	-8.679	1.00	22.30	B	C
ATOM	3725	CB	LEU	B	190	-2.900	-14.600	-8.147	1.00	21.89	B	C
ATOM	3726	CG	LEU	B	190	-3.193	-16.011	-8.652	1.00	21.53	B	C
ATOM	3727	CD1	LEU	B	190	-2.019	-16.923	-8.379	1.00	21.51	B	C
ATOM	3728	CD2	LEU	B	190	-4.431	-16.549	-7.978	1.00	22.08	B	C
ATOM	3729	C	LEU	B	190	-1.723	-13.721	-10.171	1.00	23.63	B	C
ATOM	3730	O	LEU	B	190	-1.127	-14.407	-11.028	1.00	23.87	B	O
ATOM	3731	N	ARG	B	191	-2.521	-12.709	-10.474	1.00	24.40	B	N
ATOM	3732	CA	ARG	B	191	-2.519	-12.133	-11.801	1.00	24.81	B	C
ATOM	3733	CB	ARG	B	191	-3.435	-12.925	-12.755	1.00	24.95	B	C
ATOM	3734	CG	ARG	B	191	-4.751	-13.372	-12.166	1.00	24.69	B	C
ATOM	3735	CD	ARG	B	191	-5.454	-14.478	-12.961	1.00	22.98	B	C
ATOM	3736	NE	ARG	B	191	-6.713	-14.712	-12.268	1.00	21.71	B	N
ATOM	3737	CZ	ARG	B	191	-6.947	-15.702	-11.423	1.00	22.56	B	C
ATOM	3738	NH1	ARG	B	191	-6.055	-16.663	-11.206	1.00	22.99	B	N
ATOM	3739	NH2	ARG	B	191	-8.121	-15.770	-10.827	1.00	24.08	B	N
ATOM	3740	C	ARG	B	191	-2.815	-10.632	-11.748	1.00	23.88	B	C
ATOM	3741	O	ARG	B	191	-3.248	-10.103	-10.707	1.00	23.94	B	O
ATOM	3742	N	SER	B	192	-2.488	-9.956	-12.850	1.00	22.79	B	N
ATOM	3743	CA	SER	B	192	-2.641	-8.514	-12.966	1.00	22.71	B	C
ATOM	3744	CB	SER	B	192	-1.283	-7.836	-13.169	1.00	22.27	B	C
ATOM	3745	OG	SER	B	192	-1.397	-6.423	-12.982	1.00	21.78	B	O
ATOM	3746	C	SER	B	192	-3.534	-8.165	-14.134	1.00	22.71	B	C
ATOM	3747	O	SER	B	192	-3.287	-8.605	-15.252	1.00	22.91	B	O
ATOM	3748	N	MET	B	193	-4.548	-7.347	-13.877	1.00	23.42	B	N
ATOM	3749	CA	MET	B	193	-5.441	-6.863	-14.932	1.00	24.44	B	C
ATOM	3750	CB	MET	B	193	-6.750	-6.308	-14.362	1.00	24.83	B	C
ATOM	3751	CG	MET	B	193	-7.378	-7.179	-13.277	1.00	26.13	B	C
ATOM	3752	SD	MET	B	193	-9.085	-6.776	-12.861	1.00	28.08	B	S
ATOM	3753	CE	MET	B	193	-9.889	-7.597	-14.223	1.00	28.27	B	C
ATOM	3754	C	MET	B	193	-4.739	-5.779	-15.723	1.00	25.15	B	C
ATOM	3755	O	MET	B	193	-5.018	-5.604	-16.894	1.00	27.54	B	O
ATOM	3756	N	GLU	B	194	-3.823	-5.059	-15.087	1.00	25.44	B	N
ATOM	3757	CA	GLU	B	194	-3.224	-3.908	-15.697	1.00	25.92	B	C
ATOM	3758	CB	GLU	B	194	-2.674	-2.962	-14.636	1.00	27.83	B	C
ATOM	3759	CG	GLU	B	194	-1.974	-1.743	-15.226	1.00	30.63	B	C
ATOM	3760	CD	GLU	B	194	-0.940	-1.142	-14.304	1.00	32.59	B	C
ATOM	3761	OE1	GLU	B	194	-1.326	-0.320	-13.455	1.00	33.88	B	O
ATOM	3762	OE2	GLU	B	194	0.256	-1.487	-14.441	1.00	34.79	B	O
ATOM	3763	C	GLU	B	194	-2.129	-4.387	-16.641	1.00	25.90	B	C
ATOM	3764	O	GLU	B	194	-2.014	-3.896	-17.758	1.00	26.66	B	O
ATOM	3765	N	ASN	B	195	-1.333	-5.351	-16.206	1.00	24.42	B	N
ATOM	3766	CA	ASN	B	195	-0.279	-5.876	-17.042	1.00	24.87	B	C
ATOM	3767	CB	ASN	B	195	1.032	-5.137	-16.742	1.00	26.34	B	C
ATOM	3768	CG	ASN	B	195	2.250	-5.738	-17.467	1.00	29.35	B	C
ATOM	3769	OD1	ASN	B	195	2.153	-6.336	-18.562	1.00	29.51	B	O
ATOM	3770	ND2	ASN	B	195	3.419	-5.591	-16.834	1.00	31.30	B	N
ATOM	3771	C	ASN	B	195	-0.196	-7.413	-16.888	1.00	24.24	B	C
ATOM	3772	O	ASN	B	195	0.600	-7.933	-16.101	1.00	23.20	B	O
ATOM	3773	N	PRO	B	196	-1.071	-8.139	-17.621	1.00	24.01	B	N
ATOM	3774	CA	PRO	B	196	-1.135	-9.606	-17.577	1.00	23.24	B	C
ATOM	3775	CB	PRO	B	196	-2.134	-9.929	-18.685	1.00	23.91	B	C
ATOM	3776	CG	PRO	B	196	-3.074	-8.754	-18.693	1.00	23.50	B	C
ATOM	3777	CD	PRO	B	196	-2.200	-7.569	-18.399	1.00	23.71	B	C
ATOM	3778	C	PRO	B	196	0.185	-10.321	-17.826	1.00	22.53	B	C
ATOM	3779	O	PRO	B	196	0.494	-11.282	-17.144	1.00	21.13	B	O

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ATOM   3780   N    LYS B 197      0.974  -9.836 -18.774  1.00 23.69      B   N
ATOM   3781   CA   LYS B 197      2.289 -10.419 -19.040  1.00 24.36      B   C
ATOM   3782   CB   LYS B 197      3.051  -9.624 -20.106  1.00 26.48      B   C
ATOM   3783   CG   LYS B 197      2.522  -9.758 -21.531  1.00 28.64      B   C
ATOM   3784   CD   LYS B 197      3.512  -9.183 -22.540  1.00 30.82      B   C
ATOM   3785   CE   LYS B 197      4.561 -10.244 -22.886  1.00 33.46      B   C
ATOM   3786   NZ   LYS B 197      5.890  -9.721 -23.354  1.00 34.43      B   N
ATOM   3787   C    LYS B 197      3.174 -10.537 -17.792  1.00 23.41      B   C
ATOM   3788   O    LYS B 197      4.038 -11.381 -17.745  1.00 23.66      B   O
ATOM   3789   N    LEU B 198      2.975  -9.712 -16.779  1.00 22.98      B   N
ATOM   3790   CA   LEU B 198      3.839  -9.773 -15.594  1.00 23.36      B   C
ATOM   3791   CB   LEU B 198      3.497  -8.658 -14.588  1.00 24.55      B   C
ATOM   3792   CG   LEU B 198      4.462  -8.316 -13.434  1.00 23.95      B   C
ATOM   3793   CD1  LEU B 198      5.905  -8.032 -13.877  1.00 22.89      B   C
ATOM   3794   CD2  LEU B 198      3.851  -7.126 -12.692  1.00 23.13      B   C
ATOM   3795   C    LEU B 198      3.763 -11.120 -14.903  1.00 22.24      B   C
ATOM   3796   O    LEU B 198      4.739 -11.550 -14.277  1.00 20.67      B   O
ATOM   3797   N    TYR B 199      2.609 -11.773 -15.013  1.00 22.06      B   N
ATOM   3798   CA   TYR B 199      2.432 -13.111 -14.444  1.00 22.94      B   C
ATOM   3799   CB   TYR B 199      1.500 -13.048 -13.207  1.00 23.41      B   C
ATOM   3800   CG   TYR B 199      1.901 -11.985 -12.194  1.00 23.95      B   C
ATOM   3801   CD1  TYR B 199      3.023 -12.148 -11.381  1.00 24.19      B   C
ATOM   3802   CE1  TYR B 199      3.400 -11.169 -10.474  1.00 24.03      B   C
ATOM   3803   CZ   TYR B 199      2.647 -10.011 -10.355  1.00 24.37      B   C
ATOM   3804   OH   TYR B 199      3.002  -9.038  -9.442  1.00 24.91      B   O
ATOM   3805   CE2  TYR B 199      1.543  -9.819 -11.152  1.00 24.38      B   C
ATOM   3806   CD2  TYR B 199      1.181 -10.798 -12.074  1.00 24.50      B   C
ATOM   3807   C    TYR B 199      1.975 -14.168 -15.491  1.00 22.26      B   C
ATOM   3808   O    TYR B 199      1.020 -14.929 -15.276  1.00 21.71      B   O
ATOM   3809   N    ASN B 200      2.689 -14.198 -16.614  1.00 21.60      B   N
ATOM   3810   CA   ASN B 200      2.589 -15.264 -17.620  1.00 21.13      B   C
ATOM   3811   CB   ASN B 200      3.209 -16.549 -17.072  1.00 22.32      B   C
ATOM   3812   CG   ASN B 200      4.606 -16.323 -16.485  1.00 23.87      B   C
ATOM   3813   OD1  ASN B 200      5.610 -16.490 -17.183  1.00 24.05      B   O
ATOM   3814   ND2  ASN B 200      4.675 -15.933 -15.190  1.00 24.03      B   N
ATOM   3815   C    ASN B 200      1.163 -15.477 -18.168  1.00 19.76      B   C
ATOM   3816   O    ASN B 200      0.696 -16.607 -18.388  1.00 17.76      B   O
ATOM   3817   N    GLN B 201      0.495 -14.348 -18.381  1.00 18.92      B   N
ATOM   3818   CA   GLN B 201     -0.770 -14.294 -19.088  1.00 19.24      B   C
ATOM   3819   CB   GLN B 201     -1.840 -13.585 -18.250  1.00 17.82      B   C
ATOM   3820   CG   GLN B 201     -2.373 -14.366 -17.083  1.00 16.72      B   C
ATOM   3821   CD   GLN B 201     -3.552 -13.685 -16.459  1.00 16.42      B   C
ATOM   3822   OE1  GLN B 201     -3.450 -12.553 -16.004  1.00 15.89      B   O
ATOM   3823   NE2  GLN B 201     -4.687 -14.371 -16.429  1.00 16.72      B   N
ATOM   3824   C    GLN B 201     -0.600 -13.490 -20.369  1.00 20.79      B   C
ATOM   3825   O    GLN B 201     -0.009 -12.417 -20.355  1.00 22.47      B   O
ATOM   3826   N    PRO B 202     -1.160 -13.970 -21.471  1.00 21.98      B   N
ATOM   3827   CA   PRO B 202     -1.091 -13.132 -22.622  1.00 22.64      B   C
ATOM   3828   CB   PRO B 202     -1.481 -14.079 -23.742  1.00 22.77      B   C
ATOM   3829   CG   PRO B 202     -2.452 -15.019 -23.119  1.00 22.83      B   C
ATOM   3830   CD   PRO B 202     -2.109 -15.080 -21.656  1.00 22.57      B   C
ATOM   3831   C    PRO B 202     -2.085 -11.965 -22.505  1.00 24.85      B   C
ATOM   3832   O    PRO B 202     -3.127 -12.061 -21.810  1.00 23.59      B   O
ATOM   3833   N    ASP B 203     -1.737 -10.880 -23.202  1.00 27.61      B   N
ATOM   3834   CA   ASP B 203     -2.492  -9.640 -23.199  1.00 30.45      B   C
ATOM   3835   CB   ASP B 203     -1.610  -8.492 -22.682  1.00 32.67      B   C
ATOM   3836   CG   ASP B 203     -0.356  -8.294 -23.502  1.00 34.23      B   C
ATOM   3837   OD1  ASP B 203     -0.252  -8.865 -24.613  1.00 36.10      B   O
ATOM   3838   OD2  ASP B 203      0.534  -7.576 -23.017  1.00 35.07      B   O
ATOM   3839   C    ASP B 203     -3.058  -9.284 -24.575  1.00 32.33      B   C
ATOM   3840   O    ASP B 203     -3.488  -8.154 -24.772  1.00 32.63      B   O
ATOM   3841   N    ARG B 204     -3.032 -10.235 -25.518  1.00 34.07      B   N
ATOM   3842   CA   ARG B 204     -3.744 -10.117 -26.791  1.00 34.55      B   C
ATOM   3843   CB   ARG B 204     -2.943  -9.280 -27.777  1.00 36.55      B   C
ATOM   3844   CG   ARG B 204     -1.516  -9.767 -27.975  1.00 39.06      B   C
ATOM   3845   CD   ARG B 204     -0.877  -9.151 -29.214  1.00 42.75      B   C
ATOM   3846   NE   ARG B 204      0.412  -9.771 -29.545  1.00 49.37      B   N
ATOM   3847   CZ   ARG B 204      1.388  -9.199 -30.267  1.00 53.04      B   C
ATOM   3848   NH1  ARG B 204      1.253  -7.971 -30.769  1.00 51.45      B   N
ATOM   3849   NH2  ARG B 204      2.525  -9.858 -30.482  1.00 53.50      B   N
ATOM   3850   C    ARG B 204     -4.071 -11.495 -27.408  1.00 36.34      B   C
ATOM   3851   O    ARG B 204     -3.251 -12.429 -27.360  1.00 36.07      B   O
ATOM   3852   N    TYR B 205     -5.271 -11.592 -28.001  1.00 36.40      B   N
ATOM   3853   CA   TYR B 205     -5.844 -12.829 -28.581  1.00 34.16      B   C
ATOM   3854   CB   TYR B 205     -7.022 -12.465 -29.497  1.00 34.62      B   C
ATOM   3855   CG   TYR B 205     -7.925 -13.612 -29.902  1.00 32.64      B   C
ATOM   3856   CD1  TYR B 205     -8.842 -14.136 -29.001  1.00 32.71      B   C
ATOM   3857   CE1  TYR B 205     -9.685 -15.166 -29.348  1.00 32.40      B   C
ATOM   3858   CZ   TYR B 205     -9.637 -15.671 -30.619  1.00 32.09      B   C
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ATOM	3859	OH	TYR	B	205	-10.483	-16.696	-30.926	1.00	29.46	B	O
ATOM	3860	CE2	TYR	B	205	-8.743	-15.161	-31.546	1.00	32.02	B	C
ATOM	3861	CD2	TYR	B	205	-7.898	-14.132	-31.185	1.00	31.56	B	C
ATOM	3862	C	TYR	B	205	-4.872	-13.655	-29.394	1.00	32.77	B	C
ATOM	3863	O	TYR	B	205	-4.928	-14.872	-29.361	1.00	31.27	B	O
ATOM	3864	N	GLN	B	206	-3.996	-12.993	-30.136	1.00	32.81	B	N
ATOM	3865	CA	GLN	B	206	-3.030	-13.715	-30.972	1.00	35.21	B	C
ATOM	3866	CB	GLN	B	206	-2.272	-12.841	-32.044	1.00	38.64	B	C
ATOM	3867	CG	GLN	B	206	-2.106	-11.308	-31.866	1.00	42.08	B	C
ATOM	3868	CD	GLN	B	206	-3.425	-10.488	-31.920	1.00	43.10	B	C
ATOM	3869	OE1	GLN	B	206	-3.551	-9.459	-31.249	1.00	44.46	B	O
ATOM	3870	NE2	GLN	B	206	-4.410	-10.960	-32.688	1.00	42.28	B	N
ATOM	3871	C	GLN	B	206	-2.071	-14.536	-30.129	1.00	33.13	B	C
ATOM	3872	O	GLN	B	206	-1.563	-15.534	-30.607	1.00	35.03	B	O
ATOM	3873	N	ASP	B	207	-1.855	-14.166	-28.870	1.00	31.41	B	N
ATOM	3874	CA	ASP	B	207	-0.906	-14.913	-28.018	1.00	29.64	B	C
ATOM	3875	CB	ASP	B	207	-0.053	-13.937	-27.197	1.00	29.62	B	C
ATOM	3876	CG	ASP	B	207	0.970	-13.202	-28.048	1.00	30.75	B	C
ATOM	3877	OD1	ASP	B	207	1.183	-13.628	-29.212	1.00	30.64	B	O
ATOM	3878	OD2	ASP	B	207	1.553	-12.200	-27.561	1.00	30.25	B	O
ATOM	3879	C	ASP	B	207	-1.556	-15.951	-27.101	1.00	27.81	B	C
ATOM	3880	O	ASP	B	207	-0.896	-16.513	-26.227	1.00	26.27	B	O
ATOM	3881	N	ARG	B	208	-2.836	-16.246	-27.312	1.00	26.49	B	N
ATOM	3882	CA	ARG	B	208	-3.536	-17.097	-26.368	1.00	24.72	B	C
ATOM	3883	CB	ARG	B	208	-5.010	-17.243	-26.708	1.00	24.36	B	C
ATOM	3884	CG	ARG	B	208	-5.326	-17.924	-28.024	1.00	24.48	B	C
ATOM	3885	CD	ARG	B	208	-6.755	-17.538	-28.400	1.00	25.04	B	C
ATOM	3886	NE	ARG	B	208	-7.264	-18.154	-29.617	1.00	24.76	B	N
ATOM	3887	CZ	ARG	B	208	-6.783	-17.933	-30.837	1.00	25.11	B	C
ATOM	3888	NH1	ARG	B	208	-5.750	-17.136	-31.060	1.00	25.82	B	N
ATOM	3889	NH2	ARG	B	208	-7.337	-18.534	-31.858	1.00	26.12	B	N
ATOM	3890	C	ARG	B	208	-2.920	-18.451	-26.283	1.00	24.48	B	C
ATOM	3891	O	ARG	B	208	-2.232	-18.908	-27.185	1.00	25.71	B	O
ATOM	3892	N	TYR	B	209	-3.188	-19.103	-25.167	1.00	24.84	B	N
ATOM	3893	CA	TYR	B	209	-2.840	-20.510	-25.000	1.00	22.96	B	C
ATOM	3894	CB	TYR	B	209	-2.724	-20.842	-23.521	1.00	21.57	B	C
ATOM	3895	CG	TYR	B	209	-2.520	-22.291	-23.180	1.00	19.77	B	C
ATOM	3896	CD1	TYR	B	209	-1.260	-22.868	-23.218	1.00	18.75	B	C
ATOM	3897	CE1	TYR	B	209	-1.091	-24.213	-22.858	1.00	18.78	B	C
ATOM	3898	CZ	TYR	B	209	-2.192	-24.978	-22.441	1.00	18.01	B	C
ATOM	3899	OH	TYR	B	209	-2.057	-26.288	-22.082	1.00	17.53	B	O
ATOM	3900	CE2	TYR	B	209	-3.442	-24.416	-22.391	1.00	18.24	B	C
ATOM	3901	CD2	TYR	B	209	-3.603	-23.077	-22.740	1.00	19.13	B	C
ATOM	3902	C	TYR	B	209	-3.912	-21.351	-25.673	1.00	22.56	B	C
ATOM	3903	O	TYR	B	209	-5.106	-21.048	-25.608	1.00	21.55	B	O
ATOM	3904	N	THR	B	210	-3.438	-22.421	-26.304	1.00	23.19	B	N
ATOM	3905	CA	THR	B	210	-4.190	-23.254	-27.246	1.00	21.30	B	C
ATOM	3906	CB	THR	B	210	-3.509	-23.070	-28.627	1.00	20.51	B	C
ATOM	3907	OG1	THR	B	210	-4.283	-22.128	-29.351	1.00	19.96	B	O
ATOM	3908	CG2	THR	B	210	-3.380	-24.329	-29.449	1.00	21.23	B	C
ATOM	3909	C	THR	B	210	-4.291	-24.717	-26.770	1.00	20.49	B	C
ATOM	3910	O	THR	B	210	-4.989	-25.528	-27.385	1.00	22.84	B	O
ATOM	3911	N	GLY	B	211	-3.622	-25.037	-25.662	1.00	18.65	B	N
ATOM	3912	CA	GLY	B	211	-3.502	-26.404	-25.164	1.00	17.86	B	C
ATOM	3913	C	GLY	B	211	-4.688	-26.812	-24.313	1.00	17.46	B	C
ATOM	3914	O	GLY	B	211	-5.628	-26.022	-24.134	1.00	17.51	B	O
ATOM	3915	N	PRO	B	212	-4.664	-28.052	-23.801	1.00	16.80	B	N
ATOM	3916	CA	PRO	B	212	-5.780	-28.673	-23.088	1.00	17.36	B	C
ATOM	3917	CB	PRO	B	212	-5.594	-30.156	-23.396	1.00	16.89	B	C
ATOM	3918	CG	PRO	B	212	-4.113	-30.308	-23.446	1.00	17.16	B	C
ATOM	3919	CD	PRO	B	212	-3.604	-29.030	-24.083	1.00	17.00	B	C
ATOM	3920	C	PRO	B	212	-5.769	-28.494	-21.573	1.00	18.49	B	C
ATOM	3921	O	PRO	B	212	-6.773	-28.798	-20.908	1.00	19.01	B	O
ATOM	3922	N	SER	B	213	-4.645	-28.019	-21.056	1.00	18.86	B	N
ATOM	3923	CA	SER	B	213	-4.391	-27.910	-19.645	1.00	19.95	B	C
ATOM	3924	CB	SER	B	213	-2.881	-27.698	-19.495	1.00	22.65	B	C
ATOM	3925	OG	SER	B	213	-2.471	-27.825	-18.161	1.00	26.25	B	O
ATOM	3926	C	SER	B	213	-5.168	-26.724	-19.078	1.00	18.23	B	C
ATOM	3927	O	SER	B	213	-5.345	-25.770	-19.779	1.00	16.91	B	O
ATOM	3928	N	ASP	B	214	-5.635	-26.785	-17.824	1.00	18.11	B	N
ATOM	3929	CA	ASP	B	214	-6.440	-25.689	-17.227	1.00	17.78	B	C
ATOM	3930	CB	ASP	B	214	-5.596	-24.409	-17.164	1.00	17.90	B	C
ATOM	3931	CG	ASP	B	214	-6.244	-23.295	-16.378	1.00	17.76	B	C
ATOM	3932	OD1	ASP	B	214	-7.112	-23.546	-15.494	1.00	18.10	B	O
ATOM	3933	OD2	ASP	B	214	-5.857	-22.141	-16.651	1.00	17.17	B	O
ATOM	3934	C	ASP	B	214	-7.708	-25.443	-18.049	1.00	18.13	B	C
ATOM	3935	O	ASP	B	214	-7.986	-24.311	-18.477	1.00	16.78	B	O
ATOM	3936	N	ASN	B	215	-8.446	-26.527	-18.296	1.00	18.96	B	N
ATOM	3937	CA	ASN	B	215	-9.601	-26.515	-19.196	1.00	19.63	B	C

ATOM	3938	CB	ASN	B	215	-10.848	-26.092	-18.422	1.00	20.32	B	C
ATOM	3939	CG	ASN	B	215	-11.257	-27.138	-17.405	1.00	20.81	B	C
ATOM	3940	OD1	ASN	B	215	-11.299	-28.333	-17.713	1.00	21.24	B	O
ATOM	3941	ND2	ASN	B	215	-11.492	-26.715	-16.188	1.00	21.02	B	N
ATOM	3942	C	ASN	B	215	-9.354	-25.645	-20.420	1.00	20.01	B	C
ATOM	3943	O	ASN	B	215	-10.137	-24.759	-20.766	1.00	20.66	B	O
ATOM	3944	N	GLY	B	216	-8.219	-25.896	-21.058	1.00	20.01	B	N
ATOM	3945	CA	GLY	B	216	-7.796	-25.146	-22.226	1.00	19.24	B	C
ATOM	3946	C	GLY	B	216	-7.633	-23.662	-21.985	1.00	18.69	B	C
ATOM	3947	O	GLY	B	216	-8.297	-22.859	-22.638	1.00	18.64	B	O
ATOM	3948	N	GLY	B	217	-6.775	-23.303	-21.030	1.00	18.39	B	N
ATOM	3949	CA	GLY	B	217	-6.297	-21.910	-20.845	1.00	18.17	B	C
ATOM	3950	C	GLY	B	217	-7.079	-20.998	-19.908	1.00	17.90	B	C
ATOM	3951	O	GLY	B	217	-6.747	-19.836	-19.739	1.00	18.36	B	O
ATOM	3952	N	VAL	B	218	-8.082	-21.542	-19.248	1.00	18.00	B	N
ATOM	3953	CA	VAL	B	218	-9.075	-20.757	-18.535	1.00	18.49	B	C
ATOM	3954	CB	VAL	B	218	-9.978	-21.757	-17.786	1.00	18.67	B	C
ATOM	3955	CG1	VAL	B	218	-10.669	-21.159	-16.609	1.00	19.04	B	C
ATOM	3956	CG2	VAL	B	218	-11.017	-22.288	-18.752	1.00	19.24	B	C
ATOM	3957	C	VAL	B	218	-8.520	-19.593	-17.660	1.00	19.13	B	C
ATOM	3958	O	VAL	B	218	-9.025	-18.488	-17.723	1.00	18.61	B	O
ATOM	3959	N	HIS	B	219	-7.480	-19.833	-16.865	1.00	19.66	B	N
ATOM	3960	CA	HIS	B	219	-6.885	-18.786	-16.037	1.00	19.59	B	C
ATOM	3961	CB	HIS	B	219	-6.449	-19.301	-14.641	1.00	20.15	B	C
ATOM	3962	CG	HIS	B	219	-7.529	-19.983	-13.848	1.00	19.47	B	C
ATOM	3963	ND1	HIS	B	219	-7.816	-21.327	-13.979	1.00	19.54	B	N
ATOM	3964	CE1	HIS	B	219	-8.807	-21.643	-13.163	1.00	19.59	B	C
ATOM	3965	NE2	HIS	B	219	-9.158	-20.559	-12.494	1.00	18.98	B	N
ATOM	3966	CD2	HIS	B	219	-8.361	-19.513	-12.891	1.00	19.03	B	C
ATOM	3967	C	HIS	B	219	-5.658	-18.243	-16.725	1.00	20.25	B	C
ATOM	3968	O	HIS	B	219	-5.105	-17.241	-16.283	1.00	20.29	B	O
ATOM	3969	N	ILE	B	220	-5.171	-18.915	-17.766	1.00	21.20	B	N
ATOM	3970	CA	ILE	B	220	-4.097	-18.309	-18.566	1.00	21.97	B	C
ATOM	3971	CB	ILE	B	220	-3.375	-19.323	-19.457	1.00	22.68	B	C
ATOM	3972	CG1	ILE	B	220	-2.724	-20.393	-18.595	1.00	23.99	B	C
ATOM	3973	CD1	ILE	B	220	-2.178	-21.553	-19.404	1.00	24.68	B	C
ATOM	3974	CG2	ILE	B	220	-2.293	-18.655	-20.293	1.00	22.37	B	C
ATOM	3975	C	ILE	B	220	-4.698	-17.207	-19.426	1.00	22.02	B	C
ATOM	3976	O	ILE	B	220	-4.261	-16.068	-19.344	1.00	23.21	B	O
ATOM	3977	N	ASN	B	221	-5.724	-17.545	-20.209	1.00	20.75	B	N
ATOM	3978	CA	ASN	B	221	-6.311	-16.624	-21.182	1.00	20.24	B	C
ATOM	3979	CB	ASN	B	221	-6.996	-17.406	-22.300	1.00	18.70	B	C
ATOM	3980	CG	ASN	B	221	-6.009	-18.178	-23.149	1.00	17.72	B	C
ATOM	3981	OD1	ASN	B	221	-4.883	-17.752	-23.379	1.00	17.36	B	O
ATOM	3982	ND2	ASN	B	221	-6.425	-19.321	-23.609	1.00	16.99	B	N
ATOM	3983	C	ASN	B	221	-7.291	-15.582	-20.631	1.00	21.78	B	C
ATOM	3984	O	ASN	B	221	-7.719	-14.705	-21.386	1.00	21.93	B	O
ATOM	3985	N	SER	B	222	-7.651	-15.633	-19.346	1.00	22.00	B	N
ATOM	3986	CA	SER	B	222	-8.578	-14.633	-18.860	1.00	22.02	B	C
ATOM	3987	CB	SER	B	222	-9.109	-14.959	-17.466	1.00	22.44	B	C
ATOM	3988	OG	SER	B	222	-8.090	-15.068	-16.478	1.00	23.22	B	O
ATOM	3989	C	SER	B	222	-7.852	-13.297	-18.931	1.00	23.31	B	C
ATOM	3990	O	SER	B	222	-8.481	-12.230	-19.024	1.00	22.58	B	O
ATOM	3991	N	GLY	B	223	-6.516	-13.371	-18.945	1.00	24.52	B	N
ATOM	3992	CA	GLY	B	223	-5.651	-12.186	-19.052	1.00	25.84	B	C
ATOM	3993	C	GLY	B	223	-6.008	-11.231	-20.177	1.00	26.96	B	C
ATOM	3994	O	GLY	B	223	-5.884	-10.001	-20.034	1.00	28.19	B	O
ATOM	3995	N	ILE	B	224	-6.437	-11.809	-21.296	1.00	26.49	B	N
ATOM	3996	CA	ILE	B	224	-6.923	-11.057	-22.459	1.00	25.44	B	C
ATOM	3997	CB	ILE	B	224	-7.187	-12.011	-23.637	1.00	24.70	B	C
ATOM	3998	CG1	ILE	B	224	-5.849	-12.487	-24.198	1.00	24.83	B	C
ATOM	3999	CD1	ILE	B	224	-5.956	-13.782	-24.968	1.00	25.47	B	C
ATOM	4000	CG2	ILE	B	224	-8.002	-11.327	-24.720	1.00	24.67	B	C
ATOM	4001	C	ILE	B	224	-8.172	-10.209	-22.179	1.00	24.64	B	C
ATOM	4002	O	ILE	B	224	-8.209	-9.029	-22.468	1.00	25.66	B	O
ATOM	4003	N	ASN	B	225	-9.212	-10.798	-21.637	1.00	24.78	B	N
ATOM	4004	CA	ASN	B	225	-10.377	-10.011	-21.335	1.00	24.71	B	C
ATOM	4005	CB	ASN	B	225	-11.549	-10.903	-20.978	1.00	24.55	B	C
ATOM	4006	CG	ASN	B	225	-12.869	-10.188	-21.126	1.00	24.56	B	C
ATOM	4007	OD1	ASN	B	225	-13.625	-9.979	-20.164	1.00	23.26	B	O
ATOM	4008	ND2	ASN	B	225	-13.143	-9.775	-22.347	1.00	25.30	B	N
ATOM	4009	C	ASN	B	225	-10.097	-9.051	-20.188	1.00	25.63	B	C
ATOM	4010	O	ASN	B	225	-10.577	-7.922	-20.188	1.00	25.70	B	O
ATOM	4011	N	ASN	B	226	-9.321	-9.494	-19.204	1.00	26.62	B	N
ATOM	4012	CA	ASN	B	226	-8.969	-8.608	-18.104	1.00	26.81	B	C
ATOM	4013	CB	ASN	B	226	-8.135	-9.330	-17.035	1.00	27.03	B	C
ATOM	4014	CG	ASN	B	226	-8.963	-10.256	-16.156	1.00	27.23	B	C
ATOM	4015	OD1	ASN	B	226	-10.195	-10.313	-16.254	1.00	26.96	B	O
ATOM	4016	ND2	ASN	B	226	-8.277	-11.001	-15.289	1.00	27.06	B	N

ATOM	4017	C	ASN	B	226	-8.243	-7.340	-18.594	1.00	26.48	B	C
ATOM	4018	O	ASN	B	226	-8.512	-6.254	-18.096	1.00	28.43	B	O
ATOM	4019	N	LYS	B	227	-7.343	-7.458	-19.558	1.00	24.83	B	N
ATOM	4020	CA	LYS	B	227	-6.685	-6.271	-20.081	1.00	25.45	B	C
ATOM	4021	CB	LYS	B	227	-5.631	-6.652	-21.096	1.00	25.83	B	C
ATOM	4022	CG	LYS	B	227	-4.834	-5.495	-21.646	1.00	25.86	B	C
ATOM	4023	CD	LYS	B	227	-3.856	-4.952	-20.632	1.00	27.34	B	C
ATOM	4024	CE	LYS	B	227	-3.290	-3.619	-21.118	1.00	28.38	B	C
ATOM	4025	NZ	LYS	B	227	-2.147	-3.154	-20.291	1.00	28.32	B	N
ATOM	4026	C	LYS	B	227	-7.675	-5.333	-20.742	1.00	26.25	B	C
ATOM	4027	O	LYS	B	227	-7.581	-4.130	-20.580	1.00	27.67	B	O
ATOM	4028	N	ALA	B	228	-8.605	-5.884	-21.509	1.00	26.38	B	N
ATOM	4029	CA	ALA	B	228	-9.669	-5.091	-22.101	1.00	26.22	B	C
ATOM	4030	CB	ALA	B	228	-10.670	-5.974	-22.840	1.00	26.76	B	C
ATOM	4031	C	ALA	B	228	-10.387	-4.320	-21.027	1.00	26.05	B	C
ATOM	4032	O	ALA	B	228	-10.645	-3.149	-21.190	1.00	28.08	B	O
ATOM	4033	N	PHE	B	229	-10.725	-4.969	-19.926	1.00	25.85	B	N
ATOM	4034	CA	PHE	B	229	-11.412	-4.266	-18.853	1.00	25.93	B	C
ATOM	4035	CB	PHE	B	229	-11.755	-5.203	-17.712	1.00	25.94	B	C
ATOM	4036	CG	PHE	B	229	-12.518	-4.533	-16.642	1.00	26.06	B	C
ATOM	4037	CD1	PHE	B	229	-13.890	-4.407	-16.748	1.00	26.92	B	C
ATOM	4038	CE1	PHE	B	229	-14.620	-3.758	-15.766	1.00	27.95	B	C
ATOM	4039	CZ	PHE	B	229	-13.963	-3.228	-14.661	1.00	27.83	B	C
ATOM	4040	CE2	PHE	B	229	-12.580	-3.341	-14.562	1.00	27.45	B	C
ATOM	4041	CD2	PHE	B	229	-11.868	-3.985	-15.551	1.00	26.96	B	C
ATOM	4042	C	PHE	B	229	-10.626	-3.063	-18.313	1.00	25.50	B	C
ATOM	4043	O	PHE	B	229	-11.162	-1.968	-18.214	1.00	26.44	B	O
ATOM	4044	N	TYR	B	230	-9.362	-3.262	-17.970	1.00	25.44	B	N
ATOM	4045	CA	TYR	B	230	-8.488	-2.153	-17.546	1.00	26.60	B	C
ATOM	4046	CB	TYR	B	230	-7.055	-2.645	-17.394	1.00	26.50	B	C
ATOM	4047	CG	TYR	B	230	-6.057	-1.545	-17.152	1.00	26.33	B	C
ATOM	4048	CD1	TYR	B	230	-5.980	-0.908	-15.912	1.00	25.76	B	C
ATOM	4049	CE1	TYR	B	230	-5.055	0.087	-15.667	1.00	25.25	B	C
ATOM	4050	CZ	TYR	B	230	-4.191	0.458	-16.664	1.00	26.43	B	C
ATOM	4051	OH	TYR	B	230	-3.275	1.445	-16.431	1.00	27.30	B	O
ATOM	4052	CE2	TYR	B	230	-4.237	-0.160	-17.903	1.00	27.11	B	C
ATOM	4053	CD2	TYR	B	230	-5.181	-1.149	-18.146	1.00	26.74	B	C
ATOM	4054	C	TYR	B	230	-8.455	-0.948	-18.499	1.00	26.53	B	C
ATOM	4055	O	TYR	B	230	-8.456	0.196	-18.050	1.00	26.33	B	O
ATOM	4056	N	LEU	B	231	-8.386	-1.221	-19.798	1.00	26.27	B	N
ATOM	4057	CA	LEU	B	231	-8.373	-0.180	-20.809	1.00	26.57	B	C
ATOM	4058	CB	LEU	B	231	-8.041	-0.775	-22.171	1.00	25.37	B	C
ATOM	4059	CG	LEU	B	231	-6.568	-1.208	-22.262	1.00	25.50	B	C
ATOM	4060	CD1	LEU	B	231	-6.257	-2.057	-23.476	1.00	25.18	B	C
ATOM	4061	CD2	LEU	B	231	-5.657	0.007	-22.268	1.00	26.56	B	C
ATOM	4062	C	LEU	B	231	-9.705	0.574	-20.817	1.00	28.83	B	C
ATOM	4063	O	LEU	B	231	-9.743	1.805	-20.856	1.00	30.14	B	O
ATOM	4064	N	ILE	B	232	-10.799	-0.156	-20.705	1.00	29.54	B	N
ATOM	4065	CA	ILE	B	232	-12.115	0.458	-20.640	1.00	29.21	B	C
ATOM	4066	CB	ILE	B	232	-13.197	-0.634	-20.677	1.00	28.64	B	C
ATOM	4067	CG1	ILE	B	232	-13.234	-1.247	-22.084	1.00	29.59	B	C
ATOM	4068	CD1	ILE	B	232	-14.053	-2.517	-22.206	1.00	29.92	B	C
ATOM	4069	CG2	ILE	B	232	-14.561	-0.084	-20.291	1.00	28.76	B	C
ATOM	4070	C	ILE	B	232	-12.269	1.291	-19.374	1.00	30.72	B	C
ATOM	4071	O	ILE	B	232	-13.009	2.273	-19.340	1.00	33.34	B	O
ATOM	4072	N	ALA	B	233	-11.595	0.888	-18.309	1.00	31.94	B	N
ATOM	4073	CA	ALA	B	233	-11.820	1.522	-17.007	1.00	30.90	B	C
ATOM	4074	CB	ALA	B	233	-11.604	0.509	-15.900	1.00	31.09	B	C
ATOM	4075	C	ALA	B	233	-10.896	2.715	-16.829	1.00	29.25	B	C
ATOM	4076	O	ALA	B	233	-11.338	3.839	-16.703	1.00	26.84	B	O
ATOM	4077	N	GLN	B	234	-9.601	2.438	-16.850	1.00	28.21	B	N
ATOM	4078	CA	GLN	B	234	-8.605	3.442	-16.643	1.00	27.52	B	C
ATOM	4079	CB	GLN	B	234	-7.332	2.775	-16.136	1.00	27.99	B	C
ATOM	4080	CG	GLN	B	234	-6.297	3.757	-15.629	1.00	27.70	B	C
ATOM	4081	CD	GLN	B	234	-6.901	4.805	-14.703	1.00	27.94	B	C
ATOM	4082	OE1	GLN	B	234	-7.897	4.556	-13.997	1.00	27.32	B	O
ATOM	4083	NE2	GLN	B	234	-6.301	5.988	-14.702	1.00	27.80	B	N
ATOM	4084	C	GLN	B	234	-8.257	4.222	-17.892	1.00	27.94	B	C
ATOM	4085	O	GLN	B	234	-7.823	5.377	-17.791	1.00	28.34	B	O
ATOM	4086	N	GLY	B	235	-8.417	3.590	-19.059	1.00	27.37	B	N
ATOM	4087	CA	GLY	B	235	-7.817	4.077	-20.296	1.00	25.77	B	C
ATOM	4088	C	GLY	B	235	-6.345	3.708	-20.328	1.00	25.72	B	C
ATOM	4089	O	GLY	B	235	-5.740	3.433	-19.292	1.00	25.36	B	O
ATOM	4090	N	GLY	B	236	-5.769	3.700	-21.523	1.00	25.94	B	N
ATOM	4091	CA	GLY	B	236	-4.350	3.423	-21.698	1.00	26.60	B	C
ATOM	4092	C	GLY	B	236	-4.044	3.322	-23.177	1.00	28.63	B	C
ATOM	4093	O	GLY	B	236	-4.919	3.572	-24.017	1.00	29.26	B	O
ATOM	4094	N	THR	B	237	-2.801	2.970	-23.485	1.00	29.75	B	N
ATOM	4095	CA	THR	B	237	-2.327	2.831	-24.842	1.00	31.58	B	C

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ATOM   4096  CB   THR B 237      -1.327   3.962 -25.206  1.00 33.98      B    C
ATOM   4097  OG1  THR B 237      -2.063   5.104 -25.633  1.00 37.98      B    O
ATOM   4098  CG2  THR B 237      -0.360   3.594 -26.356  1.00 34.58      B    C
ATOM   4099  C    THR B 237      -1.650   1.496 -24.899  1.00 34.03      B    C
ATOM   4100  O    THR B 237      -0.632   1.298 -24.230  1.00 34.87      B    O
ATOM   4101  N    HIS B 238      -2.184   0.602 -25.731  1.00 36.70      B    N
ATOM   4102  CA   HIS B 238      -1.747  -0.790 -25.793  1.00 37.24      B    C
ATOM   4103  CB   HIS B 238      -2.711  -1.577 -24.898  1.00 42.00      B    C
ATOM   4104  CG   HIS B 238      -2.361  -3.020 -24.728  1.00 43.70      B    C
ATOM   4105  ND1  HIS B 238      -3.268  -4.030 -24.968  1.00 43.48      B    N
ATOM   4106  CE1  HIS B 238      -2.691  -5.194 -24.734  1.00 46.45      B    C
ATOM   4107  NE2  HIS B 238      -1.445  -4.974 -24.351  1.00 47.60      B    N
ATOM   4108  CD2  HIS B 238      -1.213  -3.620 -24.335  1.00 45.16      B    C
ATOM   4109  C    HIS B 238      -1.769  -1.323 -27.239  1.00 35.71      B    C
ATOM   4110  O    HIS B 238      -2.832  -1.322 -27.876  1.00 31.39      B    O
ATOM   4111  N    TYR B 239      -0.616  -1.798 -27.743  1.00 37.49      B    N
ATOM   4112  CA   TYR B 239      -0.431  -2.163 -29.201  1.00 39.68      B    C
ATOM   4113  CB   TYR B 239      -0.973  -3.577 -29.559  1.00 38.30      B    C
ATOM   4114  CG   TYR B 239      -0.280  -4.661 -28.775  1.00 36.05      B    C
ATOM   4115  CD1  TYR B 239       1.087  -4.867 -28.915  1.00 36.03      B    C
ATOM   4116  CE1  TYR B 239       1.755  -5.830 -28.174  1.00 36.29      B    C
ATOM   4117  CZ   TYR B 239       1.042  -6.605 -27.259  1.00 37.19      B    C
ATOM   4118  OH   TYR B 239       1.707  -7.570 -26.501  1.00 34.74      B    O
ATOM   4119  CE2  TYR B 239      -0.333  -6.403 -27.104  1.00 36.29      B    C
ATOM   4120  CD2  TYR B 239      -0.975  -5.433 -27.855  1.00 35.25      B    C
ATOM   4121  C    TYR B 239      -1.026  -1.116 -30.152  1.00 41.11      B    C
ATOM   4122  O    TYR B 239      -2.046  -1.350 -30.818  1.00 40.61      B    O
ATOM   4123  N    GLY B 240      -0.401   0.057 -30.164  1.00 42.40      B    N
ATOM   4124  CA   GLY B 240      -0.862   1.165 -30.985  1.00 43.82      B    C
ATOM   4125  C    GLY B 240      -2.136   1.887 -30.549  1.00 42.06      B    C
ATOM   4126  O    GLY B 240      -2.231   3.116 -30.685  1.00 42.31      B    O
ATOM   4127  N    VAL B 241      -3.121   1.152 -30.047  1.00 38.05      B    N
ATOM   4128  CA   VAL B 241      -4.450   1.724 -29.817  1.00 37.68      B    C
ATOM   4129  CB   VAL B 241      -5.488   0.599 -29.856  1.00 35.77      B    C
ATOM   4130  CG1  VAL B 241      -6.907   1.130 -29.740  1.00 34.09      B    C
ATOM   4131  CG2  VAL B 241      -5.277  -0.194 -31.139  1.00 35.98      B    C
ATOM   4132  C    VAL B 241      -4.524   2.586 -28.519  1.00 38.81      B    C
ATOM   4133  O    VAL B 241      -3.917   2.253 -27.499  1.00 39.08      B    O
ATOM   4134  N    THR B 242      -5.204   3.732 -28.605  1.00 38.22      B    N
ATOM   4135  CA   THR B 242      -5.407   4.614 -27.465  1.00 38.17      B    C
ATOM   4136  CB   THR B 242      -5.044   6.083 -27.805  1.00 37.28      B    C
ATOM   4137  OG1  THR B 242      -3.630   6.233 -27.717  1.00 38.40      B    O
ATOM   4138  CG2  THR B 242      -5.670   7.096 -26.838  1.00 36.94      B    C
ATOM   4139  C    THR B 242      -6.865   4.458 -27.034  1.00 39.27      B    C
ATOM   4140  O    THR B 242      -7.788   4.557 -27.851  1.00 39.33      B    O
ATOM   4141  N    VAL B 243      -7.064   4.176 -25.752  1.00 38.72      B    N
ATOM   4142  CA   VAL B 243      -8.396   4.046 -25.213  1.00 38.15      B    C
ATOM   4143  CB   VAL B 243      -8.615   2.696 -24.551  1.00 36.94      B    C
ATOM   4144  CG1  VAL B 243     -10.085   2.522 -24.211  1.00 37.69      B    C
ATOM   4145  CG2  VAL B 243      -8.171   1.598 -25.492  1.00 39.28      B    C
ATOM   4146  C    VAL B 243      -8.566   5.090 -24.162  1.00 39.74      B    C
ATOM   4147  O    VAL B 243      -7.658   5.304 -23.362  1.00 40.60      B    O
ATOM   4148  N    ASN B 244      -9.727   5.736 -24.174  1.00 40.74      B    N
ATOM   4149  CA   ASN B 244     -10.041   6.753 -23.201  1.00 40.96      B    C
ATOM   4150  CB   ASN B 244     -10.781   7.919 -23.855  1.00 43.87      B    C
ATOM   4151  CG   ASN B 244      -9.999   8.560 -25.011  1.00 47.13      B    C
ATOM   4152  OD1  ASN B 244      -8.756   8.572 -25.061  1.00 44.34      B    O
ATOM   4153  ND2  ASN B 244     -10.748   9.112 -25.957  1.00 51.75      B    N
ATOM   4154  C    ASN B 244     -10.921   6.076 -22.180  1.00 38.39      B    C
ATOM   4155  O    ASN B 244     -11.998   5.629 -22.522  1.00 40.30      B    O
ATOM   4156  N    GLY B 245     -10.462   5.995 -20.936  1.00 34.92      B    N
ATOM   4157  CA   GLY B 245     -11.194   5.303 -19.883  1.00 33.21      B    C
ATOM   4158  C    GLY B 245     -12.547   5.921 -19.615  1.00 31.52      B    C
ATOM   4159  O    GLY B 245     -12.741   7.104 -19.850  1.00 32.30      B    O
ATOM   4160  N    ILE B 246     -13.476   5.110 -19.122  1.00 30.79      B    N
ATOM   4161  CA   ILE B 246     -14.800   5.578 -18.734  1.00 31.70      B    C
ATOM   4162  CB   ILE B 246     -15.907   4.792 -19.467  1.00 34.63      B    C
ATOM   4163  CG1  ILE B 246     -15.952   3.312 -19.041  1.00 35.25      B    C
ATOM   4164  CD1  ILE B 246     -17.373   2.797 -18.876  1.00 34.91      B    C
ATOM   4165  CG2  ILE B 246     -15.708   4.884 -20.976  1.00 35.49      B    C
ATOM   4166  C    ILE B 246     -15.056   5.495 -17.231  1.00 31.36      B    C
ATOM   4167  O    ILE B 246     -16.153   5.815 -16.784  1.00 29.30      B    O
ATOM   4168  N    GLY B 247     -14.038   5.076 -16.469  1.00 33.15      B    N
ATOM   4169  CA   GLY B 247     -14.103   4.926 -15.007  1.00 33.39      B    C
ATOM   4170  C    GLY B 247     -14.360   3.484 -14.662  1.00 34.14      B    C
ATOM   4171  O    GLY B 247     -14.673   2.715 -15.550  1.00 38.81      B    O
ATOM   4172  N    ARG B 248     -14.221   3.094 -13.398  1.00 35.49      B    N
ATOM   4173  CA   ARG B 248     -14.521   1.701 -13.019  1.00 34.52      B    C
ATOM   4174  CB   ARG B 248     -13.898   1.291 -11.678  1.00 34.54      B    C
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ATOM	4175	CG	ARG	B	248	-12.394	1.119	-11.670	1.00	33.03	B	C
ATOM	4176	CD	ARG	B	248	-11.942	0.463	-10.370	1.00	31.42	B	C
ATOM	4177	NE	ARG	B	248	-10.484	0.407	-10.297	1.00	30.41	B	N
ATOM	4178	CZ	ARG	B	248	-9.772	-0.522	-9.665	1.00	30.13	B	C
ATOM	4179	NH1	ARG	B	248	-10.351	-1.520	-9.018	1.00	32.14	B	N
ATOM	4180	NH2	ARG	B	248	-8.455	-0.457	-9.676	1.00	29.38	B	N
ATOM	4181	C	ARG	B	248	-16.014	1.528	-12.922	1.00	34.18	B	C
ATOM	4182	O	ARG	B	248	-16.606	0.839	-13.724	1.00	35.53	B	O
ATOM	4183	N	ASP	B	249	-16.620	2.168	-11.935	1.00	35.34	B	N
ATOM	4184	CA	ASP	B	249	-18.020	1.933	-11.609	1.00	37.30	B	C
ATOM	4185	CB	ASP	B	249	-18.584	3.108	-10.808	1.00	39.37	B	C
ATOM	4186	CG	ASP	B	249	-18.039	3.154	-9.404	1.00	40.69	B	C
ATOM	4187	OD1	ASP	B	249	-18.225	2.155	-8.689	1.00	41.67	B	O
ATOM	4188	OD2	ASP	B	249	-17.424	4.177	-9.012	1.00	43.16	B	O
ATOM	4189	C	ASP	B	249	-18.900	1.649	-12.835	1.00	36.02	B	C
ATOM	4190	O	ASP	B	249	-19.690	0.703	-12.830	1.00	35.49	B	O
ATOM	4191	N	ALA	B	250	-18.764	2.454	-13.876	1.00	33.52	B	N
ATOM	4192	CA	ALA	B	250	-19.556	2.228	-15.067	1.00	34.12	B	C
ATOM	4193	CB	ALA	B	250	-19.554	3.465	-15.932	1.00	34.74	B	C
ATOM	4194	C	ALA	B	250	-19.078	1.005	-15.872	1.00	34.00	B	C
ATOM	4195	O	ALA	B	250	-19.898	0.291	-16.453	1.00	33.32	B	O
ATOM	4196	N	ALA	B	251	-17.764	0.775	-15.914	1.00	33.23	B	N
ATOM	4197	CA	ALA	B	251	-17.192	-0.376	-16.634	1.00	32.65	B	C
ATOM	4198	CB	ALA	B	251	-15.680	-0.332	-16.595	1.00	31.92	B	C
ATOM	4199	C	ALA	B	251	-17.699	-1.735	-16.145	1.00	33.52	B	C
ATOM	4200	O	ALA	B	251	-18.037	-2.579	-16.969	1.00	33.05	B	O
ATOM	4201	N	VAL	B	252	-17.778	-1.946	-14.827	1.00	34.61	B	N
ATOM	4202	CA	VAL	B	252	-18.321	-3.223	-14.299	1.00	37.23	B	C
ATOM	4203	CB	VAL	B	252	-18.148	-3.454	-12.757	1.00	38.13	B	C
ATOM	4204	CG1	VAL	B	252	-16.734	-3.132	-12.298	1.00	39.21	B	C
ATOM	4205	CG2	VAL	B	252	-19.148	-2.657	-11.925	1.00	39.85	B	C
ATOM	4206	C	VAL	B	252	-19.791	-3.316	-14.626	1.00	38.70	B	C
ATOM	4207	O	VAL	B	252	-20.309	-4.393	-14.881	1.00	42.70	B	O
ATOM	4208	N	GLN	B	253	-20.458	-2.170	-14.596	1.00	39.66	B	N
ATOM	4209	CA	GLN	B	253	-21.882	-2.101	-14.842	1.00	38.93	B	C
ATOM	4210	CB	GLN	B	253	-22.363	-0.650	-14.690	1.00	39.08	B	C
ATOM	4211	CG	GLN	B	253	-23.849	-0.455	-14.817	1.00	38.82	B	C
ATOM	4212	CD	GLN	B	253	-24.597	-1.398	-13.925	1.00	40.50	B	C
ATOM	4213	OE1	GLN	B	253	-25.255	-2.330	-14.399	1.00	41.81	B	O
ATOM	4214	NE2	GLN	B	253	-24.472	-1.195	-12.621	1.00	39.98	B	N
ATOM	4215	C	GLN	B	253	-22.146	-2.631	-16.242	1.00	38.11	B	C
ATOM	4216	O	GLN	B	253	-23.110	-3.345	-16.462	1.00	39.28	B	O
ATOM	4217	N	ILE	B	254	-21.255	-2.307	-17.171	1.00	37.48	B	N
ATOM	4218	CA	ILE	B	254	-21.358	-2.789	-18.537	1.00	37.65	B	C
ATOM	4219	CB	ILE	B	254	-20.279	-2.163	-19.426	1.00	37.54	B	C
ATOM	4220	CG1	ILE	B	254	-20.665	-0.718	-19.712	1.00	38.79	B	C
ATOM	4221	CD1	ILE	B	254	-19.526	0.104	-20.271	1.00	40.86	B	C
ATOM	4222	CG2	ILE	B	254	-20.068	-2.972	-20.714	1.00	36.04	B	C
ATOM	4223	C	ILE	B	254	-21.210	-4.292	-18.625	1.00	38.14	B	C
ATOM	4224	O	ILE	B	254	-21.986	-4.948	-19.323	1.00	38.29	B	O
ATOM	4225	N	PHE	B	255	-20.194	-4.825	-17.950	1.00	37.29	B	N
ATOM	4226	CA	PHE	B	255	-19.928	-6.270	-17.980	1.00	35.20	B	C
ATOM	4227	CB	PHE	B	255	-18.526	-6.589	-17.464	1.00	34.13	B	C
ATOM	4228	CG	PHE	B	255	-17.464	-6.328	-18.483	1.00	33.10	B	C
ATOM	4229	CD1	PHE	B	255	-16.910	-5.080	-18.618	1.00	33.11	B	C
ATOM	4230	CE1	PHE	B	255	-15.939	-4.847	-19.585	1.00	34.35	B	C
ATOM	4231	CZ	PHE	B	255	-15.532	-5.870	-20.437	1.00	32.78	B	C
ATOM	4232	CE2	PHE	B	255	-16.107	-7.110	-20.329	1.00	31.36	B	C
ATOM	4233	CD2	PHE	B	255	-17.064	-7.332	-19.355	1.00	32.90	B	C
ATOM	4234	C	PHE	B	255	-20.993	-7.089	-17.266	1.00	33.97	B	C
ATOM	4235	O	PHE	B	255	-21.437	-8.090	-17.805	1.00	33.61	B	O
ATOM	4236	N	TYR	B	256	-21.439	-6.656	-16.091	1.00	33.92	B	N
ATOM	4237	CA	TYR	B	256	-22.584	-7.298	-15.444	1.00	33.80	B	C
ATOM	4238	CB	TYR	B	256	-22.962	-6.573	-14.186	1.00	32.62	B	C
ATOM	4239	CG	TYR	B	256	-24.124	-7.165	-13.423	1.00	32.49	B	C
ATOM	4240	CD1	TYR	B	256	-25.450	-6.822	-13.740	1.00	31.86	B	C
ATOM	4241	CE1	TYR	B	256	-26.517	-7.342	-13.024	1.00	31.32	B	C
ATOM	4242	CZ	TYR	B	256	-26.269	-8.192	-11.946	1.00	32.70	B	C
ATOM	4243	OH	TYR	B	256	-27.318	-8.694	-11.211	1.00	32.98	B	O
ATOM	4244	CE2	TYR	B	256	-24.963	-8.522	-11.588	1.00	32.52	B	C
ATOM	4245	CD2	TYR	B	256	-23.903	-8.012	-12.328	1.00	32.27	B	C
ATOM	4246	C	TYR	B	256	-23.783	-7.300	-16.360	1.00	36.90	B	C
ATOM	4247	O	TYR	B	256	-24.413	-8.325	-16.534	1.00	41.30	B	O
ATOM	4248	N	ASP	B	257	-24.117	-6.160	-16.951	1.00	39.22	B	N
ATOM	4249	CA	ASP	B	257	-25.285	-6.114	-17.840	1.00	40.23	B	C
ATOM	4250	CB	ASP	B	257	-25.574	-4.679	-18.327	1.00	42.15	B	C
ATOM	4251	CG	ASP	B	257	-26.329	-3.819	-17.279	1.00	43.41	B	C
ATOM	4252	OD1	ASP	B	257	-26.693	-4.314	-16.188	1.00	41.38	B	O
ATOM	4253	OD2	ASP	B	257	-26.567	-2.623	-17.563	1.00	46.53	B	O

ATOM	4254	C	ASP	B	257	-25.131	-7.101	-19.013	1.00	38.49	B	C
ATOM	4255	O	ASP	B	257	-26.062	-7.828	-19.341	1.00	37.98	B	O
ATOM	4256	N	ALA	B	258	-23.949	-7.150	-19.616	1.00	37.63	B	N
ATOM	4257	CA	ALA	B	258	-23.694	-8.082	-20.718	1.00	37.54	B	C
ATOM	4258	CB	ALA	B	258	-22.317	-7.832	-21.331	1.00	37.74	B	C
ATOM	4259	C	ALA	B	258	-23.833	-9.547	-20.274	1.00	36.90	B	C
ATOM	4260	O	ALA	B	258	-24.351	-10.371	-21.013	1.00	37.34	B	O
ATOM	4261	N	LEU	B	259	-23.373	-9.849	-19.067	1.00	35.49	B	N
ATOM	4262	CA	LEU	B	259	-23.468	-11.194	-18.485	1.00	36.20	B	C
ATOM	4263	CB	LEU	B	259	-22.692	-11.243	-17.149	1.00	35.03	B	C
ATOM	4264	CG	LEU	B	259	-22.789	-12.477	-16.249	1.00	33.50	B	C
ATOM	4265	CD1	LEU	B	259	-21.969	-13.599	-16.855	1.00	34.00	B	C
ATOM	4266	CD2	LEU	B	259	-22.320	-12.197	-14.830	1.00	32.11	B	C
ATOM	4267	C	LEU	B	259	-24.910	-11.618	-18.227	1.00	37.29	B	C
ATOM	4268	O	LEU	B	259	-25.238	-12.795	-18.305	1.00	37.07	B	O
ATOM	4269	N	ILE	B	260	-25.760	-10.662	-17.889	1.00	41.20	B	N
ATOM	4270	CA	ILE	B	260	-27.138	-10.968	-17.499	1.00	45.53	B	C
ATOM	4271	CB	ILE	B	260	-27.679	-9.922	-16.468	1.00	47.96	B	C
ATOM	4272	CG1	ILE	B	260	-27.242	-10.273	-15.049	1.00	49.37	B	C
ATOM	4273	CD1	ILE	B	260	-25.754	-10.302	-14.809	1.00	50.87	B	C
ATOM	4274	CG2	ILE	B	260	-29.203	-9.896	-16.425	1.00	50.61	B	C
ATOM	4275	C	ILE	B	260	-28.037	-11.059	-18.746	1.00	41.96	B	C
ATOM	4276	O	ILE	B	260	-29.047	-11.766	-18.741	1.00	37.45	B	O
ATOM	4277	N	ASN	B	261	-27.647	-10.353	-19.806	1.00	41.28	B	N
ATOM	4278	CA	ASN	B	261	-28.562	-10.065	-20.900	1.00	42.92	B	C
ATOM	4279	CB	ASN	B	261	-28.929	-8.555	-20.935	1.00	41.62	B	C
ATOM	4280	CG	ASN	B	261	-29.766	-8.108	-19.723	1.00	42.05	B	C
ATOM	4281	OD1	ASN	B	261	-29.472	-7.101	-19.087	1.00	39.28	B	O
ATOM	4282	ND2	ASN	B	261	-30.817	-8.854	-19.410	1.00	44.78	B	N
ATOM	4283	C	ASN	B	261	-28.086	-10.509	-22.266	1.00	42.09	B	C
ATOM	4284	O	ASN	B	261	-28.894	-10.541	-23.181	1.00	46.04	B	O
ATOM	4285	N	TYR	B	262	-26.811	-10.840	-22.437	1.00	40.74	B	N
ATOM	4286	CA	TYR	B	262	-26.328	-11.224	-23.775	1.00	43.37	B	C
ATOM	4287	CB	TYR	B	262	-25.645	-10.035	-24.471	1.00	45.46	B	C
ATOM	4288	CG	TYR	B	262	-26.615	-8.895	-24.720	1.00	50.69	B	C
ATOM	4289	CD1	TYR	B	262	-27.687	-9.048	-25.610	1.00	53.20	B	C
ATOM	4290	CE1	TYR	B	262	-28.603	-8.023	-25.824	1.00	51.02	B	C
ATOM	4291	CZ	TYR	B	262	-28.459	-6.829	-25.145	1.00	50.83	B	C
ATOM	4292	OH	TYR	B	262	-29.355	-5.817	-25.374	1.00	49.75	B	O
ATOM	4293	CE2	TYR	B	262	-27.406	-6.644	-24.259	1.00	51.59	B	C
ATOM	4294	CD2	TYR	B	262	-26.497	-7.676	-24.040	1.00	52.01	B	C
ATOM	4295	C	TYR	B	262	-25.448	-12.478	-23.816	1.00	42.34	B	C
