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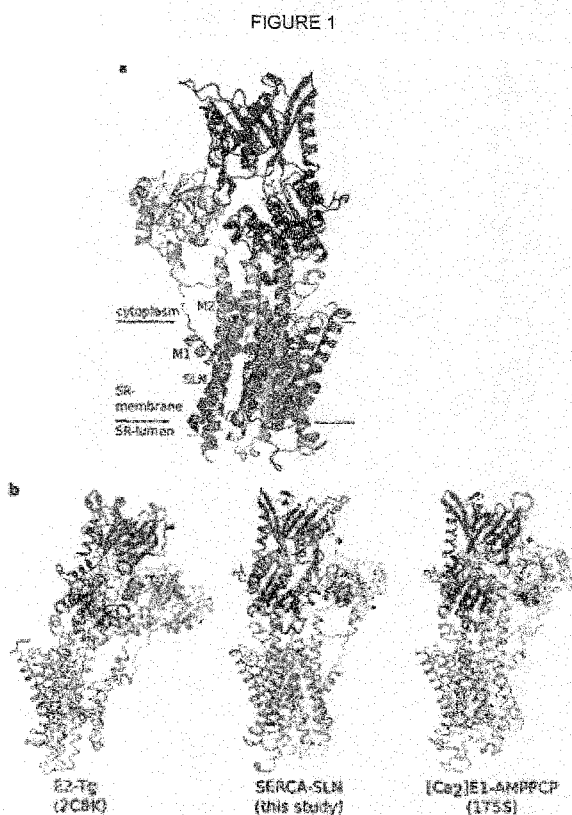
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(54) Title: CRYSTAL STRUCTURE I



(57) Abstract: The present invention provides the use of a three-dimensional structural representation of at least part of the SERCA Ca²⁺ ATPase/SLN complex as listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof, in a method for selecting or designing one or more binding partners of a Ca²⁺ ATPase and/or SLN.



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CRYSTAL STRUCTURE I

The present invention relates to protein crystal structures and their use in identifying protein binding partners and in protein structure determination. In particular, it relates to the crystal structure of the SERCA1a ATPase in complex with the regulatory protein, sarcolipin (SLN).

The listing or discussion of an apparently prior-published document in this specification should not necessarily be taken as an acknowledgement that the document is part of the state of the art or is common general knowledge.

Contraction and relaxation of muscle cells depends upon cytoplasmic Ca^{2+} levels being tightly controlled. Voltage-dependent Ca^{2+} -channels in myocytes mediate Ca^{2+} influx from the extracellular space to stimulate the opening of ryanodine receptors, which in turn release Ca^{2+} from the sarcoplasmic reticulum (SR) store, thereby triggering muscle contraction. Relaxation is initiated by Ca^{2+} efflux through the $\text{Na}^+/\text{Ca}^{2+}$ -exchanger (NCX) and Ca^{2+} resorption to the SR by the SR Ca^{2+} ATPase (SERCA), while reaching a low basal level of Ca^{2+} is achieved by plasma membrane Ca^{2+} -ATPases.

The concentration of the cytosolic Ca^{2+} levels and the duration of the Ca^{2+} increase are tightly coupled to the contractile properties, which allows for a rapid beat-to-beat control in the heart. Indeed, perturbations of this highly regulated Ca^{2+} cycling are a hallmark of human heart failure. Thus, therapeutic approaches that target the Ca^{2+} -ATPase and its regulators are highly desirable.

SERCA is a protein that is involved in determining not only the amount of Ca^{2+} available for contraction, but also controlling to a large extent the speed of relaxation. Various crystal structures are available for the SERCA Ca^{2+} -ATPase protein. From these, it is known that the 110 kDa single polypeptide chain folds into a bundle of ten transmembrane segments (M1 through M10) that together form the ion transport domain and the three cytoplasmic domains, A, P, and N (Toyshima et al., 2000) which mediate ATP hydrolysis via phosphorylation and dephosphorylation. Also, the protein undergoes large conformational changes during the Ca^{2+} transport cycle (Laursen, et al., 2009; Olesen, et al., 2007; Olesen, et al., 2004; Toyoshima, et al., 2000). The E1 state binds to Ca^{2+} and ATP to form the ADP sensitive E1P phospho-enzyme, which occludes two Ca^{2+} ions at intramembraneous sites I and II. Conversion to the ADP insensitive E2P conformation exposes a luminal exit pathway, where Ca^{2+} is exchanged for luminal H^+ .

This H^+ occlusion is accompanied by dephosphorylation and release of inorganic phosphate which leads to the E2 state.

Under physiological conditions, a major determinant of SERCA activity is its apparent Ca^{2+} affinity, which is regulated by small homologous membrane proteins called phospholamban (PLB) and sarcolipin (SLN) (James *et al.*, 1989; Odermatt *et al.*, 1989). In humans, SLN is primarily expressed in skeletal muscle, whereas PLB expression predominates in the heart. However, significant levels of SLN expression are observed in cardiac atrial muscle, indicating that SLN also plays an important role in heart physiology (Babu *et al.*, 2007). Both proteins are believed to bind to and regulate SERCA in a similar fashion. The proteins bind to the ATPase at resting Ca^{2+} concentrations (0.1 μM range), and lower its apparent Ca^{2+} affinity, i.e. modulate a threshold Ca^{2+} concentration where SERCA becomes active (Asahi *et al.*, 2002; Odermatt *et al.*, 1998; Simmerman *et al.*, 1996; Tada and Kadoma, 1989). Phosphorylation of both SLN and PLB in response to beta-adrenergic stimulation is believed to be the main cellular mechanism of regulation, with the ATPase being inhibited by the non-phosphorylated peptides (Wegener *et al.*, 1998, Gramolini *et al.*, 2006, Bhupathy *et al.*, 2009).

The structures of SLN and PLB and their interaction with SERCA have previously been studied by NMR (Buffy *et al.*, 2006; Zamoon *et al.*, 2005; Lambeth *et al.*, 2000), but a complex structure of either of the regulators bound to SERCA has so far only been observed for PLB at low-resolution by electron microscopy (Young *et al.*, 2001). As a result, the only suggestions about the placement of SLN and PLB on SERCA are those based on computerised modelling. For example, the inhibitory interaction of PLN with SERCA isoform 1 (SERCA1a) was modelled on the basis of several constraints which included: (i) spontaneous formation of SS-bridges between mutants L321C in transmembrane helix 4 (M4) of SERCA1a and N27C in PLN, and between V89C (M4) and V49C (PLN); (ii) definition of the face of the PLN transmembrane helix that interacts with SERCA; and (iii) cross-linking between Lys-3 of PLN and Lys-397 and Lys-400 of SERCA2a. The modeling was done using the crystal structure of SERCA1a in the absence of Ca^{2+} , into which an atomic model of PLN was built (Toyoshima *et al.*, 2003).

The inventors have now solved the first structure of the SERCA Ca^{2+} ATPase in complex with the regulatory protein, SLN. The structure provides new insight into the regulation of SERCA Ca^{2+} ATPase by SLN and identifies the precise binding site for SLN. The atomic coordinates of the complex may be utilised and manipulated in many different ways with

wide ranging applications including the fitting of binding partners, homology modeling and structure solution, analysis of ligand interactions and drug discovery. In particular, the structure reveals that the Ca^{2+} -ATPase adopts a novel conformation when in complex with SLN, therefore providing a novel platform for virtual screening of binding partners.

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Accordingly, a first aspect of the invention provides the use of a three-dimensional structural representation of at least part of the SERCA Ca^{2+} ATPase/SLN complex as defined by the coordinates listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof, in a method for selecting or designing one or more binding partners of a Ca^{2+} ATPase and/or SLN.

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By the term "coordinate" we include the information of the three dimensional organisation of the atoms contributing to a protein structure.

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By a 'three dimensional structural representation' we include a computer generated representation or a physical representation. Typically, in all aspects of the invention which feature a structural representation, the representation is computer generated. Computer representations can be generated or displayed by commercially available software programs. Examples of software programs include but are not limited to QUANTA (Accelrys .COPYRIGHT.2001, 2002), O (Jones et al., Acta Crystallogr. A47, pp. 110-119 (1991)) and RIBBONS (Carson, J. Appl. Crystallogr., 24, pp. 9589-961 (1991)), which are incorporated herein by reference. Examples of representations include any of a wire-frame model, a chicken-wire model, a ball-and-stick model, a space-filling model, a stick model, a ribbon model, a snake model, an arrow and cylinder model, an electron density map or a molecular surface model. Certain software programs may also imbue these three dimensional representations with physico-chemical attributes which are known from the chemical composition of the molecule, such as residue charge, hydrophobicity, torsional and rotational degrees of freedom for the residue or segment, etc. Examples of software programs for calculating chemical energies are described below.

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Typically, the coordinates of the SERCA Ca^{2+} ATPase/SLN complex used in the invention are those listed in Table (i). However, it is appreciated that it is not necessary to have recourse to the original coordinates listed in Table (i), and that any equivalent geometric representation derived from or obtained by reference to the original coordinates may be used. Thus, for the avoidance of doubt, by 'the coordinates of the

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SERCA Ca^{2+} ATPase/SLN complex listed in Table (i)', we include any equivalent representation wherein the original coordinates have been reparameterised in some way. For example, the coordinates in Table (i) may undergo any mathematical transformation known in the art, such as a geometric transformation, and the resulting transformed
5 coordinates can be used. For example, the coordinates of Table (i) may be transposed to a different origin and/or axes or may be rotated about an axis. Furthermore, it is possible to use the coordinates to calculate the psi and phi backbone torsion angles (as displayed on a Ramachandran plot) and the chi sidechain torsion angles for each residue in the protein. These angles together with the corresponding bond lengths, enable the
10 construction of a geometric representation of the protein which may be used based on the parameters of psi, phi and chi angles and bond lengths. Thus while the coordinates used are typically those in Table (i), the inventors recognise that any equivalent geometric representation of the SERCA Ca^{2+} ATPase/SLN complex structure, based on the coordinates listed in Table (i), may be used.

15 Additionally, it is appreciated that changing the number and/or positions of the ligand molecule of the Tables does not generally affect the usefulness of the coordinates in the aspects of the invention. Thus, it is also within the scope of the invention if the number and/or positions of ligand molecules of the coordinates of Table (i) is varied.

20 It will be appreciated that in all aspects of the invention which utilise the coordinates of the SERCA Ca^{2+} ATPase/SLN complex structure, it is not necessary to utilise all the coordinates of Table (i), but merely a portion of them, e.g. a set of coordinates representing atoms of particular interest in relation to a particular use. Such a portion of
25 coordinates is referred to herein as 'selected coordinates'. For example, when selecting or designing one or more binding partners of a Ca^{2+} ATPase, it may be desirable only to select those coordinates corresponding to atoms from the SERCA Ca^{2+} ATPase, and when selecting or designing one or more binding partners of SLN, it may be desirable only to select those coordinates corresponding to atoms from SLN. Also, when selecting
30 or designing binding partners that modulate the Ca^{2+} ATPase/SLN interaction, it may be convenient to select coordinates corresponding to only those atoms from one or more amino acid residues of SERCA Ca^{2+} ATPase and/or SLN within the SERCA Ca^{2+} ATPase/SLN interaction site. Further detail on which coordinates may be selected is provided below.

35 By 'selected coordinates', we include at least 5, 10 or 20 non-hydrogen protein atoms of the SERCA Ca^{2+} ATPase/SLN complex structure, more preferably at least 50, 100, 200,

300, 400, 500, 600, 700, 800 or 900 atoms and even more preferably at least 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, 2100 or 2200 non-hydrogen atoms. Preferably the selected coordinates pertain to at least 5, 10, 20 or 30 different amino acid residues (i.e. at least one atom from 5, 10, 20 or 30 different residues may be present), more preferably at least 40, 50, 60, 70, 80 or 90 residues, and even more preferably at least 100, 150, 200, 250 or 300 residues. Optionally, the selected coordinates may include one or more ligand atoms as set out in Table (i). Alternatively, the selected coordinates may exclude one or more atoms of the ligand. It will also be appreciated that the selected coordinates may pertain to atoms of only the SERCA Ca²⁺ ATPase, or that the selected coordinates may pertain to atoms of only SLN, or that the selected coordinates may pertain to atoms of both SERCA Ca²⁺ ATPase and SLN.

In one example, the selected coordinates may comprise atoms of one or more amino acid residues that contribute to the main chain or side chain atoms of a binding region of the SERCA Ca²⁺ ATPase.

For example, amino acid residues contributing to the SLN binding region include amino acid residues in helix M2, M6, M9 and the top of helix M4. Thus, the selected coordinates may comprise atoms of one or more amino acid residues selected from one or more of helices M2, M6, M9 and M4 of the SERCA Ca²⁺ ATPase, corresponding to amino acid residues M2: residues 86-122, M4: residues 288-328, M6: residues 789-809, M9: residues 931-960 according to the numbering of the SERCA Ca²⁺ ATPase as set out in Figure 8. More specifically, the SLN binding region includes amino acid residues Phe88, Phe92, Val93, Leu96, Ile97, Ala100, Ile103, Val104, Trp107, Gln108, Asn111, Tyr122, Arg324, Lys328, Trp794, Leu797, Asp800, Gly801, Leu802, Thr805, Ala806, Phe809, Trp932, Ser936, Leu939, Ser942, Leu943, Leu946, Ile947, Pro952, Leu953, Ile956, and Phe957 according to the numbering of the SERCA Ca²⁺ ATPase as set out in Figure 8. These residues are those residues of SERCA Ca²⁺ ATPase that are believed to interact with SLN. Thus the selected coordinates may comprise one or more atoms from any one or more (e.g. at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32 or 33 amino acid residues) of amino acid residues Phe88, Phe92, Val93, Leu96, Ile97, Ala100, Ile103, Val104, Trp107, Gln108, Asn111, Tyr122, Arg324, Lys328, Trp794, Leu797, Asp800, Gly801, Leu802, Thr805, Ala806, Phe809, Trp932, Ser936, Leu939, Ser942, Leu943, Leu946, Ile947, Pro952, Leu953, Ile956, and Phe957, according to the numbering of the SERCA Ca²⁺

ATPase as set out in Figure 8. Typically, coordinates of all of the atoms of the side chain of the one or more amino acid residues are selected.

In a further example, the selected coordinates may comprise atoms of one or more amino acid residues of the SLN binding pocket of SERCA Ca^{2+} ATPase which includes Val104, Trp107, Gln108, Glu109, Asn111, Ala112, Ala115, Ala118, Glu121, Tyr122, Thr317, Leu321, Arg324, Lys328, Phe760, Leu802, Thr805, Ala806 and Phe809, according to the numbering of the SERCA Ca^{2+} ATPase as set out in Figure 8. These residues are those residues of SERCA Ca^{2+} ATPase that together with residues of SLN (residues 1-11) form a pocket that represents a potential binding site. Thus the selected coordinates may comprise one or more atoms from any one or more (e.g. at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18 or 19 amino acid residues) of amino acid residues Val104, Trp107, Gln108, Glu109, Asn111, Ala112, Ala115, Ala118, Glu121, Tyr122, Thr317, Leu321, Arg324, Lys328, Phe760, Leu802, Thr805, Ala806 and Phe809, according to the numbering of the SERCA Ca^{2+} ATPase as set out in Figure 8.

In a further example, the selected coordinates may comprise atoms of one or more amino acid residues of the SERCA Ca^{2+} ATPase binding site of SLN, which includes amino acid residues Met1, Glu2, Arg3, Ser4, Thr5, Arg6, Glu7, Leu8, Cys9, Leu10 and Asn11 according to the numbering of SLN as set out in Figure 8. Thus the selected coordinates may comprise one or more atoms from any one or more of amino acid residues Met1, Glu2, Arg3, Ser4, Thr5, Arg6, Glu7, Leu8, Cys9, Leu10 and Asn11, according to the numbering of SLN as set out in Figure 8 (e.g. at least 2, 3, 4, 5, 6, 7, 8, 9, 10 or 11 of said amino acid residues).

In a yet further example, the selected coordinates may comprise atoms of one or more amino acid residues of the SERCA Ca^{2+} ATPase/SLN complex within the SERCA Ca^{2+} ATPase-SLN interaction site, which includes amino acid residues Phe88, Phe92, Val93, Leu96, Ile97, Ala100, Ile103, Val104, Trp107, Gln108, Glu109, Asn111, Ala112, Ala115, Ala118, Glu 121, Tyr122, Thr 317, Leu321, Arg324, Lys328, Phe 760, Trp794, Leu797, Asp800, Gly801, Leu802, Thr805, Ala806, Phe809, Trp932, Ser936, Leu939, Ser942, Leu943, Leu946, Ile947, Pro952, Leu953, Ile956, and Phe957 of SERCA Ca^{2+} ATPase according to the numbering of the SERCA Ca^{2+} ATPase as set out in Figure 8 and amino acids residues Met1, Arg3, Ser4, Thr5, Glu7, Leu8, Leu10, Asn11, Phe12, Val14, Val15, Leu16, Thr18, Val19, Leu21, Ile22, Trp23, Leu25, Val26, and Tyr29 according to the numbering of SLN as set out in Figure 8. Thus the selected coordinates may comprise one or more atoms from any one or more of the above amino acid residues (e.g. at least

2, 3, 4, 5, 6, 7, 8, 9 or 10 or 15 or 20 or 25 or 30 or 35 or 40 or 45 or 50 or 55 or 60 of said amino acid residues).

In another example, the selected coordinates may comprise atoms of one or more amino acid residues of the SERCA Ca^{2+} ATPase intramembranous Ca^{2+} binding sites, of which there are two: Site I and Site II. Site I involves the side chains of residues Asn 768, Glu 771, Asp 800 and Glu 908; and Site II involves the side chains of residues Asn 796, Asp 800, Gly 309, Val 304, Ala 305 and Ile 307 according to the numbering of the SERCA Ca^{2+} ATPase as set out in Figure 8. Thus the selected coordinates may comprise one or more atoms from any one or more of amino acid residues Asn 768, Glu 771, Asp 800 and Glu 908, according to the numbering of the SERCA Ca^{2+} ATPase as set out in Figure 8 (e.g. 1 or 2 or 3 of said amino acid residues), and/or one or more atoms from any one or more of amino acid residues Asn 796, Asp 800, Gly 309, Val 304, Ala 305 and Ile 307, according to the numbering of the SERCA Ca^{2+} ATPase as set out in Figure 8 (e.g. at least 1, 2, 3, 4, 5 or 6 of said amino acid residues).

In yet another example, the selected coordinates may comprise atoms of one or more amino acid residues of the SERCA Ca^{2+} ATPase Mg^{2+} binding site which involves residues Asp 800 and Glu 309 according to the numbering of the SERCA Ca^{2+} ATPase as set out in Figure 8. Thus the selected coordinates may comprise one or more atoms from any one or more of amino acid residues Asp 800 and Glu 309, according to the numbering of the SERCA Ca^{2+} ATPase as set out in Figure 8 (e.g. 1 or 2 of said amino acid residues).

It is appreciated that the selected coordinates may comprise any atoms of particular interest including atoms from amino acid residues mentioned in any one or more of the above examples, or as listed in Example 1 below.

It is also appreciated that the selected coordinates may correspond to atoms from a particular structural region (e.g. helix and/or loop) of the SERCA Ca^{2+} ATPase. Thus, the selected coordinates may correspond to atoms from one or more amino acid residues of the three cytoplasmic domains, designated P, N and A. Similarly, the selected coordinates may correspond to atoms from one or more amino acid residues of one or more of the ten transmembrane helices, designated M1-M10.

Preferably, the selected coordinates include at least 2% or 5% C- α atoms, and more preferably at least 10% C- α atoms. Alternatively or additionally, the selected coordinates

include at least 10% and more preferably at least 20% or 30% backbone atoms selected from any combination of the nitrogen, C- α , carbonyl C and carbonyl oxygen atoms.

It is appreciated that the coordinates of the SERCA Ca²⁺ ATPase used in the invention may be optionally varied and a subset of the coordinates or the varied coordinates may be selected (and constitute selected coordinates). Indeed, such variation may be necessary in various aspects of the invention, for example in the modelling of protein structures and in the fitting of various binding partners to a Ca²⁺ ATPase (e.g. SERCA Ca²⁺ ATPase) structure.

Protein structure variability and similarity is routinely expressed and measured by the root mean square deviation (rmsd), which measures the difference in positioning in space between two sets of atoms. The rmsd measures distance between equivalent atoms after their optimal superposition. The rmsd can be calculated over all atoms, over residue backbone atoms (i.e. the nitrogen-carbon-carbon backbone atoms of the protein amino acid residues), main chain atoms only (i.e. the nitrogen-carbon-oxygen-carbon backbone atoms of the protein amino acid residues), side chain atoms only or over C- α atoms only.

The least-squares algorithms used to calculate rmsd are well known in the art and include those described by Rossman and Argos (*J Biol Chem*, (1975) 250:7525), Kabsch (*Acta Cryst* (1976) A92:922; *Acta Cryst* (1978) A34:827-828), Hendrickson (*Acta Cryst* (1979) A35: 158), McLachan (*J Mol Biol* (1979) 128:49) and Kearsley (*Acta Cryst* (1989) A45:208). Both algorithms based on iteration in which one molecule is moved relative to the other, such as that described by Ferro and Hermans (*Acta Cryst* (1977) A33:345-347), and algorithms which locate the best fit directly (e.g. Kabsch's methods) may be used. Methods of comparing proteins structures are also discussed in *Methods of Enzymology*, vol 115: 397-420.

Typically, rmsd values are calculated using coordinate fitting computer programs and any suitable computer program known in the art may be used, for example MNYFIT (part of a collection of programs called COMPOSER, Sutcliffe *et al* (1987) *Protein Eng* 1:377-384). Other programs also include LSQMAN (Kleywegt & Jones (1994) A super position, CCP4/ESF-EACBM, Newsletter on Protein Crystallography, 31: 9-14), LSQKAB (Collaborative Computational Project 4. The CCP4 Suite: Programs for Protein Crystallography, *Acta Cryst* (1994) D50:760-763), QUANTA (Jones *et al*, *Acta Cryst* (1991) A47:110-119 and commercially available from Accelrys, San Diego, CA), Insight

(Commercially available from Accelrys, San Diego, CA), Sybyl® (commercially available from Tripos, Inc., St Louis) and O (Jones *et al.*, *Acta Cryst* (1991) A47:110-119).

In, for example, the programs LSQKAB and O, the user can define the residues in the two proteins that are to be paired for the purpose of the calculation. Alternatively, the pairing of residues can be determined by generating a sequence alignment of the two proteins as is well known in the art. The atomic coordinates can then be superimposed according to this alignment and an rmsd value calculated. The program Sequoia (Bruns *et al* (1999) *J Mol Biol* 288(3):427-439) performs the alignment of homologous protein sequences, and the superposition of homologous protein atomic coordinates. Once aligned, the rmsd can be calculated using programs detailed above. When the sequences are identical or highly similar, the structural alignment of proteins can be done manually or automatically as outlined above. Another approach would be to generate a superposition of protein atomic coordinates without considering the sequence.

We have conducted an rmsd analysis of C alpha atoms of the protein between the present SERCA Ca²⁺ ATPase and two known SERCA1a structures: one solved in the E1-P state (PDB code: 1T5S) and one solved in the E2 state (PDB code: 2AGV) using the program PyMol and the command Fit with specification of the C alpha atoms. The Fit command superimposes the model in the first selection on the model of the second selection (www.pymolwiki.org/index.php/Fit). Similar scripts can be used to calculate rmsd values for any other selected coordinates. Rmsd values have been calculated on C alpha atoms in the complete structure (residues 1-79, 86-883 and 887-994) and within the SLN binding site (i.e. residues Phe88, Phe92, Val93, Leu96, Ile97, Ala100, Ile103, Val104, Trp107, Gln108, Glu109, Asn111, Ala112, Ala115, Ala118, Glu 121, Tyr122, Thr 317, Leu321, Arg324, Lys328, Phe 760, Trp794, Leu797, Asp800, Gly801, Leu802, Thr805, Ala806, Phe809, Trp932, Ser936, Leu939, Ser942, Leu943, Leu946, Ile947, Pro952, Leu953, Ile956, and Phe957) as discussed below.

Conducting an rmsd analysis of C alpha atoms between the present SERCA Ca²⁺ ATPase and PDB code: 1T5S gave an rmsd value of 4.955 Å, and between the present SERCA Ca²⁺ ATPase and PDB code: 2AGV gave an rmsd valued of 9.457 Å. Thus in one embodiment, the coordinates or selected coordinates of Table (i) may be optionally varied within an rmsd of residue backbone atoms (i.e. the nitrogen-carbon-carbon backbone atoms of the protein) of not more than 4.95 Å. Preferably, the coordinates or selected coordinates are varied within an rmsd of residue backbone atoms of not more than 4.9 Å, 4.8 Å, 4.7 Å, 4.6 Å, 4.5 Å, 4.4 Å, 4.3 Å, 4.2 Å, 4.1 Å, 4.0 Å, 3.9 Å, 3.8 Å, 3.7 Å,

3.6 Å, 3.5 Å, 3.4 Å, 3.3 Å, 3.2 Å, 3.1 Å, 3.0 Å, 2.9 Å, 2.8 Å, 2.7 Å, 2.6 Å, 2.5 Å, 2.4 Å, 2.3 Å, 2.1 Å, 2.0 Å, 1.9 Å, 1.8 Å, 1.7 Å, 1.6 Å, 1.5 Å, 1.4 Å, 1.3 Å, 1.2 Å, 1.1 Å, 1.0 Å, 0.9 Å or 0.8 Å and more preferably not more than 0.7 Å, 0.6 Å, 0.5 Å, 0.4 Å, 0.3 Å, 0.2 Å or 0.1 Å. It is particularly preferred that when the selected coordinates correspond to all or some of the atoms of the SERCA Ca²⁺ ATPase, and none of the atoms of SLN, that they are optionally varied within an rmsd of residue backbone atoms of these values.

We have conducted an rmsd analysis of residue backbone atoms between the present SERCA Ca²⁺ ATPase and other SERCA Ca²⁺ ATPases represented by PDB codes: 1T5S and 2AGV, within the SLN binding site (i.e. residues Phe88, Phe92, Val93, Leu96, Ile97, Ala100, Ile103, Val104, Trp107, Gln108, Glu109, Asn111, Ala112, Ala115, Ala118, Glu 121, Tyr122, Thr 317, Leu321, Arg324, Lys328, Phe 760, Trp794, Leu797, Asp800, Gly801, Leu802, Thr805, Ala806, Phe809, Trp932, Ser936, Leu939, Ser942, Leu943, Leu946, Ile947, Pro952, Leu953, Ile956, and Phe957). The rmsd value for PDB: 1T5S is 3.581 and the rmsd value for PDB: 2AGV is 5.836 Å. Thus in an embodiment, where the coordinates or selected coordinates used in the invention are optionally varied within the SLN binding site, they are varied within an rmsd of residue backbone atoms of not more than 3.58 Å (such as not more than 3.5 Å, 3.4 Å, 3.3 Å, 3.2 Å, 3.1 Å, 3.0 Å, 2.9 Å, 2.8 Å, 2.7 Å, 2.6 Å, 2.5 Å, 2.4 Å, 2.3 Å, 2.1 Å, 2.0 Å, 1.9 Å, 1.8 Å, 1.7 Å, 1.6 Å, 1.5 Å, 1.4 Å, 1.3 Å, 1.2 Å, 1.1 Å, 1.0 Å, 0.9 Å, 0.8 Å, 0.7 Å, 0.6 Å, 0.5 Å, 0.4 Å, 0.3 Å, 0.2 Å or 0.1 Å).

We have also conducted an rmsd analysis of C alpha atoms between the present SLN and a known structure of SLN solved by NMR (PDB code: 1JDM) using the program PyMol and the command Align with specification of the C alpha atoms. Align does a BLAST-like BLOSUM62-weighted dynamic programming sequence alignment followed by a series of refinement cycles intended to improve the fit by eliminating pairing with high relative variability (e.g. >2 standard deviations from the cycle's mean deviance) (www.pymolwiki.org/index.php/Align#RMS_values). Rmsd values were calculated on C alpha atoms in the complete structure (SLN residues 5-8, 10-13, 15-21 and 23-29) and gave an rmsd value of 1.898 Å. Thus in one embodiment, the coordinates or selected coordinates of Table (i) may be optionally varied within an rmsd of C alpha atoms of not more than 1.89 Å. Preferably, the coordinates or selected coordinates are varied within an rmsd of C alpha atoms of not more than 1.8 Å, 1.7 Å, 1.6 Å, 1.5 Å, 1.4 Å, 1.3 Å, 1.2 Å, 1.1 Å, 1.0 Å, 0.9 Å or 0.8 Å and more preferably not more than 0.7 Å, 0.6 Å, 0.5 Å, 0.4 Å, 0.3 Å, 0.2 Å or 0.1 Å. It is particularly preferred that when the selected coordinates correspond to all or some of the atoms of the SLN, and none of the atoms of SERCA

Ca²⁺ ATPase, that they are optionally varied within an rmsd of C alpha atoms of these values.

It is appreciated that the coordinates of the SERCA Ca²⁺ ATPase/SLN complex of Table (i) optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof may be used in the provision, design, modification or analysis of binding partners of Ca²⁺ ATPase and/or SLN. In other words, the binding partners may be binding partners of Ca²⁺ ATPase, binding partners of SLN, or binding partners of both Ca²⁺ ATPase and SLN (i.e. the binding partner may bind to both Ca²⁺ ATPase and SLN when the two protein are in complex with one another). Such a use will be important in drug design.

By Ca²⁺ ATPase we include any Ca²⁺ ATPase which has at least 75% sequence identity with rabbit SERCA Ca²⁺ ATPase as well as Ca²⁺ ATPases (eg SERCA Ca²⁺ ATPases) from other species (eg animal species) and mutants thereof. Preferably, the Ca²⁺ ATPase has at least 80% amino acid sequence identity to rabbit SERCA Ca²⁺ ATPase, and more preferably at least 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% amino acid sequence identity. Most preferably, the Ca²⁺ ATPase is a SERCA Ca²⁺ ATPase.

By SLN we include any SLN which has at least 75% sequence identity with rabbit SLN as well as SLN from other species (eg animal species) and mutants thereof. Preferably, the SLN has at least 80% amino acid sequence identity to rabbit SLN, and more preferably at least 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% amino acid sequence identity.

By "binding partner" we mean any molecule that binds to a Ca²⁺ ATPase, or which binds to a SLN, or which binds to a Ca²⁺ ATPase/SLN complex. Preferably, the molecule binds selectively to the Ca²⁺ ATPase and/or SLN. For example, it is preferred if the binding partner has a K_d value (dissociation constant) which is at least five or ten times lower (i.e. higher affinity) than for at least one other Ca²⁺ ATPase and/or SLN, and preferably more than 100 or 500 times lower. Thus, if the binding partner is for a Ca²⁺ ATPase, it is preferred if the binding partner has a K_d value which is lower than for at least one other Ca²⁺ ATPase by the specified degree, and if the binding partner binds to both Ca²⁺ ATPase and SLN in a complex, it is preferred if the binding partner has a K_d value which is lower than for at least one other Ca²⁺ ATPase/SLN complex which complex contains a different Ca²⁺ ATPase and a different SLN. More preferably, the binding partner of a

Ca²⁺ ATPase and/or SLN has a K_d value more than 1000 or 5000 times lower than for at least one other Ca²⁺ ATPase and/or SLN. However, it will be appreciated that the limits will vary dependent upon the nature of the binding partner. Thus, typically, for small molecule binding partners, the binding partner typically has a K_d value which is at least 10 times or 50 times or 100 times lower than for at least one other Ca²⁺ ATPase and/or SLN. Typically, for antibody binding partners, the binding partner typically has a K_d value which is at least 500 or 1000 times lower than for at least one other Ca²⁺ ATPase and/or SLN.

K_d values can be determined readily using methods well known in the art and as described, for example, below.

At equilibrium $K_d = [R][L]/[RL]$

where the terms in brackets represent the concentration of

- Receptor-ligand complexes [RL],
- unbound receptor [R], and
- unbound ("free") ligand [L].

In order to determine the K_d the value of these terms must be known. Since the concentration of receptor is not usually known then the Hill-Langmuir equation is used where Fractional occupancy = $[L]/[L] + K_d$.

In order to experimentally determine a K_d then, the concentration of free ligand and bound ligand at equilibrium must be known. Typically, this can be done by using a radio-labelled or fluorescently labelled ligand which is incubated with the receptor (present in whole cells or homogenised membranes) until equilibrium is reached. The amount of free ligand vs bound ligand must then be determined by separating the signal from bound vs free ligand. In the case of a radioligand this can be done by centrifugation or filtration to separate bound ligand present on whole cells or membranes from free ligand in solution. Alternatively a scintillation proximity assay is used. In this assay the receptor (in membranes) is bound to a bead containing scintillant and a signal is only detected by the proximity of the radioligand bound to the receptor immobilised on the bead.

The binding partner may be any of a polypeptide; an anticalin; a peptide; an antibody; a chimeric antibody; a single chain antibody; an aptamer; a darpin; a Fab, F(ab')₂, Fv, ScFv or dAb antibody fragment; a small molecule; a natural product; an affibody; a peptidomimetic; a nucleic acid; a peptide nucleic acid molecule; a lipid; a carbohydrate

(eg saccharide); a protein based on a modular framework including ankyrin repeat proteins, armadillo repeat proteins, leucine rich proteins, tetrariopeptide repeat proteins or Designed Ankyrin Repeat Proteins (DARPin)s; a protein based on lipocalin or fibronectin domains or Affilin scaffolds based on either human gamma crystalline or human ubiquitin; a G protein; an RGS protein; an arrestin; a GPCR kinase; a receptor tyrosine kinase; a RAMP; a NSF; a GPCR; an NMDA receptor subunit NR1 or NR2a; calcyon; or a fragment or derivative thereof that binds to a Ca^{2+} ATPase and/or SLN. Typically, the binding partner is a small molecule or peptide.

It will be appreciated that the coordinates of the invention will also be useful in the analysis of solvent and ion interactions with a Ca^{2+} ATPase, which are important factors in drug design. Thus the binding partner may be a solvent molecule, for example water or acetonitrile, or an ion, for example a sodium ion or a protein.

It is particularly preferred if the binding partner is a small molecule with a molecule weight less than 5000 daltons, for example less than 4000, 3000, 2000 or 1000 daltons, or with a molecule weight less than 500 daltons, for example less than 450 daltons, 400 daltons, 350 daltons, 300 daltons, 250 daltons, 200 daltons, 150 daltons, 100 daltons, 50 daltons or 10 daltons.

It is further preferred if the binding partner causes a change (i.e a modulation) in the level of biological activity of the Ca^{2+} ATPase and/or SLN, and therefore may have the potential to be a candidate drug. Thus the binding partner may be a modulator of Ca^{2+} ATPase activity and/or SLN activity. In other words the binding partner may be a modulator of Ca^{2+} ATPase activity, a modulator of SLN activity, or a modulator of the activity of the Ca^{2+} ATPase/SLN complex. The activity that is modulated may be any one or more biological activities of Ca^{2+} ATPase or SLN or the Ca^{2+} ATPase/SLN complex, including binding activities, enzymatic activities and cell signalling activities. The major determinant of SERCA Ca^{2+} ATPase activity at physiological Ca^{2+} is its affinity for transported Ca^{2+} ions regulated by SLN and PLB, and so in a particularly preferred embodiment, the binding partner is a modulator of the SERCA Ca^{2+} ATPase/SLN interaction or of the SERCA Ca^{2+} ATPase/PLB interaction, and therefore also a modulator of SERCA Ca^{2+} ATPase activity. By 'modulator' we include the meaning of an agent that increases a given activity or an agent that decreases a given activity. Thus, a modulator would include an inhibitor or activator of a given activity (e.g. in the binding of

SLN or PLB to a Ca^{2+} ATPase, the modulator may act to either strengthen or diminish the interaction).

5 It will be appreciated that the binding partner may bind to an orthosteric site or to an allosteric site of either protein.

A second aspect of the invention provides a method for selecting or designing one or more binding partners of a Ca^{2+} ATPase and/or SLN, the method comprising using molecular modelling means to select or design one or more binding partners of a Ca^{2+} ATPase and/or SLN, wherein the three-dimensional structural representation of at least
10 part of the SERCA Ca^{2+} ATPase/SLN complex as listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof, is compared with a three-dimensional structural representation of one or more candidate binding partners, and one or more binding partners that are
15 predicted to interact with the Ca^{2+} ATPase and/or SLN are selected or designed.

In order to provide a three-dimensional structural representation of a candidate binding partner, the binding partner structural representation may be modelled in three dimensions using commercially available software for this purpose or, if its crystal
20 structure is available, the coordinates of the structure may be used to provide a structural representation of the binding partner.

The design of binding partners that bind to a Ca^{2+} ATPase and/or SLN generally involves consideration of two factors.

25 First, the binding partner must be capable of physically and structurally associating with parts or all of a binding region (e.g. ligand binding site or an allosteric binding site). Non-covalent molecular interactions important in this association include hydrogen bonding, van der Waals interactions, hydrophobic interactions and electrostatic interactions.

30 Second, the binding partner must be able to assume a conformation that allows it to associate with the binding region directly. Although certain portions of the binding partner will not directly participate in these associations, those portions of the binding partner may still influence the overall conformation of the molecule. This, in turn, may have a
35 significant impact on potency. Such conformational requirements include the overall three-dimensional structure and orientation of the binding partner in relation to all or a portion of the binding region, or the spacing between functional groups of a binding

partner comprising several binding partners that directly interact with the protein or protein complex. This is particularly relevant where the binding partner is a protein.

Thus it will be appreciated that selected coordinates which represent a binding region of the SERCA Ca²⁺ ATPase, or a binding region of SLN, or a binding region of the SERCA Ca²⁺ ATPase/SLN complex (eg one that spans across both proteins) may be used. For example, atoms from one or more amino acid residues contributing to the SLN binding region of SERCA Ca²⁺ ATPase, including amino acid residues Phe88, Phe92, Val93, Leu96, Ile97, Ala100, Ile103, Val104, Trp107, Gln108, Asn111, Tyr122, Arg324, Lys328, Trp794, Leu797, Asp800, Gly801, Leu802, Thr805, Ala806, Phe809, Trp932, Ser936, Leu939, Ser942, Leu943, Leu946, Ile947, Pro952, Leu953, Ile956, and Phe957 may be used, and/or atoms from one or more amino acid residues of the SLN binding pocket of SERCA Ca²⁺ ATPase, including Val104, Trp107, Gln108, Glu109, Asn111, Ala112, Ala115, Ala118, Glu121, Tyr122, Thr317, Leu321, Arg324, Lys328, Phe760, Leu802, Thr805, Ala806 and Phe809, may be used, and/or atoms of one or more amino acid residues of the SERCA Ca²⁺ ATPase binding site of SLN, including amino acid residues Met1, Arg3, Ser4, Thr5, Glu7, Leu8, Leu10, Asn11, Phe12, Val14, Val15, Leu16, Thr18, Val19, Leu21, Ile22, Trp23, Leu25, Val26, and Tyr29, may be used.

In a preferred embodiment, the one or more binding partners are predicted to bind to the SERCA Ca²⁺ ATPase/SLN interaction site. In this way, it is believed that the one or more binding partners may be modulators of the SERCA Ca²⁺ ATPase/SLN interaction, and thus modulators of Ca²⁺ ATPase activity. By the SERCA Ca²⁺ ATPase/SLN interaction site we include amino acid residues Phe88, Phe92, Val93, Leu96, Ile97, Ala100, Ile103, Val104, Trp107, Gln108, Glu109, Asn111, Ala112, Ala115, Ala118, Glu 121, Tyr122, Thr 317, Leu321, Arg324, Lys328, Phe 760, Trp794, Leu797, Asp800, Gly801, Leu802, Thr805, Ala806, Phe809, Trp932, Ser936, Leu939, Ser942, Leu943, Leu946, Ile947, Pro952, Leu953, Ile956, and Phe957 of SERCA Ca²⁺ ATPase according to the numbering of the SERCA Ca²⁺ ATPase as set out in Figure 8 and amino acids residues Met1, Arg3, Ser4, Thr5, Glu7, Leu8, Leu10, Asn11, Phe12, Val14, Val15, Leu16, Thr18, Val19, Leu21, Ile22, Trp23, Leu25, Val26, and Tyr29 according to the numbering of SLN as set out in Figure 8. Hence, the selected coordinates may correspond to atoms from one or more of these amino acid residues.

Selected coordinates representing an extracellular face would be useful to select or design for binding partners such as antibodies, and selected coordinates representing an intracellular face would be useful to select or design for agents which modulate (e.g.

increase or decrease or prevent) binding to natural binding partners such as SLN and PLB. Additional preferences for the selected coordinates, including the Ca^{2+} and Mg^{2+} binding sites, are as defined above with respect to the first aspect of the invention. It will be appreciated that any of these particular binding regions may be used to identifying
5 binding partners and potential modulators.

Designing of binding partners can generally be achieved in two ways, either by the step wise assembly of a binding partner or by the *de novo* synthesis of a binding partner. As is described in more detail below, binding partners can also be identified by virtual
10 screening.

With respect to the step-wise assembly of a binding partner, several methods may be used. Typically the process begins by visual inspection of, for example, any of the binding regions on a computer representation of the SERCA Ca^{2+} ATPase/SLN complex
15 as defined by the coordinates in Table (i), optionally varied within a rmsd of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof. Selected binding partners, or fragments or moieties thereof may then be positioned in a variety of orientations, or docked, within the binding region. Docking may be accomplished using software such as QUANTA and Sybyl (Tripos Associates, St. Louis, Mo.), followed by, or
20 performed simultaneously with, energy minimization, rigid-body minimization (Gshwend, supra) and molecular dynamics with standard molecular mechanics force fields, such as CHARMM and AMBER.

Specialized computer programs may also assist in the process of selecting binding
25 partners or fragments or moieties thereof. These include: 1. GRID (P. J. Goodford, "A Computational Procedure for Determining Energetically Favorable Binding Sites on Biologically Important Macromolecules", J. Med. Chem., 28, pp. 849-857 (1985)). GRID is available from Oxford University, Oxford, UK. 2. MCSS (A. Miranker et al., "Functionality Maps of Binding Sites: A Multiple Copy Simultaneous Search Method."
30 Proteins: Structure, Function and Genetics, 11, pp. 29-34 (1991)). MCSS is available from Molecular Simulations, San Diego, Calif. 3. AUTODOCK (D. S. Goodsell et al., "Automated Docking of Substrates to Proteins by Simulated Annealing", Proteins: Structure, Function, and Genetics, 8, pp. 195-202 (1990)). AUTODOCK is available from Scripps Research Institute, La Jolla, Calif. 4. DOCK (I. D. Kuntz et al., "A Geometric
35 Approach to Macromolecule-Ligand Interactions", J. Mol. Biol., 161, pp. 269-288 (1982)). DOCK is available from University of California, San Francisco, Calif.

Once suitable binding partners or fragments have been selected, they may be assembled into a single compound or complex. Assembly may be preceded by visual inspection of the relationship of the fragments to each other on the three-dimensional image displayed on a computer screen in relation to the structure coordinates of the SERCA Ca^{2+} ATPase and/or SLN. This would be followed by manual model building using software such as QUANTA or Sybyl.

Useful programs to aid one of skill in the art in connecting the individual chemical entities or fragments include: 1. CAVEAT (P. A. Bartlett et al., "CAVEAT: A Program to Facilitate the Structure-Derived Design of Biologically Active Molecules", in "Molecular Recognition in Chemical and Biological Problems", Special Pub., Royal Chem. Soc., 78, pp. 182-196 (1989); G. Lauri and P. A. Bartlett, "CAVEAT: a Program to Facilitate the Design of Organic Molecules", J. Comput. Aided Mol. Des., 8, pp. 51-66 (1994)). CAVEAT is available from the University of California, Berkeley, Calif; 2. 3D Database systems such as ISIS (MDL Information Systems, San Leandro, Calif.). This area is reviewed in Y. C. Martin, "3D Database Searching in Drug Design", J. Med. Chem., 35, pp. 2145-2154 (1992); and 3. HOOK (M. B. Eisen et al., "HOOK: A Program for Finding Novel Molecular Architectures that Satisfy the Chemical and Steric Requirements of a Macromolecule Binding Site", Proteins: Struct., Funct., Genet., 19, pp. 199-221 (1994). HOOK is available from Molecular Simulations, San Diego, Calif.

Thus the invention includes a method of a method for selecting or designing one or more binding partners of a Ca^{2+} ATPase and/or SLN comprising the steps of: (a) providing a structural representation of a SERCA Ca^{2+} ATPase and/or SLN binding region as defined by the coordinates of Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å or selected coordinates thereof (b) using computational means to dock a three dimensional structural representation of a first binding partner in part of the binding region; (c) docking at least a second binding partner in another part of the binding region; (d) quantifying the interaction energy between the first or second binding partner and part of the binding region; (e) repeating steps (b) to (d) with another first and second binding partner, selecting a first and a second binding partner based on the quantified interaction energy of all of said first and second binding partners; (f) optionally, visually inspecting the relationship of the first and second binding partner to each other in relation to the binding region; and (g) assembling the first and second binding partners into a one binding partner that interacts with the binding region by model building.

As an alternative to the step-wise assembly of binding partners, binding partners may be designed as a whole or "de novo" using either an empty binding region or optionally including some portion(s) of a known binding partner(s). There are many de novo ligand design methods including: 1. LUDI (H.-J. Bohm, "The Computer Program LUDI: A New
5 Method for the De Novo Design of Enzyme Inhibitors", J. Comp. Aid. Molec. Design, 6, pp. 61-78 (1992)). LUDI is available from Molecular Simulations Incorporated, San Diego, Calif; 2. LEGEND (Y. Nishibata et al., Tetrahedron, 47, p. 8985 (1991)). LEGEND is available from Molecular Simulations Incorporated, San Diego, Calif; 3. LeapFrog (available from Tripos Associates, St. Louis, Mo.); and 4. SPROUT (V. Gillet et al.,
10 "SPROUT: A Program for Structure Generation)", J. Comput. Aided Mol. Design, 7, pp. 127-153 (1993)). SPROUT is available from the University of Leeds, UK.

Other molecular modelling techniques may also be employed in accordance with this invention (see, e.g., N. C. Cohen et al., "Molecular Modeling Software and Methods for
15 Medicinal Chemistry, J. Med. Chem., 33, pp. 883-894 (1990); see also, M. A. Navia and M. A. Murcko, "The Use of Structural Information in Drug Design", Current Opinions in Structural Biology, 2, pp. 202-210 (1992); L. M. Balbes et al., "A Perspective of Modern Methods in Computer-Aided Drug Design", in Reviews in Computational Chemistry, Vol. 5, K. B. Lipkowitz and D. B. Boyd, Eds., VCH, New York, pp. 337-380 (1994); see also,
20 W. C. Guida, "Software For Structure-Based Drug Design", Curr. Opin. Struct. Biology, 4, pp. 777-781 (1994)).

In addition to the methods described above in relation to the design of binding partners, other computer-based methods are available to select for binding partners that interact
25 with Ca²⁺ ATPase and/or SLN.

For example the invention involves the computational screening of small molecule databases for binding partners that can bind in whole, or in part, to Ca²⁺ ATPase and/or SLN. In this screening, the quality of fit of such binding partners to a binding region of
30 Ca²⁺ ATPase and/or SLN as defined by the coordinates of the SERCA Ca²⁺ ATPase/SLN complex of Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å or selected coordinates thereof, may be judged either by shape complementarity or by estimated interaction energy (E. C. Meng et al., J. Comp. Chem., 13, pp. 505-524 (1992)).

For example, selection may involve using a computer for selecting an orientation of a binding partner with a favourable shape complementarity in a binding region comprising

the steps of: (a) providing the coordinates of the SERCA Ca^{2+} ATPase/SLN complex of Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å or selected coordinates thereof and a three-dimensional structural representation of one or more candidate binding partners; (b) employing computational means to dock a first binding partner in the binding region; (c) quantitating the contact score of the binding partner in different orientations; and (d) selecting an orientation with the highest contact score.

The docking may be facilitated by the contact score. The method may further comprise the step of generating a three-dimensional structural representation of the binding region and binding partner bound therein prior to step (b).

The method may further comprise the steps of: (e) repeating steps (b) through (d) with a second binding partner; and (f) selecting at least one of the first or second binding partner that has a higher contact score based on the quantitated contact score of the first or second binding partner.

In another embodiment, selection may involve using a computer for selecting an orientation of a binding partner that interacts favourably with a binding region comprising: a) providing the coordinates of the SERCA Ca^{2+} ATPase/SLN complex of Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å or selected coordinates thereof; b) employing computational means to dock a first binding partner in the binding region; c) quantitating the interaction energy between the binding partner and all or part of a binding region for different orientations of the binding partner; and d) selecting the orientation of the binding partner with the most favorable interaction energy.

The docking may be facilitated by the quantitated interaction energy and energy minimization with or without molecular dynamics simulations may be performed simultaneously with or following step (b).

The method may further comprise the steps of: (e) repeating steps (b) through (d) with a second binding partner; and (f) selecting at least one of the first or second binding partner that interacts more favourably with a binding region based on the quantitated interaction energy of the first or second binding partner.

In another embodiment, selection may involve screening a binding partner to associate at a deformation energy of binding of less than -7 kcal/mol with a binding region of a Ca^{2+} ATPase and/or SLN, comprising: (a) coordinates of the SERCA Ca^{2+} ATPase/SLN complex of Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å or selected coordinates thereof, and employing computational means which utilise coordinates to dock the binding partner into a binding region; (b) quantifying the deformation energy of binding between the binding partner and the binding region; and (d) selecting a binding partner that associates with a Ca^{2+} ATPase and/or SLN binding region at a deformation energy of binding of less than -7 kcal/mol.

Generally, the one or more binding partners are predicted to bind to at least one amino acid in a given binding region (e.g. SERCA Ca^{2+} ATPase/SLN interaction site), such as at least 2, 3, 4 or 5 amino acid residues.

Preferably, the one or more binding partners that are selected or designed according to the invention, are ones that favourably interact with a Ca^{2+} ATPase and/or SLN. Thus, the one or more binding partners may be structurally complementary to a binding region of SERCA Ca^{2+} ATPase and/or SLN, and interact with a binding region substantially free of steric interference. For example, the one or more binding partners may accommodate a three-dimensional cavity in SERCA Ca^{2+} ATPase and/or SLN without interfering in the structure of SERCA Ca^{2+} ATPase and/or SLN. Complementarity indicates that the binding partner interacts with a binding region in an energy favourable way. Thus, there should be more favourable interactions than non-favourable interactions. Favourable interactions include any non-covalent attractive forces that may exist between chemical structures such as hydrophobic or van-der-Waals interactions and polar interactions such as hydrogen bonding, salt-bridges etc. Unfavourable interactions such as hydrophobic-hydrophilic interactions should be avoided but may be accepted if they are weaker than the sum of the attractive forces. Steric interference such as clashes or overlaps with portions of the binding partner being selected or designed with protein moieties will prevent binding unless resolvable by conformation changes. The binding strength or a potential binding partner may be assessed by comparing favourable and unfavourable interactions, for example on a computer screen or by using computational methods implemented in commercial computer programs.

The invention provides a method of identifying a binding partner of a Ca^{2+} ATPase and/or SLN (e.g. a modulator of a Ca^{2+} ATPase/SLN interaction) comprising:

providing a three-dimensional structural representation of at least part of the SERCA Ca^{2+} ATPase/SLN complex as listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof;

5 providing a three-dimensional structural representation of one or more candidate binding partners,

selecting or designing of one or more binding partners that are structurally complementary to the three-dimensional structural representation of at least part of the SERCA Ca^{2+} ATPase/SLN complex.

10

The invention provides a method of identifying a binding partner of a Ca^{2+} ATPase and/or SLN (e.g. a modulator of a Ca^{2+} ATPase/SLN interaction) comprising:

providing a three-dimensional structural representation of at least part of the SERCA Ca^{2+} ATPase/SLN complex as listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof;

15 providing a three-dimensional structural representation of one or more candidate binding partners; and

selecting one or more binding partners that can bind to at least one amino acid residue of a binding region of SERCA Ca^{2+} ATPase and/or SLN without steric interference.

The invention also provides a computer-assisted method for identifying one or more binding partners of a Ca^{2+} ATPase and/or SLN (e.g. a modulator of a Ca^{2+} ATPase/SLN interaction) using a programmed computer processor, a data storage system, a data input device and a data output device, the method comprising:

25 inputting into the programmed computer, through the input device, data comprising the coordinates as listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof;

30 comparing using said processor the coordinates or selected coordinates thereof to a computer data base of low molecular weight organic chemical structures stored in the data storage system; and

selecting from said database, using computer methods, a chemical structure having a portion that is structurally complementary to the coordinates or selected coordinates thereof and being free of steric hindrance with the SERCA Ca^{2+} ATPase and/or SLN. Typically, the method makes use of selected coordinates that correspond to a particular binding region of SERCA Ca^{2+} ATPase and/or SLNs described above.

35

The invention further provides a computer-assisted method for identifying one or more binding partners of a Ca^{2+} ATPase and/or SLN (e.g. a modulator of a Ca^{2+} ATPase/SLN interaction) using a programmed computer processor, a data storage system, a data input device and a data output device, the method comprising:

inputting into the programmed computer, through the input device, data comprising the coordinates as listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof;

comparing using said processor the coordinates or selected coordinates thereof to a computer data base of low molecular weight organic chemical structures stored in the data storage system; and

constructing, using computer methods, a chemical structure having a portion that is structurally complementary to the coordinates or selected coordinates thereof and being free of steric hindrance with the SERCA Ca^{2+} ATPase and/or SLN. Typically, the method makes use of selected coordinates that correspond to a particular binding region of SERCA Ca^{2+} ATPase and/or SLN as described above.

The invention provides a method for identifying one or more binding partners of a Ca^{2+} ATPase and/or SLN (e.g. a modulator of a Ca^{2+} ATPase/SLN interaction), the method comprising:

selecting one or more candidate binding partners using atomic coordinates in conjunction with computer modelling, wherein said coordinates are the coordinates as listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof, by docking one or more candidate binding partners into a binding region of SERCA Ca^{2+} ATPase and/or SLN by computer modelling and selecting one or more candidate binding partners capable of binding to at least one amino acid in the binding region;

contacting the one or more candidate binding partners and the Ca^{2+} ATPase and/or SLN; and

assessing binding of the one or more candidate binding partners with the Ca^{2+} ATPase and/or SLN. Preferably, the method comprises assessing whether the one or more candidate binding partners modulate an activity of the Ca^{2+} ATPase and/or SLN, such that the interaction between the Ca^{2+} ATPase and SLN.

Preferences for the binding region of the SERCA Ca^{2+} ATPase and/or SLN include those defined above, such as a binding region of the SERCA Ca^{2+} ATPase, or a binding region of SLN, or a binding region of the SERCA Ca^{2+} ATPase/SLN complex (eg one that spans

across both proteins). Preferably, the one or more binding partners bind to the SERCA Ca^{2+} ATPase/SLN interaction site.

A third aspect of the invention provides a method for selecting or designing one or more
5 binding partners of a Ca^{2+} ATPase having a binding pocket in the position structurally
equivalent to the binding pocket of rabbit SERCA Ca^{2+} ATPase that is defined by
residues including Phe88, Phe92, Val93, Leu96, Ile97, Ala100, Ile103, Val104, Trp107,
Gln108, Asn111, Tyr122, Arg324, Lys328, Trp794, Leu797, Asp800, Gly801, Leu802,
Thr805, Ala806, Phe809, Trp932, Ser936, Leu939, Ser942, Leu943, Leu946, Ile947,
10 Pro952, Leu953, Ile956, and Phe957 of rabbit SERCA Ca^{2+} ATPase, the method
comprising the step of using molecular modelling means to select or design one or more
binding partners that are predicted to interact with the said Ca^{2+} ATPase, wherein a
three-dimensional structural representation of one or more candidate binding partners
are compared with a three-dimensional structural representation of the said binding
15 pocket, and one or more candidate binding partners that are predicted to interact with the
said binding pocket, are selected.

Preferably, the binding partner selected is one that is able to interact with at least one of
the amino acids that define the binding pocket (Phe88, Phe92, Val93, Leu96, Ile97,
20 Ala100, Ile103, Val104, Trp107, Gln108, Asn111, Tyr122, Arg324, Lys328, Trp794,
Leu797, Asp800, Gly801, Leu802, Thr805, Ala806, Phe809, Trp932, Ser936, Leu939,
Ser942, Leu943, Leu946, Ile947, Pro952, Leu953, Ile956, and Phe957), such as at least
2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27,
28, 29, 30, 31, 32 or all 33 of said amino acid residues.

25 A fourth aspect of the invention provides a method for selecting or designing one or more
binding partners of a SLN having a binding pocket in the position structurally equivalent
to the binding pocket of rabbit SLN that is defined by residues including Met1, Glu2,
Arg3, Ser4, Thr5, Arg6, Glu7, Leu8, Cys9, Leu10, and Asn11 of rabbit SLN, the method
30 comprising the step of using molecular modelling means to select or design one or more
binding partners that are predicted to interact with the said SLN, wherein a three-
dimensional structural representation of one or more candidate binding partners are
compared with a three-dimensional structural representation of the said binding pocket,
and one or more candidate binding partners that are predicted to interact with the said
35 binding pocket, are selected.

Preferably, the binding partner selected is one that is able to interact with at least one of amino acids that define the binding pocket (Met1, Glu2, Arg3, Ser4, Thr5, Arg6, Glu7, Leu8, Cys9, Leu10, and Asn11), such as at least 2, 3, 4, 5, 6, 7, 8, 9, 10 or all 11 of said amino acid residues.

5

By a Ca^{2+} ATPase having a binding pocket in the position structurally equivalent to the defined binding pocket, we include the meaning of a protein identifiable as that of a Ca^{2+} ATPase, and further having a predicted or determined three-dimensional structure that includes a binding pocket defined by Phe88, Phe92, Val93, Leu96, Ile97, Ala100, Ile103, Val104, Trp107, Gln108, Asn111, Tyr122, Arg324, Lys328, Trp794, Leu797, Asp800, Gly801, Leu802, Thr805, Ala806, Phe809, Trp932, Ser936, Leu939, Ser942, Leu943, Leu946, Ile947, Pro952, Leu953, Ile956, and Phe957 according to the numbering of the rabbit SERCA Ca^{2+} ATPase in Figure 8. An amino acid sequence may be identifiable as that of a Ca^{2+} ATPase by reference to sequence identity or similarities of three dimensional structure with known Ca^{2+} ATPases, as known to those skilled in the art.