ATOM	4296	O	TYR	B	262	-25.698	-13.358	-24.629	1.00	40.29	B	O
ATOM	4297	N	LEU	B	263	-24.442	-12.568	-22.943	1.00	42.79	B	N
ATOM	4298	CA	LEU	B	263	-23.480	-13.686	-22.966	1.00	40.87	B	C
ATOM	4299	CB	LEU	B	263	-22.404	-13.522	-21.890	1.00	39.39	B	C
ATOM	4300	CG	LEU	B	263	-21.392	-12.379	-22.072	1.00	39.16	B	C
ATOM	4301	CD1	LEU	B	263	-20.636	-12.135	-20.758	1.00	38.76	B	C
ATOM	4302	CD2	LEU	B	263	-20.439	-12.620	-23.251	1.00	36.77	B	C
ATOM	4303	C	LEU	B	263	-24.182	-15.025	-22.784	1.00	41.44	B	C
ATOM	4304	O	LEU	B	263	-24.950	-15.224	-21.830	1.00	43.17	B	O
ATOM	4305	N	THR	B	264	-23.920	-15.937	-23.710	1.00	39.41	B	N
ATOM	4306	CA	THR	B	264	-24.539	-17.252	-23.678	1.00	39.11	B	C
ATOM	4307	CB	THR	B	264	-25.110	-17.637	-25.071	1.00	37.81	B	C
ATOM	4308	OG1	THR	B	264	-24.209	-17.240	-26.114	1.00	34.47	B	O
ATOM	4309	CG2	THR	B	264	-26.464	-16.980	-25.291	1.00	37.47	B	C
ATOM	4310	C	THR	B	264	-23.516	-18.289	-23.180	1.00	39.71	B	C
ATOM	4311	O	THR	B	264	-22.332	-17.968	-22.988	1.00	39.63	B	O
ATOM	4312	N	PRO	B	265	-23.967	-19.534	-22.956	1.00	37.47	B	N
ATOM	4313	CA	PRO	B	265	-23.020	-20.582	-22.606	1.00	36.51	B	C
ATOM	4314	CB	PRO	B	265	-23.914	-21.815	-22.485	1.00	36.96	B	C
ATOM	4315	CG	PRO	B	265	-25.212	-21.258	-21.998	1.00	36.90	B	C
ATOM	4316	CD	PRO	B	265	-25.362	-19.978	-22.764	1.00	37.02	B	C
ATOM	4317	C	PRO	B	265	-21.889	-20.826	-23.602	1.00	34.86	B	C
ATOM	4318	O	PRO	B	265	-20.886	-21.386	-23.218	1.00	34.81	B	O
ATOM	4319	N	THR	B	266	-22.029	-20.371	-24.836	1.00	36.32	B	N
ATOM	4320	CA	THR	B	266	-21.064	-20.660	-25.909	1.00	38.58	B	C
ATOM	4321	CB	THR	B	266	-21.832	-21.113	-27.172	1.00	39.51	B	C
ATOM	4322	OG1	THR	B	266	-22.792	-22.103	-26.783	1.00	40.49	B	O
ATOM	4323	CG2	THR	B	266	-20.891	-21.667	-28.272	1.00	39.24	B	C
ATOM	4324	C	THR	B	266	-20.208	-19.477	-26.339	1.00	37.79	B	C
ATOM	4325	O	THR	B	266	-19.415	-19.606	-27.267	1.00	40.23	B	O
ATOM	4326	N	SER	B	267	-20.369	-18.324	-25.697	1.00	36.30	B	N
ATOM	4327	CA	SER	B	267	-19.731	-17.102	-26.183	1.00	34.28	B	C
ATOM	4328	CB	SER	B	267	-20.113	-15.912	-25.319	1.00	35.49	B	C
ATOM	4329	OG	SER	B	267	-21.451	-16.033	-24.828	1.00	37.99	B	O
ATOM	4330	C	SER	B	267	-18.230	-17.251	-26.190	1.00	32.77	B	C
ATOM	4331	O	SER	B	267	-17.641	-17.643	-25.208	1.00	33.92	B	O
ATOM	4332	N	ASN	B	268	-17.620	-16.986	-27.326	1.00	32.61	B	N

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ATOM   4333  CA   ASN B 268    -16.182 -16.863 -27.415  1.00 33.06      B  C
ATOM   4334  CB   ASN B 268    -15.729 -17.371 -28.773  1.00 33.54      B  C
ATOM   4335  CG   ASN B 268    -16.267 -16.536 -29.895  1.00 33.79      B  C
ATOM   4336  OD1  ASN B 268    -17.326 -15.949 -29.777  1.00 35.97      B  O
ATOM   4337  ND2  ASN B 268    -15.540 -16.461 -30.975  1.00 34.73      B  N
ATOM   4338  C    ASN B 268    -15.787 -15.390 -27.231  1.00 34.80      B  C
ATOM   4339  O    ASN B 268    -16.626 -14.538 -26.913  1.00 34.48      B  O
ATOM   4340  N    PHE B 269    -14.514 -15.079 -27.443  1.00 36.91      B  N
ATOM   4341  CA   PHE B 269    -14.026 -13.738 -27.157  1.00 38.91      B  C
ATOM   4342  CB   PHE B 269    -12.507 -13.628 -27.385  1.00 40.79      B  C
ATOM   4343  CG   PHE B 269    -11.681 -13.874 -26.141  1.00 41.78      B  C
ATOM   4344  CD1  PHE B 269    -11.418 -12.849 -25.251  1.00 41.82      B  C
ATOM   4345  CE1  PHE B 269    -10.654 -13.078 -24.112  1.00 41.04      B  C
ATOM   4346  CZ   PHE B 269    -10.135 -14.332 -23.857  1.00 38.55      B  C
ATOM   4347  CE2  PHE B 269    -10.382 -15.356 -24.732  1.00 38.41      B  C
ATOM   4348  CD2  PHE B 269    -11.155 -15.130 -25.867  1.00 41.11      B  C
ATOM   4349  C    PHE B 269    -14.805 -12.684 -27.957  1.00 38.14      B  C
ATOM   4350  O    PHE B 269    -15.419 -11.804 -27.371  1.00 37.56      B  O
ATOM   4351  N    SER B 270    -14.842 -12.803 -29.281  1.00 36.64      B  N
ATOM   4352  CA   SER B 270    -15.531 -11.802 -30.090  1.00 34.60      B  C
ATOM   4353  CB   SER B 270    -14.897 -11.695 -31.499  1.00 34.71      B  C
ATOM   4354  OG   SER B 270    -15.617 -12.383 -32.491  1.00 34.03      B  O
ATOM   4355  C    SER B 270    -17.045 -12.041 -30.114  1.00 32.63      B  C
ATOM   4356  O    SER B 270    -17.674 -11.999 -31.146  1.00 36.29      B  O
ATOM   4357  N    ALA B 271    -17.604 -12.349 -28.960  1.00 30.68      B  N
ATOM   4358  CA   ALA B 271    -19.038 -12.294 -28.730  1.00 30.92      B  C
ATOM   4359  CB   ALA B 271    -19.613 -13.701 -28.600  1.00 30.65      B  C
ATOM   4360  C    ALA B 271    -19.247 -11.507 -27.444  1.00 30.93      B  C
ATOM   4361  O    ALA B 271    -20.307 -10.917 -27.213  1.00 29.36      B  O
ATOM   4362  N    MET B 272    -18.229 -11.586 -26.584  1.00 32.20      B  N
ATOM   4363  CA   MET B 272    -18.031 -10.679 -25.460  1.00 32.76      B  C
ATOM   4364  CB   MET B 272    -16.756 -11.071 -24.673  1.00 32.48      B  C
ATOM   4365  CG   MET B 272    -16.360 -10.134 -23.533  1.00 31.70      B  C
ATOM   4366  SD   MET B 272    -17.286 -10.362 -22.001  1.00 31.29      B  S
ATOM   4367  CE   MET B 272    -18.784  -9.421 -22.293  1.00 30.09      B  C
ATOM   4368  C    MET B 272    -17.923  -9.252 -25.975  1.00 32.88      B  C
ATOM   4369  O    MET B 272    -18.662  -8.395 -25.515  1.00 32.30      B  O
ATOM   4370  N    ARG B 273    -17.011  -9.021 -26.933  1.00 34.73      B  N
ATOM   4371  CA   ARG B 273    -16.906  -7.739 -27.658  1.00 35.03      B  C
ATOM   4372  CB   ARG B 273    -16.032  -7.842 -28.925  1.00 34.92      B  C
ATOM   4373  CG   ARG B 273    -15.783  -6.483 -29.582  1.00 36.57      B  C
ATOM   4374  CD   ARG B 273    -15.352  -6.494 -31.046  1.00 38.56      B  C
ATOM   4375  NE   ARG B 273    -15.489  -5.154 -31.660  1.00 40.10      B  N
ATOM   4376  CZ   ARG B 273    -14.486  -4.289 -31.894  1.00 40.63      B  C
ATOM   4377  NH1  ARG B 273    -13.218  -4.572 -31.590  1.00 39.02      B  N
ATOM   4378  NH2  ARG B 273    -14.752  -3.107 -32.442  1.00 41.17      B  N
ATOM   4379  C    ARG B 273    -18.295  -7.267 -28.039  1.00 34.93      B  C
ATOM   4380  O    ARG B 273    -18.770  -6.252 -27.549  1.00 34.29      B  O
ATOM   4381  N    ALA B 274    -18.955  -8.045 -28.884  1.00 37.65      B  N
ATOM   4382  CA   ALA B 274    -20.304  -7.717 -29.344  1.00 37.88      B  C
ATOM   4383  CB   ALA B 274    -20.886  -8.866 -30.184  1.00 38.03      B  C
ATOM   4384  C    ALA B 274    -21.217  -7.383 -28.170  1.00 33.95      B  C
ATOM   4385  O    ALA B 274    -21.822  -6.319 -28.149  1.00 32.98      B  O
ATOM   4386  N    ALA B 275    -21.296  -8.285 -27.200  1.00 32.07      B  N
ATOM   4387  CA   ALA B 275    -22.201  -8.106 -26.070  1.00 33.08      B  C
ATOM   4388  CB   ALA B 275    -22.345  -9.407 -25.299  1.00 32.37      B  C
ATOM   4389  C    ALA B 275    -21.789  -6.962 -25.127  1.00 34.71      B  C
ATOM   4390  O    ALA B 275    -22.640  -6.437 -24.384  1.00 33.51      B  O
ATOM   4391  N    ALA B 276    -20.505  -6.581 -25.166  1.00 34.12      B  N
ATOM   4392  CA   ALA B 276    -19.991  -5.442 -24.381  1.00 34.35      B  C
ATOM   4393  CB   ALA B 276    -18.467  -5.428 -24.360  1.00 34.79      B  C
ATOM   4394  C    ALA B 276    -20.486  -4.140 -24.970  1.00 33.42      B  C
ATOM   4395  O    ALA B 276    -20.986  -3.249 -24.258  1.00 30.24      B  O
ATOM   4396  N    ILE B 277    -20.313  -4.046 -26.284  1.00 33.82      B  N
ATOM   4397  CA   ILE B 277    -20.893  -2.967 -27.069  1.00 34.25      B  C
ATOM   4398  CB   ILE B 277    -20.669  -3.167 -28.584  1.00 32.40      B  C
ATOM   4399  CG1  ILE B 277    -19.176  -2.974 -28.939  1.00 30.53      B  C
ATOM   4400  CD1  ILE B 277    -18.811  -3.402 -30.343  1.00 30.29      B  C
ATOM   4401  CG2  ILE B 277    -21.570  -2.220 -29.370  1.00 32.72      B  C
ATOM   4402  C    ILE B 277    -22.376  -2.909 -26.750  1.00 35.55      B  C
ATOM   4403  O    ILE B 277    -22.852  -1.988 -26.123  1.00 37.39      B  O
ATOM   4404  N    GLN B 278    -23.092  -3.943 -27.119  1.00 38.65      B  N
ATOM   4405  CA   GLN B 278    -24.511  -3.926 -26.950  1.00 39.92      B  C
ATOM   4406  CB   GLN B 278    -25.094  -5.290 -27.321  1.00 39.74      B  C
ATOM   4407  CG   GLN B 278    -26.606  -5.300 -27.308  1.00 39.67      B  C
ATOM   4408  CD   GLN B 278    -27.189  -4.111 -28.042  1.00 38.74      B  C
ATOM   4409  OE1  GLN B 278    -26.710  -3.731 -29.109  1.00 35.78      B  O
ATOM   4410  NE2  GLN B 278    -28.208  -3.499 -27.453  1.00 38.39      B  N
ATOM   4411  C    GLN B 278    -24.965  -3.489 -25.546  1.00 42.36      B  C
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ATOM	4412	O	GLN	B	278	-25.940	-2.757	-25.439	1.00	48.71	B	O
ATOM	4413	N	ALA	B	279	-24.285	-3.905	-24.478	1.00	45.05	B	N
ATOM	4414	CA	ALA	B	279	-24.730	-3.520	-23.108	1.00	46.98	B	C
ATOM	4415	CB	ALA	B	279	-24.072	-4.393	-22.055	1.00	46.66	B	C
ATOM	4416	C	ALA	B	279	-24.469	-2.039	-22.790	1.00	48.10	B	C
ATOM	4417	O	ALA	B	279	-25.275	-1.393	-22.123	1.00	45.73	B	O
ATOM	4418	N	ALA	B	280	-23.325	-1.529	-23.261	1.00	50.53	B	N
ATOM	4419	CA	ALA	B	280	-22.959	-0.109	-23.139	1.00	49.16	B	C
ATOM	4420	CB	ALA	B	280	-21.503	0.098	-23.531	1.00	48.26	B	C
ATOM	4421	C	ALA	B	280	-23.850	0.770	-24.006	1.00	50.26	B	C
ATOM	4422	O	ALA	B	280	-24.128	1.910	-23.647	1.00	55.46	B	O
ATOM	4423	N	THR	B	281	-24.272	0.236	-25.150	1.00	46.81	B	N
ATOM	4424	CA	THR	B	281	-25.211	0.899	-26.024	1.00	45.54	B	C
ATOM	4425	CB	THR	B	281	-25.317	0.164	-27.381	1.00	47.69	B	C
ATOM	4426	OG1	THR	B	281	-24.123	0.397	-28.143	1.00	48.16	B	O
ATOM	4427	CG2	THR	B	281	-26.488	0.648	-28.210	1.00	48.37	B	C
ATOM	4428	C	THR	B	281	-26.557	1.023	-25.310	1.00	47.32	B	C
ATOM	4429	O	THR	B	281	-27.094	2.131	-25.213	1.00	49.73	B	O
ATOM	4430	N	ASP	B	282	-27.081	-0.081	-24.771	1.00	47.65	B	N
ATOM	4431	CA	ASP	B	282	-28.330	-0.052	-23.961	1.00	49.02	B	C
ATOM	4432	CB	ASP	B	282	-28.609	-1.428	-23.343	1.00	49.93	B	C
ATOM	4433	CG	ASP	B	282	-29.000	-2.464	-24.366	1.00	51.23	B	C
ATOM	4434	OD1	ASP	B	282	-29.308	-2.090	-25.518	1.00	47.87	B	O
ATOM	4435	OD2	ASP	B	282	-28.995	-3.662	-24.005	1.00	53.69	B	O
ATOM	4436	C	ASP	B	282	-28.359	0.976	-22.811	1.00	49.83	B	C
ATOM	4437	O	ASP	B	282	-29.439	1.378	-22.350	1.00	47.84	B	O
ATOM	4438	N	LEU	B	283	-27.177	1.363	-22.329	1.00	51.88	B	N
ATOM	4439	CA	LEU	B	283	-27.052	2.309	-21.218	1.00	52.09	B	C
ATOM	4440	CB	LEU	B	283	-26.006	1.820	-20.213	1.00	52.89	B	C
ATOM	4441	CG	LEU	B	283	-26.431	0.781	-19.184	1.00	52.14	B	C
ATOM	4442	CD1	LEU	B	283	-25.348	0.710	-18.117	1.00	51.63	B	C
ATOM	4443	CD2	LEU	B	283	-27.796	1.094	-18.578	1.00	50.82	B	C
ATOM	4444	C	LEU	B	283	-26.675	3.721	-21.656	1.00	49.74	B	C
ATOM	4445	O	LEU	B	283	-27.352	4.665	-21.303	1.00	50.65	B	O
ATOM	4446	N	TYR	B	284	-25.586	3.863	-22.401	1.00	48.81	B	N
ATOM	4447	CA	TYR	B	284	-25.061	5.189	-22.727	1.00	49.44	B	C
ATOM	4448	CB	TYR	B	284	-23.556	5.262	-22.403	1.00	50.48	B	C
ATOM	4449	CG	TYR	B	284	-23.236	4.737	-21.026	1.00	49.15	B	C
ATOM	4450	CD1	TYR	B	284	-23.872	5.254	-19.903	1.00	49.52	B	C
ATOM	4451	CE1	TYR	B	284	-23.603	4.762	-18.632	1.00	50.75	B	C
ATOM	4452	CZ	TYR	B	284	-22.681	3.732	-18.471	1.00	50.38	B	C
ATOM	4453	OH	TYR	B	284	-22.404	3.229	-17.205	1.00	47.77	B	O
ATOM	4454	CE2	TYR	B	284	-22.048	3.197	-19.584	1.00	49.51	B	C
ATOM	4455	CD2	TYR	B	284	-22.333	3.695	-20.848	1.00	49.51	B	C
ATOM	4456	C	TYR	B	284	-25.315	5.610	-24.171	1.00	49.25	B	C
ATOM	4457	O	TYR	B	284	-24.821	6.647	-24.590	1.00	48.69	B	O
ATOM	4458	N	GLY	B	285	-26.074	4.821	-24.930	1.00	50.48	B	N
ATOM	4459	CA	GLY	B	285	-26.504	5.227	-26.273	1.00	49.49	B	C
ATOM	4460	C	GLY	B	285	-25.475	4.969	-27.360	1.00	48.24	B	C
ATOM	4461	O	GLY	B	285	-24.297	5.259	-27.199	1.00	44.44	B	O
ATOM	4462	N	ALA	B	286	-25.958	4.477	-28.494	1.00	49.71	B	N
ATOM	4463	CA	ALA	B	286	-25.129	3.842	-29.533	1.00	53.31	B	C
ATOM	4464	CB	ALA	B	286	-25.958	3.664	-30.805	1.00	54.01	B	C
ATOM	4465	C	ALA	B	286	-23.777	4.486	-29.893	1.00	53.88	B	C
ATOM	4466	O	ALA	B	286	-22.839	3.779	-30.282	1.00	51.19	B	O
ATOM	4467	N	ASN	B	287	-23.673	5.807	-29.803	1.00	54.40	B	N
ATOM	4468	CA	ASN	B	287	-22.489	6.464	-30.315	1.00	57.64	B	C
ATOM	4469	CB	ASN	B	287	-22.872	7.348	-31.514	1.00	60.09	B	C
ATOM	4470	CG	ASN	B	287	-22.568	6.674	-32.851	1.00	60.57	B	C
ATOM	4471	OD1	ASN	B	287	-21.399	6.491	-33.202	1.00	62.04	B	O
ATOM	4472	ND2	ASN	B	287	-23.610	6.296	-33.598	1.00	57.39	B	N
ATOM	4473	C	ASN	B	287	-21.741	7.215	-29.227	1.00	58.94	B	C
ATOM	4474	O	ASN	B	287	-21.301	8.344	-29.423	1.00	58.57	B	O
ATOM	4475	N	SER	B	288	-21.549	6.542	-28.093	1.00	58.78	B	N
ATOM	4476	CA	SER	B	288	-21.058	7.184	-26.870	1.00	54.62	B	C
ATOM	4477	CB	SER	B	288	-21.578	6.456	-25.636	1.00	53.53	B	C
ATOM	4478	OG	SER	B	288	-22.968	6.277	-25.713	1.00	53.88	B	O
ATOM	4479	C	SER	B	288	-19.554	7.219	-26.756	1.00	52.14	B	C
ATOM	4480	O	SER	B	288	-18.835	6.460	-27.428	1.00	48.93	B	O
ATOM	4481	N	SER	B	289	-19.101	8.113	-25.877	1.00	49.50	B	N
ATOM	4482	CA	SER	B	289	-17.748	8.063	-25.338	1.00	48.18	B	C
ATOM	4483	CB	SER	B	289	-17.658	8.897	-24.062	1.00	46.70	B	C
ATOM	4484	OG	SER	B	289	-17.504	10.261	-24.344	1.00	47.82	B	O
ATOM	4485	C	SER	B	289	-17.420	6.629	-24.973	1.00	45.61	B	C
ATOM	4486	O	SER	B	289	-16.363	6.096	-25.322	1.00	42.65	B	O
ATOM	4487	N	GLN	B	290	-18.371	6.033	-24.264	1.00	44.11	B	N
ATOM	4488	CA	GLN	B	290	-18.221	4.722	-23.655	1.00	45.53	B	C
ATOM	4489	CB	GLN	B	290	-19.422	4.420	-22.743	1.00	46.86	B	C
ATOM	4490	CG	GLN	B	290	-19.350	5.126	-21.390	1.00	48.38	B	C

ATOM	4491	CD	GLN	B	290	-19.890	6.548	-21.405	1.00	46.61	B	C
ATOM	4492	OE1	GLN	B	290	-20.064	7.138	-22.465	1.00	47.54	B	O
ATOM	4493	NE2	GLN	B	290	-20.156	7.098	-20.221	1.00	44.66	B	N
ATOM	4494	C	GLN	B	290	-18.081	3.619	-24.674	1.00	43.32	B	C
ATOM	4495	O	GLN	B	290	-17.141	2.838	-24.621	1.00	41.88	B	O
ATOM	4496	N	VAL	B	291	-19.029	3.562	-25.594	1.00	41.50	B	N
ATOM	4497	CA	VAL	B	291	-19.014	2.555	-26.622	1.00	40.16	B	C
ATOM	4498	CB	VAL	B	291	-20.266	2.679	-27.505	1.00	39.26	B	C
ATOM	4499	CG1	VAL	B	291	-20.219	1.674	-28.647	1.00	39.12	B	C
ATOM	4500	CG2	VAL	B	291	-21.524	2.494	-26.651	1.00	38.82	B	C
ATOM	4501	C	VAL	B	291	-17.714	2.639	-27.432	1.00	41.56	B	C
ATOM	4502	O	VAL	B	291	-17.078	1.624	-27.664	1.00	41.96	B	O
ATOM	4503	N	ASN	B	292	-17.303	3.847	-27.821	1.00	47.66	B	N
ATOM	4504	CA	ASN	B	292	-16.051	4.063	-28.595	1.00	49.69	B	C
ATOM	4505	CB	ASN	B	292	-15.801	5.576	-28.850	1.00	56.17	B	C
ATOM	4506	CG	ASN	B	292	-16.608	6.138	-30.026	1.00	59.22	B	C
ATOM	4507	OD1	ASN	B	292	-16.441	5.711	-31.179	1.00	58.08	B	O
ATOM	4508	ND2	ASN	B	292	-17.466	7.126	-29.741	1.00	57.45	B	N
ATOM	4509	C	ASN	B	292	-14.813	3.473	-27.908	1.00	44.46	B	C
ATOM	4510	O	ASN	B	292	-13.892	2.961	-28.567	1.00	40.14	B	O
ATOM	4511	N	ALA	B	293	-14.792	3.576	-26.581	1.00	42.31	B	N
ATOM	4512	CA	ALA	B	293	-13.730	2.972	-25.763	1.00	41.98	B	C
ATOM	4513	CB	ALA	B	293	-13.829	3.451	-24.321	1.00	41.43	B	C
ATOM	4514	C	ALA	B	293	-13.756	1.433	-25.810	1.00	39.16	B	C
ATOM	4515	O	ALA	B	293	-12.721	0.815	-26.082	1.00	36.57	B	O
ATOM	4516	N	VAL	B	294	-14.936	0.852	-25.539	1.00	36.84	B	N
ATOM	4517	CA	VAL	B	294	-15.177	-0.595	-25.610	1.00	35.25	B	C
ATOM	4518	CB	VAL	B	294	-16.659	-0.950	-25.468	1.00	35.72	B	C
ATOM	4519	CG1	VAL	B	294	-16.878	-2.433	-25.729	1.00	37.88	B	C
ATOM	4520	CG2	VAL	B	294	-17.176	-0.610	-24.091	1.00	36.30	B	C
ATOM	4521	C	VAL	B	294	-14.748	-1.144	-26.945	1.00	35.55	B	C
ATOM	4522	O	VAL	B	294	-13.956	-2.064	-26.995	1.00	33.54	B	O
ATOM	4523	N	LYS	B	295	-15.286	-0.587	-28.025	1.00	37.14	B	N
ATOM	4524	CA	LYS	B	295	-14.869	-0.983	-29.360	1.00	41.15	B	C
ATOM	4525	CB	LYS	B	295	-15.422	-0.035	-30.422	1.00	46.63	B	C
ATOM	4526	CG	LYS	B	295	-16.913	-0.162	-30.660	1.00	52.98	B	C
ATOM	4527	CD	LYS	B	295	-17.355	0.640	-31.874	1.00	58.56	B	C
ATOM	4528	CE	LYS	B	295	-18.834	0.407	-32.159	1.00	64.17	B	C
ATOM	4529	NZ	LYS	B	295	-19.271	1.113	-33.395	1.00	67.47	B	N
ATOM	4530	C	LYS	B	295	-13.372	-0.957	-29.481	1.00	39.83	B	C
ATOM	4531	O	LYS	B	295	-12.768	-1.874	-30.035	1.00	41.50	B	O
ATOM	4532	N	LYS	B	296	-12.786	0.118	-28.972	1.00	40.95	B	N
ATOM	4533	CA	LYS	B	296	-11.379	0.436	-29.209	1.00	42.53	B	C
ATOM	4534	CB	LYS	B	296	-11.161	1.962	-29.047	1.00	43.71	B	C
ATOM	4535	CG	LYS	B	296	-9.937	2.509	-29.771	1.00	47.26	B	C
ATOM	4536	CD	LYS	B	296	-10.251	3.670	-30.724	1.00	50.59	B	C
ATOM	4537	CE	LYS	B	296	-9.147	3.860	-31.775	1.00	51.12	B	C
ATOM	4538	NZ	LYS	B	296	-7.865	4.414	-31.217	1.00	50.10	B	N
ATOM	4539	C	LYS	B	296	-10.477	-0.407	-28.291	1.00	39.86	B	C
ATOM	4540	O	LYS	B	296	-9.340	-0.751	-28.633	1.00	39.63	B	O
ATOM	4541	N	ALA	B	297	-11.013	-0.758	-27.131	1.00	38.67	B	N
ATOM	4542	CA	ALA	B	297	-10.337	-1.648	-26.193	1.00	36.50	B	C
ATOM	4543	CB	ALA	B	297	-11.132	-1.753	-24.896	1.00	35.52	B	C
ATOM	4544	C	ALA	B	297	-10.156	-3.017	-26.823	1.00	35.43	B	C
ATOM	4545	O	ALA	B	297	-9.033	-3.437	-27.087	1.00	35.98	B	O
ATOM	4546	N	TYR	B	298	-11.266	-3.697	-27.098	1.00	33.26	B	N
ATOM	4547	CA	TYR	B	298	-11.208	-5.015	-27.703	1.00	30.77	B	C
ATOM	4548	CB	TYR	B	298	-12.615	-5.568	-27.929	1.00	29.47	B	C
ATOM	4549	CG	TYR	B	298	-13.204	-6.108	-26.644	1.00	28.38	B	C
ATOM	4550	CD1	TYR	B	298	-12.809	-7.349	-26.131	1.00	29.24	B	C
ATOM	4551	CE1	TYR	B	298	-13.318	-7.832	-24.930	1.00	28.21	B	C
ATOM	4552	CZ	TYR	B	298	-14.234	-7.070	-24.228	1.00	27.78	B	C
ATOM	4553	OH	TYR	B	298	-14.763	-7.485	-23.031	1.00	26.67	B	O
ATOM	4554	CE2	TYR	B	298	-14.638	-5.854	-24.728	1.00	27.85	B	C
ATOM	4555	CD2	TYR	B	298	-14.119	-5.381	-25.925	1.00	27.58	B	C
ATOM	4556	C	TYR	B	298	-10.332	-5.057	-28.972	1.00	31.41	B	C
ATOM	4557	O	TYR	B	298	-9.596	-6.029	-29.171	1.00	33.75	B	O
ATOM	4558	N	THR	B	299	-10.341	-4.007	-29.793	1.00	30.17	B	N
ATOM	4559	CA	THR	B	299	-9.452	-3.990	-30.981	1.00	31.63	B	C
ATOM	4560	CB	THR	B	299	-9.651	-2.727	-31.904	1.00	30.00	B	C
ATOM	4561	OG1	THR	B	299	-11.031	-2.587	-32.274	1.00	29.34	B	O
ATOM	4562	CG2	THR	B	299	-8.825	-2.848	-33.164	1.00	28.55	B	C
ATOM	4563	C	THR	B	299	-7.963	-4.124	-30.561	1.00	31.90	B	C
ATOM	4564	O	THR	B	299	-7.142	-4.745	-31.262	1.00	31.07	B	O
ATOM	4565	N	ALA	B	300	-7.641	-3.552	-29.406	1.00	32.45	B	N
ATOM	4566	CA	ALA	B	300	-6.262	-3.429	-28.966	1.00	33.91	B	C
ATOM	4567	CB	ALA	B	300	-6.157	-2.425	-27.831	1.00	35.00	B	C
ATOM	4568	C	ALA	B	300	-5.718	-4.754	-28.521	1.00	34.05	B	C
ATOM	4569	O	ALA	B	300	-4.519	-5.032	-28.722	1.00	33.41	B	O

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ATOM   4570  N   VAL B 301      -6.606  -5.551 -27.916  1.00 34.40           B   N
ATOM   4571  CA  VAL B 301      -6.294  -6.923 -27.499  1.00 35.91           B   C
ATOM   4572  CB  VAL B 301      -7.080  -7.346 -26.243  1.00 35.35           B   C
ATOM   4573  CG1 VAL B 301      -6.679  -6.467 -25.065  1.00 34.72           B   C
ATOM   4574  CG2 VAL B 301      -8.587  -7.313 -26.485  1.00 35.39           B   C
ATOM   4575  C   VAL B 301      -6.491  -7.968 -28.607  1.00 37.99           B   C
ATOM   4576  O   VAL B 301      -6.283  -9.152 -28.384  1.00 40.13           B   O
ATOM   4577  N   GLY B 302      -6.875  -7.535 -29.801  1.00 39.20           B   N
ATOM   4578  CA  GLY B 302      -6.806  -8.402 -30.975  1.00 38.61           B   C
ATOM   4579  C   GLY B 302      -8.120  -9.085 -31.268  1.00 37.68           B   C
ATOM   4580  O   GLY B 302      -8.219  -9.890 -32.206  1.00 36.97           B   O
ATOM   4581  N   VAL B 303      -9.123  -8.764 -30.457  1.00 36.46           B   N
ATOM   4582  CA  VAL B 303     -10.463  -9.269 -30.646  1.00 36.09           B   C
ATOM   4583  CB  VAL B 303     -11.186  -9.418 -29.310  1.00 34.30           B   C
ATOM   4584  CG1 VAL B 303     -12.615  -9.884 -29.525  1.00 34.12           B   C
ATOM   4585  CG2 VAL B 303     -10.413 -10.378 -28.422  1.00 34.22           B   C
ATOM   4586  C   VAL B 303     -11.210  -8.285 -31.529  1.00 39.41           B   C
ATOM   4587  O   VAL B 303     -11.410  -7.128 -31.162  1.00 39.85           B   O
ATOM   4588  N   ASN B 304     -11.623  -8.767 -32.695  1.00 42.29           B   N
ATOM   4589  CA  ASN B 304     -12.178  -7.934 -33.741  1.00 43.11           B   C
ATOM   4590  CB  ASN B 304     -11.400  -8.162 -35.039  1.00 43.44           B   C
ATOM   4591  CG  ASN B 304      -9.894  -7.915 -34.868  1.00 44.48           B   C
ATOM   4592  OD1 ASN B 304      -9.046  -8.788 -35.169  1.00 39.07           B   O
ATOM   4593  ND2 ASN B 304      -9.554  -6.727 -34.345  1.00 44.40           B   N
ATOM   4594  C   ASN B 304     -13.644  -8.265 -33.895  1.00 45.91           B   C
ATOM   4595  O   ASN B 304     -14.115  -9.329 -33.478  1.00 47.21           B   O
ATOM   4596  OXT ASN B 304     -14.398  -7.442 -34.401  1.00 50.28           B   O
HETATM 4597  O   HOH D   1     -14.453 -29.833 -15.752  1.00 11.48               O
HETATM 4598  O   HOH D   2      -3.559 -28.043  -4.163  1.00 10.41               O
HETATM 4599  O   HOH D   3       4.756 -48.667 -28.368  1.00 14.01               O
HETATM 4600  O   HOH D   4      18.017 -46.898 -29.709  1.00 17.11               O
HETATM 4601  O   HOH D   5     -18.034 -41.311 -16.195  1.00 16.89               O
HETATM 4602  O   HOH D   6       2.102 -33.576 -25.415  1.00  7.28               O
HETATM 4603  O   HOH D   7       4.340 -35.545 -22.828  1.00  6.89               O
HETATM 4604  O   HOH D   8      -1.226 -54.679  -7.110  1.00 10.35               O
HETATM 4605  O   HOH D   9     -12.874 -50.118  -9.369  1.00 13.13               O
HETATM 4606  O   HOH D  10      -1.229 -11.651 -14.935  1.00  8.69               O
HETATM 4607  O   HOH D  11     -26.802  -9.821  -2.646  1.00 34.23               O
HETATM 4608  O   HOH D  12      15.279 -23.352 -24.790  1.00 28.05               O
HETATM 4609  O   HOH D  14      -5.337 -10.672 -15.773  1.00 17.85               O
HETATM 4610  O   HOH D  15       1.182 -34.774 -17.307  1.00 14.04               O
HETATM 4611  O   HOH D  16     -10.282 -45.012   0.457  1.00  7.05               O
HETATM 4612  O   HOH D  17      -5.067 -45.950 -25.877  1.00  7.74               O
HETATM 4613  O   HOH D  18      -9.466 -22.365   4.654  1.00  9.26               O
HETATM 4614  O   HOH D  19     -14.867 -34.797 -31.110  1.00 12.29               O
HETATM 4615  O   HOH D  20      17.658 -31.345  -6.147  1.00 13.22               O
HETATM 4616  O   HOH D  21     -14.706 -66.680 -15.999  1.00 18.23               O
HETATM 4617  O   HOH D  24      22.701 -44.854 -24.508  1.00 13.43               O
HETATM 4618  O   HOH D  25      -1.606 -44.470 -24.808  1.00  4.05               O
HETATM 4619  O   HOH D  27     -14.081 -49.049 -23.938  1.00  5.85               O
HETATM 4620  O   HOH D  28      -1.406 -15.180 -13.873  1.00 20.93               O
HETATM 4621  O   HOH D  29     -18.234 -61.855 -23.352  1.00 15.81               O
HETATM 4622  O   HOH D  30      14.980 -31.161  -4.673  1.00  8.84               O
HETATM 4623  O   HOH D  31      25.232 -37.903 -28.412  1.00  7.88               O
HETATM 4624  O   HOH D  32       2.306  -3.607 -14.150  1.00 12.43               O
HETATM 4625  O   HOH D  33       8.133 -32.218 -28.553  1.00 21.62               O
HETATM 4626  O   HOH D  34      -9.785 -46.761 -10.910  1.00 11.38               O
HETATM 4627  O   HOH D  35      25.957 -51.974 -19.833  1.00 17.72               O
HETATM 4628  O   HOH D  36      -0.537 -38.406   2.660  1.00 12.52               O
HETATM 4629  O   HOH D  37      -6.253 -26.792   2.618  1.00 14.95               O
HETATM 4630  O   HOH D  38      -4.277 -32.186 -26.909  1.00 10.72               O
HETATM 4631  O   HOH D  40      -0.230 -46.981 -24.263  1.00 10.61               O
HETATM 4632  O   HOH D  41       9.113 -53.708 -16.348  1.00  8.82               O
HETATM 4633  O   HOH D  42       0.527 -57.811 -16.009  1.00  5.69               O
HETATM 4634  O   HOH D  43       7.369 -49.544 -27.875  1.00 11.17               O
HETATM 4635  O   HOH D  44      13.059 -41.050 -31.554  1.00 14.34               O
HETATM 4636  O   HOH D  45     -30.779 -55.305 -11.958  1.00 12.66               O
HETATM 4637  O   HOH D  46     -16.179 -51.696  -0.530  1.00 17.86               O
HETATM 4638  O   HOH D  47       6.739 -26.907  -6.038  1.00  8.32               O
HETATM 4639  O   HOH D  48      -1.147 -27.953  -5.319  1.00 11.94               O
HETATM 4640  O   HOH D  49     -27.771 -63.155  -6.758  1.00 25.59               O
HETATM 4641  O   HOH D  50     -22.146 -51.541 -20.878  1.00 23.93               O
HETATM 4642  O   HOH D  51      11.498 -53.494 -22.966  1.00 19.18               O
HETATM 4643  O   HOH D  52     -35.618 -17.756   3.293  1.00 30.46               O
HETATM 4644  O   HOH D  53       0.936 -10.997  -2.654  1.00 21.53               O
HETATM 4645  O   HOH D  55      -3.931 -51.435 -22.740  1.00 21.73               O
HETATM 4646  O   HOH D  56     -11.411 -49.131 -23.961  1.00  4.13               O
HETATM 4647  O   HOH D  57      10.929 -42.120  -2.629  1.00  8.04               O
HETATM 4648  O   HOH D  58      -5.258 -24.055 -13.514  1.00  7.92               O
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HETATM 4649  O   HOH D  59      -2.368  -2.482  -8.879  1.00  8.97           O
HETATM 4650  O   HOH D  60      22.320 -35.750 -12.017  1.00 10.98           O
HETATM 4651  O   HOH D  61     -19.413 -20.255 -13.553  1.00  7.71           O
HETATM 4652  O   HOH D  62      -0.658 -31.524 -23.753  1.00  8.59           O
HETATM 4653  O   HOH D  63      14.971 -39.634 -33.356  1.00 12.49           O
HETATM 4654  O   HOH D  64      -5.191 -35.793  -0.990  1.00 18.79           O
HETATM 4655  O   HOH D  65      -7.971 -52.023 -23.877  1.00  7.05           O
HETATM 4656  O   HOH D  66     -10.996 -39.555 -30.895  1.00 29.45           O
HETATM 4657  O   HOH D  67      -5.761 -28.410 -26.821  1.00 10.37           O
HETATM 4658  O   HOH D  69      -0.623 -30.084 -21.186  1.00 16.74           O
HETATM 4659  O   HOH D  70      11.237 -21.250 -19.622  1.00 12.84           O
HETATM 4660  O   HOH D  71       6.423 -13.673  -7.327  1.00  7.62           O
HETATM 4661  O   HOH D  72     -12.098   4.570  -9.813  1.00 17.86           O
HETATM 4662  O   HOH D  74     -19.719 -36.149 -15.796  1.00  6.65           O
HETATM 4663  O   HOH D  75      -7.298 -10.821   6.866  1.00 16.58           O
HETATM 4664  O   HOH D  76      24.422 -49.300  -6.907  1.00 13.05           O
HETATM 4665  O   HOH D  79       2.981 -11.284  -0.026  1.00 18.58           O
HETATM 4666  O   HOH D  80     -21.114 -35.355 -22.146  1.00 14.58           O
HETATM 4667  O   HOH D  84       1.731 -15.045 -10.266  1.00 16.73           O
HETATM 4668  O   HOH D  85     -14.299 -20.123 -30.892  1.00 18.20           O
HETATM 4669  O   HOH D  86      14.254 -53.364 -21.911  1.00  8.78           O
HETATM 4670  O   HOH D  87       1.855 -39.977  -9.636  1.00  9.12           O
HETATM 4671  O   HOH D  88       0.036 -27.584 -22.318  1.00 19.91           O
HETATM 4672  O   HOH D  89     -16.641   8.034 -21.414  1.00 28.79           O
HETATM 4673  O   HOH D  91       6.673 -19.109 -18.430  1.00 14.71           O
HETATM 4674  O   HOH D  92      15.712 -28.784 -11.584  1.00 17.47           O
HETATM 4675  O   HOH D  93     -25.882 -43.603 -12.917  1.00  9.36           O
HETATM 4676  O   HOH D  94     -13.971 -58.069  -2.171  1.00 16.23           O
HETATM 4677  O   HOH D  96      10.457 -26.740 -26.060  1.00 11.31           O
HETATM 4678  O   HOH D  97     -22.816 -38.364  -5.993  1.00 17.13           O
HETATM 4679  O   HOH D 100      -9.340 -47.635   0.235  1.00  6.76           O
HETATM 4680  O   HOH D 102       3.056 -38.032 -31.275  1.00  6.12           O
HETATM 4681  O   HOH D 103     -25.590 -42.298 -15.541  1.00 17.90           O
HETATM 4682  O   HOH D 104      10.556 -51.368 -25.973  1.00  9.26           O
HETATM 4683  O   HOH D 106     -19.882 -33.352   4.847  1.00 30.16           O
HETATM 4684  O   HOH D 107      -6.248 -27.219  -8.518  1.00 11.81           O
HETATM 4685  O   HOH D 108     -31.468 -21.088  -1.489  1.00 12.00           O
HETATM 4686  O   HOH D 111      21.684 -30.977 -26.026  1.00 23.70           O
HETATM 4687  O   HOH D 112     -31.951 -10.039   3.258  1.00 21.85           O
HETATM 4688  O   HOH D 113     -12.420 -61.104 -20.866  1.00 20.71           O
HETATM 4689  O   HOH D 115      -9.390 -46.453  -3.343  1.00 11.14           O
HETATM 4690  O   HOH D 116     -24.310  -8.827 -27.982  1.00 28.62           O
HETATM 4691  O   HOH D 118       0.928   0.943 -27.721  1.00 20.32           O
HETATM 4692  O   HOH D 119      -0.811 -22.368 -26.821  1.00 28.05           O
HETATM 4693  O   HOH D 120       2.928 -27.375  -2.252  1.00  6.28           O
HETATM 4694  O   HOH D 122      24.797 -33.048 -16.191  1.00 20.61           O
HETATM 4695  O   HOH D 123      28.116 -42.682 -17.519  1.00 20.23           O
HETATM 4696  O   HOH D 126       0.728 -11.568 -25.035  1.00 27.72           O
HETATM 4697  O   HOH D 127       5.110 -32.881   1.483  1.00  8.60           O
HETATM 4698  O   HOH D 128      -6.910  -6.512  -5.883  1.00 23.17           O
HETATM 4699  O   HOH D 129     -14.859 -32.631   4.922  1.00 20.12           O
HETATM 4700  O   HOH D 130      -9.393 -20.445 -22.229  1.00 11.44           O
HETATM 4701  O   HOH D 131       5.380 -45.506 -20.439  1.00 18.61           O
HETATM 4702  O   HOH D 132     -20.298 -17.857   4.369  1.00 24.71           O
HETATM 4703  O   HOH D 133     -13.074 -15.017 -30.254  1.00 22.69           O
HETATM 4704  O   HOH D 134     -22.544 -64.671 -13.497  1.00 18.42           O
HETATM 4705  O   HOH D 135      -4.355 -31.730 -19.579  1.00 30.49           O
HETATM 4706  O   HOH D 136      -4.978 -28.238 -15.122  1.00 22.36           O
HETATM 4707  O   HOH D 137      -7.834 -20.152   9.638  1.00 18.69           O
HETATM 4708  O   HOH D 138     -14.293 -28.356 -18.330  1.00 27.34           O
HETATM 4709  O   HOH D 139     -22.099 -32.349  -8.846  1.00 29.42           O
HETATM 4710  O   HOH D 140       8.752 -28.130  -6.857  1.00  8.09           O
HETATM 4711  O   HOH D 141      15.481 -31.534 -31.496  1.00  7.89           O
HETATM 4712  O   HOH D 142     -14.386 -25.883 -11.379  1.00 24.39           O
HETATM 4713  O   HOH D 143      -2.224 -28.207 -27.995  1.00 21.76           O
HETATM 4714  O   HOH D 144      -3.038   2.948 -18.802  1.00 17.17           O
HETATM 4715  O   HOH D 145     -17.234  -8.824 -32.860  1.00 22.34           O
HETATM 4716  O   HOH D 146     -21.972 -36.386 -17.229  1.00 15.20           O
HETATM 4717  O   HOH D 147      21.738 -50.115 -22.044  1.00 41.96           O
HETATM 4718  O   HOH D 148     -15.129 -42.497 -17.235  1.00 64.58           O
HETATM 4719  O   HOH D 149       0.499 -13.659   1.071  1.00 20.44           O
HETATM 4720  O   HOH D 150      26.656 -39.916 -12.524  1.00 28.86           O
HETATM 4721  O   HOH D 151     -26.068 -18.778  22.468  1.00 63.91           O
HETATM 4722  O   HOH D 152      17.839 -37.146  -6.365  1.00 17.05           O
HETATM 4723  O   HOH D 153      -9.872 -37.859   3.756  1.00 29.86           O
HETATM 4724  O   HOH D 154     -26.704 -13.656 -20.767  1.00 24.94           O
HETATM 4725  O   HOH D 155     -16.594 -46.356   1.735  1.00  9.02           O
HETATM 4726  O   HOH D 156      -3.278 -28.231 -11.565  1.00 15.79           O
HETATM 4727  O   HOH D 157     -13.773 -34.807   7.967  1.00 26.45           O
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HETATM 4728  O    HOH D 158      5.274 -27.734  -3.607  1.00 14.35          O
HETATM 4729  O    HOH D 159    -10.955 -62.644  -9.650  1.00 22.81          O
HETATM 4730  O    HOH D 160     19.801 -28.085 -15.802  1.00 15.92          O
HETATM 4731  O    HOH D 161     14.910 -35.916  -3.899  1.00 14.53          O
HETATM 4732  O    HOH D 162     -7.630 -39.335 -29.693  1.00 19.10          O
HETATM 4733  O    HOH D 163      8.909  -8.381  -2.714  1.00 31.11          O
HETATM 4734  O    HOH D 164    -35.136 -13.839  -9.366  1.00 19.26          O
HETATM 4735  O    HOH D 165    -28.655 -13.870  18.003  1.00 25.79          O
HETATM 4736  O    HOH D 166     -4.969 -28.077  -6.380  1.00 15.01          O
HETATM 4737  O    HOH D 167    -12.416 -58.656 -21.906  1.00 38.53          O
HETATM 4738  O    HOH D 168     -1.381 -22.000   5.296  1.00 15.16          O
HETATM 4739  O    HOH D 169    -28.073 -14.871 -23.335  1.00 29.90          O
HETATM 4740  O    HOH D 170     -5.698 -52.447 -27.051  1.00 46.81          O
HETATM 4741  O    HOH D 171     25.098 -40.710 -27.602  1.00 31.23          O
HETATM 4742  O    HOH D 172     13.253 -30.057 -31.043  1.00 25.08          O
HETATM 4743 CA    CA  C   1     -3.996 -44.763 -24.393  1.00 14.92         CA
HETATM 4744 CA    CA  C   2     -9.298 -38.014 -30.827  1.00 19.13         CA
HETATM 4745 CA    CA  C   3     -7.033  -7.984  -3.851  1.00 33.23         CA
HETATM 4746 CA    CA  C   4      3.009 -11.945  -2.235  1.00 23.81         CA
ATOM   4747  N    VAL E   1     -6.805 -32.986 -18.277  1.00 18.96          N
ATOM   4748  CA   VAL E   1     -5.543 -32.961 -17.454  1.00 19.68          C
ATOM   4749  CB   VAL E   1     -5.490 -31.747 -16.442  1.00 19.24          C
ATOM   4750  CG1  VAL E   1     -5.729 -30.417 -17.143  1.00 19.12          C
ATOM   4751  CG2  VAL E   1     -6.448 -31.893 -15.256  1.00 18.78          C
ATOM   4752  C    VAL E   1     -5.209 -34.318 -16.766  1.00 20.53          C
ATOM   4753  O    VAL E   1     -4.162 -34.931 -17.045  1.00 19.81          O
ATOM   4754  N    ARG E   2     -6.036 -34.659 -15.814  1.00 22.30          N
ATOM   4755  CA   ARG E   2     -5.893 -35.826 -14.996  1.00 22.98          C
ATOM   4756  C    ARG E   2     -5.143 -35.563 -13.709  1.00 23.10          C
ATOM   4757  O    ARG E   2     -3.987 -35.675 -13.626  1.00 21.38          O
ATOM   4758  CB   ARG E   2     -5.370 -36.923 -15.862  1.00 20.00          C
ATOM   4759  CG   ARG E   2     -6.510 -37.666 -16.472  1.00 20.00          C
ATOM   4760  CD   ARG E   2     -6.236 -37.842 -17.914  1.00 20.00          C
ATOM   4761  NE   ARG E   2     -5.023 -38.606 -18.152  1.00 20.00          N
ATOM   4762  CZ   ARG E   2     -4.700 -39.033 -19.365  1.00 20.00          C
ATOM   4763  NH1  ARG E   2     -5.498 -38.765 -20.370  1.00 20.00          N
ATOM   4764  NH2  ARG E   2     -3.590 -39.683 -19.606  1.00 20.00          N
ATOM   4765  N    ALA E   3     -5.874 -35.228 -12.682  1.00 25.76          N
ATOM   4766  CA   ALA E   3     -5.370 -34.410 -11.547  1.00 29.63          C
ATOM   4767  CB   ALA E   3     -6.254 -33.159 -11.469  1.00 30.22          C
ATOM   4768  C    ALA E   3     -5.257 -35.094 -10.105  1.00 31.58          C
ATOM   4769  O    ALA E   3     -5.874 -36.130  -9.844  1.00 31.51          O
ATOM   4770  N    ALA E   4     -4.491 -34.497  -9.169  1.00 32.55          N
ATOM   4771  CA   ALA E   4     -4.349 -35.033  -7.771  1.00 30.23          C
ATOM   4772  CB   ALA E   4     -3.660 -36.382  -7.798  1.00 28.96          C
ATOM   4773  C    ALA E   4     -3.600 -34.141  -6.772  1.00 29.50          C
ATOM   4774  O    ALA E   4     -2.820 -34.655  -5.948  1.00 27.58          O
ATOM   4775  N    ARG F   1     -8.429 -19.552  -9.416  1.00 25.91          N
ATOM   4776  CA   ARG F   1     -9.556 -20.144  -8.678  1.00 28.61          C
ATOM   4777  C    ARG F   1    -10.743 -20.675  -9.479  1.00 29.09          C
ATOM   4778  O    ARG F   1    -11.224 -20.098 -10.395  1.00 27.32          O
ATOM   4779  CB   ARG F   1    -10.034 -19.244  -7.562  1.00 20.00          C
ATOM   4780  CG   ARG F   1     -9.026 -18.241  -7.099  1.00 20.00          C
ATOM   4781  CD   ARG F   1     -9.684 -16.875  -6.961  1.00 20.00          C
ATOM   4782  NE   ARG F   1     -8.851 -15.706  -6.762  1.00 20.00          N
ATOM   4783  CZ   ARG F   1     -7.599 -15.716  -6.317  1.00 20.00          C
ATOM   4784  NH1  ARG F   1     -6.959 -16.845  -6.043  1.00 20.00          N
ATOM   4785  NH2  ARG F   1     -6.952 -14.572  -6.163  1.00 20.00          N
ATOM   4786  N    ALA F   2    -11.202 -21.816  -9.078  1.00 31.68          N
ATOM   4787  CA   ALA F   2    -11.921 -22.706  -9.931  1.00 35.91          C
ATOM   4788  CB   ALA F   2    -11.159 -24.023  -9.929  1.00 36.85          C
ATOM   4789  C    ALA F   2    -13.430 -22.961  -9.726  1.00 38.32          C
ATOM   4790  O    ALA F   2    -13.892 -23.333  -8.669  1.00 34.79          O
ATOM   4791  N    ALA F   3    -14.167 -22.664 -10.769  1.00 40.70          N
ATOM   4792  CA   ALA F   3    -15.085 -23.497 -11.515  1.00 40.16          C
ATOM   4793  CB   ALA F   3    -14.939 -24.977 -11.187  1.00 40.29          C
ATOM   4794  C    ALA F   3    -16.524 -23.097 -11.612  1.00 37.96          C
ATOM   4795  O    ALA F   3    -17.129 -23.397 -12.612  1.00 35.80          O
END
```

EXAMPLE 3

Comparison of PehPro1 with Thermolysin structure

The structure of PehPro1 was compared to that of Thermolysin (*B. thermoproteolyticus* metalloprotease, pdb 1KEI.A) [Senda, M., Senda,T. and Kidokoro,S., Crystal Structure Analyses Of Thermolysin In Complex With Its Inhibitors, Direct Submission]. The overall folding of PehPro1 is highly similar to Thermolysin and other known metalloproteases from *Bacillus (B. cereus* (pdb 1NPC.A) [Sidler,W., Niederer,E., Suter,F. and Zuber,H., The primary structure of *Bacillus cereus* neutral proteinase and comparison with thermolysin and Bacillus subtilis neutral Proteinase, Biol. Chem. Hoppe-Seyler 367 (7), 643-657 (1986)] *and B. stearothermophilus, and B. subtilis* metalloproteases,consisting of two domains and a central connecting helix. A schematic of the overall topology of PehPro1 is presented and compared with Thermolysin in Figure 2. The main differences were found in regions where there were deletions in the PehPro1 sequence relative to that of other known metalloprotease structures. Two regions of deletion occur in PehPro1, and as a consequence the main chain folding deviates from thermolysin after residue Trp58 of PehPro1 (see Figure 3), and after residue Asp170 of PehPro1 (see Figure 4). Four residues in Thermolysin are replaced by Asn59 in PehPro1 and seven residues in Thermolysin are replaced by Gly171-Lys172 in PehPro1, these deletions are indicated by arrows in Figure 2. The numbering of residues corresponds to the linear contiguous sequence of each mature enzyme, respectively.

Four calcium ions are bound in the Thermolysin structure: two at a double cation site (Ca1,2), and one in each of the single cation sites (Ca3, Ca4). In contrast to Thermolysin, the PehPro1 structure has only two calcium binding sites, a single one near the double cation site (Ca1-2) in Thermolysin and a second (Ca4) that seems to be conserved in the two molecules. One Thermolysin calcium site (Ca3) is completely absent in the PehPro1 structure. Since calcium dependence is considered to be a factor in some potential uses of these proteases, particularly as a detergent additive where builders are present specifically to reduce the hardness of water by chelating ions such as calcium and magnesium, these enzymes may prove to have reduced cation sensitivity and hence improved stability under conditions of low calcium availability.

The region around the Thermolysin double cation site (Ca1,2) is shown in Figure 5. In this figure, the structure of Thermolysin is present as black lines, with the two calcium ions shown as crosses. The superimposed structure of PehPro1 is shown as a stick figure with its single calcium ion as a non-bonding sphere. It may be seen that the two sites are substantially

different. In Thermolysin, six residues along with solvent are present to stabilize the ion pair, including side chains of Asp138, Glu177, Asp 185, Glu190, and the main chain carbonyls of residues Asn183 and Glu187 (Thermolysin numbering). In PehPro1 (numbering relative to mature PehPro1), the calcium in the same vicinity is stabilized by side chains of Asp129, Asp131, Asp170 and Asp178 along with the solvent. Only Asp131 and Asp178 in PehPro1 are homologous with side chains in Thermolysin Asp138 and Glu190, respectively.

The second calcium binding site in PehPro1 is compared with the homologous site (Ca4) in Thermolysin in Figure 6. In this instance, there is a one to one correspondence of residues forming the calcium binding site in both Thermolysin and PehPro1. In Thermolysin, the side chains of Thr194 and Asp200 (Thermolysin numbering) along with the main chain carbonyls of residues Tyr193, Thr194 and Ile197 form ligands to this calcium ion, while in PehPro1 it is the homologous residues Thr182 and Asp188 along with the carbonyl oxygen of residues Tyr181, Thr182 and Thr185 (numbering relative to mature PehPro1).

The structures of PehPro1 and Thermolysin are compared in the vicinity of the Ca3 calcium site in Thermolysin in Figure 7. In Thermolysin the Ca3 calcium site is formed in a loop containing two aspartic acids residues Asp57 and Asp59, which along with the main chain carbonyl oxygen and solvent form ligands to the calcium ion, In contrast, in PehPro1, the two (Asp) ligands are replaced with serine residues which, while in homologous conformations, will not stabilize binding of a calcium ion. In the electron density map there is no evidence of calcium binding under the conditions of crystallization.

EXAMPLE 4

Comparison of structures of PehPro1 and PpoPro2 metalloproteases

Recently, the structure of a metalloprotease from a member of the *Paenibacillus* genus, *Paenibacillus polymyxa* (PpoPro2), was reported (Ruf et al, Acta Cryst. D 69, 24-31 (2013)). The overall folding of PpoPro2 is highly homologous to Thermolysin and other known M4 metalloproteases. The PehPro1 and PpoPro2 structures consist of 304 residues that are aligned without insertions or deletions relative to each other. The PpoPro2 and PehPro1 structures therefore share a common pattern of deletions relative to that of other known metalloprotease structures. The overall folding of the PehPro1 and PpoPro2 is presented in Figure 8.

In contrast to PehPro1, the structure of PpoPro2 was found to bind three calcium ions. The first two (Ca4 and a variant of Ca1-2) described below are highly homologous between PehPro1 and PpoPro2 molecules, and the third is homologous to calcium site Ca3 site. The

common sites are compared in Figures 9 and 10. In both sites, all interactions seen in either PehProl or PpoPro2 are conserved in the other.

As mentioned above, the PpoPro2 has an additional calcium ion bound at Ca3 that is not seen in PehProl. Just as in the structure of Thermolysin (Figure 7), aspartic acid residues are found in PpoPro2 whereas in PehProl, we find Ser 53 and Ser55 instead of the aspartic acid residues (Figure 11).

EXAMPLE 5
Crystallization and structure determination of NprE

The metalloprotease NprE, obtained from *Bacillus subtilis,* is knownto perform in detergent formulations (as described in patent US 8,114,656 B2 Shaw et al and others). An NprE variant (S129I/F130L/M138L/V190I/D220P) was crystallized using the hanging drop method from a solution of protein stock at a concentration of 26.2 mg/mL in 40% Propylene Glycol + 50mM MES pH 5.4 + 1mM Calcium chloride. Aliquots of 3 µL of the protein stock and 3 µL of the crystallization solution were mixed on a plastic coverslip and inverted and sealed on a chamber containing 23% Polyethylene Glycol 4000 + 0.20M Lithium chloride + 0.09M Bis Tris Propane pH 6.5 + 12% Isopropanol + 4 mM Zinc chloride + 12.5 mM Yttrium chloride in a Linbro 6 X 4 culture plate.

Crystals grew in the hexagonal space group P6(3)22 with unit cell dimensions; a=122.9 Å, b=122.9 Å, and c=119.1 Å. Data were collected on native crystal to 2.5 Å and the structure of NprE was determined by molecular replacement using a related protein (pdb ID 1ESP) as the phasing model. The statistics of data collection are presented in Table 5.1.

Table 5.1: Statistics of NprE Data collection	
Wavelength	1.54 Å
Space group	P6322
Molecules in asymmetric unit	1
Unit cell dimensions	a=122.9 Å, b=122.9 Å and c=119.1 Å
Resolution	30.0 - 2.49 Å
Unique reflections	17969
Multiplicity	7.46 (7.36*)
Completeness	99.94% (99.9*)
R_{merge}	0.067(0.25*)
I/σ_I	17.2(5.9*)

*Value in parenthesis is that of the outermost shell of data

The model was fitted in the resulting electron density using the program COOT [Emsley, P et al (2010) Acta Cryst. D66 486-501]. After fitting and refitting adjustments, the coordinates were refined using the REFMAC program with standard defaults in the CCP4 software suite. The statistics of the current model are presented in Table 5.2.

Table 5.2: Statistics of the refined model	
R work	0.20
R free	0.23
No. protein residues	300
No. atoms	2444
rmsd Bond lengths	0.024 Å
rmsd bond angles	2.1°

The coordinates for structure of the NprE variant are provided below.

```
ATOM      1  N   ALA A   1     -50.837 -39.587 -13.317  1.00 46.97           A    N
ATOM      2  CA  ALA A   1     -51.606 -39.753 -14.634  1.00 45.97           A    C
ATOM      3  CB  ALA A   1     -52.426 -38.479 -14.961  1.00 46.00           A    C
ATOM      4  C   ALA A   1     -50.598 -40.107 -15.764  1.00 45.46           A    C
ATOM      5  O   ALA A   1     -49.808 -39.271 -16.244  1.00 43.56           A    O
ATOM      6  N   ALA A   2     -50.582 -41.387 -16.118  1.00 45.03           A    N
ATOM      7  CA  ALA A   2     -49.511 -41.916 -16.936  1.00 44.55           A    C
ATOM      8  CB  ALA A   2     -49.635 -43.447 -17.040  1.00 44.73           A    C
ATOM      9  C   ALA A   2     -49.578 -41.279 -18.307  1.00 45.19           A    C
ATOM     10  O   ALA A   2     -50.549 -41.460 -19.038  1.00 46.01           A    O
ATOM     11  N   THR A   3     -48.571 -40.506 -18.675  1.00 45.24           A    N
ATOM     12  CA  THR A   3     -48.541 -40.003 -20.048  1.00 44.84           A    C
ATOM     13  CB  THR A   3     -49.272 -38.639 -20.200  1.00 44.49           A    C
```

ATOM	14	OG1	THR	A	3	-49.432	-38.341	-21.588	1.00	42.12	A	O
ATOM	15	CG2	THR	A	3	-48.529	-37.520	-19.521	1.00	41.95	A	C
ATOM	16	C	THR	A	3	-47.144	-40.023	-20.726	1.00	45.42	A	C
ATOM	17	O	THR	A	3	-46.153	-40.548	-20.182	1.00	46.03	A	O
ATOM	18	N	THR	A	4	-47.105	-39.436	-21.913	1.00	44.79	A	N
ATOM	19	CA	THR	A	4	-45.981	-39.502	-22.803	1.00	44.31	A	C
ATOM	20	CB	THR	A	4	-46.352	-40.377	-24.023	1.00	45.17	A	C
ATOM	21	OG1	THR	A	4	-45.615	-41.611	-23.914	1.00	45.01	A	O
ATOM	22	CG2	THR	A	4	-46.117	-39.684	-25.418	1.00	46.18	A	C
ATOM	23	C	THR	A	4	-45.505	-38.090	-23.095	1.00	43.59	A	C
ATOM	24	O	THR	A	4	-46.263	-37.144	-22.990	1.00	43.13	A	O
ATOM	25	N	GLY	A	5	-44.220	-37.949	-23.385	1.00	42.62	A	N
ATOM	26	CA	GLY	A	5	-43.593	-36.642	-23.465	1.00	40.86	A	C
ATOM	27	C	GLY	A	5	-42.380	-36.751	-24.358	1.00	39.27	A	C
ATOM	28	O	GLY	A	5	-42.184	-37.762	-25.008	1.00	39.11	A	O
ATOM	29	N	THR	A	6	-41.553	-35.717	-24.347	1.00	38.05	A	N
ATOM	30	CA	THR	A	6	-40.412	-35.657	-25.213	1.00	37.20	A	C
ATOM	31	CB	THR	A	6	-40.907	-35.169	-26.624	1.00	37.93	A	C
ATOM	32	OG1	THR	A	6	-40.731	-36.218	-27.585	1.00	37.23	A	O
ATOM	33	CG2	THR	A	6	-40.272	-33.892	-27.082	1.00	37.05	A	C
ATOM	34	C	THR	A	6	-39.401	-34.748	-24.523	1.00	36.18	A	C
ATOM	35	O	THR	A	6	-39.794	-33.933	-23.690	1.00	36.69	A	O
ATOM	36	N	GLY	A	7	-38.109	-34.926	-24.791	1.00	34.95	A	N
ATOM	37	CA	GLY	A	7	-37.092	-34.018	-24.258	1.00	33.82	A	C
ATOM	38	C	GLY	A	7	-35.792	-34.134	-25.024	1.00	33.59	A	C
ATOM	39	O	GLY	A	7	-35.645	-35.006	-25.862	1.00	34.18	A	O
ATOM	40	N	THR	A	8	-34.849	-33.253	-24.732	1.00	33.90	A	N
ATOM	41	CA	THR	A	8	-33.598	-33.129	-25.464	1.00	34.22	A	C
ATOM	42	CB	THR	A	8	-33.226	-31.608	-25.718	1.00	34.37	A	C
ATOM	43	OG1	THR	A	8	-34.299	-30.920	-26.401	1.00	36.58	A	O
ATOM	44	CG2	THR	A	8	-31.947	-31.481	-26.536	1.00	33.08	A	C
ATOM	45	C	THR	A	8	-32.453	-33.790	-24.669	1.00	34.72	A	C
ATOM	46	O	THR	A	8	-32.184	-33.426	-23.489	1.00	34.25	A	O
ATOM	47	N	THR	A	9	-31.753	-34.728	-25.323	1.00	34.59	A	N
ATOM	48	CA	THR	A	9	-30.639	-35.395	-24.677	1.00	34.66	A	C
ATOM	49	CB	THR	A	9	-30.238	-36.722	-25.329	1.00	33.98	A	C
ATOM	50	OG1	THR	A	9	-29.590	-36.445	-26.559	1.00	37.28	A	O
ATOM	51	CG2	THR	A	9	-31.414	-37.551	-25.590	1.00	33.59	A	C
ATOM	52	C	THR	A	9	-29.431	-34.488	-24.559	1.00	34.50	A	C
ATOM	53	O	THR	A	9	-29.385	-33.400	-25.144	1.00	33.46	A	O
ATOM	54	N	LEU	A	10	-28.479	-34.947	-23.749	1.00	34.53	A	N
ATOM	55	CA	LEU	A	10	-27.257	-34.224	-23.481	1.00	35.27	A	C
ATOM	56	CB	LEU	A	10	-26.367	-35.131	-22.654	1.00	34.24	A	C
ATOM	57	CG	LEU	A	10	-25.892	-34.808	-21.256	1.00	33.07	A	C
ATOM	58	CD1	LEU	A	10	-26.322	-33.431	-20.727	1.00	35.04	A	C
ATOM	59	CD2	LEU	A	10	-26.213	-35.900	-20.296	1.00	29.81	A	C
ATOM	60	C	LEU	A	10	-26.539	-33.859	-24.786	1.00	37.02	A	C
ATOM	61	O	LEU	A	10	-25.854	-32.837	-24.839	1.00	36.69	A	O
ATOM	62	N	LYS	A	11	-26.672	-34.715	-25.801	1.00	38.07	A	N
ATOM	63	CA	LYS	A	11	-26.036	-34.498	-27.084	1.00	41.05	A	C
ATOM	64	CB	LYS	A	11	-25.488	-35.850	-27.666	1.00	41.74	A	C
ATOM	65	CG	LYS	A	11	-24.330	-36.532	-26.896	1.00	41.97	A	C
ATOM	66	CD	LYS	A	11	-23.014	-35.884	-27.186	1.00	40.92	A	C
ATOM	67	CE	LYS	A	11	-21.854	-36.797	-26.839	1.00	44.19	A	C
ATOM	68	NZ	LYS	A	11	-21.535	-36.808	-25.375	1.00	43.03	A	N
ATOM	69	C	LYS	A	11	-26.996	-33.861	-28.134	1.00	42.61	A	C
ATOM	70	O	LYS	A	11	-26.661	-33.822	-29.329	1.00	43.21	A	O
ATOM	71	N	GLY	A	12	-28.198	-33.427	-27.730	1.00	43.01	A	N
ATOM	72	CA	GLY	A	12	-29.046	-32.651	-28.623	1.00	42.11	A	C
ATOM	73	C	GLY	A	12	-30.002	-33.454	-29.460	1.00	42.80	A	C
ATOM	74	O	GLY	A	12	-30.566	-32.919	-30.409	1.00	43.22	A	O
ATOM	75	N	LYS	A	13	-30.208	-34.725	-29.127	1.00	43.45	A	N
ATOM	76	CA	LYS	A	13	-31.271	-35.553	-29.763	1.00	44.11	A	C
ATOM	77	CB	LYS	A	13	-30.888	-37.042	-29.814	1.00	44.72	A	C
ATOM	78	CG	LYS	A	13	-29.608	-37.376	-30.625	1.00	50.68	A	C
ATOM	79	CD	LYS	A	13	-29.503	-38.928	-30.912	1.00	59.09	A	C
ATOM	80	CE	LYS	A	13	-28.149	-39.327	-31.606	1.00	62.01	A	C
ATOM	81	NZ	LYS	A	13	-28.222	-40.646	-32.356	1.00	60.47	A	N
ATOM	82	C	LYS	A	13	-32.599	-35.440	-29.035	1.00	43.37	A	C
ATOM	83	O	LYS	A	13	-32.647	-35.028	-27.894	1.00	43.72	A	O
ATOM	84	N	THR	A	14	-33.676	-35.837	-29.697	1.00	43.02	A	N
ATOM	85	CA	THR	A	14	-35.013	-35.820	-29.126	1.00	42.26	A	C
ATOM	86	CB	THR	A	14	-36.049	-35.120	-30.099	1.00	42.99	A	C
ATOM	87	OG1	THR	A	14	-35.904	-33.701	-29.986	1.00	40.45	A	O
ATOM	88	CG2	THR	A	14	-37.519	-35.492	-29.794	1.00	41.44	A	C
ATOM	89	C	THR	A	14	-35.441	-37.241	-28.799	1.00	42.01	A	C
ATOM	90	O	THR	A	14	-35.330	-38.123	-29.644	1.00	42.35	A	O
ATOM	91	N	VAL	A	15	-35.908	-37.478	-27.569	1.00	40.90	A	N
ATOM	92	CA	VAL	A	15	-36.346	-38.846	-27.192	1.00	39.44	A	C

ATOM	93	CB	VAL	A	15	-35.297	-39.522	-26.261	1.00	39.86	A	C
ATOM	94	CG1	VAL	A	15	-34.013	-39.848	-27.046	1.00	34.51	A	C
ATOM	95	CG2	VAL	A	15	-34.997	-38.621	-24.996	1.00	37.32	A	C
ATOM	96	C	VAL	A	15	-37.779	-38.883	-26.600	1.00	39.22	A	C
ATOM	97	O	VAL	A	15	-38.288	-37.859	-26.124	1.00	38.62	A	O
ATOM	98	N	SER	A	16	-38.443	-40.034	-26.653	1.00	38.75	A	N
ATOM	99	CA	SER	A	16	-39.693	-40.193	-25.874	1.00	39.39	A	C
ATOM	100	CB	SER	A	16	-40.511	-41.380	-26.338	1.00	39.15	A	C
ATOM	101	OG	SER	A	16	-40.729	-41.230	-27.691	1.00	43.31	A	O
ATOM	102	C	SER	A	16	-39.402	-40.439	-24.405	1.00	39.11	A	C
ATOM	103	O	SER	A	16	-38.488	-41.214	-24.085	1.00	39.19	A	O
ATOM	104	N	LEU	A	17	-40.218	-39.838	-23.532	1.00	38.27	A	N
ATOM	105	CA	LEU	A	17	-40.058	-39.952	-22.081	1.00	37.35	A	C
ATOM	106	CB	LEU	A	17	-39.700	-38.582	-21.507	1.00	36.35	A	C
ATOM	107	CG	LEU	A	17	-38.308	-38.048	-21.857	1.00	33.05	A	C
ATOM	108	CD1	LEU	A	17	-38.184	-36.605	-21.514	1.00	25.83	A	C
ATOM	109	CD2	LEU	A	17	-37.189	-38.879	-21.147	1.00	31.27	A	C
ATOM	110	C	LEU	A	17	-41.371	-40.406	-21.500	1.00	37.48	A	C
ATOM	111	O	LEU	A	17	-42.378	-39.859	-21.864	1.00	38.44	A	O
ATOM	112	N	ASN	A	18	-41.383	-41.413	-20.628	1.00	37.00	A	N
ATOM	113	CA	ASN	A	18	-42.589	-41.755	-19.891	1.00	36.02	A	C
ATOM	114	CB	ASN	A	18	-42.560	-43.192	-19.444	1.00	35.98	A	C
ATOM	115	CG	ASN	A	18	-42.465	-44.148	-20.596	1.00	39.27	A	C
ATOM	116	OD1	ASN	A	18	-41.623	-45.048	-20.623	1.00	43.56	A	O
ATOM	117	ND2	ASN	A	18	-43.324	-43.971	-21.558	1.00	40.11	A	N
ATOM	118	C	ASN	A	18	-42.687	-40.812	-18.693	1.00	35.67	A	C
ATOM	119	O	ASN	A	18	-41.822	-40.804	-17.838	1.00	34.62	A	O
ATOM	120	N	ILE	A	19	-43.743	-40.004	-18.667	1.00	35.62	A	N
ATOM	121	CA	ILE	A	19	-43.935	-38.949	-17.666	1.00	35.75	A	C
ATOM	122	CB	ILE	A	19	-43.722	-37.554	-18.292	1.00	35.34	A	C
ATOM	123	CG1	ILE	A	19	-44.825	-37.201	-19.302	1.00	33.51	A	C
ATOM	124	CD1	ILE	A	19	-44.612	-35.848	-19.949	1.00	34.72	A	C
ATOM	125	CG2	ILE	A	19	-42.332	-37.528	-18.917	1.00	33.23	A	C
ATOM	126	C	ILE	A	19	-45.291	-39.046	-16.909	1.00	36.80	A	C
ATOM	127	O	ILE	A	19	-46.081	-39.965	-17.145	1.00	35.92	A	O
ATOM	128	N	SER	A	20	-45.498	-38.140	-15.963	1.00	38.36	A	N
ATOM	129	CA	SER	A	20	-46.765	-38.045	-15.189	1.00	40.90	A	C
ATOM	130	CB	SER	A	20	-46.534	-38.472	-13.726	1.00	40.17	A	C
ATOM	131	OG	SER	A	20	-47.498	-37.935	-12.855	1.00	39.41	A	O
ATOM	132	C	SER	A	20	-47.313	-36.615	-15.209	1.00	42.05	A	C
ATOM	133	O	SER	A	20	-46.530	-35.668	-14.952	1.00	42.63	A	O
ATOM	134	N	SER	A	21	-48.586	-36.438	-15.529	1.00	43.64	A	N
ATOM	135	CA	SER	A	21	-49.219	-35.132	-15.353	1.00	45.31	A	C
ATOM	136	CB	SER	A	21	-50.357	-34.872	-16.336	1.00	45.18	A	C
ATOM	137	OG	SER	A	21	-51.138	-36.000	-16.559	1.00	45.91	A	O
ATOM	138	C	SER	A	21	-49.696	-35.055	-13.949	1.00	45.77	A	C
ATOM	139	O	SER	A	21	-50.535	-35.811	-13.556	1.00	45.47	A	O
ATOM	140	N	GLU	A	22	-49.113	-34.148	-13.193	1.00	47.74	A	N
ATOM	141	CA	GLU	A	22	-49.171	-34.189	-11.767	1.00	49.15	A	C
ATOM	142	CB	GLU	A	22	-47.892	-34.769	-11.260	1.00	49.13	A	C
ATOM	143	CG	GLU	A	22	-48.016	-36.086	-10.722	1.00	46.55	A	C
ATOM	144	CD	GLU	A	22	-46.717	-36.646	-10.354	1.00	39.46	A	C
ATOM	145	OE1	GLU	A	22	-45.983	-35.997	-9.639	1.00	34.91	A	O
ATOM	146	OE2	GLU	A	22	-46.432	-37.720	-10.806	1.00	32.47	A	O
ATOM	147	C	GLU	A	22	-49.162	-32.806	-11.279	1.00	51.23	A	C
ATOM	148	O	GLU	A	22	-48.381	-32.018	-11.727	1.00	52.04	A	O
ATOM	149	N	SER	A	23	-49.996	-32.494	-10.320	1.00	52.77	A	N
ATOM	150	CA	SER	A	23	-50.001	-31.133	-9.903	1.00	54.10	A	C
ATOM	151	CB	SER	A	23	-48.649	-30.810	-9.340	1.00	54.93	A	C
ATOM	152	OG	SER	A	23	-48.179	-31.939	-8.645	1.00	54.76	A	O
ATOM	153	C	SER	A	23	-50.282	-30.272	-11.111	1.00	54.42	A	C
ATOM	154	O	SER	A	23	-51.075	-30.606	-11.970	1.00	55.29	A	O
ATOM	155	N	GLY	A	24	-49.653	-29.143	-11.212	1.00	54.60	A	N
ATOM	156	CA	GLY	A	24	-50.035	-28.344	-12.342	1.00	54.68	A	C
ATOM	157	C	GLY	A	24	-49.544	-28.801	-13.683	1.00	54.45	A	C
ATOM	158	O	GLY	A	24	-50.009	-28.324	-14.682	1.00	54.42	A	O
ATOM	159	N	LYS	A	25	-48.589	-29.717	-13.685	1.00	53.42	A	N
ATOM	160	CA	LYS	A	25	-47.626	-29.848	-14.742	1.00	51.96	A	C
ATOM	161	CB	LYS	A	25	-46.345	-29.213	-14.276	1.00	51.64	A	C
ATOM	162	CG	LYS	A	25	-46.385	-28.938	-12.870	1.00	54.15	A	C
ATOM	163	CD	LYS	A	25	-45.570	-29.847	-12.097	1.00	57.56	A	C
ATOM	164	CE	LYS	A	25	-44.768	-29.072	-11.100	1.00	60.94	A	C
ATOM	165	NZ	LYS	A	25	-44.500	-29.845	-9.858	1.00	61.61	A	N
ATOM	166	C	LYS	A	25	-47.270	-31.238	-15.143	1.00	51.03	A	C
ATOM	167	O	LYS	A	25	-48.023	-32.164	-15.011	1.00	51.65	A	O
ATOM	168	N	TYR	A	26	-46.058	-31.349	-15.644	1.00	48.55	A	N
ATOM	169	CA	TYR	A	26	-45.481	-32.609	-15.998	1.00	45.54	A	C
ATOM	170	CB	TYR	A	26	-45.266	-32.653	-17.468	1.00	45.44	A	C
ATOM	171	CG	TYR	A	26	-46.525	-32.475	-18.221	1.00	47.36	A	C

ATOM	172	CD1	TYR	A	26	-47.208	-33.550	-18.707	1.00	47.06	A	C
ATOM	173	CE1	TYR	A	26	-48.330	-33.377	-19.398	1.00	50.44	A	C
ATOM	174	CZ	TYR	A	26	-48.788	-32.124	-19.615	1.00	49.90	A	C
ATOM	175	OH	TYR	A	26	-49.922	-31.948	-20.312	1.00	52.47	A	O
ATOM	176	CE2	TYR	A	26	-48.138	-31.061	-19.143	1.00	46.84	A	C
ATOM	177	CD2	TYR	A	26	-47.028	-31.228	-18.457	1.00	46.94	A	C
ATOM	178	C	TYR	A	26	-44.191	-32.834	-15.297	1.00	43.35	A	C
ATOM	179	O	TYR	A	26	-43.380	-31.955	-15.155	1.00	42.38	A	O
ATOM	180	N	VAL	A	27	-44.026	-34.045	-14.834	1.00	40.47	A	N
ATOM	181	CA	VAL	A	27	-42.808	-34.391	-14.083	1.00	38.59	A	C
ATOM	182	CB	VAL	A	27	-43.103	-34.570	-12.556	1.00	38.99	A	C
ATOM	183	CG1	VAL	A	27	-43.789	-33.357	-12.001	1.00	38.60	A	C
ATOM	184	CG2	VAL	A	27	-43.963	-35.855	-12.313	1.00	37.66	A	C
ATOM	185	C	VAL	A	27	-42.118	-35.672	-14.643	1.00	36.60	A	C
ATOM	186	O	VAL	A	27	-42.781	-36.552	-15.270	1.00	34.97	A	O
ATOM	187	N	LEU	A	28	-40.815	-35.780	-14.379	1.00	33.39	A	N
ATOM	188	CA	LEU	A	28	-40.087	-37.030	-14.686	1.00	31.31	A	C
ATOM	189	CB	LEU	A	28	-38.592	-36.741	-14.896	1.00	30.82	A	C
ATOM	190	CG	LEU	A	28	-38.370	-35.763	-16.069	1.00	29.25	A	C
ATOM	191	CD1	LEU	A	28	-36.887	-35.614	-16.436	1.00	25.75	A	C
ATOM	192	CD2	LEU	A	28	-39.188	-36.282	-17.297	1.00	27.62	A	C
ATOM	193	C	LEU	A	28	-40.356	-38.195	-13.692	1.00	29.91	A	C
ATOM	194	O	LEU	A	28	-39.512	-38.572	-12.864	1.00	28.72	A	O
ATOM	195	N	ARG	A	29	-41.548	-38.759	-13.821	1.00	29.17	A	N
ATOM	196	CA	ARG	A	29	-41.983	-39.934	-13.093	1.00	29.07	A	C
ATOM	197	CB	ARG	A	29	-43.031	-39.566	-12.002	1.00	28.30	A	C
ATOM	198	CG	ARG	A	29	-43.815	-40.779	-11.438	1.00	29.82	A	C
ATOM	199	CD	ARG	A	29	-44.958	-40.532	-10.414	1.00	29.04	A	C
ATOM	200	NE	ARG	A	29	-44.832	-39.314	-9.598	1.00	28.43	A	N
ATOM	201	CZ	ARG	A	29	-44.170	-39.129	-8.449	1.00	27.95	A	C
ATOM	202	NH1	ARG	A	29	-43.416	-40.064	-7.875	1.00	28.57	A	N
ATOM	203	NH2	ARG	A	29	-44.232	-37.925	-7.885	1.00	29.61	A	N
ATOM	204	C	ARG	A	29	-42.556	-40.961	-14.088	1.00	29.23	A	C
ATOM	205	O	ARG	A	29	-43.510	-40.685	-14.745	1.00	28.41	A	O
ATOM	206	N	ASP	A	30	-41.990	-42.170	-14.153	1.00	30.20	A	N
ATOM	207	CA	ASP	A	30	-42.364	-43.158	-15.151	1.00	30.03	A	C
ATOM	208	CB	ASP	A	30	-41.100	-43.849	-15.701	1.00	29.34	A	C
ATOM	209	CG	ASP	A	30	-41.383	-44.840	-16.878	1.00	30.84	A	C
ATOM	210	OD1	ASP	A	30	-42.525	-45.362	-17.072	1.00	29.94	A	O
ATOM	211	OD2	ASP	A	30	-40.425	-45.107	-17.621	1.00	27.79	A	O
ATOM	212	C	ASP	A	30	-43.360	-44.123	-14.524	1.00	30.55	A	C
ATOM	213	O	ASP	A	30	-43.089	-44.784	-13.525	1.00	29.55	A	O
ATOM	214	N	LEU	A	31	-44.531	-44.182	-15.129	1.00	31.84	A	N
ATOM	215	CA	LEU	A	31	-45.673	-44.804	-14.522	1.00	33.66	A	C
ATOM	216	CB	LEU	A	31	-46.741	-43.758	-14.269	1.00	33.92	A	C
ATOM	217	CG	LEU	A	31	-47.021	-43.233	-12.839	1.00	37.06	A	C
ATOM	218	CD1	LEU	A	31	-45.876	-43.230	-11.897	1.00	35.24	A	C
ATOM	219	CD2	LEU	A	31	-47.674	-41.810	-12.854	1.00	38.45	A	C
ATOM	220	C	LEU	A	31	-46.189	-45.830	-15.479	1.00	35.24	A	C
ATOM	221	O	LEU	A	31	-47.292	-46.339	-15.306	1.00	36.18	A	O
ATOM	222	N	SER	A	32	-45.347	-46.150	-16.474	1.00	36.86	A	N
ATOM	223	CA	SER	A	32	-45.652	-47.055	-17.588	1.00	36.85	A	C
ATOM	224	CB	SER	A	32	-45.024	-46.556	-18.925	1.00	36.60	A	C
ATOM	225	OG	SER	A	32	-43.606	-46.774	-18.972	1.00	38.59	A	O
ATOM	226	C	SER	A	32	-45.197	-48.468	-17.297	1.00	37.03	A	C
ATOM	227	O	SER	A	32	-45.544	-49.365	-18.061	1.00	36.94	A	O
ATOM	228	N	LYS	A	33	-44.434	-48.691	-16.225	1.00	37.38	A	N
ATOM	229	CA	LYS	A	33	-43.866	-50.038	-16.026	1.00	38.79	A	C
ATOM	230	CB	LYS	A	33	-42.573	-50.035	-15.186	1.00	38.26	A	C
ATOM	231	CG	LYS	A	33	-41.473	-49.071	-15.689	1.00	34.67	A	C
ATOM	232	CD	LYS	A	33	-41.118	-49.392	-17.134	1.00	30.21	A	C
ATOM	233	CE	LYS	A	33	-39.984	-48.532	-17.680	1.00	29.07	A	C
ATOM	234	NZ	LYS	A	33	-39.732	-48.697	-19.185	1.00	23.25	A	N
ATOM	235	C	LYS	A	33	-44.895	-51.052	-15.503	1.00	41.30	A	C
ATOM	236	O	LYS	A	33	-45.622	-50.798	-14.530	1.00	40.23	A	O
ATOM	237	N	PRO	A	34	-44.958	-52.230	-16.147	1.00	44.22	A	N
ATOM	238	CA	PRO	A	34	-46.201	-52.950	-15.790	1.00	45.38	A	C
ATOM	239	CB	PRO	A	34	-46.352	-54.000	-16.926	1.00	47.30	A	C
ATOM	240	CG	PRO	A	34	-44.809	-54.186	-17.497	1.00	48.14	A	C
ATOM	241	CD	PRO	A	34	-43.951	-53.092	-16.834	1.00	44.53	A	C
ATOM	242	C	PRO	A	34	-46.125	-53.585	-14.377	1.00	44.92	A	C
ATOM	243	O	PRO	A	34	-47.134	-54.070	-13.845	1.00	45.69	A	O
ATOM	244	N	THR	A	35	-44.963	-53.546	-13.741	1.00	42.51	A	N
ATOM	245	CA	THR	A	35	-44.926	-54.019	-12.364	1.00	40.40	A	C
ATOM	246	CB	THR	A	35	-43.499	-54.464	-12.004	1.00	41.17	A	C
ATOM	247	OG1	THR	A	35	-42.610	-53.388	-12.332	1.00	40.39	A	O
ATOM	248	CG2	THR	A	35	-43.107	-55.773	-12.741	1.00	39.31	A	C
ATOM	249	C	THR	A	35	-45.346	-52.956	-11.315	1.00	38.28	A	C
ATOM	250	O	THR	A	35	-45.433	-53.269	-10.120	1.00	36.30	A	O

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ATOM    251  N    GLY A  36     -45.536 -51.702 -11.755  1.00 36.35          A    N
ATOM    252  CA   GLY A  36     -45.713 -50.583 -10.830  1.00 32.77          A    C
ATOM    253  C    GLY A  36     -44.426 -49.842 -10.507  1.00 31.89          A    C
ATOM    254  O    GLY A  36     -44.456 -48.780  -9.912  1.00 31.63          A    O
ATOM    255  N    THR A  37     -43.266 -50.351 -10.924  1.00 30.83          A    N
ATOM    256  CA   THR A  37     -42.003 -49.747 -10.482  1.00 27.70          A    C
ATOM    257  CB   THR A  37     -40.819 -50.642 -10.820  1.00 27.55          A    C
ATOM    258  OG1  THR A  37     -40.960 -51.876 -10.095  1.00 28.01          A    O
ATOM    259  CG2  THR A  37     -39.494 -49.979 -10.501  1.00 23.29          A    C
ATOM    260  C    THR A  37     -41.851 -48.380 -11.106  1.00 26.95          A    C
ATOM    261  O    THR A  37     -41.941 -48.260 -12.281  1.00 26.14          A    O
ATOM    262  N    GLN A  38     -41.525 -47.385 -10.329  1.00 26.09          A    N
ATOM    263  CA   GLN A  38     -41.319 -46.059 -10.826  1.00 26.76          A    C
ATOM    264  CB   GLN A  38     -41.863 -45.066  -9.816  1.00 27.60          A    C
ATOM    265  CG   GLN A  38     -43.300 -44.836  -9.957  1.00 30.56          A    C
ATOM    266  CD   GLN A  38     -43.913 -44.030  -8.864  1.00 34.02          A    C
ATOM    267  OE1  GLN A  38     -43.367 -43.074  -8.393  1.00 35.21          A    O
ATOM    268  NE2  GLN A  38     -45.077 -44.404  -8.485  1.00 31.60          A    N
ATOM    269  C    GLN A  38     -39.881 -45.752 -11.122  1.00 25.09          A    C
ATOM    270  O    GLN A  38     -39.025 -46.182 -10.432  1.00 26.13          A    O
ATOM    271  N    ILE A  39     -39.629 -45.004 -12.176  1.00 23.80          A    N
ATOM    272  CA   ILE A  39     -38.346 -44.336 -12.348  1.00 24.26          A    C
ATOM    273  CB   ILE A  39     -37.699 -44.596 -13.772  1.00 24.68          A    C
ATOM    274  CG1  ILE A  39     -37.395 -46.080 -14.014  1.00 21.84          A    C
ATOM    275  CD1  ILE A  39     -38.507 -46.858 -14.474  1.00 21.10          A    C
ATOM    276  CG2  ILE A  39     -36.388 -43.745 -13.945  1.00 24.04          A    C
ATOM    277  C    ILE A  39     -38.587 -42.826 -12.122  1.00 24.60          A    C
ATOM    278  O    ILE A  39     -39.521 -42.255 -12.681  1.00 25.49          A    O
ATOM    279  N    ILE A  40     -37.804 -42.171 -11.281  1.00 24.30          A    N
ATOM    280  CA   ILE A  40     -38.138 -40.820 -10.904  1.00 24.67          A    C
ATOM    281  CB   ILE A  40     -38.760 -40.776  -9.481  1.00 25.40          A    C
ATOM    282  CG1  ILE A  40     -39.778 -41.902  -9.248  1.00 26.78          A    C
ATOM    283  CD1  ILE A  40     -40.256 -41.969  -7.776  1.00 28.72          A    C
ATOM    284  CG2  ILE A  40     -39.456 -39.440  -9.198  1.00 25.40          A    C
ATOM    285  C    ILE A  40     -36.831 -40.033 -10.917  1.00 25.31          A    C
ATOM    286  O    ILE A  40     -35.881 -40.469 -10.303  1.00 25.86          A    O
ATOM    287  N    THR A  41     -36.785 -38.864 -11.577  1.00 25.27          A    N
ATOM    288  CA   THR A  41     -35.535 -38.168 -11.811  1.00 24.40          A    C
ATOM    289  CB   THR A  41     -35.271 -38.016 -13.322  1.00 23.99          A    C
ATOM    290  OG1  THR A  41     -35.523 -39.264 -13.986  1.00 24.89          A    O
ATOM    291  CG2  THR A  41     -33.870 -37.563 -13.592  1.00 20.66          A    C
ATOM    292  C    THR A  41     -35.545 -36.793 -11.150  1.00 26.35          A    C
ATOM    293  O    THR A  41     -36.499 -36.004 -11.319  1.00 26.67          A    O
ATOM    294  N    TYR A  42     -34.488 -36.490 -10.401  1.00 26.81          A    N
ATOM    295  CA   TYR A  42     -34.470 -35.288  -9.624  1.00 28.66          A    C
ATOM    296  CB   TYR A  42     -34.363 -35.615  -8.121  1.00 29.19          A    C
ATOM    297  CG   TYR A  42     -35.602 -36.234  -7.554  1.00 28.72          A    C
ATOM    298  CD1  TYR A  42     -35.834 -37.620  -7.674  1.00 29.76          A    C
ATOM    299  CE1  TYR A  42     -36.985 -38.198  -7.145  1.00 30.70          A    C
ATOM    300  CZ   TYR A  42     -37.913 -37.389  -6.473  1.00 32.18          A    C
ATOM    301  OH   TYR A  42     -39.044 -37.951  -5.962  1.00 34.06          A    O
ATOM    302  CE2  TYR A  42     -37.732 -36.002  -6.366  1.00 29.34          A    C
ATOM    303  CD2  TYR A  42     -36.556 -35.441  -6.883  1.00 28.41          A    C
ATOM    304  C    TYR A  42     -33.275 -34.456 -10.028  1.00 30.08          A    C
ATOM    305  O    TYR A  42     -32.293 -34.980 -10.550  1.00 29.14          A    O
ATOM    306  N    ASP A  43     -33.356 -33.160  -9.738  1.00 31.69          A    N
ATOM    307  CA   ASP A  43     -32.296 -32.216 -10.075  1.00 33.46          A    C
ATOM    308  CB   ASP A  43     -32.867 -31.090 -10.989  1.00 32.64          A    C
ATOM    309  CG   ASP A  43     -31.851 -29.958 -11.296  1.00 32.89          A    C
ATOM    310  OD1  ASP A  43     -30.696 -29.966 -10.757  1.00 30.15          A    O
ATOM    311  OD2  ASP A  43     -32.236 -29.054 -12.087  1.00 32.73          A    O
ATOM    312  C    ASP A  43     -31.740 -31.685  -8.754  1.00 34.58          A    C
ATOM    313  O    ASP A  43     -32.470 -31.124  -7.943  1.00 35.27          A    O
ATOM    314  N    LEU A  44     -30.453 -31.866  -8.521  1.00 36.27          A    N
ATOM    315  CA   LEU A  44     -29.884 -31.438  -7.245  1.00 37.65          A    C
ATOM    316  CB   LEU A  44     -28.720 -32.371  -6.881  1.00 37.26          A    C
ATOM    317  CG   LEU A  44     -28.521 -33.054  -5.509  1.00 39.07          A    C
ATOM    318  CD1  LEU A  44     -29.742 -33.120  -4.619  1.00 36.83          A    C
ATOM    319  CD2  LEU A  44     -27.831 -34.449  -5.635  1.00 37.50          A    C
ATOM    320  C    LEU A  44     -29.472 -29.939  -7.294  1.00 38.87          A    C
ATOM    321  O    LEU A  44     -29.162 -29.343  -6.279  1.00 39.39          A    O
ATOM    322  N    GLN A  45     -29.471 -29.328  -8.482  1.00 40.24          A    N
ATOM    323  CA   GLN A  45     -28.976 -27.955  -8.653  1.00 40.83          A    C
ATOM    324  CB   GLN A  45     -30.003 -26.930  -8.127  1.00 40.93          A    C
ATOM    325  CG   GLN A  45     -31.400 -27.042  -8.843  1.00 43.55          A    C
ATOM    326  CD   GLN A  45     -32.557 -26.463  -8.026  1.00 46.24          A    C
ATOM    327  OE1  GLN A  45     -32.440 -26.239  -6.825  1.00 48.19          A    O
ATOM    328  NE2  GLN A  45     -33.669 -26.215  -8.680  1.00 44.67          A    N
ATOM    329  C    GLN A  45     -27.607 -27.785  -8.002  1.00 41.18          A    C
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ATOM	330	O	GLN	A	45	-27.368	-26.809	-7.304	1.00	42.73	A	O
ATOM	331	N	ASN	A	46	-26.710	-28.738	-8.202	1.00	40.77	A	N
ATOM	332	CA	ASN	A	46	-25.305	-28.565	-7.818	1.00	41.87	A	C
ATOM	333	CB	ASN	A	46	-24.676	-27.325	-8.485	1.00	41.62	A	C
ATOM	334	CG	ASN	A	46	-24.762	-27.374	-10.029	1.00	42.52	A	C
ATOM	335	OD1	ASN	A	46	-25.384	-26.511	-10.647	1.00	42.00	A	O
ATOM	336	ND2	ASN	A	46	-24.173	-28.426	-10.642	1.00	39.75	A	N
ATOM	337	C	ASN	A	46	-24.977	-28.607	-6.340	1.00	43.16	A	C
ATOM	338	O	ASN	A	46	-23.805	-28.419	-6.002	1.00	42.88	A	O
ATOM	339	N	ARG	A	47	-25.992	-28.859	-5.485	1.00	44.54	A	N
ATOM	340	CA	ARG	A	47	-25.793	-29.192	-4.062	1.00	46.84	A	C
ATOM	341	CB	ARG	A	47	-27.013	-28.809	-3.177	1.00	47.30	A	C
ATOM	342	CG	ARG	A	47	-28.061	-27.854	-3.818	1.00	52.65	A	C
ATOM	343	CD	ARG	A	47	-28.528	-26.620	-2.951	1.00	60.12	A	C
ATOM	344	NE	ARG	A	47	-27.637	-25.455	-3.151	1.00	65.09	A	N
ATOM	345	CZ	ARG	A	47	-27.824	-24.450	-4.026	1.00	67.61	A	C
ATOM	346	NH1	ARG	A	47	-28.902	-24.400	-4.820	1.00	67.70	A	N
ATOM	347	NH2	ARG	A	47	-26.908	-23.483	-4.120	1.00	67.50	A	N
ATOM	348	C	ARG	A	47	-25.431	-30.704	-3.904	1.00	47.66	A	C
ATOM	349	O	ARG	A	47	-25.563	-31.500	-4.854	1.00	47.75	A	O
ATOM	350	N	GLU	A	48	-24.958	-31.100	-2.723	1.00	48.47	A	N
ATOM	351	CA	GLU	A	48	-24.549	-32.484	-2.482	1.00	49.38	A	C
ATOM	352	CB	GLU	A	48	-23.016	-32.618	-2.288	1.00	49.89	A	C
ATOM	353	CG	GLU	A	48	-22.140	-31.848	-3.281	1.00	53.97	A	C
ATOM	354	CD	GLU	A	48	-20.699	-32.390	-3.369	1.00	58.12	A	C
ATOM	355	OE1	GLU	A	48	-20.138	-32.504	-4.487	1.00	58.48	A	O
ATOM	356	OE2	GLU	A	48	-20.118	-32.708	-2.314	1.00	60.70	A	O
ATOM	357	C	GLU	A	48	-25.241	-33.080	-1.258	1.00	49.02	A	C
ATOM	358	O	GLU	A	48	-24.821	-34.136	-0.773	1.00	48.86	A	O
ATOM	359	N	TYR	A	49	-26.282	-32.411	-0.752	1.00	48.71	A	N
ATOM	360	CA	TYR	A	49	-26.949	-32.832	0.497	1.00	48.43	A	C
ATOM	361	CB	TYR	A	49	-26.434	-32.015	1.710	1.00	49.21	A	C
ATOM	362	CG	TYR	A	49	-26.684	-30.530	1.510	1.00	53.66	A	C
ATOM	363	CD1	TYR	A	49	-25.753	-29.740	0.794	1.00	57.40	A	C
ATOM	364	CE1	TYR	A	49	-25.994	-28.371	0.564	1.00	61.43	A	C
ATOM	365	CZ	TYR	A	49	-27.197	-27.783	1.046	1.00	63.54	A	C
ATOM	366	OH	TYR	A	49	-27.421	-26.423	0.803	1.00	65.65	A	O
ATOM	367	CE2	TYR	A	49	-28.150	-28.560	1.742	1.00	59.44	A	C
ATOM	368	CD2	TYR	A	49	-27.883	-29.918	1.975	1.00	56.66	A	C
ATOM	369	C	TYR	A	49	-28.438	-32.632	0.350	1.00	47.07	A	C
ATOM	370	O	TYR	A	49	-28.896	-31.946	-0.594	1.00	46.06	A	O
ATOM	371	N	ASN	A	50	-29.192	-33.194	1.315	1.00	46.10	A	N
ATOM	372	CA	ASN	A	50	-30.657	-33.095	1.331	1.00	43.95	A	C
ATOM	373	CB	ASN	A	50	-31.101	-31.597	1.518	1.00	44.54	A	C
ATOM	374	CG	ASN	A	50	-32.582	-31.439	1.975	1.00	46.46	A	C
ATOM	375	OD1	ASN	A	50	-33.116	-32.261	2.725	1.00	47.44	A	O
ATOM	376	ND2	ASN	A	50	-33.238	-30.373	1.511	1.00	48.73	A	N
ATOM	377	C	ASN	A	50	-31.196	-33.744	0.023	1.00	41.68	A	C
ATOM	378	O	ASN	A	50	-32.011	-33.161	-0.691	1.00	40.51	A	O
ATOM	379	N	LEU	A	51	-30.711	-34.952	-0.266	1.00	39.34	A	N
ATOM	380	CA	LEU	A	51	-31.135	-35.742	-1.434	1.00	38.05	A	C
ATOM	381	CB	LEU	A	51	-30.272	-37.011	-1.608	1.00	36.68	A	C
ATOM	382	CG	LEU	A	51	-28.736	-36.853	-1.766	1.00	38.02	A	C
ATOM	383	CD1	LEU	A	51	-28.040	-37.730	-2.821	1.00	30.41	A	C
ATOM	384	CD2	LEU	A	51	-28.301	-35.401	-1.953	1.00	38.51	A	C
ATOM	385	C	LEU	A	51	-32.609	-36.125	-1.302	1.00	37.04	A	C
ATOM	386	O	LEU	A	51	-33.115	-36.208	-0.183	1.00	38.60	A	O
ATOM	387	N	PRO	A	52	-33.296	-36.391	-2.426	1.00	35.16	A	N
ATOM	388	CA	PRO	A	52	-32.736	-36.442	-3.785	1.00	35.00	A	C
ATOM	389	CB	PRO	A	52	-33.631	-37.467	-4.472	1.00	34.76	A	C
ATOM	390	CG	PRO	A	52	-34.968	-37.210	-3.835	1.00	35.21	A	C
ATOM	391	CD	PRO	A	52	-34.680	-36.861	-2.384	1.00	33.35	A	C
ATOM	392	C	PRO	A	52	-32.741	-35.098	-4.564	1.00	34.93	A	C
ATOM	393	O	PRO	A	52	-32.065	-34.989	-5.602	1.00	35.60	A	O
ATOM	394	N	GLY	A	53	-33.486	-34.105	-4.068	1.00	34.24	A	N
ATOM	395	CA	GLY	A	53	-33.572	-32.778	-4.661	1.00	33.02	A	C
ATOM	396	C	GLY	A	53	-34.949	-32.535	-5.260	1.00	32.97	A	C
ATOM	397	O	GLY	A	53	-35.952	-33.093	-4.807	1.00	33.28	A	O
ATOM	398	N	THR	A	54	-34.967	-31.739	-6.320	1.00	32.27	A	N
ATOM	399	CA	THR	A	54	-36.160	-31.260	-6.945	1.00	32.37	A	C
ATOM	400	CB	THR	A	54	-35.947	-29.811	-7.437	1.00	32.98	A	C
ATOM	401	OG1	THR	A	54	-35.393	-29.041	-6.360	1.00	34.33	A	O
ATOM	402	CG2	THR	A	54	-37.276	-29.167	-8.007	1.00	31.11	A	C
ATOM	403	C	THR	A	54	-36.605	-32.137	-8.106	1.00	32.94	A	C
ATOM	404	O	THR	A	54	-35.878	-32.380	-9.087	1.00	31.68	A	O
ATOM	405	N	LEU	A	55	-37.838	-32.586	-7.987	1.00	33.67	A	N
ATOM	406	CA	LEU	A	55	-38.430	-33.378	-8.995	1.00	35.36	A	C
ATOM	407	CB	LEU	A	55	-39.855	-33.704	-8.577	1.00	34.52	A	C
ATOM	408	CG	LEU	A	55	-40.594	-34.680	-9.486	1.00	37.35	A	C

ATOM	409	CD1	LEU	A	55	-39.853	-36.006	-9.710	1.00	32.36	A	C
ATOM	410	CD2	LEU	A	55	-41.990	-34.945	-8.959	1.00	38.13	A	C
ATOM	411	C	LEU	A	55	-38.335	-32.533	-10.275	1.00	36.98	A	C
ATOM	412	O	LEU	A	55	-38.680	-31.346	-10.269	1.00	37.92	A	O
ATOM	413	N	VAL	A	56	-37.811	-33.123	-11.355	1.00	37.30	A	N
ATOM	414	CA	VAL	A	56	-37.657	-32.406	-12.591	1.00	36.64	A	C
ATOM	415	CB	VAL	A	56	-36.625	-33.113	-13.515	1.00	36.80	A	C
ATOM	416	CG1	VAL	A	56	-36.762	-32.623	-14.916	1.00	34.94	A	C
ATOM	417	CG2	VAL	A	56	-35.191	-32.844	-13.013	1.00	32.55	A	C
ATOM	418	C	VAL	A	56	-39.034	-32.199	-13.231	1.00	38.20	A	C
ATOM	419	O	VAL	A	56	-39.807	-33.136	-13.400	1.00	38.95	A	O
ATOM	420	N	SER	A	57	-39.370	-30.966	-13.578	1.00	40.18	A	N
ATOM	421	CA	SER	A	57	-40.712	-30.721	-14.141	1.00	42.41	A	C
ATOM	422	CB	SER	A	57	-41.729	-30.414	-13.036	1.00	41.73	A	C
ATOM	423	OG	SER	A	57	-41.165	-29.456	-12.199	1.00	42.33	A	O
ATOM	424	C	SER	A	57	-40.771	-29.642	-15.221	1.00	42.87	A	C
ATOM	425	O	SER	A	57	-39.889	-28.786	-15.312	1.00	42.53	A	O
ATOM	426	N	SER	A	58	-41.805	-29.725	-16.046	1.00	43.46	A	N
ATOM	427	CA	SER	A	58	-42.064	-28.689	-17.021	1.00	45.24	A	C
ATOM	428	CB	SER	A	58	-41.435	-29.040	-18.379	1.00	44.87	A	C
ATOM	429	OG	SER	A	58	-42.368	-28.988	-19.446	1.00	43.17	A	O
ATOM	430	C	SER	A	58	-43.572	-28.385	-17.143	1.00	46.75	A	C
ATOM	431	O	SER	A	58	-44.444	-29.258	-16.870	1.00	45.93	A	O
ATOM	432	N	THR	A	59	-43.872	-27.155	-17.572	1.00	47.81	A	N
ATOM	433	CA	THR	A	59	-45.272	-26.786	-17.788	1.00	48.79	A	C
ATOM	434	CB	THR	A	59	-45.480	-25.278	-17.829	1.00	49.03	A	C
ATOM	435	OG1	THR	A	59	-44.902	-24.807	-19.041	1.00	49.03	A	O