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By a SLN having a binding pocket in the position structurally equivalent to the defined binding pocket, we include the meaning of a protein identifiable as that of a SLN, and further having a predicted or determined three-dimensional structure that includes a binding pocket defined by Met1, Glu2, Arg3, Ser4, Thr5, Arg6, Glu7, Leu8, Cys9, Leu10, and Asn11 according to the numbering of the rabbit SLN in Figure 8. An amino acid sequence may be identifiable as that of a SLN by reference to sequence identity or similarities of three dimensional structure with known SLN, as known to those skilled in the art.

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It will be appreciated in the third and fourth aspects of the invention that the three-dimensional structural representations of the defined binding pockets may be any suitable three-dimensional structural representation. For example, it may be a three-dimensional structural representation represented by the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof. It is preferred if the selected coordinates are from one or more amino acid residues that define a binding region of SERCA Ca^{2+} ATPase and/or SLN, including those mentioned above. Alternatively, the three-dimensional structural representations of the defined binding pockets may be a three-dimensional structural representation modelled on such coordinates.

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The structural representation may then be compared with structural representations of one or more candidate binding partners and those binding partners that are predicted to interact with the binding pocket are selected.

- 5 Any suitable molecular modelling means may be employed in this selection, including those outlined above.

It is appreciated that in some instances high throughput screening of binding partners is preferred and that methods of the invention may be used as "library screening" methods,
10 a term well known to those skilled in the art. Thus, the binding partner may be a library of binding partners. For example, the library may be a peptide or protein library produced, for example, by ribosome display or an antibody library prepared either *in vivo*, *ex vivo* or *in vitro*. Methodologies for preparing and screening such libraries are known in the art.

15 Determination of the three-dimensional structure of the SERCA Ca^{2+} ATPase/SLN complex provides important information about the binding sites of SERCA Ca^{2+} ATPases and SLN, particularly when comparisons are made with other Ca^{2+} ATPases. This information may then be used for rational design and modification of Ca^{2+} ATPase and/or
20 SLN binding partners, e.g. by computational techniques which identify possible binding ligands for the binding sites, by enabling linked-fragment approaches to drug design, and by enabling the identification and location of bound ligands using X-ray crystallographic analysis. These techniques are discussed in more detail below.

25 Thus as a result of the determination of the SERCA Ca^{2+} ATPase/SLN three-dimensional structure, more purely computational techniques for rational drug design may also be used to design structures whose interaction with Ca^{2+} ATPase and/or SLN is better understood (for an overview of these techniques see e.g. Walters et al (Drug Discovery Today, Vol.3, No.4, (1998), 160-178; Abagyan, R.; Totrov, M. Curr. Opin. Chem. Biol.
30 2001 , 5, 375-382). For example, automated ligand-receptor docking programs (discussed e.g. by Jones et al. in Current Opinion in Biotechnology, Vol.6, (1995), 652-656 and Halperin, I.; Ma, B.; Wolfson, H.; Nussinov, R. Proteins 2002, 47, 409-443), which require accurate information on the atomic coordinates of target receptors may be used.

35 The aspects of the invention described herein which utilize the SERCA Ca^{2+} ATPase/SLN structure *in silico* may be equally applied to both the coordinates of the

SERCA Ca²⁺ ATPase/SLN complex of Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å or selected coordinates thereof, and to structural coordinates modelled on said coordinates, for example using the methods described below. Thus having determined a new set of structural coordinates, for example of a related Ca²⁺ ATPase, by the methods described below, such a structure may be used, for example, in a computer-based method of rational drug design as described herein. In addition, the availability of the structure of the SERCA Ca²⁺ ATPase/SLN complex will allow the generation of highly predictive pharmacophore models for virtual library screening or ligand design.

A fifth aspect of the invention provides a method for the analysis of the interaction of one or more binding partners with a Ca²⁺ ATPase and/or SLN, comprising:

providing a three dimensional structural representation of the SERCA Ca²⁺ ATPase/SLN complex as defined by the coordinates of the SERCA Ca²⁺ ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof;

providing a three dimensional structural representation of one or more binding partners to be fitted to the structural representation of the SERCA Ca²⁺ ATPase/SLN complex or selected coordinates thereof; and

fitting the one of more binding partners to said structural representation.

This method of the invention is generally applicable for the analysis of known binding partners of SERCA Ca²⁺ and/or SLN, the development or discovery of binding partners of SERCA Ca²⁺ and/or SLN, the modification of binding partners of SERCA Ca²⁺ and/or SLN e.g. to improve or modify one or more of their properties, and the like.

It will be desirable to model a sufficient number of atoms of the SERCA Ca²⁺ ATPase/SLN complex as defined by the coordinates of the SERCA Ca²⁺ ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof, which represent a binding region, e.g. atoms from amino acid residues contributing to the SLN binding region of SERCA Ca²⁺ ATPase, including amino acid residues Phe88, Phe92, Val93, Leu96, Ile97, Ala100, Ile103, Val104, Trp107, Gln108, Asn111, Tyr122, Arg324, Lys328, Trp794, Leu797, Asp800, Gly801, Leu802, Thr805, Ala806, Phe809, Trp932, Ser936, Leu939, Ser942, Leu943, Leu946, Ile947, Pro952, Leu953, Ile956, and Phe957 may be used, and/or atoms from one or more amino acid residues of the SLN binding pocket of SERCA Ca²⁺ ATPase, including Val104, Trp107, Gln108, Glu109, Asn111, Ala112,

Ala115, Ala118, Glu121, Tyr122, Thr317, Leu321, Arg324, Lys328, Phe760, Leu802, Thr805, Ala806 and Phe809, may be used, and/or atoms of one or more amino acid residues of the SERCA Ca^{2+} ATPase binding site of SLN, including amino acid residues Met1, Glu2, Arg3, Ser4, Thr5, Arg6, Glu7, Leu8, Cys9, Leu10 and Asn11. Although every different binding partner bound by SERCA Ca^{2+} ATPase and/or SLN may interact with different parts of a binding region of SERCA Ca^{2+} ATPase and/or SLN, the structure of the SERCA Ca^{2+} ATPase/SLN complex allows the identification of a number of particular sites which are likely to be involved in many of the interactions of SERCA Ca^{2+} ATPase/SLN with a drug candidate. Additional preferred selected coordinates are as described as above with respect to the first and second aspects of the invention.

In order to provide a three-dimensional structural representation of a binding partner to be fitted to the SERCA Ca^{2+} ATPase/SLN structure, the binding partner structural representation may be modelled in three dimensions using commercially available software for this purpose or, if its crystal structure is available, the coordinates of the structure may be used to provide a structural representation of the binding partner for fitting to the SERCA Ca^{2+} ATPase/SLN structure of the invention.

By "fitting", is meant determining by automatic, or semi-automatic means, interactions between one or more atoms of a candidate binding partner and at least one atom of the SERCA Ca^{2+} ATPase/SLN structure of the invention, and calculating the extent to which such interactions are stable. Interactions include attraction and repulsion, brought about by charge, steric, lipophilic, considerations and the like. Charge and steric interactions of this type can be modelled computationally. An example of such computation would be via a force field such as Amber (Cornell et al. A Second Generation Force Field for the Simulation of Proteins, Nucleic Acids, and Organic Molecules, Journal of the American Chemical Society, (1995), 117(19), 5179-97) which would assign partial charges to atoms on the protein and binding partner and evaluate the electrostatic interaction energy between a protein and binding partner atom using the Coulomb potential. The Amber force field would also assign van der Waals energy terms to assess the attractive and repulsive steric interactions between two atoms. Lipophilic interactions can be modeled using a variety of means. For example the ChemScore function (Eldridge M D; Murray C W; Auton T R; Paolini G V; Mee R P Empirical scoring functions: I. The development of a fast empirical scoring function to estimate the binding affinity of binding partners in receptor complexes, Journal of computer- aided molecular design (1997 Sep), 11 (5), 425-45) assigns protein and binding partner atoms as hydrophobic or polar, and a favourable energy term is specified for the interaction between two hydrophobic

atoms. Other methods of assessing the hydrophobic contributions to ligand binding are available and these would be known to one skilled in the art. Other methods of assessing interactions are available and would be known to one skilled in the art of designing molecules. Various computer-based methods for fitting are described further
5 herein.

More specifically, the interaction of a binding partner with the SERCA Ca^{2+} ATPase/SLN structure of the invention can be examined through the use of computer modelling using a docking program such as GOLD (Jones et al., J. Mol. Biol., 245, 43-53 (1995), Jones
10 et al., J. Mol. Biol., 267, 727-748 (1997)), GRAMM (Vakser, I.A., Proteins, Suppl., 1 :226-230 (1997)), DOCK (Kuntz et al, (1982) J. Mol. Biol., 161, 269-288; Makino et al, (1997) J.Comput.Chem., 18, 1812-1825), AUTODOCK (Goodsell et al, (1990) Proteins, 8, 195-202, Morris et al, (1998) J.Comput.Chem., 19, 1639- 1662.), FlexX, (Rarey et al, (1996) J. Mol. Biol., 261, 470-489) or ICM (Abagyan et al, (1994) J.Comput.Chem., 15,
15 488-506). This procedure can include computer fitting of binding partners to the SERCA Ca^{2+} ATPase/SLN structure to ascertain how well the shape and the chemical structure of the binding partner will bind to a Ca^{2+} ATPase and/or SLN.

Thus the invention includes a method for the analysis of the interaction of one or more
20 binding partners with a Ca^{2+} ATPase and/or SLN comprising (a) constructing a computer representation of a binding region of a Ca^{2+} ATPase and/or SLN as defined by the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof (b) selecting a binding partner to be evaluated by a method selected
25 from the group consisting of assembling said binding partner; selecting a binding partner from a small molecule database; *de novo* ligand design of the binding partner; and modifying a known agonist or inhibitor, or a portion thereof, of a Ca^{2+} ATPase and/or SLN or homologue thereof; (c) employing computational means to dock said binding partner to be evaluated in a binding region in order to provide an energy-minimized configuration
30 of the binding partner in a binding region; and (d) evaluating the results of said docking to quantify the interaction energy between said binding partner and the binding region.

Also computer-assisted, manual examination of the binding region structure of the Ca^{2+} ATPase and/or SLN may be performed. The use of programs such as GRID (Goodford,
35 (1985) J. Med. Chem., 28, 849- 857) - a program that determines probable interaction sites between molecules with various functional groups and an enzyme surface - may

also be used to analyse a binding region to predict, for example, the types of modifications which will alter the rate of metabolism of a binding partner.

Computer programs can be employed to estimate the attraction, repulsion, and steric hindrance of the a Ca^{2+} ATPase and/or SLN structure and a binding partner.

If more than one binding region is characterized and a plurality of respective smaller molecular fragments are designed or selected, a binding partner may be formed by linking the respective small molecular fragments into a single binding partner, which maintains the relative positions and orientations of the respective small molecular fragments at the binding sites. The single larger binding partner may be formed as a real molecule or by computer modelling. Detailed structural information can then be obtained about the binding of the binding partner to a Ca^{2+} ATPase and/or SLN, and in the light of this information adjustments can be made to the structure or functionality of the binding partner, e.g. to alter its interaction with a Ca^{2+} ATPase and/or SLN. The above steps may be repeated and re- repeated as necessary.

Thus, the three dimensional structural representation of the one or more binding partners of any of the above aspects of the invention may be obtained by: providing structural representations of a plurality of molecular fragments; fitting the structural representation of each of the molecular fragments to the coordinates of the structural representation of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof; and assembling the representations of the molecular fragments into one or more representations of single molecules to provide the three-dimensional structural representation of one or more candidate binding partners.

Typically the binding partner or molecule fragment is fitted to at least 5 or 10 non-hydrogen atoms of the SERCA Ca^{2+} ATPase/SLN structure, preferably at least 20, 30, 40, 50, 60, 70, 80 or 90 non-hydrogen atoms and more preferably at least 100, 150, 200, 250, 300, 350, 400, 450, or 500 atoms and even more preferably at least 600, 700, 800, 900, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, 2100 or 2200 non-hydrogen atoms.

The invention includes screening methods to identify drugs or lead compounds of use in treating a disease or condition. For example, large numbers of binding partners, for

example in a chemical database, can be screened for their ability to bind to a Ca^{2+} ATPase and/or SLN.

5 It is appreciated that in the methods described herein, which may be drug screening methods, a term well known to those skilled in the art, the binding partner may be a drug-like compound or lead compound for the development of a drug-like compound.

10 The term "drug-like compound" is well known to those skilled in the art, and may include the meaning of a compound that has characteristics that may make it suitable for use in medicine, for example as the active ingredient in a medicament. Thus, for example, a drug-like compound may be a molecule that may be synthesised by the techniques of organic chemistry, less preferably by techniques of molecular biology or biochemistry, and is preferably a small molecule, which may be of less than 5000 daltons (such as less than 500 daltons) and which may be water-soluble. A drug-like compound may
15 additionally exhibit features of selective interaction with a particular protein or proteins and be bioavailable and/or able to penetrate target cellular membranes or the blood:brain barrier, but it will be appreciated that these features are not essential.

20 The term "lead compound" is similarly well known to those skilled in the art, and may include the meaning that the compound, whilst not itself suitable for use as a drug (for example because it is only weakly potent against its intended target, non-selective in its action, unstable, poorly soluble, difficult to synthesise or has poor bioavailability) may provide a starting-point for the design of other compounds that may have more desirable characteristics.

25

Thus in one embodiment of the above methods of the invention, the methods further comprise modifying the structural representation of the binding partner so as to increase or decrease their interaction with the Ca^{2+} ATPase and/or SLN.

30 For example, once a binding partner has been designed or selected by the above methods, the efficiency with which that binding partner may bind to a Ca^{2+} ATPase and/or SLN may be tested and optimised, for example by computational evaluation. For example, a binding partner designed or selected as binding to a Ca^{2+} ATPase and/or SLN may be further computationally optimised so that in its bound state it would
35 preferably lack repulsive electrostatic interaction with the target Ca^{2+} ATPase and/or SLN and with the surrounding water molecules. Such non-complementary electrostatic interactions include repulsive charge-charge, dipole-dipole and charge-dipole

interactions. Thus, it will be appreciated that the extent to which a given binding partner can modulate the Ca^{2+} ATPase/SLN interaction may be increased or decreased.

Furthermore, it is often desired that binding partners demonstrate a relatively small difference in energy between the bound and free states (i.e., a small deformation energy of binding). Thus, binding partners may be designed with a deformation energy of binding of not greater than about 10 kcal/mole, more preferably, not greater than 7 kcal/mole. Binding partners may interact with the binding region in more than one conformation that is similar in overall binding energy. In those cases, the deformation energy of binding is taken to be the difference between the energy of the free binding partner and the average energy of the conformations observed when the binding partner binds to the protein.

Specific computer software is available in the art to evaluate compound deformation energy and electrostatic interactions. Examples of programs designed for such uses include: Gaussian 94, revision C (M. J. Frisch, Gaussian, Inc., Pittsburgh, Pa. .COPYRGT.1995); AMBER, version 4.1 (P. A. Kollman, University of California at San Francisco, .COPYRGT.1995); QUANTA/CHARMM (Molecular Simulations, Inc., San Diego, Calif. .COPYRGT.1998); Insight II/Discover (Molecular Simulations, Inc., San Diego, Calif. .COPYRGT.1998); DelPhi (Molecular Simulations, Inc., San Diego, Calif. .COPYRGT.1998); and AMSOL (Quantum Chemistry Program Exchange, Indiana University). These programs may be implemented, for instance, using a Silicon Graphics workstation such as an Indigo2 with "IMPACT" graphics. Other hardware systems and software packages will be known to those skilled in the art.

By modifying the structural representation we include, for example, adding molecular scaffolding, adding or varying functional groups, or connecting the molecule with other molecules (e.g. using a fragment linking approach) such that the chemical structure of the binding partner is changed while its original binding to Ca^{2+} ATPase and/or SLN capability is increased or decreased. Such optimisation is regularly undertaken during drug development programmes to e.g. enhance potency, promote pharmacological acceptability, increase chemical stability etc. of lead compounds.

Examples of modifications include substitutions or removal of groups containing residues which interact with the amino acid side chain groups of the SERCA Ca^{2+} ATPase/SLN structure of the invention. For example, the replacements may include the addition or removal of groups in order to decrease or increase the charge of a group in a binding

partner, the replacement of a charge group with a group of the opposite charge, or the replacement of a hydrophobic group with a hydrophilic group or vice versa. It will be understood that these are only examples of the type of substitutions considered by medicinal chemists in the development of new pharmaceutical compounds and other modifications may be made, depending upon the nature of the starting binding partner and its activity.

The potential binding effect of a binding partner on a Ca^{2+} ATPase and/or SLN may be analysed prior to its actual synthesis and testing by the use of computer modeling techniques. If the theoretical structure of the given entity suggests insufficient interaction and association between it and the Ca^{2+} ATPase and/or SLN, testing of the entity is obviated. However, if computer modelling indicates a strong interaction, the molecule may then be synthesized and tested for its ability to bind to a Ca^{2+} ATPase and/or SLN. In this manner, synthesis of inoperative compounds may be avoided.

Thus in a further embodiment of the above aspects of the invention, the methods further comprise the steps of obtaining or synthesising the one or more binding partners of a Ca^{2+} ATPase and/or SLN; and optionally contacting the one or more binding partners with a Ca^{2+} ATPase and/or SLN to determine the ability of the one or more binding partners to interact with the Ca^{2+} ATPase and/or SLN.

Various methods may be used to determine binding between a Ca^{2+} ATPase and/or SLN and a binding partner including, for example, enzyme linked immunosorbent assays (ELISA), surface plasmon resonance assays, chip-based assays, immunocytofluorescence, yeast two-hybrid technology and phage display which are common practice in the art and are described, for example, in Plant *et al* (1995) *Analyt Biochem*, 226(2), 342-348. and Sambrook *et al* (2001) *Molecular Cloning A Laboratory Manual*. Third Edition. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, New York. Other methods of detecting binding between a Ca^{2+} ATPase and/or SLN and a binding partner include ultrafiltration with ion spray mass spectroscopy/HPLC methods or other physical and analytical methods. Fluorescence Energy Resonance Transfer (FRET) methods, for example, well known to those skilled in the art, may be used, in which binding of two fluorescent labelled entities may be measured by measuring the interaction of the fluorescent labels when in close proximity to each other.

Once computer modelling has indicated that a binding partner has a strong interaction, it is appreciated that it may be desirable to crystallise a complex of the Ca^{2+} ATPase

and/or SLN with that binding partner and analyse its interaction further by X-ray crystallography.

Thus in a further embodiment, the methods of the invention further comprise the steps of
5 obtaining or synthesising the one or more binding partners of a Ca^{2+} ATPase and/or SLN; forming one or more complexes of the Ca^{2+} ATPase and/or SLN and the one or more binding partners; and analysing the one or more complexes by X-ray crystallography to determine the ability of the one or more binding partners to interact with Ca^{2+} ATPase and/or SLN.

10

Thus, it will be appreciated that another particularly useful drug design technique enabled by this invention is iterative drug design. Iterative drug design is a method for optimizing associations between a protein and a binding partner by determining and evaluating the three-dimensional structures of successive sets of protein/compound
15 complexes. In iterative drug design, crystals of a series of proteins or protein complexes are obtained and then the three-dimensional structures of each crystal are solved. Such an approach provides insight into the association between the proteins and binding partners of each complex. This is accomplished by selecting candidate binding partners, obtaining crystals of this new protein/binding partner complex, solving the three-
20 dimensional structure of the complex, and comparing the associations between the new protein/binding partner complex and previously solved protein/binding partner complexes. By observing how changes in the binding partner affected the protein/binding partner associations, these associations may be optimized.

25 In some cases, iterative drug design is carried out by forming successive protein- binding partner complexes and then crystallizing each new complex. High throughput crystallization assays may be used to find a new crystallization condition or to optimize the original protein or complex crystallization condition for the new complex. Alternatively, a pre-formed protein crystal may be soaked in the presence of a binding
30 partner, thereby forming a protein/ binding partner complex and obviating the need to crystallize each individual protein/ binding partner complex.

The ability of a binding partner to modify a function of Ca^{2+} ATPase and/or SLN may also be tested. For example the ability of a binding partner to modulate Ca^{2+} ATPase function
35 (e.g. by modulating the Ca^{2+} ATPase/SLN interaction) could be tested by a number of well known standard methods, described extensively in the prior art.

In addition to *in silico* analysis and design, the interaction of one or more binding partners with Ca^{2+} ATPase and/or SLN may be analysed directly by X-ray crystallography experiments, wherein the coordinates of the structural representation of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof, are used to analyse the a crystal complex of the Ca^{2+} ATPase and/or SLN and binding partner. This can provide high resolution information of the interaction and can also provide insights into a mechanism by which a binding partner exerts an agonistic or antagonistic function.

Accordingly, a fifth aspect of the invention provides a method for the analysis of the interaction of one or more binding partners with a Ca^{2+} ATPase and/or SLN, comprising:

obtaining or synthesising one or more binding partners;

forming one or more crystallised complexes of a binding partner with a Ca^{2+} ATPase and/or SLN; and

analysing the one or more complexes by X-ray crystallography by employing the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof, to determine the ability of the one or more binding partners to interact with the a Ca^{2+} ATPase and/or SLN.

Preferences for the selected coordinates in this and all subsequent aspects of the invention are as defined above with respect to the first aspect of the invention.

The analysis of such structures may employ X-ray crystallographic diffraction data from the complex and the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof, to generate a difference Fourier electron density map of the complex. The difference Fourier electron density map may then be analysed.

In one embodiment, the one or more crystallised complexes are formed by soaking a crystal of a Ca^{2+} ATPase and/or SLN with the binding partner to form a complex. Alternatively, the complexes may be obtained by cocrystallising the Ca^{2+} ATPase and/or SLN with the binding partner. For example a purified Ca^{2+} ATPase protein sample is incubated over a period of time (usually >1 hr) with a potential binding partner and the complex can then be screened for crystallization conditions. Alternatively, protein

crystals containing a first binding partner can be back-soaked to remove this binding partner by placing the crystals into a stabilising solution in which the binding partner is not present. The resultant crystals can then be transferred into a second solution containing a second binding partner and used to produce an X-ray diffraction pattern of

5 Ca^{2+} ATPase and/or SLN complexed with the second binding partner.

The complexes can be analysed using X-ray diffraction methods, e.g. according to the approach described by Greer et al., (J of Medicinal Chemistry, Vol. 37, (1994), 1035-1054), and difference Fourier electron density maps can be calculated based on X-ray

10 diffraction patterns of soaked or co-crystallized Ca^{2+} ATPase and/or SLN and the solved structure of uncomplexed (i.e. without binding partner) Ca^{2+} ATPase and/or SLN.

Electron density maps can be calculated using programs such as those from the CCP4 computing package (Collaborative Computational Project 4. The CCP4 Suite: Programs

15 for Protein Crystallography, Acta Crystallographica, D50, (1994), 760-763.). For map visualization and model building programs such as "O" (Jones et al., Acta Crystallographica, A47, (1991), 110-119) can be used.

This information may thus be used to optimise known classes of Ca^{2+} ATPase and/or

20 SLN binding partners and to design and synthesize novel classes of Ca^{2+} ATPase and/or SLN binding partners, particularly those which modulate Ca^{2+} ATPase function (e.g. by modulating the Ca^{2+} ATPase/SLN interaction), and to design drugs with modified Ca^{2+} ATPase and/or SLN interactions.

In one approach, the structure of a binding partner bound to a Ca^{2+} ATPase and/or SLN may be determined by experiment. This will provide a starting point in the analysis of the binding partner bound to Ca^{2+} ATPase and/or SLN thus providing those of skill in the art with a detailed insight as to how that particular binding partner interacts with Ca^{2+} ATPase and/or SLN and the mechanism by which it exerts any functional effect.

Many of the techniques and approaches applied to structure-based drug design described above rely at some stage on X-ray analysis to identify the binding position of a binding partner in a ligand-protein complex. A common way of doing this is to perform X-ray crystallography on the complex, produce a difference Fourier electron density map,

35 and associate a particular pattern of electron density with the binding partner. However, in order to produce the map (as explained e.g. by Blundell et al., in Protein Crystallography, Academic Press, New York, London and San Francisco, (1976)), it is

necessary to know beforehand the protein three dimensional structure (or at least a set of structure factors for the protein crystal). Therefore, determination of the SERCA Ca^{2+} ATPase/SLN structure also allows difference Fourier electron density maps of binding partner complexes with SERCA Ca^{2+} ATPase and/or SLN to be produced, determination
5 of the binding position of the binding partner and hence may greatly assist the process of rational drug design.

Accordingly, a sixth aspect of the invention provides a method for predicting the three dimensional structure of a binding partner of unknown structure, or part thereof, which
10 binds to a Ca^{2+} ATPase and/or SLN, comprising:

providing the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof;

providing an X-ray diffraction pattern of a Ca^{2+} ATPase and/or SLN complexed
15 with the binding partner; and

using said coordinates to predict at least part of the structure coordinates of the binding partner.

In one embodiment, the X-ray diffraction pattern is obtained from a crystal formed by
20 soaking a crystal of a Ca^{2+} ATPase and/or SLN with the binding partner to form a complex. Alternatively, the X-ray diffraction pattern is obtained from a crystal formed by cocrystallising a Ca^{2+} ATPase and/or SLN with the binding partner as described above. Alternatively, protein crystals containing a first binding partner can be back-soaked to remove this binding partner and the resultant crystals transferred into a second solution
25 containing a second binding partner as described above.

A mixture of compounds may be soaked or co-crystallized with a Ca^{2+} ATPase and/or SLN crystal (i.e. a crystal of a Ca^{2+} ATPase or of a SLN or of a Ca^{2+} ATPase/SLN complex), wherein only one or some of the compounds may be expected to bind to the
30 Ca^{2+} ATPase and/or SLN. The mixture of compounds may comprise a ligand known to bind to a Ca^{2+} ATPase and/or SLN. As well as the structure of the complex, the identity of the complexing compound(s) is/are then determined.

Preferably, the methods of the previous aspects of the invention are computer-based.
35 For example, typically the methods of the previous aspects of the invention make use of the computer systems and computer-readable storage mediums of the aspects of the invention described below.

A seventh aspect of the invention provides a method for producing a binding partner of a Ca^{2+} ATPase and/or SLN comprising: identifying a binding partner according to the methods of any of the aspects of invention described above, and synthesising the binding partner.

The binding partner may be synthesised using any suitable technique known in the art including, for example, the techniques of synthetic chemistry, organic chemistry and molecular biology.

10

It will be appreciated that it may be desirable to test the binding partner in an in vivo or in vitro biological system in order to determine its binding and/or activity and/or its effectiveness. For example, its binding to a Ca^{2+} ATPase and/or SLN may be assessed using any suitable binding assay known in the art including the examples described above. Alternatively, its ability to modulate the interaction between Ca^{2+} ATPase and SLN may be assessed. Moreover, its effect on Ca^{2+} ATPase or SLN function in an in vivo or in vitro assay may be tested. For example, the effect of the binding partner on Ca^{2+} ATPase activity may be determined. Several techniques are available in the art to detect and measure ATPase activity which would be suitable for use in the present invention. Many of these are available in kits both for determining expression in vitro and in vivo.

15

20

An eighth aspect of the invention provides a binding partner produced by the method of the seventh aspect of the invention.

25

Following identification of a binding partner, it may be manufactured and/or used in the preparation, i.e. manufacture or formulation, of a composition such as a medicament, pharmaceutical composition or drug. These may be administered to individuals.

30

Accordingly, the invention includes a method for producing a medicament, pharmaceutical composition or drug, the process comprising: (a) providing a binding partner according to the eighth aspect of the invention and (b) preparing a medicament, pharmaceutical composition or drug containing the binding partner.

35

The medicaments may be used to treat any disorder or condition ameliorated by modulation of Ca^{2+} ATPase or SLN. Malfunctioning Ca^{2+} cycling in the SR is known to play a central role in several human diseases including insulin resistance and diabetes,

muscular dystrophy, atherosclerosis, heart failure and renal disease (James et al., 1989; Odermatt et al., 1989) and recent successful clinical trials with gene delivery of SERCA in patients with heart failure have demonstrated that up-regulation of SERCA activity is an important therapeutic target (Gwathmey et al., 2011; Tilemann et al., 2012). Both
5 activators and inhibitors of SERCA activity have been suggested to be of potential therapeutic value. Thus, in an embodiment, the disorder or condition is any of cardiovascular disease, heart failure, insulin resistance, diabetes, muscular dystrophy, atherosclerosis, cancer and renal disease.

10 A ninth aspect of the invention provides a method of predicting a three dimensional structural representation of a target protein of unknown structure, or part thereof, comprising:

providing the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more
15 than 4.95 Å, or selected coordinates thereof; and

predicting the three-dimensional structural representation of the target protein, or part thereof, by modelling the structural representation on all or the selected coordinates.

In this aspect of the invention, the coordinates of the SERCA Ca^{2+} ATPase/SLN structure
20 are used to predict a three dimensional representation of a target protein of unknown structure, or part thereof, by modelling. By "modelling", we include the meaning of the prediction of structures using computer-assisted or other *de novo* prediction of structure, based upon manipulation of the coordinate data from Table (i) or selected coordinates thereof.

25 The target protein may be any protein that shares sufficient sequence identity to either the rabbit SERCA Ca^{2+} ATPase or the rabbit SLN such that its structure can be modelled by using the coordinates of Table (i). It will be appreciated that if a structural representation of only a part of the target protein is being modelled, for example a
30 particular domain, the target protein only has to share sufficient sequence identity to the SERCA Ca^{2+} ATPase or the rabbit SLN over that part. It will also be understood that the coordinates corresponding to amino acid residues of SERCA Ca^{2+} ATPase will be used to model a structure of a target protein has sufficient sequence identity to SERCA Ca^{2+} ATPase, and that coordinates corresponding to amino acid residues of SLN will be used
35 to model a structure of a target protein has sufficient sequence identity to SLN.

It has been shown for soluble protein domains that their three dimensional structure is broadly conserved above 20% amino acid sequence identity and well conserved above 30% identity, with the level of structural conservation increasing as amino acid sequence identity increases up to 100% (Ginalski, K. *Curr Op Struc Biol* (2006) **16**, 172-177).

5 Thus, it is preferred if the target protein, or part thereof, shares at least 20% amino acid sequence identity with the rabbit SERCA Ca^{2+} ATPase or the rabbit SLN sequence provided in Figure 8, and more preferably at least 30%, 40%, 50%, 60%, 70%, 80% or 90% sequence identity, and yet more preferably at least 95% or 99% sequence identity.

10 It will be appreciated therefore that the target protein may be a rabbit SERCA Ca^{2+} ATPase analogue or homologue or a rabbit SLN analogue or homologue.

Analogues are defined as proteins with similar three-dimensional structures and/or functions with little evidence of a common ancestor at a sequence level.

15

Homologues are proteins with evidence of a common ancestor, i.e. likely to be the result of evolutionary divergence and are divided into remote, medium and close sub-divisions based on the degree (usually expressed as a percentage) of sequence identity.

20 By a rabbit SERCA Ca^{2+} ATPase homologue, we include a protein with at least 20%, 25%, 30%, 35%, 40%, 45% or at least 50% amino acid sequence identity with the sequence of SERCA Ca^{2+} ATPase provided in Figure 8, preferably at least 55%, 60%, 65%, 70%, 75% or 80% amino acid sequence identity and more preferably 85%, 90%, 95% or 99% amino acid sequence identity. This includes polymorphic forms of Ca^{2+}
25 ATPases, e.g. mutants and Ca^{2+} ATPases from other species (e.g. animal species).

By a rabbit SLN homologue, we include a protein with at least 20%, 25%, 30%, 35%, 40%, 45% or at least 50% amino acid sequence identity with the sequence of SLN provided in Figure 8, preferably at least 55%, 60%, 65%, 70%, 75% or 80% amino acid
30 sequence identity and more preferably 85%, 90%, 95% or 99% amino acid sequence identity. This includes polymorphic forms of SLN, e.g. mutants and SLN from other species (e.g. animal species).

Sequence identity may be measured using any suitable method known in the art, for
35 example by the use of algorithms such as BLAST or PSI-BLAST (Altschul et al, NAR (1997), 25, 3389-3402) or methods based on Hidden Markov Models (Eddy S et al, J Comput Biol (1995) Spring 2 (1) 9-23). Typically, the percent sequence identity between

two polypeptides may be determined using any suitable computer program, for example the GAP program of the University of Wisconsin Genetic Computing Group and it will be appreciated that percent identity is calculated in relation to polypeptides whose sequence has been aligned optimally. The alignment may alternatively be carried out using the
5 Clustal W program (Thompson *et al.*, 1994). The parameters used may be as follows: Fast pairwise alignment parameters: K-tuple(word) size; 1, window size; 5, gap penalty; 3, number of top diagonals; 5. Scoring method: x percent. Multiple alignment parameters: gap open penalty; 10, gap extension penalty; 0.05. Scoring matrix: BLOSUM. Other programs include BESTFIT or FASTA in the Wisconsin Genetics
10 Software Package Release 7.0. The region of homology preferably covers at least 500 amino acids, such as 600 amino acids and more preferably 700 or 800 amino acids.

In one embodiment the target protein is an integral membrane protein. By "integral membrane protein" we mean a protein that is permanently integrated into the membrane
15 and can only be removed using detergents, non-polar solvents or denaturing agents that physically disrupt the lipid bilayer. Examples include receptors such as GPCRs, the T-cell receptor complex and growth factor receptors; transmembrane ion channels such as ligand-gated and voltage gated channels; transmembrane transporters such as neurotransmitter transporters; enzymes; carrier proteins; and ion pumps.

20 The amino acid sequences (and the nucleotide sequences of the cDNAs which encode them) of many membrane proteins are readily available, for example by reference to GenBank. It should be noted, also, that because the sequence of the human genome is substantially complete, the amino acid sequences of human membrane proteins can be
25 deduced therefrom.

Preferably, the target protein is a Ca^{2+} ATPase, or sarcolipin, or variants thereof. For example, the target protein may be a Ca^{2+} ATPase or sarcolipin from a species (eg animal species) other than rabbit, such as a human Ca^{2+} ATPase or sarcolipin.

30 Although the target protein may be derived from any source, it is particularly preferred if it is from a eukaryotic source. It is particularly preferred if it is derived from a vertebrate source such as a mammal. It is particularly preferred if the target protein is derived from rat, mouse, rabbit or dog or non-human primate or man.

35 Typically, modelling a structural representation of a target is done by homology modelling whereby homologous regions between the target protein and either the Ca^{2+} ATPase or

SLN are matched and the coordinate data of the SERCA Ca^{2+} ATPase/SLN used to predict a structural representation of the target protein.

5 The term "homologous regions" describes amino acid residues in two sequences that are identical or have similar (e.g. aliphatic, aromatic, polar, negatively charged, or positively charged) side-chain chemical groups. Identical and similar residues in homologous regions are sometimes described as being respectively "invariant" and "conserved" by those skilled in the art.

10 Typically, the method involves comparing the amino acid sequences of the SERCA Ca^{2+} ATPase or SLN with a target protein by aligning the amino acid sequences. Amino acids in the sequences are then compared and groups of amino acids that are homologous (conveniently referred to as "corresponding regions") are grouped together. This method detects conserved regions of the polypeptides and accounts for amino acid insertions or
15 deletions.

Homology between amino acid sequences can be determined using commercially available algorithms known in the art. For example, the programs BLAST, gapped BLAST, BLASTN, PSI-BLAST, BLAST 2 and WU- BLAST (provided by the National
20 Center for Biotechnology Information) can be used to align homologous regions of two, or more, amino acid sequences. These may be used with default parameters to determine the degree of homology between the amino acid sequence of the Ca^{2+} ATPase or SLN, and other target proteins which are to be modelled.

25 Preferred for use according to the present invention is the WU-BLAST (Washington University BLAST) version 2.0 software. WU-BLAST version 2.0 executable programs for several UNIX platforms can be downloaded from <ftp://blast.wustl.edu/blast/executables>. This program is based on WU-BLAST version 1.4, which in turn is based on the public domain NCBI-BLAST version 1.4 (Altschul and Gish, 1996, Local
30 alignment statistics, Doolittle ed., Methods in Enzymology 266: 460-480; Altschul et al., 1990, Basic local alignment search tool, Journal of Molecular Biology 215: 403-410; Gish and States, 1993, Identification of protein coding regions by database similarity search, Nature Genetics 3: 266-272; Karlin and Altschul, 1993, Applications and statistics for multiple high-scoring segments in molecular sequences, Proc. Natl. Acad. Sci. USA 90:
35 5873-5877; all of which are incorporated by reference herein).

In all search programs in the suite the gapped alignment routines are integral to the

database search itself. Gapping can be turned off if desired. The default penalty (Q) for a gap of length one is Q=9 for proteins and BLASTP, and Q=10 for BLASTN, but may be changed to any integer. The default per-residue penalty for extending a gap (R) is R=2 for proteins and BLASTP, and R=10 for BLASTN, but may be changed to any integer.

5 Any combination of values for Q and R can be used in order to align sequences so as to maximize overlap and identity while minimizing sequence gaps. The default amino acid comparison matrix is BLOSUM62, but other amino acid comparison matrices such as PAM can be utilized.

10 Once the amino acid sequences of the target protein of unknown structure and either of Ca²⁺ ATPase or SLN have been aligned, the structures of the conserved amino acids in the structural representation of the Ca²⁺ ATPase or SLN may be transferred to the corresponding amino acids of the target protein. For example, a tyrosine in the amino acid sequence of Ca²⁺ ATPase may be replaced by a phenylalanine, the corresponding
15 homologous amino acid in the amino acid sequence of the target protein.

The structures of amino acids located in non-conserved regions may be assigned manually by using standard peptide geometries or by molecular simulation techniques, such as molecular dynamics. The final step in the process is accomplished by refining
20 the entire structure using molecular dynamics and/or energy minimization. Typically, the predicted three dimensional structural representation will be one in which favourable interactions are formed within the target protein and/or so that a low energy conformation is formed ("High resolution structure prediction and the crystallographic phase problem" Qian *et al* (2007) *Nature* **450**; 259-264; "State of the art in studying protein folding and
25 protein structure production using molecular dynamics methods" Lee *et al* (2001) *J of Mol Graph & Modelling* **19**(1): 146-149).

Whereas it is preferred to base homology modelling on homologous amino acid sequences, it is appreciated that some proteins have low sequence identity and at the
30 same time are very similar in structure. Therefore, where at least part of the structure of the target protein is known, homologous regions can also be identified by comparing structures directly.

Homology modelling as such is a technique well known in the art (see e.g. Greer, *Science*, Vol. **228**, (1985), 1055), and Blundell *et al* (*Eur. J. Biochem*, Vol. **172**, (1988),
35 513)). The techniques described in these references, as well as other homology

modelling techniques generally available in the art, may be used in performing the present invention.

Typically, homology modelling is performed using computer programs, for example
5 SWISS-MODEL available through the Swiss Institute for Bioinformatics in Geneva, Switzerland; WHATIF available on EMBL servers; Schnare et al. (1996) J. Mol. Biol, 256: 701-719; Blundell et al. (1987) Nature 326: 347-352; Fetrow and Bryant (1993) Bio/Technology 11:479-484; Greer (1991) Methods in Enzymology 202: 239-252; and Johnson et al (1994) Crit. Rev. Biochem. Mol Biol. 29:1-68. An example of homology
10 modelling is described in Szklarz G. D (1997) Life Sci. 61: 2507-2520.

Thus, in an embodiment of the ninth aspect of the invention, the method further comprises aligning the amino acid sequence of the target protein of unknown structure with the amino acid sequence of SERCA Ca^{2+} ATPase or SLN as listed in Figure 8, to
15 match homologous regions of the amino acid sequences prior to predicting the structural representation, and wherein modelling the structural representation comprises modelling the structural representation of the matched homologous regions of the target protein on the corresponding regions of the SERCA Ca^{2+} ATPase or SLN to obtain a three dimensional structural representation for the target protein that substantially preserves
20 the structural representation of the matched homologous regions.

The invention therefore provides a method of predicting a three dimensional structural representation of a target protein of unknown structure, or part thereof, comprising:

providing the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in
25 Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof;

aligning the amino acid sequence of a target protein of unknown structure or part thereof with the amino acid sequence of SERCA Ca^{2+} ATPase or SLN as listed in Figure 8 or part thereof to match homologous regions of the amino acid sequences;

30 modelling the structure of the matched homologous regions of the target protein on the corresponding regions of the SERCA Ca^{2+} ATPase/SLN structure as defined by Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof; and

predicting a three dimensional structural representation for the target protein
35 which substantially preserves the structure of the matched homologous regions.

The coordinate data of the SERCA Ca^{2+} ATPase/SLN structure can also be used to

predict the crystal structure of target proteins where X-ray diffraction data or NMR spectroscopic data of the protein has been generated and requires interpretation in order to provide a structure.

- 5 A tenth aspect of the invention provides a method of predicting the three dimensional structural representation of a target protein of unknown structure, or part thereof, comprising: providing the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof; and either (a) positioning the coordinates in
10 the crystal unit cell of the protein so as to predict its structural representation, or (b) assigning NMR spectra peaks of the protein by manipulating the coordinates.

Thus, where X-ray crystallographic or NMR spectroscopic data is provided for a target protein of unknown structure, the coordinate data of Table (i) may be used to interpret
15 that data to predict a likely structure using techniques well known in the art including phasing, in the case of X-ray crystallography, and assisting peak assignments in the case of NMR spectra.

A three dimensional structural representation of any part of any target protein that is
20 sufficiently similar to any portion of the SERCA Ca^{2+} ATPase or SLN can be predicted by this method. Typically, the target protein or part thereof has at least 20% amino acid sequence identity with any portion of SERCA Ca^{2+} ATPase or SLN, such as at least 30% amino acid sequence identity or at least 40% or 50% or 60% or 70% or 80% or 90% sequence identity. For example, the coordinates may be used to predict the three-
25 dimensional representations of other crystal forms of SERCA Ca^{2+} ATPase or SLN, other SERCA Ca^{2+} ATPases or SLNs and mutants or co-complexes thereof. Other suitable target proteins are as defined with respect to the tenth aspect of the invention.

It will be appreciated that the coordinates corresponding to amino acid residues of
30 SERCA Ca^{2+} ATPase will be used to model a structure of a target protein has sufficient sequence identity to SERCA Ca^{2+} ATPase, and that coordinates corresponding to amino acid residues of SLN will be used to model a structure of a target protein has sufficient sequence identity to SLN.

35 One method that may be employed for the purposes of this aspect of the invention is molecular replacement which is well known in the art and described, for example, in Evans & McCoy (*Acta Cryst*, 2008, D64:1-10), McCoy (*Acta Cryst*, 2007, D63:32-42) and

McCoy *et al* (*J of App Cryst*, 2007, 40:658-674). Molecular replacement enables the solution of the crystallographic phase problem by providing initial estimates of the phases of the new structure from a previously known structure, as opposed to the other major methods for solving the phase problem, i.e. experimental methods (which measure the phase from isomorphous or anomalous differences) or direct methods (which use mathematical relationships between reflection triplets and quartets to bootstrap a phase set for all reflections from phases for a small or random 'seed' set of reflections.) Compared to molecular replacement, such methods are time consuming and generally hinder the solution of crystal structures. Thus molecular replacement provides an accurate structural form for an unknown crystal more quickly and efficiently than attempting to determine such information *ab initio*.

Accordingly, the invention involves generating a preliminary model of a target protein whose structure coordinates are unknown, by orienting and positioning the relevant portion of the SERCA Ca²⁺ ATPase/SLN structure according to Table (i) within the unit cell of a crystal of the target protein so as best to account for the observed X-ray diffraction pattern of the crystal of the target protein. Phases can be calculated from this model and combined with the observed X-ray diffraction pattern amplitudes to generate an electron density map of the target protein's structure. This, in turn, can be subjected to any well-known model building and structure refinement techniques to provide a final, accurate structural representation of the target protein (E. Lattman, "Use of the Rotation and Translation Functions", in *Meth. Enzymol.*, 115, pp. 55-77 (1985); M. G. Rossmann, ed., "The Molecular Replacement Method", *Int. Sci. Rev. Ser.*, No. 13, Gordon & Breach, New York (1972)).

Thus the invention includes a method of predicting a three dimensional structural representation of a target protein of unknown structure, or part thereof, comprising:

providing the coordinates of the SERCA Ca²⁺ ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof;

providing an X-ray diffraction pattern of the target protein; and

using the coordinates to predict at least part of the structure coordinates of the target protein.

In an embodiment, the X-ray diffraction pattern of the target protein is provided by crystallising the target protein unknown structure; and generating an X-ray diffraction pattern from the crystallised target protein. Thus, the invention also provides a method

of predicting a three dimensional structural representation of a target protein of unknown structure comprising the steps of (a) crystallising the target protein; (b) generating an X-ray diffraction pattern from the crystallised target protein; (c) applying the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof, to the X-ray diffraction pattern to generate a three-dimensional electron density map of the target protein, or part thereof; and (d) predicting a three dimensional structural representation of the target protein from the three-dimensional electron density map.

Examples of computer programs known in the art for performing molecular replacement include CNX (Brunger AT.; Adams P. D.; Rice L. M., Current Opinion in Structural Biology, Volume 8, Issue 5, October 1998, Pages 606-611 (also commercially available from Accelrys San Diego, CA), MOLREP (A.Vagin, A.Teplyakov, MOLREP: an automated program for molecular replacement, *J Appl Cryst* (1997) 30, 1022-1025, part of the CCP4 suite), AMoRe (Navaza, J. (1994). AMoRe: an automated package for molecular replacement. *Acta Cryst A* 50, 157- 163), or PHASER (part of the CCP4 suite).

Preferred selected coordinates of the SERCA Ca^{2+} ATPase/SLN complex are as defined above with respect to the first aspect of the invention.

The invention may also be used to assign peaks of NMR spectra of target proteins, by manipulation of the data of Table (i) (*J Magn Reson* (2002) **157(1)**: 119-23).

The invention also provides systems, particularly a computer system, intended to generate structures and/or perform optimisation of binding partner which interact with SERCA Ca^{2+} ATPase and/or SLN, homologues or analogues of SERCA Ca^{2+} ATPase and/or SLN, complexes of binding partners with SERCA Ca^{2+} ATPase and/or SLN, or complexes of binding partners with homologues or analogues of SERCA Ca^{2+} ATPase/SLN.

Accordingly, an eleventh aspect of the invention provides a computer system, intended to generate three dimensional structural representations of SERCA Ca^{2+} ATPase and/or SLN, homologues or analogues of SERCA Ca^{2+} ATPase and/or SLN, complexes of binding partners with SERCA Ca^{2+} ATPase and/or SLN, or complexes of binding partners with homologues or analogues of SERCA Ca^{2+} ATPase, or, to analyse or optimise binding of binding partners to SERCA Ca^{2+} ATPase and/or SLN, or homologues

or analogues or complexes thereof, the system containing computer-readable data comprising one or more of:

- 5 (a) the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof;
- (b) the coordinates of a target SERCA Ca^{2+} ATPase and/or SLN homologue or analogue generated by homology modelling of the target based on the data in (a);
- (c) the coordinates of a binding partner generated by interpreting X-ray crystallographic data or NMR data by reference to the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square
10 deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof, and
- (d) structure factor data derivable from the coordinates of (a), (b) or (c).

For example the computer system may comprise: (i) a computer-readable data storage
15 medium comprising data storage material encoded with the computer-readable data; (ii) a working memory for storing instructions for processing said computer-readable data; and (iii) a central-processing unit coupled to said working memory and to said computer-readable data storage medium for processing said computer-readable data and thereby generating structures and/or analyse or optimise binding and/or performing rational drug
20 design. The computer system may further comprise a display coupled to the central-processing unit for displaying structural representations.

The invention also provides such systems containing atomic coordinate data of target proteins of unknown structure wherein such data has been generated according to the
25 methods of the invention described herein based on the starting data provided in Table (i) optionally varied by a root mean square deviation of residue backbone atoms of not more than 4.8Å, or selected coordinates thereof.

Such data is useful for a number of purposes, including the generation of structures to
30 analyse the mechanisms of action of binding partners and/or to perform rational drug design of binding partners which interact with Ca^{2+} ATPases and/or SLN (e.g. binding partners that can modulate the Ca^{2+} ATPase/SLN interaction).

A twelfth aspect of the invention provides a computer-readable storage medium,
35 comprising a data storage material encoded with computer readable data, wherein the data comprises one or more of

(a) the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof;

5 (b) the coordinates of a target SERCA Ca^{2+} ATPase and/or SLN homologue or analogue generated by homology modelling of the target based on the data in (a);

(c) the coordinates of a binding partner generated by interpreting X-ray crystallographic data or NMR data by reference to the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof, and

10 (d) structure factor data derivable from the coordinates of (a), (b) or (c).

The invention also includes a computer-readable storage medium comprising a data storage material encoded with a first set of computer-readable data comprising a Fourier transform of at least a portion of the structural coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof; which data, when combined with a second set of machine readable data comprising an X-ray diffraction pattern of a molecule or molecular complex of unknown structure (eg a target protein of unknown structure), using a machine programmed with the instructions for using said first set of data and said second set of data, can determine at least a portion of the structure coordinates corresponding to the second set of machine readable data.

25 The invention also provides a computer-readable data storage medium comprising a data storage material encoded with a first set of computer-readable data comprising a Fourier transform of at least a portion of the structural coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof; which, when combined with a second set of machine readable data comprising an X-ray diffraction pattern of a molecule or molecular complex of unknown structure, e.g. a target protein of unknown structure, using a machine programmed with the instructions for using said first set of data and said second set of data, can determine at least a portion of the electron density corresponding to the second set of machine readable data.

35 It will be appreciated that the computer-readable storage media of the invention may comprise a data storage material encoded with any of the data generated by carrying out any of the methods of the invention relating to structure solution and selection/design of

binding partners to SERCA Ca^{2+} ATPase and/or SLN and drug design. Typically, the data is stored in PDB or CIF format, as commonly used by the person skilled in the art. The PDB and CIF formats are organized according to the instructions and guidelines given by the Research Collaboratory for Structural Bioinformatics. As an example, the data may include information on any one or more of the identity of one or more binding partners identified or selected or designed by the methods of the invention, the structure of said binding partners, details of the site of interaction, and details of how the binding partners interact with the Ca^{2+} ATPase and/or SLN.

The invention also includes a method of preparing the computer-readable storage media of the invention comprising encoding a data storage material with the computer-readable data.

As used herein, "computer readable media" refers to any medium or media, which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media such as floppy discs, hard disc storage medium and magnetic tape; optical storage media such as optical discs or CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media.

By providing such computer readable media, the atomic coordinate data of the invention can be routinely accessed to model SERCA Ca^{2+} ATPase and/or SLN or selected coordinates thereof. For example, RASMOL (Sayle et al., TIBS, Vol. 20, (1995), 374) is a publicly available computer software package, which allows access and analysis of atomic coordinate data for structure determination and/or rational drug design.

As used herein, "a computer system" refers to the hardware means, software means and data storage means used to analyse the atomic coordinate data of the invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means and data storage means. Desirably a monitor is provided to visualize structure data. The data storage means may be RAM or means for accessing computer readable media of the invention. Examples of such systems are microcomputer workstations available from Silicon Graphics Incorporated and Sun Microsystems running Unix based, Windows XP or IBM OS/2 operating systems.

A thirteenth aspect of the invention provides a method for providing data for generating three dimensional structural representations of SERCA Ca^{2+} ATPase and/or SLN, homologues or analogues of SERCA Ca^{2+} ATPase and/or SLN, or complexes of a binding partner with SERCA Ca^{2+} ATPase and/or SLN, or complexes of a binding partner with SERCA Ca^{2+} ATPase and/or SLN homologues or analogues, or for optimising binding of binding partners to said SERCA Ca^{2+} ATPase and/or SLN, or to homologues or analogues or complexes thereof, the method comprising:

(i) establishing communication with a remote device containing computer-readable data comprising at least one of:

(a) the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof;

(b) the coordinates of a target SERCA Ca^{2+} ATPase and/or SLN homologue or analogue generated by homology modelling of the target based on the data in (a);

(c) the coordinates of a binding partner generated by interpreting X-ray crystallographic data or NMR data by reference to the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof, and

(d) structure factor data derivable from the coordinates of (a), (b) or (c);
and

(ii) receiving said computer-readable data from said remote device.

The computer-readable data received from said remote device, particularly when in the form of the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof, may be used in the methods of the invention described herein, e.g. for the analysis of a binding partner interaction with the SERCA Ca^{2+} ATPase and/or SLN

Thus the remote device may comprise e.g. a computer system or computer readable media of one of the previous aspects of the invention. The device may be in a different country or jurisdiction from where the computer-readable data is received.

The communication may be via the internet, intranet, e-mail etc, transmitted through wires or by wireless means such as by terrestrial radio or by satellite. Typically the

communication will be electronic in nature, but some or all of the communication pathway may be optical, for example, over optical fibers.

A fourteenth aspect of the invention provides a method of obtaining a three dimensional structural representation of a crystal of a complex of SERCA Ca^{2+} ATPase and SLN, which method comprises providing the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof, and generating a three-dimensional structural representation of said coordinates.

For example, the structural representation may be a physical representation or a computer generated representation. Examples of representations are described above and include, for example, any of a wire-frame model, a chicken-wire model, a ball-and-stick model, a space-filling model, a stick model, a ribbon model, a snake model, an arrow and cylinder model, an electron density map or a molecular surface model.

Computer representations can be generated or displayed by commercially available software programs including for example QUANTA (Accelrys .COPYRIGHT.2001, 2002), O (Jones et al., Acta Crystallogr. A47, pp. 110-119 (1991)) and RIBBONS (Carson, J. Appl. Crystallogr., 24, pp. 9589-961 (1991)).

Typically, the computer used to generate the representation comprises (i) a computer-readable data storage medium comprising a data storage material encoded with computer-readable data, wherein said data comprise the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof; and (ii) instructions for processing the computer-readable data into a three-dimensional structural representation. The computer may further comprise a display for displaying said three-dimensional representation.

A fifteenth aspect of the invention provides a method of predicting one or more sites of interaction of SERCA Ca^{2+} ATPase and/or SLN, or homologues thereof, the method comprising:

providing the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof; and

analysing said coordinates to predict one or more sites of interaction.

For example, a binding region of a SERCA Ca^{2+} ATPase or a SLN for a particular binding partner can be predicted by modelling where the structure of the binding partner is known. Typically, the fitting and docking methods described above would be used. This method may be used, for example, to predict the site of interaction of a SERCA Ca^{2+} ATPase or a SLN of known structure.

A sixteenth aspect of the invention provides a method of predicting the location of internal and/or external parts of the structure of SERCA Ca^{2+} ATPase and/or SLN, or homologues thereof, the method comprising:

providing the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof; and

analysing said coordinates to predict the location of internal and/or external parts of the structure.

For example, from the three dimensional representation, it is possible to read off external parts of the structure, eg surface residues, as well as internal parts, eg residues within the protein core. It will be appreciated that the identification of external protein sequences will be especially useful in the generation of antibodies against a Ca^{2+} ATPase or SLN or Ca^{2+} ATPase/SLN complex.

A seventeenth aspect of the invention provides a method of producing a protein with a binding region that has substrate specificity substantially identical to that of SERCA Ca^{2+} ATPase, the method comprising

a) aligning the amino acid sequence of a target protein with the amino acid sequence of SERCA Ca^{2+} ATPase;

b) identifying the amino acid residues in the target protein that correspond to any one or more of the following positions according to the numbering of the rabbit SERCA Ca^{2+} ATPase as set out in Figure 8: Phe88, Phe92, Val93, Leu96, Ile97, Ala100, Ile103, Val104, Trp107, Gln108, Asn111, Tyr122, Arg324, Lys328, Trp794, Leu797, Asp800, Gly801, Leu802, Thr805, Ala806, Phe809, Trp932, Ser936, Leu939, Ser942, Leu943, Leu946, Ile947, Pro952, Leu953, Ile956, and Phe957; and

c) making one or more mutations in the amino acid sequence of the target protein to replace one or more identified amino acid residues with the corresponding residue in the rabbit SERCA Ca^{2+} ATPase.

Preferably, all 33 amino acids in the target portion which correspond to amino acid residues Phe88, Phe92, Val93, Leu96, Ile97, Ala100, Ile103, Val104, Trp107, Gln108, Asn111, Tyr122, Arg324, Lys328, Trp794, Leu797, Asp800, Gly801, Leu802, Thr805, Ala806, Phe809, Trp932, Ser936, Leu939, Ser942, Leu943, Leu946, Ile947, Pro952, Leu953, Ile956, and Phe957 of the SERCA Ca^{2+} ATPase are, if different, replaced. However, it will be appreciated that only 32, 31, 30, 29, 28, 27, 26, 25, 24, 23, 22, 21, 20, 19, 18, 17, 16, 15, 14, 13, 12, 11, 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 amino acid residues may be replaced.

An eighteenth aspect of the invention provides a method of producing a protein with a binding region that has substrate specificity substantially identical to that of SLN, the method comprising

a) aligning the amino acid sequence of a target protein with the amino acid sequence of SLN;

b) identifying the amino acid residues in the target protein that correspond to any one or more of the following positions according to the numbering of the rabbit SLN as set out in Figure 8: Met1, Glu2, Arg3, Ser4, Thr5, Arg6, Glu7, Leu8, Cys9, Leu10, and Asn11 ; and

c) making one or more mutations in the amino acid sequence of the target protein to replace one or more identified amino acid residues with the corresponding residue in the rabbit SLN.

Preferably, all 11 amino acids in the target portion which correspond to amino acid residues Met1, Glu2, Arg3, Ser4, Thr5, Arg6, Glu7, Leu8, Cys9, Leu10, and Asn11 of the SLN are, if different, replaced. However, it will be appreciated that only 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1 amino acid residues may be replaced.