ATOM	436	CG2	THR	A	59	-44.827	-24.562	-16.589	1.00	48.04	A	C
ATOM	437	C	THR	A	59	-45.820	-27.435	-19.055	1.00	48.93	A	C
ATOM	438	O	THR	A	59	-47.025	-27.449	-19.250	1.00	49.98	A	O
ATOM	439	N	THR	A	60	-44.956	-28.002	-19.889	1.00	48.95	A	N
ATOM	440	CA	THR	A	60	-45.416	-28.777	-21.048	1.00	49.54	A	C
ATOM	441	CB	THR	A	60	-44.976	-28.152	-22.416	1.00	50.77	A	C
ATOM	442	OG1	THR	A	60	-43.537	-27.921	-22.449	1.00	50.15	A	O
ATOM	443	CG2	THR	A	60	-45.795	-26.834	-22.706	1.00	49.54	A	C
ATOM	444	C	THR	A	60	-44.927	-30.207	-21.074	1.00	49.42	A	C
ATOM	445	O	THR	A	60	-44.079	-30.621	-20.300	1.00	49.57	A	O
ATOM	446	N	ASN	A	61	-45.521	-30.947	-21.987	1.00	48.77	A	N
ATOM	447	CA	ASN	A	61	-45.036	-32.187	-22.505	1.00	47.80	A	C
ATOM	448	CB	ASN	A	61	-45.682	-32.345	-23.885	1.00	48.54	A	C
ATOM	449	CG	ASN	A	61	-46.190	-33.713	-24.078	1.00	52.04	A	C
ATOM	450	OD1	ASN	A	61	-46.532	-34.150	-25.180	1.00	52.14	A	O
ATOM	451	ND2	ASN	A	61	-46.237	-34.448	-22.960	1.00	58.59	A	N
ATOM	452	C	ASN	A	61	-43.527	-32.339	-22.754	1.00	46.83	A	C
ATOM	453	O	ASN	A	61	-43.056	-33.455	-23.094	1.00	45.82	A	O
ATOM	454	N	GLN	A	62	-42.780	-31.234	-22.648	1.00	45.02	A	N
ATOM	455	CA	GLN	A	62	-41.465	-31.161	-23.273	1.00	43.93	A	C
ATOM	456	CB	GLN	A	62	-41.479	-30.234	-24.529	1.00	44.43	A	C
ATOM	457	CG	GLN	A	62	-42.303	-30.766	-25.762	1.00	49.48	A	C
ATOM	458	CD	GLN	A	62	-41.858	-30.185	-27.192	1.00	56.15	A	C
ATOM	459	OE1	GLN	A	62	-40.951	-29.336	-27.299	1.00	55.55	A	O
ATOM	460	NE2	GLN	A	62	-42.511	-30.683	-28.274	1.00	54.68	A	N
ATOM	461	C	GLN	A	62	-40.379	-30.760	-22.285	1.00	42.39	A	C
ATOM	462	O	GLN	A	62	-40.507	-29.738	-21.575	1.00	41.48	A	O
ATOM	463	N	PHE	A	63	-39.299	-31.553	-22.240	1.00	40.50	A	N
ATOM	464	CA	PHE	A	63	-38.183	-31.224	-21.338	1.00	39.06	A	C
ATOM	465	CB	PHE	A	63	-37.901	-32.388	-20.376	1.00	38.22	A	C
ATOM	466	CG	PHE	A	63	-39.057	-32.701	-19.488	1.00	33.68	A	C
ATOM	467	CD1	PHE	A	63	-40.184	-33.360	-20.008	1.00	26.93	A	C
ATOM	468	CE1	PHE	A	63	-41.301	-33.621	-19.216	1.00	24.98	A	C
ATOM	469	CZ	PHE	A	63	-41.285	-33.253	-17.871	1.00	23.12	A	C
ATOM	470	CE2	PHE	A	63	-40.143	-32.585	-17.311	1.00	26.49	A	C
ATOM	471	CD2	PHE	A	63	-39.044	-32.300	-18.132	1.00	30.53	A	C
ATOM	472	C	PHE	A	63	-36.977	-30.840	-22.146	1.00	39.10	A	C
ATOM	473	O	PHE	A	63	-36.152	-31.698	-22.538	1.00	38.84	A	O
ATOM	474	N	THR	A	64	-36.891	-29.544	-22.428	1.00	38.79	A	N
ATOM	475	CA	THR	A	64	-35.953	-29.061	-23.422	1.00	38.65	A	C
ATOM	476	CB	THR	A	64	-36.671	-28.406	-24.642	1.00	39.24	A	C
ATOM	477	OG1	THR	A	64	-37.175	-27.118	-24.253	1.00	36.93	A	O
ATOM	478	CG2	THR	A	64	-37.812	-29.295	-25.262	1.00	35.51	A	C
ATOM	479	C	THR	A	64	-34.986	-28.050	-22.862	1.00	39.61	A	C
ATOM	480	O	THR	A	64	-34.181	-27.525	-23.589	1.00	41.43	A	O
ATOM	481	N	THR	A	65	-35.033	-27.741	-21.586	1.00	39.94	A	N
ATOM	482	CA	THR	A	65	-34.115	-26.719	-21.101	1.00	40.84	A	C
ATOM	483	CB	THR	A	65	-34.622	-26.076	-19.777	1.00	41.39	A	C
ATOM	484	OG1	THR	A	65	-34.335	-26.930	-18.639	1.00	45.44	A	O
ATOM	485	CG2	THR	A	65	-36.149	-25.779	-19.880	1.00	39.64	A	C
ATOM	486	C	THR	A	65	-32.716	-27.304	-20.962	1.00	41.43	A	C
ATOM	487	O	THR	A	65	-32.535	-28.526	-20.920	1.00	42.73	A	O

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ATOM    488   N    SER A  66     -31.700 -26.465 -20.890  1.00 41.45           A  N
ATOM    489   CA   SER A  66     -30.363 -27.017 -20.947  1.00 41.32           A  C
ATOM    490   CB   SER A  66     -29.307 -25.956 -21.314  1.00 41.67           A  C
ATOM    491   OG   SER A  66     -28.943 -25.262 -20.148  1.00 42.16           A  O
ATOM    492   C    SER A  66     -30.011 -27.800 -19.658  1.00 40.64           A  C
ATOM    493   O    SER A  66     -29.354 -28.846 -19.737  1.00 41.27           A  O
ATOM    494   N    SER A  67     -30.456 -27.327 -18.495  1.00 38.90           A  N
ATOM    495   CA   SER A  67     -30.160 -28.045 -17.230  1.00 37.15           A  C
ATOM    496   CB   SER A  67     -30.297 -27.124 -15.998  1.00 37.36           A  C
ATOM    497   OG   SER A  67     -31.667 -26.844 -15.786  1.00 38.44           A  O
ATOM    498   C    SER A  67     -30.986 -29.349 -17.077  1.00 35.34           A  C
ATOM    499   O    SER A  67     -30.624 -30.228 -16.287  1.00 33.43           A  O
ATOM    500   N    GLN A  68     -32.039 -29.457 -17.882  1.00 33.79           A  N
ATOM    501   CA   GLN A  68     -32.809 -30.662 -18.027  1.00 34.91           A  C
ATOM    502   CB   GLN A  68     -34.204 -30.295 -18.571  1.00 34.66           A  C
ATOM    503   CG   GLN A  68     -35.212 -29.824 -17.504  1.00 38.08           A  C
ATOM    504   CD   GLN A  68     -36.542 -29.280 -18.091  1.00 42.37           A  C
ATOM    505   OE1  GLN A  68     -36.660 -28.995 -19.300  1.00 44.88           A  O
ATOM    506   NE2  GLN A  68     -37.549 -29.160 -17.230  1.00 40.98           A  N
ATOM    507   C    GLN A  68     -32.221 -31.796 -18.942  1.00 35.05           A  C
ATOM    508   O    GLN A  68     -32.826 -32.901 -19.060  1.00 34.80           A  O
ATOM    509   N    ARG A  69     -31.125 -31.505 -19.661  1.00 34.05           A  N
ATOM    510   CA   ARG A  69     -30.582 -32.456 -20.596  1.00 32.71           A  C
ATOM    511   CB   ARG A  69     -29.503 -31.788 -21.418  1.00 33.66           A  C
ATOM    512   CG   ARG A  69     -30.046 -31.047 -22.706  1.00 37.81           A  C
ATOM    513   CD   ARG A  69     -28.885 -30.461 -23.501  1.00 43.53           A  C
ATOM    514   NE   ARG A  69     -29.328 -29.621 -24.606  1.00 49.85           A  N
ATOM    515   CZ   ARG A  69     -28.711 -29.520 -25.780  1.00 50.78           A  C
ATOM    516   NH1  ARG A  69     -27.614 -30.221 -26.045  1.00 50.71           A  N
ATOM    517   NH2  ARG A  69     -29.225 -28.744 -26.717  1.00 52.55           A  N
ATOM    518   C    ARG A  69     -30.047 -33.665 -19.800  1.00 31.68           A  C
ATOM    519   O    ARG A  69     -30.369 -34.829 -20.101  1.00 31.59           A  O
ATOM    520   N    ALA A  70     -29.285 -33.386 -18.756  1.00 28.74           A  N
ATOM    521   CA   ALA A  70     -28.724 -34.423 -17.974  1.00 27.59           A  C
ATOM    522   CB   ALA A  70     -27.785 -33.868 -16.899  1.00 26.50           A  C
ATOM    523   C    ALA A  70     -29.855 -35.274 -17.389  1.00 27.63           A  C
ATOM    524   O    ALA A  70     -29.716 -36.512 -17.323  1.00 28.16           A  O
ATOM    525   N    ALA A  71     -30.997 -34.655 -17.048  1.00 26.34           A  N
ATOM    526   CA   ALA A  71     -32.130 -35.431 -16.500  1.00 25.13           A  C
ATOM    527   CB   ALA A  71     -33.162 -34.532 -15.828  1.00 26.06           A  C
ATOM    528   C    ALA A  71     -32.807 -36.303 -17.538  1.00 24.79           A  C
ATOM    529   O    ALA A  71     -33.281 -37.427 -17.215  1.00 25.17           A  O
ATOM    530   N    VAL A  72     -32.869 -35.818 -18.771  1.00 23.47           A  N
ATOM    531   CA   VAL A  72     -33.480 -36.593 -19.829  1.00 24.72           A  C
ATOM    532   CB   VAL A  72     -33.511 -35.776 -21.148  1.00 26.15           A  C
ATOM    533   CG1  VAL A  72     -34.001 -36.649 -22.334  1.00 25.93           A  C
ATOM    534   CG2  VAL A  72     -34.336 -34.478 -20.993  1.00 24.20           A  C
ATOM    535   C    VAL A  72     -32.662 -37.892 -20.057  1.00 25.57           A  C
ATOM    536   O    VAL A  72     -33.232 -38.995 -20.138  1.00 25.05           A  O
ATOM    537   N    ASP A  73     -31.322 -37.780 -20.115  1.00 25.59           A  N
ATOM    538   CA   ASP A  73     -30.561 -38.978 -20.334  1.00 25.80           A  C
ATOM    539   CB   ASP A  73     -29.082 -38.733 -20.575  1.00 26.54           A  C
ATOM    540   CG   ASP A  73     -28.799 -38.077 -21.890  1.00 25.88           A  C
ATOM    541   OD1  ASP A  73     -29.270 -36.955 -22.124  1.00 29.87           A  O
ATOM    542   OD2  ASP A  73     -28.011 -38.626 -22.658  1.00 25.27           A  O
ATOM    543   C    ASP A  73     -30.811 -39.944 -19.153  1.00 25.39           A  C
ATOM    544   O    ASP A  73     -31.104 -41.169 -19.401  1.00 23.26           A  O
ATOM    545   N    ALA A  74     -30.776 -39.386 -17.923  1.00 24.46           A  N
ATOM    546   CA   ALA A  74     -30.919 -40.211 -16.666  1.00 24.88           A  C
ATOM    547   CB   ALA A  74     -30.708 -39.411 -15.371  1.00 23.92           A  C
ATOM    548   C    ALA A  74     -32.261 -40.865 -16.648  1.00 25.23           A  C
ATOM    549   O    ALA A  74     -32.355 -42.051 -16.430  1.00 24.99           A  O
ATOM    550   N    HIS A  75     -33.305 -40.100 -16.967  1.00 26.40           A  N
ATOM    551   CA   HIS A  75     -34.655 -40.660 -16.937  1.00 26.47           A  C
ATOM    552   CB   HIS A  75     -35.729 -39.551 -17.047  1.00 25.93           A  C
ATOM    553   CG   HIS A  75     -37.106 -40.028 -16.728  1.00 26.63           A  C
ATOM    554   ND1  HIS A  75     -37.570 -40.152 -15.432  1.00 24.12           A  N
ATOM    555   CE1  HIS A  75     -38.815 -40.607 -15.458  1.00 26.83           A  C
ATOM    556   NE2  HIS A  75     -39.178 -40.775 -16.720  1.00 28.65           A  N
ATOM    557   CD2  HIS A  75     -38.119 -40.438 -17.535  1.00 28.72           A  C
ATOM    558   C    HIS A  75     -34.817 -41.735 -18.031  1.00 26.15           A  C
ATOM    559   O    HIS A  75     -35.248 -42.830 -17.754  1.00 26.75           A  O
ATOM    560   N    TYR A  76     -34.435 -41.418 -19.262  1.00 25.17           A  N
ATOM    561   CA   TYR A  76     -34.447 -42.382 -20.355  1.00 24.49           A  C
ATOM    562   CB   TYR A  76     -34.010 -41.649 -21.618  1.00 25.96           A  C
ATOM    563   CG   TYR A  76     -34.184 -42.446 -22.878  1.00 28.99           A  C
ATOM    564   CD1  TYR A  76     -35.399 -42.486 -23.521  1.00 30.72           A  C
ATOM    565   CE1  TYR A  76     -35.575 -43.211 -24.728  1.00 32.22           A  C
ATOM    566   CZ   TYR A  76     -34.509 -43.900 -25.258  1.00 35.19           A  C
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ATOM	567	OH	TYR	A	76	-34.691	-44.631	-26.403	1.00	35.34	A	O
ATOM	568	CE2	TYR	A	76	-33.273	-43.884	-24.614	1.00	33.11	A	C
ATOM	569	CD2	TYR	A	76	-33.110	-43.170	-23.432	1.00	31.42	A	C
ATOM	570	C	TYR	A	76	-33.562	-43.611	-20.148	1.00	24.10	A	C
ATOM	571	O	TYR	A	76	-33.976	-44.755	-20.350	1.00	24.86	A	O
ATOM	572	N	ASN	A	77	-32.325	-43.420	-19.724	1.00	23.91	A	N
ATOM	573	CA	ASN	A	77	-31.508	-44.603	-19.541	1.00	22.42	A	C
ATOM	574	CB	ASN	A	77	-30.023	-44.258	-19.441	1.00	22.43	A	C
ATOM	575	CG	ASN	A	77	-29.463	-43.749	-20.739	1.00	17.76	A	C
ATOM	576	OD1	ASN	A	77	-29.953	-44.040	-21.828	1.00	22.44	A	O
ATOM	577	ND2	ASN	A	77	-28.526	-42.890	-20.620	1.00	11.56	A	N
ATOM	578	C	ASN	A	77	-31.943	-45.543	-18.424	1.00	22.81	A	C
ATOM	579	O	ASN	A	77	-31.979	-46.757	-18.642	1.00	22.77	A	O
ATOM	580	N	LEU	A	78	-32.249	-45.009	-17.242	1.00	23.23	A	N
ATOM	581	CA	LEU	A	78	-32.683	-45.845	-16.123	1.00	24.06	A	C
ATOM	582	CB	LEU	A	78	-32.929	-44.983	-14.929	1.00	24.24	A	C
ATOM	583	CG	LEU	A	78	-31.961	-44.886	-13.740	1.00	27.66	A	C
ATOM	584	CD1	LEU	A	78	-30.668	-45.654	-13.841	1.00	22.27	A	C
ATOM	585	CD2	LEU	A	78	-31.740	-43.409	-13.364	1.00	29.07	A	C
ATOM	586	C	LEU	A	78	-33.950	-46.645	-16.492	1.00	24.84	A	C
ATOM	587	O	LEU	A	78	-34.119	-47.808	-16.078	1.00	24.42	A	O
ATOM	588	N	GLY	A	79	-34.816	-46.050	-17.321	1.00	25.35	A	N
ATOM	589	CA	GLY	A	79	-35.968	-46.791	-17.824	1.00	25.79	A	C
ATOM	590	C	GLY	A	79	-35.489	-47.947	-18.686	1.00	26.54	A	C
ATOM	591	O	GLY	A	79	-36.045	-49.046	-18.604	1.00	26.41	A	O
ATOM	592	N	LYS	A	80	-34.488	-47.698	-19.550	1.00	26.38	A	N
ATOM	593	CA	LYS	A	80	-33.936	-48.802	-20.369	1.00	27.32	A	C
ATOM	594	CB	LYS	A	80	-33.011	-48.302	-21.504	1.00	28.49	A	C
ATOM	595	CG	LYS	A	80	-33.782	-47.811	-22.743	1.00	33.44	A	C
ATOM	596	CD	LYS	A	80	-33.098	-48.294	-24.045	1.00	42.67	A	C
ATOM	597	CE	LYS	A	80	-32.247	-47.154	-24.682	1.00	48.39	A	C
ATOM	598	NZ	LYS	A	80	-32.366	-47.039	-26.217	1.00	49.07	A	N
ATOM	599	C	LYS	A	80	-33.271	-49.932	-19.528	1.00	25.49	A	C
ATOM	600	O	LYS	A	80	-33.395	-51.132	-19.879	1.00	25.22	A	O
ATOM	601	N	VAL	A	81	-32.626	-49.562	-18.412	1.00	23.06	A	N
ATOM	602	CA	VAL	A	81	-32.000	-50.552	-17.577	1.00	20.88	A	C
ATOM	603	CB	VAL	A	81	-30.967	-49.941	-16.655	1.00	21.65	A	C
ATOM	604	CG1	VAL	A	81	-30.409	-51.002	-15.659	1.00	19.27	A	C
ATOM	605	CG2	VAL	A	81	-29.825	-49.304	-17.481	1.00	18.92	A	C
ATOM	606	C	VAL	A	81	-33.028	-51.393	-16.828	1.00	21.39	A	C
ATOM	607	O	VAL	A	81	-32.859	-52.610	-16.699	1.00	21.09	A	O
ATOM	608	N	TYR	A	82	-34.113	-50.760	-16.375	1.00	21.90	A	N
ATOM	609	CA	TYR	A	82	-35.236	-51.463	-15.786	1.00	21.33	A	C
ATOM	610	CB	TYR	A	82	-36.373	-50.475	-15.331	1.00	22.04	A	C
ATOM	611	CG	TYR	A	82	-37.629	-51.250	-14.970	1.00	18.84	A	C
ATOM	612	CD1	TYR	A	82	-38.503	-51.665	-15.990	1.00	19.21	A	C
ATOM	613	CE1	TYR	A	82	-39.585	-52.444	-15.776	1.00	18.52	A	C
ATOM	614	CZ	TYR	A	82	-39.883	-52.874	-14.525	1.00	21.16	A	C
ATOM	615	OH	TYR	A	82	-41.020	-53.656	-14.432	1.00	24.42	A	O
ATOM	616	CE2	TYR	A	82	-39.062	-52.536	-13.457	1.00	20.05	A	C
ATOM	617	CD2	TYR	A	82	-37.855	-51.701	-13.722	1.00	16.33	A	C
ATOM	618	C	TYR	A	82	-35.781	-52.476	-16.808	1.00	22.26	A	C
ATOM	619	O	TYR	A	82	-36.007	-53.649	-16.479	1.00	22.32	A	O
ATOM	620	N	ASP	A	83	-36.041	-52.029	-18.030	1.00	22.20	A	N
ATOM	621	CA	ASP	A	83	-36.498	-52.971	-19.075	1.00	23.53	A	C
ATOM	622	CB	ASP	A	83	-36.745	-52.268	-20.416	1.00	23.02	A	C
ATOM	623	CG	ASP	A	83	-37.831	-51.196	-20.317	1.00	25.23	A	C
ATOM	624	OD1	ASP	A	83	-38.713	-51.279	-19.401	1.00	24.63	A	O
ATOM	625	OD2	ASP	A	83	-37.799	-50.280	-21.163	1.00	28.39	A	O
ATOM	626	C	ASP	A	83	-35.555	-54.134	-19.318	1.00	23.48	A	C
ATOM	627	O	ASP	A	83	-35.971	-55.249	-19.589	1.00	23.92	A	O
ATOM	628	N	TYR	A	84	-34.271	-53.874	-19.216	1.00	24.00	A	N
ATOM	629	CA	TYR	A	84	-33.326	-54.902	-19.519	1.00	23.71	A	C
ATOM	630	CB	TYR	A	84	-31.907	-54.297	-19.583	1.00	24.20	A	C
ATOM	631	CG	TYR	A	84	-30.858	-55.363	-19.629	1.00	23.19	A	C
ATOM	632	CD1	TYR	A	84	-30.519	-55.931	-20.823	1.00	22.87	A	C
ATOM	633	CE1	TYR	A	84	-29.551	-56.947	-20.875	1.00	24.91	A	C
ATOM	634	CZ	TYR	A	84	-28.992	-57.421	-19.717	1.00	20.31	A	C
ATOM	635	OH	TYR	A	84	-28.075	-58.443	-19.820	1.00	22.01	A	O
ATOM	636	CE2	TYR	A	84	-29.342	-56.869	-18.521	1.00	19.40	A	C
ATOM	637	CD2	TYR	A	84	-30.252	-55.840	-18.465	1.00	18.29	A	C
ATOM	638	C	TYR	A	84	-33.437	-56.034	-18.501	1.00	23.26	A	C
ATOM	639	O	TYR	A	84	-33.541	-57.178	-18.881	1.00	24.20	A	O
ATOM	640	N	PHE	A	85	-33.418	-55.715	-17.218	1.00	22.52	A	N
ATOM	641	CA	PHE	A	85	-33.429	-56.712	-16.173	1.00	22.03	A	C
ATOM	642	CB	PHE	A	85	-33.030	-56.067	-14.835	1.00	22.20	A	C
ATOM	643	CG	PHE	A	85	-31.531	-55.940	-14.665	1.00	20.97	A	C
ATOM	644	CD1	PHE	A	85	-30.756	-57.049	-14.344	1.00	18.41	A	C
ATOM	645	CE1	PHE	A	85	-29.382	-56.971	-14.210	1.00	17.21	A	C

ATOM	646	CZ	PHE	A	85	-28.735	-55.766	-14.418	1.00	20.03	A	C
ATOM	647	CE2	PHE	A	85	-29.477	-54.653	-14.776	1.00	21.83	A	C
ATOM	648	CD2	PHE	A	85	-30.892	-54.745	-14.895	1.00	23.45	A	C
ATOM	649	C	PHE	A	85	-34.781	-57.390	-16.087	1.00	23.25	A	C
ATOM	650	O	PHE	A	85	-34.867	-58.629	-15.837	1.00	21.25	A	O
ATOM	651	N	TYR	A	86	-35.831	-56.599	-16.381	1.00	23.68	A	N
ATOM	652	CA	TYR	A	86	-37.186	-57.146	-16.398	1.00	24.50	A	C
ATOM	653	CB	TYR	A	86	-38.259	-56.060	-16.341	1.00	25.13	A	C
ATOM	654	CG	TYR	A	86	-39.648	-56.640	-16.311	1.00	26.50	A	C
ATOM	655	CD1	TYR	A	86	-40.122	-57.303	-15.169	1.00	27.15	A	C
ATOM	656	CE1	TYR	A	86	-41.398	-57.867	-15.148	1.00	29.74	A	C
ATOM	657	CZ	TYR	A	86	-42.220	-57.763	-16.274	1.00	30.75	A	C
ATOM	658	OH	TYR	A	86	-43.463	-58.290	-16.229	1.00	33.52	A	O
ATOM	659	CE2	TYR	A	86	-41.800	-57.146	-17.414	1.00	29.62	A	C
ATOM	660	CD2	TYR	A	86	-40.477	-56.574	-17.429	1.00	29.65	A	C
ATOM	661	C	TYR	A	86	-37.438	-58.080	-17.562	1.00	24.44	A	C
ATOM	662	O	TYR	A	86	-37.906	-59.199	-17.381	1.00	25.04	A	O
ATOM	663	N	GLN	A	87	-37.088	-57.657	-18.754	1.00	24.92	A	N
ATOM	664	CA	GLN	A	87	-37.333	-58.504	-19.925	1.00	26.25	A	C
ATOM	665	CB	GLN	A	87	-37.232	-57.687	-21.197	1.00	26.93	A	C
ATOM	666	CG	GLN	A	87	-38.411	-56.771	-21.381	1.00	31.10	A	C
ATOM	667	CD	GLN	A	87	-38.085	-55.660	-22.348	1.00	39.99	A	C
ATOM	668	OE1	GLN	A	87	-37.081	-55.726	-23.071	1.00	41.78	A	O
ATOM	669	NE2	GLN	A	87	-38.922	-54.617	-22.366	1.00	42.63	A	N
ATOM	670	C	GLN	A	87	-36.420	-59.706	-20.067	1.00	26.15	A	C
ATOM	671	O	GLN	A	87	-36.831	-60.699	-20.644	1.00	24.48	A	O
ATOM	672	N	LYS	A	88	-35.153	-59.593	-19.620	1.00	25.63	A	N
ATOM	673	CA	LYS	A	88	-34.252	-60.725	-19.772	1.00	24.20	A	C
ATOM	674	CB	LYS	A	88	-32.770	-60.326	-19.777	1.00	24.42	A	C
ATOM	675	CG	LYS	A	88	-32.352	-59.286	-20.748	1.00	24.40	A	C
ATOM	676	CD	LYS	A	88	-32.523	-59.738	-22.116	1.00	26.90	A	C
ATOM	677	CE	LYS	A	88	-32.183	-58.598	-23.050	1.00	27.59	A	C
ATOM	678	NZ	LYS	A	88	-31.931	-59.174	-24.395	1.00	31.00	A	N
ATOM	679	C	LYS	A	88	-34.457	-61.711	-18.670	1.00	23.70	A	C
ATOM	680	O	LYS	A	88	-34.342	-62.871	-18.919	1.00	24.35	A	O
ATOM	681	N	PHE	A	89	-34.692	-61.267	-17.440	1.00	23.60	A	N
ATOM	682	CA	PHE	A	89	-34.576	-62.182	-16.311	1.00	23.45	A	C
ATOM	683	CB	PHE	A	89	-33.397	-61.806	-15.422	1.00	22.33	A	C
ATOM	684	CG	PHE	A	89	-32.147	-61.509	-16.191	1.00	23.28	A	C
ATOM	685	CD1	PHE	A	89	-31.498	-62.518	-16.917	1.00	19.53	A	C
ATOM	686	CE1	PHE	A	89	-30.332	-62.222	-17.674	1.00	21.34	A	C
ATOM	687	CZ	PHE	A	89	-29.809	-60.916	-17.709	1.00	20.21	A	C
ATOM	688	CE2	PHE	A	89	-30.462	-59.892	-16.997	1.00	21.28	A	C
ATOM	689	CD2	PHE	A	89	-31.634	-60.190	-16.251	1.00	21.81	A	C
ATOM	690	C	PHE	A	89	-35.845	-62.205	-15.497	1.00	24.67	A	C
ATOM	691	O	PHE	A	89	-35.910	-62.900	-14.489	1.00	23.59	A	O
ATOM	692	N	ASN	A	90	-36.848	-61.422	-15.927	1.00	25.75	A	N
ATOM	693	CA	ASN	A	90	-38.049	-61.227	-15.121	1.00	26.46	A	C
ATOM	694	CB	ASN	A	90	-38.887	-62.559	-15.076	1.00	27.00	A	C
ATOM	695	CG	ASN	A	90	-40.308	-62.371	-14.453	1.00	30.20	A	C
ATOM	696	OD1	ASN	A	90	-41.067	-61.430	-14.783	1.00	32.17	A	O
ATOM	697	ND2	ASN	A	90	-40.664	-63.284	-13.556	1.00	29.30	A	N
ATOM	698	C	ASN	A	90	-37.691	-60.676	-13.725	1.00	25.55	A	C
ATOM	699	O	ASN	A	90	-38.285	-61.086	-12.707	1.00	27.83	A	O
ATOM	700	N	ARG	A	91	-36.740	-59.751	-13.662	1.00	24.18	A	N
ATOM	701	CA	ARG	A	91	-36.398	-59.079	-12.383	1.00	24.35	A	C
ATOM	702	CB	ARG	A	91	-34.894	-58.713	-12.244	1.00	24.28	A	C
ATOM	703	CG	ARG	A	91	-34.459	-58.341	-10.821	1.00	20.60	A	C
ATOM	704	CD	ARG	A	91	-32.985	-58.061	-10.691	1.00	19.78	A	C
ATOM	705	NE	ARG	A	91	-32.656	-57.679	-9.324	1.00	16.07	A	N
ATOM	706	CZ	ARG	A	91	-32.448	-58.597	-8.355	1.00	20.75	A	C
ATOM	707	NH1	ARG	A	91	-32.544	-59.918	-8.634	1.00	14.39	A	N
ATOM	708	NH2	ARG	A	91	-32.194	-58.219	-7.091	1.00	16.44	A	N
ATOM	709	C	ARG	A	91	-37.210	-57.826	-12.208	1.00	24.66	A	C
ATOM	710	O	ARG	A	91	-37.210	-56.943	-13.073	1.00	26.57	A	O
ATOM	711	N	ASN	A	92	-37.924	-57.722	-11.102	1.00	24.72	A	N
ATOM	712	CA	ASN	A	92	-38.747	-56.532	-10.900	1.00	24.42	A	C
ATOM	713	CB	ASN	A	92	-39.951	-56.942	-10.084	1.00	24.43	A	C
ATOM	714	CG	ASN	A	92	-40.921	-55.822	-9.831	1.00	27.29	A	C
ATOM	715	OD1	ASN	A	92	-40.874	-54.757	-10.450	1.00	30.10	A	O
ATOM	716	ND2	ASN	A	92	-41.866	-56.084	-8.913	1.00	29.96	A	N
ATOM	717	C	ASN	A	92	-37.915	-55.455	-10.201	1.00	24.37	A	C
ATOM	718	O	ASN	A	92	-37.937	-55.333	-8.965	1.00	25.59	A	O
ATOM	719	N	SER	A	93	-37.175	-54.673	-10.970	1.00	22.83	A	N
ATOM	720	CA	SER	A	93	-36.336	-53.650	-10.387	1.00	22.27	A	C
ATOM	721	CB	SER	A	93	-37.090	-52.772	-9.384	1.00	21.81	A	C
ATOM	722	OG	SER	A	93	-36.335	-51.571	-9.193	1.00	20.51	A	O
ATOM	723	C	SER	A	93	-35.081	-54.191	-9.730	1.00	22.08	A	C
ATOM	724	O	SER	A	93	-34.886	-55.378	-9.638	1.00	23.02	A	O

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ATOM    725  N   TYR A  94    -34.213 -53.303  -9.254  1.00 23.13      A  N
ATOM    726  CA  TYR A  94    -32.915 -53.741  -8.709  1.00 22.74      A  C
ATOM    727  CB  TYR A  94    -32.040 -52.547  -8.387  1.00 21.69      A  C
ATOM    728  CG  TYR A  94    -32.522 -51.788  -7.184  1.00 21.77      A  C
ATOM    729  CD1 TYR A  94    -31.986 -52.046  -5.904  1.00 25.43      A  C
ATOM    730  CE1 TYR A  94    -32.444 -51.362  -4.749  1.00 21.99      A  C
ATOM    731  CZ  TYR A  94    -33.460 -50.434  -4.881  1.00 24.51      A  C
ATOM    732  OH  TYR A  94    -33.935 -49.748  -3.758  1.00 24.58      A  O
ATOM    733  CE2 TYR A  94    -34.028 -50.186  -6.162  1.00 23.54      A  C
ATOM    734  CD2 TYR A  94    -33.558 -50.857  -7.288  1.00 18.74      A  C
ATOM    735  C   TYR A  94    -33.034 -54.650  -7.501  1.00 23.34      A  C
ATOM    736  O   TYR A  94    -32.184 -55.516  -7.295  1.00 25.03      A  O
ATOM    737  N   ASP A  95    -34.077 -54.502  -6.699  1.00 24.79      A  N
ATOM    738  CA  ASP A  95    -34.229 -55.405  -5.504  1.00 25.96      A  C
ATOM    739  CB  ASP A  95    -34.718 -54.618  -4.299  1.00 25.17      A  C
ATOM    740  CG  ASP A  95    -36.080 -53.926  -4.563  1.00 26.88      A  C
ATOM    741  OD1 ASP A  95    -36.708 -54.173  -5.621  1.00 23.59      A  O
ATOM    742  OD2 ASP A  95    -36.526 -53.122  -3.710  1.00 30.47      A  O
ATOM    743  C   ASP A  95    -35.186 -56.550  -5.756  1.00 26.31      A  C
ATOM    744  O   ASP A  95    -35.570 -57.253  -4.830  1.00 28.26      A  O
ATOM    745  N   ASN A  96    -35.622 -56.705  -6.996  1.00 26.19      A  N
ATOM    746  CA  ASN A  96    -36.600 -57.726  -7.345  1.00 27.04      A  C
ATOM    747  CB  ASN A  96    -35.994 -59.141  -7.290  1.00 25.92      A  C
ATOM    748  CG  ASN A  96    -36.783 -60.126  -8.133  1.00 27.06      A  C
ATOM    749  OD1 ASN A  96    -37.509 -59.722  -9.059  1.00 28.41      A  O
ATOM    750  ND2 ASN A  96    -36.649 -61.414  -7.833  1.00 23.23      A  N
ATOM    751  C   ASN A  96    -37.868 -57.680  -6.491  1.00 27.67      A  C
ATOM    752  O   ASN A  96    -38.536 -58.706  -6.354  1.00 27.62      A  O
ATOM    753  N   LYS A  97    -38.169 -56.506  -5.911  1.00 28.43      A  N
ATOM    754  CA  LYS A  97    -39.373 -56.260  -5.095  1.00 27.97      A  C
ATOM    755  CB  LYS A  97    -39.009 -56.065  -3.606  1.00 28.01      A  C
ATOM    756  CG  LYS A  97    -38.492 -57.348  -2.937  1.00 29.56      A  C
ATOM    757  CD  LYS A  97    -38.148 -57.180  -1.435  1.00 31.10      A  C
ATOM    758  CE  LYS A  97    -36.711 -56.724  -1.178  1.00 32.30      A  C
ATOM    759  NZ  LYS A  97    -36.314 -56.990   0.232  1.00 35.76      A  N
ATOM    760  C   LYS A  97    -40.134 -55.048  -5.613  1.00 28.14      A  C
ATOM    761  O   LYS A  97    -41.135 -54.648  -5.017  1.00 28.53      A  O
ATOM    762  N   GLY A  98    -39.669 -54.447  -6.711  1.00 27.15      A  N
ATOM    763  CA  GLY A  98    -40.370 -53.299  -7.301  1.00 24.49      A  C
ATOM    764  C   GLY A  98    -39.850 -51.961  -6.793  1.00 23.46      A  C
ATOM    765  O   GLY A  98    -40.445 -50.935  -7.082  1.00 24.40      A  O
ATOM    766  N   GLY A  99    -38.776 -51.947  -6.013  1.00 21.47      A  N
ATOM    767  CA  GLY A  99    -38.290 -50.710  -5.411  1.00 20.97      A  C
ATOM    768  C   GLY A  99    -38.114 -49.600  -6.437  1.00 23.26      A  C
ATOM    769  O   GLY A  99    -37.507 -49.813  -7.495  1.00 22.85      A  O
ATOM    770  N   LYS A 100    -38.678 -48.408  -6.186  1.00 24.99      A  N
ATOM    771  CA  LYS A 100    -38.545 -47.281  -7.141  1.00 25.11      A  C
ATOM    772  CB  LYS A 100    -39.214 -46.034  -6.577  1.00 25.69      A  C
ATOM    773  CG  LYS A 100    -38.639 -45.629  -5.203  1.00 30.14      A  C
ATOM    774  CD  LYS A 100    -39.052 -44.248  -4.642  1.00 32.29      A  C
ATOM    775  CE  LYS A 100    -38.162 -43.991  -3.336  1.00 38.39      A  C
ATOM    776  NZ  LYS A 100    -38.707 -42.859  -2.443  1.00 42.60      A  N
ATOM    777  C   LYS A 100    -37.036 -47.043  -7.447  1.00 25.30      A  C
ATOM    778  O   LYS A 100    -36.150 -47.345  -6.610  1.00 24.91      A  O
ATOM    779  N   ILE A 101    -36.761 -46.564  -8.663  1.00 24.85      A  N
ATOM    780  CA  ILE A 101    -35.414 -46.283  -9.161  1.00 23.22      A  C
ATOM    781  CB  ILE A 101    -35.255 -46.923 -10.522  1.00 23.11      A  C
ATOM    782  CG1 ILE A 101    -35.219 -48.449 -10.364  1.00 20.36      A  C
ATOM    783  CD1 ILE A 101    -35.453 -49.172 -11.638  1.00 21.07      A  C
ATOM    784  CG2 ILE A 101    -33.999 -46.362 -11.287  1.00 23.99      A  C
ATOM    785  C   ILE A 101    -35.288 -44.776  -9.290  1.00 24.21      A  C
ATOM    786  O   ILE A 101    -35.944 -44.171 -10.146  1.00 26.06      A  O
ATOM    787  N   VAL A 102    -34.503 -44.153  -8.421  1.00 23.16      A  N
ATOM    788  CA  VAL A 102    -34.478 -42.727  -8.287  1.00 22.20      A  C
ATOM    789  CB  VAL A 102    -34.761 -42.340  -6.807  1.00 23.44      A  C
ATOM    790  CG1 VAL A 102    -34.424 -40.850  -6.483  1.00 19.05      A  C
ATOM    791  CG2 VAL A 102    -36.180 -42.671  -6.460  1.00 21.14      A  C
ATOM    792  C   VAL A 102    -33.084 -42.267  -8.677  1.00 23.93      A  C
ATOM    793  O   VAL A 102    -32.091 -42.941  -8.325  1.00 22.72      A  O
ATOM    794  N   SER A 103    -32.994 -41.148  -9.421  1.00 24.36      A  N
ATOM    795  CA  SER A 103    -31.708 -40.568  -9.703  1.00 25.59      A  C
ATOM    796  CB  SER A 103    -31.317 -40.856 -11.124  1.00 25.68      A  C
ATOM    797  OG  SER A 103    -31.926 -39.882 -11.946  1.00 28.96      A  O
ATOM    798  C   SER A 103    -31.654 -39.047  -9.411  1.00 26.51      A  C
ATOM    799  O   SER A 103    -32.695 -38.350  -9.383  1.00 26.56      A  O
ATOM    800  N   SER A 104    -30.442 -38.556  -9.140  1.00 26.44      A  N
ATOM    801  CA  SER A 104    -30.225 -37.140  -8.958  1.00 26.76      A  C
ATOM    802  CB  SER A 104    -29.852 -36.784  -7.518  1.00 27.23      A  C
ATOM    803  OG  SER A 104    -30.856 -37.188  -6.574  1.00 26.06      A  O
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ATOM	804	C	SER	A	104	-29.123	-36.728	-9.918	1.00	27.68	A	C
ATOM	805	O	SER	A	104	-27.979	-37.206	-9.868	1.00	27.25	A	O
ATOM	806	N	VAL	A	105	-29.495	-35.861	-10.841	1.00	28.11	A	N
ATOM	807	CA	VAL	A	105	-28.530	-35.248	-11.711	1.00	28.88	A	C
ATOM	808	CB	VAL	A	105	-29.152	-35.040	-13.083	1.00	29.18	A	C
ATOM	809	CG1	VAL	A	105	-29.569	-36.358	-13.662	1.00	27.85	A	C
ATOM	810	CG2	VAL	A	105	-30.338	-34.066	-12.990	1.00	28.33	A	C
ATOM	811	C	VAL	A	105	-28.034	-33.904	-11.141	1.00	29.60	A	C
ATOM	812	O	VAL	A	105	-28.611	-33.353	-10.151	1.00	29.63	A	O
ATOM	813	N	HIS	A	106	-27.005	-33.356	-11.782	1.00	29.73	A	N
ATOM	814	CA	HIS	A	106	-26.377	-32.102	-11.318	1.00	30.74	A	C
ATOM	815	CB	HIS	A	106	-27.287	-30.869	-11.536	1.00	30.34	A	C
ATOM	816	CG	HIS	A	106	-27.705	-30.693	-12.961	1.00	27.61	A	C
ATOM	817	ND1	HIS	A	106	-26.794	-30.645	-13.990	1.00	25.34	A	N
ATOM	818	CE1	HIS	A	106	-27.437	-30.525	-15.140	1.00	28.07	A	C
ATOM	819	NE2	HIS	A	106	-28.732	-30.482	-14.893	1.00	28.43	A	N
ATOM	820	CD2	HIS	A	106	-28.922	-30.593	-13.532	1.00	28.46	A	C
ATOM	821	C	HIS	A	106	-25.971	-32.252	-9.860	1.00	32.36	A	C
ATOM	822	O	HIS	A	106	-26.131	-31.330	-9.040	1.00	32.69	A	O
ATOM	823	N	TYR	A	107	-25.461	-33.433	-9.528	1.00	33.47	A	N
ATOM	824	CA	TYR	A	107	-24.924	-33.638	-8.211	1.00	35.05	A	C
ATOM	825	CB	TYR	A	107	-24.727	-35.116	-7.926	1.00	34.59	A	C
ATOM	826	CG	TYR	A	107	-24.107	-35.405	-6.575	1.00	35.69	A	C
ATOM	827	CD1	TYR	A	107	-24.910	-35.735	-5.483	1.00	35.84	A	C
ATOM	828	CE1	TYR	A	107	-24.339	-36.017	-4.221	1.00	36.98	A	C
ATOM	829	CZ	TYR	A	107	-22.964	-35.989	-4.073	1.00	37.15	A	C
ATOM	830	OH	TYR	A	107	-22.457	-36.265	-2.851	1.00	37.25	A	O
ATOM	831	CE2	TYR	A	107	-22.126	-35.689	-5.149	1.00	36.54	A	C
ATOM	832	CD2	TYR	A	107	-22.701	-35.393	-6.393	1.00	35.92	A	C
ATOM	833	C	TYR	A	107	-23.598	-32.924	-8.176	1.00	36.00	A	C
ATOM	834	O	TYR	A	107	-22.712	-33.209	-9.022	1.00	35.53	A	O
ATOM	835	N	GLY	A	108	-23.467	-32.001	-7.210	1.00	37.18	A	N
ATOM	836	CA	GLY	A	108	-22.178	-31.379	-6.893	1.00	38.18	A	C
ATOM	837	C	GLY	A	108	-21.753	-30.343	-7.914	1.00	40.33	A	C
ATOM	838	O	GLY	A	108	-22.577	-29.768	-8.643	1.00	40.64	A	O
ATOM	839	N	SER	A	109	-20.457	-30.086	-7.969	1.00	42.15	A	N
ATOM	840	CA	SER	A	109	-19.971	-29.038	-8.853	1.00	44.71	A	C
ATOM	841	CB	SER	A	109	-19.611	-27.751	-8.074	1.00	45.07	A	C
ATOM	842	OG	SER	A	109	-19.609	-26.644	-8.968	1.00	45.28	A	O
ATOM	843	C	SER	A	109	-18.768	-29.559	-9.638	1.00	45.55	A	C
ATOM	844	O	SER	A	109	-17.772	-30.016	-9.026	1.00	45.22	A	O
ATOM	845	N	ARG	A	110	-18.890	-29.541	-10.977	1.00	45.44	A	N
ATOM	846	CA	ARG	A	110	-17.854	-30.119	-11.821	1.00	46.27	A	C
ATOM	847	CB	ARG	A	110	-16.732	-29.064	-11.996	1.00	47.09	A	C
ATOM	848	CG	ARG	A	110	-17.316	-27.667	-12.469	1.00	53.17	A	C
ATOM	849	CD	ARG	A	110	-16.356	-26.720	-13.257	1.00	61.65	A	C
ATOM	850	NE	ARG	A	110	-14.954	-26.807	-12.807	1.00	67.59	A	N
ATOM	851	CZ	ARG	A	110	-13.906	-27.184	-13.564	1.00	70.42	A	C
ATOM	852	NH1	ARG	A	110	-14.028	-27.510	-14.865	1.00	69.00	A	N
ATOM	853	NH2	ARG	A	110	-12.704	-27.241	-13.006	1.00	71.16	A	N
ATOM	854	C	ARG	A	110	-17.354	-31.497	-11.255	1.00	44.76	A	C
ATOM	855	O	ARG	A	110	-16.167	-31.772	-11.201	1.00	44.86	A	O
ATOM	856	N	TYR	A	111	-18.284	-32.349	-10.816	1.00	43.15	A	N
ATOM	857	CA	TYR	A	111	-17.967	-33.613	-10.113	1.00	41.46	A	C
ATOM	858	CB	TYR	A	111	-19.129	-33.916	-9.167	1.00	41.36	A	C
ATOM	859	CG	TYR	A	111	-19.025	-35.147	-8.321	1.00	43.63	A	C
ATOM	860	CD1	TYR	A	111	-17.981	-35.319	-7.403	1.00	46.38	A	C
ATOM	861	CE1	TYR	A	111	-17.907	-36.482	-6.593	1.00	48.54	A	C
ATOM	862	CZ	TYR	A	111	-18.895	-37.465	-6.693	1.00	49.57	A	C
ATOM	863	OH	TYR	A	111	-18.842	-38.598	-5.909	1.00	50.97	A	O
ATOM	864	CE2	TYR	A	111	-19.946	-37.312	-7.594	1.00	48.80	A	C
ATOM	865	CD2	TYR	A	111	-20.004	-36.152	-8.405	1.00	47.79	A	C
ATOM	866	C	TYR	A	111	-17.735	-34.788	-11.088	1.00	40.02	A	C
ATOM	867	O	TYR	A	111	-18.580	-35.098	-11.906	1.00	38.85	A	O
ATOM	868	N	ASN	A	112	-16.571	-35.429	-11.013	1.00	39.72	A	N
ATOM	869	CA	ASN	A	112	-16.211	-36.473	-11.996	1.00	38.39	A	C
ATOM	870	CB	ASN	A	112	-14.688	-36.460	-12.320	1.00	38.11	A	C
ATOM	871	CG	ASN	A	112	-14.266	-35.305	-13.262	1.00	37.98	A	C
ATOM	872	OD1	ASN	A	112	-14.999	-34.901	-14.170	1.00	38.90	A	O
ATOM	873	ND2	ASN	A	112	-13.071	-34.782	-13.039	1.00	37.99	A	N
ATOM	874	C	ASN	A	112	-16.660	-37.890	-11.576	1.00	37.82	A	C
ATOM	875	O	ASN	A	112	-15.835	-38.808	-11.493	1.00	36.91	A	O
ATOM	876	N	ASN	A	113	-17.957	-38.074	-11.336	1.00	37.02	A	N
ATOM	877	CA	ASN	A	113	-18.427	-39.382	-10.923	1.00	37.51	A	C
ATOM	878	CB	ASN	A	113	-17.979	-39.699	-9.489	1.00	38.57	A	C
ATOM	879	CG	ASN	A	113	-17.709	-41.176	-9.295	1.00	43.30	A	C
ATOM	880	OD1	ASN	A	113	-16.666	-41.694	-9.683	1.00	44.68	A	O
ATOM	881	ND2	ASN	A	113	-18.682	-41.875	-8.730	1.00	50.44	A	N
ATOM	882	C	ASN	A	113	-19.941	-39.639	-11.059	1.00	36.09	A	C

ATOM	883	O	ASN	A	113	-20.717	-38.706	-11.308	1.00	35.79	A	O
ATOM	884	N	ALA	A	114	-20.316	-40.921	-10.939	1.00	33.16	A	N
ATOM	885	CA	ALA	A	114	-21.697	-41.374	-10.936	1.00	31.35	A	C
ATOM	886	CB	ALA	A	114	-22.132	-41.859	-12.322	1.00	30.10	A	C
ATOM	887	C	ALA	A	114	-21.681	-42.536	-9.981	1.00	30.28	A	C
ATOM	888	O	ALA	A	114	-20.761	-43.341	-9.971	1.00	29.89	A	O
ATOM	889	N	ALA	A	115	-22.685	-42.665	-9.152	1.00	28.73	A	N
ATOM	890	CA	ALA	A	115	-22.587	-43.775	-8.219	1.00	27.85	A	C
ATOM	891	CB	ALA	A	115	-21.783	-43.333	-6.923	1.00	26.42	A	C
ATOM	892	C	ALA	A	115	-23.951	-44.285	-7.871	1.00	27.17	A	C
ATOM	893	O	ALA	A	115	-24.932	-43.551	-7.903	1.00	26.95	A	O
ATOM	894	N	TRP	A	116	-24.017	-45.562	-7.536	1.00	27.57	A	N
ATOM	895	CA	TRP	A	116	-25.151	-46.046	-6.778	1.00	26.56	A	C
ATOM	896	CB	TRP	A	116	-25.358	-47.483	-7.083	1.00	25.55	A	C
ATOM	897	CG	TRP	A	116	-26.399	-48.130	-6.276	1.00	25.34	A	C
ATOM	898	CD1	TRP	A	116	-26.198	-48.955	-5.212	1.00	22.58	A	C
ATOM	899	NE1	TRP	A	116	-27.417	-49.374	-4.711	1.00	22.11	A	N
ATOM	900	CE2	TRP	A	116	-28.430	-48.793	-5.429	1.00	20.63	A	C
ATOM	901	CD2	TRP	A	116	-27.836	-48.012	-6.434	1.00	22.71	A	C
ATOM	902	CE3	TRP	A	116	-28.674	-47.274	-7.297	1.00	25.00	A	C
ATOM	903	CZ3	TRP	A	116	-30.096	-47.399	-7.160	1.00	20.26	A	C
ATOM	904	CH2	TRP	A	116	-30.633	-48.228	-6.183	1.00	20.58	A	C
ATOM	905	CZ2	TRP	A	116	-29.823	-48.914	-5.293	1.00	20.87	A	C
ATOM	906	C	TRP	A	116	-24.826	-45.858	-5.300	1.00	28.31	A	C
ATOM	907	O	TRP	A	116	-23.804	-46.297	-4.806	1.00	25.54	A	O
ATOM	908	N	ILE	A	117	-25.719	-45.166	-4.600	1.00	31.41	A	N
ATOM	909	CA	ILE	A	117	-25.501	-44.758	-3.224	1.00	33.35	A	C
ATOM	910	CB	ILE	A	117	-25.708	-43.237	-3.204	1.00	34.35	A	C
ATOM	911	CG1	ILE	A	117	-24.445	-42.583	-2.753	1.00	35.74	A	C
ATOM	912	CD1	ILE	A	117	-23.596	-42.437	-3.940	1.00	36.48	A	C
ATOM	913	CG2	ILE	A	117	-27.052	-42.729	-2.567	1.00	32.98	A	C
ATOM	914	C	ILE	A	117	-26.427	-45.554	-2.264	1.00	34.89	A	C
ATOM	915	O	ILE	A	117	-26.928	-45.013	-1.236	1.00	36.20	A	O
ATOM	916	N	GLY	A	118	-26.682	-46.830	-2.606	1.00	34.05	A	N
ATOM	917	CA	GLY	A	118	-27.447	-47.736	-1.741	1.00	32.89	A	C
ATOM	918	C	GLY	A	118	-28.958	-47.716	-2.031	1.00	33.33	A	C
ATOM	919	O	GLY	A	118	-29.641	-48.800	-2.057	1.00	33.11	A	O
ATOM	920	N	ASP	A	119	-29.494	-46.514	-2.243	1.00	30.79	A	N
ATOM	921	CA	ASP	A	119	-30.881	-46.411	-2.581	1.00	31.30	A	C
ATOM	922	CB	ASP	A	119	-31.688	-45.834	-1.399	1.00	33.35	A	C
ATOM	923	CG	ASP	A	119	-31.091	-44.540	-0.838	1.00	37.71	A	C
ATOM	924	OD1	ASP	A	119	-31.838	-43.790	-0.087	1.00	41.58	A	O
ATOM	925	OD2	ASP	A	119	-29.858	-44.313	-1.105	1.00	38.82	A	O
ATOM	926	C	ASP	A	119	-31.132	-45.557	-3.801	1.00	29.73	A	C
ATOM	927	O	ASP	A	119	-32.270	-45.400	-4.168	1.00	29.65	A	O
ATOM	928	N	GLN	A	120	-30.107	-44.968	-4.414	1.00	28.27	A	N
ATOM	929	CA	GLN	A	120	-30.358	-44.121	-5.565	1.00	27.33	A	C
ATOM	930	CB	GLN	A	120	-30.989	-42.784	-5.177	1.00	26.60	A	C
ATOM	931	CG	GLN	A	120	-30.031	-41.829	-4.485	1.00	25.55	A	C
ATOM	932	CD	GLN	A	120	-30.609	-40.414	-4.466	1.00	27.50	A	C
ATOM	933	OE1	GLN	A	120	-31.328	-39.981	-3.512	1.00	26.21	A	O
ATOM	934	NE2	GLN	A	120	-30.340	-39.689	-5.532	1.00	23.92	A	N
ATOM	935	C	GLN	A	120	-29.117	-43.901	-6.390	1.00	28.01	A	C
ATOM	936	O	GLN	A	120	-28.015	-44.342	-6.021	1.00	29.44	A	O
ATOM	937	N	MET	A	121	-29.299	-43.213	-7.521	1.00	27.81	A	N
ATOM	938	CA	MET	A	121	-28.212	-42.851	-8.400	1.00	26.90	A	C
ATOM	939	CB	MET	A	121	-28.639	-43.033	-9.836	1.00	26.74	A	C
ATOM	940	CG	MET	A	121	-28.830	-44.451	-10.264	1.00	28.73	A	C
ATOM	941	SD	MET	A	121	-27.203	-45.210	-10.223	1.00	33.79	A	S
ATOM	942	CE	MET	A	121	-26.289	-44.011	-11.268	1.00	35.84	A	C
ATOM	943	C	MET	A	121	-27.925	-41.400	-8.183	1.00	26.76	A	C
ATOM	944	O	MET	A	121	-28.878	-40.606	-8.009	1.00	27.02	A	O
ATOM	945	N	ILE	A	122	-26.640	-41.050	-8.198	1.00	25.38	A	N
ATOM	946	CA	ILE	A	122	-26.227	-39.676	-8.347	1.00	25.64	A	C
ATOM	947	CB	ILE	A	122	-25.493	-39.112	-7.107	1.00	25.89	A	C
ATOM	948	CG1	ILE	A	122	-24.153	-39.859	-6.849	1.00	26.78	A	C
ATOM	949	CD1	ILE	A	122	-23.210	-39.229	-5.778	1.00	28.66	A	C
ATOM	950	CG2	ILE	A	122	-26.401	-39.291	-5.890	1.00	25.18	A	C
ATOM	951	C	ILE	A	122	-25.352	-39.591	-9.585	1.00	25.99	A	C
ATOM	952	O	ILE	A	122	-24.582	-40.512	-9.892	1.00	24.65	A	O
ATOM	953	N	TYR	A	123	-25.477	-38.468	-10.292	1.00	26.83	A	N
ATOM	954	CA	TYR	A	123	-24.684	-38.214	-11.479	1.00	27.50	A	C
ATOM	955	CB	TYR	A	123	-25.620	-38.158	-12.642	1.00	26.01	A	C
ATOM	956	CG	TYR	A	123	-26.202	-39.467	-12.987	1.00	28.56	A	C