By "an amino acid residue that corresponds to" we include an amino acid residue that aligns to the given SERCA Ca^{2+} ATPase or SLN when the SERCA Ca^{2+} ATPase or SLN, and target protein are aligned using e.g. MacVector and CLUSTALW.

According to this aspect of the invention, a binding site of a particular protein may be engineered using well known molecular biology techniques to contain any one or more of these residues to give it the same substrate specificity. This technique is well known in the art and is described in, for example, Ikuta *et al* (*J Biol Chem* (2001) 276, 27548-27554) where the authors modified the active site of cdk2, for which they could obtain structural data, to resemble that of cdk4, for which no X-ray structure was available.

Preferences for the target protein are as defined above with respect to the ninth aspect of the invention.

- 5 The crystallisation of the SERCA Ca^{2+} ATPase/SLN complex has led to many interesting observations about the structure of the proteins, not least the site of interaction between the two. Thus it will be appreciated that the invention allows for the generation of mutant SERCA Ca^{2+} ATPase and mutant SLN proteins wherein residues corresponding to these areas of interest are mutated to determine their effect on protein activity.

10

Accordingly, a nineteenth aspect of the invention provides a mutant SERCA Ca^{2+} ATPase or homologue thereof, wherein any one or more of amino acid residues Phe88, Phe92, Val93, Leu96, Ile97, Ala100, Ile103, Val104, Trp107, Gln108, Asn111, Tyr122, Arg324, Lys328, Trp794, Leu797, Asp800, Gly801, Leu802, Thr805, Ala806, Phe809, 15 Trp932, Ser936, Leu939, Ser942, Leu943, Leu946, Ile947, Pro952, Leu953, Ile956, and Phe957, according to the numbering of the rabbit SERCA Ca^{2+} ATPase in Figure 8, or any one or amino acids that correspond to said residues, are mutated.

20

A twentieth aspect of the invention provides a mutant SLN or homologue thereof, wherein any one or more of amino acid residues Met1, Glu2, Arg3, Ser4, Thr5, Arg6, Glu7, Leu8, Cys9, Leu10, and Asn11, according to the numbering of the rabbit SLN in Figure 8, or any one or amino acids that correspond to said residues, are mutated.

25

It is particularly preferred if the mutant SERCA Ca^{2+} ATPase of the invention is one which has at least 20% amino acid sequence identity when compared to the given rabbit SERCA Ca^{2+} ATPase, as determined using MacVector and CLUSTALW. Preferably, the mutant SERCA Ca^{2+} ATPase has at least 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% or 99% amino acid sequence identity.

30

Similarly, it is particularly preferred if the mutant SLN of the invention is one which has at least 20% amino acid sequence identity when compared to the given rabbit SLN, as determined using MacVector and CLUSTALW. Preferably, the mutant SLN has at least 30%, 40%, 50%, 60%, 70%, 80%, 85%, 90%, 95% or 99% amino acid sequence identity.

35

The mutant SERCA Ca^{2+} ATPase or mutant SLN may be a mutant of any mutant SERCA Ca^{2+} ATPase or mutant SLN, respectively, provided that it is mutated at one or

more of the amino acid positions as stated by reference to the given rabbit SERCA Ca^{2+} ATPase or SLN amino acid sequence.

Thus, the invention includes a mutant rabbit SERCA Ca^{2+} ATPase or a mutant rabbit
5 SLN in which, compared to its parent, one or more of these amino acid residues have
been replaced by another amino acid residue. The invention also includes mutant
SERCA Ca^{2+} ATPases or SLNs from other sources (eg from another animal species
such as a human) in which one or more corresponding amino acids in the parent
receptor are replaced by another amino acid residue. For the avoidance of doubt the
10 parent may be a Ca^{2+} ATPase or SLN which has a naturally-occurring sequence, or it
may be a truncated form or it may be a fusion, either to the naturally-occurring protein or
to a fragment thereof, or it may contain mutations compared to the naturally-occurring
sequence, providing that it retains ATPase ability.

15 In an embodiment, the mutant SERCA Ca^{2+} ATPase of the invention has a combination
of 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26,
27, 28, 29, 30, 31, 32 or 33 mutations as described above.

In an embodiment, the mutant SLN of the invention has a combination of 2, 3, 4, 5, 6, 7,
20 8, 9, 10 or 11 mutations as described above.

By "an amino acid residue that corresponds to" we include an amino acid residue that
aligns to the given SERCA Ca^{2+} ATPase or SLN when the SERCA Ca^{2+} ATPase or SLN,
and target protein are aligned using e.g. MacVector and CLUSTALW.

25

Residues in proteins can be mutated using standard molecular biology techniques as are
well known in the art.

A twenty-first aspect of the invention provides a method of assessing the conformational
30 state of a structure for SERCA Ca^{2+} ATPase, comprising:

providing the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in
Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more
than 4.95 Å, or selected coordinates thereof;

performing a statistical analysis and/or a topological analysis on the coordinates;

35 and

comparing the results of the analysis with the results of an analysis of coordinates
of proteins of known conformational states.

For example, protein structures may be compared for similarity by statistical and/or topological analyses (suitable analyses are known in the art and include, for example those described in Grindley *et al* (1993) *J Mol Biol* Vol **229**: 707-721 and Holm & Sander (1997) *Nucl Acids Res* Vol **25**: 231-234). Highly similar scores would indicate a shared conformational and therefore functional state eg the open E1 state in this case.

One example of statistical analysis is multivariate analysis which is well known in the art and can be done using techniques including principal components analysis, hierarchical cluster analysis, genetic algorithms and neural networks.

By performing a multivariate analysis of the SERCA Ca²⁺ ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof, and comparing the result of the analysis with the results of the analysis performed on coordinates of proteins with known conformational states, it is possible to determine the conformational state of the coordinate set analysed. For example, the conformational state may be classified as any of E1, E1P, E2 and E2P (Laursen, et al., 2009; Olesen, et al., 2007; Olesen, et al., 2004; Toyoshima, et al., 2000). E1 refers to the pre-catalytic E1-apo state; E1P refers to the high energy ATP and Ca²⁺ bound phospho enzyme E1P; E2P refers to the low energy conformation E2P; and E2 refers to the proton occluded E2 state.

A twenty-second aspect of the invention provides a crystal comprising a Ca²⁺ ATPase/SLN complex.

It will be appreciated that the crystal may comprise rabbit SERCA Ca²⁺ ATPase and rabbit SLN, or homologues thereof as described above. It is preferred if the crystal comprises Ca²⁺ ATPase and/or a SLN that has at least 75% sequence identity with the respective sequences of the SERCA Ca²⁺ ATPase and SLN provided in Figure 8, such as at least 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% sequence identity.

Preferably, the crystal has the structure defined by the coordinates of the SERCA Ca²⁺ ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof.

The invention also includes a crystal comprising a Ca^{2+} ATPase/SLN complex and further comprising a binding partner (eg of Ca^{2+} ATPase and/or SLN). Thus the invention includes a co-crystal. It is preferred if the structure of the Ca^{2+} ATPase/SLN complex is as defined by the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table
5 (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof.

The term "crystal" refers to an ordered state of matter. Proteins, by their nature are difficult to purify to homogeneity. Even highly purified proteins may be chronically
10 heterogeneous due to modifications, structural flexibility, the binding of ligands or a host of other effects. In addition, proteins are crystallized from generally complex solutions that may include not only the target molecule but also buffers, salts, precipitating agents, water and any number of small binding proteins. It is important to note that protein crystals are composed not only of protein, but also of a large percentage of solvents
15 molecules, in particular water. These contents may vary from 30 to even 90%. Protein crystals may accumulate greater quantities and a diverse range of impurities which cannot be listed here or anticipated in detail. The skilled person knows that some crystals diffract better than others. Crystals vary in size from a barely observable micron to 1 or more 20 millimetres. Crystals useful for X- ray analysis are typically single, 0.05 mm or larger, and free of cracks and other defects.

The protein crystal diffraction pattern determines the level of detail (resolution) that can be obtained on the three-dimensional structure of a protein. The quality of a three dimensional structure is evaluated by the resolution obtained, which is an expression for
25 the minimum spacing observed in differentiation. At a resolution of about 6 Å the overall shape of molecular parts is resolved, such as α -helices that are seen as rods with strong intensity. At a resolution of about 3.5 Å the main chain is visible (usually with some ambiguities). At a resolution of about 3 Å the side chains are partly resolved. At a resolution of about 2.5 Å the side chains are well resolved. The atoms are located within
30 about 0.4 Å meaning that the lengths of hydrogen bonds calculated from a PDB file (for example, by RasMol) have at least this uncertainty. The normal limit of protein crystallography is around 1 Å or slightly less, where atoms are located at below ± 0.1 Å..

Advantageously, therefore, the crystals of the invention have a resolution of less than 6
35 Å, preferably less than 5 Å or 4 Å, and most preferably around 3.6 Å or less (eg less than 3.5, 3.4, 3.3, 3.2, 3.1, 3.0, 2.9, 2.8, 2.7, 2.6, 2.5, 2.4, 2.3, 2.2, 2.1, 2.0, 1.9, 1.8, 1.7, 1.6, 1.5, 1.4, 1.3, 1.2, 1.1 or 1.0Å) to allow a sufficiently detailed model for selecting potential

binding molecules e.g. modulators of the Ca^{2+} -ATPase Sarcolipin complex. In a particularly preferred embodiment, the crystals of the invention have a resolution of around 3.2Å or of around 3.1Å.

- 5 In one embodiment, the crystal has P21221 symmetry with unit cell dimensions 85.9 (± 10) Å, 139.5(± 10) Å, 141.6(± 10) Å, wherein $\alpha=90^\circ$, $\beta=90^\circ$, and $\gamma=90^\circ$.

The invention also includes a use of the crystals of the invention for determination of three-dimensional structures of Ca^{2+} ATPases or SLN or homologues thereof. Thus, the
10 crystals may be used in the methods of determining three-dimensional structure described above.

It will be appreciated that the crystal may contain one or more non-protein compounds such as ATP, ATP analogues, and/or ions (e.g. cations) which may have been added
15 after the protein purification process and before crystallisation. Alternatively, crystals may be submerged in a solution comprising the indicated compounds prior to crystallisation. The compounds may be one or more binding partners of Ca^{2+} ATPase and/or SLN.

20 A twenty-third aspect of the invention provides a method of making a crystal comprising a Ca^{2+} ATPase/SLN complex, the method comprising: providing a purified Ca^{2+} ATPase/SLN complex; and crystallising the complex by using the hanging drop vapour diffusion technique, using a precipitant solution comprising 15-25% (w/v) PEG6000, 100-200 mM magnesium sulphate, 4-6% glycerol and 5-7% 2-methyl-2,4-pentandiol (MPD).

25 In a particularly preferred embodiment, the precipitant solution comprises about 19.5% (w/v) PEG6000, about 150 mM magnesium sulphate, about 5% glycerol and about 6% 2-methyl-2,4-pentandiol (MPD).

30 The crystal made by the method may include one or more binding partners of Ca^{2+} ATPase and/or SLN. Thus, the method of this aspect of the invention may be a method of making a co-crystal. The one or more binding partners may be added to the purified Ca^{2+} ATPase/SLN complex, and the complex/binding partner crystallised, or a crystal of the Ca^{2+} ATPase/SLN complex may be submerged in a solution containing the one or
35 more binding partners.

The invention includes a crystal or co-crystal obtainable or obtained by the method of the twenty-third aspect of the invention.

5 The invention includes the use of the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof to solve the structure of target proteins of unknown structure.

10 The invention includes the use of the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof to identify binding partners of a Ca^{2+} ATPase and/or SLN.

15 The invention includes the use of the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof in methods of drug design where the drugs are aimed at modifying the activity of Ca^{2+} ATPase and/or SLN (e.g. modulate the Ca^{2+} ATPase/SLN interaction).

20 The invention will now be described with the aid of the following Figures and Examples.

Figure 1: Structure of the SERCA-SLN complex. (A) Overall cartoon model of the SERCA-SLN complex showing the SLN binding site between transmembrane helices M2, M6, and M9 of SERCA. Mg^{2+} is shown as magenta spheres, K^+ as purple sphere, the beta- and gamma phosphates of AMPPCP and the Ca^{2+} binding site residues are shown as ball-and-stick. (B) Comparison of E1-SLN structure (middle) with representatives of the E2 (left, PDB ID 2C8K, stabilized by thapsigargin and AMPPCP) and $[\text{Ca}_2]\text{E1P}$ (right, PDB ID 1T5S, stabilized by Ca^{2+} and AMPPCP) conformations. The arrangement of the cytoplasmic domains of the SERCA-SLN structure is E1-like, whereas transmembrane helices M1 - M4 adopt a unique configuration. The asterisk marks contacts between the N- and A-domains which are characteristic for $[\text{Ca}_2]\text{E1P}$ states but absent in SERCA-SLN.

Figure 2: SERCA-SLN interactions. (A) Omit map showing the transmembrane α -helix formed by SLN. Green mesh: unbiased Fo-Fc difference density calculated at 50-3.1 Å resolution and contoured at 2.8σ , after simulated annealing refinement omitting the SLN model. The bulky side chain density of Phe12 (asterisk) served as hallmark residue to

assign the SLN sequence. Both the very N- and C-terminal residues are poorly defined. (B) close-up view of the polar interactions between the SLN N-terminal region and SERCA. (C) close-up view of hydrophobic contacts between the C-terminal region of SLN and SERCA.

5

Figure 3: Ca^{2+} access channel and binding sites. (A) Overall surface view of the SERCA-SLN complex, showing the wide open funnel leading towards the Ca^{2+} binding sites (circle). The 'M1 kink' is depressed into the membrane, indicating a distorted membrane interface (dotted line). (B) cross-section through the continuous ion entry funnel. Yellow surface representation indicate conserved residues. The residues forming Ca^{2+} binding sites I and II (dotted circles) are projected on the cross-section plane in ball-and-stick representation (Asn 796 omitted for clarity). (C, D) the 'M1 sliding door' mechanism, depicted by the 'downward' movement of M1 relative to M3. The structures were superposed on M3. E2-Tg (PDB ID 2C8K, (C) is shown in green, $[\text{Ca}_2]\text{E1-AMPPCP}$ (PDB ID 1T5S, (D) is shown in blue. SLN bound SERCA is colored as in (A) Both in the E2 and the $[\text{Ca}_2]\text{E1P}$ states L61 and Gly257 form a 'pivot point' that anchors the M1 kink to M3, occluding the ion binding sites, while L65 shields the gating residue Glu309. In SLN-bound SERCA, the M1 kink is translocated more than 10 Å into the membrane, leaving E309 unshielded. (E, F, G) Structures of the proton/ Ca^{2+} binding sites. (E) the Ca^{2+} -free and protonated E2 state: both binding sites are distorted. (F) the E1-SLN state: site II residues are involved in Mg^{2+} binding, competing for high-affinity Ca^{2+} binding geometry. Site I is accessible for Ca^{2+} binding with only minor rearrangements. (G) the $[\text{Ca}_2]\text{E1P}$ state with the two occupied Ca^{2+} sites bound at high affinity.

25

Figure 4: Model of the regulation mechanism by SLN. Superposition of SLN in the E1-SLN structure (middle) and as modelled on the E2 (left) and $[\text{Ca}_2]\text{E1P}$ (right) states. Superposed SLN is shown in light cyan color, key residues are highlighted in yellow. The binding mode of SLN appears compatible with the E2 state, with Leu321 in close contact to the SLN helix, in support of a mutational effect on PLB binding. In contrast, tight SLN binding would be incompatible with the $[\text{Ca}_2]\text{E1P}$ conformation, where the groove is constricted by SERCA residues L96, Q108 and W107.

30

Figure 5: Transmembrane helix arrangements. Left: superposition of E2-Tg (green) with SERCA-SLN; right: superposition of E1 Ca_2 -AMPPCP (blue, Ca^{2+} in cyan) with SERCA-SLN. SERCA-SLN colouring as in Fig.1.

35

Figure 6: Sequence alignment of rabbit and human phospholamban and sarcolipin from human and rabbit. The figure was created with Jalview using the program Muscle for the sequence alignment. From NMR studies (Lamberth, S. et al.) *Helvetica Chimica Acta* 83, 2141–2152 (2000). and modeling (Toyoshima, C. et al. *Proc. Natl Acad. Sci USA* 100, 467–472 (2003), PLB consists of three subdomains: an α -helical cytoplasmic subdomain 1a (residues 1-20) a hinge region (residues 20-30) and a transmembrane alpha helix (residues 31-52).

Figure 7: Positive Fo-Fc difference density signal in the nucleotide binding site.

Figure 8: Amino acid sequences of (A) SERCA Ca^{2+} ATPase and (B) SLN as present in crystallised structure.

Figure 9: Comparison of the electrostatic surface potential of SERCA in different states. Left: E2-Tg (PDB ID 2C8K); middle: E1-SLN, right: $[\text{Ca}_2]\text{E1-AMPPCP}$ (PDB ID 1T5S). The E1-SLN state has the most prominent patch of negative surface potential around the cation entry funnel (circle). Surface electrostatics were generated with Pymol (www.pymol.org). Structures are structurally aligned on the M8-M10 segment.

Figure 10: Ca^{2+} - binding pocket in various solved structures of the SERCA Ca^{2+} -ATPase.

Figure 11: Electron density map of sarcolipin in the SERCA/sln complex.

Figure 12: Comparison of SLN and PLB. a, Helical wheel representation of the transmembrane segments of SLN and PLB. The hydrophobic side of SLN facing SERCA is indicated by a black arc. The distribution of hydrophobic (brown) and polar (green) amino acids is similar. However, SLN possesses two acidic (red) and three basic (blue) residues on the side opposite the SERCA-interface, whereas PLB only has one basic residue (Arg25, blue). b, PLB gain-of-function and loss-of-function mutations described earlier from alanine scanning experiments (Kimura et al, 1997) were plotted on the SLN structure. Loss-of function mutations (red, orange for weak effect) are proposed to be situated at the PLB-SERCA interface, whereas gain-of-function mutations (blue) are suggested to destabilize the PLB pentamer, leading to a higher concentration of inhibitory active PLB monomer. The analogous residues in SLN cluster on two opposite sides of the alpha-helix, with the PLB gain-of-function mutations pointing away from the

SLN binding groove of SERCA, and the PLB loss-of-function mutations pointing towards the interface. This further supports that SLN and PLB bind to SERCA in a similar way.

Example 1: The Sarcolipin-bound Calcium Pump exposes Calcium Sites to the Cytoplasm

Summary

Contraction and relaxation of muscle cells are controlled by the successive rise and fall of cytosolic Ca^{2+} , which in the heart is tightly coupled with contractile properties and heart beat frequency. Release of sequestered Ca^{2+} from the sarcoplasmic reticulum (SR) store initiates contraction while a rapid removal of the cytosolic Ca^{2+} leads to relaxation. Re-sequestration of Ca^{2+} into the SR lumen is the main mechanism of Ca^{2+} removal and is catalyzed by the SR Ca^{2+} -ATPase (SERCA), which therefore plays a key role in muscle and cardiovascular physiology. A major determinant of SERCA activity is its apparent Ca^{2+} affinity, which is regulated by two small and homologous membrane proteins called phospholamban (PLB) and sarcolipin (SLN)^{1,2}. Detailed structural information explaining how these regulatory proteins reduce the apparent Ca^{2+} -affinity has however been missing, and the structural features that characterize a proper, cytoplasmic entry pathway for Ca^{2+} leading to the intramembraneous binding sites of SERCA have remained unknown. Here we report the crystal structure of SERCA in complex with SLN at 3.1 Å resolution. The regulatory SLN traps the Ca^{2+} -ATPase in an open E1 state with cytoplasmic exposure of the Ca^{2+} sites through a pathway further stabilized by Mg^{2+} . The structure suggests a mechanism for selective Ca^{2+} loading and activation of SERCA and provides novel insight on SLN/PLB inhibition by an E1 intermediate state stabilization. We find an intriguing analogy to how autoinhibitory domains of other ion pumps may modulate transport across biological membranes.

In humans, SLN is primarily expressed in skeletal muscle, whereas PLB expression predominates in heart, although significant levels of SLN expression are also observed in cardiac atrial muscle³. Both SLN and PLB are believed to bind to, and regulate SERCA in a similar fashion. Binding of SLN or PLB to SERCA lowers the apparent Ca^{2+} affinity thus modulating the threshold Ca^{2+} concentration at which SERCA gains transport activity^{2,4-7}. Phosphorylation of SLN and PLB in response to beta-adrenergic stimulation is a main cellular pathway of regulation of heart activity, as SERCA is inhibited by the non-phosphorylated proteins at resting Ca^{2+} conditions⁷⁻⁸ (typically in the 0.1 μM range).

The structures of SLN and PLB and their interactions with SERCA have previously been studied by NMR^{9,10}, but a complex structure of either of the regulators bound to SERCA has so far only been observed for PLB at low-resolution by electron microscopy¹¹. Numerous crystal structures have on the other hand provided a thorough description of SERCA at atomic detail^{12,13}. The 110 kDa single polypeptide chain folds into a bundle of ten transmembrane segments (M1 through M10) that form the ion transport domain, and three cytoplasmic domains (A, P, and N), which mediate ATP hydrolysis via phosphorylation and dephosphorylation. SERCA undergoes large conformational changes during the Ca^{2+} transport cycle: the E1 state binds Ca^{2+} and ATP to form the ADP sensitive E1P phospho-enzyme, which occludes two Ca^{2+} ions at intramembraneous sites I and II. Conversion to the ADP insensitive E2P conformation exposes a luminal exit pathway, where Ca^{2+} is exchanged for luminal protons. Dephosphorylation accompanies proton occlusion, and release of inorganic phosphate leads to the E2 state. An open question remains, however, on how the E2 to $[\text{Ca}_2]\text{E1P}$ transition occurs; a structure of a physiologically relevant, ion exchanging E1 intermediate state is missing.

Results and Discussion

Structure of the SERCA-SLN complex: a new E1 conformation.

Rabbit SERCA1a was solubilized from native SR membranes and crystallized in the presence of approx. 75 mM Mg^{2+} and no Ca^{2+} . The structure was determined at 3.1 Å resolution by molecular replacement revealing a novel conformation and clear indication of a SLN-bound complex (Fig. 1, Fig. 2a). Forming a slightly curved and membrane-spanning helix, SLN associates to SERCA in a groove between M2, M6 and M9 (Fig. 1a). This is consistent with earlier models based on computational docking to the E2 form of SERCA⁵. However, the crystal structure is significantly different from the Ca^{2+} -free E2 state (RMSD ~6.6 Å, E2 representing thapsigargin-bound E2 forms) and despite being a Ca^{2+} -free state it resembles much closer the Ca^{2+} -occluded E1P states (RMSD ~4.9 Å, $[\text{Ca}_2]\text{E1P}$ representing calcium-occluded AMPPCP and ADP- AlF_4^- forms and the AMPPNP phosphorylated enzyme). Hence, we propose that the SLN complex represents a genuine E1 intermediate between the proton-occluded E2 and the Ca^{2+} -occluded E1P states – in functional analogy to the E2P state that allows $\text{Ca}^{2+}/\text{H}^+$ exchange of ions on the luminal side^{12,13}. The positions of the P- and the N-domain relative to the transmembrane domain are clearly E1-like, whereas the A-domain is at the trajectory from the E2 to the $[\text{Ca}_2]\text{E1P}$ position (approx. 100° and -15° rotation, respectively). Characteristic contacts between the A- and the N-domain of the $[\text{Ca}_2]\text{E1P}$

states (e.g. Arg134, Ser136, Arg139, Thr171, and Lys218 interacting with Asp426, Asn469, Glu435, Glu486, and Asp422, respectively) have not yet formed in the SLN bound state (Fig. 1b), and compared to the [Ca₂]E1P states, the N-domain is in a slightly outward rotated position (~17°) relative to the phosphorylation site of the P-domain. The side chain conformation of the Asp351 phosphorylation site is still E2-like, i.e. interacting with Lys684 and Thr701, and not pointing towards the N-domain introducing the adenine binding pocket. We observed, however, electron density, which overlaps with the position of a divalent cation and the β,γ-phosphates of bound AMPPCP in the Ca²⁺-occluded state. Accordingly, we assigned this density to a partially ordered AMPPCP molecule (present in the crystal) coordinated by Arg560 and Thr353 of SERCA.

SERCA-SLN interactions

The SLN molecule is traced in its complete 31 amino acid length, although N- and C-terminal residues are rather poorly defined in the electron density maps (Fig. 2a). The assignment of the SLN sequence is validated by the overall quality of fit to the electron density maps. Most of the observed SERCA-SLN contacts (4 Å distance criterion) involve highly conserved amino-acid residues (Table 1), and the binding site is in accordance with previous observations and models based on mutational studies for both SLN and PLB^{4,5,14-16}. The SERCA-M4 segment bends at the unwound region of the ion binding cavity within the membrane and it crosses diagonally over the N-terminal end of SLN at the cytoplasmic interface. The intermolecular contacts show however only few, intimate interactions: three hydrogen bonds (SLN-Thr5 to Trp932 of SERCA M9, and SLN-Asn11 to Thr805 and the main chain carbonyl of Gly801 of M6, Fig. 2b), and a hydrophobic cluster of SLN-Val19 and Ile22 to Leu953 of M9 (Fig. 2c; Table 2). SLN release in response to conformational changes of SERCA therefore seems only moderately restricted. A suggestion that the C-terminal YQY motif stacks with aromatic residues of SERCA in the M1-M2 luminal loop⁵, is not directly supported, although we note that this SLN motif is rather disordered in our structure.

SLN is homologous to the membrane-spanning, C-terminal segment of phospholamban (PLB). Since mutations in SERCA that affect interactions with PLB also affect SLN binding and equivalent mutations of PLB and SLN reduce functional interactions with SERCA similarly, it is expected that PLB and SLN use analogous mechanisms for SERCA interactions. Indeed, the interactions we observe between SLN and SERCA agree with crosslinking studies to PLB by Chen et al.¹⁷ who predicted ~10 Å and ~15 Å distances between SERCA2b-Lys328 and Cys-mutations of PLB-Asn27 (SLN-Ser4) and

PLB-Asn30 (SLN-Glu7), respectively – distances that measure 10 and 13 Å in our structure (Lys328 side chain nitrogen to Ser4 and Glu7 side chain oxygens, respectively).

The Ca²⁺ access channel and binding sites

5 Relative movements of M1 against M2, M3 and M4 act like a 'sliding door' that generates a wide-open access pathway leading from the cytoplasm to the Ca²⁺ binding sites in the membrane (Fig. 3a+b, Suppl. Movie M1). Compared to the [Ca₂]E1P states, helices M1, M2, M3 and M4 are all shifted away from the central M6, and most importantly, M1 describes a 'downward' translocation (towards the lumen) by almost two turns relative to
10 M4 and ~12 Å along the membrane normal (Fig. 3c+d). This leads to an opening of a wide funnel above the characteristic M1 kink at Leu61 and a distorted membrane interface. Glu309 is typically associated with a key role in Ca²⁺ binding and release^{12,13,18,19}. Similarly, the conserved pair of the hydrophobic Leu61 (M1) and small Gly257 (M3) has been described as a 'pivot point' for the kink, and the conserved Leu65
15 as a 'gate-lock' residue, restricting Glu309 mobility as required for Ca²⁺ occlusion²⁰. However, in our E1-SLN structure, the Leu61-Gly257 pair is separated: Leu61 now opposes Ala303 (M4) and Leu65 packs against Val300 (both also conserved). The M1 kink is therefore translocated from "above" to "below" the unwound, central part of M4 around the conserved Pro308 and Glu309, i.e. diving deeply into the membrane. The
20 consequence is a large distortion of the membrane interface, through which Glu309 and other Ca²⁺ binding residues become accessible from the cytoplasmic environment (Fig. 3a-e).

The two intramembraneous Ca²⁺ sites I and II are also involved in the counter-transport
25 of 2-3 protons. Site I involves the side chains of residues Asn768, Glu771, Asp800, and Glu908, and site II comprises those of Asn796, Asp800, Glu309 and the main chain carbonyl oxygens of Val304, Ala305 and Ile307 (Fig. 3 e-g). Kinetic evidence points to a sequential and cooperative mechanism of Ca²⁺ binding to SERCA, where binding of the first Ca²⁺ ion leads to an increased affinity for the second²². In further support of this
30 kinetic model, single mutations at site I prevent binding of Ca²⁺ to both sites I and II, while single mutations at site II only interfere with site II²³.

With the M1 'sliding door' open, the side chains of Asp800 and Glu309 as well as the main chain carbonyl groups of Val304 and Ile307 are exposed to the surface of the entry
35 funnel formed by SERCA M1, M3 and M4 (Fig. 3b). These are all part of Ca²⁺ binding site II. Several other highly conserved residues (Gln56, Asn101, Gln109) line the Ca²⁺ entry funnel, indicating that an ion selective environment for Ca²⁺ recruitment and binding

is exposed at the membrane interface. Indeed, a comparison of the electrostatic surface potential of the E2, E1-SLN and [Ca₂]E1P states shows that only the E1-SLN structure displays such a deep, funnel-shaped and negatively charged path leading to the Ca²⁺ sites. Phospholipid head groups attracting Ca²⁺ ions²¹ may further assist Ca²⁺ entry.

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Probing the molecular contact surface for Ca²⁺ ions (ionic radius of 1.14 Å), the calcium entry pathway connects through a distorted site II all the way to site I. Interestingly, Asp800 (site I+II) and Glu309 (site II) are associated with Mg²⁺ ions in our structure, one of which is also in close vicinity to the exposed main chain carbonyls of Val304, Ala305, and Ile307 (Fig. 3b+f). We assume that Mg²⁺ ions bound at low affinity (but saturated at the ~100 mM concentration in the crystal) stabilize a deprotonated, open structure of site II with exposed carbonyl groups of the unwound part of M4 and deprotonated side chains of Glu309 and Asp800. It grants access for cytoplasmic Ca²⁺ to reach site I through site II. Ca²⁺ binding at site I is likely to engage Asp800, thus distorting the Mg²⁺ sites and preparing also site II for Ca²⁺ binding as a basis for cooperativity. The involvement of Mg²⁺ in Ca²⁺ exchange is in line with a "gating function" proposed earlier²⁴, and places an important role of Mg²⁺ in SLN/PLB mediated myocardial control. In further support of an open, deprotonated E1 state, Glu771 is separated from the hydrogen bond to Asn796 observed in the E2 conformation.

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Mechanism of regulation

Besides the cytoplasmic calcium concentration and the lipid environment (see above), SLN and PLB activity is regulated by their expression level and phosphorylation status^{2,4,6,7}. Both SLN and PLB have been proposed to exist in biological membranes in monomeric and multimeric free forms and as monomeric and dimeric SERCA-bound forms²⁵. When plotting the gain-of-function and loss-of-function mutations of PLB^{4,15,26} onto the SLN structure, the mutations clearly cluster on opposite sides of the helix: loss-of-function mutations at the PLB-SERCA-interface, and gain-of-function mutations (presumably impaired PLB pentamerization leading to more active monomer) at the outside. This also supports the notion that SERCA can interact at least in part with PLB pentamers²⁷.

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During beta-adrenergic stimulation, PLB is phosphorylated by Protein Kinase A or Ca²⁺/calmodulin-dependent protein kinase II (CaMKII). This results in a rapid increase in Ca²⁺ uptake to SR and has a strong impact on relaxation and contraction^{6,7}. SLN is also phosphorylated by CaMKII at Thr5. A study using adult rat ventricular myocytes showed that the point mutation Thr5Glu, mimicking phosphorylation, abolishes the inhibitory

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function of SLN. Furthermore, a block in CaMKII activity in SLN overexpressing myocytes completely eliminates beta-adrenergic responses⁸. Thr5 faces Trp932 of SERCA at approx. 2.6 Å distance, indicating a hydrogen bond, while a phosphothreonine at this site would clash with Trp932 and probably destabilize binding. At the same time, SLN-Thr5 is not deeply buried at the interface, but accessible at a lateral position at the membrane interface allowing CaMKII phosphorylation possibly even when SLN is associated with SERCA.

Both non-dissociative and dissociative models for SLN and PLB interaction with SERCA have been suggested^{5,17}. Superimposing our structure to the E2 state of SERCA, we find that the SLN binding groove is wider (Fig. 4) and thus compatible with also an E2-bound form of the complex. The E2 conformation would offer a more extensive contact to M4 rather than to M2, and the superpositioning suggests a close contact of SLN-Glu7 (PLB-Asn30) to Leu321 of M4. This may explain that mutation at Leu321 reduces PLB binding⁵. In the occluded [Ca₂]E1P conformation, M1, M2, M3 and M4 have moved significantly, destroying the SLN binding groove. In particular residues Leu96, Trp107 and Glu108 constrict the groove at the N-terminal region of SLN, where all of the few polar interactions are located (Fig. 4). We therefore find it likely that the complex dissociates upon Ca²⁺-activation of SERCA.

A common regulation-sensitive surface?

The identified E1-SLN form of SERCA candidates as a genuine intermediate of the catalytic cycle, required for Ca²⁺ loading and therefore essential for the transport of ions across the SR membrane. SLN and PLB reduce the apparent affinity for Ca²⁺ by stabilization of this probably otherwise dynamic intermediate, which is also stabilized by Mg²⁺. Many P-type ATPases are regulated by autoinhibitory extensions/domains, such as the plasma-membrane Ca²⁺ATPases (PMCAs), which are activated by Ca²⁺-calmodulin binding to the autoinhibitory element in a Ca²⁺dependent way^{28,29}. Interestingly, a conserved groove of the cytoplasmic domains that is linked to autoinhibition of PMCA²⁹ represents the extension of the SLN/PLB binding site observed here. Additionally, it overlaps also with a conserved site of interaction of heavy-metal binding domains mapped to the heavy-metal transporting P1B-ATPase^{30,31}. This groove is conserved for different P-type ion pumps as a core feature of ATPase coupled conformational changes; maximally exposed in E2 states and buried in E1P states. It implicates this conserved surface in different mechanisms of binding, inhibition or regulation of P-type ATPases, and hints at therapeutic potential for ion pump targeting.

Methods Summary

The SERCA1a-SLN complex was obtained from rabbit hind leg muscle. Solubilization and purification were performed with the detergent octaethylene glycol monododecyl ether (C₁₂E₈) and crystals were obtained using PEG6000 as the precipitant and with approx. 75 mM MgSO₄ in the crystallization drop. Crystals were cryoprotected by addition of 20% glycerol in crystallization buffer. Crystallographic data were collected at the beam lines 911-3 at MaxLab in Lund, Sweden and X06SA of the Swiss Light Source (SLS) in Villigen, Switzerland. Phases were determined by molecular replacement using individual domains of SERCA E2 (pdb:2AGV) as structural search models. Refinement using data extending to 3.1 Å resolution produced a model with a crystallographic R-factor of 19.1 % and a free R-factor of 24.6 %.

Table 1: Serca residues facing the SLN binding groove (any atom within a distance of ≤4 Å)

TM helix	SERCA residue	Conservation (%) among Ca ²⁺ - ATPases*
M2	Phe88	74
	Val93	70
	Leu96	74
	Ala100	56
	Val104	92
	Trp107	62
M4	Arg324	66
	Lys328	76 (12% R)
M6	Trp794	98 (2% F)
	Leu797	72
	Gly801	92
	Leu802	62
	Thr805	72
	Ala806	72
	Phe809	70
M9	Trp932	68
	Ser936	54 (50% A)
	Leu939	52 (10% V)
	Leu943	74
	Leu946	52 (20% V)
	Pro952	68
	Leu953	82

*based on a sequence alignment of 50 Ca²⁺ ATPase structures

Table 2: SLN residues facing the SERCA binding groove (any atom within a

distance of ≤ 4 Å)

SLN residue	Facing SERCA TM helix
Met1	M4
Ser4	M6
Thr5	M9
Glu7	M2, M6
Leu8	M6, M9
Asn11	M6
Phe12	M9
Val14	M2
Val15	M6
Thr18	M2
Val19	M6, M9
Ile22	M2
Trp23	M9-M10 loop
Val26	M9-M10 loop
Tyr29	M2

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Example 2 : Crystallisation of Ca^{2+} ATPase/SLN structure complex

SERCA 1a isoform was prepared from sarcoplasmic reticulum vesicles isolated from rabbit skeletal muscle. The membranes were further extracted and purified with low concentration of deoxycholate according to established procedures³². The membrane preparation was washed in 100 mM MOPS-Tris pH 6.8 (3-[N-morpholino]propanesulfonic acid titrated by tris[hydroxymethyl]aminomethane) and 80 mM KCl followed by a centrifugation at 40,000 rpm for 35 minutes at 4° C (TLS-55 rotor). The purified membranes were incubated for 80 minutes with 1% DMSO, 100 mM MOPS-KOH pH 6.8, 15 20% glycerol, 80 mM KCl, 3 mM MgCl_2 , 3.9 mM EGTA, and SERCA and SLN were solubilized with 35 mM octaethyleneglycol dodecylether (C_{12}E_8) for 10 minutes followed by centrifugation (TLA-55 rotor, 50,000 rpm, 35 minutes, 4° C). The protein concentration was 12 mg/ml of the final supernatant and 1 mM AMPPCP was added. Crystallization was obtained by vapour diffusion using hanging drops equilibrated at 23°C from 1 + 1 μl of protein and crystallization buffer (19.5% (w/v) PEG6000, 5% glycerol, 150 mM MgSO_4 and 6% MPD). Under these conditions the equilibrated drops maintain an approximately 2 μl volume. Single crystals appeared after few days and grew within a week to a final size of 250 x 250 x 50 microns. Experiments initially aimed for cocrystallization with inhibitory compounds, which however were not bound in the E1-SLN crystal structure presented here, and crystallization was later reproduced without inhibitors. Crystals were 25 cryo-protected by addition of 1 μl of cryobuffer (20% glycerol, 19.5% PEG6000, 150 mM MgSO_4 and 6% MPD) to a 2 μl drop. Crystals were mounted in litho-loops and flash-cooled in liquid nitrogen.

Example 3: Use of coordinates of Ca^{2+} ATPase/SLN structure

According to the invention various strategies can be followed to identify and generate selective modulators of the Ca^{2+} -ATPase sarcolipin interaction based on the structural information described herein. Potential modulators can be identified through virtual screening of chemical databases. Virtual screening are performed with different 35 database docking programs (for instance Dock, FlexX, Gold, Flo, Fred, Glide, LigFit, MOE or MVP, but not limited to these) and used with different scoring functions (e.g.

Warren *et al*, 2005; Jain, 2006; Seifert *et al*, 2007). The scoring functions may include, but are not limited to force-field scoring functions (affinities estimated by summing Van der Waals and electrostatic interactions of all atoms in the complex between the Ca^{2+} -ATPase and Sarcolipin and the ligand), empirical scoring functions (counting the number of various interactions, for instance number of hydrogen bonds, hydrophobic-hydrophobic contacts and hydrophilic-hydrophobic contacts, between the complex and the ligand), and knowledge based scoring functions (with basis on statistical findings of intermolecular contacts involving certain types of atoms or functional groups). Scoring functions involving terms from any of the two of the mentioned scoring functions may also be combined into a single function used in database virtual screening of chemical libraries. Identified potential modulators are confirmed by *in vitro* and *in vivo* experiments before further developments. The binding of modulators may further be confirmed by x-ray experiments. Even when inhibitory activity is confirmed further drug development may be required before a compound suitable as a drug is identified. As seen from the above and the three dimensional structure described herein, based on this knowledge potential modulators of a Ca^{2+} -ATPase/Sarcolipin complex can be identified.

Such methods are preferable performed using computers, whereby the atomic coordinates are introduced into the computer, allowing generation of a model on the computer screen which allows visual selection of binding molecules.

Table (i)

Table (i) shows the x, y and z coordinates by amino acid residue of each non-hydrogen atom in the polypeptide structure for SLN bound SERCA1a.

The third column indicates whether the atom is from an amino acid residue of one of SERCA1a or SLN (differentiated by A and B, respectively, in fourth column), a diphosphate (ACP), a potassium ion (K), water (HOH), or a magnesium ion (MG).

30

Data collection and structure determination

Crystallographic data were collected at the beam lines 911-3 at MaxLab in Lund, Sweden and X06SA of the Swiss Light Source (SLS) in Villigen, Switzerland. The data were collected at 100 K and a wavelength of 0.97935 Å. XDS was used for dataprocessing³³ and phases were determined by molecular replacement using individual domains of SERCA (pdb:2AGV and 3N5K) as search models³⁴. Sarcolipin was originally traced as a poly-alanine model. Placing the 'distinct hallmark' side chain of SLN

(Phe12 in the central part of SLN) into the largest unbiased side chain density yielded a reasonable fit of all other side chains in this helix register and satisfactory difference maps, while model refinement of alternative registers (shifted in both N- and C-terminal directions) increased the noise features of difference maps significantly. Phenix was used for refinement³⁵ and Coot for model building³⁶. Molprobity was used for model validation³⁷. The Ramachandran plot shows 93% of residues in favored regions and 0.79 % outliers (8 residues), with the latter emerging in poorly resolved loops upon reciprocal space refinement. Several structural reports were included in model analysis³⁸⁻⁴⁵ and atomic coordinates used for specific purposes (pdb: 1T5S, 2AGV, 2C8K, 3BA6)

10

Methods Table: Data collection and refinement statistics

SERCA E1-SLN	
Data collection	
Space group	P2 ₁ 22 ₁
Cell dimensions	
<i>a</i> , <i>b</i> , <i>c</i> (Å)	85.9, 139.5, 141.6
α , β , γ (°)	90, 90, 90
Resolution (Å)	50 - 3.1 (3.2-3.1) ⁱ
<i>R</i> _{sym}	27.3 (> 100)
<i>I</i> / σ <i>I</i>	14.19 (2.2)
CC ^{*ii}	99.9 (82.2)
Completeness (%)	99.3 (99.2)
Redundancy	22.6 (23.96)
Refinement	
Resolution (Å)	43 - 3.1 (3.2 - 3.1)
Unique reflections	31,391 (3060)
<i>R</i> _{work} / <i>R</i> _{free}	0.191 (0.272) / 0.246 (0.320)
No. atoms	7890
Protein	7869
AMPPCP	9 (β , γ -phosphates)
Mg ²⁺	3
K ⁺	1
Water	8
Av. <i>B</i> -factors (Å ²)	
Protein	105.3

AMPPCP	144.9 (β,γ -phosphates)
Mg ²⁺	144.0
K ⁺	69.3
Water	98.6
R.m.s. deviations	
Bond lengths (Å)	0.009
Bond angles	1.41°

ⁱ Highest resolution shell is shown in parenthesis

ⁱⁱ CC* = percentage of correlation between intensities from random half-datasets⁴⁶

5	ATOM	1	N	MET A	1	-2.148	59.175	154.520	1.00	65.93	N
	ATOM	2	CA	MET A	1	-2.102	60.598	154.146	1.00	77.59	C
	ATOM	3	C	MET A	1	-0.982	60.974	153.160	1.00	85.02	C
	ATOM	4	O	MET A	1	0.208	60.772	153.441	1.00	91.71	O
10	ATOM	5	CB	MET A	1	-1.969	61.478	155.387	1.00	77.42	C
	ATOM	6	CG	MET A	1	-1.908	62.953	155.050	1.00	81.44	C
	ATOM	7	SD	MET A	1	-1.830	64.086	156.457	1.00	86.56	S
	ATOM	8	CE	MET A	1	-2.046	65.638	155.561	1.00	59.73	C
	ATOM	9	N	GLU A	2	-1.348	61.555	152.022	1.00	75.32	N
15	ATOM	10	CA	GLU A	2	-0.352	61.833	150.985	1.00	69.63	C
	ATOM	11	C	GLU A	2	0.241	63.237	150.970	1.00	73.85	C
	ATOM	12	O	GLU A	2	-0.472	64.240	151.039	1.00	78.46	O
	ATOM	13	CB	GLU A	2	-0.898	61.525	149.607	1.00	68.79	C
	ATOM	14	CG	GLU A	2	-0.114	60.496	148.874	1.00	83.35	C
20	ATOM	15	CD	GLU A	2	-0.584	60.369	147.448	1.00	104.91	C
	ATOM	16	OE1	GLU A	2	-1.725	60.815	147.163	1.00	111.73	O
	ATOM	17	OE2	GLU A	2	0.184	59.835	146.616	1.00	111.17	O
	ATOM	18	N	ALA A	3	1.561	63.273	150.813	1.00	74.53	N
	ATOM	19	CA	ALA A	3	2.335	64.500	150.815	1.00	73.76	C
25	ATOM	20	C	ALA A	3	2.051	65.252	152.094	1.00	74.61	C
	ATOM	21	O	ALA A	3	1.715	66.441	152.061	1.00	74.94	O
	ATOM	22	CB	ALA A	3	2.022	65.349	149.621	1.00	67.27	C
	ATOM	23	N	ALA A	4	2.177	64.546	153.216	1.00	66.81	N
	ATOM	24	CA	ALA A	4	2.091	65.180	154.520	1.00	67.78	C
30	ATOM	25	C	ALA A	4	3.075	66.340	154.632	1.00	67.43	C
	ATOM	26	O	ALA A	4	2.752	67.387	155.190	1.00	64.64	O
	ATOM	27	CB	ALA A	4	2.345	64.166	155.615	1.00	70.43	C

	ATOM	28	N	HIS	A	5	4.268	66.151	154.076	1.00	71.31	N
	ATOM	29	CA	HIS	A	5	5.358	67.116	154.201	1.00	78.45	C
	ATOM	30	C	HIS	A	5	5.021	68.463	153.570	1.00	78.86	C
	ATOM	31	O	HIS	A	5	5.669	69.482	153.855	1.00	69.46	O
5	ATOM	32	CB	HIS	A	5	6.605	66.571	153.510	1.00	82.03	C
	ATOM	33	CG	HIS	A	5	6.482	66.518	152.021	1.00	79.75	C
	ATOM	34	ND1	HIS	A	5	6.027	65.402	151.357	1.00	77.12	N
	ATOM	35	CD2	HIS	A	5	6.723	67.452	151.072	1.00	65.35	C
	ATOM	36	CE1	HIS	A	5	6.006	65.650	150.058	1.00	81.03	C
10	ATOM	37	NE2	HIS	A	5	6.417	66.889	149.862	1.00	67.32	N
	ATOM	38	N	SER	A	6	4.029	68.451	152.684	1.00	81.22	N
	ATOM	39	CA	SER	A	6	3.633	69.655	151.974	1.00	81.64	C
	ATOM	40	C	SER	A	6	2.445	70.296	152.668	1.00	73.34	C
	ATOM	41	O	SER	A	6	2.248	71.513	152.586	1.00	71.99	O
15	ATOM	42	CB	SER	A	6	3.295	69.340	150.523	1.00	90.76	C
	ATOM	43	OG	SER	A	6	2.206	68.439	150.469	1.00	101.85	O
	ATOM	44	N	LYS	A	7	1.649	69.477	153.351	1.00	67.75	N
	ATOM	45	CA	LYS	A	7	0.578	70.016	154.178	1.00	70.15	C
	ATOM	46	C	LYS	A	7	1.254	70.675	155.370	1.00	72.02	C
20	ATOM	47	O	LYS	A	7	2.341	70.278	155.783	1.00	60.52	O
	ATOM	48	CB	LYS	A	7	-0.430	68.938	154.602	1.00	62.10	C
	ATOM	49	CG	LYS	A	7	-1.159	68.286	153.434	1.00	105.69	C
	ATOM	50	CD	LYS	A	7	-1.910	69.334	152.598	1.00	104.03	C
	ATOM	51	CE	LYS	A	7	-1.831	69.078	151.090	1.00	94.92	C
25	ATOM	52	NZ	LYS	A	7	-1.515	70.347	150.377	1.00	82.64	N
	ATOM	53	N	SER	A	8	0.622	71.715	155.892	1.00	77.60	N
	ATOM	54	CA	SER	A	8	1.110	72.390	157.074	1.00	69.19	C
	ATOM	55	C	SER	A	8	0.720	71.575	158.277	1.00	70.84	C
	ATOM	56	O	SER	A	8	0.143	70.499	158.166	1.00	76.05	O
30	ATOM	57	CB	SER	A	8	0.468	73.751	157.198	1.00	70.16	C
	ATOM	58	OG	SER	A	8	-0.859	73.592	157.622	1.00	64.60	O
	ATOM	59	N	THR	A	9	1.019	72.098	159.448	1.00	74.06	N
	ATOM	60	CA	THR	A	9	0.937	71.268	160.630	1.00	70.02	C
	ATOM	61	C	THR	A	9	-0.491	71.159	161.187	1.00	76.58	C
35	ATOM	62	O	THR	A	9	-0.909	70.079	161.592	1.00	71.87	O
	ATOM	63	CB	THR	A	9	1.974	71.710	161.660	1.00	68.21	C
	ATOM	64	OG1	THR	A	9	1.949	70.818	162.777	1.00	73.26	O
	ATOM	65	CG2	THR	A	9	1.731	73.150	162.094	1.00	67.03	C
	ATOM	66	N	GLU	A	10	-1.243	72.262	161.169	1.00	85.03	N
40	ATOM	67	CA	GLU	A	10	-2.663	72.231	161.518	1.00	79.32	C

	ATOM	68	C	GLU A 10	-3.389	71.266	160.601	1.00	73.71	C
	ATOM	69	O	GLU A 10	-4.283	70.528	161.018	1.00	79.36	O
	ATOM	70	CB	GLU A 10	-3.289	73.630	161.431	1.00	89.05	C
	ATOM	71	CG	GLU A 10	-2.694	74.545	160.355	1.00	108.67	C
5	ATOM	72	CD	GLU A 10	-3.304	75.962	160.344	1.00	130.87	C
	ATOM	73	OE1	GLU A 10	-4.548	76.096	160.472	1.00	138.55	O
	ATOM	74	OE2	GLU A 10	-2.534	76.948	160.208	1.00	134.12	O
	ATOM	75	N	GLU A 11	-2.962	71.259	159.346	1.00	66.89	N
	ATOM	76	CA	GLU A 11	-3.620	70.506	158.292	1.00	69.04	C
10	ATOM	77	C	GLU A 11	-3.455	69.002	158.416	1.00	71.57	C
	ATOM	78	O	GLU A 11	-4.318	68.238	157.994	1.00	77.02	O
	ATOM	79	CB	GLU A 11	-3.089	70.970	156.947	1.00	68.26	C
	ATOM	80	CG	GLU A 11	-3.540	72.355	156.608	1.00	73.70	C
	ATOM	81	CD	GLU A 11	-3.011	72.841	155.286	1.00	77.56	C
15	ATOM	82	OE1	GLU A 11	-2.103	72.190	154.712	1.00	69.82	O
	ATOM	83	OE2	GLU A 11	-3.516	73.887	154.835	1.00	86.21	O
	ATOM	84	N	CYS A 12	-2.333	68.574	158.971	1.00	64.83	N
	ATOM	85	CA	CYS A 12	-2.111	67.157	159.172	1.00	67.57	C
	ATOM	86	C	CYS A 12	-2.967	66.658	160.331	1.00	76.80	C
20	ATOM	87	O	CYS A 12	-3.505	65.553	160.295	1.00	83.18	O
	ATOM	88	CB	CYS A 12	-0.631	66.882	159.439	1.00	57.16	C
	ATOM	89	SG	CYS A 12	0.363	66.911	157.963	1.00	74.43	S
	ATOM	90	N	LEU A 13	-3.084	67.480	161.363	1.00	73.26	N
	ATOM	91	CA	LEU A 13	-3.878	67.112	162.517	1.00	71.32	C
25	ATOM	92	C	LEU A 13	-5.304	67.049	162.026	1.00	74.55	C
	ATOM	93	O	LEU A 13	-6.040	66.090	162.289	1.00	67.46	O
	ATOM	94	CB	LEU A 13	-3.729	68.142	163.637	1.00	57.57	C
	ATOM	95	CG	LEU A 13	-2.335	68.297	164.239	1.00	95.05	C
	ATOM	96	CD1	LEU A 13	-2.178	69.589	164.995	1.00	57.46	C
30	ATOM	97	CD2	LEU A 13	-2.072	67.132	165.129	1.00	55.00	C
	ATOM	98	N	ALA A 14	-5.679	68.064	161.261	1.00	77.01	N
	ATOM	99	CA	ALA A 14	-7.037	68.158	160.783	1.00	62.93	C
	ATOM	100	C	ALA A 14	-7.407	66.974	159.895	1.00	63.05	C
	ATOM	101	O	ALA A 14	-8.521	66.493	159.940	1.00	86.38	O
35	ATOM	102	CB	ALA A 14	-7.231	69.452	160.069	1.00	84.29	C
	ATOM	103	N	TYR A 15	-6.471	66.497	159.095	1.00	77.04	N
	ATOM	104	CA	TYR A 15	-6.799	65.512	158.077	1.00	71.91	C
	ATOM	105	C	TYR A 15	-7.279	64.212	158.723	1.00	67.91	C
	ATOM	106	O	TYR A 15	-8.186	63.527	158.225	1.00	65.19	O
40	ATOM	107	CB	TYR A 15	-5.578	65.278	157.176	1.00	66.70	C

	ATOM	108	CG	TYR A 15	-5.759	64.236	156.095	1.00	63.29	C
	ATOM	109	CD2	TYR A 15	-6.237	64.582	154.831	1.00	66.32	C
	ATOM	110	CD1	TYR A 15	-5.433	62.912	156.329	1.00	62.41	C
	ATOM	111	CE2	TYR A 15	-6.400	63.628	153.845	1.00	66.47	C
5	ATOM	112	CE1	TYR A 15	-5.601	61.957	155.354	1.00	62.85	C
	ATOM	113	CZ	TYR A 15	-6.087	62.317	154.123	1.00	75.64	C
	ATOM	114	OH	TYR A 15	-6.240	61.343	153.174	1.00	81.08	O
	ATOM	115	N	PHE A 16	-6.673	63.890	159.852	1.00	60.17	N
	ATOM	116	CA	PHE A 16	-6.977	62.650	160.540	1.00	79.24	C
10	ATOM	117	C	PHE A 16	-7.922	62.896	161.718	1.00	77.88	C
	ATOM	118	O	PHE A 16	-8.279	61.958	162.436	1.00	79.46	O
	ATOM	119	CB	PHE A 16	-5.695	62.024	161.080	1.00	77.65	C
	ATOM	120	CG	PHE A 16	-4.863	61.320	160.055	1.00	79.46	C
	ATOM	121	CD1	PHE A 16	-5.344	60.196	159.406	1.00	74.00	C
15	ATOM	122	CD2	PHE A 16	-3.567	61.747	159.786	1.00	77.84	C
	ATOM	123	CE1	PHE A 16	-4.567	59.524	158.497	1.00	65.95	C
	ATOM	124	CE2	PHE A 16	-2.777	61.085	158.868	1.00	68.51	C
	ATOM	125	CZ	PHE A 16	-3.278	59.970	158.231	1.00	70.05	C
	ATOM	126	N	GLY A 17	-8.293	64.158	161.928	1.00	70.65	N
20	ATOM	127	CA	GLY A 17	-9.194	64.533	163.004	1.00	68.88	C
	ATOM	128	C	GLY A 17	-8.673	64.168	164.380	1.00	69.45	C
	ATOM	129	O	GLY A 17	-9.395	63.611	165.197	1.00	72.97	O
	ATOM	130	N	VAL A 18	-7.416	64.496	164.641	1.00	72.09	N
	ATOM	131	CA	VAL A 18	-6.735	64.064	165.856	1.00	73.55	C
25	ATOM	132	C	VAL A 18	-6.278	65.279	166.646	1.00	75.58	C
	ATOM	133	O	VAL A 18	-5.930	66.302	166.065	1.00	85.64	O
	ATOM	134	CB	VAL A 18	-5.525	63.138	165.507	1.00	61.40	C
	ATOM	135	CG1	VAL A 18	-4.971	63.482	164.153	1.00	65.40	C
	ATOM	136	CG2	VAL A 18	-4.425	63.235	166.526	1.00	59.53	C
30	ATOM	137	N	SER A 19	-6.300	65.182	167.968	1.00	73.77	N
	ATOM	138	CA	SER A 19	-5.804	66.266	168.796	1.00	75.68	C
	ATOM	139	C	SER A 19	-4.351	66.070	169.231	1.00	85.04	C
	ATOM	140	O	SER A 19	-3.956	64.983	169.663	1.00	88.46	O
	ATOM	141	CB	SER A 19	-6.672	66.426	170.023	1.00	76.52	C
35	ATOM	142	OG	SER A 19	-6.346	67.643	170.650	1.00	88.57	O
	ATOM	143	N	GLU A 20	-3.564	67.136	169.138	1.00	87.30	N
	ATOM	144	CA	GLU A 20	-2.171	67.096	169.556	1.00	85.24	C
	ATOM	145	C	GLU A 20	-2.106	66.902	171.062	1.00	86.80	C
	ATOM	146	O	GLU A 20	-1.182	66.275	171.590	1.00	85.10	O
40	ATOM	147	CB	GLU A 20	-1.488	68.406	169.175	1.00	91.22	C

	ATOM	148	CG	GLU A 20	0.020	68.391	169.272	1.00100.63	C
	ATOM	149	CD	GLU A 20	0.638	69.639	168.661	1.00118.23	C
	ATOM	150	OE1	GLU A 20	0.006	70.218	167.761	1.00117.31	O
	ATOM	151	OE2	GLU A 20	1.745	70.052	169.076	1.00130.58	O
5	ATOM	152	N	THR A 21	-3.111	67.443	171.747	1.00 86.16	N
	ATOM	153	CA	THR A 21	-3.148	67.449	173.204	1.00 72.52	C
	ATOM	154	C	THR A 21	-3.456	66.089	173.783	1.00 71.81	C
	ATOM	155	O	THR A 21	-3.003	65.780	174.874	1.00 81.79	O
	ATOM	156	CB	THR A 21	-4.185	68.435	173.736	1.00 68.63	C
10	ATOM	157	OG1	THR A 21	-4.179	69.602	172.915	1.00 79.11	O
	ATOM	158	CG2	THR A 21	-3.849	68.841	175.148	1.00 71.40	C
	ATOM	159	N	THR A 22	-4.224	65.273	173.070	1.00 69.49	N
	ATOM	160	CA	THR A 22	-4.630	63.981	173.623	1.00 74.54	C
	ATOM	161	C	THR A 22	-4.213	62.788	172.773	1.00 69.32	C
15	ATOM	162	O	THR A 22	-3.885	61.729	173.313	1.00 67.21	O
	ATOM	163	CB	THR A 22	-6.146	63.926	173.858	1.00 78.35	C
	ATOM	164	OG1	THR A 22	-6.824	63.776	172.609	1.00 78.99	O
	ATOM	165	CG2	THR A 22	-6.610	65.206	174.507	1.00 86.62	C
	ATOM	166	N	GLY A 23	-4.223	62.975	171.453	1.00 61.97	N
20	ATOM	167	CA	GLY A 23	-3.994	61.896	170.508	1.00 64.46	C
	ATOM	168	C	GLY A 23	-5.271	61.168	170.101	1.00 77.47	C
	ATOM	169	O	GLY A 23	-6.398	61.601	170.387	1.00 80.97	O
	ATOM	170	N	LEU A 24	-5.100	60.047	169.416	1.00 79.37	N
	ATOM	171	CA	LEU A 24	-6.250	59.276	168.966	1.00 77.52	C
25	ATOM	172	C	LEU A 24	-6.998	58.718	170.149	1.00 76.08	C
	ATOM	173	O	LEU A 24	-6.388	58.289	171.120	1.00 84.80	O
	ATOM	174	CB	LEU A 24	-5.804	58.110	168.083	1.00 70.26	C
	ATOM	175	CG	LEU A 24	-5.109	58.477	166.778	1.00 63.20	C
	ATOM	176	CD1	LEU A 24	-5.048	57.263	165.877	1.00 61.29	C
30	ATOM	177	CD2	LEU A 24	-5.835	59.636	166.112	1.00 63.56	C
	ATOM	178	N	THR A 25	-8.319	58.706	170.074	1.00 68.68	N
	ATOM	179	CA	THR A 25	-9.077	57.951	171.055	1.00 75.10	C
	ATOM	180	C	THR A 25	-8.962	56.477	170.676	1.00 77.81	C
	ATOM	181	O	THR A 25	-8.573	56.170	169.556	1.00 86.31	O
35	ATOM	182	CB	THR A 25	-10.524	58.352	171.033	1.00 77.99	C
	ATOM	183	OG1	THR A 25	-11.102	57.835	169.840	1.00 86.68	O
	ATOM	184	CG2	THR A 25	-10.644	59.847	171.056	1.00 66.97	C
	ATOM	185	N	PRO A 26	-9.280	55.561	171.610	1.00 75.78	N
	ATOM	186	CA	PRO A 26	-9.340	54.121	171.333	1.00 74.93	C
40	ATOM	187	C	PRO A 26	-10.111	53.754	170.052	1.00 82.12	C

	ATOM	188	O	PRO A 26	-9.684	52.842	169.339	1.00	80.53	O
	ATOM	189	CB	PRO A 26	-10.105	53.576	172.542	1.00	72.75	C
	ATOM	190	CG	PRO A 26	-9.799	54.487	173.616	1.00	74.25	C
	ATOM	191	CD	PRO A 26	-9.541	55.840	173.032	1.00	77.45	C
5	ATOM	192	N	ASP A 27	-11.228	54.434	169.784	1.00	79.80	N
	ATOM	193	CA	ASP A 27	-12.044	54.129	168.615	1.00	85.42	C
	ATOM	194	C	ASP A 27	-11.301	54.489	167.349	1.00	84.15	C
	ATOM	195	O	ASP A 27	-11.193	53.671	166.435	1.00	90.15	O
	ATOM	196	CB	ASP A 27	-13.386	54.865	168.658	1.00	100.30	C
10	ATOM	197	CG	ASP A 27	-14.232	54.643	167.393	1.00	106.81	C
	ATOM	198	OD1	ASP A 27	-14.680	53.496	167.142	1.00	107.07	O
	ATOM	199	OD2	ASP A 27	-14.470	55.632	166.664	1.00	106.51	O
	ATOM	200	N	GLN A 28	-10.797	55.716	167.301	1.00	75.24	N
	ATOM	201	CA	GLN A 28	-10.024	56.185	166.167	1.00	64.31	C
15	ATOM	202	C	GLN A 28	-8.920	55.197	165.818	1.00	74.76	C
	ATOM	203	O	GLN A 28	-8.668	54.936	164.640	1.00	73.20	O
	ATOM	204	CB	GLN A 28	-9.400	57.539	166.483	1.00	65.13	C
	ATOM	205	CG	GLN A 28	-10.276	58.730	166.226	1.00	63.99	C
	ATOM	206	CD	GLN A 28	-9.729	59.983	166.859	1.00	72.76	C
20	ATOM	207	OE1	GLN A 28	-9.355	59.991	168.033	1.00	75.03	O
	ATOM	208	NE2	GLN A 28	-9.673	61.050	166.089	1.00	62.77	N
	ATOM	209	N	VAL A 29	-8.264	54.650	166.846	1.00	67.55	N
	ATOM	210	CA	VAL A 29	-7.148	53.726	166.645	1.00	64.07	C
	ATOM	211	C	VAL A 29	-7.635	52.468	165.971	1.00	68.78	C
25	ATOM	212	O	VAL A 29	-7.035	52.009	165.004	1.00	73.89	O
	ATOM	213	CB	VAL A 29	-6.485	53.321	167.959	1.00	65.06	C
	ATOM	214	CG1	VAL A 29	-5.408	52.279	167.701	1.00	60.17	C
	ATOM	215	CG2	VAL A 29	-5.914	54.542	168.670	1.00	64.46	C
	ATOM	216	N	LYS A 30	-8.734	51.921	166.490	1.00	72.37	N
30	ATOM	217	CA	LYS A 30	-9.370	50.749	165.907	1.00	67.54	C
	ATOM	218	C	LYS A 30	-9.714	51.004	164.442	1.00	78.12	C
	ATOM	219	O	LYS A 30	-9.343	50.216	163.571	1.00	81.55	O
	ATOM	220	CB	LYS A 30	-10.622	50.395	166.682	1.00	70.32	C
	ATOM	221	CG	LYS A 30	-11.438	49.290	166.055	1.00	135.09	C
35	ATOM	222	CD	LYS A 30	-12.912	49.365	166.486	1.00	135.57	C
	ATOM	223	CE	LYS A 30	-13.766	48.408	165.668	1.00	139.61	C
	ATOM	224	NZ	LYS A 30	-15.214	48.484	166.010	1.00	145.23	N
	ATOM	225	N	ARG A 31	-10.410	52.109	164.174	1.00	79.10	N
	ATOM	226	CA	ARG A 31	-10.793	52.461	162.808	1.00	81.43	C
40	ATOM	227	C	ARG A 31	-9.566	52.542	161.931	1.00	67.06	C

	ATOM	228	O	ARG A 31	-9.489	51.835	160.935	1.00	82.01	O
	ATOM	229	CB	ARG A 31	-11.576	53.779	162.749	1.00	69.49	C
	ATOM	230	CG	ARG A 31	-13.047	53.671	163.101	1.00	111.20	C
	ATOM	231	CD	ARG A 31	-13.619	55.005	163.524	1.00	72.90	C
5	ATOM	232	NE	ARG A 31	-12.853	56.126	163.011	1.00	70.65	N
	ATOM	233	CZ	ARG A 31	-13.008	57.381	163.419	1.00	91.22	C
	ATOM	234	NH1	ARG A 31	-13.904	57.665	164.350	1.00	92.97	N
	ATOM	235	NH2	ARG A 31	-12.267	58.356	162.905	1.00	87.89	N
	ATOM	236	N	HIS A 32	-8.593	53.373	162.316	1.00	64.39	N
10	ATOM	237	CA	HIS A 32	-7.363	53.535	161.522	1.00	73.96	C
	ATOM	238	C	HIS A 32	-6.548	52.239	161.393	1.00	74.95	C
	ATOM	239	O	HIS A 32	-5.844	52.040	160.409	1.00	70.95	O
	ATOM	240	CB	HIS A 32	-6.463	54.645	162.065	1.00	60.19	C
	ATOM	241	CG	HIS A 32	-7.103	55.995	162.108	1.00	60.22	C
15	ATOM	242	ND1	HIS A 32	-6.373	57.154	162.286	1.00	58.50	N
	ATOM	243	CD2	HIS A 32	-8.396	56.383	162.026	1.00	62.47	C
	ATOM	244	CE1	HIS A 32	-7.189	58.192	162.303	1.00	72.39	C
	ATOM	245	NE2	HIS A 32	-8.426	57.754	162.141	1.00	61.52	N
	ATOM	246	N	LEU A 33	-6.641	51.357	162.378	1.00	63.37	N
20	ATOM	247	CA	LEU A 33	-5.956	50.081	162.280	1.00	70.00	C
	ATOM	248	C	LEU A 33	-6.723	49.139	161.357	1.00	77.97	C
	ATOM	249	O	LEU A 33	-6.132	48.282	160.689	1.00	77.45	O
	ATOM	250	CB	LEU A 33	-5.778	49.454	163.661	1.00	66.39	C
	ATOM	251	CG	LEU A 33	-4.709	48.368	163.806	1.00	64.74	C
25	ATOM	252	CD1	LEU A 33	-3.859	48.658	165.014	1.00	66.00	C
	ATOM	253	CD2	LEU A 33	-5.364	47.008	163.935	1.00	67.15	C
	ATOM	254	N	GLU A 34	-8.043	49.296	161.327	1.00	77.53	N
	ATOM	255	CA	GLU A 34	-8.874	48.529	160.418	1.00	86.56	C
	ATOM	256	C	GLU A 34	-8.508	48.921	158.996	1.00	87.19	C
30	ATOM	257	O	GLU A 34	-8.383	48.075	158.113	1.00	73.95	O
	ATOM	258	CB	GLU A 34	-10.347	48.835	160.679	1.00	100.00	C
	ATOM	259	CG	GLU A 34	-11.315	48.270	159.649	1.00	113.39	C
	ATOM	260	CD	GLU A 34	-11.587	46.795	159.862	1.00	124.01	C
	ATOM	261	OE1	GLU A 34	-11.186	46.270	160.929	1.00	122.22	O
35	ATOM	262	OE2	GLU A 34	-12.201	46.165	158.967	1.00	129.44	O
	ATOM	263	N	LYS A 35	-8.300	50.220	158.810	1.00	85.22	N
	ATOM	264	CA	LYS A 35	-8.176	50.841	157.495	1.00	83.47	C
	ATOM	265	C	LYS A 35	-6.779	50.762	156.904	1.00	83.66	C
	ATOM	266	O	LYS A 35	-6.618	50.526	155.714	1.00	86.71	O
40	ATOM	267	CB	LYS A 35	-8.592	52.312	157.588	1.00	84.42	C

	ATOM	268	CG	LYS A 35	-8.474	53.067	156.289	1.00	93.82	C
	ATOM	269	CD	LYS A 35	-9.183	54.406	156.331	1.00	103.28	C
	ATOM	270	CE	LYS A 35	-9.158	55.048	154.949	1.00	121.29	C
	ATOM	271	NZ	LYS A 35	-9.531	56.491	154.969	1.00	132.72	N
5	ATOM	272	N	TYR A 36	-5.769	50.971	157.742	1.00	80.26	N
	ATOM	273	CA	TYR A 36	-4.390	51.048	157.286	1.00	77.29	C
	ATOM	274	C	TYR A 36	-3.569	49.812	157.656	1.00	81.30	C
	ATOM	275	O	TYR A 36	-2.448	49.624	157.182	1.00	65.39	O
	ATOM	276	CB	TYR A 36	-3.739	52.314	157.835	1.00	62.43	C
10	ATOM	277	CG	TYR A 36	-4.444	53.574	157.427	1.00	62.38	C
	ATOM	278	CD1	TYR A 36	-4.558	53.910	156.103	1.00	70.74	C
	ATOM	279	CD2	TYR A 36	-4.996	54.433	158.364	1.00	88.11	C
	ATOM	280	CE1	TYR A 36	-5.201	55.061	155.703	1.00	69.64	C
	ATOM	281	CE2	TYR A 36	-5.649	55.605	157.970	1.00	80.34	C
15	ATOM	282	CZ	TYR A 36	-5.746	55.900	156.630	1.00	68.49	C
	ATOM	283	OH	TYR A 36	-6.374	57.031	156.179	1.00	65.90	O
	ATOM	284	N	GLY A 37	-4.121	48.960	158.500	1.00	66.43	N
	ATOM	285	CA	GLY A 37	-3.417	47.750	158.864	1.00	82.08	C
	ATOM	286	C	GLY A 37	-2.311	48.015	159.865	1.00	77.04	C
20	ATOM	287	O	GLY A 37	-2.137	49.140	160.368	1.00	69.02	O
	ATOM	288	N	HIS A 38	-1.546	46.974	160.162	1.00	78.47	N
	ATOM	289	CA	HIS A 38	-0.457	47.116	161.115	1.00	76.88	C
	ATOM	290	C	HIS A 38	0.789	47.782	160.524	1.00	75.35	C
	ATOM	291	O	HIS A 38	1.009	47.767	159.326	1.00	84.68	O
25	ATOM	292	CB	HIS A 38	-0.118	45.760	161.710	1.00	77.94	C
	ATOM	293	CG	HIS A 38	-1.207	45.192	162.562	1.00	79.78	C
	ATOM	294	ND1	HIS A 38	-1.271	45.395	163.924	1.00	81.95	N
	ATOM	295	CD2	HIS A 38	-2.276	44.420	162.247	1.00	71.01	C
	ATOM	296	CE1	HIS A 38	-2.326	44.772	164.416	1.00	77.27	C
30	ATOM	297	NE2	HIS A 38	-2.952	44.174	163.417	1.00	75.20	N
	ATOM	298	N	ASN A 39	1.605	48.374	161.380	1.00	78.85	N
	ATOM	299	CA	ASN A 39	2.873	48.950	160.959	1.00	74.43	C
	ATOM	300	C	ASN A 39	3.946	47.901	160.716	1.00	72.02	C
	ATOM	301	O	ASN A 39	4.932	47.865	161.440	1.00	74.12	O
35	ATOM	302	CB	ASN A 39	3.379	49.881	162.039	1.00	70.45	C
	ATOM	303	CG	ASN A 39	4.345	50.876	161.509	1.00	67.35	C
	ATOM	304	OD1	ASN A 39	4.659	50.860	160.330	1.00	57.98	O
	ATOM	305	ND2	ASN A 39	4.802	51.775	162.360	1.00	68.16	N
	ATOM	306	N	GLU A 40	3.750	47.056	159.709	1.00	71.01	N
40	ATOM	307	CA	GLU A 40	4.605	45.904	159.458	1.00	73.47	C

	ATOM	308	C	GLU A 40	4.731	45.738	157.960	1.00	88.78	C
	ATOM	309	O	GLU A 40	4.017	46.388	157.192	1.00	89.57	O
	ATOM	310	CB	GLU A 40	3.954	44.616	159.978	1.00	74.95	C
	ATOM	311	CG	GLU A 40	3.768	44.490	161.483	1.00	87.18	C
5	ATOM	312	CD	GLU A 40	3.063	43.187	161.881	1.00	96.52	C
	ATOM	313	OE1	GLU A 40	3.382	42.630	162.954	1.00	102.96	O
	ATOM	314	OE2	GLU A 40	2.189	42.717	161.121	1.00	92.70	O
	ATOM	315	N	LEU A 41	5.626	44.845	157.547	1.00	96.87	N
	ATOM	316	CA	LEU A 41	5.638	44.340	156.176	1.00	94.65	C
10	ATOM	317	C	LEU A 41	5.058	42.927	156.222	1.00	99.71	C
	ATOM	318	O	LEU A 41	5.165	42.253	157.247	1.00	103.11	O
	ATOM	319	CB	LEU A 41	7.061	44.315	155.620	1.00	88.42	C
	ATOM	320	CG	LEU A 41	7.954	45.548	155.800	1.00	85.68	C
	ATOM	321	CD2	LEU A 41	7.322	46.847	155.288	1.00	79.64	C
15	ATOM	322	CD1	LEU A 41	9.287	45.294	155.125	1.00	85.97	C
	ATOM	323	N	PRO A 42	4.436	42.471	155.124	1.00	120.25	N
	ATOM	324	CA	PRO A 42	3.801	41.147	155.126	1.00	119.45	C
	ATOM	325	C	PRO A 42	4.830	40.039	155.272	1.00	115.66	C
	ATOM	326	O	PRO A 42	5.907	40.125	154.689	1.00	96.69	O
20	ATOM	327	CB	PRO A 42	3.161	41.059	153.738	1.00	129.61	C
	ATOM	328	CG	PRO A 42	3.137	42.459	153.218	1.00	134.90	C
	ATOM	329	CD	PRO A 42	4.321	43.132	153.817	1.00	129.59	C
	ATOM	330	N	ALA A 43	4.500	39.010	156.041	1.00	115.78	N
	ATOM	331	CA	ALA A 43	5.423	37.907	156.248	1.00	125.74	C
25	ATOM	332	C	ALA A 43	5.520	37.079	154.976	1.00	138.39	C
	ATOM	333	O	ALA A 43	4.568	36.392	154.609	1.00	140.13	O
	ATOM	334	CB	ALA A 43	4.971	37.048	157.420	1.00	124.12	C
	ATOM	335	N	GLU A 44	6.671	37.156	154.307	1.00	148.80	N
	ATOM	336	CA	GLU A 44	6.883	36.491	153.017	1.00	158.32	C
30	ATOM	337	C	GLU A 44	6.672	34.975	153.107	1.00	166.61	C
	ATOM	338	O	GLU A 44	5.763	34.429	152.475	1.00	167.95	O
	ATOM	339	CB	GLU A 44	8.279	36.822	152.468	1.00	157.91	C
	ATOM	340	CG	GLU A 44	8.615	36.199	151.110	1.00	158.03	C
	ATOM	341	CD	GLU A 44	8.079	36.996	149.926	1.00	155.78	C
35	ATOM	342	OE1	GLU A 44	6.924	37.470	149.999	1.00	156.11	O
	ATOM	343	OE2	GLU A 44	8.816	37.146	148.922	1.00	150.93	O
	ATOM	344	N	GLU A 45	7.521	34.309	153.889	1.00	169.92	N
	ATOM	345	CA	GLU A 45	7.352	32.893	154.233	1.00	171.58	C
	ATOM	346	C	GLU A 45	7.227	31.941	153.037	1.00	167.79	C
40	ATOM	347	O	GLU A 45	6.298	31.137	152.971	1.00	166.71	O

	ATOM	348	CB	GLU A 45	6.151	32.722	155.171	1.00175.07	C
	ATOM	349	CG	GLU A 45	6.286	33.475	156.490	1.00178.47	C
	ATOM	350	CD	GLU A 45	5.005	33.467	157.305	1.00179.98	C
	ATOM	351	OE1	GLU A 45	3.925	33.276	156.704	1.00182.91	O
5	ATOM	352	OE2	GLU A 45	5.079	33.651	158.542	1.00176.90	O
	ATOM	353	N	GLY A 46	8.171	32.025	152.105	1.00164.81	N
	ATOM	354	CA	GLY A 46	8.132	31.194	150.916	1.00164.37	C
	ATOM	355	C	GLY A 46	9.129	30.046	150.907	1.00166.73	C
	ATOM	356	O	GLY A 46	10.276	30.222	150.500	1.00171.20	O
10	ATOM	357	O	LYS A 47	7.327	26.749	151.972	1.00149.97	O
	ATOM	358	N	LYS A 47	8.678	28.874	151.355	1.00162.01	N
	ATOM	359	CA	LYS A 47	9.450	27.626	151.329	1.00154.37	C
	ATOM	360	C	LYS A 47	8.462	26.494	151.570	1.00147.56	C
	ATOM	361	CB	LYS A 47	10.496	27.607	152.442	1.00154.67	C
15	ATOM	362	CG	LYS A 47	11.850	28.192	152.083	1.00155.53	C
	ATOM	363	CD	LYS A 47	12.771	28.170	153.290	1.00157.62	C
	ATOM	364	CE	LYS A 47	14.108	28.816	152.990	1.00160.68	C
	ATOM	365	NZ	LYS A 47	15.030	28.719	154.156	1.00164.90	N
	ATOM	366	N	SER A 48	8.874	25.251	151.345	1.00140.89	N
20	ATOM	367	CA	SER A 48	8.012	24.122	151.705	1.00144.93	C
	ATOM	368	C	SER A 48	8.773	22.822	151.964	1.00154.17	C
	ATOM	369	O	SER A 48	9.820	22.579	151.372	1.00158.46	O
	ATOM	370	CB	SER A 48	6.930	23.896	150.648	1.00146.14	C
	ATOM	371	OG	SER A 48	7.349	22.954	149.680	1.00152.05	O
25	ATOM	372	N	LEU A 49	8.233	21.992	152.854	1.00158.25	N
	ATOM	373	CA	LEU A 49	8.839	20.704	153.194	1.00165.37	C
	ATOM	374	C	LEU A 49	8.863	19.771	151.987	1.00172.20	C
	ATOM	375	O	LEU A 49	9.783	18.970	151.819	1.00167.75	O
	ATOM	376	CB	LEU A 49	8.071	20.045	154.343	1.00166.25	C
30	ATOM	377	CG	LEU A 49	8.286	18.545	154.573	1.00169.42	C
	ATOM	378	CD1	LEU A 49	9.666	18.271	155.144	1.00170.71	C
	ATOM	379	CD2	LEU A 49	7.202	17.977	155.476	1.00171.94	C
	ATOM	380	N	TRP A 50	7.832	19.883	151.155	1.00147.56	N
	ATOM	381	CA	TRP A 50	7.739	19.110	149.927	1.00157.06	C
35	ATOM	382	C	TRP A 50	8.902	19.493	149.024	1.00149.12	C
	ATOM	383	O	TRP A 50	9.647	18.637	148.560	1.00148.00	O
	ATOM	384	CB	TRP A 50	6.421	19.400	149.194	1.00174.04	C
	ATOM	385	CG	TRP A 50	5.167	19.382	150.052	1.00188.09	C
	ATOM	386	CD1	TRP A 50	4.820	20.283	151.023	1.00191.08	C
40	ATOM	387	CD2	TRP A 50	4.082	18.440	149.978	1.00196.02	C

	ATOM	388	NE1 TRP A 50	3.602	19.948	151.569	1.00194.31	N
	ATOM	389	CE2 TRP A 50	3.127	18.824	150.944	1.00196.84	C
	ATOM	390	CE3 TRP A 50	3.831	17.306	149.196	1.00198.92	C
	ATOM	391	CZ2 TRP A 50	1.943	18.114	151.149	1.00198.35	C
5	ATOM	392	CZ3 TRP A 50	2.653	16.604	149.402	1.00200.45	C
	ATOM	393	CH2 TRP A 50	1.725	17.011	150.370	1.00200.09	C
	ATOM	394	N GLU A 51	9.052	20.794	148.794	1.00144.01	N
	ATOM	395	CA GLU A 51	10.041	21.316	147.857	1.00142.26	C
	ATOM	396	C GLU A 51	11.469	20.989	148.288	1.00141.34	C
10	ATOM	397	O GLU A 51	12.300	20.602	147.466	1.00144.84	O
	ATOM	398	CB GLU A 51	9.875	22.833	147.711	1.00146.19	C
	ATOM	399	CG GLU A 51	10.161	23.382	146.316	1.00156.61	C
	ATOM	400	CD GLU A 51	11.588	23.129	145.855	1.00166.04	C
	ATOM	401	OE2 GLU A 51	11.765	22.605	144.730	1.00168.98	O
15	ATOM	402	OE1 GLU A 51	12.529	23.446	146.617	1.00168.73	O
	ATOM	403	N LEU A 52	11.744	21.133	149.580	1.00137.47	N
	ATOM	404	CA LEU A 52	13.107	21.020	150.091	1.00130.51	C
	ATOM	405	C LEU A 52	13.698	19.608	150.002	1.00132.73	C
	ATOM	406	O LEU A 52	14.899	19.454	149.778	1.00136.88	O
20	ATOM	407	CB LEU A 52	13.200	21.585	151.513	1.00120.41	C
	ATOM	408	CG LEU A 52	12.988	23.103	151.580	1.00113.99	C
	ATOM	409	CD2 LEU A 52	14.213	23.852	151.075	1.00114.41	C
	ATOM	410	CD1 LEU A 52	12.626	23.563	152.977	1.00107.53	C
	ATOM	411	N VAL A 53	12.870	18.579	150.164	1.00130.88	N
25	ATOM	412	CA VAL A 53	13.363	17.216	149.982	1.00129.39	C
	ATOM	413	C VAL A 53	13.661	16.954	148.508	1.00129.29	C
	ATOM	414	O VAL A 53	14.591	16.219	148.176	1.00132.21	O
	ATOM	415	CB VAL A 53	12.399	16.134	150.533	1.00100.04	C
	ATOM	416	CG1 VAL A 53	12.221	16.287	152.037	1.00102.19	C
30	ATOM	417	CG2 VAL A 53	11.061	16.184	149.824	1.00101.29	C
	ATOM	418	N ILE A 54	12.876	17.564	147.626	1.00125.12	N
	ATOM	419	CA ILE A 54	13.113	17.441	146.198	1.00124.59	C
	ATOM	420	C ILE A 54	14.404	18.169	145.866	1.00127.93	C
	ATOM	421	O ILE A 54	15.233	17.673	145.102	1.00131.65	O
35	ATOM	422	CB ILE A 54	11.939	18.014	145.366	1.00125.30	C
	ATOM	423	CG1 ILE A 54	10.715	17.101	145.458	1.00123.65	C
	ATOM	424	CG2 ILE A 54	12.325	18.165	143.905	1.00125.64	C
	ATOM	425	CD1 ILE A 54	9.506	17.628	144.700	1.00124.24	C
	ATOM	426	N GLU A 55	14.587	19.338	146.468	1.00129.26	N
40	ATOM	427	CA GLU A 55	15.771	20.141	146.202	1.00136.90	C

	ATOM	428	C	GLU A 55	17.026	19.441	146.715	1.00133.60	C
	ATOM	429	O	GLU A 55	18.131	19.715	146.258	1.00135.78	O
	ATOM	430	CB	GLU A 55	15.638	21.531	146.828	1.00146.23	C
	ATOM	431	CG	GLU A 55	16.666	22.534	146.328	1.00152.08	C
5	ATOM	432	CD	GLU A 55	16.988	23.599	147.357	1.00154.60	C
	ATOM	433	OE1	GLU A 55	16.042	24.169	147.943	1.00154.37	O
	ATOM	434	OE2	GLU A 55	18.191	23.855	147.585	1.00155.33	O
	ATOM	435	N	GLN A 56	16.855	18.530	147.664	1.00128.92	N
	ATOM	436	CA	GLN A 56	17.990	17.776	148.172	1.00126.28	C
10	ATOM	437	C	GLN A 56	18.421	16.706	147.172	1.00130.03	C
	ATOM	438	O	GLN A 56	19.608	16.408	147.040	1.00129.10	O
	ATOM	439	CB	GLN A 56	17.671	17.165	149.537	1.00121.11	C
	ATOM	440	CG	GLN A 56	18.827	17.253	150.503	1.00122.67	C
	ATOM	441	CD	GLN A 56	19.466	18.631	150.496	1.00128.85	C
15	ATOM	442	OE1	GLN A 56	18.773	19.649	150.450	1.00129.61	O
	ATOM	443	NE2	GLN A 56	20.796	18.670	150.526	1.00131.06	N
	ATOM	444	N	PHE A 57	17.447	16.152	146.454	1.00132.14	N
	ATOM	445	CA	PHE A 57	17.703	15.120	145.451	1.00127.21	C
	ATOM	446	C	PHE A 57	18.149	15.696	144.116	1.00140.12	C
20	ATOM	447	O	PHE A 57	17.947	15.071	143.071	1.00143.01	O
	ATOM	448	CB	PHE A 57	16.452	14.272	145.223	1.00110.03	C
	ATOM	449	CG	PHE A 57	16.271	13.195	146.231	1.00101.04	C
	ATOM	450	CD2	PHE A 57	15.518	13.414	147.368	1.00100.47	C
	ATOM	451	CD1	PHE A 57	16.864	11.960	146.048	1.00102.81	C
25	ATOM	452	CE2	PHE A 57	15.353	12.415	148.315	1.00104.16	C
	ATOM	453	CE1	PHE A 57	16.710	10.954	146.983	1.00108.29	C
	ATOM	454	CZ	PHE A 57	15.950	11.182	148.122	1.00107.42	C
	ATOM	455	N	GLU A 58	18.748	16.883	144.139	1.00143.56	N
	ATOM	456	CA	GLU A 58	19.169	17.515	142.898	1.00145.61	C
30	ATOM	457	C	GLU A 58	20.686	17.500	142.750	1.00147.01	C
	ATOM	458	O	GLU A 58	21.210	17.808	141.679	1.00149.85	O
	ATOM	459	CB	GLU A 58	18.619	18.937	142.792	1.00143.84	C
	ATOM	460	CG	GLU A 58	19.464	19.985	143.476	1.00144.23	C
	ATOM	461	CD	GLU A 58	18.790	21.339	143.491	1.00147.07	C
35	ATOM	462	OE1	GLU A 58	17.627	21.418	143.041	1.00148.76	O
	ATOM	463	OE2	GLU A 58	19.419	22.317	143.953	1.00146.14	O
	ATOM	464	N	ASP A 59	21.389	17.135	143.819	1.00144.35	N
	ATOM	465	CA	ASP A 59	22.841	17.013	143.747	1.00145.76	C
	ATOM	466	C	ASP A 59	23.209	15.736	143.000	1.00148.53	C
40	ATOM	467	O	ASP A 59	22.455	14.760	143.006	1.00150.86	O

	ATOM	468	CB	ASP	A	59	23.482	17.033	145.137	1.00143.01	C
	ATOM	469	CG	ASP	A	59	23.371	15.702	145.850	1.00140.97	C
	ATOM	470	OD2	ASP	A	59	24.340	15.312	146.538	1.00137.04	O
	ATOM	471	OD1	ASP	A	59	22.314	15.049	145.721	1.00142.37	O
5	ATOM	472	N	LEU	A	60	24.375	15.745	142.365	1.00146.98	N
	ATOM	473	CA	LEU	A	60	24.734	14.694	141.419	1.00145.82	C
	ATOM	474	C	LEU	A	60	24.894	13.311	142.044	1.00136.56	C
	ATOM	475	O	LEU	A	60	24.296	12.344	141.569	1.00136.16	O
	ATOM	476	CB	LEU	A	60	25.990	15.080	140.632	1.00149.98	C
10	ATOM	477	CG	LEU	A	60	25.885	16.371	139.811	1.00154.93	C
	ATOM	478	CD1	LEU	A	60	26.349	17.595	140.614	1.00157.18	C
	ATOM	479	CD2	LEU	A	60	26.645	16.246	138.496	1.00153.44	C
	ATOM	480	N	LEU	A	61	25.695	13.224	143.101	1.00128.10	N
	ATOM	481	CA	LEU	A	61	26.009	11.942	143.721	1.00126.29	C
15	ATOM	482	C	LEU	A	61	24.774	11.107	144.015	1.00131.98	C
	ATOM	483	O	LEU	A	61	24.747	9.907	143.742	1.00138.63	O
	ATOM	484	CB	LEU	A	61	26.795	12.146	145.010	1.00121.36	C
	ATOM	485	CG	LEU	A	61	28.304	12.304	144.870	1.00113.90	C
	ATOM	486	CD1	LEU	A	61	28.972	11.965	146.199	1.00112.37	C
20	ATOM	487	CD2	LEU	A	61	28.841	11.435	143.734	1.00105.96	C
	ATOM	488	N	VAL	A	62	23.751	11.751	144.559	1.00130.32	N
	ATOM	489	CA	VAL	A	62	22.519	11.061	144.913	1.00129.72	C
	ATOM	490	C	VAL	A	62	21.780	10.546	143.672	1.00131.20	C
	ATOM	491	O	VAL	A	62	21.206	9.455	143.687	1.00128.53	O
25	ATOM	492	CB	VAL	A	62	21.624	11.964	145.771	1.00126.15	C
	ATOM	493	CG1	VAL	A	62	20.238	11.372	145.925	1.00128.09	C
	ATOM	494	CG2	VAL	A	62	22.273	12.170	147.121	1.00123.08	C
	ATOM	495	N	ARG	A	63	21.819	11.324	142.596	1.00131.89	N
	ATOM	496	CA	ARG	A	63	21.224	10.897	141.336	1.00131.99	C
30	ATOM	497	C	ARG	A	63	21.999	9.722	140.741	1.00132.59	C
	ATOM	498	O	ARG	A	63	21.402	8.759	140.261	1.00134.26	O
	ATOM	499	CB	ARG	A	63	21.177	12.053	140.334	1.00130.14	C
	ATOM	500	CG	ARG	A	63	20.255	13.201	140.718	1.00130.74	C
	ATOM	501	CD	ARG	A	63	20.106	14.174	139.557	1.00137.74	C
35	ATOM	502	NE	ARG	A	63	19.199	15.283	139.849	1.00144.61	N
	ATOM	503	CZ	ARG	A	63	17.891	15.271	139.602	1.00146.25	C
	ATOM	504	NH1	ARG	A	63	17.323	14.199	139.066	1.00146.07	N
	ATOM	505	NH2	ARG	A	63	17.145	16.329	139.897	1.00145.73	N
	ATOM	506	N	ILE	A	64	23.328	9.812	140.780	1.00131.06	N
40	ATOM	507	CA	ILE	A	64	24.205	8.778	140.227	1.00129.51	C

	ATOM	508	C	ILE A 64	23.920	7.409	140.830	1.00131.32	C
	ATOM	509	O	ILE A 64	23.719	6.435	140.100	1.00136.04	O
	ATOM	510	CB	ILE A 64	25.696	9.120	140.438	1.00123.19	C
	ATOM	511	CG1	ILE A 64	26.125	10.248	139.498	1.00122.65	C
5	ATOM	512	CG2	ILE A 64	26.568	7.902	140.201	1.00118.36	C
	ATOM	513	CD1	ILE A 64	27.571	10.679	139.678	1.00119.54	C
	ATOM	514	N	LEU A 65	23.905	7.345	142.159	1.00123.92	N
	ATOM	515	CA	LEU A 65	23.579	6.118	142.873	1.00125.78	C
	ATOM	516	C	LEU A 65	22.236	5.550	142.396	1.00132.97	C
10	ATOM	517	O	LEU A 65	22.106	4.342	142.168	1.00136.87	O
	ATOM	518	CB	LEU A 65	23.563	6.376	144.384	1.00125.70	C
	ATOM	519	CG	LEU A 65	23.357	5.209	145.358	1.00126.10	C
	ATOM	520	CD2	LEU A 65	23.104	5.729	146.764	1.00124.23	C
	ATOM	521	CD1	LEU A 65	24.540	4.246	145.348	1.00124.38	C
15	ATOM	522	N	LEU A 66	21.248	6.427	142.223	1.00134.05	N
	ATOM	523	CA	LEU A 66	19.937	6.025	141.712	1.00131.74	C
	ATOM	524	C	LEU A 66	20.025	5.519	140.275	1.00132.63	C
	ATOM	525	O	LEU A 66	19.290	4.615	139.884	1.00137.10	O
	ATOM	526	CB	LEU A 66	18.936	7.182	141.800	1.00128.46	C
20	ATOM	527	CG	LEU A 66	18.580	7.678	143.204	1.00124.79	C
	ATOM	528	CD2	LEU A 66	18.039	6.548	144.068	1.00119.94	C
	ATOM	529	CD1	LEU A 66	17.584	8.823	143.129	1.00127.10	C
	ATOM	530	N	LEU A 67	20.926	6.104	139.492	1.00128.20	N
	ATOM	531	CA	LEU A 67	21.146	5.646	138.126	1.00129.87	C
25	ATOM	532	C	LEU A 67	21.843	4.283	138.115	1.00138.60	C
	ATOM	533	O	LEU A 67	21.441	3.376	137.381	1.00140.66	O
	ATOM	534	CB	LEU A 67	21.956	6.673	137.335	1.00125.26	C
	ATOM	535	CG	LEU A 67	22.354	6.275	135.912	1.00126.59	C
	ATOM	536	CD1	LEU A 67	21.959	7.350	134.907	1.00120.04	C
30	ATOM	537	CD2	LEU A 67	23.852	5.987	135.828	1.00131.41	C
	ATOM	538	N	ALA A 68	22.884	4.147	138.935	1.00142.26	N
	ATOM	539	CA	ALA A 68	23.598	2.880	139.085	1.00143.94	C
	ATOM	540	C	ALA A 68	22.630	1.762	139.455	1.00147.83	C
	ATOM	541	O	ALA A 68	22.672	0.675	138.875	1.00153.23	O
35	ATOM	542	CB	ALA A 68	24.698	3.004	140.138	1.00139.25	C
	ATOM	543	N	ALA A 69	21.753	2.049	140.414	1.00144.19	N
	ATOM	544	CA	ALA A 69	20.745	1.099	140.871	1.00143.76	C
	ATOM	545	C	ALA A 69	19.771	0.688	139.762	1.00149.53	C
	ATOM	546	O	ALA A 69	19.444	-0.493	139.623	1.00154.06	O
40	ATOM	547	CB	ALA A 69	19.991	1.671	142.050	1.00139.92	C

	ATOM	548	N	CYS A 70	19.312	1.661	138.978	1.00148.68	N
	ATOM	549	CA	CYS A 70	18.393	1.390	137.873	1.00150.94	C
	ATOM	550	C	CYS A 70	19.034	0.501	136.825	1.00157.29	C
	ATOM	551	O	CYS A 70	18.472	-0.529	136.435	1.00161.42	O
5	ATOM	552	CB	CYS A 70	17.940	2.690	137.215	1.00146.96	C
	ATOM	553	SG	CYS A 70	16.775	3.641	138.199	1.00125.90	S
	ATOM	554	N	ILE A 71	20.213	0.914	136.371	1.00156.98	N
	ATOM	555	CA	ILE A 71	20.952	0.171	135.360	1.00157.91	C
	ATOM	556	C	ILE A 71	21.224	-1.271	135.790	1.00165.04	C
10	ATOM	557	O	ILE A 71	21.030	-2.203	135.006	1.00172.35	O
	ATOM	558	CB	ILE A 71	22.287	0.856	135.012	1.00147.82	C
	ATOM	559	CG1	ILE A 71	22.045	2.264	134.470	1.00142.78	C
	ATOM	560	CG2	ILE A 71	23.047	0.033	133.997	1.00146.85	C
	ATOM	561	CD1	ILE A 71	23.299	2.943	133.964	1.00139.83	C
15	ATOM	562	O	SER A 72	20.875	-4.877	137.125	1.00175.41	O
	ATOM	563	N	SER A 72	21.662	-1.452	137.033	1.00161.54	N
	ATOM	564	CA	SER A 72	21.974	-2.785	137.536	1.00161.60	C
	ATOM	565	C	SER A 72	20.755	-3.700	137.472	1.00170.01	C
	ATOM	566	CB	SER A 72	22.508	-2.718	138.964	1.00157.38	C
20	ATOM	567	OG	SER A 72	21.490	-2.325	139.861	1.00157.67	O
	ATOM	568	O	PHE A 73	17.579	-5.484	136.068	1.00186.37	O
	ATOM	569	N	PHE A 73	19.582	-3.155	137.786	1.00172.52	N
	ATOM	570	CA	PHE A 73	18.349	-3.939	137.745	1.00180.15	C
	ATOM	571	C	PHE A 73	17.940	-4.330	136.323	1.00182.72	C
25	ATOM	572	CB	PHE A 73	17.195	-3.206	138.436	1.00185.60	C
	ATOM	573	CG	PHE A 73	15.853	-3.836	138.192	1.00195.55	C
	ATOM	574	CD1	PHE A 73	15.602	-5.141	138.591	1.00201.42	C
	ATOM	575	CD2	PHE A 73	14.845	-3.131	137.556	1.00200.33	C
	ATOM	576	CE1	PHE A 73	14.371	-5.733	138.355	1.00206.73	C
30	ATOM	577	CE2	PHE A 73	13.609	-3.714	137.325	1.00206.40	C
	ATOM	578	CZ	PHE A 73	13.371	-5.016	137.728	1.00208.80	C
	ATOM	579	O	VAL A 74	17.995	-5.584	132.702	1.00182.00	O
	ATOM	580	N	VAL A 74	17.992	-3.365	135.406	1.00178.26	N
	ATOM	581	CA	VAL A 74	17.615	-3.602	134.013	1.00174.35	C
35	ATOM	582	C	VAL A 74	18.493	-4.671	133.364	1.00177.20	C
	ATOM	583	CB	VAL A 74	17.679	-2.302	133.182	1.00162.60	C
	ATOM	584	CG1	VAL A 74	17.425	-2.591	131.711	1.00161.05	C
	ATOM	585	CG2	VAL A 74	16.678	-1.292	133.709	1.00158.85	C
	ATOM	586	O	LEU A 75	20.484	-7.838	132.621	1.00187.93	O
40	ATOM	587	N	LEU A 75	19.799	-4.560	133.576	1.00174.48	N

	ATOM	588	CA	LEU A 75	20.755	-5.481	132.978	1.00177.28	C
	ATOM	589	C	LEU A 75	20.574	-6.925	133.443	1.00183.25	C
	ATOM	590	CB	LEU A 75	22.186	-5.010	133.241	1.00172.37	C
	ATOM	591	CG	LEU A 75	22.615	-3.759	132.471	1.00169.88	C
5	ATOM	592	CD1	LEU A 75	24.035	-3.363	132.846	1.00163.31	C
	ATOM	593	CD2	LEU A 75	22.486	-3.969	130.961	1.00173.46	C
	ATOM	594	O	ALA A 76	18.758	-10.120	135.874	1.00197.50	O
	ATOM	595	N	ALA A 76	20.513	-7.134	134.755	1.00183.41	N
	ATOM	596	CA	ALA A 76	20.432	-8.488	135.299	1.00187.52	C
10	ATOM	597	C	ALA A 76	19.019	-9.086	135.256	1.00195.25	C
	ATOM	598	CB	ALA A 76	20.998	-8.528	136.716	1.00184.40	C
	ATOM	599	O	TRP A 77	15.703	-10.974	133.608	1.00208.49	O
	ATOM	600	N	TRP A 77	18.122	-8.441	134.514	1.00199.35	N
	ATOM	601	CA	TRP A 77	16.751	-8.925	134.329	1.00205.04	C
15	ATOM	602	C	TRP A 77	16.696	-10.244	133.544	1.00205.35	C
	ATOM	603	CB	TRP A 77	15.906	-7.850	133.625	1.00210.09	C
	ATOM	604	CG	TRP A 77	14.549	-8.314	133.157	1.00219.23	C
	ATOM	605	CD1	TRP A 77	13.377	-8.256	133.855	1.00221.55	C
	ATOM	606	CD2	TRP A 77	14.226	-8.896	131.882	1.00227.62	C
20	ATOM	607	NE1	TRP A 77	12.349	-8.770	133.100	1.00228.50	N
	ATOM	608	CE2	TRP A 77	12.843	-9.170	131.885	1.00232.27	C
	ATOM	609	CE3	TRP A 77	14.974	-9.217	130.742	1.00229.11	C
	ATOM	610	CZ2	TRP A 77	12.190	-9.750	130.791	1.00236.66	C
	ATOM	611	CZ3	TRP A 77	14.323	-9.792	129.656	1.00232.73	C
25	ATOM	612	CH2	TRP A 77	12.946	-10.051	129.691	1.00235.98	C
	ATOM	613	O	PHE A 78	16.755	-13.838	131.919	1.00192.52	O
	ATOM	614	N	PHE A 78	17.773	-10.550	132.824	1.00199.50	N
	ATOM	615	CA	PHE A 78	17.794	-11.664	131.874	1.00194.00	C
	ATOM	616	C	PHE A 78	17.451	-13.016	132.520	1.00190.37	C
30	ATOM	617	CB	PHE A 78	19.145	-11.736	131.137	1.00190.07	C
	ATOM	618	CG	PHE A 78	19.506	-10.480	130.360	1.00190.71	C
	ATOM	619	CD1	PHE A 78	18.607	-9.428	130.219	1.00192.68	C
	ATOM	620	CD2	PHE A 78	20.751	-10.365	129.758	1.00189.40	C
	ATOM	621	CE1	PHE A 78	18.949	-8.285	129.512	1.00192.51	C
35	ATOM	622	CE2	PHE A 78	21.100	-9.224	129.045	1.00188.95	C
	ATOM	623	CZ	PHE A 78	20.197	-8.183	128.921	1.00191.02	C
	ATOM	624	O	GLU A 79	18.455	-13.491	136.488	1.00167.22	O
	ATOM	625	N	GLU A 79	17.928	-13.240	133.743	1.00184.68	N
	ATOM	626	CA	GLU A 79	17.645	-14.489	134.452	1.00179.94	C
40	ATOM	627	C	GLU A 79	17.706	-14.320	135.969	1.00173.17	C

	ATOM	628	CB	GLU A 79	18.612	-15.591	134.009	1.00178.68	C
	ATOM	629	CG	GLU A 79	20.013	-15.498	134.612	1.00175.28	C
	ATOM	630	CD	GLU A 79	20.898	-14.448	133.950	1.00171.29	C
	ATOM	631	OE1	GLU A 79	22.080	-14.757	133.690	1.00167.54	O
5	ATOM	632	OE2	GLU A 79	20.428	-13.318	133.698	1.00171.01	O
	ATOM	633	O	THR A 86	18.636	-7.895	145.648	1.00157.40	O
	ATOM	634	N	THR A 86	16.095	-9.096	144.039	1.00154.73	N
	ATOM	635	CA	THR A 86	16.456	-7.839	144.687	1.00152.39	C
	ATOM	636	C	THR A 86	17.974	-7.620	144.648	1.00156.26	C
10	ATOM	637	CB	THR A 86	16.001	-7.824	146.155	1.00144.58	C
	ATOM	638	OG1	THR A 86	17.116	-8.056	147.024	1.00140.27	O
	ATOM	639	CG2	THR A 86	14.928	-8.878	146.414	1.00143.70	C
	ATOM	640	O	ALA A 87	17.459	-4.323	142.614	1.00168.26	O
	ATOM	641	N	ALA A 87	18.559	-7.129	143.547	1.00157.82	N
15	ATOM	642	CA	ALA A 87	17.916	-6.647	142.307	1.00163.61	C
	ATOM	643	C	ALA A 87	16.988	-5.433	142.418	1.00170.33	C
	ATOM	644	CB	ALA A 87	17.289	-7.786	141.461	1.00199.04	C
	ATOM	645	O	PHE A 88	14.054	-2.580	143.297	1.00185.36	O
	ATOM	646	N	PHE A 88	15.685	-5.648	142.285	1.00180.65	N
20	ATOM	647	CA	PHE A 88	14.733	-4.546	142.116	1.00189.31	C
	ATOM	648	C	PHE A 88	14.366	-3.768	143.378	1.00185.40	C
	ATOM	649	CB	PHE A 88	13.447	-5.046	141.461	1.00201.60	C
	ATOM	650	CG	PHE A 88	12.808	-6.181	142.190	1.00210.59	C
	ATOM	651	CD1	PHE A 88	11.755	-5.956	143.060	1.00215.49	C
25	ATOM	652	CD2	PHE A 88	13.270	-7.476	142.017	1.00212.51	C
	ATOM	653	CE1	PHE A 88	11.168	-7.005	143.734	1.00218.78	C
	ATOM	654	CE2	PHE A 88	12.695	-8.524	142.691	1.00215.90	C
	ATOM	655	CZ	PHE A 88	11.645	-8.289	143.553	1.00219.24	C
	ATOM	656	N	VAL A 89	14.368	-4.419	144.534	1.00180.21	N
30	ATOM	657	CA	VAL A 89	13.994	-3.701	145.745	1.00175.37	C
	ATOM	658	C	VAL A 89	15.101	-2.743	146.170	1.00165.77	C
	ATOM	659	O	VAL A 89	14.831	-1.730	146.818	1.00163.08	O
	ATOM	660	CB	VAL A 89	13.632	-4.642	146.909	1.00178.74	C
	ATOM	661	CG1	VAL A 89	12.947	-5.880	146.387	1.00181.13	C
35	ATOM	662	CG2	VAL A 89	14.864	-5.009	147.709	1.00178.94	C
	ATOM	663	N	GLU A 90	16.340	-3.058	145.797	1.00159.64	N
	ATOM	664	CA	GLU A 90	17.474	-2.227	146.186	1.00154.76	C
	ATOM	665	C	GLU A 90	17.332	-0.768	145.735	1.00150.06	C
	ATOM	666	O	GLU A 90	17.478	0.136	146.558	1.00152.18	O
40	ATOM	667	CB	GLU A 90	18.819	-2.836	145.762	1.00158.55	C

	ATOM	668	CG	GLU A 90	19.332	-3.915	146.706	1.00167.06	C
	ATOM	669	CD	GLU A 90	20.847	-3.893	146.862	1.00171.17	C
	ATOM	670	OE1	GLU A 90	21.525	-3.168	146.095	1.00168.95	O
	ATOM	671	OE2	GLU A 90	21.356	-4.591	147.768	1.00173.15	O
5	ATOM	672	N	PRO A 91	17.020	-0.527	144.445	1.00140.71	N
	ATOM	673	CA	PRO A 91	16.821	0.864	144.023	1.00137.01	C
	ATOM	674	C	PRO A 91	15.672	1.550	144.752	1.00134.24	C
	ATOM	675	O	PRO A 91	15.700	2.763	144.952	1.00126.62	O
	ATOM	676	CB	PRO A 91	16.468	0.724	142.543	1.00134.34	C
10	ATOM	677	CG	PRO A 91	17.119	-0.521	142.132	1.00133.50	C
	ATOM	678	CD	PRO A 91	16.961	-1.438	143.293	1.00135.25	C
	ATOM	679	N	PHE A 92	14.671	0.774	145.143	1.00139.31	N
	ATOM	680	CA	PHE A 92	13.512	1.330	145.822	1.00139.92	C
	ATOM	681	C	PHE A 92	13.796	1.670	147.280	1.00135.43	C
15	ATOM	682	O	PHE A 92	13.354	2.709	147.764	1.00133.08	O
	ATOM	683	CB	PHE A 92	12.316	0.385	145.703	1.00144.20	C
	ATOM	684	CG	PHE A 92	11.628	0.448	144.365	1.00145.22	C
	ATOM	685	CD1	PHE A 92	11.588	1.637	143.646	1.00140.52	C
	ATOM	686	CD2	PHE A 92	11.025	-0.678	143.825	1.00145.29	C
20	ATOM	687	CE1	PHE A 92	10.957	1.703	142.419	1.00137.71	C
	ATOM	688	CE2	PHE A 92	10.392	-0.618	142.598	1.00144.59	C
	ATOM	689	CZ	PHE A 92	10.359	0.577	141.894	1.00141.53	C
	ATOM	690	N	VAL A 93	14.536	0.807	147.974	1.00135.61	N
	ATOM	691	CA	VAL A 93	14.878	1.069	149.374	1.00136.23	C
25	ATOM	692	C	VAL A 93	15.972	2.132	149.512	1.00137.35	C
	ATOM	693	O	VAL A 93	15.996	2.879	150.493	1.00139.71	O
	ATOM	694	CB	VAL A 93	15.276	-0.213	150.145	1.00133.83	C
	ATOM	695	CG1	VAL A 93	14.233	-1.298	149.946	1.00134.99	C
	ATOM	696	CG2	VAL A 93	16.648	-0.698	149.720	1.00133.69	C
30	ATOM	697	N	ILE A 94	16.872	2.195	148.534	1.00133.05	N
	ATOM	698	CA	ILE A 94	17.843	3.279	148.468	1.00126.88	C
	ATOM	699	C	ILE A 94	17.100	4.620	148.460	1.00129.69	C
	ATOM	700	O	ILE A 94	17.349	5.485	149.300	1.00132.39	O
	ATOM	701	CB	ILE A 94	18.752	3.146	147.224	1.00119.74	C
35	ATOM	702	CG1	ILE A 94	19.773	2.028	147.433	1.00117.04	C
	ATOM	703	CG2	ILE A 94	19.472	4.455	146.918	1.00115.09	C
	ATOM	704	CD1	ILE A 94	20.779	1.906	146.300	1.00115.03	C
	ATOM	705	N	LEU A 95	16.166	4.766	147.527	1.00127.65	N
	ATOM	706	CA	LEU A 95	15.354	5.969	147.430	1.00121.56	C
40	ATOM	707	C	LEU A 95	14.686	6.273	148.759	1.00117.89	C

	ATOM	708	O	LEU A 95	14.775	7.390	149.252	1.00122.86	O
	ATOM	709	CB	LEU A 95	14.292	5.812	146.339	1.00125.49	C
	ATOM	710	CG	LEU A 95	13.353	7.003	146.126	1.00122.32	C
	ATOM	711	CD1	LEU A 95	14.153	8.230	145.702	1.00120.31	C
5	ATOM	712	CD2	LEU A 95	12.252	6.674	145.112	1.00117.92	C
	ATOM	713	N	LEU A 96	14.038	5.271	149.343	1.00115.87	N
	ATOM	714	CA	LEU A 96	13.282	5.467	150.577	1.00120.32	C
	ATOM	715	C	LEU A 96	14.157	5.959	151.725	1.00129.05	C
	ATOM	716	O	LEU A 96	13.797	6.913	152.412	1.00134.52	O
10	ATOM	717	CB	LEU A 96	12.547	4.187	150.988	1.00116.79	C
	ATOM	718	CG	LEU A 96	11.268	3.828	150.227	1.00110.82	C
	ATOM	719	CD1	LEU A 96	10.791	2.436	150.616	1.00110.63	C
	ATOM	720	CD2	LEU A 96	10.186	4.862	150.481	1.00103.79	C
	ATOM	721	N	ILE A 97	15.298	5.309	151.936	1.00128.50	N
15	ATOM	722	CA	ILE A 97	16.229	5.747	152.970	1.00126.56	C
	ATOM	723	C	ILE A 97	16.730	7.160	152.673	1.00124.51	C
	ATOM	724	O	ILE A 97	16.805	8.002	153.574	1.00123.81	O
	ATOM	725	CB	ILE A 97	17.425	4.791	153.099	1.00129.01	C
	ATOM	726	CG1	ILE A 97	16.974	3.455	153.680	1.00134.52	C
20	ATOM	727	CG2	ILE A 97	18.502	5.389	153.989	1.00128.99	C
	ATOM	728	CD1	ILE A 97	18.119	2.495	153.930	1.00138.22	C
	ATOM	729	N	LEU A 98	17.057	7.414	151.406	1.00120.91	N
	ATOM	730	CA	LEU A 98	17.518	8.731	150.978	1.00117.63	C
	ATOM	731	C	LEU A 98	16.438	9.789	151.144	1.00124.04	C
25	ATOM	732	O	LEU A 98	16.733	10.938	151.471	1.00129.49	O
	ATOM	733	CB	LEU A 98	17.996	8.702	149.530	1.00113.21	C
	ATOM	734	CG	LEU A 98	19.336	8.012	149.294	1.00115.96	C
	ATOM	735	CD1	LEU A 98	19.923	8.469	147.975	1.00119.37	C
	ATOM	736	CD2	LEU A 98	20.309	8.257	150.440	1.00113.88	C
30	ATOM	737	N	ILE A 99	15.189	9.399	150.908	1.00122.49	N
	ATOM	738	CA	ILE A 99	14.052	10.278	151.158	1.00117.11	C
	ATOM	739	C	ILE A 99	13.860	10.457	152.662	1.00111.71	C
	ATOM	740	O	ILE A 99	13.562	11.550	153.134	1.00108.84	O
	ATOM	741	CB	ILE A 99	12.757	9.738	150.504	1.00113.99	C
35	ATOM	742	CG1	ILE A 99	12.840	9.884	148.980	1.00107.66	C
	ATOM	743	CG2	ILE A 99	11.529	10.460	151.056	1.00114.11	C
	ATOM	744	CD1	ILE A 99	11.606	9.456	148.234	1.00103.28	C
	ATOM	745	N	ALA A 100	14.058	9.378	153.409	1.00114.69	N
	ATOM	746	CA	ALA A 100	13.957	9.413	154.865	1.00119.18	C
40	ATOM	747	C	ALA A 100	14.997	10.352	155.464	1.00118.39	C

	ATOM	748	O	ALA A 100	14.672	11.225	156.273	1.00117.23	O
	ATOM	749	CB	ALA A 100	14.119	8.011	155.439	1.00120.41	C
	ATOM	750	N	ASN A 101	16.249	10.159	155.059	1.00115.41	N
	ATOM	751	CA	ASN A 101	17.348	10.968	155.558	1.00110.85	C
5	ATOM	752	C	ASN A 101	17.153	12.430	155.191	1.00110.36	C
	ATOM	753	O	ASN A 101	17.419	13.321	156.000	1.00105.85	O
	ATOM	754	CB	ASN A 101	18.680	10.452	155.016	1.00106.81	C
	ATOM	755	CG	ASN A 101	19.864	10.981	155.791	1.00108.18	C
	ATOM	756	OD1	ASN A 101	20.099	10.587	156.936	1.00106.93	O
10	ATOM	757	ND2	ASN A 101	20.624	11.875	155.171	1.00110.72	N
	ATOM	758	N	ALA A 102	16.668	12.661	153.972	1.00110.43	N
	ATOM	759	CA	ALA A 102	16.406	14.008	153.475	1.00111.11	C
	ATOM	760	C	ALA A 102	15.430	14.766	154.369	1.00120.41	C
	ATOM	761	O	ALA A 102	15.732	15.873	154.810	1.00124.83	O
15	ATOM	762	CB	ALA A 102	15.881	13.958	152.060	1.00109.52	C
	ATOM	763	N	ILE A 103	14.266	14.171	154.632	1.00122.11	N
	ATOM	764	CA	ILE A 103	13.243	14.808	155.467	1.00120.36	C
	ATOM	765	C	ILE A 103	13.802	15.178	156.831	1.00124.33	C
	ATOM	766	O	ILE A 103	13.599	16.292	157.308	1.00130.63	O
20	ATOM	767	CB	ILE A 103	12.003	13.909	155.674	1.00112.56	C
	ATOM	768	CG1	ILE A 103	11.329	13.604	154.342	1.00111.58	C
	ATOM	769	CG2	ILE A 103	10.998	14.584	156.591	1.00107.87	C
	ATOM	770	CD1	ILE A 103	10.125	12.724	154.480	1.00112.15	C
	ATOM	771	N	VAL A 104	14.510	14.240	157.454	1.00120.55	N
25	ATOM	772	CA	VAL A 104	15.123	14.489	158.752	1.00116.62	C
	ATOM	773	C	VAL A 104	16.068	15.677	158.655	1.00116.43	C
	ATOM	774	O	VAL A 104	16.037	16.578	159.490	1.00120.89	O
	ATOM	775	CB	VAL A 104	15.898	13.262	159.257	1.00115.42	C
	ATOM	776	CG1	VAL A 104	16.557	13.563	160.590	1.00112.26	C
30	ATOM	777	CG2	VAL A 104	14.971	12.068	159.387	1.00118.98	C
	ATOM	778	N	GLY A 105	16.891	15.681	157.614	1.00112.98	N
	ATOM	779	CA	GLY A 105	17.808	16.776	157.372	1.00112.53	C
	ATOM	780	C	GLY A 105	17.127	18.106	157.108	1.00113.73	C
	ATOM	781	O	GLY A 105	17.680	19.156	157.414	1.00115.24	O
35	ATOM	782	N	VAL A 106	15.930	18.078	156.533	1.00114.99	N
	ATOM	783	CA	VAL A 106	15.223	19.323	156.242	1.00118.39	C
	ATOM	784	C	VAL A 106	14.637	19.925	157.513	1.00119.24	C
	ATOM	785	O	VAL A 106	14.749	21.131	157.741	1.00121.73	O
	ATOM	786	CB	VAL A 106	14.095	19.138	155.203	1.00122.91	C
40	ATOM	787	CG1	VAL A 106	13.376	20.456	154.970	1.00124.36	C