ATOM	957	CD1	TYR	A	123	-25.458	-40.424	-13.696	1.00	26.12	A	C
ATOM	958	CE1	TYR	A	123	-26.016	-41.621	-14.047	1.00	27.49	A	C
ATOM	959	CZ	TYR	A	123	-27.340	-41.890	-13.696	1.00	29.40	A	C
ATOM	960	OH	TYR	A	123	-27.940	-43.075	-14.048	1.00	29.36	A	O
ATOM	961	CE2	TYR	A	123	-28.089	-40.965	-12.974	1.00	29.36	A	C

ATOM	962	CD2	TYR	A	123	-27.525	-39.761	-12.637	1.00	28.86	A	C
ATOM	963	C	TYR	A	123	-24.000	-36.866	-11.410	1.00	27.64	A	C
ATOM	964	O	TYR	A	123	-24.682	-35.864	-11.416	1.00	27.65	A	O
ATOM	965	N	GLY	A	124	-22.675	-36.814	-11.397	1.00	28.67	A	N
ATOM	966	CA	GLY	A	124	-21.985	-35.522	-11.636	1.00	29.95	A	C
ATOM	967	C	GLY	A	124	-22.156	-34.939	-13.056	1.00	32.16	A	C
ATOM	968	O	GLY	A	124	-22.633	-35.631	-14.029	1.00	31.54	A	O
ATOM	969	N	ASP	A	125	-21.774	-33.667	-13.197	1.00	32.99	A	N
ATOM	970	CA	ASP	A	125	-21.679	-33.034	-14.514	1.00	34.33	A	C
ATOM	971	CB	ASP	A	125	-21.971	-31.562	-14.386	1.00	34.40	A	C
ATOM	972	CG	ASP	A	125	-23.380	-31.287	-13.965	1.00	37.99	A	C
ATOM	973	OD1	ASP	A	125	-24.336	-31.852	-14.549	1.00	38.07	A	O
ATOM	974	OD2	ASP	A	125	-23.520	-30.455	-13.045	1.00	44.23	A	O
ATOM	975	C	ASP	A	125	-20.288	-33.194	-15.165	1.00	34.98	A	C
ATOM	976	O	ASP	A	125	-20.102	-32.863	-16.340	1.00	34.73	A	O
ATOM	977	N	GLY	A	126	-19.312	-33.685	-14.397	1.00	35.47	A	N
ATOM	978	CA	GLY	A	126	-17.931	-33.785	-14.893	1.00	36.66	A	C
ATOM	979	C	GLY	A	126	-17.350	-32.381	-15.012	1.00	37.88	A	C
ATOM	980	O	GLY	A	126	-18.083	-31.394	-14.794	1.00	38.63	A	O
ATOM	981	N	ASP	A	127	-16.060	-32.284	-15.376	1.00	37.62	A	N
ATOM	982	CA	ASP	A	127	-15.330	-31.004	-15.363	1.00	37.72	A	C
ATOM	983	CB	ASP	A	127	-13.996	-31.138	-14.637	1.00	37.18	A	C
ATOM	984	CG	ASP	A	127	-13.106	-32.173	-15.272	1.00	37.42	A	C
ATOM	985	OD1	ASP	A	127	-13.431	-32.597	-16.405	1.00	36.84	A	O
ATOM	986	OD2	ASP	A	127	-12.107	-32.578	-14.631	1.00	35.38	A	O
ATOM	987	C	ASP	A	127	-15.057	-30.433	-16.756	1.00	37.76	A	C
ATOM	988	O	ASP	A	127	-14.229	-29.510	-16.877	1.00	37.23	A	O
ATOM	989	N	GLY	A	128	-15.750	-30.980	-17.767	1.00	37.19	A	N
ATOM	990	CA	GLY	A	128	-15.485	-30.716	-19.179	1.00	37.16	A	C
ATOM	991	C	GLY	A	128	-14.082	-31.007	-19.715	1.00	38.07	A	C
ATOM	992	O	GLY	A	128	-13.859	-30.746	-20.890	1.00	39.17	A	O
ATOM	993	N	ILE	A	129	-13.139	-31.495	-18.880	1.00	37.52	A	N
ATOM	994	CA	ILE	A	129	-11.811	-31.964	-19.309	1.00	36.84	A	C
ATOM	995	CB	ILE	A	129	-10.651	-31.606	-18.310	1.00	37.50	A	C
ATOM	996	CG1	ILE	A	129	-10.767	-30.184	-17.642	1.00	38.34	A	C
ATOM	997	CD1	ILE	A	129	-10.877	-28.983	-18.606	1.00	42.13	A	C
ATOM	998	CG2	ILE	A	129	-9.254	-31.938	-18.942	1.00	33.49	A	C
ATOM	999	C	ILE	A	129	-11.819	-33.512	-19.349	1.00	37.57	A	C
ATOM	1000	O	ILE	A	129	-11.514	-34.142	-20.378	1.00	38.01	A	O
ATOM	1001	N	LEU	A	130	-12.150	-34.132	-18.216	1.00	36.97	A	N
ATOM	1002	CA	LEU	A	130	-12.229	-35.595	-18.099	1.00	36.57	A	C
ATOM	1003	CB	LEU	A	130	-11.936	-35.959	-16.669	1.00	37.18	A	C
ATOM	1004	CG	LEU	A	130	-10.659	-36.632	-16.212	1.00	43.85	A	C
ATOM	1005	CD1	LEU	A	130	-10.785	-38.205	-16.580	1.00	46.49	A	C
ATOM	1006	CD2	LEU	A	130	-9.269	-35.957	-16.695	1.00	47.25	A	C
ATOM	1007	C	LEU	A	130	-13.599	-36.199	-18.584	1.00	35.25	A	C
ATOM	1008	O	LEU	A	130	-13.644	-37.081	-19.447	1.00	33.76	A	O
ATOM	1009	N	PHE	A	131	-14.713	-35.687	-18.074	1.00	34.61	A	N
ATOM	1010	CA	PHE	A	131	-16.039	-36.253	-18.388	1.00	34.15	A	C
ATOM	1011	CB	PHE	A	131	-16.657	-36.934	-17.161	1.00	34.95	A	C
ATOM	1012	CG	PHE	A	131	-15.891	-38.104	-16.672	1.00	38.14	A	C
ATOM	1013	CD1	PHE	A	131	-15.883	-39.308	-17.404	1.00	41.58	A	C
ATOM	1014	CE1	PHE	A	131	-15.151	-40.406	-16.966	1.00	44.73	A	C
ATOM	1015	CZ	PHE	A	131	-14.387	-40.309	-15.767	1.00	48.86	A	C
ATOM	1016	CE2	PHE	A	131	-14.398	-39.106	-15.023	1.00	47.18	A	C
ATOM	1017	CD2	PHE	A	131	-15.162	-38.011	-15.501	1.00	41.75	A	C
ATOM	1018	C	PHE	A	131	-17.011	-35.199	-18.809	1.00	32.89	A	C
ATOM	1019	O	PHE	A	131	-16.964	-34.096	-18.280	1.00	33.01	A	O
ATOM	1020	N	SER	A	132	-17.907	-35.526	-19.737	1.00	30.84	A	N
ATOM	1021	CA	SER	A	132	-19.070	-34.702	-19.916	1.00	29.80	A	C
ATOM	1022	CB	SER	A	132	-19.624	-34.804	-21.323	1.00	29.21	A	C
ATOM	1023	OG	SER	A	132	-19.674	-36.134	-21.697	1.00	30.42	A	O
ATOM	1024	C	SER	A	132	-20.048	-35.190	-18.859	1.00	29.53	A	C
ATOM	1025	O	SER	A	132	-19.685	-36.006	-18.008	1.00	30.08	A	O
ATOM	1026	N	PRO	A	133	-21.272	-34.647	-18.817	1.00	29.36	A	N
ATOM	1027	CA	PRO	A	133	-22.190	-35.114	-17.725	1.00	27.74	A	C
ATOM	1028	CB	PRO	A	133	-23.429	-34.274	-17.954	1.00	27.87	A	C
ATOM	1029	CG	PRO	A	133	-22.824	-32.907	-18.594	1.00	28.87	A	C
ATOM	1030	CD	PRO	A	133	-21.681	-33.354	-19.443	1.00	28.76	A	C
ATOM	1031	C	PRO	A	133	-22.473	-36.640	-17.708	1.00	27.79	A	C
ATOM	1032	O	PRO	A	133	-22.816	-37.261	-18.724	1.00	28.94	A	O
ATOM	1033	N	LEU	A	134	-22.333	-37.266	-16.551	1.00	27.55	A	N
ATOM	1034	CA	LEU	A	134	-22.239	-38.723	-16.535	1.00	26.30	A	C
ATOM	1035	CB	LEU	A	134	-21.559	-39.226	-15.287	1.00	26.50	A	C
ATOM	1036	CG	LEU	A	134	-20.106	-38.765	-15.416	1.00	26.04	A	C
ATOM	1037	CD1	LEU	A	134	-19.838	-37.590	-14.496	1.00	24.48	A	C
ATOM	1038	CD2	LEU	A	134	-19.191	-39.925	-15.156	1.00	25.59	A	C
ATOM	1039	C	LEU	A	134	-23.503	-39.514	-16.841	1.00	26.32	A	C
ATOM	1040	O	LEU	A	134	-23.407	-40.717	-17.164	1.00	26.47	A	O

ATOM	1041	N	SER	A	135	-24.671	-38.862	-16.804	1.00	24.53	A	N
ATOM	1042	CA	SER	A	135	-25.889	-39.545	-17.217	1.00	23.28	A	C
ATOM	1043	CB	SER	A	135	-27.116	-38.743	-16.855	1.00	23.25	A	C
ATOM	1044	OG	SER	A	135	-26.917	-37.361	-17.117	1.00	25.21	A	O
ATOM	1045	C	SER	A	135	-25.899	-39.891	-18.701	1.00	22.93	A	C
ATOM	1046	O	SER	A	135	-26.695	-40.741	-19.145	1.00	21.32	A	O
ATOM	1047	N	GLY	A	136	-24.986	-39.272	-19.467	1.00	23.76	A	N
ATOM	1048	CA	GLY	A	136	-25.006	-39.438	-20.917	1.00	24.14	A	C
ATOM	1049	C	GLY	A	136	-24.621	-40.823	-21.457	1.00	24.78	A	C
ATOM	1050	O	GLY	A	136	-24.722	-41.048	-22.656	1.00	26.30	A	O
ATOM	1051	N	SER	A	137	-24.240	-41.758	-20.584	1.00	24.70	A	N
ATOM	1052	CA	SER	A	137	-23.777	-43.079	-20.985	1.00	24.83	A	C
ATOM	1053	CB	SER	A	137	-22.367	-43.311	-20.477	1.00	24.69	A	C
ATOM	1054	OG	SER	A	137	-22.103	-44.685	-20.366	1.00	25.08	A	O
ATOM	1055	C	SER	A	137	-24.685	-44.169	-20.437	1.00	25.13	A	C
ATOM	1056	O	SER	A	137	-24.759	-44.368	-19.222	1.00	24.93	A	O
ATOM	1057	N	LEU	A	138	-25.412	-44.849	-21.328	1.00	24.00	A	N
ATOM	1058	CA	LEU	A	138	-26.252	-45.962	-20.897	1.00	22.97	A	C
ATOM	1059	CB	LEU	A	138	-27.032	-46.501	-22.064	1.00	21.65	A	C
ATOM	1060	CG	LEU	A	138	-27.858	-47.765	-21.927	1.00	22.78	A	C
ATOM	1061	CD1	LEU	A	138	-28.727	-47.666	-20.674	1.00	21.27	A	C
ATOM	1062	CD2	LEU	A	138	-28.726	-47.916	-23.246	1.00	18.55	A	C
ATOM	1063	C	LEU	A	138	-25.439	-47.092	-20.237	1.00	22.85	A	C
ATOM	1064	O	LEU	A	138	-25.874	-47.701	-19.254	1.00	23.50	A	O
ATOM	1065	N	ASP	A	139	-24.260	-47.382	-20.755	1.00	22.10	A	N
ATOM	1066	CA	ASP	A	139	-23.512	-48.490	-20.171	1.00	21.45	A	C
ATOM	1067	CB	ASP	A	139	-22.459	-49.121	-21.135	1.00	21.46	A	C
ATOM	1068	CG	ASP	A	139	-21.378	-48.184	-21.548	1.00	20.87	A	C
ATOM	1069	OD1	ASP	A	139	-20.693	-47.613	-20.695	1.00	19.56	A	O
ATOM	1070	OD2	ASP	A	139	-21.230	-48.006	-22.768	1.00	26.03	A	O
ATOM	1071	C	ASP	A	139	-22.996	-48.153	-18.787	1.00	20.85	A	C
ATOM	1072	O	ASP	A	139	-22.941	-49.032	-17.951	1.00	20.86	A	O
ATOM	1073	N	VAL	A	140	-22.708	-46.881	-18.518	1.00	20.51	A	N
ATOM	1074	CA	VAL	A	140	-22.297	-46.459	-17.184	1.00	20.92	A	C
ATOM	1075	CB	VAL	A	140	-21.593	-45.074	-17.222	1.00	21.74	A	C
ATOM	1076	CG1	VAL	A	140	-21.631	-44.384	-15.832	1.00	21.41	A	C
ATOM	1077	CG2	VAL	A	140	-20.164	-45.249	-17.728	1.00	21.41	A	C
ATOM	1078	C	VAL	A	140	-23.476	-46.498	-16.156	1.00	22.07	A	C
ATOM	1079	O	VAL	A	140	-23.291	-46.870	-14.941	1.00	21.54	A	O
ATOM	1080	N	THR	A	141	-24.676	-46.178	-16.641	1.00	20.44	A	N
ATOM	1081	CA	THR	A	141	-25.833	-46.224	-15.813	1.00	20.85	A	C
ATOM	1082	CB	THR	A	141	-26.984	-45.523	-16.496	1.00	21.74	A	C
ATOM	1083	OG1	THR	A	141	-26.849	-44.113	-16.306	1.00	23.68	A	O
ATOM	1084	CG2	THR	A	141	-28.304	-45.978	-15.950	1.00	23.15	A	C
ATOM	1085	C	THR	A	141	-26.163	-47.695	-15.559	1.00	21.53	A	C
ATOM	1086	O	THR	A	141	-26.583	-48.086	-14.444	1.00	21.87	A	O
ATOM	1087	N	ALA	A	142	-25.964	-48.547	-16.552	1.00	20.30	A	N
ATOM	1088	CA	ALA	A	142	-26.249	-49.949	-16.264	1.00	20.29	A	C
ATOM	1089	CB	ALA	A	142	-26.338	-50.784	-17.552	1.00	18.91	A	C
ATOM	1090	C	ALA	A	142	-25.177	-50.503	-15.260	1.00	20.38	A	C
ATOM	1091	O	ALA	A	142	-25.511	-51.271	-14.311	1.00	19.43	A	O
ATOM	1092	N	HIS	A	143	-23.912	-50.094	-15.455	1.00	19.82	A	N
ATOM	1093	CA	HIS	A	143	-22.832	-50.454	-14.479	1.00	20.46	A	C
ATOM	1094	CB	HIS	A	143	-21.554	-49.725	-14.830	1.00	19.52	A	C
ATOM	1095	CG	HIS	A	143	-20.477	-49.854	-13.814	1.00	20.81	A	C
ATOM	1096	ND1	HIS	A	143	-19.292	-50.509	-14.068	1.00	20.20	A	N
ATOM	1097	CE1	HIS	A	143	-18.521	-50.442	-12.994	1.00	21.05	A	C
ATOM	1098	NE2	HIS	A	143	-19.171	-49.786	-12.044	1.00	20.22	A	N
ATOM	1099	CD2	HIS	A	143	-20.378	-49.370	-12.548	1.00	23.25	A	C
ATOM	1100	C	HIS	A	143	-23.266	-50.149	-13.024	1.00	20.74	A	C
ATOM	1101	O	HIS	A	143	-23.219	-50.990	-12.137	1.00	20.11	A	O
ATOM	1102	N	GLU	A	144	-23.722	-48.929	-12.824	1.00	22.35	A	N
ATOM	1103	CA	GLU	A	144	-24.156	-48.452	-11.507	1.00	24.02	A	C
ATOM	1104	CB	GLU	A	144	-24.237	-46.884	-11.486	1.00	23.44	A	C
ATOM	1105	CG	GLU	A	144	-22.935	-46.184	-11.827	1.00	23.80	A	C
ATOM	1106	CD	GLU	A	144	-21.806	-46.396	-10.835	1.00	31.05	A	C
ATOM	1107	OE1	GLU	A	144	-20.600	-46.173	-11.189	1.00	37.21	A	O
ATOM	1108	OE2	GLU	A	144	-22.093	-46.768	-9.676	1.00	33.01	A	O
ATOM	1109	C	GLU	A	144	-25.452	-49.143	-11.015	1.00	23.04	A	C
ATOM	1110	O	GLU	A	144	-25.530	-49.577	-9.873	1.00	24.42	A	O
ATOM	1111	N	MET	A	145	-26.441	-49.319	-11.863	1.00	22.79	A	N
ATOM	1112	CA	MET	A	145	-27.614	-50.030	-11.390	1.00	23.27	A	C
ATOM	1113	CB	MET	A	145	-28.698	-50.127	-12.442	1.00	23.04	A	C
ATOM	1114	CG	MET	A	145	-29.845	-49.154	-12.293	1.00	30.13	A	C
ATOM	1115	SD	MET	A	145	-30.091	-48.329	-10.642	1.00	38.83	A	S
ATOM	1116	CE	MET	A	145	-28.992	-46.995	-10.984	1.00	30.09	A	C
ATOM	1117	C	MET	A	145	-27.255	-51.425	-10.899	1.00	23.43	A	C
ATOM	1118	O	MET	A	145	-27.820	-51.930	-9.890	1.00	23.83	A	O
ATOM	1119	N	THR	A	146	-26.308	-52.042	-11.602	1.00	22.59	A	N

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ATOM   1120  CA   THR A 146     -25.933 -53.408 -11.333  1.00 22.67      A    C
ATOM   1121  CB   THR A 146     -25.012 -53.943 -12.471  1.00 23.17      A    C
ATOM   1122  OG1  THR A 146     -25.757 -53.956 -13.691  1.00 21.92      A    O
ATOM   1123  CG2  THR A 146     -24.520 -55.370 -12.182  1.00 22.76      A    C
ATOM   1124  C    THR A 146     -25.310 -53.564  -9.938  1.00 23.21      A    C
ATOM   1125  O    THR A 146     -25.425 -54.655  -9.340  1.00 23.05      A    O
ATOM   1126  N    HIS A 147     -24.658 -52.502  -9.417  1.00 22.84      A    N
ATOM   1127  CA   HIS A 147     -24.120 -52.535  -8.034  1.00 23.53      A    C
ATOM   1128  CB   HIS A 147     -23.409 -51.247  -7.640  1.00 23.43      A    C
ATOM   1129  CG   HIS A 147     -22.024 -51.094  -8.195  1.00 25.63      A    C
ATOM   1130  ND1  HIS A 147     -21.056 -52.081  -8.097  1.00 22.45      A    N
ATOM   1131  CE1  HIS A 147     -19.935 -51.638  -8.662  1.00 23.31      A    C
ATOM   1132  NE2  HIS A 147     -20.139 -50.412  -9.125  1.00 22.19      A    N
ATOM   1133  CD2  HIS A 147     -21.432 -50.042  -8.838  1.00 24.54      A    C
ATOM   1134  C    HIS A 147     -25.274 -52.736  -7.045  1.00 23.74      A    C
ATOM   1135  O    HIS A 147     -25.099 -53.368  -6.037  1.00 22.83      A    O
ATOM   1136  N    GLY A 148     -26.454 -52.192  -7.379  1.00 24.04      A    N
ATOM   1137  CA   GLY A 148     -27.645 -52.306  -6.567  1.00 23.86      A    C
ATOM   1138  C    GLY A 148     -28.157 -53.715  -6.634  1.00 24.32      A    C
ATOM   1139  O    GLY A 148     -28.523 -54.294  -5.597  1.00 26.05      A    O
ATOM   1140  N    VAL A 149     -28.141 -54.301  -7.825  1.00 23.92      A    N
ATOM   1141  CA   VAL A 149     -28.526 -55.705  -7.988  1.00 22.96      A    C
ATOM   1142  CB   VAL A 149     -28.493 -56.127  -9.460  1.00 22.83      A    C
ATOM   1143  CG1  VAL A 149     -28.656 -57.615  -9.564  1.00 18.85      A    C
ATOM   1144  CG2  VAL A 149     -29.512 -55.358 -10.259  1.00 20.25      A    C
ATOM   1145  C    VAL A 149     -27.569 -56.616  -7.200  1.00 24.15      A    C
ATOM   1146  O    VAL A 149     -27.990 -57.541  -6.453  1.00 25.47      A    O
ATOM   1147  N    THR A 150     -26.278 -56.343  -7.332  1.00 23.75      A    N
ATOM   1148  CA   THR A 150     -25.284 -57.085  -6.559  1.00 24.24      A    C
ATOM   1149  CB   THR A 150     -23.863 -56.666  -6.946  1.00 23.99      A    C
ATOM   1150  OG1  THR A 150     -23.602 -57.125  -8.283  1.00 22.23      A    O
ATOM   1151  CG2  THR A 150     -22.845 -57.248  -6.005  1.00 20.09      A    C
ATOM   1152  C    THR A 150     -25.514 -56.948  -5.041  1.00 25.81      A    C
ATOM   1153  O    THR A 150     -25.448 -57.939  -4.305  1.00 26.18      A    O
ATOM   1154  N    GLN A 151     -25.802 -55.731  -4.594  1.00 26.07      A    N
ATOM   1155  CA   GLN A 151     -25.946 -55.438  -3.194  1.00 27.46      A    C
ATOM   1156  CB   GLN A 151     -26.045 -53.951  -3.078  1.00 28.06      A    C
ATOM   1157  CG   GLN A 151     -26.508 -53.295  -1.761  1.00 34.50      A    C
ATOM   1158  CD   GLN A 151     -26.880 -51.784  -2.065  1.00 38.36      A    C
ATOM   1159  OE1  GLN A 151     -28.045 -51.379  -1.940  1.00 37.38      A    O
ATOM   1160  NE2  GLN A 151     -25.886 -51.007  -2.557  1.00 37.31      A    N
ATOM   1161  C    GLN A 151     -27.146 -56.201  -2.585  1.00 27.11      A    C
ATOM   1162  O    GLN A 151     -27.025 -56.777  -1.499  1.00 26.88      A    O
ATOM   1163  N    GLU A 152     -28.218 -56.308  -3.358  1.00 25.84      A    N
ATOM   1164  CA   GLU A 152     -29.411 -57.045  -2.979  1.00 26.00      A    C
ATOM   1165  CB   GLU A 152     -30.601 -56.525  -3.811  1.00 24.38      A    C
ATOM   1166  CG   GLU A 152     -30.962 -55.115  -3.474  1.00 28.24      A    C
ATOM   1167  CD   GLU A 152     -31.418 -55.027  -2.050  1.00 30.02      A    C
ATOM   1168  OE1  GLU A 152     -32.452 -55.626  -1.757  1.00 33.64      A    O
ATOM   1169  OE2  GLU A 152     -30.694 -54.464  -1.202  1.00 32.95      A    O
ATOM   1170  C    GLU A 152     -29.337 -58.566  -3.183  1.00 25.65      A    C
ATOM   1171  O    GLU A 152     -30.318 -59.303  -2.924  1.00 25.43      A    O
ATOM   1172  N    THR A 153     -28.193 -59.026  -3.670  1.00 24.78      A    N
ATOM   1173  CA   THR A 153     -28.036 -60.395  -4.148  1.00 23.39      A    C
ATOM   1174  CB   THR A 153     -28.026 -60.258  -5.660  1.00 24.08      A    C
ATOM   1175  OG1  THR A 153     -29.320 -60.620  -6.229  1.00 27.23      A    O
ATOM   1176  CG2  THR A 153     -27.026 -60.967  -6.210  1.00 21.52      A    C
ATOM   1177  C    THR A 153     -26.756 -60.999  -3.519  1.00 23.00      A    C
ATOM   1178  O    THR A 153     -26.707 -61.211  -2.325  1.00 22.29      A    O
ATOM   1179  N    ALA A 154     -25.685 -61.182  -4.301  1.00 22.49      A    N
ATOM   1180  CA   ALA A 154     -24.415 -61.685  -3.835  1.00 20.07      A    C
ATOM   1181  CB   ALA A 154     -23.506 -61.833  -4.985  1.00 19.57      A    C
ATOM   1182  C    ALA A 154     -23.744 -60.845  -2.758  1.00 20.31      A    C
ATOM   1183  O    ALA A 154     -22.986 -61.382  -1.911  1.00 19.99      A    O
ATOM   1184  N    ASN A 155     -23.935 -59.540  -2.840  1.00 19.80      A    N
ATOM   1185  CA   ASN A 155     -23.290 -58.608  -1.924  1.00 20.54      A    C
ATOM   1186  CB   ASN A 155     -23.959 -58.712  -0.525  1.00 20.57      A    C
ATOM   1187  CG   ASN A 155     -23.827 -57.429   0.321  1.00 21.69      A    C
ATOM   1188  OD1  ASN A 155     -24.120 -57.444   1.545  1.00 24.14      A    O
ATOM   1189  ND2  ASN A 155     -23.340 -56.352  -0.283  1.00 18.66      A    N
ATOM   1190  C    ASN A 155     -21.753 -58.751  -1.853  1.00 20.95      A    C
ATOM   1191  O    ASN A 155     -21.134 -58.840  -0.755  1.00 21.27      A    O
ATOM   1192  N    LEU A 156     -21.109 -58.792  -3.009  1.00 21.01      A    N
ATOM   1193  CA   LEU A 156     -19.650 -58.923  -3.002  1.00 20.82      A    C
ATOM   1194  CB   LEU A 156     -19.137 -58.933  -4.433  1.00 20.60      A    C
ATOM   1195  CG   LEU A 156     -19.621 -60.098  -5.269  1.00 19.99      A    C
ATOM   1196  CD1  LEU A 156     -19.739 -59.645  -6.739  1.00 18.05      A    C
ATOM   1197  CD2  LEU A 156     -18.615 -61.191  -5.062  1.00 15.60      A    C
ATOM   1198  C    LEU A 156     -18.998 -57.809  -2.193  1.00 20.75      A    C
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ATOM	1199	O	LEU	A	156	-19.303	-56.638	-2.377	1.00	21.10	A	O
ATOM	1200	N	ASN	A	157	-18.135	-58.188	-1.268	1.00	21.00	A	N
ATOM	1201	CA	ASN	A	157	-17.314	-57.263	-0.529	1.00	21.48	A	C
ATOM	1202	CB	ASN	A	157	-16.367	-58.077	0.293	1.00	20.96	A	C
ATOM	1203	CG	ASN	A	157	-17.026	-58.748	1.430	1.00	19.87	A	C
ATOM	1204	OD1	ASN	A	157	-18.154	-58.388	1.838	1.00	24.09	A	O
ATOM	1205	ND2	ASN	A	157	-16.337	-59.738	1.977	1.00	14.00	A	N
ATOM	1206	C	ASN	A	157	-16.458	-56.356	-1.436	1.00	24.39	A	C
ATOM	1207	O	ASN	A	157	-15.973	-56.793	-2.498	1.00	24.92	A	O
ATOM	1208	N	TYR	A	158	-16.273	-55.110	-1.031	1.00	26.83	A	N
ATOM	1209	CA	TYR	A	158	-15.597	-54.138	-1.874	1.00	29.99	A	C
ATOM	1210	CB	TYR	A	158	-16.133	-52.730	-1.625	1.00	30.74	A	C
ATOM	1211	CG	TYR	A	158	-16.036	-51.870	-2.854	1.00	37.88	A	C
ATOM	1212	CD1	TYR	A	158	-16.756	-52.240	-4.013	1.00	44.29	A	C
ATOM	1213	CE1	TYR	A	158	-16.708	-51.472	-5.186	1.00	46.05	A	C
ATOM	1214	CZ	TYR	A	158	-15.952	-50.285	-5.215	1.00	46.84	A	C
ATOM	1215	OH	TYR	A	158	-15.988	-49.585	-6.428	1.00	48.74	A	O
ATOM	1216	CE2	TYR	A	158	-15.219	-49.856	-4.067	1.00	41.11	A	C
ATOM	1217	CD2	TYR	A	158	-15.267	-50.674	-2.884	1.00	41.50	A	C
ATOM	1218	C	TYR	A	158	-14.104	-54.136	-1.551	1.00	29.47	A	C
ATOM	1219	O	TYR	A	158	-13.627	-53.206	-0.945	1.00	30.04	A	O
ATOM	1220	N	GLU	A	159	-13.385	-55.186	-1.925	1.00	28.99	A	N
ATOM	1221	CA	GLU	A	159	-11.976	-55.272	-1.641	1.00	28.82	A	C
ATOM	1222	CB	GLU	A	159	-11.768	-55.340	-0.127	1.00	29.92	A	C
ATOM	1223	CG	GLU	A	159	-12.306	-56.655	0.403	1.00	37.72	A	C
ATOM	1224	CD	GLU	A	159	-12.378	-56.771	1.908	1.00	46.55	A	C
ATOM	1225	OE1	GLU	A	159	-12.816	-57.862	2.360	1.00	50.45	A	O
ATOM	1226	OE2	GLU	A	159	-11.985	-55.828	2.625	1.00	48.20	A	O
ATOM	1227	C	GLU	A	159	-11.430	-56.526	-2.312	1.00	26.90	A	C
ATOM	1228	O	GLU	A	159	-12.135	-57.520	-2.455	1.00	25.63	A	O
ATOM	1229	N	ASN	A	160	-10.175	-56.458	-2.749	1.00	25.86	A	N
ATOM	1230	CA	ASN	A	160	-9.476	-57.603	-3.289	1.00	24.72	A	C
ATOM	1231	CB	ASN	A	160	-9.059	-58.529	-2.121	1.00	25.81	A	C
ATOM	1232	CG	ASN	A	160	-8.197	-57.765	-1.025	1.00	27.32	A	C
ATOM	1233	OD1	ASN	A	160	-7.376	-56.910	-1.343	1.00	31.59	A	O
ATOM	1234	ND2	ASN	A	160	-8.415	-58.075	0.224	1.00	26.78	A	N
ATOM	1235	C	ASN	A	160	-10.273	-58.290	-4.423	1.00	24.15	A	C
ATOM	1236	O	ASN	A	160	-10.980	-57.617	-5.193	1.00	24.63	A	O
ATOM	1237	N	GLN	A	161	-10.171	-59.597	-4.565	1.00	23.15	A	N
ATOM	1238	CA	GLN	A	161	-10.906	-60.268	-5.611	1.00	22.89	A	C
ATOM	1239	CB	GLN	A	161	-10.611	-61.755	-5.633	1.00	23.27	A	C
ATOM	1240	CG	GLN	A	161	-9.261	-62.087	-6.309	1.00	25.24	A	C
ATOM	1241	CD	GLN	A	161	-8.807	-63.524	-6.096	1.00	24.45	A	C
ATOM	1242	OE1	GLN	A	161	-7.827	-63.747	-5.430	1.00	28.68	A	O
ATOM	1243	NE2	GLN	A	161	-9.507	-64.484	-6.661	1.00	23.13	A	N
ATOM	1244	C	GLN	A	161	-12.409	-60.032	-5.552	1.00	22.22	A	C
ATOM	1245	O	GLN	A	161	-12.998	-59.792	-6.604	1.00	23.02	A	O
ATOM	1246	N	PRO	A	162	-13.039	-60.085	-4.344	1.00	20.98	A	N
ATOM	1247	CA	PRO	A	162	-14.502	-59.890	-4.417	1.00	19.36	A	C
ATOM	1248	CB	PRO	A	162	-14.975	-60.120	-2.987	1.00	18.81	A	C
ATOM	1249	CG	PRO	A	162	-13.912	-60.912	-2.337	1.00	18.86	A	C
ATOM	1250	CD	PRO	A	162	-12.606	-60.623	-3.033	1.00	19.79	A	C
ATOM	1251	C	PRO	A	162	-14.857	-58.470	-4.924	1.00	19.83	A	C
ATOM	1252	O	PRO	A	162	-15.809	-58.341	-5.670	1.00	19.72	A	O
ATOM	1253	N	GLY	A	163	-14.068	-57.436	-4.605	1.00	18.23	A	N
ATOM	1254	CA	GLY	A	163	-14.331	-56.114	-5.191	1.00	17.64	A	C
ATOM	1255	C	GLY	A	163	-14.089	-56.028	-6.705	1.00	18.03	A	C
ATOM	1256	O	GLY	A	163	-14.854	-55.382	-7.478	1.00	17.09	A	O
ATOM	1257	N	ALA	A	164	-13.025	-56.674	-7.161	1.00	16.65	A	N
ATOM	1258	CA	ALA	A	164	-12.727	-56.654	-8.580	1.00	16.33	A	C
ATOM	1259	CB	ALA	A	164	-11.406	-57.419	-8.845	1.00	14.77	A	C
ATOM	1260	C	ALA	A	164	-13.938	-57.339	-9.278	1.00	17.55	A	C
ATOM	1261	O	ALA	A	164	-14.455	-56.837	-10.268	1.00	18.28	A	O
ATOM	1262	N	LEU	A	165	-14.420	-58.448	-8.707	1.00	17.14	A	N
ATOM	1263	CA	LEU	A	165	-15.608	-59.097	-9.196	1.00	17.89	A	C
ATOM	1264	CB	LEU	A	165	-15.877	-60.287	-8.315	1.00	16.99	A	C
ATOM	1265	CG	LEU	A	165	-15.729	-61.677	-8.900	1.00	19.04	A	C
ATOM	1266	CD1	LEU	A	165	-14.973	-61.795	-10.252	1.00	15.06	A	C
ATOM	1267	CD2	LEU	A	165	-15.198	-62.613	-7.856	1.00	13.97	A	C
ATOM	1268	C	LEU	A	165	-16.847	-58.169	-9.210	1.00	18.52	A	C
ATOM	1269	O	LEU	A	165	-17.639	-58.204	-10.166	1.00	19.03	A	O
ATOM	1270	N	ASN	A	166	-16.998	-57.340	-8.177	1.00	17.89	A	N
ATOM	1271	CA	ASN	A	166	-18.166	-56.480	-8.021	1.00	18.38	A	C
ATOM	1272	CB	ASN	A	166	-18.079	-55.783	-6.670	1.00	18.80	A	C
ATOM	1273	CG	ASN	A	166	-19.340	-54.998	-6.315	1.00	22.37	A	C
ATOM	1274	OD1	ASN	A	166	-19.843	-55.100	-5.194	1.00	27.99	A	O
ATOM	1275	ND2	ASN	A	166	-19.845	-54.238	-7.231	1.00	23.69	A	N
ATOM	1276	C	ASN	A	166	-18.122	-55.478	-9.184	1.00	18.27	A	C
ATOM	1277	O	ASN	A	166	-19.090	-55.312	-9.911	1.00	16.89	A	O

ATOM	1278	N	GLU	A	167	-16.956	-54.845	-9.378	1.00	18.74	A	N
ATOM	1279	CA	GLU	A	167	-16.739	-53.911	-10.509	1.00	19.05	A	C
ATOM	1280	CB	GLU	A	167	-15.330	-53.278	-10.479	1.00	19.22	A	C
ATOM	1281	CG	GLU	A	167	-15.166	-52.277	-9.341	1.00	18.04	A	C
ATOM	1282	CD	GLU	A	167	-16.188	-51.122	-9.491	1.00	26.42	A	C
ATOM	1283	OE1	GLU	A	167	-16.420	-50.721	-10.651	1.00	23.23	A	O
ATOM	1284	OE2	GLU	A	167	-16.758	-50.618	-8.458	1.00	31.20	A	O
ATOM	1285	C	GLU	A	167	-16.989	-54.607	-11.845	1.00	19.13	A	C
ATOM	1286	O	GLU	A	167	-17.653	-54.030	-12.724	1.00	18.28	A	O
ATOM	1287	N	SER	A	168	-16.521	-55.853	-11.965	1.00	18.00	A	N
ATOM	1288	CA	SER	A	168	-16.599	-56.564	-13.230	1.00	18.98	A	C
ATOM	1289	CB	SER	A	168	-15.698	-57.800	-13.208	1.00	19.87	A	C
ATOM	1290	OG	SER	A	168	-15.795	-58.557	-14.402	1.00	21.32	A	O
ATOM	1291	C	SER	A	168	-18.005	-56.948	-13.640	1.00	19.25	A	C
ATOM	1292	O	SER	A	168	-18.367	-56.783	-14.817	1.00	20.90	A	O
ATOM	1293	N	PHE	A	169	-18.794	-57.485	-12.710	1.00	18.94	A	N
ATOM	1294	CA	PHE	A	169	-20.217	-57.729	-12.980	1.00	18.08	A	C
ATOM	1295	CB	PHE	A	169	-20.900	-58.365	-11.790	1.00	17.52	A	C
ATOM	1296	CG	PHE	A	169	-20.691	-59.855	-11.744	1.00	18.33	A	C
ATOM	1297	CD1	PHE	A	169	-21.599	-60.729	-12.369	1.00	20.04	A	C
ATOM	1298	CE1	PHE	A	169	-21.384	-62.140	-12.368	1.00	18.87	A	C
ATOM	1299	CZ	PHE	A	169	-20.211	-62.664	-11.775	1.00	16.77	A	C
ATOM	1300	CE2	PHE	A	169	-19.287	-61.777	-11.188	1.00	15.44	A	C
ATOM	1301	CD2	PHE	A	169	-19.556	-60.391	-11.156	1.00	15.38	A	C
ATOM	1302	C	PHE	A	169	-20.892	-56.445	-13.414	1.00	18.51	A	C
ATOM	1303	O	PHE	A	169	-21.651	-56.464	-14.360	1.00	18.82	A	O
ATOM	1304	N	SER	A	170	-20.574	-55.317	-12.778	1.00	18.28	A	N
ATOM	1305	CA	SER	A	170	-21.139	-54.034	-13.214	1.00	18.86	A	C
ATOM	1306	CB	SER	A	170	-20.808	-52.909	-12.207	1.00	19.58	A	C
ATOM	1307	OG	SER	A	170	-21.680	-52.939	-11.063	1.00	18.44	A	O
ATOM	1308	C	SER	A	170	-20.703	-53.636	-14.648	1.00	19.35	A	C
ATOM	1309	O	SER	A	170	-21.548	-53.179	-15.481	1.00	19.84	A	O
ATOM	1310	N	ASP	A	171	-19.419	-53.836	-14.973	1.00	18.01	A	N
ATOM	1311	CA	ASP	A	171	-18.950	-53.628	-16.357	1.00	17.49	A	C
ATOM	1312	CB	ASP	A	171	-17.426	-53.709	-16.481	1.00	17.01	A	C
ATOM	1313	CG	ASP	A	171	-16.753	-52.437	-15.954	1.00	19.97	A	C
ATOM	1314	OD1	ASP	A	171	-17.486	-51.457	-15.784	1.00	23.37	A	O
ATOM	1315	OD2	ASP	A	171	-15.541	-52.393	-15.672	1.00	21.12	A	O
ATOM	1316	C	ASP	A	171	-19.625	-54.597	-17.318	1.00	17.10	A	C
ATOM	1317	O	ASP	A	171	-19.989	-54.225	-18.390	1.00	16.94	A	O
ATOM	1318	N	VAL	A	172	-19.821	-55.841	-16.929	1.00	17.31	A	N
ATOM	1319	CA	VAL	A	172	-20.311	-56.797	-17.915	1.00	17.03	A	C
ATOM	1320	CB	VAL	A	172	-20.175	-58.274	-17.436	1.00	17.29	A	C
ATOM	1321	CG1	VAL	A	172	-20.952	-59.218	-18.390	1.00	10.63	A	C
ATOM	1322	CG2	VAL	A	172	-18.727	-58.633	-17.292	1.00	12.24	A	C
ATOM	1323	C	VAL	A	172	-21.769	-56.540	-18.178	1.00	17.87	A	C
ATOM	1324	O	VAL	A	172	-22.186	-56.570	-19.320	1.00	20.15	A	O
ATOM	1325	N	PHE	A	173	-22.566	-56.286	-17.139	1.00	17.61	A	N
ATOM	1326	CA	PHE	A	173	-23.938	-55.837	-17.384	1.00	16.74	A	C
ATOM	1327	CB	PHE	A	173	-24.788	-55.923	-16.129	1.00	15.90	A	C
ATOM	1328	CG	PHE	A	173	-25.200	-57.319	-15.836	1.00	16.63	A	C
ATOM	1329	CD1	PHE	A	173	-26.192	-57.945	-16.615	1.00	15.84	A	C
ATOM	1330	CE1	PHE	A	173	-26.541	-59.316	-16.394	1.00	15.38	A	C
ATOM	1331	CZ	PHE	A	173	-25.920	-60.041	-15.400	1.00	12.78	A	C
ATOM	1332	CE2	PHE	A	173	-24.915	-59.420	-14.624	1.00	15.12	A	C
ATOM	1333	CD2	PHE	A	173	-24.547	-58.063	-14.864	1.00	14.07	A	C
ATOM	1334	C	PHE	A	173	-23.980	-54.476	-18.083	1.00	16.64	A	C
ATOM	1335	O	PHE	A	173	-24.859	-54.210	-18.881	1.00	16.87	A	O
ATOM	1336	N	GLY	A	174	-23.012	-53.618	-17.829	1.00	16.88	A	N
ATOM	1337	CA	GLY	A	174	-22.910	-52.412	-18.676	1.00	17.01	A	C
ATOM	1338	C	GLY	A	174	-22.824	-52.773	-20.129	1.00	15.87	A	C
ATOM	1339	O	GLY	A	174	-23.639	-52.364	-20.946	1.00	16.39	A	O
ATOM	1340	N	TYR	A	175	-21.850	-53.597	-20.440	1.00	16.21	A	N
ATOM	1341	CA	TYR	A	175	-21.672	-54.101	-21.818	1.00	16.33	A	C
ATOM	1342	CB	TYR	A	175	-20.505	-55.135	-21.929	1.00	15.56	A	C
ATOM	1343	CG	TYR	A	175	-20.634	-55.868	-23.242	1.00	16.30	A	C
ATOM	1344	CD1	TYR	A	175	-20.244	-55.242	-24.446	1.00	15.97	A	C
ATOM	1345	CE1	TYR	A	175	-20.412	-55.874	-25.660	1.00	15.05	A	C
ATOM	1346	CZ	TYR	A	175	-20.993	-57.103	-25.692	1.00	12.27	A	C
ATOM	1347	OH	TYR	A	175	-21.122	-57.668	-26.889	1.00	19.05	A	O
ATOM	1348	CE2	TYR	A	175	-21.447	-57.760	-24.541	1.00	15.27	A	C
ATOM	1349	CD2	TYR	A	175	-21.266	-57.140	-23.315	1.00	16.32	A	C
ATOM	1350	C	TYR	A	175	-22.940	-54.727	-22.397	1.00	16.62	A	C
ATOM	1351	O	TYR	A	175	-23.255	-54.468	-23.558	1.00	17.16	A	O
ATOM	1352	N	PHE	A	176	-23.635	-55.601	-21.634	1.00	16.39	A	N
ATOM	1353	CA	PHE	A	176	-24.897	-56.208	-22.145	1.00	16.88	A	C
ATOM	1354	CB	PHE	A	176	-25.520	-57.206	-21.179	1.00	15.95	A	C
ATOM	1355	CG	PHE	A	176	-24.676	-58.450	-20.932	1.00	17.51	A	C
ATOM	1356	CD1	PHE	A	176	-23.993	-59.092	-21.990	1.00	17.21	A	C

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ATOM   1357  CE1 PHE A 176     -23.200 -60.253 -21.776  1.00 14.72      A    C
ATOM   1358  CZ  PHE A 176     -23.112 -60.805 -20.542  1.00 13.49      A    C
ATOM   1359  CE2 PHE A 176     -23.805 -60.198 -19.455  1.00 16.22      A    C
ATOM   1360  CD2 PHE A 176     -24.583 -59.005 -19.657  1.00 12.99      A    C
ATOM   1361  C   PHE A 176     -25.969 -55.159 -22.503  1.00 18.52      A    C
ATOM   1362  O   PHE A 176     -26.918 -55.487 -23.240  1.00 19.58      A    O
ATOM   1363  N   ASN A 177     -25.867 -53.935 -21.969  1.00 18.66      A    N
ATOM   1364  CA  ASN A 177     -26.812 -52.883 -22.349  1.00 20.84      A    C
ATOM   1365  CB  ASN A 177     -27.074 -51.973 -21.158  1.00 21.25      A    C
ATOM   1366  CG  ASN A 177     -28.132 -52.547 -20.240  1.00 23.82      A    C
ATOM   1367  OD1 ASN A 177     -29.337 -52.292 -20.447  1.00 26.73      A    O
ATOM   1368  ND2 ASN A 177     -27.713 -53.430 -19.304  1.00 19.14      A    N
ATOM   1369  C   ASN A 177     -26.349 -52.026 -23.528  1.00 22.09      A    C
ATOM   1370  O   ASN A 177     -27.098 -51.180 -24.026  1.00 22.65      A    O
ATOM   1371  N   ASP A 178     -25.096 -52.227 -23.949  1.00 22.56      A    N
ATOM   1372  CA  ASP A 178     -24.585 -51.613 -25.167  1.00 22.81      A    C
ATOM   1373  CB  ASP A 178     -23.717 -50.419 -24.795  1.00 22.90      A    C
ATOM   1374  CG  ASP A 178     -23.211 -49.690 -26.009  1.00 24.04      A    C
ATOM   1375  OD1 ASP A 178     -23.707 -50.024 -27.136  1.00 23.24      A    O
ATOM   1376  OD2 ASP A 178     -22.320 -48.827 -25.821  1.00 23.69      A    O
ATOM   1377  C   ASP A 178     -23.756 -52.589 -25.997  1.00 22.85      A    C
ATOM   1378  O   ASP A 178     -22.551 -52.517 -25.957  1.00 22.00      A    O
ATOM   1379  N   THR A 179     -24.373 -53.519 -26.733  1.00 23.82      A    N
ATOM   1380  CA  THR A 179     -23.587 -54.582 -27.357  1.00 23.81      A    C
ATOM   1381  CB  THR A 179     -24.382 -55.843 -27.549  1.00 23.60      A    C
ATOM   1382  OG1 THR A 179     -25.444 -55.583 -28.454  1.00 22.97      A    O
ATOM   1383  CG2 THR A 179     -24.988 -56.319 -26.217  1.00 23.48      A    C
ATOM   1384  C   THR A 179     -22.874 -54.197 -28.652  1.00 25.94      A    C
ATOM   1385  O   THR A 179     -22.231 -55.060 -29.276  1.00 28.95      A    O
ATOM   1386  N   GLU A 180     -22.905 -52.916 -29.011  1.00 25.67      A    N
ATOM   1387  CA  GLU A 180     -22.389 -52.446 -30.283  1.00 26.89      A    C
ATOM   1388  CB  GLU A 180     -23.122 -51.171 -30.761  1.00 26.98      A    C
ATOM   1389  CG  GLU A 180     -24.670 -51.330 -30.837  1.00 35.87      A    C
ATOM   1390  CD  GLU A 180     -25.179 -52.083 -32.100  1.00 42.93      A    C
ATOM   1391  OE1 GLU A 180     -25.040 -51.571 -33.253  1.00 44.91      A    O
ATOM   1392  OE2 GLU A 180     -25.746 -53.192 -31.912  1.00 46.19      A    O
ATOM   1393  C   GLU A 180     -20.879 -52.186 -30.191  1.00 25.23      A    C
ATOM   1394  O   GLU A 180     -20.239 -52.040 -31.212  1.00 23.83      A    O
ATOM   1395  N   ASP A 181     -20.348 -52.112 -28.967  1.00 23.52      A    N
ATOM   1396  CA  ASP A 181     -18.938 -51.832 -28.760  1.00 22.58      A    C
ATOM   1397  CB  ASP A 181     -18.655 -50.340 -28.850  1.00 21.01      A    C
ATOM   1398  CG  ASP A 181     -19.321 -49.522 -27.710  1.00 22.57      A    C
ATOM   1399  OD1 ASP A 181     -18.851 -49.707 -26.552  1.00 18.34      A    O
ATOM   1400  OD2 ASP A 181     -20.243 -48.665 -27.982  1.00 16.82      A    O
ATOM   1401  C   ASP A 181     -18.475 -52.504 -27.448  1.00 22.44      A    C
ATOM   1402  O   ASP A 181     -19.320 -52.946 -26.690  1.00 23.47      A    O
ATOM   1403  N   TRP A 182     -17.171 -52.683 -27.223  1.00 20.84      A    N
ATOM   1404  CA  TRP A 182     -16.721 -53.385 -26.028  1.00 20.90      A    C
ATOM   1405  CB  TRP A 182     -15.592 -54.408 -26.332  1.00 20.47      A    C
ATOM   1406  CG  TRP A 182     -15.970 -55.461 -27.334  1.00 22.13      A    C
ATOM   1407  CD1 TRP A 182     -15.669 -55.448 -28.650  1.00 22.17      A    C
ATOM   1408  NE1 TRP A 182     -16.166 -56.554 -29.262  1.00 23.53      A    N
ATOM   1409  CE2 TRP A 182     -16.785 -57.337 -28.332  1.00 21.98      A    C
ATOM   1410  CD2 TRP A 182     -16.686 -56.673 -27.101  1.00 20.26      A    C
ATOM   1411  CE3 TRP A 182     -17.205 -57.286 -25.966  1.00 23.99      A    C
ATOM   1412  CZ3 TRP A 182     -17.855 -58.507 -26.101  1.00 22.34      A    C
ATOM   1413  CH2 TRP A 182     -17.953 -59.143 -27.362  1.00 21.91      A    C
ATOM   1414  CZ2 TRP A 182     -17.419 -58.583 -28.483  1.00 20.01      A    C
ATOM   1415  C   TRP A 182     -16.261 -52.469 -24.900  1.00 20.55      A    C
ATOM   1416  O   TRP A 182     -15.597 -52.916 -23.924  1.00 20.79      A    O
ATOM   1417  N   ASP A 183     -16.572 -51.197 -25.029  1.00 20.24      A    N
ATOM   1418  CA  ASP A 183     -16.041 -50.196 -24.082  1.00 20.11      A    C
ATOM   1419  CB  ASP A 183     -15.603 -48.958 -24.837  1.00 22.04      A    C
ATOM   1420  CG  ASP A 183     -14.519 -49.243 -25.853  1.00 22.53      A    C
ATOM   1421  OD1 ASP A 183     -13.631 -50.058 -25.566  1.00 22.42      A    O
ATOM   1422  OD2 ASP A 183     -14.559 -48.640 -26.931  1.00 28.89      A    O
ATOM   1423  C   ASP A 183     -17.103 -49.771 -23.098  1.00 19.38      A    C
ATOM   1424  O   ASP A 183     -18.305 -49.994 -23.280  1.00 18.81      A    O
ATOM   1425  N   ILE A 184     -16.634 -49.198 -22.016  1.00 19.19      A    N
ATOM   1426  CA  ILE A 184     -17.472 -48.656 -21.008  1.00 17.88      A    C
ATOM   1427  CB  ILE A 184     -17.207 -49.273 -19.633  1.00 17.96      A    C
ATOM   1428  CG1 ILE A 184     -17.542 -50.770 -19.598  1.00 15.40      A    C
ATOM   1429  CD1 ILE A 184     -19.003 -51.161 -20.100  1.00 11.93      A    C
ATOM   1430  CG2 ILE A 184     -17.982 -48.453 -18.531  1.00 17.15      A    C
ATOM   1431  C   ILE A 184     -17.137 -47.196 -20.953  1.00 19.24      A    C
ATOM   1432  O   ILE A 184     -15.951 -46.792 -20.858  1.00 18.87      A    O
ATOM   1433  N   GLY A 185     -18.188 -46.389 -21.023  1.00 21.21      A    N
ATOM   1434  CA  GLY A 185     -18.053 -44.959 -20.843  1.00 21.03      A    C
ATOM   1435  C   GLY A 185     -17.689 -44.215 -22.100  1.00 22.01      A    C
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ATOM	1436	O	GLY	A	185	-17.408	-43.045	-21.967	1.00	24.52	A	O
ATOM	1437	N	GLU	A	186	-17.654	-44.826	-23.304	1.00	22.73	A	N
ATOM	1438	CA	GLU	A	186	-17.326	-44.039	-24.564	1.00	23.37	A	C
ATOM	1439	CB	GLU	A	186	-17.879	-44.589	-25.903	1.00	22.89	A	C
ATOM	1440	CG	GLU	A	186	-18.056	-45.939	-26.167	1.00	25.12	A	C
ATOM	1441	CD	GLU	A	186	-19.138	-46.652	-25.424	1.00	22.33	A	C
ATOM	1442	OE1	GLU	A	186	-20.284	-46.845	-25.960	1.00	21.68	A	O
ATOM	1443	OE2	GLU	A	186	-18.737	-47.213	-24.397	1.00	22.18	A	O
ATOM	1444	C	GLU	A	186	-18.099	-42.696	-24.596	1.00	22.60	A	C
ATOM	1445	O	GLU	A	186	-17.618	-41.754	-25.165	1.00	20.62	A	O
ATOM	1446	N	ASP	A	187	-19.369	-42.720	-24.167	1.00	22.32	A	N
ATOM	1447	CA	ASP	A	187	-20.271	-41.596	-24.391	1.00	23.51	A	C
ATOM	1448	CB	ASP	A	187	-21.713	-42.035	-24.268	1.00	23.08	A	C
ATOM	1449	CG	ASP	A	187	-22.113	-42.937	-25.376	1.00	25.22	A	C
ATOM	1450	OD1	ASP	A	187	-22.001	-42.509	-26.563	1.00	30.20	A	O
ATOM	1451	OD2	ASP	A	187	-22.524	-44.071	-25.076	1.00	23.02	A	O
ATOM	1452	C	ASP	A	187	-20.027	-40.439	-23.465	1.00	23.38	A	C
ATOM	1453	O	ASP	A	187	-20.566	-39.384	-23.691	1.00	23.91	A	O
ATOM	1454	N	ILE	A	188	-19.201	-40.619	-22.438	1.00	23.41	A	N
ATOM	1455	CA	ILE	A	188	-18.961	-39.496	-21.533	1.00	23.94	A	C
ATOM	1456	CB	ILE	A	188	-19.559	-39.732	-20.159	1.00	23.51	A	C
ATOM	1457	CG1	ILE	A	188	-18.854	-40.951	-19.557	1.00	23.55	A	C
ATOM	1458	CD1	ILE	A	188	-19.426	-41.402	-18.274	1.00	32.06	A	C
ATOM	1459	CG2	ILE	A	188	-21.052	-39.892	-20.310	1.00	22.40	A	C
ATOM	1460	C	ILE	A	188	-17.497	-39.168	-21.316	1.00	23.80	A	C
ATOM	1461	O	ILE	A	188	-17.230	-38.262	-20.549	1.00	23.43	A	O
ATOM	1462	N	THR	A	189	-16.566	-39.889	-21.943	1.00	24.69	A	N
ATOM	1463	CA	THR	A	189	-15.119	-39.571	-21.732	1.00	26.63	A	C
ATOM	1464	CB	THR	A	189	-14.162	-40.770	-21.846	1.00	26.40	A	C
ATOM	1465	OG1	THR	A	189	-14.423	-41.478	-23.060	1.00	27.13	A	O
ATOM	1466	CG2	THR	A	189	-14.341	-41.690	-20.690	1.00	23.01	A	C
ATOM	1467	C	THR	A	189	-14.682	-38.528	-22.714	1.00	28.64	A	C
ATOM	1468	O	THR	A	189	-15.058	-38.577	-23.901	1.00	29.97	A	O
ATOM	1469	N	ILE	A	190	-13.958	-37.531	-22.231	1.00	30.38	A	N
ATOM	1470	CA	ILE	A	190	-13.570	-36.450	-23.129	1.00	32.28	A	C
ATOM	1471	CB	ILE	A	190	-13.879	-35.064	-22.516	1.00	34.01	A	C
ATOM	1472	CG1	ILE	A	190	-15.423	-34.848	-22.441	1.00	32.91	A	C
ATOM	1473	CD1	ILE	A	190	-15.854	-33.566	-21.723	1.00	31.28	A	C
ATOM	1474	CG2	ILE	A	190	-13.060	-33.922	-23.296	1.00	32.95	A	C
ATOM	1475	C	ILE	A	190	-12.094	-36.542	-23.563	1.00	32.73	A	C
ATOM	1476	O	ILE	A	190	-11.803	-36.448	-24.738	1.00	32.45	A	O
ATOM	1477	N	SER	A	191	-11.169	-36.751	-22.627	1.00	33.19	A	N
ATOM	1478	CA	SER	A	191	-9.775	-36.805	-23.025	1.00	33.49	A	C
ATOM	1479	CB	SER	A	191	-8.920	-36.253	-21.920	1.00	33.14	A	C
ATOM	1480	OG	SER	A	191	-9.041	-37.100	-20.809	1.00	36.97	A	O
ATOM	1481	C	SER	A	191	-9.306	-38.202	-23.382	1.00	34.18	A	C
ATOM	1482	O	SER	A	191	-8.091	-38.453	-23.467	1.00	35.06	A	O
ATOM	1483	N	GLN	A	192	-10.228	-39.146	-23.573	1.00	33.35	A	N
ATOM	1484	CA	GLN	A	192	-9.783	-40.462	-23.989	1.00	32.23	A	C
ATOM	1485	CB	GLN	A	192	-9.101	-41.218	-22.838	1.00	33.39	A	C
ATOM	1486	CG	GLN	A	192	-9.988	-41.561	-21.702	1.00	38.13	A	C
ATOM	1487	CD	GLN	A	192	-9.247	-42.255	-20.544	1.00	43.66	A	C
ATOM	1488	OE1	GLN	A	192	-8.231	-41.748	-20.087	1.00	47.31	A	O
ATOM	1489	NE2	GLN	A	192	-9.778	-43.396	-20.052	1.00	41.63	A	N
ATOM	1490	C	GLN	A	192	-10.937	-41.186	-24.580	1.00	30.01	A	C
ATOM	1491	O	GLN	A	192	-12.071	-40.805	-24.353	1.00	30.89	A	O
ATOM	1492	N	PRO	A	193	-10.678	-42.212	-25.372	1.00	27.78	A	N
ATOM	1493	CA	PRO	A	193	-11.870	-42.698	-26.109	1.00	26.45	A	C
ATOM	1494	CB	PRO	A	193	-11.270	-43.631	-27.207	1.00	26.27	A	C
ATOM	1495	CG	PRO	A	193	-9.795	-43.281	-27.236	1.00	27.16	A	C
ATOM	1496	CD	PRO	A	193	-9.408	-42.778	-25.858	1.00	26.09	A	C
ATOM	1497	C	PRO	A	193	-12.923	-43.471	-25.273	1.00	25.90	A	C
ATOM	1498	O	PRO	A	193	-14.023	-43.682	-25.773	1.00	27.07	A	O
ATOM	1499	N	ALA	A	194	-12.554	-43.950	-24.072	1.00	24.70	A	N
ATOM	1500	CA	ALA	A	194	-13.440	-44.762	-23.204	1.00	23.36	A	C
ATOM	1501	CB	ALA	A	194	-13.575	-46.154	-23.742	1.00	22.19	A	C
ATOM	1502	C	ALA	A	194	-12.818	-44.815	-21.812	1.00	24.00	A	C
ATOM	1503	O	ALA	A	194	-11.698	-44.385	-21.593	1.00	24.86	A	O
ATOM	1504	N	LEU	A	195	-13.539	-45.349	-20.857	1.00	23.81	A	N
ATOM	1505	CA	LEU	A	195	-13.018	-45.520	-19.534	1.00	24.41	A	C
ATOM	1506	CB	LEU	A	195	-14.229	-45.511	-18.651	1.00	25.95	A	C
ATOM	1507	CG	LEU	A	195	-14.275	-44.996	-17.236	1.00	30.68	A	C
ATOM	1508	CD1	LEU	A	195	-13.317	-43.838	-17.055	1.00	33.65	A	C
ATOM	1509	CD2	LEU	A	195	-15.726	-44.586	-16.969	1.00	30.18	A	C
ATOM	1510	C	LEU	A	195	-12.270	-46.863	-19.403	1.00	24.08	A	C
ATOM	1511	O	LEU	A	195	-11.192	-46.935	-18.804	1.00	23.41	A	O
ATOM	1512	N	ARG	A	196	-12.841	-47.922	-20.014	1.00	23.67	A	N
ATOM	1513	CA	ARG	A	196	-12.370	-49.296	-19.891	1.00	22.76	A	C
ATOM	1514	CB	ARG	A	196	-12.961	-49.963	-18.629	1.00	23.02	A	C

ATOM	1515	CG	ARG	A	196	-12.367	-49.426	-17.342	1.00	21.73	A	C
ATOM	1516	CD	ARG	A	196	-12.813	-50.233	-16.158	1.00	23.25	A	C
ATOM	1517	NE	ARG	A	196	-14.264	-50.087	-15.937	1.00	24.59	A	N
ATOM	1518	CZ	ARG	A	196	-14.837	-49.069	-15.282	1.00	20.86	A	C
ATOM	1519	NH1	ARG	A	196	-14.092	-48.100	-14.791	1.00	17.04	A	N
ATOM	1520	NH2	ARG	A	196	-16.159	-49.037	-15.109	1.00	21.02	A	N
ATOM	1521	C	ARG	A	196	-12.807	-50.069	-21.114	1.00	22.52	A	C
ATOM	1522	O	ARG	A	196	-13.819	-49.727	-21.723	1.00	21.99	A	O
ATOM	1523	N	SER	A	197	-12.018	-51.090	-21.485	1.00	22.05	A	N
ATOM	1524	CA	SER	A	197	-12.362	-51.996	-22.573	1.00	21.00	A	C
ATOM	1525	CB	SER	A	197	-11.229	-52.025	-23.613	1.00	20.95	A	C
ATOM	1526	OG	SER	A	197	-11.566	-52.922	-24.687	1.00	18.92	A	O
ATOM	1527	C	SER	A	197	-12.544	-53.422	-22.020	1.00	21.27	A	C
ATOM	1528	O	SER	A	197	-11.708	-53.882	-21.198	1.00	21.38	A	O
ATOM	1529	N	LEU	A	198	-13.585	-54.117	-22.484	1.00	19.82	A	N
ATOM	1530	CA	LEU	A	198	-13.686	-55.557	-22.248	1.00	19.79	A	C
ATOM	1531	CB	LEU	A	198	-15.145	-56.034	-22.319	1.00	19.75	A	C
ATOM	1532	CG	LEU	A	198	-15.904	-56.087	-20.985	1.00	21.07	A	C
ATOM	1533	CD1	LEU	A	198	-16.178	-54.692	-20.481	1.00	21.88	A	C
ATOM	1534	CD2	LEU	A	198	-17.157	-56.815	-21.298	1.00	21.91	A	C
ATOM	1535	C	LEU	A	198	-12.806	-56.434	-23.166	1.00	19.74	A	C
ATOM	1536	O	LEU	A	198	-12.344	-57.508	-22.740	1.00	19.53	A	O
ATOM	1537	N	SER	A	199	-12.609	-56.013	-24.424	1.00	19.06	A	N
ATOM	1538	CA	SER	A	199	-11.884	-56.819	-25.395	1.00	19.27	A	C
ATOM	1539	CB	SER	A	199	-12.216	-56.441	-26.825	1.00	18.43	A	C
ATOM	1540	OG	SER	A	199	-11.972	-55.055	-27.037	1.00	20.70	A	O
ATOM	1541	C	SER	A	199	-10.433	-56.637	-25.153	1.00	19.83	A	C
ATOM	1542	O	SER	A	199	-9.659	-57.529	-25.360	1.00	20.84	A	O
ATOM	1543	N	ASN	A	200	-10.032	-55.478	-24.689	1.00	21.41	A	N
ATOM	1544	CA	ASN	A	200	-8.634	-55.334	-24.362	1.00	21.87	A	C
ATOM	1545	CB	ASN	A	200	-7.791	-54.832	-25.537	1.00	21.65	A	C
ATOM	1546	CG	ASN	A	200	-6.249	-54.889	-25.231	1.00	27.06	A	C
ATOM	1547	OD1	ASN	A	200	-5.475	-54.393	-26.049	1.00	30.41	A	O
ATOM	1548	ND2	ASN	A	200	-5.809	-55.501	-24.039	1.00	24.34	A	N
ATOM	1549	C	ASN	A	200	-8.422	-54.438	-23.181	1.00	21.54	A	C
ATOM	1550	O	ASN	A	200	-8.158	-53.253	-23.359	1.00	22.88	A	O
ATOM	1551	N	PRO	A	201	-8.456	-55.035	-21.969	1.00	20.76	A	N
ATOM	1552	CA	PRO	A	201	-8.386	-54.221	-20.767	1.00	19.97	A	C
ATOM	1553	CB	PRO	A	201	-8.583	-55.233	-19.649	1.00	20.04	A	C
ATOM	1554	CG	PRO	A	201	-9.418	-56.297	-20.256	1.00	17.27	A	C
ATOM	1555	CD	PRO	A	201	-8.940	-56.400	-21.672	1.00	20.21	A	C
ATOM	1556	C	PRO	A	201	-7.119	-53.460	-20.605	1.00	20.08	A	C
ATOM	1557	O	PRO	A	201	-7.154	-52.398	-19.957	1.00	20.34	A	O
ATOM	1558	N	THR	A	202	-6.013	-53.952	-21.165	1.00	20.30	A	N
ATOM	1559	CA	THR	A	202	-4.687	-53.266	-20.959	1.00	20.87	A	C
ATOM	1560	CB	THR	A	202	-3.423	-54.140	-21.428	1.00	21.44	A	C
ATOM	1561	OG1	THR	A	202	-3.517	-54.431	-22.817	1.00	20.58	A	O
ATOM	1562	CG2	THR	A	202	-3.344	-55.458	-20.668	1.00	20.68	A	C
ATOM	1563	C	THR	A	202	-4.593	-51.904	-21.646	1.00	21.36	A	C
ATOM	1564	O	THR	A	202	-3.792	-51.104	-21.320	1.00	22.47	A	O
ATOM	1565	N	LYS	A	203	-5.450	-51.641	-22.592	1.00	22.15	A	N
ATOM	1566	CA	LYS	A	203	-5.507	-50.383	-23.264	1.00	23.44	A	C
ATOM	1567	CB	LYS	A	203	-6.710	-50.552	-24.145	1.00	23.94	A	C
ATOM	1568	CG	LYS	A	203	-6.858	-49.774	-25.356	1.00	27.38	A	C
ATOM	1569	CD	LYS	A	203	-8.155	-50.373	-25.996	1.00	33.35	A	C
ATOM	1570	CE	LYS	A	203	-8.589	-49.721	-27.299	1.00	34.69	A	C
ATOM	1571	NZ	LYS	A	203	-9.750	-50.462	-27.851	1.00	28.98	A	N
ATOM	1572	C	LYS	A	203	-5.760	-49.217	-22.295	1.00	24.00	A	C
ATOM	1573	O	LYS	A	203	-5.411	-48.078	-22.598	1.00	24.08	A	O
ATOM	1574	N	TYR	A	204	-6.439	-49.493	-21.165	1.00	23.80	A	N
ATOM	1575	CA	TYR	A	204	-6.757	-48.477	-20.131	1.00	22.53	A	C
ATOM	1576	CB	TYR	A	204	-8.279	-48.163	-19.987	1.00	21.98	A	C
ATOM	1577	CG	TYR	A	204	-8.883	-47.674	-21.292	1.00	21.51	A	C
ATOM	1578	CD1	TYR	A	204	-8.557	-46.403	-21.813	1.00	22.54	A	C
ATOM	1579	CE1	TYR	A	204	-9.011	-45.973	-23.036	1.00	20.99	A	C
ATOM	1580	CZ	TYR	A	204	-9.841	-46.786	-23.781	1.00	26.90	A	C
ATOM	1581	OH	TYR	A	204	-10.293	-46.348	-25.000	1.00	29.43	A	O
ATOM	1582	CE2	TYR	A	204	-10.178	-48.064	-23.333	1.00	25.65	A	C
ATOM	1583	CD2	TYR	A	204	-9.663	-48.503	-22.069	1.00	24.69	A	C
ATOM	1584	C	TYR	A	204	-6.159	-48.892	-18.820	1.00	22.27	A	C
ATOM	1585	O	TYR	A	204	-6.671	-48.521	-17.794	1.00	21.04	A	O
ATOM	1586	N	GLY	A	205	-5.058	-49.650	-18.870	1.00	22.10	A	N
ATOM	1587	CA	GLY	A	205	-4.262	-49.918	-17.675	1.00	22.18	A	C
ATOM	1588	C	GLY	A	205	-4.809	-50.989	-16.730	1.00	22.79	A	C
ATOM	1589	O	GLY	A	205	-4.430	-50.991	-15.582	1.00	23.60	A	O
ATOM	1590	N	GLN	A	206	-5.648	-51.923	-17.219	1.00	21.26	A	N
ATOM	1591	CA	GLN	A	206	-6.107	-53.065	-16.447	1.00	19.18	A	C
ATOM	1592	CB	GLN	A	206	-7.630	-53.235	-16.524	1.00	18.15	A	C
ATOM	1593	CG	GLN	A	206	-8.377	-52.048	-16.028	1.00	17.17	A	C

ATOM	1594	CD	GLN	A	206	-9.904	-52.209	-16.063	1.00	21.79	A	C
ATOM	1595	OE1	GLN	A	206	-10.523	-52.330	-17.135	1.00	18.29	A	O
ATOM	1596	NE2	GLN	A	206	-10.525	-52.152	-14.883	1.00	20.04	A	N
ATOM	1597	C	GLN	A	206	-5.450	-54.321	-16.974	1.00	19.36	A	C
ATOM	1598	O	GLN	A	206	-5.357	-54.518	-18.186	1.00	19.20	A	O
ATOM	1599	N	PRO	A	207	-5.012	-55.210	-16.056	1.00	19.13	A	N
ATOM	1600	CA	PRO	A	207	-4.493	-56.519	-16.465	1.00	17.37	A	C
ATOM	1601	CB	PRO	A	207	-4.123	-57.151	-15.119	1.00	17.34	A	C
ATOM	1602	CG	PRO	A	207	-4.994	-56.447	-14.112	1.00	16.68	A	C
ATOM	1603	CD	PRO	A	207	-5.103	-55.070	-14.581	1.00	17.24	A	C
ATOM	1604	C	PRO	A	207	-5.609	-57.340	-17.104	1.00	19.09	A	C
ATOM	1605	O	PRO	A	207	-6.823	-57.179	-16.786	1.00	18.40	A	O
ATOM	1606	N	ASP	A	208	-5.242	-58.267	-17.982	1.00	19.79	A	N
ATOM	1607	CA	ASP	A	208	-6.287	-59.043	-18.617	1.00	19.30	A	C
ATOM	1608	CB	ASP	A	208	-6.405	-58.653	-20.118	1.00	20.08	A	C
ATOM	1609	CG	ASP	A	208	-5.187	-59.120	-20.946	1.00	21.13	A	C
ATOM	1610	OD1	ASP	A	208	-4.286	-59.708	-20.379	1.00	20.02	A	O
ATOM	1611	OD2	ASP	A	208	-5.120	-58.915	-22.167	1.00	29.06	A	O
ATOM	1612	C	ASP	A	208	-5.899	-60.513	-18.392	1.00	19.37	A	C
ATOM	1613	O	ASP	A	208	-6.395	-61.433	-19.078	1.00	19.60	A	O
ATOM	1614	N	ASN	A	209	-4.972	-60.727	-17.455	1.00	18.32	A	N
ATOM	1615	CA	ASN	A	209	-4.466	-62.070	-17.169	1.00	17.32	A	C
ATOM	1616	CB	ASN	A	209	-3.246	-62.433	-18.071	1.00	15.81	A	C
ATOM	1617	CG	ASN	A	209	-2.821	-63.952	-17.937	1.00	18.79	A	C
ATOM	1618	OD1	ASN	A	209	-2.149	-64.383	-16.941	1.00	17.96	A	O
ATOM	1619	ND2	ASN	A	209	-3.226	-64.760	-18.938	1.00	16.61	A	N
ATOM	1620	C	ASN	A	209	-4.108	-62.160	-15.700	1.00	16.81	A	C
ATOM	1621	O	ASN	A	209	-3.563	-61.188	-15.078	1.00	18.22	A	O
ATOM	1622	N	PHE	A	210	-4.332	-63.314	-15.130	1.00	15.27	A	N
ATOM	1623	CA	PHE	A	210	-4.271	-63.352	-13.695	1.00	16.31	A	C
ATOM	1624	CB	PHE	A	210	-5.023	-64.587	-13.159	1.00	15.05	A	C
ATOM	1625	CG	PHE	A	210	-5.035	-64.702	-11.635	1.00	18.41	A	C
ATOM	1626	CD1	PHE	A	210	-5.798	-63.830	-10.847	1.00	17.35	A	C
ATOM	1627	CE1	PHE	A	210	-5.823	-63.930	-9.476	1.00	14.09	A	C
ATOM	1628	CZ	PHE	A	210	-5.139	-64.956	-8.821	1.00	18.23	A	C
ATOM	1629	CE2	PHE	A	210	-4.398	-65.832	-9.542	1.00	22.42	A	C
ATOM	1630	CD2	PHE	A	210	-4.331	-65.726	-10.982	1.00	22.85	A	C
ATOM	1631	C	PHE	A	210	-2.805	-63.235	-13.180	1.00	16.82	A	C
ATOM	1632	O	PHE	A	210	-2.584	-62.770	-12.078	1.00	18.49	A	O
ATOM	1633	N	LYS	A	211	-1.820	-63.679	-13.963	1.00	16.71	A	N
ATOM	1634	CA	LYS	A	211	-0.456	-63.522	-13.587	1.00	16.11	A	C
ATOM	1635	CB	LYS	A	211	0.520	-64.063	-14.628	1.00	15.62	A	C
ATOM	1636	CG	LYS	A	211	0.349	-65.592	-14.816	1.00	18.60	A	C
ATOM	1637	CD	LYS	A	211	1.446	-66.227	-15.594	1.00	18.76	A	C
ATOM	1638	CE	LYS	A	211	1.391	-65.839	-17.100	1.00	22.01	A	C
ATOM	1639	NZ	LYS	A	211	0.075	-66.030	-17.786	1.00	23.18	A	N
ATOM	1640	C	LYS	A	211	-0.191	-62.056	-13.365	1.00	16.71	A	C
ATOM	1641	O	LYS	A	211	0.733	-61.781	-12.666	1.00	18.56	A	O
ATOM	1642	N	ASN	A	212	-0.989	-61.139	-13.917	1.00	16.09	A	N
ATOM	1643	CA	ASN	A	212	-0.705	-59.723	-13.783	1.00	17.44	A	C
ATOM	1644	CB	ASN	A	212	-0.759	-59.008	-15.168	1.00	15.91	A	C
ATOM	1645	CG	ASN	A	212	0.176	-59.639	-16.156	1.00	18.08	A	C
ATOM	1646	OD1	ASN	A	212	1.287	-60.089	-15.768	1.00	20.31	A	O
ATOM	1647	ND2	ASN	A	212	-0.239	-59.719	-17.437	1.00	13.44	A	N
ATOM	1648	C	ASN	A	212	-1.638	-58.995	-12.839	1.00	18.72	A	C
ATOM	1649	O	ASN	A	212	-1.699	-57.779	-12.907	1.00	20.55	A	O
ATOM	1650	N	TYR	A	213	-2.417	-59.718	-12.041	1.00	20.14	A	N
ATOM	1651	CA	TYR	A	213	-3.203	-59.181	-10.941	1.00	22.18	A	C
ATOM	1652	CB	TYR	A	213	-3.678	-60.382	-10.076	1.00	21.74	A	C
ATOM	1653	CG	TYR	A	213	-4.569	-60.001	-8.895	1.00	22.28	A	C
ATOM	1654	CD1	TYR	A	213	-5.960	-60.034	-9.009	1.00	21.52	A	C
ATOM	1655	CE1	TYR	A	213	-6.771	-59.682	-7.945	1.00	25.23	A	C
ATOM	1656	CZ	TYR	A	213	-6.199	-59.285	-6.716	1.00	24.59	A	C
ATOM	1657	OH	TYR	A	213	-7.033	-58.937	-5.676	1.00	25.57	A	O
ATOM	1658	CE2	TYR	A	213	-4.841	-59.229	-6.572	1.00	20.07	A	C
ATOM	1659	CD2	TYR	A	213	-4.020	-59.585	-7.679	1.00	23.48	A	C
ATOM	1660	C	TYR	A	213	-2.325	-58.231	-10.096	1.00	23.86	A	C
ATOM	1661	O	TYR	A	213	-1.247	-58.629	-9.696	1.00	24.04	A	O
ATOM	1662	N	LYS	A	214	-2.769	-56.999	-9.862	1.00	26.34	A	N
ATOM	1663	CA	LYS	A	214	-1.988	-55.999	-9.139	1.00	29.23	A	C
ATOM	1664	CB	LYS	A	214	-2.379	-54.571	-9.560	1.00	28.88	A	C
ATOM	1665	CG	LYS	A	214	-1.891	-54.173	-10.948	1.00	34.77	A	C
ATOM	1666	CD	LYS	A	214	-0.472	-54.771	-11.307	1.00	42.59	A	C
ATOM	1667	CE	LYS	A	214	0.018	-54.429	-12.759	1.00	46.77	A	C
ATOM	1668	NZ	LYS	A	214	-0.563	-55.320	-13.814	1.00	44.75	A	N
ATOM	1669	C	LYS	A	214	-2.153	-56.159	-7.638	1.00	30.36	A	C
ATOM	1670	O	LYS	A	214	-3.239	-55.937	-7.112	1.00	29.56	A	O
ATOM	1671	N	ASN	A	215	-1.087	-56.456	-6.949	1.00	32.59	A	N
ATOM	1672	CA	ASN	A	215	-1.146	-56.618	-5.534	1.00	35.97	A	C

ATOM	1673	CB	ASN	A	215	-0.024	-57.504	-5.121	1.00	37.03	A	C
ATOM	1674	CG	ASN	A	215	-0.447	-58.524	-4.182	1.00	45.30	A	C
ATOM	1675	OD1	ASN	A	215	-1.581	-58.963	-4.202	1.00	55.68	A	O
ATOM	1676	ND2	ASN	A	215	0.460	-58.920	-3.309	1.00	48.95	A	N
ATOM	1677	C	ASN	A	215	-1.097	-55.333	-4.736	1.00	35.60	A	C
ATOM	1678	O	ASN	A	215	-0.160	-55.071	-4.071	1.00	37.05	A	O
ATOM	1679	N	LEU	A	216	-2.142	-54.545	-4.803	1.00	35.58	A	N
ATOM	1680	CA	LEU	A	216	-2.245	-53.342	-4.006	1.00	34.88	A	C
ATOM	1681	CB	LEU	A	216	-3.192	-52.367	-4.683	1.00	33.33	A	C
ATOM	1682	CG	LEU	A	216	-2.645	-51.966	-6.042	1.00	33.49	A	C
ATOM	1683	CD1	LEU	A	216	-1.328	-51.060	-5.941	1.00	30.51	A	C
ATOM	1684	CD2	LEU	A	216	-3.737	-51.333	-6.956	1.00	30.71	A	C
ATOM	1685	C	LEU	A	216	-2.672	-53.627	-2.544	1.00	35.63	A	C
ATOM	1686	O	LEU	A	216	-3.253	-54.695	-2.238	1.00	34.93	A	O
ATOM	1687	N	PRO	A	217	-2.313	-52.703	-1.617	1.00	36.04	A	N
ATOM	1688	CA	PRO	A	217	-2.773	-52.946	-0.251	1.00	34.97	A	C
ATOM	1689	CB	PRO	A	217	-1.826	-52.085	0.598	1.00	34.61	A	C
ATOM	1690	CG	PRO	A	217	-1.400	-50.968	-0.374	1.00	36.58	A	C
ATOM	1691	CD	PRO	A	217	-1.221	-51.699	-1.661	1.00	36.55	A	C
ATOM	1692	C	PRO	A	217	-4.268	-52.572	-0.092	1.00	34.04	A	C
ATOM	1693	O	PRO	A	217	-4.858	-51.753	-0.843	1.00	33.03	A	O
ATOM	1694	N	ASN	A	218	-4.876	-53.226	0.879	1.00	32.61	A	N
ATOM	1695	CA	ASN	A	218	-6.270	-53.043	1.126	1.00	31.31	A	C
ATOM	1696	CB	ASN	A	218	-6.832	-54.318	1.763	1.00	29.93	A	C
ATOM	1697	CG	ASN	A	218	-8.318	-54.301	1.829	1.00	27.40	A	C
ATOM	1698	OD1	ASN	A	218	-8.947	-53.358	1.320	1.00	26.18	A	O
ATOM	1699	ND2	ASN	A	218	-8.911	-55.309	2.494	1.00	19.83	A	N
ATOM	1700	C	ASN	A	218	-6.520	-51.815	1.987	1.00	31.62	A	C
ATOM	1701	O	ASN	A	218	-6.790	-51.939	3.153	1.00	31.01	A	O
ATOM	1702	N	THR	A	219	-6.450	-50.630	1.382	1.00	32.99	A	N
ATOM	1703	CA	THR	A	219	-6.485	-49.327	2.093	1.00	33.63	A	C
ATOM	1704	CB	THR	A	219	-5.053	-48.809	2.427	1.00	34.29	A	C
ATOM	1705	OG1	THR	A	219	-4.364	-48.497	1.191	1.00	36.98	A	O
ATOM	1706	CG2	THR	A	219	-4.243	-49.832	3.250	1.00	33.05	A	C
ATOM	1707	C	THR	A	219	-7.013	-48.315	1.104	1.00	33.34	A	C
ATOM	1708	O	THR	A	219	-6.959	-48.567	-0.089	1.00	33.10	A	O
ATOM	1709	N	PRO	A	220	-7.484	-47.146	1.562	1.00	33.55	A	N
ATOM	1710	CA	PRO	A	220	-7.957	-46.213	0.490	1.00	34.11	A	C
ATOM	1711	CB	PRO	A	220	-8.394	-44.943	1.263	1.00	33.67	A	C
ATOM	1712	CG	PRO	A	220	-8.401	-45.295	2.659	1.00	32.53	A	C
ATOM	1713	CD	PRO	A	220	-7.794	-46.666	2.911	1.00	32.53	A	C
ATOM	1714	C	PRO	A	220	-6.879	-45.880	-0.591	1.00	34.21	A	C
ATOM	1715	O	PRO	A	220	-7.205	-45.756	-1.779	1.00	34.70	A	O
ATOM	1716	N	ALA	A	221	-5.621	-45.743	-0.178	1.00	33.57	A	N
ATOM	1717	CA	ALA	A	221	-4.528	-45.392	-1.112	1.00	33.92	A	C
ATOM	1718	CB	ALA	A	221	-3.157	-45.124	-0.344	1.00	33.52	A	C
ATOM	1719	C	ALA	A	221	-4.353	-46.519	-2.148	1.00	33.79	A	C
ATOM	1720	O	ALA	A	221	-4.193	-46.233	-3.326	1.00	35.18	A	O
ATOM	1721	N	GLY	A	222	-4.375	-47.779	-1.694	1.00	32.11	A	N
ATOM	1722	CA	GLY	A	222	-4.400	-48.959	-2.550	1.00	30.09	A	C
ATOM	1723	C	GLY	A	222	-5.687	-49.271	-3.346	1.00	29.61	A	C
ATOM	1724	O	GLY	A	222	-5.760	-50.308	-4.010	1.00	28.33	A	O
ATOM	1725	N	ASP	A	223	-6.692	-48.385	-3.349	1.00	28.45	A	N
ATOM	1726	CA	ASP	A	223	-7.980	-48.764	-4.003	1.00	28.35	A	C
ATOM	1727	CB	ASP	A	223	-7.787	-48.802	-5.520	1.00	27.61	A	C
ATOM	1728	CG	ASP	A	223	-9.098	-48.814	-6.281	1.00	30.68	A	C
ATOM	1729	OD1	ASP	A	223	-9.101	-49.747	-7.448	1.00	32.09	A	O
ATOM	1730	OD2	ASP	A	223	-10.127	-48.359	-5.724	1.00	36.19	A	O
ATOM	1731	C	ASP	A	223	-8.530	-50.124	-3.459	1.00	27.02	A	C
ATOM	1732	O	ASP	A	223	-8.979	-51.018	-4.195	1.00	25.89	A	O
ATOM	1733	N	TYR	A	224	-8.429	-50.276	-2.148	1.00	26.54	A	N
ATOM	1734	CA	TYR	A	224	-8.894	-51.485	-1.451	1.00	26.72	A	C
ATOM	1735	CB	TYR	A	224	-10.425	-51.446	-1.256	1.00	25.59	A	C
ATOM	1736	CG	TYR	A	224	-10.803	-50.163	-0.604	1.00	25.61	A	C
ATOM	1737	CD1	TYR	A	224	-10.450	-49.932	0.719	1.00	26.00	A	C
ATOM	1738	CE1	TYR	A	224	-10.759	-48.717	1.364	1.00	26.61	A	C
ATOM	1739	CZ	TYR	A	224	-11.426	-47.718	0.670	1.00	28.65	A	C
ATOM	1740	OH	TYR	A	224	-11.695	-46.564	1.364	1.00	31.55	A	O
ATOM	1741	CE2	TYR	A	224	-11.778	-47.884	-0.680	1.00	24.77	A	C
ATOM	1742	CD2	TYR	A	224	-11.448	-49.132	-1.315	1.00	26.18	A	C
ATOM	1743	C	TYR	A	224	-8.455	-52.742	-2.151	1.00	26.55	A	C
ATOM	1744	O	TYR	A	224	-9.255	-53.616	-2.386	1.00	27.97	A	O
ATOM	1745	N	GLY	A	225	-7.174	-52.825	-2.484	1.00	26.70	A	N
ATOM	1746	CA	GLY	A	225	-6.604	-54.038	-3.046	1.00	24.99	A	C
ATOM	1747	C	GLY	A	225	-6.686	-54.032	-4.576	1.00	24.95	A	C
ATOM	1748	O	GLY	A	225	-6.602	-55.087	-5.173	1.00	25.97	A	O
ATOM	1749	N	GLY	A	226	-6.881	-52.879	-5.206	1.00	22.96	A	N
ATOM	1750	CA	GLY	A	226	-6.876	-52.794	-6.658	1.00	23.27	A	C
ATOM	1751	C	GLY	A	226	-8.208	-53.065	-7.380	1.00	23.87	A	C

ATOM	1752	O	GLY	A	226	-8.258	-53.513	-8.540	1.00	24.79	A	O
ATOM	1753	N	VAL	A	227	-9.290	-52.745	-6.710	1.00	23.04	A	N
ATOM	1754	CA	VAL	A	227	-10.625	-53.162	-7.073	1.00	22.69	A	C
ATOM	1755	CB	VAL	A	227	-11.553	-52.701	-5.895	1.00	23.09	A	C
ATOM	1756	CG1	VAL	A	227	-12.761	-52.005	-6.310	1.00	20.90	A	C
ATOM	1757	CG2	VAL	A	227	-11.769	-53.815	-4.873	1.00	22.17	A	C
ATOM	1758	C	VAL	A	227	-11.033	-52.668	-8.467	1.00	23.44	A	C
ATOM	1759	O	VAL	A	227	-11.670	-53.398	-9.206	1.00	23.58	A	O
ATOM	1760	N	HIS	A	228	-10.608	-51.461	-8.843	1.00	23.13	A	N
ATOM	1761	CA	HIS	A	228	-10.921	-50.876	-10.133	1.00	23.87	A	C
ATOM	1762	CB	HIS	A	228	-10.907	-49.340	-10.010	1.00	24.16	A	C
ATOM	1763	CG	HIS	A	228	-12.028	-48.829	-9.173	1.00	29.12	A	C
ATOM	1764	ND1	HIS	A	228	-11.909	-48.651	-7.803	1.00	27.92	A	N
ATOM	1765	CE1	HIS	A	228	-13.076	-48.251	-7.325	1.00	29.37	A	C
ATOM	1766	NE2	HIS	A	228	-13.939	-48.169	-8.327	1.00	29.73	A	N
ATOM	1767	CD2	HIS	A	228	-13.315	-48.522	-9.498	1.00	26.55	A	C
ATOM	1768	C	HIS	A	228	-9.905	-51.230	-11.202	1.00	23.76	A	C
ATOM	1769	O	HIS	A	228	-10.149	-50.923	-12.372	1.00	23.21	A	O
ATOM	1770	N	THR	A	229	-8.734	-51.751	-10.819	1.00	22.54	A	N
ATOM	1771	CA	THR	A	229	-7.830	-52.122	-11.846	1.00	23.69	A	C
ATOM	1772	CB	THR	A	229	-6.389	-51.542	-11.723	1.00	25.20	A	C
ATOM	1773	OG1	THR	A	229	-5.400	-52.578	-11.619	1.00	28.21	A	O
ATOM	1774	CG2	THR	A	229	-6.279	-50.571	-10.632	1.00	24.20	A	C
ATOM	1775	C	THR	A	229	-7.947	-53.613	-12.134	1.00	23.03	A	C
ATOM	1776	O	THR	A	229	-8.152	-53.971	-13.277	1.00	22.94	A	O
ATOM	1777	N	ASN	A	230	-7.940	-54.455	-11.100	1.00	22.15	A	N
ATOM	1778	CA	ASN	A	230	-8.058	-55.904	-11.271	1.00	21.10	A	C
ATOM	1779	CB	ASN	A	230	-7.726	-56.621	-9.992	1.00	19.61	A	C
ATOM	1780	CG	ASN	A	230	-6.306	-56.361	-9.574	1.00	22.93	A	C
ATOM	1781	OD1	ASN	A	230	-5.397	-56.225	-10.416	1.00	25.85	A	O
ATOM	1782	ND2	ASN	A	230	-6.084	-56.287	-8.289	1.00	24.86	A	N
ATOM	1783	C	ASN	A	230	-9.353	-56.449	-11.870	1.00	20.93	A	C
ATOM	1784	O	ASN	A	230	-9.417	-57.628	-12.232	1.00	21.10	A	O
ATOM	1785	N	SER	A	231	-10.353	-55.601	-12.040	1.00	19.41	A	N
ATOM	1786	CA	SER	A	231	-11.594	-56.083	-12.603	1.00	19.21	A	C
ATOM	1787	CB	SER	A	231	-12.638	-54.982	-12.525	1.00	19.11	A	C
ATOM	1788	OG	SER	A	231	-12.088	-53.760	-13.008	1.00	20.47	A	O
ATOM	1789	C	SER	A	231	-11.362	-56.457	-14.053	1.00	19.87	A	C
ATOM	1790	O	SER	A	231	-12.201	-57.153	-14.688	1.00	22.04	A	O
ATOM	1791	N	GLY	A	232	-10.239	-56.000	-14.607	1.00	18.34	A	N
ATOM	1792	CA	GLY	A	232	-9.908	-56.335	-15.989	1.00	17.71	A	C
ATOM	1793	C	GLY	A	232	-9.746	-57.827	-16.229	1.00	17.62	A	C
ATOM	1794	O	GLY	A	232	-9.950	-58.302	-17.370	1.00	18.95	A	O
ATOM	1795	N	ILE	A	233	-9.433	-58.587	-15.169	1.00	16.84	A	N
ATOM	1796	CA	ILE	A	233	-9.226	-60.005	-15.346	1.00	15.89	A	C
ATOM	1797	CB	ILE	A	233	-8.370	-60.622	-14.217	1.00	16.51	A	C
ATOM	1798	CG1	ILE	A	233	-6.945	-60.055	-14.326	1.00	16.48	A	C
ATOM	1799	CD1	ILE	A	233	-6.233	-59.984	-12.977	1.00	17.92	A	C
ATOM	1800	CG2	ILE	A	233	-8.355	-62.182	-14.255	1.00	12.46	A	C
ATOM	1801	C	ILE	A	233	-10.523	-60.704	-15.579	1.00	16.17	A	C
ATOM	1802	O	ILE	A	233	-10.652	-61.379	-16.578	1.00	16.06	A	O
ATOM	1803	N	PRO	A	234	-11.503	-60.554	-14.674	1.00	16.91	A	N
ATOM	1804	CA	PRO	A	234	-12.803	-61.186	-14.959	1.00	16.88	A	C
ATOM	1805	CB	PRO	A	234	-13.588	-61.028	-13.663	1.00	17.47	A	C
ATOM	1806	CG	PRO	A	234	-12.874	-59.914	-12.897	1.00	17.44	A	C
ATOM	1807	CD	PRO	A	234	-11.413	-60.111	-13.282	1.00	16.92	A	C
ATOM	1808	C	PRO	A	234	-13.540	-60.494	-16.103	1.00	17.34	A	C
ATOM	1809	O	PRO	A	234	-14.370	-61.164	-16.763	1.00	17.89	A	O
ATOM	1810	N	ASN	A	235	-13.213	-59.230	-16.421	1.00	16.49	A	N
ATOM	1811	CA	ASN	A	235	-13.880	-58.615	-17.615	1.00	16.69	A	C
ATOM	1812	CB	ASN	A	235	-13.571	-57.150	-17.771	1.00	16.50	A	C
ATOM	1813	CG	ASN	A	235	-14.452	-56.279	-16.873	1.00	17.42	A	C
ATOM	1814	OD1	ASN	A	235	-15.346	-56.800	-16.177	1.00	16.73	A	O
ATOM	1815	ND2	ASN	A	235	-14.217	-54.948	-16.890	1.00	14.95	A	N
ATOM	1816	C	ASN	A	235	-13.467	-59.334	-18.849	1.00	17.37	A	C
ATOM	1817	O	ASN	A	235	-14.303	-59.692	-19.699	1.00	17.84	A	O
ATOM	1818	N	LYS	A	236	-12.159	-59.618	-18.927	1.00	17.83	A	N
ATOM	1819	CA	LYS	A	236	-11.641	-60.409	-20.021	1.00	16.30	A	C
ATOM	1820	CB	LYS	A	236	-10.143	-60.479	-19.933	1.00	16.14	A	C
ATOM	1821	CG	LYS	A	236	-9.520	-61.075	-21.131	1.00	13.45	A	C
ATOM	1822	CD	LYS	A	236	-9.677	-60.098	-22.339	1.00	19.20	A	C
ATOM	1823	CE	LYS	A	236	-8.565	-60.313	-23.457	1.00	24.27	A	C
ATOM	1824	NZ	LYS	A	236	-9.006	-61.451	-24.142	1.00	25.04	A	N
ATOM	1825	C	LYS	A	236	-12.232	-61.820	-20.059	1.00	17.07	A	C
ATOM	1826	O	LYS	A	236	-12.539	-62.351	-21.166	1.00	16.49	A	O
ATOM	1827	N	ALA	A	237	-12.404	-62.457	-18.887	1.00	16.60	A	N
ATOM	1828	CA	ALA	A	237	-12.982	-63.842	-18.917	1.00	15.77	A	C
ATOM	1829	CB	ALA	A	237	-12.995	-64.516	-17.535	1.00	13.36	A	C
ATOM	1830	C	ALA	A	237	-14.408	-63.738	-19.500	1.00	15.82	A	C

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ATOM   1831  O    ALA A 237     -14.820 -64.585 -20.294  1.00 15.89      A   O
ATOM   1832  N    ALA A 238     -15.122 -62.664 -19.148  1.00 14.96      A   N
ATOM   1833  CA   ALA A 238     -16.455 -62.493 -19.616  1.00 14.72      A   C
ATOM   1834  CB   ALA A 238     -17.103 -61.346 -18.843  1.00 15.43      A   C
ATOM   1835  C    ALA A 238     -16.482 -62.242 -21.142  1.00 14.97      A   C
ATOM   1836  O    ALA A 238     -17.297 -62.807 -21.866  1.00 15.12      A   O
ATOM   1837  N    TYR A 239     -15.574 -61.427 -21.633  1.00 15.89      A   N
ATOM   1838  CA   TYR A 239     -15.480 -61.143 -23.068  1.00 17.95      A   C
ATOM   1839  CB   TYR A 239     -14.410 -60.061 -23.352  1.00 18.82      A   C
ATOM   1840  CG   TYR A 239     -13.741 -60.115 -24.716  1.00 19.94      A   C
ATOM   1841  CD1  TYR A 239     -14.213 -59.292 -25.773  1.00 21.70      A   C
ATOM   1842  CE1  TYR A 239     -13.606 -59.300 -27.001  1.00 19.11      A   C
ATOM   1843  CZ   TYR A 239     -12.507 -60.154 -27.212  1.00 19.40      A   C
ATOM   1844  OH   TYR A 239     -11.959 -60.182 -28.450  1.00 20.23      A   O
ATOM   1845  CE2  TYR A 239     -12.015 -60.996 -26.200  1.00 16.51      A   C
ATOM   1846  CD2  TYR A 239     -12.640 -60.970 -24.960  1.00 17.39      A   C
ATOM   1847  C    TYR A 239     -15.126 -62.428 -23.754  1.00 19.06      A   C
ATOM   1848  O    TYR A 239     -15.687 -62.740 -24.802  1.00 21.37      A   O
ATOM   1849  N    ASN A 240     -14.229 -63.216 -23.175  1.00 18.84      A   N
ATOM   1850  CA   ASN A 240     -13.906 -64.501 -23.817  1.00 17.95      A   C
ATOM   1851  CB   ASN A 240     -12.789 -65.267 -23.125  1.00 17.02      A   C
ATOM   1852  CG   ASN A 240     -11.459 -64.609 -23.259  1.00 16.24      A   C
ATOM   1853  OD1  ASN A 240     -11.195 -63.810 -24.179  1.00 18.47      A   O
ATOM   1854  ND2  ASN A 240     -10.575 -64.965 -22.360  1.00 13.19      A   N
ATOM   1855  C    ASN A 240     -15.126 -65.358 -23.841  1.00 17.29      A   C
ATOM   1856  O    ASN A 240     -15.321 -66.126 -24.820  1.00 17.61      A   O
ATOM   1857  N    THR A 241     -15.960 -65.253 -22.803  1.00 16.40      A   N
ATOM   1858  CA   THR A 241     -17.108 -66.151 -22.843  1.00 16.12      A   C
ATOM   1859  CB   THR A 241     -17.653 -66.698 -21.463  1.00 16.69      A   C
ATOM   1860  OG1  THR A 241     -19.095 -66.600 -21.334  1.00 18.84      A   O
ATOM   1861  CG2  THR A 241     -16.875 -66.395 -20.334  1.00  5.55      A   C
ATOM   1862  C    THR A 241     -18.214 -65.732 -23.801  1.00 16.89      A   C
ATOM   1863  O    THR A 241     -18.763 -66.561 -24.531  1.00 17.17      A   O
ATOM   1864  N    ILE A 242     -18.475 -64.435 -23.829  1.00 16.90      A   N
ATOM   1865  CA   ILE A 242     -19.404 -63.861 -24.758  1.00 16.79      A   C
ATOM   1866  CB   ILE A 242     -19.520 -62.366 -24.521  1.00 17.11      A   C
ATOM   1867  CG1  ILE A 242     -20.083 -62.103 -23.129  1.00 13.60      A   C
ATOM   1868  CD1  ILE A 242     -19.869 -60.607 -22.655  1.00 17.41      A   C
ATOM   1869  CG2  ILE A 242     -20.358 -61.731 -25.622  1.00 13.89      A   C
ATOM   1870  C    ILE A 242     -19.070 -64.125 -26.232  1.00 17.41      A   C
ATOM   1871  O    ILE A 242     -19.983 -64.398 -27.051  1.00 17.82      A   O
ATOM   1872  N    THR A 243     -17.793 -64.041 -26.583  1.00 17.72      A   N
ATOM   1873  CA   THR A 243     -17.392 -64.274 -27.982  1.00 18.06      A   C
ATOM   1874  CB   THR A 243     -15.931 -63.774 -28.295  1.00 17.72      A   C
ATOM   1875  OG1  THR A 243     -15.019 -64.485 -27.481  1.00 17.90      A   O
ATOM   1876  CG2  THR A 243     -15.758 -62.235 -27.989  1.00 14.22      A   C
ATOM   1877  C    THR A 243     -17.501 -65.747 -28.366  1.00 20.21      A   C
ATOM   1878  O    THR A 243     -17.439 -66.072 -29.545  1.00 20.40      A   O
ATOM   1879  N    LYS A 244     -17.602 -66.650 -27.377  1.00 21.24      A   N
ATOM   1880  CA   LYS A 244     -17.624 -68.092 -27.650  1.00 21.87      A   C
ATOM   1881  CB   LYS A 244     -16.972 -68.936 -26.509  1.00 21.68      A   C
ATOM   1882  CG   LYS A 244     -15.628 -69.561 -26.846  1.00 27.48      A   C
ATOM   1883  CD   LYS A 244     -14.538 -69.622 -25.605  1.00 35.73      A   C
ATOM   1884  CE   LYS A 244     -13.219 -70.459 -25.990  1.00 38.68      A   C
ATOM   1885  NZ   LYS A 244     -13.444 -72.043 -26.349  1.00 33.65      A   N
ATOM   1886  C    LYS A 244     -19.073 -68.462 -27.796  1.00 21.76      A   C
ATOM   1887  O    LYS A 244     -19.422 -69.182 -28.721  1.00 21.38      A   O
ATOM   1888  N    ILE A 245     -19.918 -67.949 -26.884  1.00 21.31      A   N
ATOM   1889  CA   ILE A 245     -21.286 -68.479 -26.727  1.00 20.42      A   C
ATOM   1890  CB   ILE A 245     -21.520 -69.132 -25.334  1.00 20.57      A   C
ATOM   1891  CG1  ILE A 245     -21.640 -68.087 -24.227  1.00 18.94      A   C
ATOM   1892  CD1  ILE A 245     -22.106 -68.673 -22.920  1.00 17.00      A   C
ATOM   1893  CG2  ILE A 245     -20.419 -70.121 -24.984  1.00 20.88      A   C
ATOM   1894  C    ILE A 245     -22.407 -67.471 -27.044  1.00 20.62      A   C
ATOM   1895  O    ILE A 245     -23.554 -67.877 -27.233  1.00 21.25      A   O
ATOM   1896  N    GLY A 246     -22.076 -66.182 -27.160  1.00 19.44      A   N
ATOM   1897  CA   GLY A 246     -23.054 -65.205 -27.613  1.00 20.30      A   C
ATOM   1898  C    GLY A 246     -23.672 -64.532 -26.400  1.00 20.27      A   C
ATOM   1899  O    GLY A 246     -23.565 -65.092 -25.298  1.00 19.99      A   O
ATOM   1900  N    VAL A 247     -24.275 -63.348 -26.583  1.00 19.71      A   N
ATOM   1901  CA   VAL A 247     -24.808 -62.615 -25.468  1.00 20.66      A   C
ATOM   1902  CB   VAL A 247     -24.838 -61.037 -25.578  1.00 21.06      A   C
ATOM   1903  CG1  VAL A 247     -24.159 -60.493 -26.787  1.00 20.58      A   C
ATOM   1904  CG2  VAL A 247     -26.206 -60.431 -25.285  1.00 21.14      A   C
ATOM   1905  C    VAL A 247     -26.030 -63.180 -24.828  1.00 21.73      A   C
ATOM   1906  O    VAL A 247     -26.071 -63.239 -23.616  1.00 23.82      A   O
ATOM   1907  N    ASN A 248     -26.975 -63.695 -25.594  1.00 21.97      A   N
ATOM   1908  CA   ASN A 248     -28.169 -64.283 -25.003  1.00 23.02      A   C
ATOM   1909  CB   ASN A 248     -29.082 -64.962 -26.087  1.00 23.95      A   C
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ATOM   1910  CG   ASN A 248    -29.794 -63.932 -27.012  1.00 29.57      A    C
ATOM   1911  OD1  ASN A 248    -30.030 -64.209 -28.217  1.00 42.08      A    O
ATOM   1912  ND2  ASN A 248    -30.108 -62.755 -26.485  1.00 30.06      A    N
ATOM   1913  C    ASN A 248    -27.822 -65.295 -23.931  1.00 21.63      A    C
ATOM   1914  O    ASN A 248    -28.454 -65.298 -22.887  1.00 22.73      A    O
ATOM   1915  N    LYS A 249    -26.903 -66.221 -24.226  1.00 19.62      A    N
ATOM   1916  CA   LYS A 249    -26.557 -67.246 -23.272  1.00 18.79      A    C
ATOM   1917  CB   LYS A 249    -25.866 -68.406 -23.961  1.00 18.46      A    C
ATOM   1918  CG   LYS A 249    -26.757 -69.173 -24.902  1.00 19.59      A    C
ATOM   1919  CD   LYS A 249    -26.019 -70.451 -25.276  1.00 23.34      A    C
ATOM   1920  CE   LYS A 249    -26.834 -71.447 -26.132  1.00 23.02      A    C
ATOM   1921  NZ   LYS A 249    -25.958 -72.544 -26.700  1.00 24.35      A    N
ATOM   1922  C    LYS A 249    -25.692 -66.650 -22.150  1.00 18.27      A    C
ATOM   1923  O    LYS A 249    -25.931 -66.895 -20.964  1.00 18.67      A    O
ATOM   1924  N    ALA A 250    -24.728 -65.812 -22.511  1.00 18.25      A    N
ATOM   1925  CA   ALA A 250    -23.781 -65.288 -21.533  1.00 18.63      A    C
ATOM   1926  CB   ALA A 250    -22.612 -64.563 -22.178  1.00 16.62      A    C
ATOM   1927  C    ALA A 250    -24.490 -64.403 -20.508  1.00 19.22      A    C
ATOM   1928  O    ALA A 250    -24.128 -64.419 -19.319  1.00 19.71      A    O
ATOM   1929  N    GLU A 251    -25.513 -63.667 -20.930  1.00 19.16      A    N
ATOM   1930  CA   GLU A 251    -26.133 -62.772 -19.962  1.00 18.90      A    C
ATOM   1931  CB   GLU A 251    -26.864 -61.637 -20.610  1.00 17.73      A    C
ATOM   1932  CG   GLU A 251    -28.130 -62.056 -21.261  1.00 19.93      A    C
ATOM   1933  CD   GLU A 251    -28.718 -60.975 -22.197  1.00 20.89      A    C
ATOM   1934  OE1  GLU A 251    -28.226 -59.813 -22.204  1.00 16.53      A    O
ATOM   1935  OE2  GLU A 251    -29.671 -61.319 -22.925  1.00 22.41      A    O
ATOM   1936  C    GLU A 251    -27.018 -63.599 -18.987  1.00 19.67      A    C
ATOM   1937  O    GLU A 251    -27.126 -63.256 -17.811  1.00 18.68      A    O
ATOM   1938  N    GLN A 252    -27.591 -64.720 -19.450  1.00 18.71      A    N
ATOM   1939  CA   GLN A 252    -28.298 -65.580 -18.502  1.00 17.84      A    C
ATOM   1940  CB   GLN A 252    -29.096 -66.642 -19.250  1.00 17.39      A    C
ATOM   1941  CG   GLN A 252    -30.141 -66.048 -20.183  1.00 17.73      A    C
ATOM   1942  CD   GLN A 252    -31.265 -65.373 -19.427  1.00 23.25      A    C
ATOM   1943  OE1  GLN A 252    -31.531 -65.695 -18.253  1.00 24.70      A    O
ATOM   1944  NE2  GLN A 252    -31.902 -64.382 -20.068  1.00 21.47      A    N
ATOM   1945  C    GLN A 252    -27.316 -66.222 -17.496  1.00 18.12      A    C
ATOM   1946  O    GLN A 252    -27.576 -66.284 -16.292  1.00 18.70      A    O
ATOM   1947  N    ILE A 253    -26.167 -66.661 -17.983  1.00 17.81      A    N
ATOM   1948  CA   ILE A 253    -25.181 -67.356 -17.153  1.00 16.02      A    C
ATOM   1949  CB   ILE A 253    -24.079 -67.899 -18.093  1.00 15.55      A    C
ATOM   1950  CG1  ILE A 253    -24.629 -69.145 -18.832  1.00 15.24      A    C
ATOM   1951  CD1  ILE A 253    -23.758 -69.590 -20.013  1.00 15.45      A    C
ATOM   1952  CG2  ILE A 253    -22.759 -68.151 -17.353  1.00 11.68      A    C
ATOM   1953  C    ILE A 253    -24.659 -66.419 -16.024  1.00 16.62      A    C
ATOM   1954  O    ILE A 253    -24.695 -66.802 -14.828  1.00 15.86      A    O
ATOM   1955  N    TYR A 254    -24.283 -65.187 -16.423  1.00 16.13      A    N
ATOM   1956  CA   TYR A 254    -23.859 -64.098 -15.561  1.00 16.69      A    C
ATOM   1957  CB   TYR A 254    -23.426 -62.842 -16.387  1.00 15.61      A    C
ATOM   1958  CG   TYR A 254    -21.977 -62.980 -16.659  1.00 16.81      A    C
ATOM   1959  CD1  TYR A 254    -21.025 -62.441 -15.767  1.00 15.95      A    C
ATOM   1960  CE1  TYR A 254    -19.660 -62.726 -15.920  1.00 16.12      A    C
ATOM   1961  CZ   TYR A 254    -19.265 -63.540 -16.983  1.00 16.40      A    C
ATOM   1962  OH   TYR A 254    -17.933 -63.797 -17.199  1.00 15.02      A    O
ATOM   1963  CE2  TYR A 254    -20.194 -64.080 -17.871  1.00 15.41      A    C
ATOM   1964  CD2  TYR A 254    -21.529 -63.828 -17.700  1.00 13.73      A    C
ATOM   1965  C    TYR A 254    -24.888 -63.742 -14.479  1.00 18.24      A    C
ATOM   1966  O    TYR A 254    -24.514 -63.497 -13.318  1.00 18.18      A    O
ATOM   1967  N    TYR A 255    -26.160 -63.727 -14.863  1.00 18.34      A    N
ATOM   1968  CA   TYR A 255    -27.226 -63.290 -13.994  1.00 18.95      A    C
ATOM   1969  CB   TYR A 255    -28.510 -62.998 -14.805  1.00 17.25      A    C
ATOM   1970  CG   TYR A 255    -29.636 -62.557 -13.921  1.00 16.18      A    C
ATOM   1971  CD1  TYR A 255    -29.658 -61.279 -13.396  1.00 14.41      A    C
ATOM   1972  CE1  TYR A 255    -30.653 -60.865 -12.553  1.00 17.82      A    C
ATOM   1973  CZ   TYR A 255    -31.640 -61.758 -12.173  1.00 19.38      A    C
ATOM   1974  OH   TYR A 255    -32.618 -61.323 -11.341  1.00 20.14      A    O
ATOM   1975  CE2  TYR A 255    -31.642 -63.055 -12.644  1.00 18.82      A    C
ATOM   1976  CD2  TYR A 255    -30.620 -63.447 -13.526  1.00 17.58      A    C
ATOM   1977  C    TYR A 255    -27.441 -64.415 -12.940  1.00 20.84      A    C
ATOM   1978  O    TYR A 255    -27.610 -64.166 -11.724  1.00 20.60      A    O
ATOM   1979  N    ARG A 256    -27.438 -65.652 -13.423  1.00 21.16      A    N
ATOM   1980  CA   ARG A 256    -27.617 -66.775 -12.554  1.00 21.24      A    C
ATOM   1981  CB   ARG A 256    -27.617 -68.057 -13.402  1.00 20.10      A    C
ATOM   1982  CG   ARG A 256    -27.889 -69.310 -12.614  1.00 20.46      A    C
ATOM   1983  CD   ARG A 256    -28.636 -70.402 -13.386  1.00 22.52      A    C
ATOM   1984  NE   ARG A 256    -29.042 -71.451 -12.449  1.00 25.65      A    N
ATOM   1985  CZ   ARG A 256    -30.190 -71.448 -11.756  1.00 24.08      A    C
ATOM   1986  NH1  ARG A 256    -31.107 -70.479 -11.918  1.00 18.40      A    N
ATOM   1987  NH2  ARG A 256    -30.395 -72.414 -10.890  1.00 18.20      A    N
ATOM   1988  C    ARG A 256    -26.455 -66.748 -11.539  1.00 21.58      A    C
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ATOM   1989  O    ARG A 256     -26.664 -66.813 -10.345  1.00 23.44           A    O