	ATOM	788	CG2 VAL A 106	14.648	18.610	153.895	1.00125.00	C
	ATOM	789	N TRP A 107	14.006	19.081	158.329	1.00118.34	N
	ATOM	790	CA TRP A 107	13.463	19.509	159.613	1.00120.72	C
	ATOM	791	C TRP A 107	14.590	20.067	160.476	1.00119.66	C
5	ATOM	792	O TRP A 107	14.444	21.114	161.113	1.00118.71	O
	ATOM	793	CB TRP A 107	12.780	18.343	160.336	1.00125.18	C
	ATOM	794	CG TRP A 107	11.466	17.920	159.745	1.00133.75	C
	ATOM	795	CD1 TRP A 107	10.750	18.570	158.781	1.00138.86	C
	ATOM	796	CD2 TRP A 107	10.712	16.743	160.078	1.00139.13	C
10	ATOM	797	NE1 TRP A 107	9.598	17.870	158.491	1.00142.33	N
	ATOM	798	CE2 TRP A 107	9.552	16.747	159.273	1.00140.37	C
	ATOM	799	CE3 TRP A 107	10.907	15.689	160.977	1.00139.08	C
	ATOM	800	CZ2 TRP A 107	8.590	15.738	159.344	1.00136.51	C
	ATOM	801	CZ3 TRP A 107	9.948	14.688	161.045	1.00137.53	C
15	ATOM	802	CH2 TRP A 107	8.806	14.721	160.233	1.00135.96	C
	ATOM	803	N GLN A 108	15.716	19.359	160.481	1.00115.50	N
	ATOM	804	CA GLN A 108	16.900	19.797	161.199	1.00112.24	C
	ATOM	805	C GLN A 108	17.258	21.218	160.787	1.00111.67	C
	ATOM	806	O GLN A 108	17.310	22.111	161.624	1.00118.08	O
20	ATOM	807	CB GLN A 108	18.071	18.856	160.919	1.00119.03	C
	ATOM	808	CG GLN A 108	19.132	18.838	162.011	1.00129.23	C
	ATOM	809	CD GLN A 108	19.677	20.222	162.336	1.00133.35	C
	ATOM	810	OE1 GLN A 108	20.278	20.882	161.478	1.00135.37	O
	ATOM	811	NE2 GLN A 108	19.451	20.679	163.575	1.00125.90	N
25	ATOM	812	N GLU A 109	17.494	21.423	159.498	1.00112.51	N
	ATOM	813	CA GLU A 109	17.860	22.743	158.993	1.00118.38	C
	ATOM	814	C GLU A 109	16.833	23.839	159.308	1.00119.72	C
	ATOM	815	O GLU A 109	17.216	24.934	159.722	1.00119.79	O
	ATOM	816	CB GLU A 109	18.137	22.703	157.483	1.00124.43	C
30	ATOM	817	CG GLU A 109	19.527	22.210	157.103	1.00130.58	C
	ATOM	818	CD GLU A 109	19.899	22.552	155.668	1.00140.66	C
	ATOM	819	OE1 GLU A 109	20.512	23.621	155.457	1.00147.69	O
	ATOM	820	OE2 GLU A 109	19.584	21.759	154.752	1.00140.74	O
	ATOM	821	N ARG A 110	15.543	23.558	159.121	1.00116.53	N
35	ATOM	822	CA ARG A 110	14.534	24.611	159.248	1.00113.93	C
	ATOM	823	C ARG A 110	14.275	25.041	160.696	1.00113.28	C
	ATOM	824	O ARG A 110	14.055	26.225	160.964	1.00110.79	O
	ATOM	825	CB ARG A 110	13.224	24.237	158.552	1.00116.71	C
	ATOM	826	CG ARG A 110	12.231	25.403	158.476	1.00130.63	C
40	ATOM	827	CD ARG A 110	10.885	25.015	157.854	1.00146.12	C

	ATOM	828	NE	ARG A 110	10.234	23.925	158.580	1.00158.70	N
	ATOM	829	CZ	ARG A 110	9.397	24.090	159.601	1.00163.61	C
	ATOM	830	NH1	ARG A 110	9.091	25.310	160.025	1.00164.63	N
	ATOM	831	NH2	ARG A 110	8.863	23.029	160.199	1.00163.29	N
5	ATOM	832	N	ASN A 111	14.301	24.089	161.625	1.00111.35	N
	ATOM	833	CA	ASN A 111	14.107	24.412	163.036	1.00105.19	C
	ATOM	834	C	ASN A 111	15.197	25.342	163.514	1.00105.52	C
	ATOM	835	O	ASN A 111	14.947	26.279	164.280	1.00108.74	O
	ATOM	836	CB	ASN A 111	14.106	23.151	163.894	1.00102.44	C
10	ATOM	837	CG	ASN A 111	12.875	22.306	163.674	1.00104.73	C
	ATOM	838	OD1	ASN A 111	11.841	22.810	163.231	1.00109.57	O
	ATOM	839	ND2	ASN A 111	12.973	21.014	163.981	1.00100.20	N
	ATOM	840	N	ALA A 112	16.413	25.073	163.050	1.00100.56	N
	ATOM	841	CA	ALA A 112	17.557	25.905	163.382	1.00 91.63	C
15	ATOM	842	C	ALA A 112	17.372	27.314	162.827	1.00 91.79	C
	ATOM	843	O	ALA A 112	17.620	28.293	163.524	1.00 94.95	O
	ATOM	844	CB	ALA A 112	18.835	25.284	162.868	1.00 78.05	C
	ATOM	845	N	GLU A 113	16.920	27.417	161.583	1.00 88.21	N
	ATOM	846	CA	GLU A 113	16.696	28.724	160.989	1.00 96.67	C
20	ATOM	847	C	GLU A 113	15.642	29.489	161.779	1.00104.41	C
	ATOM	848	O	GLU A 113	15.865	30.637	162.164	1.00109.18	O
	ATOM	849	CB	GLU A 113	16.271	28.599	159.529	1.00107.66	C
	ATOM	850	CG	GLU A 113	16.026	29.932	158.841	1.00121.70	C
	ATOM	851	CD	GLU A 113	15.217	29.796	157.556	1.00136.58	C
25	ATOM	852	OE1	GLU A 113	15.436	28.813	156.806	1.00137.24	O
	ATOM	853	OE2	GLU A 113	14.356	30.673	157.303	1.00143.61	O
	ATOM	854	N	ASN A 114	14.504	28.843	162.035	1.00107.66	N
	ATOM	855	CA	ASN A 114	13.390	29.484	162.740	1.00107.05	C
	ATOM	856	C	ASN A 114	13.767	29.962	164.136	1.00104.39	C
30	ATOM	857	O	ASN A 114	13.428	31.077	164.538	1.00105.07	O
	ATOM	858	CB	ASN A 114	12.186	28.546	162.827	1.00108.03	C
	ATOM	859	CG	ASN A 114	11.585	28.239	161.468	1.00111.64	C
	ATOM	860	OD1	ASN A 114	11.059	27.147	161.244	1.00111.70	O
	ATOM	861	ND2	ASN A 114	11.664	29.199	160.552	1.00113.27	N
35	ATOM	862	N	ALA A 115	14.463	29.102	164.869	1.00 98.82	N
	ATOM	863	CA	ALA A 115	15.011	29.463	166.165	1.00 94.32	C
	ATOM	864	C	ALA A 115	15.817	30.755	166.067	1.00 90.18	C
	ATOM	865	O	ALA A 115	15.584	31.698	166.821	1.00 94.53	O
	ATOM	866	CB	ALA A 115	15.883	28.331	166.698	1.00 95.21	C
40	ATOM	867	N	ILE A 116	16.762	30.802	165.133	1.00 82.66	N

	ATOM	868	CA	ILE A 116	17.630	31.965	165.009	1.00	82.24	C
	ATOM	869	C	ILE A 116	16.812	33.207	164.717	1.00	86.73	C
	ATOM	870	O	ILE A 116	17.042	34.284	165.282	1.00	79.98	O
	ATOM	871	CB	ILE A 116	18.634	31.801	163.877	1.00	78.43	C
5	ATOM	872	CG1	ILE A 116	19.494	30.562	164.098	1.00	77.20	C
	ATOM	873	CG2	ILE A 116	19.521	33.029	163.812	1.00	80.56	C
	ATOM	874	CD1	ILE A 116	20.545	30.748	165.159	1.00	81.83	C
	ATOM	875	N	GLU A 117	15.854	33.027	163.815	1.00	93.27	N
	ATOM	876	CA	GLU A 117	14.952	34.084	163.404	1.00	95.51	C
10	ATOM	877	C	GLU A 117	14.072	34.497	164.576	1.00	93.73	C
	ATOM	878	O	GLU A 117	13.717	35.668	164.723	1.00	97.85	O
	ATOM	879	CB	GLU A 117	14.096	33.598	162.238	1.00	99.26	C
	ATOM	880	CG	GLU A 117	13.096	34.616	161.745	1.00	107.95	C
	ATOM	881	CD	GLU A 117	13.762	35.890	161.288	1.00	111.79	C
15	ATOM	882	OE2	GLU A 117	14.681	35.803	160.441	1.00	119.56	O
	ATOM	883	OE1	GLU A 117	13.363	36.974	161.770	1.00	108.27	O
	ATOM	884	N	ALA A 118	13.737	33.528	165.421	1.00	86.89	N
	ATOM	885	CA	ALA A 118	12.867	33.784	166.562	1.00	81.28	C
	ATOM	886	C	ALA A 118	13.517	34.691	167.595	1.00	73.56	C
20	ATOM	887	O	ALA A 118	12.823	35.262	168.432	1.00	78.23	O
	ATOM	888	CB	ALA A 118	12.435	32.485	167.203	1.00	74.86	C
	ATOM	889	N	LEU A 119	14.841	34.827	167.537	1.00	80.80	N
	ATOM	890	CA	LEU A 119	15.553	35.677	168.488	1.00	80.42	C
	ATOM	891	C	LEU A 119	15.058	37.109	168.411	1.00	83.12	C
25	ATOM	892	O	LEU A 119	15.242	37.884	169.345	1.00	81.52	O
	ATOM	893	CB	LEU A 119	17.060	35.679	168.234	1.00	79.28	C
	ATOM	894	CG	LEU A 119	17.965	34.558	168.733	1.00	78.27	C
	ATOM	895	CD1	LEU A 119	19.395	34.991	168.551	1.00	78.19	C
	ATOM	896	CD2	LEU A 119	17.703	34.247	170.178	1.00	75.84	C
30	ATOM	897	N	LYS A 120	14.446	37.469	167.289	1.00	76.59	N
	ATOM	898	CA	LYS A 120	13.996	38.835	167.110	1.00	78.25	C
	ATOM	899	C	LYS A 120	12.762	39.079	167.959	1.00	77.65	C
	ATOM	900	O	LYS A 120	12.371	40.221	168.168	1.00	83.24	O
	ATOM	901	CB	LYS A 120	13.698	39.127	165.638	1.00	104.30	C
35	ATOM	902	CG	LYS A 120	14.895	38.960	164.713	1.00	106.84	C
	ATOM	903	CD	LYS A 120	14.557	39.336	163.274	1.00	110.69	C
	ATOM	904	CE	LYS A 120	15.714	38.989	162.339	1.00	116.52	C
	ATOM	905	NZ	LYS A 120	15.382	39.182	160.896	1.00	121.04	N
	ATOM	906	N	GLU A 121	12.151	38.002	168.447	1.00	87.73	N
40	ATOM	907	CA	GLU A 121	10.903	38.104	169.200	1.00	88.63	C

	ATOM	908	C	GLU A 121	11.181	38.628	170.603	1.00	94.50	C
	ATOM	909	O	GLU A 121	10.333	39.284	171.223	1.00	75.04	O
	ATOM	910	CB	GLU A 121	10.178	36.757	169.251	1.00	86.65	C
	ATOM	911	CG	GLU A 121	9.336	36.457	168.019	1.00	96.03	C
5	ATOM	912	CD	GLU A 121	9.087	34.963	167.818	1.00	110.30	C
	ATOM	913	OE1	GLU A 121	8.050	34.593	167.219	1.00	116.62	O
	ATOM	914	OE2	GLU A 121	9.935	34.152	168.246	1.00	114.47	O
	ATOM	915	N	TYR A 122	12.391	38.352	171.086	1.00	93.54	N
	ATOM	916	CA	TYR A 122	12.832	38.836	172.389	1.00	84.61	C
10	ATOM	917	C	TYR A 122	13.001	40.350	172.413	1.00	89.50	C
	ATOM	918	O	TYR A 122	13.234	40.923	173.474	1.00	93.22	O
	ATOM	919	CB	TYR A 122	14.137	38.158	172.818	1.00	77.98	C
	ATOM	920	CG	TYR A 122	13.990	36.705	173.202	1.00	78.15	C
	ATOM	921	CD2	TYR A 122	14.399	35.695	172.338	1.00	83.50	C
15	ATOM	922	CD1	TYR A 122	13.461	36.339	174.436	1.00	79.50	C
	ATOM	923	CE2	TYR A 122	14.269	34.350	172.682	1.00	89.16	C
	ATOM	924	CE1	TYR A 122	13.324	34.996	174.794	1.00	87.27	C
	ATOM	925	CZ	TYR A 122	13.733	34.003	173.910	1.00	93.62	C
	ATOM	926	OH	TYR A 122	13.606	32.665	174.245	1.00	95.76	O
20	ATOM	927	N	GLU A 123	12.917	41.002	171.258	1.00	81.58	N
	ATOM	928	CA	GLU A 123	12.890	42.463	171.251	1.00	85.39	C
	ATOM	929	C	GLU A 123	12.197	43.101	170.060	1.00	81.40	C
	ATOM	930	O	GLU A 123	12.852	43.549	169.111	1.00	81.08	O
	ATOM	931	CB	GLU A 123	14.270	43.082	171.452	1.00	82.90	C
25	ATOM	932	CG	GLU A 123	15.411	42.366	170.821	1.00	87.27	C
	ATOM	933	CD	GLU A 123	16.704	43.079	171.123	1.00	96.22	C
	ATOM	934	OE1	GLU A 123	17.782	42.613	170.678	1.00	100.07	O
	ATOM	935	OE2	GLU A 123	16.619	44.120	171.814	1.00	94.37	O
	ATOM	936	N	PRO A 124	10.861	43.153	170.128	1.00	77.64	N
30	ATOM	937	CA	PRO A 124	9.969	43.826	169.184	1.00	78.89	C
	ATOM	938	C	PRO A 124	10.227	45.323	169.074	1.00	77.48	C
	ATOM	939	O	PRO A 124	10.468	45.981	170.084	1.00	77.58	O
	ATOM	940	CB	PRO A 124	8.577	43.596	169.797	1.00	77.28	C
	ATOM	941	CG	PRO A 124	8.816	43.134	171.176	1.00	79.36	C
35	ATOM	942	CD	PRO A 124	10.103	42.408	171.141	1.00	75.09	C
	ATOM	943	N	GLU A 125	10.167	45.848	167.855	1.00	76.66	N
	ATOM	944	CA	GLU A 125	10.232	47.289	167.640	1.00	80.03	C
	ATOM	945	C	GLU A 125	9.099	48.017	168.374	1.00	78.78	C
	ATOM	946	O	GLU A 125	7.927	47.677	168.217	1.00	83.29	O
40	ATOM	947	CB	GLU A 125	10.181	47.598	166.145	1.00	81.75	C

	ATOM	948	CG	GLU A 125	11.303	46.971	165.342	1.00	87.42	C
	ATOM	949	CD	GLU A 125	12.222	48.020	164.759	1.00	95.41	C
	ATOM	950	OE1	GLU A 125	11.798	49.201	164.724	1.00	100.63	O
	ATOM	951	OE2	GLU A 125	13.355	47.671	164.348	1.00	93.61	O
5	ATOM	952	N	MET A 126	9.462	49.015	169.178	1.00	71.63	N
	ATOM	953	CA	MET A 126	8.503	49.757	169.988	1.00	64.70	C
	ATOM	954	C	MET A 126	8.553	51.243	169.668	1.00	64.00	C
	ATOM	955	O	MET A 126	9.582	51.756	169.236	1.00	67.18	O
	ATOM	956	CB	MET A 126	8.833	49.575	171.460	1.00	67.21	C
10	ATOM	957	CG	MET A 126	9.236	48.177	171.832	1.00	66.86	C
	ATOM	958	SD	MET A 126	7.800	47.234	172.305	1.00	116.33	S
	ATOM	959	CE	MET A 126	7.128	48.361	173.507	1.00	64.01	C
	ATOM	960	N	GLY A 127	7.446	51.941	169.896	1.00	61.91	N
	ATOM	961	CA	GLY A 127	7.405	53.378	169.678	1.00	59.90	C
15	ATOM	962	C	GLY A 127	6.689	54.029	170.841	1.00	65.84	C
	ATOM	963	O	GLY A 127	6.045	53.334	171.627	1.00	78.51	O
	ATOM	964	N	LYS A 128	6.796	55.349	170.968	1.00	57.76	N
	ATOM	965	CA	LYS A 128	6.065	56.052	172.026	1.00	62.44	C
	ATOM	966	C	LYS A 128	4.944	56.913	171.455	1.00	66.40	C
20	ATOM	967	O	LYS A 128	5.204	57.781	170.623	1.00	66.21	O
	ATOM	968	CB	LYS A 128	7.004	56.938	172.833	1.00	60.56	C
	ATOM	969	CG	LYS A 128	8.091	56.233	173.537	1.00	56.84	C
	ATOM	970	CD	LYS A 128	9.118	57.272	173.899	1.00	60.29	C
	ATOM	971	CE	LYS A 128	10.530	56.789	173.539	1.00	63.79	C
25	ATOM	972	NZ	LYS A 128	11.499	57.912	173.510	1.00	61.14	N
	ATOM	973	N	VAL A 129	3.708	56.686	171.900	1.00	66.14	N
	ATOM	974	CA	VAL A 129	2.570	57.495	171.431	1.00	63.61	C
	ATOM	975	C	VAL A 129	1.865	58.196	172.571	1.00	61.74	C
	ATOM	976	O	VAL A 129	2.089	57.868	173.725	1.00	57.34	O
30	ATOM	977	CB	VAL A 129	1.512	56.649	170.740	1.00	53.21	C
	ATOM	978	CG1	VAL A 129	2.053	56.070	169.447	1.00	52.47	C
	ATOM	979	CG2	VAL A 129	1.045	55.563	171.685	1.00	61.22	C
	ATOM	980	N	TYR A 130	1.031	59.176	172.236	1.00	67.40	N
	ATOM	981	CA	TYR A 130	0.058	59.731	173.171	1.00	71.30	C
35	ATOM	982	C	TYR A 130	-1.326	59.443	172.651	1.00	73.05	C
	ATOM	983	O	TYR A 130	-1.660	59.768	171.519	1.00	82.44	O
	ATOM	984	CB	TYR A 130	0.198	61.228	173.322	1.00	55.65	C
	ATOM	985	CG	TYR A 130	1.461	61.652	174.000	1.00	71.36	C
	ATOM	986	CD1	TYR A 130	1.578	61.609	175.379	1.00	76.68	C
40	ATOM	987	CD2	TYR A 130	2.533	62.119	173.267	1.00	75.33	C

	ATOM	988	CE1 TYR A 130	2.736	62.015	176.010	1.00	82.02	C
	ATOM	989	CE2 TYR A 130	3.694	62.524	173.888	1.00	81.28	C
	ATOM	990	CZ TYR A 130	3.790	62.464	175.253	1.00	82.53	C
	ATOM	991	OH TYR A 130	4.952	62.856	175.855	1.00	88.66	O
5	ATOM	992	N ARG A 131	-2.127	58.814	173.489	1.00	73.42	N
	ATOM	993	CA ARG A 131	-3.499	58.491	173.168	1.00	75.19	C
	ATOM	994	C ARG A 131	-4.353	58.908	174.364	1.00	80.03	C
	ATOM	995	O ARG A 131	-3.818	59.230	175.429	1.00	87.31	O
	ATOM	996	CB ARG A 131	-3.614	57.007	172.859	1.00	58.47	C
10	ATOM	997	CG ARG A 131	-2.776	56.606	171.694	1.00	56.67	C
	ATOM	998	CD ARG A 131	-2.890	55.139	171.386	1.00	71.36	C
	ATOM	999	NE ARG A 131	-2.323	54.848	170.075	1.00	70.23	N
	ATOM	1000	CZ ARG A 131	-2.138	53.626	169.596	1.00	74.05	C
	ATOM	1001	NH1 ARG A 131	-2.469	52.576	170.324	1.00	77.27	N
15	ATOM	1002	NH2 ARG A 131	-1.622	53.456	168.387	1.00	80.67	N
	ATOM	1003	N ALA A 132	-5.670	58.916	174.191	1.00	74.36	N
	ATOM	1004	CA ALA A 132	-6.505	59.736	175.051	1.00	75.97	C
	ATOM	1005	C ALA A 132	-6.840	59.038	176.345	1.00	85.81	C
	ATOM	1006	O ALA A 132	-7.278	59.676	177.311	1.00	91.59	O
20	ATOM	1007	CB ALA A 132	-7.756	60.160	174.330	1.00	65.27	C
	ATOM	1008	N ASP A 133	-6.612	57.730	176.375	1.00	85.66	N
	ATOM	1009	CA ASP A 133	-7.039	56.937	177.521	1.00	83.88	C
	ATOM	1010	C ASP A 133	-6.033	56.986	178.669	1.00	82.12	C
	ATOM	1011	O ASP A 133	-6.275	56.412	179.729	1.00	85.17	O
25	ATOM	1012	CB ASP A 133	-7.351	55.500	177.098	1.00	87.14	C
	ATOM	1013	CG ASP A 133	-6.168	54.816	176.473	1.00	100.38	C
	ATOM	1014	OD1 ASP A 133	-5.232	55.523	176.033	1.00	104.32	O
	ATOM	1015	OD2 ASP A 133	-6.174	53.570	176.425	1.00	106.49	O
	ATOM	1016	N ARG A 134	-4.915	57.674	178.449	1.00	82.25	N
30	ATOM	1017	CA ARG A 134	-3.892	57.911	179.461	1.00	68.64	C
	ATOM	1018	C ARG A 134	-3.243	59.277	179.196	1.00	83.04	C
	ATOM	1019	O ARG A 134	-2.969	59.637	178.045	1.00	72.25	O
	ATOM	1020	CB ARG A 134	-2.850	56.782	179.456	1.00	93.97	C
	ATOM	1021	CG ARG A 134	-3.411	55.411	179.857	1.00	102.19	C
35	ATOM	1022	CD ARG A 134	-2.400	54.264	179.823	1.00	107.68	C
	ATOM	1023	NE ARG A 134	-1.041	54.688	180.138	1.00	117.82	N
	ATOM	1024	CZ ARG A 134	-0.624	55.065	181.343	1.00	129.82	C
	ATOM	1025	NH1 ARG A 134	-1.465	55.095	182.377	1.00	133.48	N
	ATOM	1026	NH2 ARG A 134	0.641	55.428	181.509	1.00	131.61	N
40	ATOM	1027	N LYS A 135	-3.002	60.052	180.246	1.00	88.56	N

	ATOM	1028	CA	LYS A 135	-2.458	61.398	180.072	1.00	68.73	C
	ATOM	1029	C	LYS A 135	-0.969	61.355	179.746	1.00	74.31	C
	ATOM	1030	O	LYS A 135	-0.469	62.184	178.988	1.00	73.29	O
	ATOM	1031	CB	LYS A 135	-2.723	62.262	181.313	1.00	100.41	C
5	ATOM	1032	CG	LYS A 135	-2.221	63.709	181.222	1.00	72.08	C
	ATOM	1033	CD	LYS A 135	-2.979	64.618	182.187	1.00	115.97	C
	ATOM	1034	CE	LYS A 135	-2.866	64.154	183.650	1.00	119.49	C
	ATOM	1035	NZ	LYS A 135	-3.868	64.810	184.561	1.00	120.62	N
	ATOM	1036	N	SER A 136	-0.283	60.363	180.312	1.00	72.97	N
10	ATOM	1037	CA	SER A 136	1.150	60.137	180.123	1.00	75.51	C
	ATOM	1038	C	SER A 136	1.483	59.585	178.743	1.00	77.68	C
	ATOM	1039	O	SER A 136	0.591	59.126	178.013	1.00	89.34	O
	ATOM	1040	CB	SER A 136	1.616	59.079	181.108	1.00	80.35	C
	ATOM	1041	OG	SER A 136	1.228	57.794	180.627	1.00	75.69	O
15	ATOM	1042	N	VAL A 137	2.775	59.591	178.405	1.00	65.57	N
	ATOM	1043	CA	VAL A 137	3.250	58.906	177.206	1.00	60.17	C
	ATOM	1044	C	VAL A 137	3.126	57.372	177.325	1.00	60.68	C
	ATOM	1045	O	VAL A 137	3.271	56.804	178.398	1.00	62.74	O
	ATOM	1046	CB	VAL A 137	4.689	59.319	176.840	1.00	60.57	C
20	ATOM	1047	CG1	VAL A 137	5.703	58.546	177.664	1.00	70.26	C
	ATOM	1048	CG2	VAL A 137	4.941	59.081	175.373	1.00	57.29	C
	ATOM	1049	N	GLN A 138	2.818	56.709	176.221	1.00	59.15	N
	ATOM	1050	CA	GLN A 138	2.616	55.275	176.249	1.00	70.02	C
	ATOM	1051	C	GLN A 138	3.602	54.635	175.306	1.00	77.24	C
25	ATOM	1052	O	GLN A 138	3.835	55.136	174.202	1.00	86.09	O
	ATOM	1053	CB	GLN A 138	1.206	54.898	175.804	1.00	64.43	C
	ATOM	1054	CG	GLN A 138	0.079	55.743	176.368	1.00	68.32	C
	ATOM	1055	CD	GLN A 138	-1.250	55.077	176.131	1.00	78.70	C
	ATOM	1056	OE1	GLN A 138	-1.338	53.844	176.123	1.00	62.30	O
30	ATOM	1057	NE2	GLN A 138	-2.290	55.876	175.919	1.00	77.56	N
	ATOM	1058	N	ARG A 139	4.164	53.514	175.735	1.00	69.76	N
	ATOM	1059	CA	ARG A 139	5.193	52.842	174.968	1.00	64.73	C
	ATOM	1060	C	ARG A 139	4.630	51.542	174.435	1.00	67.99	C
	ATOM	1061	O	ARG A 139	4.629	50.538	175.120	1.00	66.42	O
35	ATOM	1062	CB	ARG A 139	6.411	52.588	175.843	1.00	64.75	C
	ATOM	1063	CG	ARG A 139	7.605	52.054	175.102	1.00	76.30	C
	ATOM	1064	CD	ARG A 139	8.892	52.118	175.937	1.00	81.88	C
	ATOM	1065	NE	ARG A 139	9.933	51.316	175.303	1.00	82.68	N
	ATOM	1066	CZ	ARG A 139	10.179	50.053	175.627	1.00	92.68	C
40	ATOM	1067	NH1	ARG A 139	9.474	49.472	176.600	1.00	94.41	N

	ATOM	1068	NH2 ARG A 139	11.137	49.379	174.998	1.00	94.11	N
	ATOM	1069	N ILE A 140	4.152	51.579	173.195	1.00	72.09	N
	ATOM	1070	CA ILE A 140	3.467	50.452	172.586	1.00	69.96	C
	ATOM	1071	C ILE A 140	4.314	49.786	171.514	1.00	74.00	C
5	ATOM	1072	O ILE A 140	5.256	50.378	170.988	1.00	72.12	O
	ATOM	1073	CB ILE A 140	2.185	50.919	171.911	1.00	66.77	C
	ATOM	1074	CG1 ILE A 140	2.524	51.856	170.756	1.00	59.10	C
	ATOM	1075	CG2 ILE A 140	1.296	51.639	172.905	1.00	63.33	C
	ATOM	1076	CD1 ILE A 140	1.303	52.318	170.022	1.00	56.83	C
10	ATOM	1077	N LYS A 141	3.965	48.542	171.202	1.00	81.12	N
	ATOM	1078	CA LYS A 141	4.581	47.829	170.107	1.00	82.18	C
	ATOM	1079	C LYS A 141	4.348	48.660	168.860	1.00	86.25	C
	ATOM	1080	O LYS A 141	3.241	49.165	168.648	1.00	83.08	O
	ATOM	1081	CB LYS A 141	3.945	46.455	169.957	1.00	63.36	C
15	ATOM	1082	CG LYS A 141	4.592	45.389	170.790	1.00	75.75	C
	ATOM	1083	CD LYS A 141	4.079	44.011	170.413	1.00	68.18	C
	ATOM	1084	CE LYS A 141	4.931	42.910	171.029	1.00	82.81	C
	ATOM	1085	NZ LYS A 141	4.321	41.565	170.850	1.00	86.00	N
	ATOM	1086	N ALA A 142	5.390	48.815	168.044	1.00	85.95	N
20	ATOM	1087	CA ALA A 142	5.351	49.757	166.932	1.00	72.35	C
	ATOM	1088	C ALA A 142	4.423	49.293	165.824	1.00	74.50	C
	ATOM	1089	O ALA A 142	3.922	50.108	165.054	1.00	79.76	O
	ATOM	1090	CB ALA A 142	6.731	50.007	166.403	1.00	69.04	C
	ATOM	1091	N ARG A 143	4.179	47.989	165.754	1.00	67.52	N
25	ATOM	1092	CA ARG A 143	3.224	47.460	164.787	1.00	66.49	C
	ATOM	1093	C ARG A 143	1.778	47.853	165.122	1.00	73.68	C
	ATOM	1094	O ARG A 143	0.851	47.510	164.390	1.00	76.46	O
	ATOM	1095	CB ARG A 143	3.314	45.941	164.737	1.00	67.42	C
	ATOM	1096	CG ARG A 143	2.842	45.261	166.011	1.00	66.03	C
30	ATOM	1097	CD ARG A 143	2.869	43.764	165.846	1.00	68.42	C
	ATOM	1098	NE ARG A 143	1.946	43.321	164.813	1.00	72.40	N
	ATOM	1099	CZ ARG A 143	0.765	42.791	165.091	1.00	93.79	C
	ATOM	1100	NH1 ARG A 143	0.418	42.649	166.365	1.00	108.35	N
	ATOM	1101	NH2 ARG A 143	-0.062	42.401	164.124	1.00	96.10	N
35	ATOM	1102	N ASP A 144	1.574	48.541	166.239	1.00	66.65	N
	ATOM	1103	CA ASP A 144	0.230	48.952	166.612	1.00	68.22	C
	ATOM	1104	C ASP A 144	0.085	50.468	166.490	1.00	66.90	C
	ATOM	1105	O ASP A 144	-0.879	51.068	166.985	1.00	69.32	O
	ATOM	1106	CB ASP A 144	-0.103	48.458	168.016	1.00	74.15	C
40	ATOM	1107	CG ASP A 144	-0.040	46.942	168.126	1.00	80.62	C

	ATOM	1108	OD1 ASP A 144	-0.345	46.263	167.126	1.00	87.30	O
	ATOM	1109	OD2 ASP A 144	0.300	46.424	169.212	1.00	82.13	O
	ATOM	1110	N ILE A 145	1.067	51.070	165.826	1.00	59.12	N
	ATOM	1111	CA ILE A 145	1.063	52.488	165.525	1.00	61.73	C
5	ATOM	1112	C ILE A 145	0.306	52.679	164.205	1.00	72.14	C
	ATOM	1113	O ILE A 145	0.534	51.973	163.219	1.00	75.39	O
	ATOM	1114	CB ILE A 145	2.522	53.044	165.459	1.00	61.59	C
	ATOM	1115	CG1 ILE A 145	3.198	52.884	166.825	1.00	65.21	C
	ATOM	1116	CG2 ILE A 145	2.566	54.505	165.007	1.00	52.28	C
10	ATOM	1117	CD1 ILE A 145	4.474	53.710	167.028	1.00	52.97	C
	ATOM	1118	N VAL A 146	-0.627	53.618	164.197	1.00	69.97	N
	ATOM	1119	CA VAL A 146	-1.465	53.825	163.030	1.00	66.70	C
	ATOM	1120	C VAL A 146	-1.309	55.258	162.538	1.00	67.55	C
	ATOM	1121	O VAL A 146	-0.823	56.120	163.263	1.00	66.59	O
15	ATOM	1122	CB VAL A 146	-2.943	53.521	163.356	1.00	67.31	C
	ATOM	1123	CG1 VAL A 146	-3.119	52.044	163.724	1.00	57.95	C
	ATOM	1124	CG2 VAL A 146	-3.427	54.412	164.470	1.00	68.53	C
	ATOM	1125	N PRO A 147	-1.675	55.514	161.282	1.00	68.84	N
	ATOM	1126	CA PRO A 147	-1.645	56.902	160.819	1.00	67.50	C
20	ATOM	1127	C PRO A 147	-2.516	57.812	161.675	1.00	73.57	C
	ATOM	1128	O PRO A 147	-3.665	57.488	161.976	1.00	74.58	O
	ATOM	1129	CB PRO A 147	-2.211	56.796	159.409	1.00	58.60	C
	ATOM	1130	CG PRO A 147	-1.761	55.453	158.961	1.00	58.75	C
	ATOM	1131	CD PRO A 147	-1.838	54.565	160.168	1.00	62.38	C
25	ATOM	1132	N GLY A 148	-1.953	58.943	162.079	1.00	71.36	N
	ATOM	1133	CA GLY A 148	-2.696	59.928	162.829	1.00	64.61	C
	ATOM	1134	C GLY A 148	-2.344	59.864	164.289	1.00	66.25	C
	ATOM	1135	O GLY A 148	-2.852	60.655	165.077	1.00	70.31	O
	ATOM	1136	N ASP A 149	-1.481	58.916	164.648	1.00	66.47	N
30	ATOM	1137	CA ASP A 149	-0.970	58.798	166.013	1.00	62.12	C
	ATOM	1138	C ASP A 149	-0.069	59.970	166.321	1.00	62.11	C
	ATOM	1139	O ASP A 149	0.631	60.463	165.446	1.00	72.21	O
	ATOM	1140	CB ASP A 149	-0.189	57.490	166.194	1.00	57.16	C
	ATOM	1141	CG ASP A 149	-0.934	56.467	167.054	1.00	61.87	C
35	ATOM	1142	OD1 ASP A 149	-1.675	56.880	167.999	1.00	54.90	O
	ATOM	1143	OD2 ASP A 149	-0.770	55.251	166.777	1.00	61.01	O
	ATOM	1144	N ILE A 150	-0.112	60.444	167.556	1.00	58.44	N
	ATOM	1145	CA ILE A 150	0.875	61.422	168.010	1.00	59.91	C
	ATOM	1146	C ILE A 150	2.026	60.660	168.619	1.00	56.89	C
40	ATOM	1147	O ILE A 150	1.884	60.113	169.708	1.00	58.75	O

	ATOM	1148	CB	ILE A 150	0.316	62.335	169.110	1.00	61.09	C
	ATOM	1149	CG1	ILE A 150	-0.996	63.005	168.659	1.00	60.82	C
	ATOM	1150	CG2	ILE A 150	1.387	63.311	169.584	1.00	52.21	C
	ATOM	1151	CD1	ILE A 150	-0.911	63.756	167.372	1.00	52.50	C
5	ATOM	1152	N	VAL A 151	3.155	60.596	167.924	1.00	54.59	N
	ATOM	1153	CA	VAL A 151	4.312	59.886	168.465	1.00	58.41	C
	ATOM	1154	C	VAL A 151	5.357	60.841	168.974	1.00	50.88	C
	ATOM	1155	O	VAL A 151	5.415	61.994	168.562	1.00	56.78	O
	ATOM	1156	CB	VAL A 151	4.975	58.975	167.452	1.00	59.26	C
10	ATOM	1157	CG1	VAL A 151	4.017	57.890	167.042	1.00	69.48	C
	ATOM	1158	CG2	VAL A 151	5.370	59.771	166.271	1.00	57.73	C
	ATOM	1159	N	GLU A 152	6.169	60.349	169.898	1.00	68.84	N
	ATOM	1160	CA	GLU A 152	7.253	61.129	170.472	1.00	65.31	C
	ATOM	1161	C	GLU A 152	8.584	60.440	170.197	1.00	67.24	C
15	ATOM	1162	O	GLU A 152	8.693	59.206	170.254	1.00	69.49	O
	ATOM	1163	CB	GLU A 152	7.049	61.289	171.968	1.00	61.83	C
	ATOM	1164	CG	GLU A 152	8.049	62.203	172.620	1.00	73.11	C
	ATOM	1165	CD	GLU A 152	7.762	62.412	174.087	1.00	80.86	C
	ATOM	1166	OE1	GLU A 152	7.964	61.452	174.857	1.00	85.55	O
20	ATOM	1167	OE2	GLU A 152	7.329	63.529	174.464	1.00	82.83	O
	ATOM	1168	N	VAL A 153	9.590	61.242	169.871	1.00	64.30	N
	ATOM	1169	CA	VAL A 153	10.935	60.724	169.669	1.00	66.70	C
	ATOM	1170	C	VAL A 153	11.945	61.546	170.462	1.00	66.76	C
	ATOM	1171	O	VAL A 153	11.796	62.757	170.656	1.00	56.15	O
25	ATOM	1172	CB	VAL A 153	11.325	60.725	168.178	1.00	53.86	C
	ATOM	1173	CG1	VAL A 153	10.496	59.704	167.407	1.00	52.89	C
	ATOM	1174	CG2	VAL A 153	11.131	62.106	167.592	1.00	74.99	C
	ATOM	1175	N	ALA A 154	12.979	60.878	170.936	1.00	65.04	N
	ATOM	1176	CA	ALA A 154	14.079	61.594	171.553	1.00	69.59	C
30	ATOM	1177	C	ALA A 154	15.401	60.907	171.237	1.00	71.10	C
	ATOM	1178	O	ALA A 154	15.424	59.805	170.686	1.00	71.32	O
	ATOM	1179	CB	ALA A 154	13.867	61.687	173.026	1.00	76.41	C
	ATOM	1180	N	VAL A 155	16.497	61.563	171.601	1.00	67.13	N
	ATOM	1181	CA	VAL A 155	17.840	61.105	171.241	1.00	69.36	C
35	ATOM	1182	C	VAL A 155	18.129	59.640	171.567	1.00	66.07	C
	ATOM	1183	O	VAL A 155	18.016	59.206	172.703	1.00	67.07	O
	ATOM	1184	CB	VAL A 155	18.905	62.004	171.862	1.00	67.83	C
	ATOM	1185	CG1	VAL A 155	18.570	62.264	173.301	1.00	68.79	C
	ATOM	1186	CG2	VAL A 155	20.259	61.378	171.716	1.00	70.46	C
40	ATOM	1187	N	GLY A 156	18.481	58.886	170.536	1.00	66.03	N

	ATOM	1188	CA	GLY A 156	18.786	57.481	170.687	1.00	79.10	C
	ATOM	1189	C	GLY A 156	17.736	56.570	170.091	1.00	77.69	C
	ATOM	1190	O	GLY A 156	17.999	55.384	169.850	1.00	73.79	O
	ATOM	1191	N	ASP A 157	16.547	57.129	169.855	1.00	74.76	N
5	ATOM	1192	CA	ASP A 157	15.398	56.368	169.371	1.00	78.17	C
	ATOM	1193	C	ASP A 157	15.523	55.954	167.915	1.00	75.23	C
	ATOM	1194	O	ASP A 157	16.168	56.629	167.128	1.00	83.90	O
	ATOM	1195	CB	ASP A 157	14.118	57.190	169.515	1.00	87.27	C
	ATOM	1196	CG	ASP A 157	13.653	57.318	170.949	1.00	91.56	C
10	ATOM	1197	OD1	ASP A 157	14.229	56.638	171.835	1.00	91.31	O
	ATOM	1198	OD2	ASP A 157	12.691	58.094	171.170	1.00	88.91	O
	ATOM	1199	N	LYS A 158	14.877	54.851	167.555	1.00	73.98	N
	ATOM	1200	CA	LYS A 158	14.753	54.454	166.155	1.00	72.61	C
	ATOM	1201	C	LYS A 158	13.329	54.765	165.697	1.00	72.58	C
15	ATOM	1202	O	LYS A 158	12.392	54.098	166.127	1.00	77.70	O
	ATOM	1203	CB	LYS A 158	15.064	52.962	165.997	1.00	66.54	C
	ATOM	1204	CG	LYS A 158	14.874	52.384	164.609	1.00	67.93	C
	ATOM	1205	CD	LYS A 158	15.166	50.871	164.619	1.00	81.85	C
	ATOM	1206	CE	LYS A 158	15.760	50.349	163.291	1.00	94.59	C
20	ATOM	1207	NZ	LYS A 158	17.197	50.748	163.058	1.00	98.75	N
	ATOM	1208	N	VAL A 159	13.185	55.776	164.836	1.00	64.53	N
	ATOM	1209	CA	VAL A 159	11.892	56.280	164.358	1.00	66.70	C
	ATOM	1210	C	VAL A 159	10.926	55.198	163.823	1.00	71.26	C
	ATOM	1211	O	VAL A 159	11.255	54.488	162.872	1.00	71.52	O
25	ATOM	1212	CB	VAL A 159	12.095	57.389	163.303	1.00	55.09	C
	ATOM	1213	CG1	VAL A 159	10.760	57.920	162.837	1.00	53.66	C
	ATOM	1214	CG2	VAL A 159	12.940	58.522	163.872	1.00	55.45	C
	ATOM	1215	N	PRO A 160	9.725	55.083	164.444	1.00	71.27	N
	ATOM	1216	CA	PRO A 160	8.803	53.942	164.301	1.00	65.30	C
30	ATOM	1217	C	PRO A 160	7.907	53.933	163.071	1.00	66.92	C
	ATOM	1218	O	PRO A 160	7.445	52.853	162.721	1.00	55.09	O
	ATOM	1219	CB	PRO A 160	7.923	54.061	165.542	1.00	57.36	C
	ATOM	1220	CG	PRO A 160	7.842	55.520	165.759	1.00	60.48	C
	ATOM	1221	CD	PRO A 160	9.235	56.032	165.462	1.00	68.54	C
35	ATOM	1222	N	ALA A 161	7.642	55.094	162.472	1.00	66.97	N
	ATOM	1223	CA	ALA A 161	6.820	55.212	161.259	1.00	67.12	C
	ATOM	1224	C	ALA A 161	7.276	56.452	160.487	1.00	80.60	C
	ATOM	1225	O	ALA A 161	8.014	57.270	161.029	1.00	89.83	O
	ATOM	1226	CB	ALA A 161	5.330	55.345	161.625	1.00	55.01	C
40	ATOM	1227	N	ASP A 162	6.858	56.596	159.231	1.00	72.53	N

	ATOM	1228	CA	ASP A 162	6.982	57.887	158.562	1.00	61.97	C
	ATOM	1229	C	ASP A 162	6.124	58.924	159.307	1.00	64.20	C
	ATOM	1230	O	ASP A 162	4.927	58.723	159.503	1.00	71.01	O
	ATOM	1231	CB	ASP A 162	6.539	57.781	157.113	1.00	68.69	C
5	ATOM	1232	CG	ASP A 162	7.664	57.371	156.178	1.00	80.17	C
	ATOM	1233	OD1	ASP A 162	8.751	56.994	156.664	1.00	83.84	O
	ATOM	1234	OD2	ASP A 162	7.446	57.418	154.944	1.00	87.73	O
	ATOM	1235	N	ILE A 163	6.726	60.035	159.714	1.00	52.20	N
	ATOM	1236	CA	ILE A 163	6.082	60.943	160.659	1.00	56.71	C
10	ATOM	1237	C	ILE A 163	6.245	62.400	160.251	1.00	60.59	C
	ATOM	1238	O	ILE A 163	7.368	62.842	160.011	1.00	63.69	O
	ATOM	1239	CB	ILE A 163	6.728	60.758	162.064	1.00	58.77	C
	ATOM	1240	CG1	ILE A 163	6.382	59.378	162.614	1.00	50.60	C
	ATOM	1241	CG2	ILE A 163	6.311	61.851	163.036	1.00	50.28	C
15	ATOM	1242	CD1	ILE A 163	7.311	58.911	163.623	1.00	50.78	C
	ATOM	1243	N	ARG A 164	5.147	63.156	160.167	1.00	56.12	N
	ATOM	1244	CA	ARG A 164	5.269	64.622	160.042	1.00	59.52	C
	ATOM	1245	C	ARG A 164	5.666	65.178	161.407	1.00	67.42	C
	ATOM	1246	O	ARG A 164	5.121	64.765	162.429	1.00	76.50	O
20	ATOM	1247	CB	ARG A 164	3.965	65.279	159.554	1.00	60.17	C
	ATOM	1248	CG	ARG A 164	3.991	66.820	159.425	1.00	53.71	C
	ATOM	1249	CD	ARG A 164	4.666	67.276	158.125	1.00	60.73	C
	ATOM	1250	NE	ARG A 164	4.494	68.695	157.756	1.00	56.53	N
	ATOM	1251	CZ	ARG A 164	4.877	69.747	158.486	1.00	65.56	C
25	ATOM	1252	NH1	ARG A 164	5.432	69.587	159.680	1.00	63.54	N
	ATOM	1253	NH2	ARG A 164	4.690	70.978	158.034	1.00	58.61	N
	ATOM	1254	N	ILE A 165	6.619	66.100	161.430	1.00	66.31	N
	ATOM	1255	CA	ILE A 165	7.022	66.716	162.685	1.00	66.43	C
	ATOM	1256	C	ILE A 165	6.066	67.847	163.100	1.00	74.37	C
30	ATOM	1257	O	ILE A 165	5.721	68.721	162.293	1.00	80.28	O
	ATOM	1258	CB	ILE A 165	8.466	67.223	162.611	1.00	63.67	C
	ATOM	1259	CG1	ILE A 165	9.417	66.051	162.408	1.00	60.83	C
	ATOM	1260	CG2	ILE A 165	8.850	67.943	163.882	1.00	66.82	C
	ATOM	1261	CD1	ILE A 165	10.788	66.477	161.999	1.00	67.65	C
35	ATOM	1262	N	LEU A 166	5.638	67.820	164.362	1.00	67.61	N
	ATOM	1263	CA	LEU A 166	4.686	68.802	164.866	1.00	65.16	C
	ATOM	1264	C	LEU A 166	5.346	69.928	165.650	1.00	70.52	C
	ATOM	1265	O	LEU A 166	5.025	71.107	165.448	1.00	72.40	O
	ATOM	1266	CB	LEU A 166	3.657	68.126	165.766	1.00	62.97	C
40	ATOM	1267	CG	LEU A 166	2.602	67.218	165.162	1.00	64.01	C

	ATOM	1268	CD1 LEU A 166	1.867	66.557	166.300	1.00	64.09	C
	ATOM	1269	CD2 LEU A 166	1.662	68.031	164.297	1.00	68.06	C
	ATOM	1270	N SER A 167	6.245	69.562	166.563	1.00	54.87	N
	ATOM	1271	CA SER A 167	6.886	70.543	167.426	1.00	56.50	C
5	ATOM	1272	C SER A 167	8.225	70.059	167.941	1.00	66.39	C
	ATOM	1273	O SER A 167	8.346	68.918	168.390	1.00	69.07	O
	ATOM	1274	CB SER A 167	5.985	70.846	168.607	1.00	64.64	C
	ATOM	1275	OG SER A 167	6.685	71.571	169.598	1.00	68.11	O
	ATOM	1276	N ILE A 168	9.227	70.931	167.892	1.00	63.50	N
10	ATOM	1277	CA ILE A 168	10.583	70.547	168.286	1.00	69.71	C
	ATOM	1278	C ILE A 168	10.909	71.022	169.710	1.00	71.74	C
	ATOM	1279	O ILE A 168	11.066	72.221	169.966	1.00	78.47	O
	ATOM	1280	CB ILE A 168	11.628	71.038	167.246	1.00	75.60	C
	ATOM	1281	CG1 ILE A 168	11.722	70.062	166.093	1.00	58.55	C
15	ATOM	1282	CG2 ILE A 168	13.008	71.168	167.848	1.00	77.29	C
	ATOM	1283	CD1 ILE A 168	12.337	70.673	164.873	1.00	106.25	C
	ATOM	1284	N LYS A 169	10.996	70.070	170.635	1.00	69.25	N
	ATOM	1285	CA LYS A 169	11.102	70.392	172.061	1.00	74.52	C
	ATOM	1286	C LYS A 169	12.510	70.837	172.422	1.00	80.84	C
20	ATOM	1287	O LYS A 169	12.720	71.472	173.452	1.00	85.42	O
	ATOM	1288	CB LYS A 169	10.692	69.196	172.930	1.00	73.11	C
	ATOM	1289	CG LYS A 169	9.326	68.617	172.590	1.00	78.83	C
	ATOM	1290	CD LYS A 169	8.211	69.352	173.318	1.00	88.52	C
	ATOM	1291	CE LYS A 169	6.877	69.213	172.610	1.00	81.67	C
25	ATOM	1292	NZ LYS A 169	6.674	70.335	171.651	1.00	79.73	N
	ATOM	1293	N SER A 170	13.470	70.502	171.565	1.00	82.51	N
	ATOM	1294	CA SER A 170	14.865	70.878	171.773	1.00	86.31	C
	ATOM	1295	C SER A 170	15.118	72.273	171.236	1.00	97.05	C
	ATOM	1296	O SER A 170	14.181	72.983	170.873	1.00	103.25	O
30	ATOM	1297	CB SER A 170	15.774	69.893	171.045	1.00	79.79	C
	ATOM	1298	OG SER A 170	15.197	68.598	171.045	1.00	71.76	O
	ATOM	1299	N THR A 171	16.384	72.676	171.197	1.00	102.47	N
	ATOM	1300	CA THR A 171	16.747	73.878	170.452	1.00	103.19	C
	ATOM	1301	C THR A 171	17.021	73.417	169.034	1.00	96.84	C
35	ATOM	1302	O THR A 171	17.032	74.214	168.101	1.00	103.00	O
	ATOM	1303	CB THR A 171	17.978	74.648	171.044	1.00	131.75	C
	ATOM	1304	OG1 THR A 171	18.984	73.717	171.467	1.00	131.69	O
	ATOM	1305	CG2 THR A 171	17.567	75.556	172.228	1.00	78.97	C
	ATOM	1306	N THR A 172	17.214	72.109	168.887	1.00	84.82	N
40	ATOM	1307	CA THR A 172	17.541	71.504	167.602	1.00	81.49	C

	ATOM	1308	C	THR A 172	17.166	70.044	167.631	1.00	85.53	C
	ATOM	1309	O	THR A 172	17.498	69.334	168.576	1.00	95.00	O
	ATOM	1310	CB	THR A 172	19.052	71.523	167.325	1.00	82.21	C
	ATOM	1311	OG1	THR A 172	19.750	71.301	168.555	1.00	98.52	O
5	ATOM	1312	CG2	THR A 172	19.503	72.847	166.733	1.00	78.35	C
	ATOM	1313	N	LEU A 173	16.486	69.588	166.587	1.00	81.10	N
	ATOM	1314	CA	LEU A 173	16.320	68.160	166.370	1.00	71.65	C
	ATOM	1315	C	LEU A 173	17.300	67.773	165.285	1.00	75.76	C
	ATOM	1316	O	LEU A 173	17.480	68.515	164.329	1.00	89.96	O
10	ATOM	1317	CB	LEU A 173	14.901	67.825	165.934	1.00	66.13	C
	ATOM	1318	CG	LEU A 173	14.770	66.350	165.584	1.00	67.03	C
	ATOM	1319	CD1	LEU A 173	15.032	65.523	166.831	1.00	59.04	C
	ATOM	1320	CD2	LEU A 173	13.415	66.039	164.962	1.00	63.51	C
	ATOM	1321	N	ARG A 174	17.936	66.620	165.436	1.00	70.35	N
15	ATOM	1322	CA	ARG A 174	19.021	66.223	164.556	1.00	71.83	C
	ATOM	1323	C	ARG A 174	18.915	64.720	164.295	1.00	68.21	C
	ATOM	1324	O	ARG A 174	18.827	63.927	165.224	1.00	68.97	O
	ATOM	1325	CB	ARG A 174	20.349	66.607	165.202	1.00	68.89	C
	ATOM	1326	CG	ARG A 174	21.553	66.380	164.345	1.00	107.86	C
20	ATOM	1327	CD	ARG A 174	22.727	67.239	164.802	1.00	115.57	C
	ATOM	1328	NE	ARG A 174	22.876	68.443	163.982	1.00	124.18	N
	ATOM	1329	CZ	ARG A 174	23.589	68.501	162.857	1.00	129.80	C
	ATOM	1330	NH1	ARG A 174	24.222	67.425	162.410	1.00	131.58	N
	ATOM	1331	NH2	ARG A 174	23.671	69.635	162.170	1.00	130.54	N
25	ATOM	1332	N	VAL A 175	18.890	64.325	163.028	1.00	69.37	N
	ATOM	1333	CA	VAL A 175	18.487	62.963	162.680	1.00	70.06	C
	ATOM	1334	C	VAL A 175	19.514	62.219	161.812	1.00	78.95	C
	ATOM	1335	O	VAL A 175	20.167	62.826	160.969	1.00	86.01	O
	ATOM	1336	CB	VAL A 175	17.138	62.991	161.943	1.00	66.84	C
30	ATOM	1337	CG1	VAL A 175	16.552	61.645	161.891	1.00	67.52	C
	ATOM	1338	CG2	VAL A 175	16.157	63.912	162.642	1.00	65.37	C
	ATOM	1339	N	ASP A 176	19.658	60.911	162.028	1.00	75.85	N
	ATOM	1340	CA	ASP A 176	20.546	60.076	161.218	1.00	76.89	C
	ATOM	1341	C	ASP A 176	19.733	59.267	160.219	1.00	83.71	C
35	ATOM	1342	O	ASP A 176	19.302	58.159	160.517	1.00	92.91	O
	ATOM	1343	CB	ASP A 176	21.367	59.132	162.109	1.00	74.54	C
	ATOM	1344	CG	ASP A 176	22.260	58.149	161.314	1.00	82.14	C
	ATOM	1345	OD1	ASP A 176	22.197	58.084	160.071	1.00	84.44	O
	ATOM	1346	OD2	ASP A 176	23.029	57.397	161.950	1.00	90.77	O
40	ATOM	1347	N	GLN A 177	19.557	59.795	159.016	1.00	80.43	N

	ATOM	1348	CA	GLN A 177	18.809	59.067	158.004	1.00	77.96	C
	ATOM	1349	C	GLN A 177	19.731	58.491	156.932	1.00	82.61	C
	ATOM	1350	O	GLN A 177	19.397	58.489	155.754	1.00	89.81	O
	ATOM	1351	CB	GLN A 177	17.704	59.950	157.400	1.00	66.29	C
5	ATOM	1352	CG	GLN A 177	18.171	61.278	156.841	1.00	70.40	C
	ATOM	1353	CD	GLN A 177	17.052	62.290	156.686	1.00	69.13	C
	ATOM	1354	OE1	GLN A 177	16.117	62.321	157.469	1.00	63.18	O
	ATOM	1355	NE2	GLN A 177	17.153	63.129	155.675	1.00	77.36	N
	ATOM	1356	N	SER A 178	20.889	57.988	157.342	1.00	86.79	N
10	ATOM	1357	CA	SER A 178	21.867	57.460	156.391	1.00	94.64	C
	ATOM	1358	C	SER A 178	21.367	56.205	155.690	1.00	98.23	C
	ATOM	1359	O	SER A 178	21.529	56.043	154.482	1.00	103.83	O
	ATOM	1360	CB	SER A 178	23.140	57.086	157.122	1.00	97.37	C
	ATOM	1361	OG	SER A 178	23.000	55.781	157.655	1.00	100.19	O
15	ATOM	1362	N	ILE A 179	20.782	55.312	156.480	1.00	97.18	N
	ATOM	1363	CA	ILE A 179	20.214	54.051	156.015	1.00	94.81	C
	ATOM	1364	C	ILE A 179	19.162	54.306	154.926	1.00	91.25	C
	ATOM	1365	O	ILE A 179	18.842	53.439	154.104	1.00	82.52	O
	ATOM	1366	CB	ILE A 179	19.601	53.298	157.225	1.00	87.82	C
20	ATOM	1367	CG1	ILE A 179	18.824	52.051	156.792	1.00	91.32	C
	ATOM	1368	CG2	ILE A 179	18.743	54.255	158.060	1.00	75.90	C
	ATOM	1369	CD1	ILE A 179	18.181	51.292	157.930	1.00	89.41	C
	ATOM	1370	N	LEU A 180	18.647	55.527	154.911	1.00	95.33	N
	ATOM	1371	CA	LEU A 180	17.659	55.921	153.927	1.00	94.61	C
25	ATOM	1372	C	LEU A 180	18.210	56.793	152.784	1.00	96.29	C
	ATOM	1373	O	LEU A 180	18.103	56.426	151.618	1.00	101.27	O
	ATOM	1374	CB	LEU A 180	16.497	56.628	154.614	1.00	88.61	C
	ATOM	1375	CG	LEU A 180	15.405	56.962	153.608	1.00	96.77	C
	ATOM	1376	CD1	LEU A 180	14.908	55.688	152.929	1.00	98.80	C
30	ATOM	1377	CD2	LEU A 180	14.279	57.679	154.293	1.00	96.75	C
	ATOM	1378	N	THR A 181	18.785	57.948	153.116	1.00	91.27	N
	ATOM	1379	CA	THR A 181	19.155	58.935	152.104	1.00	86.10	C
	ATOM	1380	C	THR A 181	20.637	58.863	151.733	1.00	96.84	C
	ATOM	1381	O	THR A 181	21.067	59.433	150.722	1.00	109.07	O
35	ATOM	1382	CB	THR A 181	18.825	60.370	152.564	1.00	80.62	C
	ATOM	1383	OG1	THR A 181	19.804	60.798	153.515	1.00	77.69	O
	ATOM	1384	CG2	THR A 181	17.411	60.457	153.191	1.00	71.39	C
	ATOM	1385	N	GLY A 182	21.419	58.166	152.550	1.00	87.50	N
	ATOM	1386	CA	GLY A 182	22.834	58.030	152.283	1.00	91.61	C
40	ATOM	1387	C	GLY A 182	23.626	59.195	152.842	1.00	105.38	C