ATOM   1990  N    ALA A 257     -25.226 -66.616 -12.003  1.00 21.29           A    N
ATOM   1991  CA   ALA A 257     -24.070 -66.707 -11.091  1.00 20.37           A    C
ATOM   1992  CB   ALA A 257     -22.807 -66.514 -11.846  1.00 18.20           A    C
ATOM   1993  C    ALA A 257     -24.154 -65.660  -9.994  1.00 20.56           A    C
ATOM   1994  O    ALA A 257     -23.861 -65.947  -8.809  1.00 20.92           A    O
ATOM   1995  N    LEU A 258     -24.536 -64.448 -10.406  1.00 20.17           A    N
ATOM   1996  CA   LEU A 258     -24.565 -63.313  -9.543  1.00 20.36           A    C
ATOM   1997  CB   LEU A 258     -24.787 -62.029 -10.315  1.00 19.99           A    C
ATOM   1998  CG   LEU A 258     -24.858 -60.759  -9.436  1.00 20.59           A    C
ATOM   1999  CD1  LEU A 258     -23.600 -60.617  -8.588  1.00 16.80           A    C
ATOM   2000  CD2  LEU A 258     -25.098 -59.441 -10.256  1.00 18.81           A    C
ATOM   2001  C    LEU A 258     -25.643 -63.493  -8.471  1.00 21.49           A    C
ATOM   2002  O    LEU A 258     -25.359 -63.253  -7.290  1.00 20.13           A    O
ATOM   2003  N    THR A 259     -26.814 -64.018  -8.861  1.00 21.25           A    N
ATOM   2004  CA   THR A 259     -27.954 -63.957  -8.010  1.00 22.14           A    C
ATOM   2005  CB   THR A 259     -29.256 -63.572  -8.813  1.00 22.89           A    C
ATOM   2006  OG1  THR A 259     -29.521 -64.589  -9.777  1.00 21.97           A    O
ATOM   2007  CG2  THR A 259     -29.109 -62.251  -9.512  1.00 21.29           A    C
ATOM   2008  C    THR A 259     -28.188 -65.287  -7.337  1.00 23.10           A    C
ATOM   2009  O    THR A 259     -29.019 -65.396  -6.446  1.00 22.98           A    O
ATOM   2010  N    VAL A 260     -27.497 -66.334  -7.749  1.00 23.70           A    N
ATOM   2011  CA   VAL A 260     -27.751 -67.645  -7.104  1.00 22.78           A    C
ATOM   2012  CB   VAL A 260     -28.299 -68.684  -8.114  1.00 22.81           A    C
ATOM   2013  CG1  VAL A 260     -28.313 -70.064  -7.524  1.00 21.92           A    C
ATOM   2014  CG2  VAL A 260     -29.712 -68.253  -8.612  1.00 22.11           A    C
ATOM   2015  C    VAL A 260     -26.561 -68.217  -6.345  1.00 22.91           A    C
ATOM   2016  O    VAL A 260     -26.741 -68.754  -5.252  1.00 23.99           A    O
ATOM   2017  N    TYR A 261     -25.366 -68.069  -6.897  1.00 21.81           A    N
ATOM   2018  CA   TYR A 261     -24.181 -68.768  -6.417  1.00 21.43           A    C
ATOM   2019  CB   TYR A 261     -23.470 -69.511  -7.565  1.00 20.42           A    C
ATOM   2020  CG   TYR A 261     -24.256 -70.683  -8.061  1.00 19.92           A    C
ATOM   2021  CD1  TYR A 261     -24.485 -71.807  -7.226  1.00 20.08           A    C
ATOM   2022  CE1  TYR A 261     -25.248 -72.907  -7.649  1.00 19.11           A    C
ATOM   2023  CZ   TYR A 261     -25.785 -72.870  -8.926  1.00 23.20           A    C
ATOM   2024  OH   TYR A 261     -26.510 -73.952  -9.382  1.00 21.60           A    O
ATOM   2025  CE2  TYR A 261     -25.539 -71.750  -9.788  1.00 18.76           A    C
ATOM   2026  CD2  TYR A 261     -24.775 -70.695  -9.342  1.00 17.58           A    C
ATOM   2027  C    TYR A 261     -23.165 -67.922  -5.704  1.00 21.41           A    C
ATOM   2028  O    TYR A 261     -22.458 -68.423  -4.888  1.00 23.70           A    O
ATOM   2029  N    LEU A 262     -23.052 -66.646  -6.011  1.00 21.84           A    N
ATOM   2030  CA   LEU A 262     -21.933 -65.876  -5.498  1.00 20.81           A    C
ATOM   2031  CB   LEU A 262     -21.499 -64.783  -6.525  1.00 20.64           A    C
ATOM   2032  CG   LEU A 262     -20.712 -65.319  -7.777  1.00 17.72           A    C
ATOM   2033  CD1  LEU A 262     -20.347 -64.218  -8.742  1.00 15.44           A    C
ATOM   2034  CD2  LEU A 262     -19.485 -66.126  -7.488  1.00 13.13           A    C
ATOM   2035  C    LEU A 262     -22.211 -65.361  -4.075  1.00 21.67           A    C
ATOM   2036  O    LEU A 262     -23.357 -65.179  -3.681  1.00 21.61           A    O
ATOM   2037  N    THR A 263     -21.153 -65.179  -3.288  1.00 22.08           A    N
ATOM   2038  CA   THR A 263     -21.296 -64.852  -1.855  1.00 22.85           A    C
ATOM   2039  CB   THR A 263     -20.821 -66.011  -0.975  1.00 22.90           A    C
ATOM   2040  OG1  THR A 263     -19.435 -66.202  -1.246  1.00 24.49           A    O
ATOM   2041  CG2  THR A 263     -21.591 -67.324  -1.303  1.00 20.75           A    C
ATOM   2042  C    THR A 263     -20.430 -63.596  -1.581  1.00 23.07           A    C
ATOM   2043  O    THR A 263     -19.704 -63.163  -2.461  1.00 23.16           A    O
ATOM   2044  N    PRO A 264     -20.524 -62.984  -0.381  1.00 22.93           A    N
ATOM   2045  CA   PRO A 264     -19.713 -61.734  -0.268  1.00 21.80           A    C
ATOM   2046  CB   PRO A 264     -20.013 -61.259   1.168  1.00 20.85           A    C
ATOM   2047  CG   PRO A 264     -21.494 -61.677   1.307  1.00 20.96           A    C
ATOM   2048  CD   PRO A 264     -21.548 -63.073   0.686  1.00 21.37           A    C
ATOM   2049  C    PRO A 264     -18.219 -61.927  -0.449  1.00 21.95           A    C
ATOM   2050  O    PRO A 264     -17.527 -60.980  -0.854  1.00 21.74           A    O
ATOM   2051  N    SER A 265     -17.689 -63.107  -0.155  1.00 21.51           A    N
ATOM   2052  CA   SER A 265     -16.245 -63.202  -0.203  1.00 22.77           A    C
ATOM   2053  CB   SER A 265     -15.708 -63.723   1.131  1.00 23.22           A    C
ATOM   2054  OG   SER A 265     -16.294 -64.984   1.338  1.00 27.76           A    O
ATOM   2055  C    SER A 265     -15.714 -64.054  -1.385  1.00 22.08           A    C
ATOM   2056  O    SER A 265     -14.572 -64.565  -1.337  1.00 21.37           A    O
ATOM   2057  N    SER A 266     -16.554 -64.203  -2.402  1.00 21.31           A    N
ATOM   2058  CA   SER A 266     -16.239 -64.941  -3.615  1.00 21.74           A    C
ATOM   2059  CB   SER A 266     -17.390 -64.849  -4.624  1.00 20.96           A    C
ATOM   2060  OG   SER A 266     -18.465 -65.654  -4.203  1.00 23.84           A    O
ATOM   2061  C    SER A 266     -14.949 -64.428  -4.260  1.00 21.37           A    C
ATOM   2062  O    SER A 266     -14.822 -63.246  -4.543  1.00 21.41           A    O
ATOM   2063  N    THR A 267     -13.993 -65.334  -4.447  1.00 19.86           A    N
ATOM   2064  CA   THR A 267     -12.823 -65.083  -5.229  1.00 18.51           A    C
ATOM   2065  CB   THR A 267     -11.802 -66.126  -4.784  1.00 19.66           A    C
ATOM   2066  OG1  THR A 267     -12.308 -67.447  -5.103  1.00 19.50           A    O
ATOM   2067  CG2  THR A 267     -11.539 -66.029  -3.234  1.00 17.09           A    C
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ATOM	2068	C	THR	A	267	-13.116	-65.295	-6.759	1.00	19.26	A	C
ATOM	2069	O	THR	A	267	-14.219	-65.810	-7.179	1.00	18.49	A	O
ATOM	2070	N	PHE	A	268	-12.140	-64.915	-7.597	1.00	18.40	A	N
ATOM	2071	CA	PHE	A	268	-12.115	-65.257	-9.035	1.00	17.62	A	C
ATOM	2072	CB	PHE	A	268	-10.766	-64.858	-9.626	1.00	17.69	A	C
ATOM	2073	CG	PHE	A	268	-10.559	-63.372	-9.729	1.00	15.59	A	C
ATOM	2074	CD1	PHE	A	268	-11.476	-62.467	-9.151	1.00	15.00	A	C
ATOM	2075	CE1	PHE	A	268	-11.320	-61.031	-9.284	1.00	14.29	A	C
ATOM	2076	CZ	PHE	A	268	-10.192	-60.528	-9.924	1.00	10.88	A	C
ATOM	2077	CE2	PHE	A	268	-9.224	-61.438	-10.418	1.00	16.00	A	C
ATOM	2078	CD2	PHE	A	268	-9.422	-62.870	-10.339	1.00	12.08	A	C
ATOM	2079	C	PHE	A	268	-12.310	-66.753	-9.254	1.00	18.07	A	C
ATOM	2080	O	PHE	A	268	-13.080	-67.204	-10.110	1.00	18.45	A	O
ATOM	2081	N	LYS	A	269	-11.604	-67.547	-8.493	1.00	18.34	A	N
ATOM	2082	CA	LYS	A	269	-11.833	-68.966	-8.606	1.00	20.19	A	C
ATOM	2083	CB	LYS	A	269	-10.924	-69.711	-7.635	1.00	20.91	A	C
ATOM	2084	CG	LYS	A	269	-10.228	-70.808	-8.311	1.00	24.31	A	C
ATOM	2085	CD	LYS	A	269	-8.941	-70.383	-8.907	1.00	23.96	A	C
ATOM	2086	CE	LYS	A	269	-8.774	-71.095	-10.196	1.00	24.14	A	C
ATOM	2087	NZ	LYS	A	269	-7.867	-72.214	-10.403	1.00	20.27	A	N
ATOM	2088	C	LYS	A	269	-13.302	-69.340	-8.328	1.00	20.16	A	C
ATOM	2089	O	LYS	A	269	-13.864	-70.209	-9.017	1.00	19.03	A	O
ATOM	2090	N	ASP	A	270	-13.942	-68.678	-7.342	1.00	20.01	A	N
ATOM	2091	CA	ASP	A	270	-15.339	-69.019	-7.061	1.00	19.27	A	C
ATOM	2092	CB	ASP	A	270	-15.851	-68.360	-5.764	1.00	18.81	A	C
ATOM	2093	CG	ASP	A	270	-15.108	-68.810	-4.541	1.00	21.89	A	C
ATOM	2094	OD1	ASP	A	270	-14.949	-70.010	-4.345	1.00	23.08	A	O
ATOM	2095	OD2	ASP	A	270	-14.667	-67.973	-3.738	1.00	25.68	A	O
ATOM	2096	C	ASP	A	270	-16.226	-68.573	-8.236	1.00	18.97	A	C
ATOM	2097	O	ASP	A	270	-17.210	-69.268	-8.563	1.00	20.23	A	O
ATOM	2098	N	ALA	A	271	-15.938	-67.397	-8.818	1.00	17.67	A	N
ATOM	2099	CA	ALA	A	271	-16.789	-66.827	-9.864	1.00	17.60	A	C
ATOM	2100	CB	ALA	A	271	-16.341	-65.408	-10.223	1.00	17.75	A	C
ATOM	2101	C	ALA	A	271	-16.719	-67.744	-11.122	1.00	18.15	A	C
ATOM	2102	O	ALA	A	271	-17.742	-68.120	-11.703	1.00	15.72	A	O
ATOM	2103	N	LYS	A	272	-15.491	-68.135	-11.474	1.00	17.71	A	N
ATOM	2104	CA	LYS	A	272	-15.259	-69.255	-12.392	1.00	18.86	A	C
ATOM	2105	CB	LYS	A	272	-13.796	-69.746	-12.312	1.00	18.42	A	C
ATOM	2106	CG	LYS	A	272	-13.494	-70.766	-13.309	1.00	17.22	A	C
ATOM	2107	CD	LYS	A	272	-12.161	-71.342	-13.061	1.00	15.91	A	C
ATOM	2108	CE	LYS	A	272	-11.739	-72.203	-14.227	1.00	14.80	A	C
ATOM	2109	NZ	LYS	A	272	-10.791	-73.326	-13.827	1.00	15.95	A	N
ATOM	2110	C	LYS	A	272	-16.188	-70.425	-12.144	1.00	18.82	A	C
ATOM	2111	O	LYS	A	272	-16.921	-70.829	-13.044	1.00	20.76	A	O
ATOM	2112	N	ALA	A	273	-16.160	-70.970	-10.941	1.00	18.23	A	N
ATOM	2113	CA	ALA	A	273	-16.998	-72.154	-10.623	1.00	19.13	A	C
ATOM	2114	CB	ALA	A	273	-16.647	-72.807	-9.192	1.00	16.62	A	C
ATOM	2115	C	ALA	A	273	-18.471	-71.778	-10.703	1.00	19.05	A	C
ATOM	2116	O	ALA	A	273	-19.307	-72.577	-11.169	1.00	20.74	A	O
ATOM	2117	N	ALA	A	274	-18.813	-70.577	-10.278	1.00	17.40	A	N
ATOM	2118	CA	ALA	A	274	-20.247	-70.246	-10.346	1.00	17.80	A	C
ATOM	2119	CB	ALA	A	274	-20.571	-69.077	-9.474	1.00	15.47	A	C
ATOM	2120	C	ALA	A	274	-20.745	-70.018	-11.791	1.00	17.78	A	C
ATOM	2121	O	ALA	A	274	-21.911	-70.319	-12.089	1.00	19.25	A	O
ATOM	2122	N	LEU	A	275	-19.896	-69.473	-12.671	1.00	16.84	A	N
ATOM	2123	CA	LEU	A	275	-20.292	-69.266	-14.053	1.00	17.21	A	C
ATOM	2124	CB	LEU	A	275	-19.396	-68.234	-14.730	1.00	16.62	A	C
ATOM	2125	CG	LEU	A	275	-19.504	-66.851	-14.062	1.00	16.84	A	C
ATOM	2126	CD1	LEU	A	275	-18.140	-66.091	-14.152	1.00	8.70	A	C
ATOM	2127	CD2	LEU	A	275	-20.648	-66.083	-14.679	1.00	14.58	A	C
ATOM	2128	C	LEU	A	275	-20.316	-70.642	-14.817	1.00	17.79	A	C
ATOM	2129	O	LEU	A	275	-21.207	-70.909	-15.632	1.00	16.56	A	O
ATOM	2130	N	ILE	A	276	-19.383	-71.542	-14.501	1.00	17.59	A	N
ATOM	2131	CA	ILE	A	276	-19.467	-72.859	-15.076	1.00	17.24	A	C
ATOM	2132	CB	ILE	A	276	-18.225	-73.656	-14.721	1.00	17.48	A	C
ATOM	2133	CG1	ILE	A	276	-17.017	-73.094	-15.440	1.00	13.52	A	C
ATOM	2134	CD1	ILE	A	276	-15.754	-73.748	-14.901	1.00	3.30	A	C
ATOM	2135	CG2	ILE	A	276	-18.402	-75.137	-15.034	1.00	17.60	A	C
ATOM	2136	C	ILE	A	276	-20.749	-73.565	-14.630	1.00	18.56	A	C
ATOM	2137	O	ILE	A	276	-21.492	-74.148	-15.449	1.00	19.97	A	O
ATOM	2138	N	GLN	A	277	-21.057	-73.506	-13.341	1.00	18.86	A	N
ATOM	2139	CA	GLN	A	277	-22.182	-74.275	-12.870	1.00	18.92	A	C
ATOM	2140	CB	GLN	A	277	-22.273	-74.263	-11.334	1.00	19.61	A	C
ATOM	2141	CG	GLN	A	277	-23.503	-74.991	-10.746	1.00	21.40	A	C
ATOM	2142	CD	GLN	A	277	-23.470	-76.498	-11.075	1.00	23.90	A	C
ATOM	2143	OE1	GLN	A	277	-22.447	-77.138	-10.868	1.00	25.80	A	O
ATOM	2144	NE2	GLN	A	277	-24.577	-77.045	-11.614	1.00	18.38	A	N
ATOM	2145	C	GLN	A	277	-23.427	-73.656	-13.481	1.00	19.42	A	C
ATOM	2146	O	GLN	A	277	-24.344	-74.397	-13.839	1.00	21.09	A	O

ATOM	2147	N	SER	A	278	-23.488	-72.323	-13.581	1.00	18.34	A	N
ATOM	2148	CA	SER	A	278	-24.692	-71.660	-14.126	1.00	18.25	A	C
ATOM	2149	CB	SER	A	278	-24.629	-70.154	-13.977	1.00	17.87	A	C
ATOM	2150	OG	SER	A	278	-24.503	-69.758	-12.604	1.00	16.50	A	O
ATOM	2151	C	SER	A	278	-24.939	-72.068	-15.578	1.00	19.54	A	C
ATOM	2152	O	SER	A	278	-26.084	-72.350	-15.980	1.00	20.47	A	O
ATOM	2153	N	ALA	A	279	-23.860	-72.206	-16.337	1.00	19.79	A	N
ATOM	2154	CA	ALA	A	279	-23.960	-72.760	-17.666	1.00	21.00	A	C
ATOM	2155	CB	ALA	A	279	-22.615	-72.646	-18.398	1.00	20.07	A	C
ATOM	2156	C	ALA	A	279	-24.516	-74.211	-17.734	1.00	21.50	A	C
ATOM	2157	O	ALA	A	279	-25.345	-74.508	-18.588	1.00	21.44	A	O
ATOM	2158	N	ARG	A	280	-24.019	-75.117	-16.894	1.00	22.65	A	N
ATOM	2159	CA	ARG	A	280	-24.598	-76.453	-16.826	1.00	23.31	A	C
ATOM	2160	CB	ARG	A	280	-23.966	-77.278	-15.740	1.00	23.89	A	C
ATOM	2161	CG	ARG	A	280	-22.545	-77.418	-15.885	1.00	26.68	A	C
ATOM	2162	CD	ARG	A	280	-22.073	-78.462	-14.928	1.00	35.43	A	C
ATOM	2163	NE	ARG	A	280	-21.148	-79.273	-15.687	1.00	44.20	A	N
ATOM	2164	CZ	ARG	A	280	-19.848	-79.206	-15.520	1.00	46.31	A	C
ATOM	2165	NH1	ARG	A	280	-19.351	-78.425	-14.558	1.00	44.34	A	N
ATOM	2166	NH2	ARG	A	280	-19.073	-79.932	-16.307	1.00	50.17	A	N
ATOM	2167	C	ARG	A	280	-26.050	-76.405	-16.479	1.00	23.26	A	C
ATOM	2168	O	ARG	A	280	-26.803	-77.133	-17.062	1.00	23.68	A	O
ATOM	2169	N	ASP	A	281	-26.446	-75.567	-15.519	1.00	23.26	A	N
ATOM	2170	CA	ASP	A	281	-27.850	-75.536	-15.101	1.00	23.49	A	C
ATOM	2171	CB	ASP	A	281	-28.145	-74.472	-14.012	1.00	24.21	A	C
ATOM	2172	CG	ASP	A	281	-27.444	-74.729	-12.668	1.00	26.18	A	C
ATOM	2173	OD1	ASP	A	281	-26.972	-75.873	-12.401	1.00	24.91	A	O
ATOM	2174	OD2	ASP	A	281	-27.406	-73.738	-11.864	1.00	26.85	A	O
ATOM	2175	C	ASP	A	281	-28.701	-75.177	-16.315	1.00	22.86	A	C
ATOM	2176	O	ASP	A	281	-29.726	-75.776	-16.535	1.00	21.44	A	O
ATOM	2177	N	LEU	A	282	-28.284	-74.155	-17.063	1.00	22.26	A	N
ATOM	2178	CA	LEU	A	282	-29.152	-73.538	-18.067	1.00	22.50	A	C
ATOM	2179	CB	LEU	A	282	-28.882	-72.041	-18.151	1.00	21.78	A	C
ATOM	2180	CG	LEU	A	282	-29.252	-71.174	-16.961	1.00	22.74	A	C
ATOM	2181	CD1	LEU	A	282	-28.603	-69.829	-17.165	1.00	19.04	A	C
ATOM	2182	CD2	LEU	A	282	-30.773	-71.069	-16.821	1.00	20.56	A	C
ATOM	2183	C	LEU	A	282	-29.018	-74.180	-19.462	1.00	22.63	A	C
ATOM	2184	O	LEU	A	282	-30.002	-74.340	-20.151	1.00	21.89	A	O
ATOM	2185	N	TYR	A	283	-27.809	-74.605	-19.842	1.00	22.88	A	N
ATOM	2186	CA	TYR	A	283	-27.545	-75.030	-21.212	1.00	22.90	A	C
ATOM	2187	CB	TYR	A	283	-26.845	-73.929	-22.020	1.00	21.85	A	C
ATOM	2188	CG	TYR	A	283	-27.559	-72.574	-21.968	1.00	21.84	A	C
ATOM	2189	CD1	TYR	A	283	-28.816	-72.417	-22.547	1.00	18.80	A	C
ATOM	2190	CE1	TYR	A	283	-29.461	-71.200	-22.491	1.00	20.76	A	C
ATOM	2191	CZ	TYR	A	283	-28.874	-70.092	-21.858	1.00	20.12	A	C
ATOM	2192	OH	TYR	A	283	-29.586	-68.908	-21.854	1.00	20.69	A	O
ATOM	2193	CE2	TYR	A	283	-27.652	-70.195	-21.253	1.00	15.68	A	C
ATOM	2194	CD2	TYR	A	283	-26.983	-71.454	-21.307	1.00	17.76	A	C
ATOM	2195	C	TYR	A	283	-26.777	-76.314	-21.367	1.00	23.64	A	C
ATOM	2196	O	TYR	A	283	-26.744	-76.821	-22.465	1.00	23.90	A	O
ATOM	2197	N	GLY	A	284	-26.149	-76.846	-20.308	1.00	24.18	A	N
ATOM	2198	CA	GLY	A	284	-25.490	-78.146	-20.441	1.00	23.74	A	C
ATOM	2199	C	GLY	A	284	-23.995	-78.012	-20.547	1.00	25.56	A	C
ATOM	2200	O	GLY	A	284	-23.429	-76.878	-20.400	1.00	26.07	A	O
ATOM	2201	N	SER	A	285	-23.367	-79.169	-20.765	1.00	25.64	A	N
ATOM	2202	CA	SER	A	285	-21.924	-79.403	-20.789	1.00	26.97	A	C
ATOM	2203	CB	SER	A	285	-21.644	-80.813	-21.289	1.00	27.65	A	C
ATOM	2204	OG	SER	A	285	-21.679	-81.599	-20.147	1.00	30.68	A	O
ATOM	2205	C	SER	A	285	-21.060	-78.586	-21.678	1.00	26.93	A	C
ATOM	2206	O	SER	A	285	-19.949	-78.197	-21.282	1.00	27.19	A	O
ATOM	2207	N	GLN	A	286	-21.517	-78.384	-22.892	1.00	26.76	A	N
ATOM	2208	CA	GLN	A	286	-20.648	-77.835	-23.874	1.00	28.08	A	C
ATOM	2209	CB	GLN	A	286	-21.265	-78.047	-25.242	1.00	30.00	A	C
ATOM	2210	CG	GLN	A	286	-20.317	-78.539	-26.290	1.00	39.99	A	C
ATOM	2211	CD	GLN	A	286	-21.093	-79.305	-27.400	1.00	52.85	A	C
ATOM	2212	OE1	GLN	A	286	-22.302	-79.063	-27.620	1.00	56.21	A	O
ATOM	2213	NE2	GLN	A	286	-20.401	-80.226	-28.097	1.00	54.74	A	N
ATOM	2214	C	GLN	A	286	-20.490	-76.349	-23.594	1.00	26.64	A	C
ATOM	2215	O	GLN	A	286	-19.363	-75.804	-23.701	1.00	26.48	A	O
ATOM	2216	N	ASP	A	287	-21.589	-75.686	-23.203	1.00	24.40	A	N
ATOM	2217	CA	ASP	A	287	-21.488	-74.240	-22.904	1.00	22.97	A	C
ATOM	2218	CB	ASP	A	287	-22.865	-73.495	-22.906	1.00	21.60	A	C
ATOM	2219	CG	ASP	A	287	-23.535	-73.501	-24.311	1.00	24.04	A	C
ATOM	2220	OD1	ASP	A	287	-24.782	-73.687	-24.383	1.00	27.03	A	O
ATOM	2221	OD2	ASP	A	287	-22.824	-73.346	-25.351	1.00	23.58	A	O
ATOM	2222	C	ASP	A	287	-20.686	-74.062	-21.631	1.00	21.52	A	C
ATOM	2223	O	ASP	A	287	-19.872	-73.146	-21.556	1.00	20.96	A	O
ATOM	2224	N	ALA	A	288	-20.869	-74.979	-20.663	1.00	21.28	A	N
ATOM	2225	CA	ALA	A	288	-19.968	-75.095	-19.491	1.00	20.85	A	C

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ATOM   2226  CB  ALA A 288   -20.373 -76.242 -18.555  1.00 20.98      A  C
ATOM   2227  C   ALA A 288   -18.502 -75.224 -19.849  1.00 20.23      A  C
ATOM   2228  O   ALA A 288   -17.687 -74.457 -19.337  1.00 23.40      A  O
ATOM   2229  N   ALA A 289   -18.134 -76.136 -20.728  1.00 18.74      A  N
ATOM   2230  CA  ALA A 289   -16.734 -76.188 -21.224  1.00 18.20      A  C
ATOM   2231  CB  ALA A 289   -16.517 -77.355 -22.253  1.00 15.30      A  C
ATOM   2232  C   ALA A 289   -16.224 -74.821 -21.797  1.00 18.09      A  C
ATOM   2233  O   ALA A 289   -15.079 -74.402 -21.525  1.00 19.17      A  O
ATOM   2234  N   SER A 290   -17.035 -74.145 -22.592  1.00 17.27      A  N
ATOM   2235  CA  SER A 290   -16.602 -72.866 -23.165  1.00 18.01      A  C
ATOM   2236  CB  SER A 290   -17.574 -72.332 -24.200  1.00 17.59      A  C
ATOM   2237  OG  SER A 290   -17.978 -73.398 -25.030  1.00 17.68      A  O
ATOM   2238  C   SER A 290   -16.430 -71.814 -22.096  1.00 17.84      A  C
ATOM   2239  O   SER A 290   -15.458 -71.040 -22.161  1.00 18.11      A  O
ATOM   2240  N   VAL A 291   -17.347 -71.766 -21.119  1.00 17.53      A  N
ATOM   2241  CA  VAL A 291   -17.137 -70.846 -19.979  1.00 16.01      A  C
ATOM   2242  CB  VAL A 291   -18.259 -70.906 -18.946  1.00 16.40      A  C
ATOM   2243  CG1 VAL A 291   -17.867 -70.159 -17.668  1.00 12.35      A  C
ATOM   2244  CG2 VAL A 291   -19.547 -70.364 -19.535  1.00 14.61      A  C
ATOM   2245  C   VAL A 291   -15.790 -71.192 -19.360  1.00 16.98      A  C
ATOM   2246  O   VAL A 291   -14.935 -70.295 -19.156  1.00 17.93      A  O
ATOM   2247  N   GLU A 292   -15.554 -72.485 -19.084  1.00 17.26      A  N
ATOM   2248  CA  GLU A 292   -14.285 -72.893 -18.404  1.00 17.43      A  C
ATOM   2249  CB  GLU A 292   -14.296 -74.410 -18.184  1.00 16.88      A  C
ATOM   2250  CG  GLU A 292   -13.056 -74.909 -17.514  1.00 18.64      A  C
ATOM   2251  CD  GLU A 292   -13.160 -76.349 -17.130  1.00 21.95      A  C
ATOM   2252  OE1 GLU A 292   -13.129 -77.179 -18.042  1.00 22.49      A  O
ATOM   2253  OE2 GLU A 292   -13.281 -76.658 -15.926  1.00 21.17      A  O
ATOM   2254  C   GLU A 292   -13.009 -72.459 -19.221  1.00 17.74      A  C
ATOM   2255  O   GLU A 292   -12.023 -71.872 -18.666  1.00 19.53      A  O
ATOM   2256  N   ALA A 293   -13.031 -72.732 -20.521  1.00 15.97      A  N
ATOM   2257  CA  ALA A 293   -11.959 -72.339 -21.435  1.00 16.10      A  C
ATOM   2258  CB  ALA A 293   -12.266 -72.836 -22.889  1.00 13.76      A  C
ATOM   2259  C   ALA A 293   -11.743 -70.814 -21.410  1.00 17.14      A  C
ATOM   2260  O   ALA A 293   -10.569 -70.319 -21.455  1.00 17.89      A  O
ATOM   2261  N   ALA A 294   -12.849 -70.063 -21.330  1.00 16.60      A  N
ATOM   2262  CA  ALA A 294   -12.746 -68.599 -21.268  1.00 17.10      A  C
ATOM   2263  CB  ALA A 294   -14.098 -67.948 -21.258  1.00 16.35      A  C
ATOM   2264  C   ALA A 294   -11.953 -68.177 -20.039  1.00 17.40      A  C
ATOM   2265  O   ALA A 294   -11.212 -67.221 -20.121  1.00 17.93      A  O
ATOM   2266  N   TRP A 295   -12.058 -68.906 -18.916  1.00 17.09      A  N
ATOM   2267  CA  TRP A 295   -11.301 -68.546 -17.702  1.00 16.03      A  C
ATOM   2268  CB  TRP A 295   -12.029 -69.018 -16.423  1.00 16.23      A  C
ATOM   2269  CG  TRP A 295   -13.219 -68.152 -16.073  1.00 13.59      A  C
ATOM   2270  CD1 TRP A 295   -14.511 -68.249 -16.584  1.00 12.53      A  C
ATOM   2271  NE1 TRP A 295   -15.301 -67.226 -16.047  1.00 16.35      A  N
ATOM   2272  CE2 TRP A 295   -14.543 -66.484 -15.161  1.00 14.53      A  C
ATOM   2273  CD2 TRP A 295   -13.226 -67.016 -15.169  1.00 12.86      A  C
ATOM   2274  CE3 TRP A 295   -12.249 -66.411 -14.357  1.00 12.83      A  C
ATOM   2275  CZ3 TRP A 295   -12.591 -65.298 -13.575  1.00 11.80      A  C
ATOM   2276  CH2 TRP A 295   -13.910 -64.782 -13.569  1.00 12.57      A  C
ATOM   2277  CZ2 TRP A 295   -14.894 -65.343 -14.376  1.00 15.73      A  C
ATOM   2278  C   TRP A 295    -9.895 -69.097 -17.803  1.00 17.18      A  C
ATOM   2279  O   TRP A 295    -8.914 -68.446 -17.386  1.00 18.22      A  O
ATOM   2280  N   ASN A 296    -9.749 -70.269 -18.417  1.00 16.56      A  N
ATOM   2281  CA  ASN A 296    -8.391 -70.769 -18.692  1.00 15.21      A  C
ATOM   2282  CB  ASN A 296    -8.457 -72.131 -19.424  1.00 14.65      A  C
ATOM   2283  CG  ASN A 296    -9.033 -73.285 -18.512  1.00 16.77      A  C
ATOM   2284  OD1 ASN A 296    -9.175 -73.141 -17.276  1.00 20.24      A  O
ATOM   2285  ND2 ASN A 296    -9.387 -74.380 -19.120  1.00 14.16      A  N
ATOM   2286  C   ASN A 296    -7.521 -69.729 -19.432  1.00 16.44      A  C
ATOM   2287  O   ASN A 296    -6.303 -69.529 -19.113  1.00 16.54      A  O
ATOM   2288  N   ALA A 297    -8.126 -69.035 -20.406  1.00 16.57      A  N
ATOM   2289  CA  ALA A 297    -7.355 -68.195 -21.309  1.00 16.69      A  C
ATOM   2290  CB  ALA A 297    -8.181 -67.747 -22.564  1.00 15.79      A  C
ATOM   2291  C   ALA A 297    -6.858 -66.990 -20.556  1.00 17.86      A  C
ATOM   2292  O   ALA A 297    -5.951 -66.356 -21.041  1.00 19.04      A  O
ATOM   2293  N   VAL A 298    -7.426 -66.663 -19.388  1.00 18.30      A  N
ATOM   2294  CA  VAL A 298    -6.891 -65.550 -18.595  1.00 19.09      A  C
ATOM   2295  CB  VAL A 298    -7.981 -64.544 -18.074  1.00 19.27      A  C
ATOM   2296  CG1 VAL A 298    -8.904 -64.123 -19.182  1.00 18.35      A  C
ATOM   2297  CG2 VAL A 298    -8.752 -65.155 -16.892  1.00 17.14      A  C
ATOM   2298  C   VAL A 298    -6.069 -66.035 -17.372  1.00 20.71      A  C
ATOM   2299  O   VAL A 298    -5.776 -65.201 -16.456  1.00 21.47      A  O
ATOM   2300  N   GLY A 299    -5.710 -67.337 -17.362  1.00 18.91      A  N
ATOM   2301  CA  GLY A 299    -4.856 -67.900 -16.345  1.00 18.24      A  C
ATOM   2302  C   GLY A 299    -5.536 -68.500 -15.113  1.00 19.14      A  C
ATOM   2303  O   GLY A 299    -4.903 -68.602 -14.071  1.00 19.70      A  O
ATOM   2304  N   LEU A 300    -6.801 -68.912 -15.215  1.00 19.37      A  N
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ATOM   2305  CA   LEU A 300      -7.579 -69.370 -14.049  1.00 19.59      A    C
ATOM   2306  CB   LEU A 300      -8.594 -68.309 -13.572  1.00 18.80      A    C
ATOM   2307  CG   LEU A 300      -8.010 -67.213 -12.664  1.00 20.17      A    C
ATOM   2308  CD1  LEU A 300      -8.820 -65.889 -12.682  1.00 14.68      A    C
ATOM   2309  CD2  LEU A 300      -7.730 -67.747 -11.152  1.00 15.80      A    C
ATOM   2310  C    LEU A 300      -8.321 -70.657 -14.342  1.00 20.21      A    C
ATOM   2311  O    LEU A 300      -8.607 -70.984 -15.546  1.00 19.40      A    O
ATOM   2312  OXT  LEU A 300      -8.659 -71.329 -13.331  1.00 19.54      A    O
ATOM   2313  ZN   ZN  A 325     -18.474 -49.581 -10.110  1.00 26.57      A    ZN
ATOM   2314  CA   CA  A 326     -20.141 -49.094 -24.614  1.00 21.37      A    CA
ATOM   2315  CA   CA  A 327     -21.620 -47.425 -27.379  1.00 13.56      A    CA
ATOM   2316  O8   BTB A 401     -25.754 -64.686  -4.944  1.00 33.84           O
ATOM   2317  C8   BTB A 401     -27.177 -64.941  -4.724  1.00 49.20           C
ATOM   2318  C7   BTB A 401     -27.961 -64.219  -3.595  1.00 48.31           C
ATOM   2319  N    BTB A 401     -28.068 -65.122  -2.424  1.00 50.93           N
ATOM   2320  C5   BTB A 401     -29.458 -65.487  -2.106  1.00 53.08           C
ATOM   2321  C6   BTB A 401     -30.027 -64.461  -1.056  1.00 54.37           C
ATOM   2322  O6   BTB A 401     -29.100 -63.396  -0.674  1.00 51.50           O
ATOM   2323  C2   BTB A 401     -26.911 -65.600  -1.545  1.00 50.97           C
ATOM   2324  C4   BTB A 401     -25.924 -64.439  -1.315  1.00 49.99           C
ATOM   2325  O4   BTB A 401     -25.290 -64.470  -0.033  1.00 50.81           O
ATOM   2326  C3   BTB A 401     -26.124 -66.761  -2.205  1.00 49.77           C
ATOM   2327  O3   BTB A 401     -25.471 -67.594  -1.239  1.00 49.48           O
ATOM   2328  C1   BTB A 401     -27.471 -66.012  -0.165  1.00 51.74           C
ATOM   2329  O1   BTB A 401     -28.588 -66.951  -0.241  1.00 51.00           O
ATOM   2330  O    HOH C   2      -2.711 -67.592 -19.132  1.00 29.87           O
ATOM   2331  O    HOH C   3     -16.211 -62.592 -15.497  1.00 13.75           O
ATOM   2332  O    HOH C   5     -13.080 -72.566  -9.617  1.00 25.61           O
ATOM   2333  O    HOH C   6     -12.806 -53.340 -28.915  1.00 18.86           O
ATOM   2334  O    HOH C   7      -2.312 -58.186 -18.387  1.00 21.39           O
ATOM   2335  O    HOH C   8     -17.631 -66.593 -17.691  1.00 14.22           O
ATOM   2336  O    HOH C   9     -35.936 -48.250  -3.867  1.00 19.09           O
ATOM   2337  O    HOH C  10     -20.260 -73.864 -26.521  1.00 21.53           O
ATOM   2338  O    HOH C  11      -7.569 -64.056 -22.670  1.00 16.33           O
ATOM   2339  O    HOH C  12     -41.422 -26.102 -22.458  1.00 36.88           O
ATOM   2340  O    HOH C  13      -2.583 -67.718 -13.855  1.00 19.81           O
ATOM   2341  O    HOH C  14     -42.378 -48.644 -20.422  1.00 24.29           O
ATOM   2342  O    HOH C  15     -40.574 -61.262 -18.180  1.00 38.06           O
ATOM   2343  O    HOH C  16     -30.259 -66.532 -15.709  1.00 21.74           O
ATOM   2344  O    HOH C  17     -28.285 -38.912 -27.320  1.00 17.16           O
ATOM   2345  O    HOH C  18     -32.187 -62.257  -7.228  1.00 16.83           O
ATOM   2346  O    HOH C  19     -25.078 -44.158 -23.968  1.00 14.65           O
ATOM   2347  O    HOH C  20     -23.895 -46.936 -23.545  1.00 16.14           O
ATOM   2348  O    HOH C  21     -41.667 -48.219  -7.746  1.00 34.18           O
ATOM   2349  O    HOH C  22     -40.068 -48.275  -3.726  1.00 19.95           O
ATOM   2350  O    HOH C  23     -35.010 -62.824 -11.601  1.00 26.66           O
ATOM   2351  O    HOH C  24     -13.021 -76.519 -21.028  1.00 30.07           O
ATOM   2352  O    HOH C  25     -19.087 -36.433 -24.374  1.00 34.42           O
ATOM   2353  O    HOH C  26     -24.793 -80.040 -12.678  1.00 29.84           O
ATOM   2354  O    HOH C  27     -30.660 -63.583 -22.716  1.00 19.99           O
ATOM   2355  O    HOH C  28     -24.403 -76.833 -24.011  1.00 25.02           O
ATOM   2356  O    HOH C  29      -1.256 -55.688 -17.362  1.00 25.31           O
ATOM   2357  O    HOH C  30     -31.120 -63.745  -5.118  1.00 25.53           O
ATOM   2358  O    HOH C  31     -32.816 -71.675  -9.104  1.00 42.94           O
ATOM   2359  O    HOH C  32     -25.511 -47.418 -25.772  1.00 30.04           O
ATOM   2360  O    HOH C  33       2.080 -61.199  -7.018  1.00 32.19           O
ATOM   2361  O    HOH C  34     -10.798 -60.304   0.807  1.00 34.30           O
ATOM   2362  O    HOH C  35     -13.969 -52.276 -13.493  1.00 22.29           O
ATOM   2363  O    HOH C  36     -26.801 -37.860 -24.720  1.00 24.12           O
ATOM   2364  O    HOH C  37     -20.776 -45.215 -22.957  1.00 21.88           O
ATOM   2365  O    HOH C  38       1.055 -57.909 -10.764  1.00 16.66           O
ATOM   2366  O    HOH C  39     -32.697 -59.896  -4.934  1.00 23.95           O
ATOM   2367  O    HOH C  40     -33.179 -53.385 -12.401  1.00 27.60           O
ATOM   2368  O    HOH C  41      -7.976 -52.645 -29.054  1.00 32.74           O
ATOM   2369  O    HOH C  42     -24.307 -79.767 -24.391  1.00 35.33           O
ATOM   2370  O    HOH C  43     -38.839 -42.447 -20.245  1.00 21.37           O
ATOM   2371  O    HOH C  44     -52.198 -32.387 -13.024  1.00 34.97           O
ATOM   2372  O    HOH C  45     -33.718 -45.777  -6.287  1.00 21.53           O
ATOM   2373  O    HOH C  46      -5.504 -62.986 -21.066  1.00 33.17           O
ATOM   2374  O    HOH C  47     -18.734 -64.795   2.288  1.00 34.55           O
ATOM   2375  O    HOH C  48     -24.367 -38.933 -24.187  1.00 26.39           O
ATOM   2376  O    HOH C  49     -43.788 -47.175 -13.701  1.00 27.38           O
ATOM   2377  O    HOH C  50     -26.131 -66.593 -26.975  1.00 31.01           O
ATOM   2378  O    HOH C  51     -22.554 -53.372  -4.818  1.00 25.37           O
ATOM   2379  O    HOH C  52     -38.611 -43.353 -22.739  1.00 28.58           O
ATOM   2380  O    HOH C  53       1.781 -56.450  -8.391  1.00 20.44           O
ATOM   2381  O    HOH C  54      -9.763 -51.219 -19.497  1.00 21.78           O
ATOM   2382  O    HOH C  55     -35.947 -54.526 -13.693  1.00 29.02           O
ATOM   2383  O    HOH C  56     -34.353 -65.294 -14.056  1.00 32.29           O
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ATOM   2384  O   HOH C  57      0.430 -61.703  -8.963  1.00 31.79           O
ATOM   2385  O   HOH C  58    -46.066 -43.418 -20.148  1.00 39.75           O
ATOM   2386  O   HOH C  59     -9.719 -55.069 -28.478  1.00 22.91           O
ATOM   2387  O   HOH C  60    -11.594 -47.814 -26.606  1.00 28.37           O
ATOM   2388  O   HOH C  61    -27.425 -59.413  -0.115  1.00 30.47           O
ATOM   2389  O   HOH C  62    -25.237 -34.589 -13.754  1.00 25.20           O
ATOM   2390  O   HOH C  63    -24.889 -76.446 -26.846  1.00 39.30           O
ATOM   2391  O   HOH C  64    -28.189 -67.960 -28.520  1.00  9.69           O
ATOM   2392  O   HOH C  65      2.279 -57.488 -13.341  1.00 22.09           O
ATOM   2393  O   HOH C  66     -9.170 -66.952  -6.893  1.00 17.86           O
ATOM   2394  O   HOH C  67    -18.314 -47.411  -9.661  1.00 20.32           O
ATOM   2395  O   HOH C  68    -31.399 -68.090 -23.976  1.00 28.09           O
ATOM   2396  O   HOH C  69    -12.106 -51.680 -27.036  1.00 14.12           O
ATOM   2397  O   HOH C  70    -17.481 -60.702 -14.176  1.00 25.54           O
ATOM   2398  O   HOH C  71     -1.207 -68.518 -16.338  1.00 21.45           O
ATOM   2399  O   HOH C  72    -40.653 -60.453 -10.248  1.00 45.50           O
ATOM   2400  O   HOH C  73    -17.827 -46.310 -13.499  1.00 31.29           O
ATOM   2401  O   HOH C  74    -23.273 -80.385 -17.437  1.00 38.60           O
ATOM   2402  O   HOH C  75    -11.710 -54.235 -18.487  1.00 12.63           O
ATOM   2403  O   HOH C  76    -37.268 -63.184 -10.316  1.00 34.47           O
ATOM   2404  O   HOH C  77    -40.855 -53.336 -19.367  1.00 40.20           O
ATOM   2405  O   HOH C  78    -15.231 -52.071 -29.251  1.00 14.34           O
ATOM   2406  O   HOH C  79    -18.374 -75.243 -10.951  1.00 32.51           O
ATOM   2407  O   HOH C  80     -8.556 -71.510 -23.158  1.00 27.00           O
ATOM   2408  O   HOH C  81    -39.663 -31.157  -5.844  1.00 41.74           O
ATOM   2409  O   HOH C  82    -27.219 -53.428 -26.557  1.00 32.84           O
ATOM   2410  O   HOH C  83    -14.922 -49.381 -29.521  1.00 26.74           O
ATOM   2411  O   HOH C  84     -9.883 -70.265 -25.549  1.00 31.60           O
ATOM   2412  O   HOH C  85     -6.047 -71.565 -22.212  1.00 27.12           O
ATOM   2413  O   HOH C  86     -4.894 -73.457 -20.619  1.00 24.66           O
ATOM   2414  O   HOH C  87     -9.284 -61.962  -2.485  1.00 18.79           O
ATOM   2415  O   HOH C  88    -22.712 -48.116 -28.995  1.00 23.45           O
ATOM   2416  O   HOH C  89    -20.620 -51.414 -24.485  1.00 19.66           O
ATOM   2417  O   HOH C  90    -23.556 -62.487 -29.443  1.00 22.98           O
ATOM   2418  O   HOH C  91    -20.711 -46.214 -28.623  1.00 18.98           O
ATOM   2419  O   HOH C  92     -8.725 -56.266  -6.821  1.00 31.39           O
ATOM   2420  O   HOH C  93    -22.021 -55.134  -9.353  1.00 26.24           O
ATOM   2421  O   HOH C  94    -23.737 -28.744  -1.310  1.00 41.74           O
ATOM   2422  O   HOH C  95     -6.811 -49.921  -8.253  1.00 35.42           O
ATOM   2423  O   HOH C  96    -25.425 -53.168 -35.560  1.00 24.85           O
ATOM   2424  O   HOH C  97    -31.444 -62.742  -2.659  1.00 35.46           O
ATOM   2425  O   HOH C  98     -6.736 -58.471 -24.600  1.00 38.37           O
ATOM   2426  O   HOH C  99    -28.262 -30.941 -18.263  1.00 25.36           O
ATOM   2427  O   HOH C 100    -25.294 -36.174 -16.058  1.00 28.89           O
ATOM   2428  O   HOH C 101    -34.158 -41.383 -12.513  1.00 36.88           O
ATOM   2429  O   HOH C 102    -20.678 -59.982 -28.773  1.00 32.58           O
ATOM   2430  O   HOH C 103    -23.104 -45.976 -26.531  1.00 19.37           O
ATOM   2431  O   HOH C 104    -14.860 -50.263 -12.303  1.00 37.60           O
ATOM   2432  O   HOH C 105    -21.078 -29.119 -12.350  1.00 40.95           O
ATOM   2433  O   HOH C 106    -38.049 -43.845 -18.170  1.00 28.92           O
ATOM   2434  O   HOH C 107    -20.238 -77.224 -12.325  1.00 29.15           O
ATOM   2435  O   HOH C 108     -1.438 -48.204   1.601  1.00 28.53           O
ATOM   2436  O   HOH C 109     -5.758 -57.592  -3.844  1.00 37.72           O
ATOM   2438  O   HOH C 111    -36.779 -29.048 -13.433  1.00 33.74           O
ATOM   2439  O   HOH C 112    -31.245 -68.295 -13.382  1.00 27.31           O
ATOM   2440  O   HOH C 113     -4.425 -45.328   2.720  1.00 36.16           O
ATOM   2441  O   HOH C 114    -13.705 -60.485   1.229  1.00 34.26           O
ATOM   2442  O   HOH C 115    -21.165 -32.036 -10.846  1.00 44.52           O
ATOM   2444  O   HOH C 117    -38.547 -52.247  -2.195  1.00 23.00           O
END
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EXAMPLE 6

Comparison of NprE variant structure with Thermolysin

A structure based sequence alignment of NprE variant with other metalloproteases is shown in Figure 12. Mature protein sequences of metalloproteases *Thermolysin* (*Bacillus thermoproteolyticus, protein 1*), PbaPro1 (*Paenibacillus barcinonensis, protein 1*), PhuPro1 (*Paenibacillus hunanensis, protein 1*), PhuPro2 (*Paenibacillus hunanensis, protein 2*), PehPro1

((*Paenibacillus ehimensis, protein 1*, Peh1.A crystal structure) , PpoPro1 (*Paenibacillus polymyxa, protein 1*), PspPro3 (*Paenibacillus sp., protein 3*), and PspPro2 (*Paenibacillus sp., protein 2*), and BbrPro1 (*Brevibacillus brevis, protein 1*) were aligned with sequences of known *Paenibacillus* metalloproteases from *P. polymyxa* (PpoPro2, YP_003872179.1), *P. peoriae* (PpePro1, ZP_10241029.1), *P. terrae* (PtePro1, F5LRG4) and known neutral protease homologs 1NPC.A (*Bacillus cereus* metalloprotease) and 1 KEI.A (Thermolysin, *Bacillus thermoproteolyticus*) . This alignment shows that the NprE variant shares a common deletion with PehPro1 and PpoPro2 relative to Thermolysin (pdb entry 1KEI).