	ATOM	1388	O	GLY A 182	24.865	59.159	152.855	1.00118.22	O
	ATOM	1389	N	GLU A 183	22.918	60.234	153.291	1.00100.93	N
	ATOM	1390	CA	GLU A 183	23.554	61.351	153.992	1.00106.05	C
	ATOM	1391	C	GLU A 183	24.257	60.761	155.220	1.00118.69	C
5	ATOM	1392	O	GLU A 183	23.596	60.399	156.204	1.00118.45	O
	ATOM	1393	CB	GLU A 183	22.519	62.402	154.436	1.00 98.79	C
	ATOM	1394	CG	GLU A 183	21.828	63.242	153.351	1.00 80.00	C
	ATOM	1395	CD	GLU A 183	20.440	63.753	153.798	1.00 93.10	C
	ATOM	1396	OE1	GLU A 183	20.125	64.944	153.590	1.00 94.49	O
10	ATOM	1397	OE2	GLU A 183	19.654	62.963	154.364	1.00 73.60	O
	ATOM	1398	N	SER A 184	25.584	60.636	155.165	1.00126.71	N
	ATOM	1399	CA	SER A 184	26.311	59.983	156.257	1.00130.96	C
	ATOM	1400	C	SER A 184	26.330	60.827	157.538	1.00125.15	C
	ATOM	1401	O	SER A 184	26.276	60.294	158.656	1.00122.20	O
15	ATOM	1402	CB	SER A 184	27.730	59.614	155.831	1.00138.48	C
	ATOM	1403	OG	SER A 184	28.297	58.694	156.751	1.00141.70	O
	ATOM	1404	N	VAL A 185	26.401	62.144	157.361	1.00115.79	N
	ATOM	1405	CA	VAL A 185	26.298	63.081	158.472	1.00106.94	C
	ATOM	1406	C	VAL A 185	24.841	63.175	158.933	1.00104.03	C
20	ATOM	1407	O	VAL A 185	23.933	62.753	158.221	1.00110.87	O
	ATOM	1408	CB	VAL A 185	26.781	64.471	158.044	1.00100.97	C
	ATOM	1409	CG1	VAL A 185	27.133	65.321	159.261	1.00 99.30	C
	ATOM	1410	CG2	VAL A 185	27.982	64.336	157.128	1.00101.91	C
	ATOM	1411	N	SER A 186	24.612	63.711	160.127	1.00 95.80	N
25	ATOM	1412	CA	SER A 186	23.253	63.937	160.598	1.00 84.09	C
	ATOM	1413	C	SER A 186	22.737	65.247	160.039	1.00 78.57	C
	ATOM	1414	O	SER A 186	23.502	66.184	159.825	1.00 79.96	O
	ATOM	1415	CB	SER A 186	23.200	63.972	162.117	1.00 86.41	C
	ATOM	1416	OG	SER A 186	23.924	65.082	162.607	1.00 94.01	O
30	ATOM	1417	N	VAL A 187	21.429	65.298	159.809	1.00 80.49	N
	ATOM	1418	CA	VAL A 187	20.771	66.427	159.175	1.00 71.64	C
	ATOM	1419	C	VAL A 187	19.877	67.058	160.219	1.00 91.54	C
	ATOM	1420	O	VAL A 187	19.508	66.402	161.193	1.00 67.72	O
	ATOM	1421	CB	VAL A 187	19.914	65.918	158.045	1.00125.88	C
35	ATOM	1422	CG1	VAL A 187	20.740	65.023	157.158	1.00 72.79	C
	ATOM	1423	CG2	VAL A 187	18.754	65.117	158.603	1.00 67.33	C
	ATOM	1424	N	ILE A 188	19.536	68.330	160.051	1.00 69.66	N
	ATOM	1425	CA	ILE A 188	18.586	68.938	160.981	1.00 90.86	C
	ATOM	1426	C	ILE A 188	17.173	68.955	160.402	1.00 65.55	C
40	ATOM	1427	O	ILE A 188	16.973	68.781	159.199	1.00110.92	O

	ATOM	1428	CB	ILE A 188	19.026	70.340	161.481	1.00	69.77	C
	ATOM	1429	CG1	ILE A 188	19.028	71.358	160.362	1.00	95.02	C
	ATOM	1430	CG2	ILE A 188	20.400	70.283	162.113	1.00	72.31	C
	ATOM	1431	CD1	ILE A 188	17.812	72.251	160.386	1.00	99.78	C
5	ATOM	1432	N	LYS A 189	16.185	69.136	161.262	1.00	72.04	N
	ATOM	1433	CA	LYS A 189	14.802	69.188	160.815	1.00	61.88	C
	ATOM	1434	C	LYS A 189	14.109	70.465	161.294	1.00	81.69	C
	ATOM	1435	O	LYS A 189	14.516	71.074	162.276	1.00	86.90	O
	ATOM	1436	CB	LYS A 189	14.047	67.957	161.313	1.00	59.60	C
10	ATOM	1437	CG	LYS A 189	14.644	66.631	160.881	1.00	67.81	C
	ATOM	1438	CD	LYS A 189	14.395	66.343	159.411	1.00	65.67	C
	ATOM	1439	CE	LYS A 189	14.702	64.895	159.074	1.00	63.84	C
	ATOM	1440	NZ	LYS A 189	14.543	64.618	157.618	1.00	68.58	N
	ATOM	1441	N	HIS A 190	13.074	70.882	160.583	1.00	61.55	N
15	ATOM	1442	CA	HIS A 190	12.227	71.959	161.061	1.00	82.84	C
	ATOM	1443	C	HIS A 190	10.763	71.492	161.047	1.00	77.95	C
	ATOM	1444	O	HIS A 190	10.496	70.289	160.927	1.00	71.62	O
	ATOM	1445	CB	HIS A 190	12.428	73.213	160.214	1.00	85.56	C
	ATOM	1446	CG	HIS A 190	12.243	72.981	158.751	1.00	93.23	C
20	ATOM	1447	ND1	HIS A 190	11.005	72.975	158.148	1.00	98.83	N
	ATOM	1448	CD2	HIS A 190	13.141	72.729	157.769	1.00	100.51	C
	ATOM	1449	CE1	HIS A 190	11.147	72.740	156.856	1.00	106.11	C
	ATOM	1450	NE2	HIS A 190	12.435	72.587	156.602	1.00	107.03	N
	ATOM	1451	N	THR A 191	9.824	72.434	161.177	1.00	71.97	N
25	ATOM	1452	CA	THR A 191	8.409	72.088	161.263	1.00	65.29	C
	ATOM	1453	C	THR A 191	7.543	72.886	160.304	1.00	75.45	C
	ATOM	1454	O	THR A 191	6.324	72.675	160.265	1.00	82.95	O
	ATOM	1455	CB	THR A 191	7.835	72.271	162.697	1.00	59.64	C
	ATOM	1456	OG1	THR A 191	7.997	73.629	163.111	1.00	60.41	O
30	ATOM	1457	CG2	THR A 191	8.524	71.366	163.695	1.00	57.46	C
	ATOM	1458	N	GLU A 192	8.153	73.809	159.551	1.00	79.84	N
	ATOM	1459	CA	GLU A 192	7.432	74.551	158.503	1.00	80.74	C
	ATOM	1460	C	GLU A 192	7.206	73.585	157.332	1.00	76.61	C
	ATOM	1461	O	GLU A 192	7.877	72.548	157.256	1.00	76.51	O
35	ATOM	1462	CB	GLU A 192	8.187	75.813	158.057	1.00	66.41	C
	ATOM	1463	CG	GLU A 192	8.553	76.793	159.149	1.00	128.93	C
	ATOM	1464	CD	GLU A 192	7.369	77.215	160.001	1.00	131.73	C
	ATOM	1465	OE1	GLU A 192	6.283	77.432	159.425	1.00	134.44	O
	ATOM	1466	OE2	GLU A 192	7.524	77.327	161.245	1.00	130.60	O
40	ATOM	1467	N	PRO A 193	6.259	73.899	156.425	1.00	69.40	N

	ATOM	1468	CA	PRO A 193	5.980	72.952	155.342	1.00	73.56	C
	ATOM	1469	C	PRO A 193	6.937	73.079	154.156	1.00	83.35	C
	ATOM	1470	O	PRO A 193	7.476	74.168	153.894	1.00	68.08	O
	ATOM	1471	CB	PRO A 193	4.569	73.343	154.908	1.00	65.04	C
5	ATOM	1472	CG	PRO A 193	4.521	74.803	155.131	1.00	73.14	C
	ATOM	1473	CD	PRO A 193	5.383	75.082	156.345	1.00	71.00	C
	ATOM	1474	N	VAL A 194	7.133	71.951	153.466	1.00	83.02	N
	ATOM	1475	CA	VAL A 194	7.895	71.866	152.219	1.00	77.31	C
	ATOM	1476	C	VAL A 194	6.901	71.870	151.075	1.00	84.48	C
10	ATOM	1477	O	VAL A 194	6.314	70.832	150.750	1.00	89.41	O
	ATOM	1478	CB	VAL A 194	8.678	70.554	152.135	1.00	68.48	C
	ATOM	1479	CG1	VAL A 194	9.339	70.413	150.783	1.00	71.05	C
	ATOM	1480	CG2	VAL A 194	9.696	70.472	153.247	1.00	65.55	C
	ATOM	1481	N	PRO A 195	6.697	73.046	150.467	1.00	79.45	N
15	ATOM	1482	CA	PRO A 195	5.669	73.305	149.452	1.00	79.57	C
	ATOM	1483	C	PRO A 195	5.585	72.299	148.304	1.00	81.91	C
	ATOM	1484	O	PRO A 195	4.470	71.998	147.890	1.00	85.19	O
	ATOM	1485	CB	PRO A 195	6.054	74.684	148.926	1.00	77.25	C
	ATOM	1486	CG	PRO A 195	6.630	75.345	150.106	1.00	80.91	C
20	ATOM	1487	CD	PRO A 195	7.411	74.280	150.832	1.00	74.00	C
	ATOM	1488	N	ASP A 196	6.709	71.798	147.801	1.00	76.06	N
	ATOM	1489	CA	ASP A 196	6.682	70.922	146.631	1.00	77.91	C
	ATOM	1490	C	ASP A 196	6.164	69.549	146.997	1.00	75.60	C
	ATOM	1491	O	ASP A 196	6.749	68.878	147.833	1.00	75.94	O
25	ATOM	1492	CB	ASP A 196	8.084	70.802	146.042	1.00	101.66	C
	ATOM	1493	CG	ASP A 196	8.117	70.022	144.743	1.00	104.42	C
	ATOM	1494	OD1	ASP A 196	7.355	69.041	144.595	1.00	81.81	O
	ATOM	1495	OD2	ASP A 196	8.932	70.392	143.868	1.00	111.97	O
	ATOM	1496	N	PRO A 197	5.061	69.119	146.372	1.00	76.66	N
30	ATOM	1497	CA	PRO A 197	4.545	67.779	146.672	1.00	92.03	C
	ATOM	1498	C	PRO A 197	5.491	66.692	146.190	1.00	98.79	C
	ATOM	1499	O	PRO A 197	5.757	65.713	146.900	1.00	73.40	O
	ATOM	1500	CB	PRO A 197	3.256	67.722	145.871	1.00	77.07	C
	ATOM	1501	CG	PRO A 197	2.855	69.133	145.710	1.00	136.86	C
35	ATOM	1502	CD	PRO A 197	4.110	69.909	145.580	1.00	79.40	C
	ATOM	1503	N	ARG A 198	6.010	66.883	144.984	1.00	79.01	N
	ATOM	1504	CA	ARG A 198	6.875	65.902	144.362	1.00	94.18	C
	ATOM	1505	C	ARG A 198	8.285	65.849	144.982	1.00	93.16	C
	ATOM	1506	O	ARG A 198	9.183	65.221	144.409	1.00	83.02	O
40	ATOM	1507	CB	ARG A 198	7.016	66.230	142.884	1.00	100.17	C

	ATOM	1508	CG	ARG A 198	5.738	66.429	142.125	1.00	87.23	C
	ATOM	1509	CD	ARG A 198	5.286	65.116	141.519	1.00	117.77	C
	ATOM	1510	NE	ARG A 198	4.267	65.279	140.479	1.00	92.17	N
	ATOM	1511	CZ	ARG A 198	4.535	65.253	139.187	1.00	97.43	C
5	ATOM	1512	NH1	ARG A 198	5.790	65.086	138.778	1.00	103.74	N
	ATOM	1513	NH2	ARG A 198	3.561	65.402	138.309	1.00	104.01	N
	ATOM	1514	N	ALA A 199	8.486	66.507	146.127	1.00	93.29	N
	ATOM	1515	CA	ALA A 199	9.820	66.634	146.722	1.00	76.04	C
	ATOM	1516	C	ALA A 199	10.480	65.297	147.029	1.00	75.26	C
10	ATOM	1517	O	ALA A 199	9.824	64.274	147.222	1.00	80.44	O
	ATOM	1518	CB	ALA A 199	9.802	67.523	147.965	1.00	73.49	C
	ATOM	1519	N	VAL A 200	11.805	65.330	147.062	1.00	79.83	N
	ATOM	1520	CA	VAL A 200	12.638	64.149	147.230	1.00	76.58	C
	ATOM	1521	C	VAL A 200	13.018	64.015	148.721	1.00	83.50	C
15	ATOM	1522	O	VAL A 200	13.132	65.029	149.419	1.00	87.74	O
	ATOM	1523	CB	VAL A 200	13.852	64.287	146.289	1.00	80.43	C
	ATOM	1524	CG1	VAL A 200	14.648	65.533	146.639	1.00	114.32	C
	ATOM	1525	CG2	VAL A 200	14.703	63.046	146.297	1.00	108.09	C
	ATOM	1526	N	ASN A 201	13.167	62.782	149.215	1.00	76.22	N
20	ATOM	1527	CA	ASN A 201	13.253	62.521	150.667	1.00	72.98	C
	ATOM	1528	C	ASN A 201	14.127	63.495	151.406	1.00	69.21	C
	ATOM	1529	O	ASN A 201	13.750	64.053	152.418	1.00	80.94	O
	ATOM	1530	CB	ASN A 201	13.781	61.125	150.957	1.00	69.72	C
	ATOM	1531	CG	ASN A 201	12.810	60.045	150.592	1.00	80.30	C
25	ATOM	1532	OD1	ASN A 201	11.606	60.225	150.695	1.00	67.98	O
	ATOM	1533	ND2	ASN A 201	13.327	58.898	150.174	1.00	85.04	N
	ATOM	1534	N	GLN A 202	15.303	63.716	150.850	1.00	88.60	N
	ATOM	1535	CA	GLN A 202	16.312	64.553	151.465	1.00	82.19	C
	ATOM	1536	C	GLN A 202	15.898	66.029	151.538	1.00	78.83	C
30	ATOM	1537	O	GLN A 202	16.598	66.853	152.120	1.00	76.29	O
	ATOM	1538	CB	GLN A 202	17.626	64.381	150.707	1.00	83.44	C
	ATOM	1539	CG	GLN A 202	18.044	65.584	149.931	1.00	84.86	C
	ATOM	1540	CD	GLN A 202	19.507	65.842	150.070	1.00	86.64	C
	ATOM	1541	OE1	GLN A 202	20.320	64.935	149.881	1.00	88.81	O
35	ATOM	1542	NE2	GLN A 202	19.863	67.077	150.421	1.00	86.51	N
	ATOM	1543	N	ASP A 203	14.745	66.363	150.968	1.00	81.63	N
	ATOM	1544	CA	ASP A 203	14.300	67.748	150.986	1.00	71.80	C
	ATOM	1545	C	ASP A 203	13.059	67.942	151.827	1.00	76.78	C
	ATOM	1546	O	ASP A 203	12.609	69.071	152.032	1.00	77.39	O
40	ATOM	1547	CB	ASP A 203	14.099	68.267	149.583	1.00	74.67	C

	ATOM	1548	CG	ASP A 203	15.316	68.982	149.071	1.00	93.96	C
	ATOM	1549	OD1	ASP A 203	15.915	69.720	149.902	1.00	90.46	O
	ATOM	1550	OD2	ASP A 203	15.671	68.799	147.861	1.00	86.61	O
	ATOM	1551	N	LYS A 204	12.533	66.824	152.320	1.00	66.73	N
5	ATOM	1552	CA	LYS A 204	11.451	66.811	153.290	1.00	79.59	C
	ATOM	1553	C	LYS A 204	12.019	67.028	154.698	1.00	72.15	C
	ATOM	1554	O	LYS A 204	11.946	66.154	155.571	1.00	63.46	O
	ATOM	1555	CB	LYS A 204	10.718	65.477	153.232	1.00	62.83	C
	ATOM	1556	CG	LYS A 204	10.100	65.144	151.896	1.00	85.96	C
10	ATOM	1557	CD	LYS A 204	9.780	63.686	151.881	1.00	63.90	C
	ATOM	1558	CE	LYS A 204	9.344	63.192	150.557	1.00	66.07	C
	ATOM	1559	NZ	LYS A 204	9.077	61.742	150.696	1.00	99.16	N
	ATOM	1560	N	LYS A 205	12.572	68.211	154.927	1.00	63.68	N
	ATOM	1561	CA	LYS A 205	13.231	68.510	156.184	1.00	63.09	C
15	ATOM	1562	C	LYS A 205	12.243	68.590	157.321	1.00	67.64	C
	ATOM	1563	O	LYS A 205	12.604	68.969	158.430	1.00	66.72	O
	ATOM	1564	CB	LYS A 205	14.012	69.814	156.067	1.00	65.31	C
	ATOM	1565	CG	LYS A 205	14.996	69.786	154.923	1.00	68.01	C
	ATOM	1566	CD	LYS A 205	15.963	70.946	154.950	1.00	90.50	C
20	ATOM	1567	CE	LYS A 205	17.016	70.785	153.864	1.00	73.55	C
	ATOM	1568	NZ	LYS A 205	17.614	72.090	153.474	1.00	112.63	N
	ATOM	1569	N	ASN A 206	10.989	68.241	157.050	1.00	67.57	N
	ATOM	1570	CA	ASN A 206	9.967	68.241	158.090	1.00	63.32	C
	ATOM	1571	C	ASN A 206	9.404	66.855	158.383	1.00	59.23	C
25	ATOM	1572	O	ASN A 206	8.421	66.728	159.095	1.00	58.61	O
	ATOM	1573	CB	ASN A 206	8.853	69.240	157.773	1.00	58.24	C
	ATOM	1574	CG	ASN A 206	8.054	68.859	156.552	1.00	72.89	C
	ATOM	1575	OD1	ASN A 206	8.132	67.730	156.070	1.00	70.96	O
	ATOM	1576	ND2	ASN A 206	7.255	69.800	156.050	1.00	77.76	N
30	ATOM	1577	N	MET A 207	10.041	65.820	157.837	1.00	64.70	N
	ATOM	1578	CA	MET A 207	9.616	64.436	158.066	1.00	64.50	C
	ATOM	1579	C	MET A 207	10.660	63.634	158.829	1.00	63.42	C
	ATOM	1580	O	MET A 207	11.845	63.903	158.708	1.00	64.76	O
	ATOM	1581	CB	MET A 207	9.322	63.742	156.731	1.00	64.37	C
35	ATOM	1582	CG	MET A 207	8.201	64.395	155.944	1.00	56.87	C
	ATOM	1583	SD	MET A 207	6.600	64.207	156.732	1.00	67.96	S
	ATOM	1584	CE	MET A 207	6.541	62.420	156.848	1.00	54.74	C
	ATOM	1585	N	LEU A 208	10.217	62.665	159.627	1.00	54.20	N
	ATOM	1586	CA	LEU A 208	11.113	61.643	160.168	1.00	62.14	C
40	ATOM	1587	C	LEU A 208	10.679	60.305	159.583	1.00	56.64	C

	ATOM	1588	O	LEU A 208	9.577	59.846	159.840	1.00	55.10	O
	ATOM	1589	CB	LEU A 208	11.086	61.597	161.700	1.00	53.64	C
	ATOM	1590	CG	LEU A 208	11.183	62.945	162.411	1.00	63.55	C
	ATOM	1591	CD1	LEU A 208	10.561	62.908	163.810	1.00	55.82	C
5	ATOM	1592	CD2	LEU A 208	12.620	63.399	162.489	1.00	69.18	C
	ATOM	1593	N	PHE A 209	11.535	59.687	158.781	1.00	59.70	N
	ATOM	1594	CA	PHE A 209	11.167	58.436	158.134	1.00	68.23	C
	ATOM	1595	C	PHE A 209	11.440	57.260	159.074	1.00	69.34	C
	ATOM	1596	O	PHE A 209	12.298	57.355	159.950	1.00	72.80	O
10	ATOM	1597	CB	PHE A 209	11.933	58.257	156.805	1.00	69.60	C
	ATOM	1598	CG	PHE A 209	12.024	59.512	155.971	1.00	63.30	C
	ATOM	1599	CD1	PHE A 209	10.980	59.886	155.134	1.00	65.12	C
	ATOM	1600	CD2	PHE A 209	13.153	60.311	156.018	1.00	64.72	C
	ATOM	1601	CE1	PHE A 209	11.066	61.033	154.361	1.00	70.86	C
15	ATOM	1602	CE2	PHE A 209	13.238	61.463	155.256	1.00	72.78	C
	ATOM	1603	CZ	PHE A 209	12.194	61.823	154.424	1.00	74.80	C
	ATOM	1604	N	SER A 210	10.735	56.150	158.862	1.00	65.65	N
	ATOM	1605	CA	SER A 210	10.899	54.934	159.664	1.00	71.52	C
	ATOM	1606	C	SER A 210	12.325	54.377	159.587	1.00	74.67	C
20	ATOM	1607	O	SER A 210	13.092	54.780	158.735	1.00	68.86	O
	ATOM	1608	CB	SER A 210	9.905	53.876	159.184	1.00	77.56	C
	ATOM	1609	OG	SER A 210	9.432	53.054	160.234	1.00	75.81	O
	ATOM	1610	N	GLY A 211	12.684	53.460	160.484	1.00	83.46	N
	ATOM	1611	CA	GLY A 211	14.014	52.851	160.475	1.00	87.15	C
25	ATOM	1612	C	GLY A 211	15.225	53.764	160.674	1.00	81.85	C
	ATOM	1613	O	GLY A 211	16.364	53.343	160.514	1.00	85.85	O
	ATOM	1614	N	THR A 212	14.968	55.004	161.067	1.00	74.93	N
	ATOM	1615	CA	THR A 212	15.965	56.059	161.139	1.00	68.45	C
	ATOM	1616	C	THR A 212	16.216	56.462	162.594	1.00	76.82	C
30	ATOM	1617	O	THR A 212	15.291	56.467	163.384	1.00	92.12	O
	ATOM	1618	CB	THR A 212	15.421	57.258	160.363	1.00	66.07	C
	ATOM	1619	OG1	THR A 212	15.629	57.040	158.970	1.00	65.11	O
	ATOM	1620	CG2	THR A 212	16.088	58.512	160.752	1.00	61.15	C
	ATOM	1621	N	ASN A 213	17.460	56.790	162.947	1.00	80.56	N
35	ATOM	1622	CA	ASN A 213	17.844	57.155	164.318	1.00	79.52	C
	ATOM	1623	C	ASN A 213	17.736	58.653	164.595	1.00	78.00	C
	ATOM	1624	O	ASN A 213	17.893	59.465	163.692	1.00	83.89	O
	ATOM	1625	CB	ASN A 213	19.298	56.755	164.588	1.00	86.63	C
	ATOM	1626	CG	ASN A 213	19.526	55.265	164.503	1.00	103.72	C
40	ATOM	1627	OD1	ASN A 213	18.601	54.475	164.674	1.00	111.97	O

	ATOM	1628	ND2 ASN A 213	20.777	54.867	164.252	1.00110.98	N
	ATOM	1629	N ILE A 214	17.508	59.023	165.849	1.00 72.14	N
	ATOM	1630	CA ILE A 214	17.679	60.410	166.256	1.00 62.19	C
	ATOM	1631	C ILE A 214	19.042	60.592	166.916	1.00 78.91	C
5	ATOM	1632	O ILE A 214	19.392	59.876	167.856	1.00 66.08	O
	ATOM	1633	CB ILE A 214	16.594	60.862	167.231	1.00 63.71	C
	ATOM	1634	CG1 ILE A 214	15.211	60.500	166.683	1.00 61.51	C
	ATOM	1635	CG2 ILE A 214	16.731	62.352	167.519	1.00 60.89	C
	ATOM	1636	CD1 ILE A 214	14.413	61.671	166.160	1.00 56.88	C
10	ATOM	1637	N ALA A 215	19.806	61.560	166.424	1.00 66.35	N
	ATOM	1638	CA ALA A 215	21.164	61.789	166.887	1.00 69.47	C
	ATOM	1639	C ALA A 215	21.229	62.784	168.043	1.00 83.27	C
	ATOM	1640	O ALA A 215	22.110	62.696	168.904	1.00 80.72	O
	ATOM	1641	CB ALA A 215	21.987	62.280	165.745	1.00 71.19	C
15	ATOM	1642	N ALA A 216	20.299	63.735	168.041	1.00 81.91	N
	ATOM	1643	CA ALA A 216	20.215	64.780	169.055	1.00 69.06	C
	ATOM	1644	C ALA A 216	18.793	65.330	169.073	1.00 74.67	C
	ATOM	1645	O ALA A 216	18.185	65.526	168.029	1.00 80.35	O
	ATOM	1646	CB ALA A 216	21.185	65.887	168.741	1.00 71.57	C
20	ATOM	1647	N GLY A 217	18.247	65.573	170.253	1.00 75.10	N
	ATOM	1648	CA GLY A 217	16.964	66.248	170.330	1.00 68.38	C
	ATOM	1649	C GLY A 217	15.767	65.432	170.788	1.00 66.35	C
	ATOM	1650	O GLY A 217	15.841	64.221	171.016	1.00 65.47	O
	ATOM	1651	N LYS A 218	14.646	66.126	170.933	1.00 66.87	N
25	ATOM	1652	CA LYS A 218	13.380	65.508	171.290	1.00 69.81	C
	ATOM	1653	C LYS A 218	12.346	66.207	170.428	1.00 69.00	C
	ATOM	1654	O LYS A 218	12.454	67.418	170.187	1.00 70.77	O
	ATOM	1655	CB LYS A 218	13.069	65.733	172.777	1.00 60.99	C
	ATOM	1656	CG LYS A 218	11.854	64.976	173.312	1.00 65.40	C
30	ATOM	1657	CD LYS A 218	11.597	65.307	174.775	1.00 76.62	C
	ATOM	1658	CE LYS A 218	10.323	64.653	175.302	1.00 87.38	C
	ATOM	1659	NZ LYS A 218	9.999	65.042	176.722	1.00 93.94	N
	ATOM	1660	N ALA A 219	11.355	65.457	169.950	1.00 62.44	N
	ATOM	1661	CA ALA A 219	10.312	66.051	169.126	1.00 60.82	C
35	ATOM	1662	C ALA A 219	9.023	65.262	169.173	1.00 62.79	C
	ATOM	1663	O ALA A 219	9.015	64.072	169.515	1.00 62.06	O
	ATOM	1664	CB ALA A 219	10.785	66.203	167.686	1.00 59.60	C
	ATOM	1665	N LEU A 220	7.941	65.956	168.818	1.00 64.45	N
	ATOM	1666	CA LEU A 220	6.595	65.398	168.742	1.00 56.73	C
40	ATOM	1667	C LEU A 220	6.084	65.513	167.304	1.00 59.20	C

	ATOM	1668	O	LEU A 220	6.292	66.545	166.650	1.00	63.51	O
	ATOM	1669	CB	LEU A 220	5.678	66.194	169.655	1.00	60.48	C
	ATOM	1670	CG	LEU A 220	4.344	65.550	170.003	1.00	70.04	C
	ATOM	1671	CD1	LEU A 220	4.556	64.486	171.060	1.00	70.66	C
5	ATOM	1672	CD2	LEU A 220	3.334	66.600	170.452	1.00	74.93	C
	ATOM	1673	N	GLY A 221	5.420	64.469	166.805	1.00	57.47	N
	ATOM	1674	CA	GLY A 221	4.878	64.500	165.455	1.00	58.70	C
	ATOM	1675	C	GLY A 221	3.621	63.680	165.252	1.00	62.44	C
	ATOM	1676	O	GLY A 221	3.199	62.959	166.159	1.00	71.20	O
10	ATOM	1677	N	ILE A 222	3.013	63.798	164.068	1.00	56.55	N
	ATOM	1678	CA	ILE A 222	1.849	62.969	163.695	1.00	59.46	C
	ATOM	1679	C	ILE A 222	2.200	61.945	162.612	1.00	62.88	C
	ATOM	1680	O	ILE A 222	2.858	62.262	161.608	1.00	68.16	O
	ATOM	1681	CB	ILE A 222	0.626	63.818	163.236	1.00	65.80	C
15	ATOM	1682	CG1	ILE A 222	-0.617	62.948	163.076	1.00	65.24	C
	ATOM	1683	CG2	ILE A 222	0.897	64.548	161.920	1.00	62.94	C
	ATOM	1684	CD1	ILE A 222	-1.785	63.688	162.411	1.00	63.72	C
	ATOM	1685	N	VAL A 223	1.774	60.709	162.827	1.00	56.52	N
	ATOM	1686	CA	VAL A 223	2.090	59.635	161.898	1.00	55.33	C
20	ATOM	1687	C	VAL A 223	1.326	59.770	160.584	1.00	58.98	C
	ATOM	1688	O	VAL A 223	0.106	59.766	160.579	1.00	73.66	O
	ATOM	1689	CB	VAL A 223	1.769	58.288	162.507	1.00	50.97	C
	ATOM	1690	CG1	VAL A 223	1.925	57.214	161.478	1.00	76.82	C
	ATOM	1691	CG2	VAL A 223	2.677	58.037	163.690	1.00	50.46	C
25	ATOM	1692	N	ALA A 224	2.046	59.876	159.471	1.00	57.69	N
	ATOM	1693	CA	ALA A 224	1.408	60.069	158.175	1.00	62.28	C
	ATOM	1694	C	ALA A 224	1.193	58.759	157.415	1.00	68.89	C
	ATOM	1695	O	ALA A 224	0.152	58.574	156.755	1.00	67.30	O
	ATOM	1696	CB	ALA A 224	2.205	61.053	157.325	1.00	54.12	C
30	ATOM	1697	N	THR A 225	2.194	57.877	157.442	1.00	54.78	N
	ATOM	1698	CA	THR A 225	2.074	56.571	156.789	1.00	56.26	C
	ATOM	1699	C	THR A 225	2.870	55.494	157.528	1.00	63.59	C
	ATOM	1700	O	THR A 225	3.917	55.770	158.088	1.00	60.70	O
	ATOM	1701	CB	THR A 225	2.429	56.604	155.242	1.00	65.69	C
35	ATOM	1702	OG1	THR A 225	3.689	55.972	154.979	1.00	60.04	O
	ATOM	1703	CG2	THR A 225	2.454	58.025	154.670	1.00	58.26	C
	ATOM	1704	N	THR A 226	2.357	54.269	157.540	1.00	64.70	N
	ATOM	1705	CA	THR A 226	3.031	53.154	158.200	1.00	63.76	C
	ATOM	1706	C	THR A 226	3.275	52.011	157.219	1.00	69.59	C
40	ATOM	1707	O	THR A 226	3.299	52.248	156.026	1.00	75.79	O

	ATOM	1708	CB	THR A 226	2.220	52.680	159.389	1.00	71.80	C
	ATOM	1709	OG1	THR A 226	0.870	52.412	158.983	1.00	82.13	O
	ATOM	1710	CG2	THR A 226	2.200	53.762	160.440	1.00	77.18	C
	ATOM	1711	N	GLY A 227	3.484	50.793	157.710	1.00	60.55	N
5	ATOM	1712	CA	GLY A 227	3.652	49.621	156.852	1.00	73.10	C
	ATOM	1713	C	GLY A 227	4.469	49.772	155.568	1.00	69.22	C
	ATOM	1714	O	GLY A 227	5.402	50.565	155.514	1.00	66.94	O
	ATOM	1715	N	VAL A 228	4.120	49.019	154.527	1.00	67.54	N
	ATOM	1716	CA	VAL A 228	4.764	49.183	153.219	1.00	92.05	C
10	ATOM	1717	C	VAL A 228	4.681	50.602	152.647	1.00	88.55	C
	ATOM	1718	O	VAL A 228	5.476	50.961	151.787	1.00	89.00	O
	ATOM	1719	CB	VAL A 228	4.191	48.227	152.156	1.00	73.10	C
	ATOM	1720	CG1	VAL A 228	4.864	46.873	152.222	1.00	85.78	C
	ATOM	1721	CG2	VAL A 228	2.710	48.096	152.339	1.00	73.32	C
15	ATOM	1722	N	SER A 229	3.736	51.412	153.107	1.00	66.50	N
	ATOM	1723	CA	SER A 229	3.576	52.749	152.540	1.00	71.01	C
	ATOM	1724	C	SER A 229	4.717	53.692	152.883	1.00	69.80	C
	ATOM	1725	O	SER A 229	4.891	54.714	152.230	1.00	75.86	O
	ATOM	1726	CB	SER A 229	2.238	53.369	152.944	1.00	74.44	C
20	ATOM	1727	OG	SER A 229	1.171	52.488	152.639	1.00	75.71	O
	ATOM	1728	N	THR A 230	5.486	53.343	153.909	1.00	73.28	N
	ATOM	1729	CA	THR A 230	6.645	54.134	154.336	1.00	61.85	C
	ATOM	1730	C	THR A 230	7.737	54.182	153.276	1.00	70.62	C
	ATOM	1731	O	THR A 230	7.838	53.294	152.423	1.00	73.32	O
25	ATOM	1732	CB	THR A 230	7.277	53.539	155.577	1.00	60.84	C
	ATOM	1733	OG1	THR A 230	7.597	52.171	155.321	1.00	82.85	O
	ATOM	1734	CG2	THR A 230	6.332	53.612	156.746	1.00	58.84	C
	ATOM	1735	N	GLU A 231	8.558	55.226	153.348	1.00	73.07	N
	ATOM	1736	CA	GLU A 231	9.710	55.393	152.467	1.00	77.72	C
30	ATOM	1737	C	GLU A 231	10.636	54.192	152.470	1.00	82.90	C
	ATOM	1738	O	GLU A 231	11.186	53.811	151.437	1.00	91.64	O
	ATOM	1739	CB	GLU A 231	10.511	56.634	152.863	1.00	75.67	C
	ATOM	1740	CG	GLU A 231	9.986	57.894	152.238	1.00	80.16	C
	ATOM	1741	CD	GLU A 231	9.702	57.705	150.766	1.00	89.59	C
35	ATOM	1742	OE1	GLU A 231	10.627	57.265	150.034	1.00	101.03	O
	ATOM	1743	OE2	GLU A 231	8.551	57.974	150.350	1.00	81.06	O
	ATOM	1744	N	ILE A 232	10.818	53.608	153.642	1.00	79.73	N
	ATOM	1745	CA	ILE A 232	11.688	52.456	153.778	1.00	79.24	C
	ATOM	1746	C	ILE A 232	10.936	51.175	153.409	1.00	79.37	C
40	ATOM	1747	O	ILE A 232	11.535	50.227	152.875	1.00	79.00	O

	ATOM	1748	CB	ILE A 232	12.341	52.389	155.197	1.00	71.93	C
	ATOM	1749	CG1	ILE A 232	13.138	51.109	155.359	1.00	77.92	C
	ATOM	1750	CG2	ILE A 232	11.317	52.521	156.314	1.00	63.92	C
	ATOM	1751	CD1	ILE A 232	13.650	50.936	156.737	1.00	86.91	C
5	ATOM	1752	N	GLY A 233	9.622	51.171	153.658	1.00	74.66	N
	ATOM	1753	CA	GLY A 233	8.759	50.071	153.254	1.00	81.64	C
	ATOM	1754	C	GLY A 233	8.800	49.792	151.751	1.00	92.12	C
	ATOM	1755	O	GLY A 233	8.900	48.638	151.313	1.00	90.86	O
	ATOM	1756	N	LYS A 234	8.717	50.855	150.959	1.00	73.06	N
10	ATOM	1757	CA	LYS A 234	8.851	50.755	149.516	1.00	76.47	C
	ATOM	1758	C	LYS A 234	10.191	50.125	149.121	1.00	81.34	C
	ATOM	1759	O	LYS A 234	10.291	49.379	148.148	1.00	87.66	O
	ATOM	1760	CB	LYS A 234	8.727	52.142	148.892	1.00	75.95	C
	ATOM	1761	CG	LYS A 234	7.431	52.862	149.219	1.00	74.08	C
15	ATOM	1762	CD	LYS A 234	7.376	54.234	148.557	1.00	75.86	C
	ATOM	1763	CE	LYS A 234	6.175	55.044	149.040	1.00	80.30	C
	ATOM	1764	NZ	LYS A 234	6.278	56.467	148.603	1.00	86.33	N
	ATOM	1765	N	ILE A 235	11.224	50.423	149.891	1.00	83.07	N
	ATOM	1766	CA	ILE A 235	12.551	49.909	149.611	1.00	93.05	C
20	ATOM	1767	C	ILE A 235	12.729	48.474	150.118	1.00	104.91	C
	ATOM	1768	O	ILE A 235	13.255	47.620	149.402	1.00	101.03	O
	ATOM	1769	CB	ILE A 235	13.613	50.839	150.208	1.00	90.26	C
	ATOM	1770	CG1	ILE A 235	13.662	52.133	149.395	1.00	79.67	C
	ATOM	1771	CG2	ILE A 235	14.967	50.142	150.273	1.00	82.40	C
25	ATOM	1772	CD1	ILE A 235	14.338	53.284	150.092	1.00	77.92	C
	ATOM	1773	N	ARG A 236	12.273	48.204	151.341	1.00	115.38	N
	ATOM	1774	CA	ARG A 236	12.412	46.864	151.917	1.00	120.96	C
	ATOM	1775	C	ARG A 236	11.553	45.826	151.189	1.00	118.49	C
	ATOM	1776	O	ARG A 236	11.898	44.647	151.148	1.00	117.82	O
30	ATOM	1777	CB	ARG A 236	12.117	46.858	153.425	1.00	120.89	C
	ATOM	1778	CG	ARG A 236	13.206	47.469	154.299	1.00	124.76	C
	ATOM	1779	CD	ARG A 236	13.397	46.673	155.590	1.00	138.48	C
	ATOM	1780	NE	ARG A 236	13.754	47.534	156.720	1.00	148.86	N
	ATOM	1781	CZ	ARG A 236	14.068	47.097	157.938	1.00	151.96	C
35	ATOM	1782	NH1	ARG A 236	14.085	45.795	158.199	1.00	156.65	N
	ATOM	1783	NH2	ARG A 236	14.372	47.966	158.897	1.00	147.06	N
	ATOM	1784	O	ASP A 237	10.138	43.680	148.217	1.00	128.06	O
	ATOM	1785	N	ASP A 237	10.440	46.272	150.616	1.00	121.68	N
	ATOM	1786	CA	ASP A 237	9.576	45.404	149.815	1.00	133.14	C
40	ATOM	1787	C	ASP A 237	10.310	44.848	148.578	1.00	130.26	C

	ATOM	1788	CB	ASP A 237	8.303	46.159	149.398	1.00138.31	C
	ATOM	1789	CG	ASP A 237	7.038	45.326	149.556	1.00133.74	C
	ATOM	1790	OD1	ASP A 237	6.792	44.816	150.672	1.00126.54	O
	ATOM	1791	OD2	ASP A 237	6.294	45.189	148.558	1.00133.46	O
5	ATOM	1792	O	GLN A 238	13.583	44.858	148.676	1.00188.11	O
	ATOM	1793	N	GLN A 238	11.113	45.693	147.933	1.00181.16	N
	ATOM	1794	CA	GLN A 238	12.044	45.249	146.893	1.00183.08	C
	ATOM	1795	C	GLN A 238	13.180	44.484	147.573	1.00183.65	C
	ATOM	1796	CB	GLN A 238	12.587	46.457	146.127	1.00184.61	C
10	ATOM	1797	CG	GLN A 238	13.529	46.116	144.987	1.00189.67	C
	ATOM	1798	CD	GLN A 238	13.757	47.293	144.049	1.00192.85	C
	ATOM	1799	OE1	GLN A 238	13.373	48.427	144.353	1.00193.90	O
	ATOM	1800	NE2	GLN A 238	14.378	47.026	142.899	1.00190.43	N
	ATOM	1801	O	MET A 239	12.556	41.761	148.542	1.00257.43	O
15	ATOM	1802	N	MET A 239	13.679	43.421	146.935	1.00180.46	N
	ATOM	1803	CA	MET A 239	14.603	42.480	147.585	1.00182.84	C
	ATOM	1804	C	MET A 239	13.782	41.697	148.656	1.00257.42	C
	ATOM	1805	CB	MET A 239	15.864	43.220	148.042	1.00187.22	C
	ATOM	1806	CG	MET A 239	17.053	43.030	147.108	1.00189.35	C
20	ATOM	1807	SD	MET A 239	18.483	43.998	147.622	1.00224.09	S
	ATOM	1808	CE	MET A 239	19.814	42.920	147.108	1.00215.08	C
	ATOM	1809	O	ALA A 240	16.625	39.727	148.399	1.00252.43	O
	ATOM	1810	N	ALA A 240	14.296	40.966	149.669	1.00256.61	N
	ATOM	1811	CA	ALA A 240	15.646	40.863	150.263	1.00255.86	C
25	ATOM	1812	C	ALA A 240	16.813	40.516	149.324	1.00254.77	C
	ATOM	1813	CB	ALA A 240	15.605	39.885	151.442	1.00255.57	C
	ATOM	1814	O	ALA A 241	18.346	41.562	153.082	1.00253.07	O
	ATOM	1815	N	ALA A 241	18.023	41.068	149.533	1.00255.59	N
	ATOM	1816	CA	ALA A 241	18.522	41.867	150.696	1.00255.95	C
30	ATOM	1817	C	ALA A 241	18.730	41.105	152.004	1.00254.07	C
	ATOM	1818	CB	ALA A 241	17.770	43.217	150.923	1.00286.50	C
	ATOM	1819	O	THR A 242	21.951	38.740	152.075	1.00249.32	O
	ATOM	1820	N	THR A 242	19.364	39.945	151.886	1.00253.02	N
	ATOM	1821	CA	THR A 242	19.788	39.179	153.048	1.00251.11	C
35	ATOM	1822	C	THR A 242	21.316	39.061	153.085	1.00249.25	C
	ATOM	1823	CB	THR A 242	19.120	37.790	153.090	1.00249.82	C
	ATOM	1824	OG1	THR A 242	19.063	37.247	151.765	1.00248.67	O
	ATOM	1825	CG2	THR A 242	17.705	37.908	153.641	1.00247.92	C
	ATOM	1826	O	GLU A 243	24.967	37.791	153.626	1.00242.51	O
40	ATOM	1827	N	GLU A 243	21.887	39.351	154.253	1.00245.87	N

	ATOM	1828	CA	GLU A 243	23.329	39.323	154.468	1.00239.74	C
	ATOM	1829	C	GLU A 243	23.861	37.942	154.145	1.00241.01	C
	ATOM	1830	CB	GLU A 243	23.639	39.659	155.924	1.00231.62	C
	ATOM	1831	CG	GLU A 243	22.826	40.819	156.469	1.00222.03	C
5	ATOM	1832	CD	GLU A 243	22.789	40.838	157.981	1.00215.53	C
	ATOM	1833	OE1	GLU A 243	23.044	39.782	158.594	1.00212.06	O
	ATOM	1834	OE2	GLU A 243	22.507	41.909	158.555	1.00215.92	O
	ATOM	1835	O	GLN A 244	25.346	34.393	153.678	1.00245.35	O
	ATOM	1836	N	GLN A 244	23.056	36.939	154.483	1.00241.48	N
10	ATOM	1837	CA	GLN A 244	23.286	35.556	154.076	1.00241.97	C
	ATOM	1838	C	GLN A 244	24.622	34.946	154.511	1.00244.62	C
	ATOM	1839	CB	GLN A 244	23.097	35.407	152.561	1.00238.84	C
	ATOM	1840	CG	GLN A 244	21.641	35.405	152.121	1.00234.42	C
	ATOM	1841	CD	GLN A 244	21.482	35.418	150.613	1.00231.52	C
15	ATOM	1842	OE1	GLN A 244	22.463	35.520	149.876	1.00231.98	O
	ATOM	1843	NE2	GLN A 244	20.242	35.315	150.146	1.00229.08	N
	ATOM	1844	O	ASP A 245	27.489	35.554	155.064	1.00179.07	O
	ATOM	1845	N	ASP A 245	24.943	35.054	155.802	1.00244.95	N
	ATOM	1846	CA	ASP A 245	25.995	34.232	156.405	1.00243.99	C
20	ATOM	1847	C	ASP A 245	27.397	34.589	155.826	1.00178.92	C
	ATOM	1848	CB	ASP A 245	25.587	32.756	156.236	1.00241.19	C
	ATOM	1849	CG	ASP A 245	24.367	32.390	157.060	1.00238.57	C
	ATOM	1850	OD1	ASP A 245	24.532	32.083	158.259	1.00238.55	O
	ATOM	1851	OD2	ASP A 245	23.246	32.412	156.509	1.00236.92	O
25	ATOM	1852	O	LYS A 246	30.402	34.234	158.073	1.00175.01	O
	ATOM	1853	N	LYS A 246	28.496	33.910	156.194	1.00178.84	N
	ATOM	1854	CA	LYS A 246	28.604	32.889	157.239	1.00176.80	C
	ATOM	1855	C	LYS A 246	29.622	33.310	158.289	1.00175.08	C
	ATOM	1856	CB	LYS A 246	29.050	31.549	156.644	1.00179.41	C
30	ATOM	1857	CG	LYS A 246	28.406	31.162	155.318	1.00181.64	C
	ATOM	1858	CD	LYS A 246	27.844	29.741	155.352	1.00185.38	C
	ATOM	1859	CE	LYS A 246	26.622	29.597	154.444	1.00185.86	C
	ATOM	1860	NZ	LYS A 246	26.023	28.227	154.390	1.00185.38	N
	ATOM	1861	N	THR A 247	29.620	32.615	159.421	1.00176.53	N
35	ATOM	1862	CA	THR A 247	30.557	32.900	160.502	1.00182.21	C
	ATOM	1863	C	THR A 247	31.996	32.587	160.068	1.00187.72	C
	ATOM	1864	O	THR A 247	32.210	31.729	159.214	1.00186.70	O
	ATOM	1865	CB	THR A 247	30.183	32.121	161.789	1.00196.54	C
	ATOM	1866	OG1	THR A 247	29.817	30.780	161.451	1.00196.12	O
40	ATOM	1867	CG2	THR A 247	29.011	32.782	162.506	1.00163.76	C

	ATOM	1868	N	PRO A 248	32.984	33.302	160.636	1.00103.41	N
	ATOM	1869	CA	PRO A 248	34.393	33.119	160.262	1.00117.73	C
	ATOM	1870	C	PRO A 248	34.894	31.722	160.593	1.00127.64	C
	ATOM	1871	O	PRO A 248	35.736	31.168	159.884	1.00134.29	O
5	ATOM	1872	CB	PRO A 248	35.124	34.154	161.122	1.00119.14	C
	ATOM	1873	CG	PRO A 248	34.178	34.450	162.244	1.00116.54	C
	ATOM	1874	CD	PRO A 248	32.826	34.382	161.621	1.00108.77	C
	ATOM	1875	N	LEU A 249	34.380	31.159	161.675	1.00128.50	N
	ATOM	1876	CA	LEU A 249	34.743	29.806	162.053	1.00127.72	C
10	ATOM	1877	C	LEU A 249	34.122	28.841	161.063	1.00128.60	C
	ATOM	1878	O	LEU A 249	34.667	27.772	160.810	1.00128.62	O
	ATOM	1879	CB	LEU A 249	34.258	29.493	163.469	1.00119.32	C
	ATOM	1880	CG	LEU A 249	34.748	28.210	164.132	1.00105.17	C
	ATOM	1881	CD1	LEU A 249	36.261	28.243	164.296	1.00111.23	C
15	ATOM	1882	CD2	LEU A 249	34.067	28.047	165.464	1.00 92.10	C
	ATOM	1883	N	GLN A 250	32.985	29.234	160.495	1.00132.92	N
	ATOM	1884	CA	GLN A 250	32.263	28.381	159.559	1.00137.02	C
	ATOM	1885	C	GLN A 250	33.071	28.166	158.293	1.00139.50	C
	ATOM	1886	O	GLN A 250	32.915	27.150	157.618	1.00135.55	O
20	ATOM	1887	CB	GLN A 250	30.916	28.998	159.200	1.00136.51	C
	ATOM	1888	CG	GLN A 250	29.790	28.003	159.064	1.00133.33	C
	ATOM	1889	CD	GLN A 250	28.452	28.635	159.366	1.00133.73	C
	ATOM	1890	OE1	GLN A 250	28.304	29.857	159.313	1.00134.76	O
	ATOM	1891	NE2	GLN A 250	27.472	27.810	159.700	1.00133.01	N
25	ATOM	1892	N	GLN A 251	33.934	29.130	157.985	1.00142.49	N
	ATOM	1893	CA	GLN A 251	34.772	29.066	156.796	1.00142.66	C
	ATOM	1894	C	GLN A 251	36.030	28.249	157.057	1.00135.43	C
	ATOM	1895	O	GLN A 251	36.422	27.422	156.233	1.00134.58	O
	ATOM	1896	CB	GLN A 251	35.142	30.473	156.327	1.00151.84	C
30	ATOM	1897	CG	GLN A 251	35.914	30.501	155.022	1.00162.71	C
	ATOM	1898	CD	GLN A 251	36.065	31.905	154.474	1.00175.28	C
	ATOM	1899	OE1	GLN A 251	35.553	32.863	155.054	1.00181.05	O
	ATOM	1900	NE2	GLN A 251	36.766	32.035	153.351	1.00177.21	N
	ATOM	1901	N	LYS A 252	36.653	28.480	158.210	1.00129.33	N
35	ATOM	1902	CA	LYS A 252	37.868	27.765	158.577	1.00123.89	C
	ATOM	1903	C	LYS A 252	37.582	26.273	158.642	1.00112.65	C
	ATOM	1904	O	LYS A 252	38.437	25.444	158.336	1.00109.44	O
	ATOM	1905	CB	LYS A 252	38.397	28.254	159.927	1.00124.93	C
	ATOM	1906	CG	LYS A 252	38.589	29.758	160.025	1.00130.57	C
40	ATOM	1907	CD	LYS A 252	39.157	30.135	161.386	1.00136.46	C

	ATOM	1908	CE	LYS A 252	39.074	31.633	161.652	1.00136.84	C
	ATOM	1909	NZ	LYS A 252	37.692	32.062	161.989	1.00129.63	N
	ATOM	1910	N	LEU A 253	36.360	25.945	159.034	1.00108.51	N
	ATOM	1911	CA	LEU A 253	35.938	24.559	159.157	1.00110.24	C
5	ATOM	1912	C	LEU A 253	35.373	24.063	157.833	1.00111.53	C
	ATOM	1913	O	LEU A 253	35.386	22.865	157.552	1.00107.99	O
	ATOM	1914	CB	LEU A 253	34.917	24.416	160.296	1.00112.14	C
	ATOM	1915	CG	LEU A 253	34.097	23.137	160.475	1.00111.07	C
	ATOM	1916	CD1	LEU A 253	33.791	22.902	161.932	1.00112.63	C
10	ATOM	1917	CD2	LEU A 253	32.800	23.250	159.713	1.00113.29	C
	ATOM	1918	N	ASP A 254	34.874	24.995	157.026	1.00119.64	N
	ATOM	1919	CA	ASP A 254	34.395	24.681	155.685	1.00123.25	C
	ATOM	1920	C	ASP A 254	35.563	24.214	154.820	1.00119.92	C
	ATOM	1921	O	ASP A 254	35.464	23.212	154.102	1.00116.50	O
15	ATOM	1922	CB	ASP A 254	33.747	25.913	155.051	1.00129.31	C
	ATOM	1923	CG	ASP A 254	32.901	25.571	153.847	1.00134.73	C
	ATOM	1924	OD1	ASP A 254	32.368	24.441	153.801	1.00137.85	O
	ATOM	1925	OD2	ASP A 254	32.770	26.433	152.947	1.00136.09	O
	ATOM	1926	N	GLU A 255	36.665	24.954	154.897	1.00117.64	N
20	ATOM	1927	CA	GLU A 255	37.877	24.620	154.160	1.00118.42	C
	ATOM	1928	C	GLU A 255	38.363	23.218	154.522	1.00112.61	C
	ATOM	1929	O	GLU A 255	38.780	22.451	153.657	1.00110.45	O
	ATOM	1930	CB	GLU A 255	38.968	25.665	154.431	1.00127.13	C
	ATOM	1931	CG	GLU A 255	38.573	27.088	154.039	1.00134.60	C
25	ATOM	1932	CD	GLU A 255	39.628	28.119	154.396	1.00143.49	C
	ATOM	1933	OE1	GLU A 255	39.252	29.245	154.792	1.00143.37	O
	ATOM	1934	OE2	GLU A 255	40.833	27.808	154.269	1.00150.70	O
	ATOM	1935	N	PHE A 256	38.294	22.884	155.805	1.00112.91	N
	ATOM	1936	CA	PHE A 256	38.661	21.552	156.271	1.00109.01	C
30	ATOM	1937	C	PHE A 256	37.686	20.519	155.737	1.00114.56	C
	ATOM	1938	O	PHE A 256	38.025	19.346	155.594	1.00114.61	O
	ATOM	1939	CB	PHE A 256	38.669	21.509	157.792	1.00101.76	C
	ATOM	1940	CG	PHE A 256	38.843	20.135	158.357	1.00100.23	C
	ATOM	1941	CD1	PHE A 256	40.106	19.614	158.565	1.00103.61	C
35	ATOM	1942	CD2	PHE A 256	37.744	19.364	158.697	1.00 99.57	C
	ATOM	1943	CE1	PHE A 256	40.271	18.346	159.099	1.00105.27	C
	ATOM	1944	CE2	PHE A 256	37.903	18.099	159.222	1.00101.11	C
	ATOM	1945	CZ	PHE A 256	39.167	17.589	159.425	1.00104.46	C
	ATOM	1946	N	GLY A 257	36.465	20.960	155.461	1.00122.96	N
40	ATOM	1947	CA	GLY A 257	35.462	20.096	154.870	1.00125.40	C

	ATOM	1948	C	GLY A 257	35.839	19.768	153.444	1.00123.33	C
	ATOM	1949	O	GLY A 257	35.760	18.611	153.026	1.00120.84	O
	ATOM	1950	N	GLU A 258	36.261	20.796	152.709	1.00124.15	N
	ATOM	1951	CA	GLU A 258	36.711	20.636	151.333	1.00127.28	C
5	ATOM	1952	C	GLU A 258	37.883	19.670	151.269	1.00127.76	C
	ATOM	1953	O	GLU A 258	37.837	18.699	150.519	1.00130.95	O
	ATOM	1954	CB	GLU A 258	37.126	21.982	150.744	1.00140.70	C
	ATOM	1955	CG	GLU A 258	36.165	23.131	151.035	1.00155.49	C
	ATOM	1956	CD	GLU A 258	34.985	23.187	150.077	1.00164.56	C
10	ATOM	1957	OE1	GLU A 258	34.783	22.213	149.316	1.00167.01	O
	ATOM	1958	OE2	GLU A 258	34.265	24.214	150.085	1.00166.09	O
	ATOM	1959	N	GLN A 259	38.924	19.945	152.059	1.00127.37	N
	ATOM	1960	CA	GLN A 259	40.108	19.080	152.151	1.00123.29	C
	ATOM	1961	C	GLN A 259	39.727	17.613	152.335	1.00116.45	C
15	ATOM	1962	O	GLN A 259	40.079	16.765	151.517	1.00112.99	O
	ATOM	1963	CB	GLN A 259	41.028	19.519	153.305	1.00127.28	C
	ATOM	1964	CG	GLN A 259	42.155	18.511	153.623	1.00131.47	C
	ATOM	1965	CD	GLN A 259	42.792	18.695	155.011	1.00131.07	C
	ATOM	1966	OE1	GLN A 259	42.934	19.818	155.506	1.00134.77	O
20	ATOM	1967	NE2	GLN A 259	43.177	17.581	155.638	1.00121.90	N
	ATOM	1968	N	LEU A 260	38.996	17.331	153.410	1.00118.18	N
	ATOM	1969	CA	LEU A 260	38.579	15.973	153.750	1.00113.39	C
	ATOM	1970	C	LEU A 260	37.715	15.353	152.657	1.00106.62	C
	ATOM	1971	O	LEU A 260	37.948	14.216	152.242	1.00104.19	O
25	ATOM	1972	CB	LEU A 260	37.827	15.965	155.086	1.00109.59	C
	ATOM	1973	CG	LEU A 260	37.545	14.597	155.712	1.00107.17	C
	ATOM	1974	CD1	LEU A 260	38.795	13.746	155.715	1.00108.15	C
	ATOM	1975	CD2	LEU A 260	37.034	14.755	157.129	1.00105.32	C
	ATOM	1976	N	SER A 261	36.724	16.108	152.193	1.00102.69	N
30	ATOM	1977	CA	SER A 261	35.843	15.640	151.131	1.00104.75	C
	ATOM	1978	C	SER A 261	36.619	15.165	149.899	1.00112.93	C
	ATOM	1979	O	SER A 261	36.272	14.153	149.285	1.00115.04	O
	ATOM	1980	CB	SER A 261	34.850	16.728	150.744	1.00101.97	C
	ATOM	1981	OG	SER A 261	34.153	16.349	149.579	1.00105.88	O
35	ATOM	1982	N	LYS A 262	37.674	15.898	149.557	1.00117.07	N
	ATOM	1983	CA	LYS A 262	38.570	15.522	148.467	1.00115.64	C
	ATOM	1984	C	LYS A 262	39.192	14.138	148.705	1.00109.32	C
	ATOM	1985	O	LYS A 262	39.033	13.228	147.887	1.00108.38	O
	ATOM	1986	CB	LYS A 262	39.660	16.589	148.284	1.00118.86	C
40	ATOM	1987	CG	LYS A 262	40.714	16.259	147.231	1.00128.20	C

	ATOM	1988	CD	LYS A 262	41.798	17.338	147.158	1.00137.04	C
	ATOM	1989	CE	LYS A 262	42.921	16.970	146.175	1.00138.51	C
	ATOM	1990	NZ	LYS A 262	43.724	15.791	146.619	1.00135.93	N
	ATOM	1991	N	VAL A 263	39.885	13.982	149.830	1.00102.62	N
5	ATOM	1992	CA	VAL A 263	40.585	12.735	150.133	1.00102.37	C
	ATOM	1993	C	VAL A 263	39.628	11.546	150.138	1.00110.94	C
	ATOM	1994	O	VAL A 263	40.021	10.424	149.817	1.00110.40	O
	ATOM	1995	CB	VAL A 263	41.324	12.801	151.493	1.00 93.52	C
	ATOM	1996	CG1	VAL A 263	42.156	11.535	151.725	1.00 85.33	C
10	ATOM	1997	CG2	VAL A 263	42.194	14.045	151.573	1.00 89.76	C
	ATOM	1998	N	ILE A 264	38.369	11.790	150.492	1.00115.70	N
	ATOM	1999	CA	ILE A 264	37.384	10.714	150.499	1.00118.26	C
	ATOM	2000	C	ILE A 264	37.005	10.348	149.066	1.00116.72	C
	ATOM	2001	O	ILE A 264	36.778	9.176	148.753	1.00120.54	O
15	ATOM	2002	CB	ILE A 264	36.135	11.064	151.333	1.00115.30	C
	ATOM	2003	CG1	ILE A 264	36.519	11.304	152.794	1.00111.01	C
	ATOM	2004	CG2	ILE A 264	35.113	9.943	151.269	1.00115.73	C
	ATOM	2005	CD1	ILE A 264	35.334	11.592	153.697	1.00107.14	C
	ATOM	2006	N	SER A 265	36.966	11.352	148.195	1.00109.23	N
20	ATOM	2007	CA	SER A 265	36.721	11.113	146.780	1.00112.46	C
	ATOM	2008	C	SER A 265	37.812	10.230	146.172	1.00116.17	C
	ATOM	2009	O	SER A 265	37.517	9.258	145.470	1.00116.96	O
	ATOM	2010	CB	SER A 265	36.631	12.433	146.019	1.00117.68	C
	ATOM	2011	OG	SER A 265	35.618	13.259	146.562	1.00123.84	O
25	ATOM	2012	N	LEU A 266	39.069	10.568	146.449	1.00115.59	N
	ATOM	2013	CA	LEU A 266	40.197	9.783	145.957	1.00113.87	C
	ATOM	2014	C	LEU A 266	40.090	8.344	146.433	1.00112.04	C
	ATOM	2015	O	LEU A 266	40.212	7.419	145.638	1.00117.55	O
	ATOM	2016	CB	LEU A 266	41.524	10.386	146.412	1.00118.96	C
30	ATOM	2017	CG	LEU A 266	41.679	11.887	146.138	1.00127.51	C
	ATOM	2018	CD1	LEU A 266	42.995	12.427	146.713	1.00130.91	C
	ATOM	2019	CD2	LEU A 266	41.549	12.207	144.644	1.00125.50	C
	ATOM	2020	N	ILE A 267	39.837	8.159	147.725	1.00105.39	N
	ATOM	2021	CA	ILE A 267	39.737	6.819	148.301	1.00102.98	C
35	ATOM	2022	C	ILE A 267	38.526	6.058	147.756	1.00110.56	C
	ATOM	2023	O	ILE A 267	38.535	4.824	147.672	1.00114.55	O
	ATOM	2024	CB	ILE A 267	39.733	6.866	149.845	1.00 95.87	C
	ATOM	2025	CG1	ILE A 267	41.033	7.502	150.342	1.00 98.16	C
	ATOM	2026	CG2	ILE A 267	39.588	5.471	150.435	1.00 91.81	C
40	ATOM	2027	CD1	ILE A 267	41.049	7.847	151.812	1.00 97.76	C

	ATOM	2028	N	CYS A 268	37.498	6.801	147.357	1.00113.69	N
	ATOM	2029	CA	CYS A 268	36.324	6.202	146.730	1.00121.14	C
	ATOM	2030	C	CYS A 268	36.614	5.692	145.322	1.00129.11	C
	ATOM	2031	O	CYS A 268	36.196	4.594	144.951	1.00134.95	O
5	ATOM	2032	CB	CYS A 268	35.171	7.196	146.690	1.00118.11	C
	ATOM	2033	SG	CYS A 268	34.223	7.221	148.197	1.00126.06	S
	ATOM	2034	N	VAL A 269	37.317	6.495	144.531	1.00123.12	N
	ATOM	2035	CA	VAL A 269	37.710	6.059	143.200	1.00115.61	C
	ATOM	2036	C	VAL A 269	38.677	4.884	143.291	1.00119.38	C
10	ATOM	2037	O	VAL A 269	38.611	3.946	142.501	1.00122.55	O
	ATOM	2038	CB	VAL A 269	38.392	7.180	142.428	1.00104.69	C
	ATOM	2039	CG1	VAL A 269	38.740	6.706	141.042	1.00103.15	C
	ATOM	2040	CG2	VAL A 269	37.494	8.398	142.370	1.00102.17	C
	ATOM	2041	N	ALA A 270	39.569	4.937	144.273	1.00120.10	N
15	ATOM	2042	CA	ALA A 270	40.600	3.921	144.420	1.00123.36	C
	ATOM	2043	C	ALA A 270	40.038	2.562	144.828	1.00131.41	C
	ATOM	2044	O	ALA A 270	40.654	1.534	144.554	1.00137.99	O
	ATOM	2045	CB	ALA A 270	41.668	4.375	145.401	1.00120.77	C
	ATOM	2046	N	VAL A 271	38.878	2.544	145.478	1.00129.83	N
20	ATOM	2047	CA	VAL A 271	38.270	1.265	145.834	1.00132.13	C
	ATOM	2048	C	VAL A 271	37.721	0.605	144.569	1.00129.72	C
	ATOM	2049	O	VAL A 271	37.553	-0.620	144.502	1.00128.20	O
	ATOM	2050	CB	VAL A 271	37.172	1.403	146.922	1.00112.26	C
	ATOM	2051	CG1	VAL A 271	35.903	2.000	146.354	1.00109.17	C
25	ATOM	2052	CG2	VAL A 271	36.862	0.055	147.520	1.00117.26	C
	ATOM	2053	N	TRP A 272	37.473	1.433	143.558	1.00123.45	N
	ATOM	2054	CA	TRP A 272	36.940	0.964	142.290	1.00119.90	C
	ATOM	2055	C	TRP A 272	38.027	0.286	141.465	1.00121.43	C
	ATOM	2056	O	TRP A 272	37.801	-0.786	140.897	1.00129.78	O
30	ATOM	2057	CB	TRP A 272	36.330	2.131	141.531	1.00115.50	C
	ATOM	2058	CG	TRP A 272	35.494	1.756	140.359	1.00119.38	C
	ATOM	2059	CD1	TRP A 272	34.201	1.315	140.375	1.00120.58	C
	ATOM	2060	CD2	TRP A 272	35.876	1.828	138.983	1.00121.87	C
	ATOM	2061	NE1	TRP A 272	33.760	1.097	139.092	1.00122.06	N
35	ATOM	2062	CE2	TRP A 272	34.771	1.407	138.220	1.00121.29	C
	ATOM	2063	CE3	TRP A 272	37.050	2.205	138.324	1.00120.11	C
	ATOM	2064	CZ2	TRP A 272	34.805	1.349	136.832	1.00119.60	C
	ATOM	2065	CZ3	TRP A 272	37.081	2.148	136.948	1.00117.79	C
	ATOM	2066	CH2	TRP A 272	35.966	1.723	136.216	1.00118.28	C
40	ATOM	2067	N	LEU A 273	39.210	0.895	141.407	1.00112.94	N

	ATOM	2068	CA	LEU A 273	40.333	0.261	140.719	1.00112.38	C
	ATOM	2069	C	LEU A 273	40.828	-1.026	141.392	1.00115.34	C
	ATOM	2070	O	LEU A 273	41.398	-1.876	140.725	1.00121.00	O
	ATOM	2071	CB	LEU A 273	41.520	1.210	140.519	1.00111.18	C
5	ATOM	2072	CG	LEU A 273	41.508	2.706	140.848	1.00110.64	C
	ATOM	2073	CD1	LEU A 273	42.935	2.766	141.560	1.00235.80	C
	ATOM	2074	CD2	LEU A 273	40.718	3.427	139.748	1.00101.76	C
	ATOM	2075	N	ILE A 274	40.637	-1.176	142.700	1.00115.48	N
	ATOM	2076	CA	ILE A 274	41.046	-2.418	143.346	1.00128.78	C
10	ATOM	2077	C	ILE A 274	40.257	-3.558	142.738	1.00136.12	C
	ATOM	2078	O	ILE A 274	40.748	-4.680	142.590	1.00140.22	O
	ATOM	2079	CB	ILE A 274	40.755	-2.431	144.843	1.00140.20	C
	ATOM	2080	CG1	ILE A 274	41.363	-1.213	145.530	1.00141.41	C
	ATOM	2081	CG2	ILE A 274	41.286	-3.723	145.465	1.00148.39	C
15	ATOM	2082	CD1	ILE A 274	41.008	-1.120	146.997	1.00146.92	C
	ATOM	2083	N	ASN A 275	39.015	-3.255	142.390	1.00137.59	N
	ATOM	2084	CA	ASN A 275	38.150	-4.242	141.771	1.00142.48	C
	ATOM	2085	C	ASN A 275	38.290	-4.251	140.251	1.00143.40	C
	ATOM	2086	O	ASN A 275	37.850	-5.185	139.598	1.00151.69	O
20	ATOM	2087	CB	ASN A 275	36.692	-4.032	142.189	1.00138.12	C
	ATOM	2088	CG	ASN A 275	36.424	-4.466	143.621	1.00130.69	C
	ATOM	2089	OD1	ASN A 275	35.997	-3.663	144.455	1.00126.51	O
	ATOM	2090	ND2	ASN A 275	36.660	-5.745	143.909	1.00126.79	N
	ATOM	2091	N	ILE A 276	38.927	-3.229	139.689	1.00132.71	N
25	ATOM	2092	CA	ILE A 276	39.035	-3.129	138.234	1.00130.83	C
	ATOM	2093	C	ILE A 276	39.685	-4.358	137.570	1.00136.60	C
	ATOM	2094	O	ILE A 276	39.546	-4.552	136.363	1.00140.12	O
	ATOM	2095	CB	ILE A 276	39.795	-1.871	137.816	1.00128.33	C
	ATOM	2096	CG1	ILE A 276	39.226	-1.302	136.517	1.00122.77	C
30	ATOM	2097	CG2	ILE A 276	41.263	-2.175	137.653	1.00133.95	C
	ATOM	2098	CD1	ILE A 276	39.895	-0.014	136.084	1.00119.22	C
	ATOM	2099	N	GLY A 277	40.397	-5.173	138.349	1.00136.44	N
	ATOM	2100	CA	GLY A 277	40.892	-6.446	137.857	1.00141.61	C
	ATOM	2101	C	GLY A 277	39.908	-7.556	138.175	1.00148.23	C
35	ATOM	2102	O	GLY A 277	39.951	-8.638	137.587	1.00151.85	O
	ATOM	2103	N	HIS A 278	39.010	-7.271	139.110	1.00149.37	N
	ATOM	2104	CA	HIS A 278	38.051	-8.249	139.614	1.00153.24	C
	ATOM	2105	C	HIS A 278	36.709	-8.135	138.876	1.00150.92	C
	ATOM	2106	O	HIS A 278	35.784	-8.897	139.152	1.00152.93	O
40	ATOM	2107	CB	HIS A 278	37.843	-8.000	141.116	1.00151.49	C

	ATOM	2108	CG	HIS A 278	37.669	-9.242	141.934	1.00156.47	C
	ATOM	2109	ND1	HIS A 278	36.489	-9.952	141.971	1.00162.53	N
	ATOM	2110	CD2	HIS A 278	38.516	-9.878	142.778	1.00159.09	C
	ATOM	2111	CE1	HIS A 278	36.620	-10.981	142.789	1.00166.00	C
5	ATOM	2112	NE2	HIS A 278	37.841	-10.960	143.293	1.00164.87	N
	ATOM	2113	N	PHE A 279	36.609	-7.186	137.945	1.00144.07	N
	ATOM	2114	CA	PHE A 279	35.351	-6.902	137.251	1.00141.17	C
	ATOM	2115	C	PHE A 279	34.771	-8.093	136.494	1.00154.38	C
	ATOM	2116	O	PHE A 279	33.551	-8.203	136.340	1.00155.48	O
10	ATOM	2117	CB	PHE A 279	35.524	-5.743	136.274	1.00131.30	C
	ATOM	2118	CG	PHE A 279	35.360	-4.389	136.899	1.00127.52	C
	ATOM	2119	CD2	PHE A 279	35.004	-3.298	136.126	1.00123.42	C
	ATOM	2120	CD1	PHE A 279	35.547	-4.207	138.254	1.00125.21	C
	ATOM	2121	CE2	PHE A 279	34.862	-2.054	136.686	1.00116.21	C
15	ATOM	2122	CE1	PHE A 279	35.408	-2.960	138.830	1.00121.00	C
	ATOM	2123	CZ	PHE A 279	35.054	-1.881	138.040	1.00117.04	C
	ATOM	2124	N	ASN A 280	35.644	-8.969	136.002	1.00161.87	N
	ATOM	2125	CA	ASN A 280	35.189	-10.120	135.228	1.00168.46	C
	ATOM	2126	C	ASN A 280	34.986	-11.414	136.030	1.00174.16	C
20	ATOM	2127	O	ASN A 280	34.563	-12.430	135.479	1.00182.03	O
	ATOM	2128	CB	ASN A 280	36.046	-10.344	133.963	1.00168.68	C
	ATOM	2129	CG	ASN A 280	37.522	-10.578	134.263	1.00168.19	C
	ATOM	2130	OD1	ASN A 280	37.900	-10.950	135.373	1.00173.41	O
	ATOM	2131	ND2	ASN A 280	38.363	-10.369	133.256	1.00162.52	N
25	ATOM	2132	N	ASP A 281	35.278	-11.375	137.328	1.00169.95	N
	ATOM	2133	CA	ASP A 281	34.927	-12.483	138.211	1.00173.70	C
	ATOM	2134	C	ASP A 281	33.399	-12.508	138.279	1.00175.73	C
	ATOM	2135	O	ASP A 281	32.763	-11.461	138.140	1.00173.58	O
	ATOM	2136	CB	ASP A 281	35.547	-12.265	139.599	1.00175.21	C
30	ATOM	2137	CG	ASP A 281	35.369	-13.462	140.532	1.00183.79	C
	ATOM	2138	OD1	ASP A 281	36.126	-14.446	140.395	1.00186.60	O
	ATOM	2139	OD2	ASP A 281	34.475	-13.417	141.406	1.00186.18	O
	ATOM	2140	N	PRO A 282	32.800	-13.701	138.455	1.00178.37	N
	ATOM	2141	CA	PRO A 282	31.336	-13.826	138.511	1.00177.06	C
35	ATOM	2142	C	PRO A 282	30.595	-12.940	139.529	1.00168.94	C
	ATOM	2143	O	PRO A 282	30.405	-13.329	140.684	1.00164.02	O
	ATOM	2144	CB	PRO A 282	31.117	-15.313	138.838	1.00181.74	C
	ATOM	2145	CG	PRO A 282	32.464	-15.841	139.237	1.00183.24	C
	ATOM	2146	CD	PRO A 282	33.444	-15.022	138.468	1.00179.96	C
40	ATOM	2147	N	VAL A 283	30.164	-11.762	139.077	1.00162.66	N

	ATOM	2148	CA	VAL A 283	29.101	-11.030	139.763	1.00162.59	C
	ATOM	2149	C	VAL A 283	27.826	-10.703	138.940	1.00246.49	C
	ATOM	2150	O	VAL A 283	27.247	-9.642	139.178	1.00245.00	O
	ATOM	2151	CB	VAL A 283	29.612	-9.686	140.400	1.00141.56	C
5	ATOM	2152	CG1	VAL A 283	30.472	-9.931	141.633	1.00138.07	C
	ATOM	2153	CG2	VAL A 283	30.362	-8.860	139.385	1.00138.14	C
	ATOM	2154	N	HIS A 284	27.348	-11.534	137.996	1.00250.31	N
	ATOM	2155	CA	HIS A 284	27.934	-12.780	137.476	1.00253.30	C
	ATOM	2156	C	HIS A 284	27.364	-13.050	136.070	1.00247.51	C
10	ATOM	2157	O	HIS A 284	26.290	-12.549	135.744	1.00249.68	O
	ATOM	2158	CB	HIS A 284	27.672	-13.965	138.425	1.00264.64	C
	ATOM	2159	CG	HIS A 284	26.273	-14.496	138.384	1.00273.86	C
	ATOM	2160	ND1	HIS A 284	25.280	-14.041	139.227	1.00275.28	N
	ATOM	2161	CD2	HIS A 284	25.706	-15.464	137.625	1.00280.08	C
15	ATOM	2162	CE1	HIS A 284	24.159	-14.695	138.976	1.00281.24	C
	ATOM	2163	NE2	HIS A 284	24.391	-15.564	138.009	1.00284.28	N
	ATOM	2164	O	GLY A 285	31.325	-13.868	134.209	1.00220.81	O
	ATOM	2165	N	GLY A 285	28.070	-13.802	135.225	1.00239.54	N
	ATOM	2166	CA	GLY A 285	29.380	-14.347	135.520	1.00231.55	C
20	ATOM	2167	C	GLY A 285	30.489	-13.453	135.010	1.00220.87	C
	ATOM	2168	N	GLY A 286	30.484	-12.208	135.468	1.00210.37	N
	ATOM	2169	CA	GLY A 286	31.576	-11.300	135.195	1.00199.57	C
	ATOM	2170	C	GLY A 286	31.518	-10.587	133.861	1.00190.87	C
	ATOM	2171	O	GLY A 286	32.554	-10.170	133.345	1.00189.02	O
25	ATOM	2172	N	SER A 287	30.325	-10.453	133.291	1.00186.50	N
	ATOM	2173	CA	SER A 287	30.161	-9.562	132.152	1.00179.56	C
	ATOM	2174	C	SER A 287	30.608	-8.181	132.617	1.00169.85	C
	ATOM	2175	O	SER A 287	30.240	-7.739	133.707	1.00169.04	O
	ATOM	2176	CB	SER A 287	28.712	-9.540	131.680	1.00183.68	C
30	ATOM	2177	OG	SER A 287	27.833	-9.345	132.769	1.00186.67	O
	ATOM	2178	N	TRP A 288	31.421	-7.514	131.805	1.00161.98	N
	ATOM	2179	CA	TRP A 288	32.142	-6.335	132.271	1.00155.85	C
	ATOM	2180	C	TRP A 288	31.243	-5.201	132.756	1.00152.37	C
	ATOM	2181	O	TRP A 288	31.571	-4.517	133.722	1.00147.79	O
35	ATOM	2182	CB	TRP A 288	33.111	-5.822	131.206	1.00157.43	C
	ATOM	2183	CG	TRP A 288	34.293	-5.115	131.809	1.00157.48	C
	ATOM	2184	CD1	TRP A 288	34.287	-3.910	132.461	1.00153.85	C
	ATOM	2185	CD2	TRP A 288	35.652	-5.573	131.824	1.00156.88	C
	ATOM	2186	NE1	TRP A 288	35.559	-3.592	132.877	1.00150.40	N
40	ATOM	2187	CE2	TRP A 288	36.415	-4.595	132.500	1.00151.08	C

	ATOM	2188	CE3 TRP A 288	36.300	-6.711	131.330	1.00158.89	C
	ATOM	2189	CZ2 TRP A 288	37.791	-4.725	132.695	1.00146.66	C
	ATOM	2190	CZ3 TRP A 288	37.667	-6.837	131.526	1.00156.00	C
	ATOM	2191	CH2 TRP A 288	38.397	-5.848	132.203	1.00149.62	C
5	ATOM	2192	N ILE A 289	30.110	-5.003	132.092	1.00153.61	N
	ATOM	2193	CA ILE A 289	29.207	-3.921	132.472	1.00149.30	C
	ATOM	2194	C ILE A 289	28.514	-4.196	133.810	1.00145.85	C
	ATOM	2195	O ILE A 289	28.312	-3.280	134.602	1.00139.14	O
	ATOM	2196	CB ILE A 289	28.154	-3.640	131.381	1.00153.01	C
10	ATOM	2197	CG1 ILE A 289	28.827	-3.490	130.013	1.00153.86	C
	ATOM	2198	CG2 ILE A 289	27.346	-2.396	131.726	1.00148.52	C
	ATOM	2199	CD1 ILE A 289	27.853	-3.295	128.870	1.00157.39	C
	ATOM	2200	N ARG A 290	28.158	-5.453	134.068	1.00149.65	N
	ATOM	2201	CA ARG A 290	27.545	-5.802	135.348	1.00151.89	C
15	ATOM	2202	C ARG A 290	28.562	-5.767	136.469	1.00148.32	C
	ATOM	2203	O ARG A 290	28.266	-5.320	137.576	1.00147.73	O
	ATOM	2204	CB ARG A 290	26.876	-7.172	135.301	1.00159.97	C
	ATOM	2205	CG ARG A 290	25.549	-7.151	134.589	1.00169.62	C
	ATOM	2206	CD ARG A 290	24.859	-8.500	134.668	1.00183.24	C
20	ATOM	2207	NE ARG A 290	23.918	-8.672	133.565	1.00193.79	N
	ATOM	2208	CZ ARG A 290	23.305	-9.816	133.284	1.00204.13	C
	ATOM	2209	NH1 ARG A 290	23.533	-10.888	134.029	1.00209.14	N
	ATOM	2210	NH2 ARG A 290	22.467	-9.891	132.262	1.00208.67	N
	ATOM	2211	N GLY A 291	29.762	-6.253	136.179	1.00147.27	N
25	ATOM	2212	CA GLY A 291	30.842	-6.206	137.143	1.00147.58	C
	ATOM	2213	C GLY A 291	31.212	-4.776	137.486	1.00145.14	C
	ATOM	2214	O GLY A 291	31.612	-4.473	138.607	1.00142.13	O
	ATOM	2215	N ALA A 292	31.069	-3.885	136.513	1.00144.88	N
	ATOM	2216	CA ALA A 292	31.481	-2.502	136.692	1.00138.92	C
30	ATOM	2217	C ALA A 292	30.539	-1.750	137.607	1.00131.83	C
	ATOM	2218	O ALA A 292	30.964	-1.103	138.557	1.00122.44	O
	ATOM	2219	CB ALA A 292	31.574	-1.801	135.350	1.00142.11	C
	ATOM	2220	N ILE A 293	29.253	-1.852	137.307	1.00136.77	N
	ATOM	2221	CA ILE A 293	28.233	-1.067	137.983	1.00136.44	C
35	ATOM	2222	C ILE A 293	28.017	-1.533	139.420	1.00139.36	C
	ATOM	2223	O ILE A 293	27.691	-0.730	140.297	1.00143.25	O
	ATOM	2224	CB ILE A 293	26.935	-1.049	137.151	1.00137.41	C
	ATOM	2225	CG1 ILE A 293	27.118	-0.105	135.967	1.00136.34	C
	ATOM	2226	CG2 ILE A 293	25.743	-0.604	137.965	1.00139.70	C
40	ATOM	2227	CD1 ILE A 293	26.466	-0.595	134.713	1.00145.99	C

	ATOM	2228	N	TYR A 294	28.245	-2.816	139.676	1.00138.93	N
	ATOM	2229	CA	TYR A 294	28.170	-3.313	141.044	1.00139.95	C
	ATOM	2230	C	TYR A 294	29.178	-2.598	141.927	1.00134.93	C
	ATOM	2231	O	TYR A 294	28.807	-1.879	142.852	1.00135.45	O
5	ATOM	2232	CB	TYR A 294	28.437	-4.805	141.099	1.00145.51	C
	ATOM	2233	CG	TYR A 294	28.292	-5.385	142.486	1.00150.94	C
	ATOM	2234	CD1	TYR A 294	27.042	-5.720	142.988	1.00161.91	C
	ATOM	2235	CD2	TYR A 294	29.402	-5.605	143.290	1.00148.47	C
	ATOM	2236	CE1	TYR A 294	26.898	-6.260	144.251	1.00168.28	C
10	ATOM	2237	CE2	TYR A 294	29.270	-6.146	144.552	1.00155.44	C
	ATOM	2238	CZ	TYR A 294	28.014	-6.471	145.032	1.00165.35	C
	ATOM	2239	OH	TYR A 294	27.863	-7.011	146.293	1.00168.39	O
	ATOM	2240	N	TYR A 295	30.458	-2.772	141.614	1.00130.69	N
	ATOM	2241	CA	TYR A 295	31.535	-2.123	142.358	1.00125.43	C
15	ATOM	2242	C	TYR A 295	31.538	-0.603	142.211	1.00121.54	C
	ATOM	2243	O	TYR A 295	32.489	0.063	142.617	1.00118.57	O
	ATOM	2244	CB	TYR A 295	32.886	-2.683	141.919	1.00124.96	C
	ATOM	2245	CG	TYR A 295	33.047	-4.146	142.235	1.00132.92	C
	ATOM	2246	CD2	TYR A 295	33.483	-5.043	141.269	1.00140.10	C
20	ATOM	2247	CD1	TYR A 295	32.739	-4.640	143.495	1.00136.27	C
	ATOM	2248	CE2	TYR A 295	33.624	-6.399	141.555	1.00143.26	C
	ATOM	2249	CE1	TYR A 295	32.879	-5.991	143.790	1.00141.41	C
	ATOM	2250	CZ	TYR A 295	33.320	-6.863	142.815	1.00138.45	C
	ATOM	2251	OH	TYR A 295	33.456	-8.200	143.092	1.00132.56	O
25	ATOM	2252	N	PHE A 296	30.475	-0.061	141.629	1.00121.96	N
	ATOM	2253	CA	PHE A 296	30.362	1.369	141.407	1.00116.37	C
	ATOM	2254	C	PHE A 296	29.224	1.899	142.236	1.00126.68	C
	ATOM	2255	O	PHE A 296	29.171	3.090	142.529	1.00134.66	O
	ATOM	2256	CB	PHE A 296	30.106	1.664	139.936	1.00110.30	C
30	ATOM	2257	CG	PHE A 296	29.840	3.108	139.644	1.00104.81	C
	ATOM	2258	CD1	PHE A 296	30.818	4.061	139.847	1.00 99.27	C
	ATOM	2259	CD2	PHE A 296	28.611	3.511	139.147	1.00109.30	C
	ATOM	2260	CE1	PHE A 296	30.571	5.395	139.567	1.00 99.53	C
	ATOM	2261	CE2	PHE A 296	28.358	4.844	138.862	1.00105.13	C
35	ATOM	2262	CZ	PHE A 296	29.339	5.785	139.072	1.00100.05	C
	ATOM	2263	N	LYS A 297	28.297	1.018	142.602	1.00128.69	N
	ATOM	2264	CA	LYS A 297	27.284	1.379	143.582	1.00127.60	C
	ATOM	2265	C	LYS A 297	27.987	1.533	144.929	1.00119.49	C
	ATOM	2266	O	LYS A 297	27.768	2.507	145.644	1.00111.95	O
40	ATOM	2267	CB	LYS A 297	26.174	0.327	143.659	1.00133.85	C

	ATOM	2268	CG	LYS A 297	25.307	0.229	142.409	1.00137.47	C
	ATOM	2269	CD	LYS A 297	23.948	-0.412	142.708	1.00143.07	C
	ATOM	2270	CE	LYS A 297	24.071	-1.847	143.217	1.00145.08	C
	ATOM	2271	NZ	LYS A 297	24.428	-2.811	142.138	1.00145.25	N
5	ATOM	2272	N	ILE A 298	28.851	0.572	145.248	1.00117.93	N
	ATOM	2273	CA	ILE A 298	29.664	0.611	146.455	1.00113.42	C
	ATOM	2274	C	ILE A 298	30.457	1.899	146.527	1.00117.28	C
	ATOM	2275	O	ILE A 298	30.405	2.618	147.523	1.00121.52	O
	ATOM	2276	CB	ILE A 298	30.695	-0.520	146.463	1.00111.05	C
10	ATOM	2277	CG1	ILE A 298	30.009	-1.890	146.484	1.00114.26	C
	ATOM	2278	CG2	ILE A 298	31.654	-0.346	147.634	1.00108.62	C
	ATOM	2279	CD1	ILE A 298	29.528	-2.315	147.832	1.00116.19	C
	ATOM	2280	N	ALA A 299	31.198	2.181	145.463	1.00117.13	N
	ATOM	2281	CA	ALA A 299	32.087	3.333	145.443	1.00116.48	C
15	ATOM	2282	C	ALA A 299	31.342	4.647	145.686	1.00119.76	C
	ATOM	2283	O	ALA A 299	31.822	5.512	146.417	1.00122.41	O
	ATOM	2284	CB	ALA A 299	32.862	3.384	144.139	1.00111.53	C
	ATOM	2285	N	VAL A 300	30.166	4.793	145.087	1.00119.68	N
	ATOM	2286	CA	VAL A 300	29.414	6.033	145.231	1.00118.01	C
20	ATOM	2287	C	VAL A 300	28.491	6.000	146.454	1.00120.68	C
	ATOM	2288	O	VAL A 300	28.083	7.049	146.953	1.00119.30	O
	ATOM	2289	CB	VAL A 300	28.634	6.393	143.944	1.00121.05	C
	ATOM	2290	CG1	VAL A 300	27.464	5.467	143.748	1.00126.99	C
	ATOM	2291	CG2	VAL A 300	28.150	7.830	143.994	1.00124.21	C
25	ATOM	2292	N	ALA A 301	28.176	4.802	146.947	1.00122.27	N
	ATOM	2293	CA	ALA A 301	27.413	4.681	148.191	1.00118.22	C
	ATOM	2294	C	ALA A 301	28.232	5.246	149.344	1.00114.52	C
	ATOM	2295	O	ALA A 301	27.785	6.148	150.058	1.00109.53	O
	ATOM	2296	CB	ALA A 301	27.037	3.235	148.470	1.00115.85	C
30	ATOM	2297	N	LEU A 302	29.440	4.715	149.507	1.00115.74	N
	ATOM	2298	CA	LEU A 302	30.385	5.228	150.491	1.00117.33	C
	ATOM	2299	C	LEU A 302	30.569	6.724	150.313	1.00114.44	C
	ATOM	2300	O	LEU A 302	30.763	7.451	151.277	1.00113.58	O
	ATOM	2301	CB	LEU A 302	31.741	4.538	150.339	1.00119.72	C
35	ATOM	2302	CG	LEU A 302	32.851	5.021	151.278	1.00115.55	C
	ATOM	2303	CD1	LEU A 302	32.676	4.412	152.653	1.00118.31	C
	ATOM	2304	CD2	LEU A 302	34.227	4.698	150.723	1.00113.15	C
	ATOM	2305	N	ALA A 303	30.506	7.176	149.066	1.00114.95	N
	ATOM	2306	CA	ALA A 303	30.686	8.583	148.758	1.00112.85	C
40	ATOM	2307	C	ALA A 303	29.567	9.408	149.368	1.00116.90	C

	ATOM	2308	O	ALA A 303	29.822	10.299	150.167	1.00117.31	O
	ATOM	2309	CB	ALA A 303	30.745	8.788	147.263	1.00112.29	C
	ATOM	2310	N	VAL A 304	28.328	9.096	148.999	1.00122.31	N
	ATOM	2311	CA	VAL A 304	27.163	9.836	149.482	1.00121.58	C
5	ATOM	2312	C	VAL A 304	27.048	9.786	151.004	1.00121.53	C
	ATOM	2313	O	VAL A 304	26.741	10.789	151.650	1.00123.62	O
	ATOM	2314	CB	VAL A 304	25.857	9.295	148.861	1.00122.69	C
	ATOM	2315	CG1	VAL A 304	24.644	9.904	149.544	1.00123.90	C
	ATOM	2316	CG2	VAL A 304	25.822	9.568	147.364	1.00122.03	C
10	ATOM	2317	N	ALA A 305	27.318	8.618	151.574	1.00119.22	N
	ATOM	2318	CA	ALA A 305	27.130	8.418	153.003	1.00118.94	C
	ATOM	2319	C	ALA A 305	28.249	9.006	153.860	1.00117.63	C
	ATOM	2320	O	ALA A 305	28.026	9.356	155.017	1.00122.85	O
	ATOM	2321	CB	ALA A 305	26.946	6.938	153.310	1.00123.61	C
15	ATOM	2322	N	ALA A 306	29.449	9.124	153.302	1.00115.84	N
	ATOM	2323	CA	ALA A 306	30.604	9.511	154.117	1.00116.26	C
	ATOM	2324	C	ALA A 306	31.204	10.887	153.817	1.00108.22	C
	ATOM	2325	O	ALA A 306	31.947	11.422	154.636	1.00105.66	O
	ATOM	2326	CB	ALA A 306	31.684	8.430	154.075	1.00122.26	C
20	ATOM	2327	N	ILE A 307	30.903	11.452	152.651	1.00106.68	N
	ATOM	2328	CA	ILE A 307	31.308	12.829	152.378	1.00108.43	C
	ATOM	2329	C	ILE A 307	30.588	13.750	153.357	1.00113.59	C
	ATOM	2330	O	ILE A 307	29.354	13.834	153.349	1.00117.25	O
	ATOM	2331	CB	ILE A 307	30.996	13.274	150.934	1.00103.70	C
25	ATOM	2332	CG1	ILE A 307	31.886	12.531	149.937	1.00110.23	C
	ATOM	2333	CG2	ILE A 307	31.229	14.761	150.782	1.00 93.39	C
	ATOM	2334	CD1	ILE A 307	33.349	12.862	150.067	1.00111.98	C
	ATOM	2335	N	PRO A 308	31.361	14.435	154.214	1.00108.16	N
	ATOM	2336	CA	PRO A 308	30.814	15.258	155.292	1.00101.55	C
30	ATOM	2337	C	PRO A 308	30.574	16.727	154.913	1.00103.21	C
	ATOM	2338	O	PRO A 308	31.556	17.459	154.906	1.00105.21	O
	ATOM	2339	CB	PRO A 308	31.907	15.166	156.356	1.00 92.46	C
	ATOM	2340	CG	PRO A 308	33.168	15.045	155.575	1.00 92.01	C
	ATOM	2341	CD	PRO A 308	32.831	14.347	154.288	1.00101.41	C
35	ATOM	2342	N	GLU A 309	29.355	17.205	154.642	1.00108.65	N
	ATOM	2343	CA	GLU A 309	28.040	16.564	154.751	1.00122.29	C
	ATOM	2344	C	GLU A 309	27.168	17.796	154.762	1.00132.07	C
	ATOM	2345	O	GLU A 309	26.058	17.841	154.219	1.00138.81	O
	ATOM	2346	CB	GLU A 309	27.802	15.887	156.108	1.00122.20	C
40	ATOM	2347	CG	GLU A 309	26.506	15.102	156.205	1.00125.48	C

	ATOM	2348	CD	GLU A 309	26.746	13.604	156.269	1.00137.42	C
	ATOM	2349	OE1	GLU A 309	26.634	12.934	155.218	1.00142.42	O
	ATOM	2350	OE2	GLU A 309	27.048	13.097	157.372	1.00140.75	O
	ATOM	2351	N	GLY A 310	27.747	18.817	155.376	1.00129.10	N
5	ATOM	2352	CA	GLY A 310	27.021	19.881	156.019	1.00129.94	C
	ATOM	2353	C	GLY A 310	27.637	19.912	157.406	1.00129.07	C
	ATOM	2354	O	GLY A 310	27.022	19.531	158.404	1.00134.37	O
	ATOM	2355	N	LEU A 311	28.905	20.295	157.445	1.00119.93	N
	ATOM	2356	CA	LEU A 311	29.553	20.681	158.684	1.00112.04	C
10	ATOM	2357	C	LEU A 311	29.183	22.116	159.074	1.00115.04	C
	ATOM	2358	O	LEU A 311	29.091	22.417	160.259	1.00125.27	O
	ATOM	2359	CB	LEU A 311	31.071	20.534	158.588	1.00107.53	C
	ATOM	2360	CG	LEU A 311	31.715	19.219	158.999	1.00105.55	C
	ATOM	2361	CD1	LEU A 311	31.185	18.107	158.127	1.00111.62	C
15	ATOM	2362	CD2	LEU A 311	33.220	19.320	158.880	1.00 97.22	C
	ATOM	2363	N	PRO A 312	28.988	23.017	158.090	1.00109.10	N
	ATOM	2364	CA	PRO A 312	28.446	24.315	158.516	1.00117.23	C
	ATOM	2365	C	PRO A 312	27.039	24.197	159.099	1.00121.16	C
	ATOM	2366	O	PRO A 312	26.622	25.054	159.882	1.00122.92	O
20	ATOM	2367	CB	PRO A 312	28.420	25.119	157.219	1.00122.75	C
	ATOM	2368	CG	PRO A 312	29.552	24.551	156.433	1.00121.00	C
	ATOM	2369	CD	PRO A 312	29.529	23.083	156.720	1.00108.50	C
	ATOM	2370	N	ALA A 313	26.324	23.142	158.717	1.00119.80	N
	ATOM	2371	CA	ALA A 313	25.040	22.819	159.328	1.00111.93	C
25	ATOM	2372	C	ALA A 313	25.199	22.680	160.842	1.00112.02	C
	ATOM	2373	O	ALA A 313	24.352	23.140	161.608	1.00116.00	O
	ATOM	2374	CB	ALA A 313	24.479	21.535	158.732	1.00101.45	C
	ATOM	2375	N	VAL A 314	26.300	22.053	161.253	1.00106.54	N
	ATOM	2376	CA	VAL A 314	26.637	21.831	162.660	1.00 98.67	C
30	ATOM	2377	C	VAL A 314	26.917	23.122	163.436	1.00 99.80	C
	ATOM	2378	O	VAL A 314	26.468	23.284	164.573	1.00 98.77	O
	ATOM	2379	CB	VAL A 314	27.847	20.890	162.772	1.00 89.45	C
	ATOM	2380	CG1	VAL A 314	28.434	20.912	164.171	1.00 79.67	C
	ATOM	2381	CG2	VAL A 314	27.448	19.479	162.358	1.00 97.51	C
35	ATOM	2382	N	ILE A 315	27.655	24.040	162.823	1.00 99.09	N
	ATOM	2383	CA	ILE A 315	27.894	25.345	163.432	1.00102.35	C
	ATOM	2384	C	ILE A 315	26.593	26.150	163.551	1.00107.97	C
	ATOM	2385	O	ILE A 315	26.384	26.879	164.523	1.00107.46	O
	ATOM	2386	CB	ILE A 315	28.968	26.143	162.657	1.00 97.48	C
40	ATOM	2387	CG1	ILE A 315	30.325	25.467	162.817	1.00 99.23	C

	ATOM	2388	CG2 ILE A 315	29.059	27.572	163.154	1.00	96.20	C
	ATOM	2389	CD1 ILE A 315	30.680	25.165	164.260	1.00	99.74	C
	ATOM	2390	N THR A 316	25.705	25.989	162.575	1.00	108.27	N
	ATOM	2391	CA THR A 316	24.454	26.739	162.561	1.00	109.43	C
5	ATOM	2392	C THR A 316	23.353	26.014	163.336	1.00	107.60	C
	ATOM	2393	O THR A 316	22.175	26.341	163.218	1.00	114.31	O
	ATOM	2394	CB THR A 316	24.001	27.023	161.117	1.00	112.20	C
	ATOM	2395	OG1 THR A 316	25.150	27.328	160.320	1.00	121.36	O
	ATOM	2396	CG2 THR A 316	23.055	28.211	161.065	1.00	110.53	C
10	ATOM	2397	N THR A 317	23.746	25.029	164.134	1.00	98.59	N
	ATOM	2398	CA THR A 317	22.802	24.287	164.956	1.00	98.18	C
	ATOM	2399	C THR A 317	23.148	24.525	166.410	1.00	110.85	C
	ATOM	2400	O THR A 317	22.268	24.748	167.248	1.00	117.86	O
	ATOM	2401	CB THR A 317	22.852	22.773	164.660	1.00	92.53	C
15	ATOM	2402	OG1 THR A 317	22.382	22.534	163.329	1.00	103.85	O
	ATOM	2403	CG2 THR A 317	21.991	21.983	165.643	1.00	78.64	C
	ATOM	2404	N CYS A 318	24.443	24.482	166.704	1.00	109.64	N
	ATOM	2405	CA CYS A 318	24.931	24.757	168.046	1.00	101.58	C
	ATOM	2406	C CYS A 318	24.645	26.202	168.399	1.00	95.49	C
20	ATOM	2407	O CYS A 318	24.268	26.505	169.528	1.00	93.92	O
	ATOM	2408	CB CYS A 318	26.417	24.457	168.132	1.00	100.59	C
	ATOM	2409	SG CYS A 318	26.743	22.714	167.907	1.00	103.80	S
	ATOM	2410	N LEU A 319	24.814	27.082	167.416	1.00	95.27	N
	ATOM	2411	CA LEU A 319	24.352	28.463	167.518	1.00	95.65	C
25	ATOM	2412	C LEU A 319	22.877	28.524	167.920	1.00	98.29	C
	ATOM	2413	O LEU A 319	22.540	29.092	168.962	1.00	94.55	O
	ATOM	2414	CB LEU A 319	24.563	29.203	166.189	1.00	88.51	C
	ATOM	2415	CG LEU A 319	25.949	29.817	165.970	1.00	82.78	C
	ATOM	2416	CD1 LEU A 319	26.176	30.171	164.521	1.00	82.55	C
30	ATOM	2417	CD2 LEU A 319	26.117	31.045	166.836	1.00	81.63	C
	ATOM	2418	N ALA A 320	22.018	27.921	167.094	1.00	97.72	N
	ATOM	2419	CA ALA A 320	20.565	27.917	167.295	1.00	90.93	C
	ATOM	2420	C ALA A 320	20.155	27.416	168.670	1.00	88.67	C
	ATOM	2421	O ALA A 320	19.227	27.948	169.284	1.00	96.33	O
35	ATOM	2422	CB ALA A 320	19.882	27.095	166.211	1.00	90.67	C
	ATOM	2423	N LEU A 321	20.842	26.384	169.143	1.00	80.56	N
	ATOM	2424	CA LEU A 321	20.639	25.893	170.496	1.00	82.90	C
	ATOM	2425	C LEU A 321	21.130	26.910	171.525	1.00	81.07	C
	ATOM	2426	O LEU A 321	20.361	27.409	172.348	1.00	81.86	O
40	ATOM	2427	CB LEU A 321	21.381	24.576	170.685	1.00	88.17	C

	ATOM	2428	CG	LEU A 321	20.776	23.373	169.968	1.00	93.51	C
	ATOM	2429	CD1	LEU A 321	21.714	22.194	170.050	1.00	96.70	C
	ATOM	2430	CD2	LEU A 321	19.438	23.019	170.584	1.00	97.73	C
	ATOM	2431	N	GLY A 322	22.416	27.222	171.460	1.00	80.46	N
5	ATOM	2432	CA	GLY A 322	23.035	28.132	172.406	1.00	85.18	C
	ATOM	2433	C	GLY A 322	22.467	29.541	172.478	1.00	83.92	C
	ATOM	2434	O	GLY A 322	22.287	30.073	173.572	1.00	82.78	O
	ATOM	2435	N	THR A 323	22.200	30.162	171.333	1.00	77.70	N
	ATOM	2436	CA	THR A 323	21.595	31.489	171.349	1.00	80.14	C
10	ATOM	2437	C	THR A 323	20.202	31.469	171.967	1.00	85.45	C
	ATOM	2438	O	THR A 323	19.763	32.470	172.545	1.00	86.34	O
	ATOM	2439	CB	THR A 323	21.504	32.141	169.952	1.00	80.04	C
	ATOM	2440	OG1	THR A 323	21.080	31.170	168.989	1.00	92.66	O
	ATOM	2441	CG2	THR A 323	22.835	32.735	169.539	1.00	63.80	C
15	ATOM	2442	N	ARG A 324	19.505	30.340	171.841	1.00	86.92	N
	ATOM	2443	CA	ARG A 324	18.192	30.209	172.462	1.00	92.13	C
	ATOM	2444	C	ARG A 324	18.366	30.269	173.966	1.00	87.42	C
	ATOM	2445	O	ARG A 324	17.708	31.056	174.647	1.00	81.37	O
	ATOM	2446	CB	ARG A 324	17.495	28.912	172.055	1.00	102.84	C
20	ATOM	2447	CG	ARG A 324	16.059	28.823	172.563	1.00	121.70	C
	ATOM	2448	CD	ARG A 324	15.242	27.772	171.816	1.00	138.33	C
	ATOM	2449	NE	ARG A 324	15.785	26.427	171.991	1.00	149.01	N
	ATOM	2450	CZ	ARG A 324	15.189	25.317	171.563	1.00	156.57	C
	ATOM	2451	NH1	ARG A 324	14.019	25.387	170.936	1.00	160.76	N
25	ATOM	2452	NH2	ARG A 324	15.761	24.135	171.768	1.00	156.29	N
	ATOM	2453	N	ARG A 325	19.283	29.442	174.463	1.00	88.95	N
	ATOM	2454	CA	ARG A 325	19.645	29.411	175.878	1.00	87.17	C
	ATOM	2455	C	ARG A 325	20.009	30.791	176.415	1.00	82.70	C
	ATOM	2456	O	ARG A 325	19.517	31.203	177.464	1.00	82.04	O
30	ATOM	2457	CB	ARG A 325	20.810	28.444	176.100	1.00	86.10	C
	ATOM	2458	CG	ARG A 325	20.393	27.081	176.620	1.00	93.78	C
	ATOM	2459	CD	ARG A 325	21.080	25.940	175.877	1.00	100.64	C
	ATOM	2460	NE	ARG A 325	22.522	26.136	175.754	1.00	104.44	N
	ATOM	2461	CZ	ARG A 325	23.282	25.542	174.838	1.00	107.95	C
35	ATOM	2462	NH1	ARG A 325	22.742	24.707	173.956	1.00	104.24	N
	ATOM	2463	NH2	ARG A 325	24.584	25.790	174.800	1.00	113.79	N
	ATOM	2464	N	MET A 326	20.869	31.502	175.691	1.00	74.19	N
	ATOM	2465	CA	MET A 326	21.334	32.800	176.152	1.00	67.28	C
	ATOM	2466	C	MET A 326	20.170	33.789	176.259	1.00	67.24	C
40	ATOM	2467	O	MET A 326	20.160	34.645	177.133	1.00	61.81	O

	ATOM	2468	CB	MET A 326	22.433	33.370	175.246	1.00	59.86	C
	ATOM	2469	CG	MET A 326	23.697	32.511	175.042	1.00	68.02	C
	ATOM	2470	SD	MET A 326	24.801	33.157	173.719	1.00	70.14	S
	ATOM	2471	CE	MET A 326	26.368	32.411	174.147	1.00	214.46	C
5	ATOM	2472	N	ALA A 327	19.187	33.684	175.375	1.00	68.06	N
	ATOM	2473	CA	ALA A 327	18.072	34.629	175.415	1.00	76.67	C
	ATOM	2474	C	ALA A 327	17.173	34.346	176.623	1.00	89.02	C
	ATOM	2475	O	ALA A 327	16.687	35.273	177.295	1.00	94.21	O
	ATOM	2476	CB	ALA A 327	17.281	34.571	174.130	1.00	78.85	C
10	ATOM	2477	N	LYS A 328	16.963	33.058	176.898	1.00	87.00	N
	ATOM	2478	CA	LYS A 328	16.249	32.632	178.096	1.00	82.33	C
	ATOM	2479	C	LYS A 328	16.994	33.031	179.373	1.00	75.91	C
	ATOM	2480	O	LYS A 328	16.409	33.102	180.437	1.00	78.85	O
	ATOM	2481	CB	LYS A 328	15.985	31.125	178.069	1.00	86.50	C
15	ATOM	2482	CG	LYS A 328	14.907	30.707	177.082	1.00	96.52	C
	ATOM	2483	CD	LYS A 328	14.324	29.353	177.455	1.00	109.59	C
	ATOM	2484	CE	LYS A 328	13.005	29.099	176.739	1.00	120.22	C
	ATOM	2485	NZ	LYS A 328	12.199	28.011	177.380	1.00	124.41	N
	ATOM	2486	N	LYS A 329	18.288	33.296	179.261	1.00	76.73	N
20	ATOM	2487	CA	LYS A 329	19.052	33.869	180.365	1.00	73.42	C
	ATOM	2488	C	LYS A 329	19.356	35.358	180.137	1.00	70.78	C
	ATOM	2489	O	LYS A 329	20.451	35.815	180.442	1.00	72.49	O
	ATOM	2490	CB	LYS A 329	20.370	33.112	180.539	1.00	74.62	C
	ATOM	2491	CG	LYS A 329	20.240	31.603	180.651	1.00	73.88	C
25	ATOM	2492	CD	LYS A 329	21.610	30.991	180.865	1.00	79.46	C
	ATOM	2493	CE	LYS A 329	21.550	29.478	180.946	1.00	89.41	C
	ATOM	2494	NZ	LYS A 329	22.916	28.889	181.138	1.00	96.88	N
	ATOM	2495	N	ASN A 330	18.406	36.094	179.563	1.00	73.62	N
	ATOM	2496	CA	ASN A 330	18.537	37.542	179.345	1.00	70.07	C
30	ATOM	2497	C	ASN A 330	19.714	38.066	178.515	1.00	74.18	C
	ATOM	2498	O	ASN A 330	20.042	39.256	178.604	1.00	75.69	O
	ATOM	2499	CB	ASN A 330	18.522	38.272	180.680	1.00	70.63	C
	ATOM	2500	CG	ASN A 330	17.274	38.003	181.455	1.00	74.53	C
	ATOM	2501	OD1	ASN A 330	16.207	37.789	180.877	1.00	81.42	O
35	ATOM	2502	ND2	ASN A 330	17.388	38.004	182.772	1.00	69.45	N
	ATOM	2503	N	ALA A 331	20.342	37.198	177.719	1.00	73.61	N
	ATOM	2504	CA	ALA A 331	21.407	37.613	176.795	1.00	65.77	C
	ATOM	2505	C	ALA A 331	20.926	37.504	175.356	1.00	70.96	C
	ATOM	2506	O	ALA A 331	21.020	36.448	174.721	1.00	80.72	O
40	ATOM	2507	CB	ALA A 331	22.653	36.770	176.991	1.00	60.74	C

	ATOM	2508	N	ILE A 332	20.420	38.606	174.832	1.00	63.80	N
	ATOM	2509	CA	ILE A 332	19.846	38.603	173.499	1.00	66.52	C
	ATOM	2510	C	ILE A 332	20.898	38.855	172.406	1.00	72.00	C
	ATOM	2511	O	ILE A 332	21.389	39.979	172.237	1.00	80.59	O
5	ATOM	2512	CB	ILE A 332	18.726	39.614	173.462	1.00	62.40	C
	ATOM	2513	CG1	ILE A 332	17.667	39.176	174.464	1.00	64.50	C
	ATOM	2514	CG2	ILE A 332	18.163	39.734	172.070	1.00	68.02	C
	ATOM	2515	CD1	ILE A 332	16.681	40.255	174.814	1.00	146.25	C
	ATOM	2516	N	VAL A 333	21.267	37.804	171.679	1.00	67.09	N
10	ATOM	2517	CA	VAL A 333	22.354	37.926	170.695	1.00	65.96	C
	ATOM	2518	C	VAL A 333	21.921	38.571	169.371	1.00	71.41	C
	ATOM	2519	O	VAL A 333	20.963	38.128	168.726	1.00	74.57	O
	ATOM	2520	CB	VAL A 333	23.028	36.558	170.412	1.00	76.16	C
	ATOM	2521	CG1	VAL A 333	23.869	36.625	169.149	1.00	59.55	C
15	ATOM	2522	CG2	VAL A 333	23.864	36.107	171.619	1.00	71.92	C
	ATOM	2523	N	ARG A 334	22.628	39.625	168.972	1.00	68.56	N
	ATOM	2524	CA	ARG A 334	22.341	40.291	167.705	1.00	69.38	C
	ATOM	2525	C	ARG A 334	23.276	39.848	166.583	1.00	75.66	C
	ATOM	2526	O	ARG A 334	22.841	39.618	165.459	1.00	80.82	O
20	ATOM	2527	CB	ARG A 334	22.389	41.801	167.867	1.00	58.78	C
	ATOM	2528	CG	ARG A 334	21.198	42.344	168.578	1.00	59.66	C
	ATOM	2529	CD	ARG A 334	20.869	43.729	168.094	1.00	68.88	C
	ATOM	2530	NE	ARG A 334	19.621	44.200	168.679	1.00	68.78	N
	ATOM	2531	CZ	ARG A 334	19.120	45.412	168.481	1.00	75.62	C
25	ATOM	2532	NH1	ARG A 334	19.760	46.280	167.703	1.00	75.96	N
	ATOM	2533	NH2	ARG A 334	17.982	45.758	169.064	1.00	78.41	N
	ATOM	2534	N	SER A 335	24.564	39.730	166.887	1.00	79.87	N
	ATOM	2535	CA	SER A 335	25.529	39.214	165.920	1.00	77.70	C
	ATOM	2536	C	SER A 335	25.905	37.765	166.219	1.00	75.95	C
30	ATOM	2537	O	SER A 335	26.422	37.463	167.284	1.00	78.00	O
	ATOM	2538	CB	SER A 335	26.782	40.075	165.920	1.00	77.17	C
	ATOM	2539	OG	SER A 335	27.907	39.294	165.576	1.00	81.80	O
	ATOM	2540	N	LEU A 336	25.637	36.867	165.282	1.00	78.22	N
	ATOM	2541	CA	LEU A 336	25.987	35.463	165.470	1.00	84.92	C
35	ATOM	2542	C	LEU A 336	27.498	35.158	165.424	1.00	89.13	C
	ATOM	2543	O	LEU A 336	27.966	34.274	166.149	1.00	93.87	O
	ATOM	2544	CB	LEU A 336	25.217	34.569	164.494	1.00	91.38	C
	ATOM	2545	CG	LEU A 336	23.918	33.955	165.008	1.00	96.29	C
	ATOM	2546	CD1	LEU A 336	22.859	35.026	165.188	1.00	103.23	C
40	ATOM	2547	CD2	LEU A 336	23.436	32.879	164.061	1.00	97.06	C