In the sequence of native NprE and NprE variant (shown), this five residue deletion occurs after residue Asp178 (NprE numbering). Seven residues in Thermolysin are replaced by Thr179-Glu180 of NprE. In addition, NprE variant manifests three other deletions, a 3-residues deletion after Ser191, a 10-residues deletion after Thr243 and a 2-residues deletion after Gly284, and three insertions of two residues after Lys33, one residue after Tyr49 and four residues after Pro217 (NprE numbering) not common with PehPro1 and PpoPro2. Nevertheless, the overall topology between NprE variant and Thermolysin is highly conserved as shown in Figure 16, and also conserved in PehPro1 and PpoPro2 (not shown).

EXAMPLE 7

Differences in Calcium Binding sites between various metalloproteases

In the electron density from the crystal of the NprE variant, there is density for two calcium ions, corresponding to Ca1,2 (the double calcium in Thermolysin described above). There is no electron density for calcium ions at sites Ca3 or Ca4 that are seen in Thermolysin. Note that the Ca4 site is conserved in both PehPro1 and PpoPro2, and the Ca3 site is also seen in the PpoPro2 structure as noted previously.

In the vicinity of the Thermolysin double calcium site (Ca1,2) the structure of the NprE variant retains a similar binding pattern as shown in Figure 13. Despite having similar deletions as seen in PehPro1 and PpoPro2, the constellation of ligands is with one exception maintained by the presence of Asp181 which along with Glu186 (NprE numbering) forms ligands to both calcium ions. The single exception is that the carbonyl O of residue 183 in Thermolysin is absent owing to the deletion that is present in the NprE and common to PehPro1 and PpoPro2 structures. The carboxylates of Asp185 and Glu190 in Thermolysin form ligands to both calcium ions in Thermolysin and this pattern is retained in NprE with Asp181 and Glu186.

Referring back to Figure 9, the difference in calcium binding seen between Thermolysin, NprE variant, PpoPro2 and PehPro1 can be attributed to the specific sequence differences as

well as the presence of the five residue deletion. In Thermolysin, the Ca1-2 site is created by six ligands, while in NprE five of these ligands are retained, the last being removed due to the five residue deletion. Specifically, Asp181 in NprE and Asp185 in Thermolysin are replaced by Asn173 in PehPro1 and PpoPro2, Glu 186 in NprE and Glu190 in Thermolysin are replaced by Asn178 in PehPro1 and PpoPro2 (PehPro1 or PpoPro2 numbering, mature sequence). This deletion in PehPro1 and PpoPro2 removes three potential ligands. In addition, there is the removal of a main chain carbonyl (Asn183 in Thermolysin) and the presence of a new ligand (Asp129) in PehPro1 and PpoPro2 results in an altered calcium binding site in the PehPro1 and PpoPro2 enzyme structures, instead of the previously observed double site Ca1-2. In PehPro1 and PpoPro2, Asp129 replaces Gly and Ser found in Thermolysin and the NprE variant respectively. This site in PehPro1 and PpoPro2 has effectively been re-sculpted to form a single Ca binding site arising from the reduction of six to four calcium ligands.

It is interesting that with the replacement of Asp57 and Asp59 (thermolysin numbering) in PehPro1 the DxD motif present in the majority of the M4 metalloprotease is now replaced by SSS/N at the "Ca3" site andPehPro1 does not have calcium binding at this site (Figure 7 and Figure 11). While the main chain conformation is conserved at the DxD site, aspartic acids at these positions are replaced with serine residues in PehPro1. In the structure of the NprE variant (Figure 14), although the main chain conformation is again conserved, the aspartic acid residues observed in Thermolysin are now replaced by Ser and Thr residues, and calcium binding is absent.

From multiple sequence alignment shown in Figure 12, it is apparent that based on the presence of the DxD motif (the Ca3 site in Thermolysin and the third calcium site in PpoPro2), there seem to be different subsets of metalloproteases. Metalloproteases that have the DxD motif are exemplified by Thermolysin, the *Bacillus cereus* neutral protease and PpoPro2, while those that do not have the DxD motif have members such as PehPro1 and NprE. We see that several of proteases that contain the double delete lack the DxD motif (Figure 15- blowup of Figure 12).

Thermolysin, PpoPro2 and PehPro1 all share one common Ca binding site, the Ca4 site in Thermolysin (See Figures 6 and 10). In the NprE variant, this site is absent owing to a deletion of three residues following Ser191 in the NprE variant relative to Thermolysin, PehPro1 and PpoPro2. A comparison of the structure of Thermolysin and the NprE variant are shown in Figure 17.

EXAMPLE 8

Strategy to eliminate calcium dependence in metalloproteases

The fundamental teaching derived from attempts to remove calcium from proteases such as subtilisin and Thermolysin is that removal of calcium is detrimental to stability folding and function of these enzymes. However, to use these proteases in detergents, one desires that the proteases function in a low calcium environment. Presence of calcium in high concentration is considered undesirable as it affects the hardness of water. Detergent manufacturers add chelating agent to remove dissolved calcium. Not wishing to be bound by theory, it is proposed that calcium dependence may be a primary contributor to the instability of metalloproteases, such as Thermolysin, in detergent solutions. Thus, a metalloprotease that requires less calcium for folding and stability would likely be more stable in detergent formulations.

One approach would be to begin with an enzyme that naturally had fewer calcium ions bound such as those manifesting the pattern of double delete metalloproteases or one lacking DxD motif.

In one embodiment, the strategy for removing the Thermolysin Ca4 calcium would follow the homology seen for NprE, namely, to replace residues at sites equivalent to residues 193-200 (YTPGISGD (SEQ ID NO:17)) in Thermolysin with the sequence TISQP (SEQ ID NO:18) present in NprE resulting in a three residue deletion.

The strategy for removing the site corresponding to Ca3 in Thermolysin would be to replace residues at sites equivalent to residues 55-66 (WADADNQFFASY (SEQ ID NO:19)) in Thermolysin with either a sequence replacing the DxD motif (i.e. WASSSNQFFASY (SEQ ID NO:20)) or replacing the DxD motif in Thermolysin along with the PehPro1 type deletion (i.e. LTSSSNIWN (SEQ ID NO:21)).

The strategy for removing the double calcium site in Thermolysin (Ca1,2) could be staged, first to replace the double site with a single site as found in PehPro1 and PpoPro2. Replacing the residues in Thermolysin at sites equivalent to residues 177-185 (EFYANKNPD (SEQ ID NO:22)) with DGKN (SEQ ID NO:23) in PehPro1 (resulting in a five residue deletion) along with the substitutions of the residue equivalent to Thermolysin position 136 (G) with Asp and Thermolysin position 190 (E) to Asp would result in the loss of one calcium.

To replace the remaining calcium ion, one additional step would be to replace the residue equivalent to Thermolysin position 136 with Lys or Arg so as to stabilize the negative charge present at the position equivalent to position 190 now an Asp. An additional step may be

required to replace the residues equivalent to Thermolysin residues 177 (now Asp from above) to Asn or Ser and Thermolysin 138 (Asp) to Ser.

PROTEIN SEQUENCES FOR SEQUENCE LISTING:

PehPro1 (*Paenibacillus ehimensis, protein 1*)
ATGTGKGVLGDTKSFTTTQSGSTYQLKDTTRGQGIVTYSAGNRSSLPGTLLTSSSNIWN
DGAAVDAHAYTAKVYDYYKNKFGRNSIDGNGFQLKSTVHYSSRYNNAFWNGVQMV
YGDGDGVTFIPFSADPDVIGHELTHGVTEHTAGLEYYGESGALNESISDIIGNAIDGKNW
LIGDLIYTPNTPGDALRSMENPKLYNQPDRYQDRYTGPSDNGGVHINSGINNKAFYLIA
QGGTHYGVTVNGIGRDAAVQIFYDALINYLTPTSNFSAMRAAAIQAATDLYGANSSQV
NAVKKAYTAVGVN (SEQ ID NO:1)

PbaPro1 (*Paenibacillus barcinonensis, protein 1*)
ATGTGTGVHGDTKTLTTTQSGSTYQLKDTTRGKGIQTYTANNRSSLPGSLSTSSNNVWT
DRAAVDAHAYAAATYDFYKNKFNRNGIDGNGLLIRSTVHYGSNYKNAFWNGAQIVYG
DGDGIEFGPFSGDLDVVGHELTHGVIEYTANLEYRNEPGALNEAFADIMGNTIESKNWL
LGDGIYTPNIPGDALRSLSDPTLYNQPDKYSDRYTGSQDNGGVHINSGIINKAYYLAAQ
GGTHNGVTVSGIGRDKAVRIFYSTLVNYLTPTSKFAAAKTATIQAAKDLYGANSAEAT
AITKAYQAVGL (SEQ ID NO:2)

PhuPro1 (*Paenibacillus hunanensis, protein 1*)
ATGTGKGVLGDTKSFTVGTSGSSYVMTDSTRGKGIQTYTASNRTSLPGSTVTSSSSTFN
DPASVDAHAYAQKVYDFYKSNFNRNSIDGNGLAIRSTTHYSTRYNNAFWNGSQMVYG
DGDGSQFIAFSGDLDVVGHELTHGVTEYTANLEYYGQSGALNESISDIFGNTIEGKNWM
VGDAIYTPGVSGDALRYMDDPTKGGQPARMADYNNTSADNGGVHTNSGIPNKAYYLL
AQGGTFGGVNVTGIGRSQAIQIVYRALTYYLTSTSNFSNYRSAMVQASTDLYGANSTQT
TAVKNSLSAVGIN (SEQ ID NO:3)

PpoPro2 (*Paenibacillus polymyxa, protein 2*)
ATGTGKGVLGDTKSFTTTASGSSYQLKDTTRGNGIVTYTASNRQSIPGTLLTDADNVWNDPAGV
DAHAYAAKTYDYYKSKFGRDSVDGRGLQLRSTVHYGSRYNNAFWNGSQMTYGDGDGSTFIAF
SGDPDVVGHELTHGVTEYTSNLEYYGESGALNEAFSDVIGNDIQRKNWLVGDDIYTPNIAGDAL
RSMSNPTLYDQPDHYSNLYKGSSDNGGVHTNSGIINKAYYLLAQGGTFHGVAVNGIGRDAAVQ
IYYSAFTNYLTSSSDFSNARAAVIQAAKDLYGANSAEATAAAKSFDAVGVN (SEQ ID NO:4)

PpoPro1 (*Paenibacillus polymyxa, protein 1*)
ATGTGKGVLGDSKSFTTTASGSSYQLKDTTRGNGIVTYTASNRQSIPGTILTDADNVWN
DPAGVDAHAYAAKTYDYYKAKFGRNSIDGRGLQLRSTVHYGSRYNNAFWNGSQMTY
GDGDGSTFIAFSGDPDVVGHELTHGVTEYTSNLEYYGESGALNEAFSDVIGNDIQRKNW
LVGDDIYTPNIAGDALRSMSNPTLYDQPDHYSNLYRGSSDNGGVHTNSGIINKAYYLLA
QGGNFHGVTVNGIGRDAAVQIYYSAFTNYLTSSSDFSNARAAVIQAAKDLYGANSAEA
TAAAKSFDAVGVN (SEQ ID NO:5)

PamPro1 (*Paenibacillus amylolyticus, protein 1*)
ATGTGTGVLGDTKTLTTTQSGSTFQLKDTTRGNGIQTYTANNGSSLPGSLLTDSDNVWT
DRAGVDAHAHAAATYDFYKNKFNRNGINGNGLLIRSTVHYGSNYNNAFWNGAQIVFG
DGDGTMFRSLSGDLDVVGHELTHGVIEYTANLEYRNEPGALNEAFADIFGNTIQSKNW
LLGDDIYTPNTPGDALRSLSNPTLYGQPDKYSDRYTGSQDNGGVHINSGIINKAYFLAA
QGGTHNGVTVTGIGRDKAIQIFYSTLVNYLTPTSKFAAAKTATIQAAKDLYGATSAEAT
AITKAYQAVGL (SEQ ID NO:6)

PhuPro2 (*Paenibacillus hunanensis, protein 2*)
ATGSGTGVLGDNKTFQTTLSGSTYQLKDTTRGNGIYTYTASNRTTIPGTLLTDADNVWT
DGAAVDAHTYAGKVYDFYKTKFGRNSLDGNGLLIRSSVHYSSRYNNAFWNGTQIVFG
DGDGSTFIPLSGDLDVVGHELSHGVIEYTSNLQYLNESGALNESYADVLGNSIQAKNWL
IGDDVYTPGISGDALRSMSNPTLYGQPDNYANRYTGSSDNGGVHTNSGITNKAFYLLA
QGGTQNGVTVAGIGRDAAVNIFYNTVAYYLTSTSNFAAAKNASIQAAKDLYGTGSSYV
TSVTNAFRAVGL (SEQ ID NO:7)

PspPro2 (*Paenibacillus sp., protein 2*)
ATGTGRGVDGKTKSFTTTASGNRYQLKDTTRSNGIVTYTAGNRQTTPGTILTDTDNVW
EDPAAVDAHAYAIKTYDYYKNKFGRDSIDGRGMQIRSTVHYGKKYNNAFWNGSQMT
YGDGDGSTFTFFSGDPDVVGHELTHGVTEFTSNLEYYGESGALNEAFSDIIGNDIDGTS
WLLGDGIYTPNIPGDALRSLSDPTRFGQPDHYSNFYPDPNNDDEGGVHTNSGIINKAYY
LLAQGGTSHGVTVTGIGREAAVFIYYNAFTNYLTSTSNFSNARAAVIQAAKDFYGADSL
AVTSAIQSFDAVGIK (SEQ ID NO:8)

PspPro3 (*Paenibacillus sp., protein 3*)
ATGTGKGVLGDTKTFNTTASGSSYQLRDTTRGNGIVTYTASNRQSIPGTILTDADNVWN
DPAGVDAHAYAAKTYDYYKEKFNRNSIDGRGLQLRSTVHYGNRYNNAFWNGSQMTY
GDGDGTTFIAFSGDPDVVGHELTHGVTEYTSNLEYYGESGALNEAFSDIIGNDIQRKNW
LVGDDIYTPRIAGDALRSMSNPTLYDQPDHYSNLYRGSSDNGGVHTNSGIINKAYYLLA
QGGTFHGVTVNGIGRDAAVQIYYSAFTNYLTSSSDFSNARDAVVQAAKDLYGASSAQA
TAAAKSFDAVGVN (SEQ ID NO:9)

PpePro1 (*Paenibacillus peoriae, protein 1*)
ATGTGRGVDGVTKSFTTTASGNGYQLKDTTRSNGIVTYTANNRQTTPGTIMTDADNVWNDPAA
VDAHAYAIKTYDYYKNKFGRDSIDGRGMQIRSTVHYGKKYVNAFWNGSQMTYGDGDGSTFTF
FSGDPDVVGHELTHGVTEFTSNLEYYGESGALNEAFSDIIGNDIDGANWLLGDGIYTPGIPGDAL
RSLSDPTRFGQPDHYSNFYPDPNNDDEGGVHTNSGIINKAYYLLAQGGTSHGVKVTGIGREAAV
FIYYNAFTNYLTSTSNFSNARAAVIQAAKDFYGADSLAVTSAIKSFDAVGIK (SEQ ID NO:10)

PtePro1 (*Paenibacillus terrae, protein 1*)
ATGTGVGVLGDTKTFTTTQSGTQYVMQDTTRGGGIVTYSAGNTQSLPGTLMRDTDNV
WTDPAAVDAHAYAAVVYDYFKNNFNRDSLDGRGMAIKSTVHYGSRYNNAFWNGTQI
AYGDGDGTTFRAFSGDLDVIGHELTHGITEKTAGLIYQGESGALNESISDVFGNTIQGKN
WLIGDDIYTPSIPGDALRSMENPTLFNQPDHYSNIYRGSDDNGGVHTNSGIPNKAFYLLA
QGGTHRGVSVTGIGRGDAAKIVYKALTYYLTSTSNFAAMRQAAISSATDLFGANSAQV
NSVKAAYAAVGI (SEQ ID NO:11)

BbrProl *(Brevibacillus brevis, protein 1)*
VTATGKGVLGDTKQFETTKQGSTYMLKDTTRGKGIETYTANNRTSLPGTLMTDSDNY
WTDGAAVDAHAHAQKTYDYFRNVHNRNSYDGNGAVIRSTVHYSTRYNNAFWNGSQ
MVYGDGDGTTFLPLSGGLDVVAHELTHAVTERTAGLVYQNESGALNESMSDIFGAMV
DNDDWLMGEDIYTPGRSGDALRSLQDPAAYGDPDHYSKRYTGSQDNGGVHTNSGINN
KAAYLLAEGGTHYGVRVNGIGRTDTAKIYYHALTHYLTPYSNFSAMRRAAVLSATDLF
GANSRQVQAVNAAYDAVGVK (SEQ ID NO:12)

1KEI.A *(Bacillus thermoproteolyticus, thermolysin)*
ITGTSTVGVGRGVLGDQKNINTTYSTYYYLQDNTRGNGIFTYDAKYRTTLPGSLWADA
DNQFFASYDAPAVDAHYYAGVTYDYYKNVHNRLSYDGNNAAIRSSVHYSQGYNNAF
WNGSQMVYGDGDGQTFIPLSGGIDVVAHELTHAVTDYTAGLIYQNESGAINEAISDIFG
TLVEFYANKNPDWEIGEDVYTPGISGDSLRSMSDPAKYGDPDHYSKRYTGTQDNGGVH
INSGIINKAAYLISQGGTHYGVSVVGIGRDKLGKIFYRALTQYLTPTSNFSQLRAAAVQS
ATDLYGSTSQEVASVKQAFDAVGVK (SEQ ID NO:13)

1NPC.A *(Bacillus cereus)*
VTGTNKVGTGKGVLGDTKSLNTTLSGSSYYLQDNTRGATIFTYDAKNRSTLPGTLWAD
ADNVFNAAYDAAAVDAHYYAGKTYDYYKATFNRNSINDAGAPLKSTVHYGSNYNNA
FWNGSQMVYGDGDGVTFTSLSGGIDVIGHELTHAVTENSSNLIYQNESGALNEAISDIFG
TLVEFYDNRNPDWEIGEDIYTPGKAGDALRSMSDPTKYGDPDHYSKRYTGSSDNGGVH
TNSGIINKQAYLLANGGTHYGVTVTGIGKDKLGAIYYRANTQYFTQSTTFSQARAGAV
QAAADLYGANSAEVAAVKQSFSAVGVN (SEQ ID NO:14)

NprE_var *(Bacillus subtilis)*
AATTGTGTTLKGKTVSLNISSESGKYVLRDLSKPTGTQIITYDLQNREYNLPGTLVSSTT
NQFTTSSQRAAVDAHYNLGKVYDYFYQKFNRNSYDNKGGKIVSSVHYGSRYNNAAWI
GDQMIYGDGDGILFSPLSGSLDVTAHEMTHGVTQETANLNYENQPGALNESFSDVFGY
FNDTEDWDIGEDITISQPALRSLSNPTKYGQPDNFKNYKNLPNTPAGDYGGVHTNSGIP
NKAAYNTITKIGVNKAEQIYYRALTVYLTPSSTFKDAKAALIQSARDLYGSQDAASVEA
AWNAVGL (SEQ ID NO:15)

NprE *(Bacillus subtilis)*
AATTGTGTTLKGKTVSLNISSESGKYVLRDLSKPTGTQIITYDLQNREYNLPGTLVSSTT
NQFTTSSQRAAVDAHYNLGKVYDYFYQKFNRNSYDNKGGKIVSSVHYGSRYNNAAWI
GDQMIYGDGDGSFFSPLSGSMDVTAHEMTHGVTQETANLNYENQPGALNESFSDVFGY
FNDTEDWDIGEDITVSQPALRSLSNPTKYGQPDNFKNYKNLPNTDAGDYGGVHTNSGIP
NKAAYNTITKIGVNKAEQIYYRALTVYLTPSSTFKDAKAALIQSARDLYGSQDAASVEA
AWNAVGL (SEQ ID NO:16)

CLAIMS:

1.   A metalloprotease polypeptide comprising a calcium binding region.

2.   The polypeptide of claim 1, wherein the polypeptide comprises a modification in at least
        one amino acid residue in one of the calcium binding regions, Ca1-2, Ca3 and Ca4,
        (including residues 55-66, 136, 138, 177-190, and 193-200) of the polypeptide, wherein
        the amino acid positions of the polypeptide are numbered by correspondence with the
        amino acid sequence of *Bacillus thermoproteolyticus* metalloprotease set forth in SEQ
        ID NO: 13.

3.   The polypeptide of claim 2, wherein the polypeptide comprises a modification in at least
        one amino acid residue in a calcium binding region 1-2 of residues 177-190, 136 and 138
        of the polypeptide.

4.   The polypeptide of any of the above claims, wherein the polypeptide comprises an amino
        acid at position 184 selected from the group consisting of lysine, threonine, alanine,
        glutamic acid and aspartic acid.

5.   The polypeptide of any of the above claims, wherein the amino acid at position 185 is an
        amino acid other than aspartic acid.

6.   The polypeptide of claim 5, wherein the amino acid at position 185 is a non-negatively
        charged residue.

7.   The polypeptide of any of claims 5 or 6, wherein the amino acid at position 185 is a
        neutrally charged residue.

8.   The polypeptide of any of claims 5-7, wherein the amino acid at position 185 is an
        asparagine or serine.

9.   The polypeptide of any of the above claims, wherein the amino acid at position 187 is a
        non-negatively charged residue.

10.   The polypeptide of claim 9, wherein the amino acid at position 187 is a neutrally charged
        residue.

11.   The polypeptide of any of claims 9 or 10, wherein the amino acid at position 187 is a
        leucine or methionine.

12.   The polypeptide of any of claims 1-8, wherein the amino acid at position 187 is an
        aspartic acid.

13.   The polypeptide of any of the above claims, wherein the amino acid at position 188 is a
        leucine, valine or methionine.

14.   The polypeptide of any of the above claims, wherein the amino acid at position 190 is a residue other than glutamic acid.

15.   The polypeptide of claim 14, wherein the amino acid at position 190 is aspartic acid.

16.   The polypeptide of any of the above claims, wherein the polypeptide comprises a deletion at amino acid residue positions 179-183.

17.   The polypeptide of any of the above claims, wherein the amino acid at position 177 is a neutrally charged residue or aspartic acid.

18.   The polypeptide of any of the above claims, wherein the amino acid at position 177 is glutamine or aspartic acid.

19.   The polypeptide of any of the above claims, wherein the amino acid at position 178 is a residue selected from the group consisting of glycine, serine, arginine, alanine, asparagine, and threonine.

20.   The polypeptide of any of the above claims, wherein the amino acid at position 136 is an aspartic acid or serine.

21.   The polypeptide of any of the above claims, comprising a modification in at least one amino acid residue in a calcium binding region 3 of residues 55-66, wherein the amino acid positions of the polypeptide are numbered by correspondence with the amino acid sequence of *Bacillus thermoproteolyticus* metalloprotease set forth in SEQ ID NO: 13.

22.   The polypeptide of any of the above claims, wherein the amino acid at position 55 is a residue selected from the group consisting of leucine, serine, valine, and methionine.

23.   The polypeptide of any of the above claims, wherein the amino acid at position 56 is a residue selected from the group consisting of serine, arginine and threonine.

24.   The polypeptide of any of the above claims, wherein the amino acid at position 57 is a serine.

25.   The polypeptide of any of the above claims, wherein the amino acid at position 58 is a serine or threonine.

26.   The polypeptide of any of the above claims, wherein the amino acid at position 59 is a residue selected from the group consisting of serine, threonine, and asparagine.

27.   The polypeptide of any of the above claims, wherein the amino acid at position 60 is a serine.

28.   The polypeptide of any of the above claims, wherein the amino acid at position 61 is a residue selected from the group consisting of isoleucine, valine, and threonine.

29.   The polypeptide of any of the above claims, wherein the amino acid at position 62 is a residue selected from the group consisting of tryptophan and phenylalanine.

30.   The polypeptide of any of the above claims, wherein the amino acid at position 63 is a residue selected from the group consisting of asparagine, glutamic acid, and threonine.

31.   The polypeptide of any of the above claims, wherein the polypeptide comprises a deletion at amino acid residue positions 64-66.

32.   The polypeptide of any of the above claims, comprising a modification in at least one amino acid residue in a calcium binding region 4 of residues 193-200, wherein the amino acid positions of the polypeptide are numbered by correspondence with the amino acid sequence of *Bacillus thermoproteolyticus* metalloprotease set forth in SEQ ID NO: 13.

33.   The polypeptide of any of the above claims, wherein the amino acid at position 193 is a threonine.

34.   The polypeptide of any of the above claims, wherein the amino acid at position 194 is an isoleucine.

35.   The polypeptide of any of the above claims, wherein the amino acid at position 195 is a serine.

36.   The polypeptide of any of the above claims, wherein the polypeptide comprises a deletion at amino acid residue positions 196-198.

37.   The polypeptide of any of the above claims, wherein the amino acid at position 199 is a glutamine.

38.   The polypeptide of any of the above claims, wherein the amino acid at position 200 is a proline.

39.   The polypeptide of any of the above claims, wherein the calcium binding region 1-2 binds fewer than two calcium ions.

40.   The polypeptide of any of the above claims, wherein the calcium binding region 3 binds fewer than one calcium ion.

41.   The polypeptide of any of the above claims, wherein the calcium binding region 4 binds fewer than one calcium ion.

42.   The polypeptide of any of the previous claims, wherein the polypeptide is a variant of a parent polypeptide.

43.   The polypeptide of claim 42, wherein the variant comprises a modification in a calcium binding region of the parent polypeptide.

44.   The polypepide of claim 43, wherein the modification is to any of the amino acids listed in claims 4-38.

45.   The polypeptide of any of the previous claims, wherein the parent polypeptide is an M4 metalloprotease.

46.   The polypeptide of any of the previous claims, wherein the polypeptide has at least 60% sequence identity to the parent polypeptide.

47.   The polypeptide of any of the previous claims, wherein the polypeptide has at least 60% sequence identity to any one of SEQ ID NOs: 1-15.

48.   The polypeptide of any of the previous claims, wherein the polypeptide has at least 60% sequence identity to SEQ ID NOs: 13.

49.   The polypeptide of any of the previous claims, wherein the polypeptide has metalloprotease activity.

50.   A composition comprising any of the polypeptides of claims 1-49.

51.   The composition of claim 50, wherein said composition is a cleaning composition.

52.   The composition of claim 51, wherein said composition is a detergent composition.

53.   The composition of claim 52, wherein said detergent composition is selected from the group consisting of a laundry detergent, a fabric softening detergent, a dishwashing detergent, and a hard-surface cleaning detergent.

54.   The composition of any of claims 50 to 53, wherein said composition further comprises a surfactant.

55.   The composition of claim 54, wherein said surfactant is selected from the group consisting of an anionic surfactant, a cationic surfactant, a zwitterionic surfactant, a ampholytic surfactant, a semi-polar non-ionic surfactant, and a combination thereof.

56.   The composition of claim 55, wherein said surfactant is an ionic surfactant.

57.   The composition of claim 55, wherein said surfactant is a non-ionic surfactant.

58.   The composition of any of claims 50-57, wherein said composition further comprises at least one stabilizer.

59.   The composition of any of claims 50-58, wherein said composition comprises from about 0.001 to about 10 weight % of said polypeptide.

60.   The composition of any of claims 50-59, further comprising at least one bleaching agent.

61.   The composition of any of claims 50-60, wherein said cleaning composition is phosphate-free.

62.   The composition of any of claims 50-60, wherein said cleaning composition contains phosphate.

63.   The composition of any of claims 50-62, further comprising at least one adjunct ingredient.

64.   The composition of any of claims 50-63, wherein said composition is a granular, powder, solid, bar, liquid, tablet, gel, unit dose or paste composition.

65.   The composition of any of claims 50-64, further comprising one or more additional enzymes or enzyme derivatives selected from the group consisting of acyl transferases, alpha-amylases, beta-amylases, alpha-galactosidases, arabinosidases, aryl esterases, beta-galactosidases, carrageenases, catalases, cellobiohydrolases, cellulases, chondroitinases, cutinases, endo-beta-1, 4-glucanases, endo-beta-mannanases, esterases, exo-mannanases, galactanases, glucoamylases, hemicellulases, hyaluronidases, keratinases, laccases, lactases, ligninases, lipases, lipoxygenases,

mannanases, oxidases, pectate lyases, pectin acetyl esterases, pectinases, pentosanases, peroxidases, phenoloxidases, phosphatases, phospholipases, phytases, polygalacturonases, proteases, pullulanases, reductases, rhamnogalacturonases, beta-glucanases, tannases, transglutaminases, xylan acetyl-esterases, xylanases, xyloglucanases, and xylosidases, additional metallopotease enzymes and combinations thereof.

66.   The composition of any of claims 50-65, wherein said composition is formulated at a pH of from about 5.0 to about 12.0.

67.   A method of cleaning, comprising contacting a surface or an item with a composition comprising the variant of any one of claims 1-49.

68.   A method of cleaning comprising contacting a surface or an item with the composition of any one of claims 50-66.

69.   The method of claim 67 or 68, further comprising rinsing said surface or item after contacting said surface or item, respectively, with said composition.

70.   The method of any one of claims 67-69, wherein said item is dishware.

71.   The method of any one of claims 67-70, wherein said item is fabric.

72.   The method of any one of claims 67-71, further comprising the step of rinsing said surface or item after contacting said surface or item with said composition.

73.   The method of claim 72, further comprising the step of drying said surface or item after said rinsing of said surface or item.

74.   A method of cleaning a surface or item, comprising: providing the composition of any of claims 50-66 and a surface or item in need of cleaning; and contacting said composition with said surface or item in need of cleaning under conditions suitable for the cleansing of said surface of said surface or item, to produce a cleansed surface or item.

75.   The method of claim 74, further comprising the step of rinsing said cleansed surface or item to produce a rinsed surface or item.

76.   The method of any of claims 74 or 75, further comprising the step of drying said rinsed surface or item.

77.   A method for producing the variant of any of claims 1-49 comprising:

        a.   stably transforming a host cell with an expression vector comprising a polynucleotide encoding the variant of any of claims 1-49;

        b.   cultivating said transformed host cell under conditions suitable for said host cell to produce said protease; and

        c.   recovering said protease.

78.   The method of claim 77, wherein said host cell is a filamentous fungus or bacterial cell.

79.   The method of any of claims 77 or 78, wherein said host cell is selected from *Bacillus spp., Streptomyces spp., Escherichia spp., Aspergillus spp., Trichoderma spp., Pseudomonas spp., Corynebacterium spp., Saccharomyces spp.,* or *Pichia spp.*

80.   A textile processing composition comprising the variant of any one of claims 1-49.

81.   An animal feed composition comprising the variant of any one of claims 1-49.

82.   A leather processing composition comprising the variant of any one of claims 1-49.

83.   A feather processing composition comprising the variant or recombinant polypeptide of any one
       of claims 1-49.

84.   A lens cleaning composition comprising the variant of any one of claims 1-49.

85.   A tissue debridement composition comprising the variant of any one of claims 1-49.

86.   A tissue cell culture additive composition comprising the variant of any one of claims 1-49.

Figure 1 A schematic showing the arrangement of the two independent molecules of PehPro1 in the asymmetric unit of the crystal unit cell.

Figure 2 Stereo diagram showing a schematic of the Thermolysin main chain folding (black) and the schematic of PehPro1 (light gray).

Figure 3 Close-up 3 residue deletion in PehPro1 structure.

Figure 4 Close-up of 5 residue deletion in PehPro1 structure.

PehPro1 site1
lt gray
Asp 129
Asp 131
Asp 170
Asp 178

Thermolysin Ca1, Ca2 site
Black lines
Asp 138
Glu 177
C=O (183)
Asp 185
C=O (187)
Glu 190

Figure 5 Comparison of the calcium binding sitein PehPro1 that superimposes on the Ca1,2 calcium binding site in Thermolysin. Single Ca ion in PehPro1 shown as sphere, while 2 Ca ions in Thermolysin shown as crosses.

PehPro1 site2
gray lines
C=O (181)
Thr 182 OH
Thr 182 C=O
C=O (185)
Asp 188

Thermolysin Ca4 site
Black lines
C=O (193)
Thr 194 OH
Thr 194 C=O
C=O (197)
Asp 200

Figure 6 Schematic comparing Thermolysin (black lines) with PehPro1 (light gray sticks) in the vicinity of calcium binding site Ca4 in PehPro1.

Thermolysin Ca3 site
C=O (61)
Asp 59
Asp 57

Peh Pro1 equivalents
C=O (57)
Ser 55
Ser 53

Figure 7 A comparison of the structures of Thermolysin (black lines) and PehPro1
(light gray sticks) in the region of calcium binding Ca3 present in Thermolysin

Figure 8 Schematic comparing the main chain folding of PehPro1 (dark gray) and PpoPro2 (light gray).

Figure 9 Comparison of the first common calcium binding site between PehPro1 (light gray) and PpoPro2 (dark gray).

PehPro1 site2
light gray
C=O (181)
Thr 182 OH
Thr 182 O
C=O (185)
Asp 188

PpoPro2
dark gray
C=O (181)
Thr 182 OH
Thr 182 O
C=O (185)
Asp 188

Figure 10 Comparison of the structure of PehPro1 (light gray) and PpoPro2 (dark gray) at the second common calcium site, Ca4.

PpoPro2 Ca3
C=O (57)
Asp 55
Asp 53

Peh Pro1 equivalents
C=O (57)
Ser 55
Ser 53

Figure 11 Comparison of the third calcium binding site (Ca3) seen in PpoPro2 (dark gray) as compared to PehPro1 (light gray) where it is devoid of a calcium ion.

```
                5         10        15        20        25        30        35        40        45        50
  Consensus   ITGTSTVGVGRGVLGDQKNINTTYS-TYYYLQDNTR--GNGIFTYDAKYRTT-LP
2:Peh1_A      ATGTGKGVLGDTKSFTTTQSGSTYQLKDTTR--GQGIVTYSAGNRSS-LP
3:PbaPrc1     ATGTGVHGDTKTLTTTQSGSTYQLKDTTR·GKGIQTYTANNRSS-LP
4:PbsPrc1     ATGTGKGVLGDTKSFTVGTSGSSYVMTDSTR·GKGIQTYTASNRTS-LP
5:PboPrc2     ATGTGKGVLGDTKSFTTTASGSSYQLKDTTR--GNGVVTYTASNRQS-IP
6:PbePrc1     ATGTGKGVLGDSKSFTTTASGSSYQLKDTTR·GNGIVTYTASNRQS-IP
7:PamPrc1     ATGTGVLGDTKTLTTTQSGSTFQLKDTTR·GNGIQTYTANNGSS-LP
8:PbuPrc2     ATGSGTGVLGDNKTFQTTLSGSTYQLKDTTR·GNGIYTYTASNRTT-IP
9:PspPrc3     ATGTGRGVDGKTKSFTTTASGNRYQLKDTTR·GNGIVTYTAGNRQT-TP
10:PspPrc3    ATGTGKGVLGDTKTFNTTASGSSYQLRDTTR·SNGIVTYTASNRQS-IP
11:PpePrc1    ATGTGRGVDGVTKSFTTTASGNGYQLKDTTR·SNGIVTYTANNRQT-TP
12:PfePrc1    ATGTGVLGDTKQFETTKQGSTYMLKDTTR·GKGIETYTANNRTS-LP
13:BsrPrc1    VTATGKGVLGDTKQFETTKQGSTYMLKDTTR·GKGIETYTANNRTS-LP
14:Rona_var   AATTGTGTTLKGKTVSLNISSESGKYVLRDLSKPTGTQIITYDLQNREYNLP
15:tNPC_A     VTGTNKVGTGKGVLGDTKSLNTTLSGSSYYLQDNTR--GATIFTYDAKNRST-LP
```

Figure 12a

Figure 12b

Figure 12c

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            155      160      165      170      175      180      185      190      195      200      205      210      215
1:PehlA      GALNEAISDIFGTLVEFYANKNPDWEIGEDVYTPGISGDSLRSMSDPAKYGDPDH
2:PbaPro1    GALNESISDIIGNAIDG- - - -KNWLIGDLIYTPNTPGDALRSMENPKLYNQPDR
3:PbaPro1    GALNEAFADIMGNTIES· · · · ·KNWLLGDGIYTPNIPGDALRSLSDPTLYNQPDK
4:PhuPro1    GALNESISDIFGNTIEG· · · · ·KNWMVGDAIYTPGVSGDALRYMDDPTKGGQPAR
5:PpoPro2    GALNEAFSDVIGNDIQR- - - - -KNWLVGDDIYTPNIAGDALRSMSNPTLYDQPDH
6:PpoPro1    GALNEAFSDVIGNDIQR· · · · ·KNWLVGDDIYTPNIAGDALRSMSNPTLYDQPDH
7:PsmPro1    GALNEAFADIFGNTIQS· · · · ·KNWLLGDDIYTPNTPGDALRSLSNPTLYGQPDK
8:PhuPro2    GALNESYADVLGNSIQA· · · · ·KNWLIGDDVYTPGISGDALRSMSNPTLYGQPDN
9:PspPro2    GALNEAFSDIIGNDIDG· · · · ·TSWLLGDGIYTPNIPGDALRSLSDPTRFGQPDH
10:PspPro3   GALNEAFSDIIGNDIQR· · · · ·KNWLVGDDIYTPRIAGDALRSMSNPTLYDQPDH
11:PtePro1   GALNEAFSDIIGNDIDG· · · · ·ANWLLGDGIYTPGIPGDALRSLSDPTRFGQPDH
12:PtePro1   GALNESISDVFGNTIQG· · · · ·KNWLIGDDIYTPSIPGDALRSMENPTLFNQPDH
13:BbRo1     GALNESMSDIFGAMVDN· · · ·DDWLMGEDIYTPGRSGDALRSLQDPAAYGDPDH
14:Npre_bar  GALNESFSDVFGYFNDT- - - - -EDWDIGEDITIS- - -QPALRSLSNPTKYGQPDN
15:PCA       GALNEAISDIFGTLVEFYDNRNPDWEIGEDIYTPGKAGDALRSMSDPTKYGDPDH
```

Figure 12d

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1:Psh1.A     YSKRYTGT----QDNGGVHINSGIINKAAYLISQGGTHYGVSVVGIGRDKLGKIF
2:PbaPro1    YQDRYTGP----SDNGGVHINSGINNKAFYLIAQGGTHYGVTVNGIGRDAAVQIF
3:PhuPro1    YSDRYTGS...QDNGGVHINSGIINKAYYLAAQGGTHNGVTVSGIGRDKAVRIF
4:PhuPro1    MADYNNTS...ADNGGVHTNSGIPNKAYYLLAQGGTFGGVNVTGIGRSQAIQIV
5:PhpPro2    YSNLYTGS----SDNGGVHTNSGIINKAYYLLAQGGTFHGVTVNGIGRDAAVQIY
6:PhpPro1    YSNLYRGS...SDNGGVHTNSGIINKAYYLLAQGGNFHGVTVNGIGRDAAVQIY
7:PamPro1    YSDRYTGS...QDNGGVHINSGIINKAYFLAAQGGTHNGVTVTGIGRDKAIQIF
8:PhpPro2    YANRYTGS...SDNGGVHTNSGITNKAFYLLAQGGTQNGVTVAGIGRDAAVNIF
9:PspPro2    YSNFYPDPN..NDDEGGVHTNSGIINKAYYLLAQGGTSHGVTVTGIGREAAVFIY
10:PspPro3   YSNLYRGS...SDNGGVHTNSGIINKAYYLLAQGGTFHGVTVNGIGRDAAVQIY
11:PbePro1   YSNFYPDPN..NDDEGGVHTNSGIINKAYYLLAQGGTSHGVKVTGIGREAAVFIY
12:PhpPro1   YSNIYRGS...DDNGGVHTNSGIPNKAFYLLAQGGTHRGVSVTGIGRGDAAKIV
13:BalPro1   YSKRYTGS...QDNGGVHTNSGINNKAAYLLAEGGTHYGVRVNGIGRTDTAKIY
14:Rppe_car  FKNYKNLPNTPAGDYGGVHTNSGIPNKAAYNTIT-------KIGVNKAEQIY
15:1NPC-A    YSKRYTGS----SDNGGVHTNSGIINKQAYLLANGGTHYGVTVTGIGKDKLGAIY
```

Figure 12e

Consensus YRALTQYLTPTSNFSQLRAAAVQSATDLYGSTSQEVASVKQAFDAVGVK

1:Fth1A   YDALINYLTPTSNFSAMRAAAIQAATDLYGANSSQVNAVKKAYTAVGVN

2:FbaPro1   YSTLVNYLTPTSKFAAAKTATIQAAKDLYGANSAEATAITKAYQAVGL

3:PhuPro1   YRALTYYLTSTSNFSNYRSAMVQASTDLYGANSTQTTAVKNSLSAVGIN

4:FppPro2   YSAFTNYLTSSSDFSNARAAVIQAAKDQYGANSAEATAAAKSFDAVGVN

5:FppPro2   YSAFTNYLTSSSDFSNARAAVIQAAKDLYGANSAEATAAAKSFDAVGVN

6:PpsPro1   YSTLVNYLTPTSKFAAAKTATIQAAKDLYGATSAEATAITKAYQAVGL

7:FsmPro1   YNTVAYYLTSTSNFAAAKNASIQAAKDLYGTGSSYVTSVTNAFRAVGL

8:PhuPro2   YNAFTNYLTSTSNFSNARAAVIQAAKDFYGADSLAVTSAIQSFDAVGIK

9:FspPro2   YSAFTNYLTSSSDFSNARDAVVQAAKDLYGASSAQATAAAKSFDAVGVN

10:FgtPro3 YNAFTNYLTSTSNFSNARAAVIQAAKDFYGADSLAVTSAIKSFDAVGIK

11:FbePro1 YKALTYYLTSTSNFAAMRQAAISSATDLFGANSAQVNSVKAAYAAVGI

12:FtePro1 YHALTHYLTPYSNFSAMRRAAVLSATDLFGANSRQVQAVNAAYDAVGVK

13:BbkPro1 YRALTVVLTPSSTFKDAKAALIQSARDLYG--SQDAASVEAAWNAVGL

14:Nbre_ser YRANTQYFTQSTTFSQARAGAVQAAADLYGANSAEVAAVKQSFSAVGVN

15:MPCA

Figure 12f

NprE Ca sites
Gray sticks
Asp 139
Asp 178
Asp 181
C=O (183)
Glu 186

Thermolysin
Ca1, Ca2 sites
Black lines
Asp 138
Glu 177
C=O (183) *
Asp 185
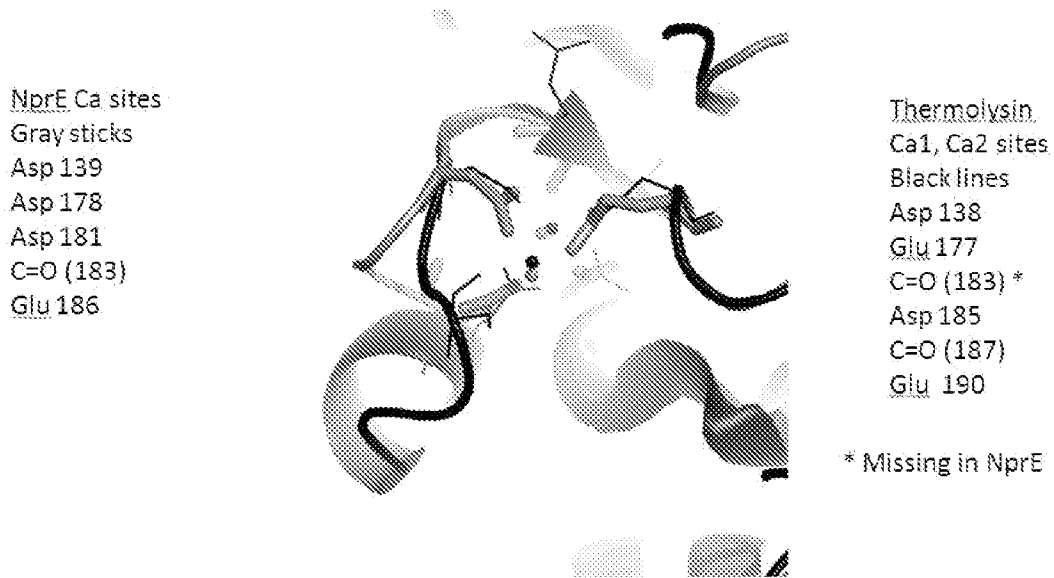C=O (187)
Glu 190

* Missing in NprE

Figure 13 Comparison of the calcium binding sites (Ca1,2) present in NprE (gray sticks) and Thermolysin (black lines).
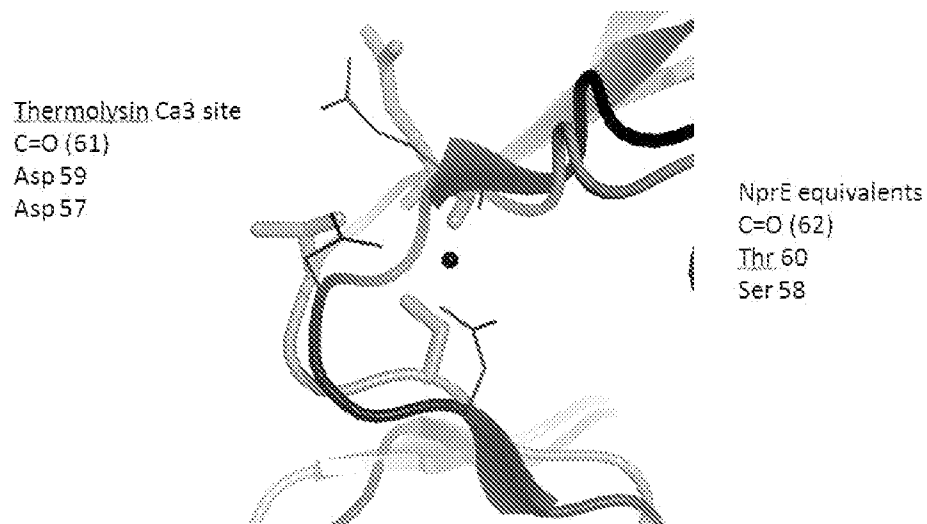
Figure 14 Comparison of NprE variant with Thermolysin at the region of Ca3 site, showing Caicion ion bound to Thermolysin as a sphere, while NprE lacks calcium ion.

Figure 15 Sequence alignment of several M4 metalloproteases showing the lack of the DxD motif (rectangle) among some members of *Paenibacillus* genus.
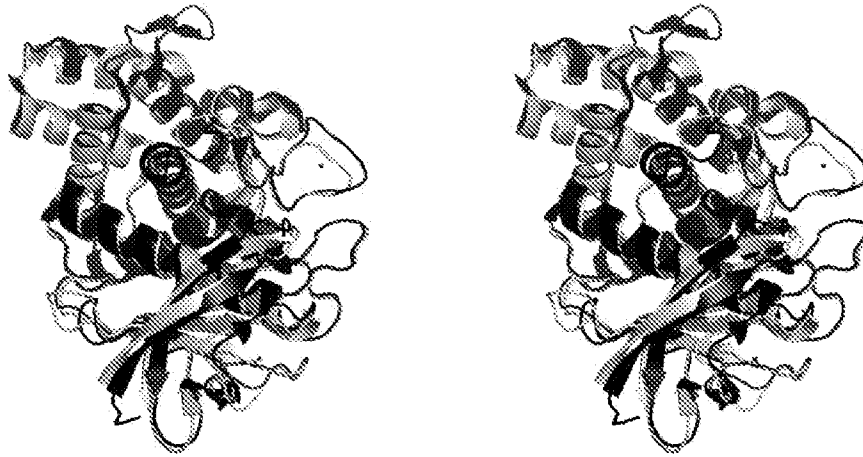
Figure 16 Stereodiagram comparing the overall main chain folding pattern of Thermolysin (black) with the NprE variant (gray) structures.

NprE variant
Light gray
Residues
189-192

Thermolysin Ca4 site
Black lines
C=O (193)
T194 OH
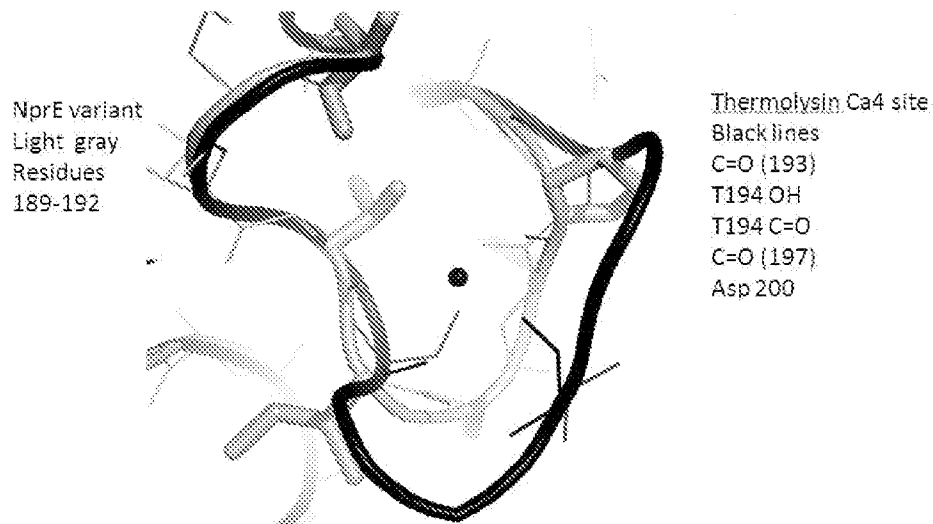T194 C=O
C=O (197)
Asp 200

Figure 17 Comparison of the structures of the NprE variant and Thermolysin at the Ca4 binding site of Thermolysin. The deletion of three residues in NprE relative to Thermolysin results in the elimination of a calcium binding site.