	ATOM	2548	N	PRO A 337	28.260	35.856	164.555	1.00	81.31	N
	ATOM	2549	CA	PRO A 337	29.720	35.805	164.631	1.00	78.47	C
	ATOM	2550	C	PRO A 337	30.265	35.936	166.048	1.00	83.25	C
	ATOM	2551	O	PRO A 337	31.131	35.158	166.427	1.00	96.18	O
5	ATOM	2552	CB	PRO A 337	30.125	37.035	163.835	1.00	71.82	C
	ATOM	2553	CG	PRO A 337	29.120	37.103	162.774	1.00	71.51	C
	ATOM	2554	CD	PRO A 337	27.835	36.550	163.327	1.00	77.81	C
	ATOM	2555	N	SER A 338	29.759	36.893	166.817	1.00	75.15	N
	ATOM	2556	CA	SER A 338	30.287	37.147	168.156	1.00	75.78	C
10	ATOM	2557	C	SER A 338	30.152	35.978	169.144	1.00	75.22	C
	ATOM	2558	O	SER A 338	30.949	35.877	170.075	1.00	81.36	O
	ATOM	2559	CB	SER A 338	29.715	38.446	168.753	1.00	78.73	C
	ATOM	2560	OG	SER A 338	28.332	38.334	169.030	1.00	83.34	O
	ATOM	2561	N	VAL A 339	29.172	35.100	168.940	1.00	71.82	N
15	ATOM	2562	CA	VAL A 339	28.999	33.922	169.806	1.00	75.14	C
	ATOM	2563	C	VAL A 339	30.287	33.091	169.916	1.00	77.68	C
	ATOM	2564	O	VAL A 339	30.602	32.570	170.983	1.00	75.77	O
	ATOM	2565	CB	VAL A 339	27.813	33.018	169.340	1.00	81.10	C
	ATOM	2566	CG1	VAL A 339	27.682	31.767	170.196	1.00	69.89	C
20	ATOM	2567	CG2	VAL A 339	26.517	33.789	169.353	1.00	85.45	C
	ATOM	2568	N	GLU A 340	31.034	32.992	168.818	1.00	85.23	N
	ATOM	2569	CA	GLU A 340	32.320	32.289	168.800	1.00	91.92	C
	ATOM	2570	C	GLU A 340	33.397	33.030	169.573	1.00	89.51	C
	ATOM	2571	O	GLU A 340	34.107	32.435	170.389	1.00	96.03	O
25	ATOM	2572	CB	GLU A 340	32.797	32.109	167.368	1.00	103.80	C
	ATOM	2573	CG	GLU A 340	31.759	31.468	166.484	1.00	119.78	C
	ATOM	2574	CD	GLU A 340	32.136	31.520	165.024	1.00	125.62	C
	ATOM	2575	OE1	GLU A 340	31.470	30.814	164.234	1.00	126.99	O
	ATOM	2576	OE2	GLU A 340	33.090	32.260	164.673	1.00	122.41	O
30	ATOM	2577	N	THR A 341	33.521	34.328	169.308	1.00	79.63	N
	ATOM	2578	CA	THR A 341	34.524	35.144	169.979	1.00	78.68	C
	ATOM	2579	C	THR A 341	34.102	35.522	171.387	1.00	83.51	C
	ATOM	2580	O	THR A 341	34.839	36.199	172.096	1.00	85.87	O
	ATOM	2581	CB	THR A 341	34.827	36.449	169.221	1.00	74.26	C
35	ATOM	2582	OG1	THR A 341	33.720	37.348	169.349	1.00	65.37	O
	ATOM	2583	CG2	THR A 341	35.124	36.176	167.746	1.00	81.45	C
	ATOM	2584	N	LEU A 342	32.912	35.095	171.790	1.00	88.92	N
	ATOM	2585	CA	LEU A 342	32.408	35.425	173.118	1.00	86.61	C
	ATOM	2586	C	LEU A 342	33.091	34.586	174.192	1.00	90.99	C
40	ATOM	2587	O	LEU A 342	33.432	35.102	175.253	1.00	91.36	O

	ATOM	2588	CB	LEU A 342	30.895	35.242	173.183	1.00	82.28	C
	ATOM	2589	CG	LEU A 342	30.198	35.977	174.323	1.00	77.08	C
	ATOM	2590	CD1	LEU A 342	30.393	37.466	174.193	1.00	69.80	C
	ATOM	2591	CD2	LEU A 342	28.728	35.634	174.314	1.00	82.99	C
5	ATOM	2592	N	GLY A 343	33.303	33.300	173.908	1.00	93.15	N
	ATOM	2593	CA	GLY A 343	34.036	32.423	174.806	1.00	93.56	C
	ATOM	2594	C	GLY A 343	35.536	32.689	174.799	1.00	94.12	C
	ATOM	2595	O	GLY A 343	36.324	31.903	175.330	1.00	100.71	O
	ATOM	2596	N	CYS A 344	35.928	33.801	174.187	1.00	85.38	N
10	ATOM	2597	CA	CYS A 344	37.313	34.237	174.164	1.00	82.30	C
	ATOM	2598	C	CYS A 344	37.516	35.487	175.004	1.00	89.26	C
	ATOM	2599	O	CYS A 344	38.648	35.924	175.182	1.00	101.24	O
	ATOM	2600	CB	CYS A 344	37.750	34.531	172.733	1.00	79.87	C
	ATOM	2601	SG	CYS A 344	38.189	33.076	171.773	1.00	85.24	S
15	ATOM	2602	N	THR A 345	36.418	36.061	175.500	1.00	84.28	N
	ATOM	2603	CA	THR A 345	36.438	37.297	176.294	1.00	75.85	C
	ATOM	2604	C	THR A 345	37.432	37.185	177.425	1.00	73.80	C
	ATOM	2605	O	THR A 345	37.452	36.175	178.126	1.00	72.94	O
	ATOM	2606	CB	THR A 345	35.053	37.598	176.909	1.00	71.48	C
20	ATOM	2607	OG1	THR A 345	34.063	37.603	175.876	1.00	74.48	O
	ATOM	2608	CG2	THR A 345	35.051	38.939	177.614	1.00	65.49	C
	ATOM	2609	N	SER A 346	38.263	38.212	177.592	1.00	77.83	N
	ATOM	2610	CA	SER A 346	39.354	38.172	178.576	1.00	80.41	C
	ATOM	2611	C	SER A 346	39.335	39.368	179.525	1.00	77.54	C
25	ATOM	2612	O	SER A 346	40.035	39.367	180.542	1.00	83.98	O
	ATOM	2613	CB	SER A 346	40.712	38.112	177.881	1.00	75.39	C
	ATOM	2614	OG	SER A 346	41.036	39.368	177.307	1.00	70.49	O
	ATOM	2615	N	VAL A 347	38.547	40.383	179.171	1.00	62.75	N
	ATOM	2616	CA	VAL A 347	38.404	41.598	179.953	1.00	56.54	C
30	ATOM	2617	C	VAL A 347	36.977	42.062	179.750	1.00	64.71	C
	ATOM	2618	O	VAL A 347	36.484	42.046	178.627	1.00	67.93	O
	ATOM	2619	CB	VAL A 347	39.305	42.743	179.420	1.00	67.17	C
	ATOM	2620	CG1	VAL A 347	39.112	44.016	180.233	1.00	71.51	C
	ATOM	2621	CG2	VAL A 347	40.752	42.349	179.406	1.00	63.54	C
35	ATOM	2622	N	ILE A 348	36.310	42.478	180.820	1.00	61.35	N
	ATOM	2623	CA	ILE A 348	35.000	43.108	180.696	1.00	64.68	C
	ATOM	2624	C	ILE A 348	35.002	44.486	181.350	1.00	72.36	C
	ATOM	2625	O	ILE A 348	35.145	44.595	182.571	1.00	82.18	O
	ATOM	2626	CB	ILE A 348	33.898	42.278	181.378	1.00	65.16	C
40	ATOM	2627	CG1	ILE A 348	33.809	40.884	180.776	1.00	58.97	C

	ATOM	2628	CG2 ILE A 348	32.560	42.980	181.262	1.00	51.61	C
	ATOM	2629	CD1 ILE A 348	33.103	39.901	181.660	1.00	55.08	C
	ATOM	2630	N CYS A 349	34.855	45.539	180.551	1.00	66.05	N
	ATOM	2631	CA CYS A 349	34.603	46.853	181.128	1.00	68.64	C
5	ATOM	2632	C CYS A 349	33.109	46.966	181.300	1.00	69.25	C
	ATOM	2633	O CYS A 349	32.367	46.801	180.340	1.00	72.55	O
	ATOM	2634	CB CYS A 349	35.060	47.994	180.219	1.00	61.95	C
	ATOM	2635	SG CYS A 349	36.603	47.764	179.388	1.00	85.22	S
	ATOM	2636	N SER A 350	32.663	47.250	182.515	1.00	65.55	N
10	ATOM	2637	CA SER A 350	31.241	47.426	182.761	1.00	68.75	C
	ATOM	2638	C SER A 350	30.947	48.788	183.349	1.00	63.59	C
	ATOM	2639	O SER A 350	31.769	49.371	184.059	1.00	65.57	O
	ATOM	2640	CB SER A 350	30.722	46.343	183.706	1.00	74.21	C
	ATOM	2641	OG SER A 350	29.363	46.569	184.013	1.00	71.97	O
15	ATOM	2642	N ASP A 351	29.767	49.307	183.066	1.00	52.88	N
	ATOM	2643	CA ASP A 351	29.382	50.516	183.749	1.00	58.87	C
	ATOM	2644	C ASP A 351	28.856	50.136	185.115	1.00	66.03	C
	ATOM	2645	O ASP A 351	28.502	48.987	185.352	1.00	67.28	O
	ATOM	2646	CB ASP A 351	28.348	51.285	182.960	1.00	69.93	C
20	ATOM	2647	CG ASP A 351	28.959	52.070	181.846	1.00	76.19	C
	ATOM	2648	OD1 ASP A 351	29.492	53.161	182.151	1.00	78.46	O
	ATOM	2649	OD2 ASP A 351	28.914	51.601	180.681	1.00	76.20	O
	ATOM	2650	N LYS A 352	28.838	51.099	186.022	1.00	70.64	N
	ATOM	2651	CA LYS A 352	28.398	50.841	187.375	1.00	69.82	C
25	ATOM	2652	C LYS A 352	26.877	50.966	187.394	1.00	66.72	C
	ATOM	2653	O LYS A 352	26.180	49.976	187.258	1.00	62.46	O
	ATOM	2654	CB LYS A 352	29.078	51.821	188.359	1.00	68.80	C
	ATOM	2655	CG LYS A 352	29.080	51.402	189.847	1.00	65.55	C
	ATOM	2656	CD LYS A 352	29.028	52.618	190.781	1.00	58.65	C
30	ATOM	2657	CE LYS A 352	27.666	53.292	190.677	1.00	74.13	C
	ATOM	2658	NZ LYS A 352	27.311	54.219	191.794	1.00	83.84	N
	ATOM	2659	N THR A 353	26.381	52.191	187.528	1.00	55.70	N
	ATOM	2660	CA THR A 353	24.957	52.464	187.745	1.00	66.47	C
	ATOM	2661	C THR A 353	23.966	51.628	186.935	1.00	57.41	C
35	ATOM	2662	O THR A 353	23.857	51.771	185.738	1.00	65.47	O
	ATOM	2663	CB THR A 353	24.649	53.936	187.483	1.00	70.96	C
	ATOM	2664	OG1 THR A 353	25.549	54.752	188.245	1.00	69.55	O
	ATOM	2665	CG2 THR A 353	23.215	54.249	187.856	1.00	75.09	C
	ATOM	2666	N GLY A 354	23.255	50.742	187.612	1.00	81.96	N
40	ATOM	2667	CA GLY A 354	22.248	49.938	186.965	1.00	72.89	C

	ATOM	2668	C	GLY A 354	22.760	48.689	186.274	1.00	73.99	C
	ATOM	2669	O	GLY A 354	21.972	47.966	185.676	1.00	81.56	O
	ATOM	2670	N	THR A 355	24.060	48.424	186.334	1.00	56.60	N
	ATOM	2671	CA	THR A 355	24.601	47.182	185.766	1.00	67.92	C
5	ATOM	2672	C	THR A 355	25.366	46.348	186.801	1.00	73.53	C
	ATOM	2673	O	THR A 355	25.193	45.133	186.883	1.00	77.67	O
	ATOM	2674	CB	THR A 355	25.508	47.435	184.542	1.00	61.77	C
	ATOM	2675	OG1	THR A 355	24.769	48.125	183.523	1.00	56.23	O
	ATOM	2676	CG2	THR A 355	26.042	46.113	183.991	1.00	53.22	C
10	ATOM	2677	N	LEU A 356	26.228	47.005	187.570	1.00	74.80	N
	ATOM	2678	CA	LEU A 356	26.860	46.385	188.728	1.00	73.25	C
	ATOM	2679	C	LEU A 356	26.001	46.661	189.950	1.00	73.78	C
	ATOM	2680	O	LEU A 356	26.009	45.907	190.912	1.00	76.93	O
	ATOM	2681	CB	LEU A 356	28.250	46.961	188.949	1.00	62.34	C
15	ATOM	2682	CG	LEU A 356	29.224	46.556	187.861	1.00	58.56	C
	ATOM	2683	CD1	LEU A 356	30.459	47.422	187.909	1.00	58.70	C
	ATOM	2684	CD2	LEU A 356	29.564	45.094	188.043	1.00	57.26	C
	ATOM	2685	N	THR A 357	25.271	47.769	189.897	1.00	68.70	N
	ATOM	2686	CA	THR A 357	24.344	48.125	190.941	1.00	74.68	C
20	ATOM	2687	C	THR A 357	22.963	47.895	190.375	1.00	80.62	C
	ATOM	2688	O	THR A 357	22.819	47.158	189.404	1.00	79.29	O
	ATOM	2689	CB	THR A 357	24.520	49.581	191.392	1.00	74.10	C
	ATOM	2690	OG1	THR A 357	24.395	50.451	190.269	1.00	60.76	O
	ATOM	2691	CG2	THR A 357	25.890	49.780	192.023	1.00	72.30	C
25	ATOM	2692	N	THR A 358	21.951	48.524	190.966	1.00	83.70	N
	ATOM	2693	CA	THR A 358	20.571	48.227	190.596	1.00	84.11	C
	ATOM	2694	C	THR A 358	19.755	49.437	190.162	1.00	67.24	C
	ATOM	2695	O	THR A 358	18.627	49.284	189.720	1.00	73.93	O
	ATOM	2696	CB	THR A 358	19.813	47.525	191.740	1.00	87.04	C
30	ATOM	2697	OG1	THR A 358	19.837	48.347	192.915	1.00	89.13	O
	ATOM	2698	CG2	THR A 358	20.419	46.176	192.050	1.00	69.88	C
	ATOM	2699	N	ASN A 359	20.318	50.628	190.303	1.00	73.90	N
	ATOM	2700	CA	ASN A 359	19.616	51.869	189.991	1.00	70.91	C
	ATOM	2701	C	ASN A 359	18.319	52.091	190.783	1.00	87.60	C
35	ATOM	2702	O	ASN A 359	17.450	52.860	190.370	1.00	92.74	O
	ATOM	2703	CB	ASN A 359	19.335	51.980	188.498	1.00	71.98	C
	ATOM	2704	CG	ASN A 359	19.216	53.403	188.045	1.00	123.99	C
	ATOM	2705	OD1	ASN A 359	19.869	54.290	188.595	1.00	68.50	O
	ATOM	2706	ND2	ASN A 359	18.375	53.641	187.049	1.00	70.89	N
40	ATOM	2707	N	GLN A 360	18.177	51.422	191.920	1.00	79.45	N

	ATOM	2708	CA	GLN A 360	17.073	51.730	192.803	1.00	72.57	C
	ATOM	2709	C	GLN A 360	17.573	52.757	193.811	1.00	74.06	C
	ATOM	2710	O	GLN A 360	18.070	52.383	194.870	1.00	78.89	O
	ATOM	2711	CB	GLN A 360	16.613	50.485	193.541	1.00	74.29	C
5	ATOM	2712	CG	GLN A 360	16.869	49.194	192.832	1.00	86.89	C
	ATOM	2713	CD	GLN A 360	15.622	48.617	192.203	1.00	100.22	C
	ATOM	2714	OE1	GLN A 360	14.929	49.297	191.447	1.00	106.85	O
	ATOM	2715	NE2	GLN A 360	15.327	47.352	192.511	1.00	100.55	N
	ATOM	2716	N	MET A 361	17.465	54.044	193.488	1.00	67.56	N
10	ATOM	2717	CA	MET A 361	17.954	55.079	194.391	1.00	66.53	C
	ATOM	2718	C	MET A 361	17.026	55.234	195.593	1.00	73.81	C
	ATOM	2719	O	MET A 361	15.859	54.875	195.529	1.00	79.66	O
	ATOM	2720	CB	MET A 361	18.083	56.436	193.692	1.00	70.70	C
	ATOM	2721	CG	MET A 361	18.819	56.445	192.385	1.00	76.49	C
15	ATOM	2722	SD	MET A 361	20.458	55.780	192.523	1.00	69.36	S
	ATOM	2723	CE	MET A 361	21.309	57.079	193.404	1.00	172.16	C
	ATOM	2724	N	SER A 362	17.565	55.787	196.677	1.00	77.51	N
	ATOM	2725	CA	SER A 362	16.814	56.077	197.889	1.00	75.88	C
	ATOM	2726	C	SER A 362	17.639	56.969	198.803	1.00	73.95	C
20	ATOM	2727	O	SER A 362	18.713	56.581	199.236	1.00	76.53	O
	ATOM	2728	CB	SER A 362	16.472	54.785	198.625	1.00	78.76	C
	ATOM	2729	OG	SER A 362	17.578	53.918	198.626	1.00	64.17	O
	ATOM	2730	N	VAL A 363	17.133	58.167	199.082	1.00	72.90	N
	ATOM	2731	CA	VAL A 363	17.774	59.097	199.997	1.00	65.82	C
25	ATOM	2732	C	VAL A 363	17.705	58.524	201.387	1.00	73.60	C
	ATOM	2733	O	VAL A 363	16.618	58.238	201.879	1.00	85.49	O
	ATOM	2734	CB	VAL A 363	17.051	60.436	200.017	1.00	57.09	C
	ATOM	2735	CG1	VAL A 363	17.710	61.347	201.003	1.00	69.91	C
	ATOM	2736	CG2	VAL A 363	17.079	61.059	198.649	1.00	78.08	C
30	ATOM	2737	N	CYS A 364	18.854	58.351	202.033	1.00	74.92	N
	ATOM	2738	CA	CYS A 364	18.868	57.637	203.306	1.00	71.53	C
	ATOM	2739	C	CYS A 364	19.791	58.248	204.367	1.00	66.98	C
	ATOM	2740	O	CYS A 364	19.979	57.665	205.436	1.00	63.67	O
	ATOM	2741	CB	CYS A 364	19.209	56.171	203.077	1.00	70.64	C
35	ATOM	2742	SG	CYS A 364	20.950	55.901	202.908	1.00	62.45	S
	ATOM	2743	N	LYS A 365	20.385	59.395	204.035	1.00	59.05	N
	ATOM	2744	CA	LYS A 365	20.877	60.373	205.009	1.00	58.77	C
	ATOM	2745	C	LYS A 365	20.634	61.752	204.409	1.00	63.37	C
	ATOM	2746	O	LYS A 365	20.426	61.876	203.207	1.00	64.00	O
40	ATOM	2747	CB	LYS A 365	22.372	60.203	205.306	1.00	62.52	C

	ATOM	2748	CG	LYS A 365	22.747	58.970	206.136	1.00	74.88	C
	ATOM	2749	CD	LYS A 365	24.195	59.013	206.619	1.00	72.48	C
	ATOM	2750	CE	LYS A 365	24.691	57.622	206.964	1.00	67.36	C
	ATOM	2751	NZ	LYS A 365	26.101	57.634	207.451	1.00	71.88	N
5	ATOM	2752	N	MET A 366	20.649	62.787	205.233	1.00	57.12	N
	ATOM	2753	CA	MET A 366	20.576	64.155	204.737	1.00	59.20	C
	ATOM	2754	C	MET A 366	20.935	65.076	205.863	1.00	66.69	C
	ATOM	2755	O	MET A 366	20.764	64.730	207.029	1.00	69.60	O
	ATOM	2756	CB	MET A 366	19.175	64.515	204.238	1.00	57.97	C
10	ATOM	2757	CG	MET A 366	18.080	64.388	205.291	1.00	56.05	C
	ATOM	2758	SD	MET A 366	16.425	64.762	204.686	1.00	71.78	S
	ATOM	2759	CE	MET A 366	15.389	64.011	205.933	1.00	56.93	C
	ATOM	2760	N	PHE A 367	21.428	66.256	205.532	1.00	55.90	N
	ATOM	2761	CA	PHE A 367	21.694	67.207	206.582	1.00	66.01	C
15	ATOM	2762	C	PHE A 367	21.292	68.619	206.232	1.00	63.59	C
	ATOM	2763	O	PHE A 367	21.082	68.924	205.074	1.00	60.75	O
	ATOM	2764	CB	PHE A 367	23.140	67.104	207.070	1.00	57.40	C
	ATOM	2765	CG	PHE A 367	24.172	67.639	206.131	1.00	56.99	C
	ATOM	2766	CD2	PHE A 367	25.046	66.777	205.498	1.00	100.97	C
20	ATOM	2767	CD1	PHE A 367	24.347	68.996	205.963	1.00	63.66	C
	ATOM	2768	CE2	PHE A 367	26.029	67.250	204.674	1.00	57.32	C
	ATOM	2769	CE1	PHE A 367	25.320	69.473	205.130	1.00	64.97	C
	ATOM	2770	CZ	PHE A 367	26.161	68.599	204.486	1.00	73.51	C
	ATOM	2771	N	ILE A 368	21.143	69.458	207.247	1.00	56.40	N
25	ATOM	2772	CA	ILE A 368	20.933	70.884	207.050	1.00	72.30	C
	ATOM	2773	C	ILE A 368	21.786	71.583	208.088	1.00	74.70	C
	ATOM	2774	O	ILE A 368	22.346	70.933	208.958	1.00	70.91	O
	ATOM	2775	CB	ILE A 368	19.469	71.301	207.272	1.00	64.97	C
	ATOM	2776	CG1	ILE A 368	18.921	70.610	208.509	1.00	57.08	C
30	ATOM	2777	CG2	ILE A 368	18.622	70.916	206.114	1.00	55.40	C
	ATOM	2778	CD1	ILE A 368	17.981	71.464	209.303	1.00	146.02	C
	ATOM	2779	N	ILE A 369	21.881	72.902	208.008	1.00	73.04	N
	ATOM	2780	CA	ILE A 369	22.652	73.646	208.989	1.00	69.54	C
	ATOM	2781	C	ILE A 369	21.913	73.693	210.326	1.00	65.59	C
35	ATOM	2782	O	ILE A 369	20.684	73.731	210.365	1.00	68.28	O
	ATOM	2783	CB	ILE A 369	22.953	75.051	208.468	1.00	72.78	C
	ATOM	2784	CG1	ILE A 369	23.853	74.954	207.239	1.00	75.35	C
	ATOM	2785	CG2	ILE A 369	23.592	75.907	209.528	1.00	60.79	C
	ATOM	2786	CD1	ILE A 369	25.196	74.357	207.489	1.00	59.16	C
40	ATOM	2787	N	ASP A 370	22.661	73.658	211.420	1.00	68.90	N

	ATOM	2788	CA	ASP A 370	22.079	73.676	212.757	1.00	71.74	C
	ATOM	2789	C	ASP A 370	22.402	75.007	213.448	1.00	70.66	C
	ATOM	2790	O	ASP A 370	21.620	75.936	213.379	1.00	72.52	O
	ATOM	2791	CB	ASP A 370	22.562	72.441	213.531	1.00	74.43	C
5	ATOM	2792	CG	ASP A 370	22.084	72.398	214.967	1.00	85.18	C
	ATOM	2793	OD1	ASP A 370	21.253	73.237	215.376	1.00	81.83	O
	ATOM	2794	OD2	ASP A 370	22.556	71.491	215.691	1.00	94.13	O
	ATOM	2795	N	LYS A 371	23.557	75.118	214.086	1.00	65.51	N
	ATOM	2796	CA	LYS A 371	23.980	76.401	214.633	1.00	67.14	C
10	ATOM	2797	C	LYS A 371	25.108	76.958	213.780	1.00	70.13	C
	ATOM	2798	O	LYS A 371	25.759	76.209	213.068	1.00	66.03	O
	ATOM	2799	CB	LYS A 371	24.445	76.248	216.080	1.00	69.37	C
	ATOM	2800	CG	LYS A 371	23.402	75.693	217.017	1.00	83.10	C
	ATOM	2801	CD	LYS A 371	22.151	76.547	217.018	1.00	85.90	C
15	ATOM	2802	CE	LYS A 371	21.352	76.334	218.301	1.00	96.90	C
	ATOM	2803	NZ	LYS A 371	21.234	74.889	218.679	1.00	102.90	N
	ATOM	2804	N	VAL A 372	25.312	78.271	213.837	1.00	71.57	N
	ATOM	2805	CA	VAL A 372	26.425	78.940	213.160	1.00	76.01	C
	ATOM	2806	C	VAL A 372	27.031	80.030	214.065	1.00	84.50	C
20	ATOM	2807	O	VAL A 372	26.489	81.131	214.188	1.00	93.02	O
	ATOM	2808	CB	VAL A 372	25.991	79.562	211.809	1.00	73.27	C
	ATOM	2809	CG1	VAL A 372	27.091	80.426	211.228	1.00	75.49	C
	ATOM	2810	CG2	VAL A 372	25.635	78.493	210.829	1.00	64.86	C
	ATOM	2811	N	ASP A 373	28.149	79.715	214.707	1.00	81.52	N
25	ATOM	2812	CA	ASP A 373	28.794	80.648	215.622	1.00	81.34	C
	ATOM	2813	C	ASP A 373	30.042	81.207	214.980	1.00	85.59	C
	ATOM	2814	O	ASP A 373	30.970	80.458	214.701	1.00	92.21	O
	ATOM	2815	CB	ASP A 373	29.173	79.937	216.920	1.00	84.97	C
	ATOM	2816	CG	ASP A 373	28.138	80.112	217.998	1.00	101.09	C
30	ATOM	2817	OD1	ASP A 373	27.607	81.235	218.107	1.00	110.52	O
	ATOM	2818	OD2	ASP A 373	27.849	79.139	218.732	1.00	106.81	O
	ATOM	2819	N	GLY A 374	30.077	82.514	214.750	1.00	91.76	N
	ATOM	2820	CA	GLY A 374	31.216	83.128	214.088	1.00	105.46	C
	ATOM	2821	C	GLY A 374	31.502	82.553	212.705	1.00	116.69	C
35	ATOM	2822	O	GLY A 374	30.845	82.913	211.716	1.00	118.47	O
	ATOM	2823	N	ASP A 375	32.477	81.645	212.634	1.00	117.95	N
	ATOM	2824	CA	ASP A 375	32.848	81.012	211.366	1.00	112.54	C
	ATOM	2825	C	ASP A 375	32.625	79.500	211.324	1.00	104.10	C
	ATOM	2826	O	ASP A 375	32.801	78.880	210.284	1.00	104.18	O
40	ATOM	2827	CB	ASP A 375	34.309	81.312	211.028	1.00	115.78	C

	ATOM	2828	CG	ASP A 375	34.495	82.678	210.400	1.00116.03	C
	ATOM	2829	OD2	ASP A 375	35.603	82.937	209.878	1.00117.92	O
	ATOM	2830	OD1	ASP A 375	33.540	83.489	210.437	1.00112.18	O
	ATOM	2831	N	PHE A 376	32.238	78.907	212.445	1.00 94.57	N
5	ATOM	2832	CA	PHE A 376	32.015	77.467	212.496	1.00 82.78	C
	ATOM	2833	C	PHE A 376	30.520	77.155	212.529	1.00 83.20	C
	ATOM	2834	O	PHE A 376	29.699	78.032	212.801	1.00 86.03	O
	ATOM	2835	CB	PHE A 376	32.737	76.879	213.700	1.00 80.59	C
	ATOM	2836	CG	PHE A 376	34.132	77.408	213.865	1.00 85.14	C
10	ATOM	2837	CD1	PHE A 376	34.355	78.630	214.475	1.00 88.70	C
	ATOM	2838	CD2	PHE A 376	35.217	76.704	213.383	1.00 88.62	C
	ATOM	2839	CE1	PHE A 376	35.625	79.127	214.608	1.00 93.26	C
	ATOM	2840	CE2	PHE A 376	36.488	77.199	213.514	1.00 89.02	C
	ATOM	2841	CZ	PHE A 376	36.695	78.409	214.126	1.00 94.31	C
15	ATOM	2842	N	CYS A 377	30.162	75.915	212.221	1.00 81.85	N
	ATOM	2843	CA	CYS A 377	28.761	75.551	212.170	1.00 66.96	C
	ATOM	2844	C	CYS A 377	28.509	74.158	212.733	1.00 79.94	C
	ATOM	2845	O	CYS A 377	29.391	73.301	212.748	1.00 71.87	O
	ATOM	2846	CB	CYS A 377	28.193	75.709	210.754	1.00 64.93	C
20	ATOM	2847	SG	CYS A 377	28.612	74.423	209.501	1.00 74.42	S
	ATOM	2848	N	SER A 378	27.294	73.968	213.231	1.00 87.60	N
	ATOM	2849	CA	SER A 378	26.835	72.703	213.760	1.00 66.24	C
	ATOM	2850	C	SER A 378	26.022	72.147	212.620	1.00 69.30	C
	ATOM	2851	O	SER A 378	25.454	72.927	211.857	1.00 64.07	O
25	ATOM	2852	CB	SER A 378	25.932	72.998	214.944	1.00 67.26	C
	ATOM	2853	OG	SER A 378	25.577	71.828	215.650	1.00113.96	O
	ATOM	2854	N	LEU A 379	25.965	70.830	212.449	1.00 63.65	N
	ATOM	2855	CA	LEU A 379	25.042	70.303	211.431	1.00 61.85	C
	ATOM	2856	C	LEU A 379	23.884	69.533	212.032	1.00 85.89	C
30	ATOM	2857	O	LEU A 379	24.054	68.762	212.981	1.00 96.06	O
	ATOM	2858	CB	LEU A 379	25.729	69.419	210.396	1.00 61.20	C
	ATOM	2859	CG	LEU A 379	26.737	70.082	209.457	1.00 74.20	C
	ATOM	2860	CD1	LEU A 379	27.219	69.096	208.413	1.00 74.97	C
	ATOM	2861	CD2	LEU A 379	26.144	71.284	208.801	1.00 60.06	C
35	ATOM	2862	N	ASN A 380	22.698	69.762	211.483	1.00 81.42	N
	ATOM	2863	CA	ASN A 380	21.532	68.945	211.796	1.00 77.21	C
	ATOM	2864	C	ASN A 380	21.412	67.807	210.794	1.00 74.74	C
	ATOM	2865	O	ASN A 380	21.266	68.038	209.597	1.00 72.63	O
	ATOM	2866	CB	ASN A 380	20.275	69.794	211.778	1.00 74.90	C
40	ATOM	2867	CG	ASN A 380	19.727	70.010	213.138	1.00 79.88	C

	ATOM	2868	OD1 ASN A 380	19.823	69.129	213.977	1.00	62.81	O
	ATOM	2869	ND2 ASN A 380	19.145	71.186	213.380	1.00	85.37	N
	ATOM	2870	N GLU A 381	21.458	66.579	211.283	1.00	70.41	N
	ATOM	2871	CA GLU A 381	21.723	65.459	210.404	1.00	59.99	C
5	ATOM	2872	C GLU A 381	20.861	64.239	210.710	1.00	69.37	C
	ATOM	2873	O GLU A 381	20.824	63.744	211.850	1.00	75.88	O
	ATOM	2874	CB GLU A 381	23.198	65.141	210.512	1.00	60.80	C
	ATOM	2875	CG GLU A 381	23.656	63.915	209.805	1.00	66.61	C
	ATOM	2876	CD GLU A 381	25.137	63.708	209.998	1.00	80.54	C
10	ATOM	2877	OE1 GLU A 381	25.873	64.708	210.234	1.00	62.26	O
	ATOM	2878	OE2 GLU A 381	25.556	62.536	209.930	1.00	93.34	O
	ATOM	2879	N PHE A 382	20.167	63.752	209.682	1.00	61.01	N
	ATOM	2880	CA PHE A 382	19.106	62.771	209.895	1.00	65.41	C
	ATOM	2881	C PHE A 382	19.331	61.582	209.008	1.00	67.80	C
15	ATOM	2882	O PHE A 382	20.136	61.645	208.109	1.00	59.60	O
	ATOM	2883	CB PHE A 382	17.743	63.372	209.567	1.00	65.19	C
	ATOM	2884	CG PHE A 382	17.547	64.755	210.092	1.00	65.61	C
	ATOM	2885	CD1 PHE A 382	18.115	65.842	209.455	1.00	58.39	C
	ATOM	2886	CD2 PHE A 382	16.788	64.971	211.210	1.00	60.40	C
20	ATOM	2887	CE1 PHE A 382	17.943	67.116	209.937	1.00	74.41	C
	ATOM	2888	CE2 PHE A 382	16.608	66.248	211.688	1.00	74.92	C
	ATOM	2889	CZ PHE A 382	17.189	67.321	211.047	1.00	71.51	C
	ATOM	2890	N SER A 383	18.616	60.499	209.252	1.00	61.17	N
	ATOM	2891	CA SER A 383	18.672	59.379	208.341	1.00	74.30	C
25	ATOM	2892	C SER A 383	17.244	58.928	208.002	1.00	72.37	C
	ATOM	2893	O SER A 383	16.301	59.342	208.659	1.00	61.72	O
	ATOM	2894	CB SER A 383	19.569	58.270	208.906	1.00	62.96	C
	ATOM	2895	OG SER A 383	18.908	57.436	209.834	1.00	64.50	O
	ATOM	2896	N ILE A 384	17.066	58.143	206.947	1.00	61.56	N
30	ATOM	2897	CA ILE A 384	15.723	57.719	206.563	1.00	75.30	C
	ATOM	2898	C ILE A 384	15.672	56.215	206.287	1.00	73.70	C
	ATOM	2899	O ILE A 384	16.548	55.680	205.622	1.00	74.01	O
	ATOM	2900	CB ILE A 384	15.175	58.500	205.339	1.00	60.61	C
	ATOM	2901	CG1 ILE A 384	15.238	60.019	205.543	1.00	81.75	C
35	ATOM	2902	CG2 ILE A 384	13.725	58.151	205.117	1.00	75.80	C
	ATOM	2903	CD1 ILE A 384	16.501	60.714	205.075	1.00	58.32	C
	ATOM	2904	N THR A 385	14.658	55.529	206.809	1.00	64.75	N
	ATOM	2905	CA THR A 385	14.525	54.088	206.591	1.00	66.49	C
	ATOM	2906	C THR A 385	13.637	53.761	205.392	1.00	75.51	C
40	ATOM	2907	O THR A 385	12.873	54.604	204.910	1.00	70.73	O

	ATOM	2908	CB	THR A 385	13.931	53.402	207.791	1.00	68.35	C
	ATOM	2909	OG1	THR A 385	12.663	54.002	208.078	1.00	68.40	O
	ATOM	2910	CG2	THR A 385	14.841	53.556	208.989	1.00	68.75	C
	ATOM	2911	N	GLY A 386	13.737	52.523	204.922	1.00	76.48	N
5	ATOM	2912	CA	GLY A 386	13.030	52.101	203.725	1.00	79.91	C
	ATOM	2913	C	GLY A 386	13.830	52.451	202.490	1.00	78.71	C
	ATOM	2914	O	GLY A 386	14.211	53.602	202.302	1.00	80.38	O
	ATOM	2915	N	SER A 387	14.086	51.461	201.645	1.00	81.28	N
	ATOM	2916	CA	SER A 387	15.002	51.644	200.528	1.00	78.02	C
10	ATOM	2917	C	SER A 387	14.386	51.270	199.192	1.00	78.85	C
	ATOM	2918	O	SER A 387	15.095	51.121	198.206	1.00	85.09	O
	ATOM	2919	CB	SER A 387	16.228	50.781	200.745	1.00	84.61	C
	ATOM	2920	OG	SER A 387	15.821	49.428	200.760	1.00	94.74	O
	ATOM	2921	N	THR A 388	13.075	51.077	199.163	1.00	79.14	N
15	ATOM	2922	CA	THR A 388	12.371	50.948	197.902	1.00	77.35	C
	ATOM	2923	C	THR A 388	11.778	52.312	197.587	1.00	77.94	C
	ATOM	2924	O	THR A 388	12.141	53.300	198.220	1.00	78.63	O
	ATOM	2925	CB	THR A 388	11.271	49.895	197.950	1.00	72.57	C
	ATOM	2926	OG1	THR A 388	10.174	50.395	198.711	1.00	72.33	O
20	ATOM	2927	CG2	THR A 388	11.783	48.615	198.563	1.00	74.43	C
	ATOM	2928	N	TYR A 389	10.895	52.383	196.597	1.00	77.51	N
	ATOM	2929	CA	TYR A 389	10.329	53.673	196.224	1.00	73.65	C
	ATOM	2930	C	TYR A 389	9.082	53.929	197.042	1.00	74.76	C
	ATOM	2931	O	TYR A 389	8.518	55.020	196.990	1.00	76.20	O
25	ATOM	2932	CB	TYR A 389	10.015	53.752	194.725	1.00	71.38	C
	ATOM	2933	CG	TYR A 389	11.229	53.927	193.852	1.00	73.25	C
	ATOM	2934	CD1	TYR A 389	11.985	55.096	193.888	1.00	74.33	C
	ATOM	2935	CD2	TYR A 389	11.625	52.925	192.991	1.00	72.44	C
	ATOM	2936	CE1	TYR A 389	13.105	55.246	193.081	1.00	69.88	C
30	ATOM	2937	CE2	TYR A 389	12.731	53.068	192.192	1.00	72.12	C
	ATOM	2938	CZ	TYR A 389	13.467	54.220	192.236	1.00	70.36	C
	ATOM	2939	OH	TYR A 389	14.569	54.320	191.420	1.00	74.69	O
	ATOM	2940	N	ALA A 390	8.661	52.909	197.790	1.00	71.03	N
	ATOM	2941	CA	ALA A 390	7.455	52.983	198.604	1.00	75.26	C
35	ATOM	2942	C	ALA A 390	7.590	54.140	199.563	1.00	73.36	C
	ATOM	2943	O	ALA A 390	8.688	54.397	200.066	1.00	79.00	O
	ATOM	2944	CB	ALA A 390	7.246	51.691	199.365	1.00	72.63	C
	ATOM	2945	N	PRO A 391	6.494	54.877	199.795	1.00	68.92	N
	ATOM	2946	CA	PRO A 391	6.611	55.984	200.744	1.00	77.78	C
40	ATOM	2947	C	PRO A 391	6.516	55.489	202.168	1.00	85.69	C

	ATOM	2948	O	PRO A 391	5.930	56.171	202.995	1.00	95.03	O
	ATOM	2949	CB	PRO A 391	5.415	56.867	200.408	1.00	69.69	C
	ATOM	2950	CG	PRO A 391	4.452	55.960	199.747	1.00	72.21	C
	ATOM	2951	CD	PRO A 391	5.245	54.938	199.022	1.00	70.27	C
5	ATOM	2952	N	GLU A 392	7.094	54.328	202.447	1.00	69.22	N
	ATOM	2953	CA	GLU A 392	7.034	53.750	203.773	1.00	81.11	C
	ATOM	2954	C	GLU A 392	8.387	53.790	204.452	1.00	82.01	C
	ATOM	2955	O	GLU A 392	9.305	53.082	204.052	1.00	90.11	O
	ATOM	2956	CB	GLU A 392	6.525	52.312	203.684	1.00	95.10	C
10	ATOM	2957	CG	GLU A 392	5.055	52.215	203.282	1.00	113.65	C
	ATOM	2958	CD	GLU A 392	4.806	51.158	202.222	1.00	129.17	C
	ATOM	2959	OE1	GLU A 392	5.711	50.320	202.011	1.00	134.20	O
	ATOM	2960	OE2	GLU A 392	3.713	51.167	201.603	1.00	132.75	O
	ATOM	2961	N	GLY A 393	8.506	54.620	205.484	1.00	78.05	N
15	ATOM	2962	CA	GLY A 393	9.717	54.687	206.286	1.00	73.18	C
	ATOM	2963	C	GLY A 393	9.711	55.899	207.200	1.00	72.74	C
	ATOM	2964	O	GLY A 393	8.794	56.714	207.149	1.00	66.74	O
	ATOM	2965	N	GLU A 394	10.732	56.043	208.035	1.00	66.68	N
	ATOM	2966	CA	GLU A 394	10.794	57.230	208.885	1.00	83.87	C
20	ATOM	2967	C	GLU A 394	12.092	58.005	208.800	1.00	79.65	C
	ATOM	2968	O	GLU A 394	13.137	57.458	208.462	1.00	83.61	O
	ATOM	2969	CB	GLU A 394	10.499	56.882	210.339	1.00	89.43	C
	ATOM	2970	CG	GLU A 394	11.020	55.543	210.744	1.00	97.33	C
	ATOM	2971	CD	GLU A 394	10.166	54.931	211.807	1.00	114.97	C
25	ATOM	2972	OE1	GLU A 394	9.086	55.500	212.096	1.00	119.36	O
	ATOM	2973	OE2	GLU A 394	10.574	53.890	212.360	1.00	125.86	O
	ATOM	2974	N	VAL A 395	11.995	59.297	209.091	1.00	73.43	N
	ATOM	2975	CA	VAL A 395	13.154	60.140	209.270	1.00	72.16	C
	ATOM	2976	C	VAL A 395	13.544	59.997	210.734	1.00	76.18	C
30	ATOM	2977	O	VAL A 395	12.738	60.242	211.634	1.00	75.45	O
	ATOM	2978	CB	VAL A 395	12.823	61.593	208.969	1.00	61.24	C
	ATOM	2979	CG1	VAL A 395	14.000	62.465	209.206	1.00	60.41	C
	ATOM	2980	CG2	VAL A 395	12.371	61.730	207.569	1.00	60.35	C
	ATOM	2981	N	LEU A 396	14.776	59.559	210.964	1.00	75.73	N
35	ATOM	2982	CA	LEU A 396	15.291	59.392	212.303	1.00	74.93	C
	ATOM	2983	C	LEU A 396	16.255	60.520	212.625	1.00	76.80	C
	ATOM	2984	O	LEU A 396	16.765	61.186	211.730	1.00	63.00	O
	ATOM	2985	CB	LEU A 396	16.011	58.054	212.401	1.00	76.13	C
	ATOM	2986	CG	LEU A 396	15.194	56.843	211.957	1.00	82.59	C
40	ATOM	2987	CD1	LEU A 396	15.926	55.564	212.294	1.00	83.39	C

	ATOM	2988	CD2 LEU A 396	13.824	56.846	212.602	1.00	87.07	C
	ATOM	2989	N LYS A 397	16.468	60.762	213.911	1.00	73.43	N
	ATOM	2990	CA LYS A 397	17.612	61.551	214.365	1.00	75.94	C
	ATOM	2991	C LYS A 397	18.173	60.915	215.620	1.00	73.08	C
5	ATOM	2992	O LYS A 397	17.458	60.722	216.595	1.00	79.75	O
	ATOM	2993	CB LYS A 397	17.254	63.010	214.631	1.00	79.98	C
	ATOM	2994	CG LYS A 397	18.397	63.760	215.265	1.00	65.68	C
	ATOM	2995	CD LYS A 397	18.337	65.239	214.983	1.00	64.68	C
	ATOM	2996	CE LYS A 397	19.414	65.946	215.785	1.00	84.69	C
10	ATOM	2997	NZ LYS A 397	19.335	67.420	215.670	1.00	84.28	N
	ATOM	2998	N ASN A 398	19.451	60.581	215.577	1.00	68.22	N
	ATOM	2999	CA ASN A 398	20.069	59.762	216.599	1.00	70.45	C
	ATOM	3000	C ASN A 398	19.273	58.490	216.825	1.00	79.64	C
	ATOM	3001	O ASN A 398	19.002	58.098	217.941	1.00	89.80	O
15	ATOM	3002	CB ASN A 398	20.265	60.569	217.873	1.00	82.68	C
	ATOM	3003	CG ASN A 398	21.179	61.759	217.661	1.00	91.21	C
	ATOM	3004	OD1 ASN A 398	20.731	62.901	217.566	1.00	88.27	O
	ATOM	3005	ND2 ASN A 398	22.473	61.490	217.562	1.00	103.53	N
	ATOM	3006	N ASP A 399	18.895	57.861	215.726	1.00	82.14	N
20	ATOM	3007	CA ASP A 399	18.067	56.654	215.712	1.00	87.39	C
	ATOM	3008	C ASP A 399	16.722	56.754	216.424	1.00	86.11	C
	ATOM	3009	O ASP A 399	16.061	55.744	216.647	1.00	93.26	O
	ATOM	3010	CB ASP A 399	18.865	55.412	216.118	1.00	98.69	C
	ATOM	3011	CG ASP A 399	19.665	54.840	214.951	1.00	113.78	C
25	ATOM	3012	OD1 ASP A 399	20.727	55.414	214.619	1.00	121.14	O
	ATOM	3013	OD2 ASP A 399	19.225	53.832	214.348	1.00	114.87	O
	ATOM	3014	N LYS A 400	16.319	57.982	216.745	1.00	84.25	N
	ATOM	3015	CA LYS A 400	15.000	58.276	217.298	1.00	85.20	C
	ATOM	3016	C LYS A 400	14.104	58.874	216.209	1.00	79.31	C
30	ATOM	3017	O LYS A 400	14.458	59.903	215.637	1.00	75.19	O
	ATOM	3018	CB LYS A 400	15.138	59.264	218.467	1.00	91.10	C
	ATOM	3019	CG LYS A 400	13.800	59.784	219.024	1.00	113.25	C
	ATOM	3020	CD LYS A 400	13.910	60.218	220.500	1.00	121.28	C
	ATOM	3021	CE LYS A 400	12.560	60.132	221.231	1.00	114.34	C
35	ATOM	3022	NZ LYS A 400	12.676	60.414	222.702	1.00	108.30	N
	ATOM	3023	N PRO A 401	12.950	58.229	215.905	1.00	76.65	N
	ATOM	3024	CA PRO A 401	12.005	58.802	214.944	1.00	72.79	C
	ATOM	3025	C PRO A 401	11.709	60.242	215.299	1.00	73.11	C
	ATOM	3026	O PRO A 401	11.726	60.585	216.473	1.00	70.67	O
40	ATOM	3027	CB PRO A 401	10.757	57.937	215.132	1.00	71.62	C

	ATOM	3028	CG	PRO A 401	11.276	56.637	215.492	1.00	73.12	C
	ATOM	3029	CD	PRO A 401	12.485	56.910	216.368	1.00	82.28	C
	ATOM	3030	N	ILE A 402	11.500	61.082	214.299	1.00	67.58	N
	ATOM	3031	CA	ILE A 402	11.208	62.486	214.527	1.00	79.83	C
5	ATOM	3032	C	ILE A 402	10.319	62.995	213.410	1.00	75.10	C
	ATOM	3033	O	ILE A 402	10.271	62.415	212.322	1.00	74.00	O
	ATOM	3034	CB	ILE A 402	12.488	63.381	214.563	1.00	86.85	C
	ATOM	3035	CG1	ILE A 402	13.240	63.336	213.222	1.00	84.96	C
	ATOM	3036	CG2	ILE A 402	13.387	63.013	215.717	1.00	67.39	C
10	ATOM	3037	CD1	ILE A 402	12.965	64.506	212.301	1.00	62.71	C
	ATOM	3038	N	ARG A 403	9.640	64.102	213.685	1.00	72.89	N
	ATOM	3039	CA	ARG A 403	8.763	64.738	212.718	1.00	71.87	C
	ATOM	3040	C	ARG A 403	9.477	65.864	211.946	1.00	70.67	C
	ATOM	3041	O	ARG A 403	9.868	66.884	212.519	1.00	64.00	O
15	ATOM	3042	CB	ARG A 403	7.477	65.203	213.422	1.00	67.35	C
	ATOM	3043	CG	ARG A 403	6.801	66.393	212.807	1.00	113.38	C
	ATOM	3044	CD	ARG A 403	5.594	66.760	213.618	1.00	109.15	C
	ATOM	3045	NE	ARG A 403	4.739	65.599	213.806	1.00	70.47	N
	ATOM	3046	CZ	ARG A 403	3.560	65.639	214.408	1.00	84.93	C
20	ATOM	3047	NH1	ARG A 403	3.093	66.786	214.883	1.00	73.50	N
	ATOM	3048	NH2	ARG A 403	2.856	64.529	214.526	1.00	79.09	N
	ATOM	3049	N	SER A 404	9.634	65.669	210.638	1.00	62.58	N
	ATOM	3050	CA	SER A 404	10.492	66.545	209.833	1.00	64.21	C
	ATOM	3051	C	SER A 404	10.019	67.998	209.710	1.00	64.49	C
25	ATOM	3052	O	SER A 404	10.813	68.871	209.410	1.00	71.48	O
	ATOM	3053	CB	SER A 404	10.755	65.954	208.436	1.00	59.90	C
	ATOM	3054	OG	SER A 404	11.038	64.571	208.506	1.00	74.46	O
	ATOM	3055	N	GLY A 405	8.739	68.267	209.923	1.00	66.73	N
	ATOM	3056	CA	GLY A 405	8.241	69.622	209.748	1.00	69.24	C
30	ATOM	3057	C	GLY A 405	8.658	70.547	210.881	1.00	69.29	C
	ATOM	3058	O	GLY A 405	8.570	71.783	210.781	1.00	67.64	O
	ATOM	3059	N	GLN A 406	9.113	69.942	211.973	1.00	67.79	N
	ATOM	3060	CA	GLN A 406	9.534	70.703	213.134	1.00	69.89	C
	ATOM	3061	C	GLN A 406	10.813	71.470	212.815	1.00	69.11	C
35	ATOM	3062	O	GLN A 406	11.139	72.445	213.472	1.00	79.44	O
	ATOM	3063	CB	GLN A 406	9.710	69.780	214.335	1.00	70.43	C
	ATOM	3064	CG	GLN A 406	8.411	69.427	215.051	1.00	80.57	C
	ATOM	3065	CD	GLN A 406	8.596	68.291	216.057	1.00	100.25	C
	ATOM	3066	OE1	GLN A 406	9.642	67.605	216.060	1.00	101.55	O
40	ATOM	3067	NE2	GLN A 406	7.581	68.077	216.915	1.00	97.70	N

	ATOM	3068	N	PHE A 407	11.516	71.034	211.777	1.00	66.22	N
	ATOM	3069	CA	PHE A 407	12.699	71.722	211.284	1.00	61.11	C
	ATOM	3070	C	PHE A 407	12.398	72.555	210.014	1.00	75.39	C
	ATOM	3071	O	PHE A 407	12.210	71.998	208.923	1.00	72.48	O
5	ATOM	3072	CB	PHE A 407	13.759	70.680	210.958	1.00	60.15	C
	ATOM	3073	CG	PHE A 407	14.113	69.783	212.109	1.00	65.87	C
	ATOM	3074	CD1	PHE A 407	13.370	68.644	212.374	1.00	61.69	C
	ATOM	3075	CD2	PHE A 407	15.219	70.068	212.922	1.00	62.79	C
	ATOM	3076	CE1	PHE A 407	13.713	67.820	213.435	1.00	62.83	C
10	ATOM	3077	CE2	PHE A 407	15.561	69.249	213.969	1.00	62.87	C
	ATOM	3078	CZ	PHE A 407	14.815	68.125	214.225	1.00	73.79	C
	ATOM	3079	N	ASP A 408	12.370	73.882	210.143	1.00	75.69	N
	ATOM	3080	CA	ASP A 408	12.133	74.764	208.997	1.00	72.52	C
	ATOM	3081	C	ASP A 408	13.159	74.568	207.892	1.00	71.47	C
15	ATOM	3082	O	ASP A 408	12.882	74.812	206.709	1.00	78.36	O
	ATOM	3083	CB	ASP A 408	12.138	76.221	209.432	1.00	61.53	C
	ATOM	3084	CG	ASP A 408	11.038	76.526	210.411	1.00	89.12	C
	ATOM	3085	OD1	ASP A 408	9.877	76.133	210.144	1.00	87.73	O
	ATOM	3086	OD2	ASP A 408	11.333	77.137	211.462	1.00	95.46	O
20	ATOM	3087	N	GLY A 409	14.354	74.146	208.287	1.00	69.09	N
	ATOM	3088	CA	GLY A 409	15.379	73.782	207.336	1.00	62.81	C
	ATOM	3089	C	GLY A 409	14.925	72.577	206.546	1.00	65.61	C
	ATOM	3090	O	GLY A 409	15.039	72.567	205.317	1.00	69.71	O
	ATOM	3091	N	LEU A 410	14.401	71.565	207.239	1.00	65.23	N
25	ATOM	3092	CA	LEU A 410	13.914	70.370	206.560	1.00	65.82	C
	ATOM	3093	C	LEU A 410	12.734	70.680	205.662	1.00	64.09	C
	ATOM	3094	O	LEU A 410	12.564	70.047	204.611	1.00	65.28	O
	ATOM	3095	CB	LEU A 410	13.548	69.262	207.535	1.00	57.28	C
	ATOM	3096	CG	LEU A 410	14.725	68.474	208.105	1.00	57.29	C
30	ATOM	3097	CD1	LEU A 410	14.280	67.107	208.588	1.00	73.18	C
	ATOM	3098	CD2	LEU A 410	15.836	68.330	207.102	1.00	56.30	C
	ATOM	3099	N	VAL A 411	11.919	71.651	206.071	1.00	63.48	N
	ATOM	3100	CA	VAL A 411	10.758	72.029	205.272	1.00	67.91	C
	ATOM	3101	C	VAL A 411	11.231	72.512	203.918	1.00	75.32	C
35	ATOM	3102	O	VAL A 411	10.748	72.036	202.893	1.00	77.26	O
	ATOM	3103	CB	VAL A 411	9.885	73.096	205.957	1.00	62.73	C
	ATOM	3104	CG1	VAL A 411	8.585	73.279	205.205	1.00	59.87	C
	ATOM	3105	CG2	VAL A 411	9.570	72.657	207.343	1.00	67.95	C
	ATOM	3106	N	GLU A 412	12.201	73.422	203.914	1.00	72.68	N
40	ATOM	3107	CA	GLU A 412	12.734	73.944	202.663	1.00	65.36	C

	ATOM	3108	C	GLU A 412	13.523	72.929	201.859	1.00	64.90	C
	ATOM	3109	O	GLU A 412	13.513	72.968	200.638	1.00	63.95	O
	ATOM	3110	CB	GLU A 412	13.612	75.148	202.907	1.00	61.36	C
	ATOM	3111	CG	GLU A 412	14.130	75.739	201.632	1.00	56.06	C
5	ATOM	3112	CD	GLU A 412	14.818	77.039	201.870	1.00	64.43	C
	ATOM	3113	OE1	GLU A 412	15.145	77.320	203.037	1.00	66.43	O
	ATOM	3114	OE2	GLU A 412	15.036	77.781	200.901	1.00	63.60	O
	ATOM	3115	N	LEU A 413	14.220	72.024	202.536	1.00	66.64	N
	ATOM	3116	CA	LEU A 413	14.949	70.979	201.824	1.00	63.80	C
10	ATOM	3117	C	LEU A 413	13.964	70.043	201.112	1.00	65.77	C
	ATOM	3118	O	LEU A 413	14.238	69.518	200.034	1.00	68.75	O
	ATOM	3119	CB	LEU A 413	15.861	70.202	202.773	1.00	54.14	C
	ATOM	3120	CG	LEU A 413	16.569	69.013	202.142	1.00	53.81	C
	ATOM	3121	CD1	LEU A 413	17.914	68.884	202.737	1.00	53.81	C
15	ATOM	3122	CD2	LEU A 413	15.788	67.718	202.328	1.00	57.13	C
	ATOM	3123	N	ALA A 414	12.810	69.838	201.726	1.00	55.04	N
	ATOM	3124	CA	ALA A 414	11.792	69.010	201.122	1.00	74.72	C
	ATOM	3125	C	ALA A 414	11.089	69.773	199.997	1.00	74.31	C
	ATOM	3126	O	ALA A 414	10.704	69.169	198.999	1.00	69.55	O
20	ATOM	3127	CB	ALA A 414	10.819	68.534	202.169	1.00	56.37	C
	ATOM	3128	N	THR A 415	10.954	71.094	200.144	1.00	56.07	N
	ATOM	3129	CA	THR A 415	10.295	71.920	199.136	1.00	71.71	C
	ATOM	3130	C	THR A 415	11.112	71.904	197.847	1.00	72.09	C
	ATOM	3131	O	THR A 415	10.583	71.888	196.727	1.00	67.81	O
25	ATOM	3132	CB	THR A 415	10.137	73.359	199.627	1.00	57.21	C
	ATOM	3133	OG1	THR A 415	9.081	73.425	200.588	1.00	69.61	O
	ATOM	3134	CG2	THR A 415	9.770	74.264	198.508	1.00	57.87	C
	ATOM	3135	N	ILE A 416	12.424	71.904	198.022	1.00	69.31	N
	ATOM	3136	CA	ILE A 416	13.350	71.873	196.912	1.00	60.89	C
30	ATOM	3137	C	ILE A 416	13.259	70.534	196.206	1.00	62.69	C
	ATOM	3138	O	ILE A 416	13.091	70.490	194.992	1.00	65.15	O
	ATOM	3139	CB	ILE A 416	14.762	72.170	197.400	1.00	56.30	C
	ATOM	3140	CG1	ILE A 416	14.942	73.680	197.519	1.00	56.12	C
	ATOM	3141	CG2	ILE A 416	15.789	71.607	196.466	1.00	65.96	C
35	ATOM	3142	CD1	ILE A 416	16.142	74.093	198.334	1.00	54.32	C
	ATOM	3143	N	CYS A 417	13.326	69.444	196.960	1.00	59.16	N
	ATOM	3144	CA	CYS A 417	13.258	68.116	196.352	1.00	63.67	C
	ATOM	3145	C	CYS A 417	11.960	67.840	195.589	1.00	69.98	C
	ATOM	3146	O	CYS A 417	11.939	66.969	194.717	1.00	85.02	O
40	ATOM	3147	CB	CYS A 417	13.505	67.003	197.371	1.00	63.52	C

	ATOM	3148	SG	CYS A 417	15.136	67.047	198.147	1.00	70.62	S
	ATOM	3149	N	ALA A 418	10.890	68.579	195.890	1.00	63.59	N
	ATOM	3150	CA	ALA A 418	9.617	68.407	195.177	1.00	65.51	C
	ATOM	3151	C	ALA A 418	9.519	69.239	193.921	1.00	58.36	C
5	ATOM	3152	O	ALA A 418	8.960	68.796	192.939	1.00	117.55	O
	ATOM	3153	CB	ALA A 418	8.441	68.693	196.086	1.00	58.52	C
	ATOM	3154	N	LEU A 419	10.051	70.450	193.947	1.00	75.30	N
	ATOM	3155	CA	LEU A 419	10.010	71.311	192.760	1.00	71.64	C
	ATOM	3156	C	LEU A 419	11.157	71.123	191.727	1.00	70.94	C
10	ATOM	3157	O	LEU A 419	10.910	71.251	190.536	1.00	69.13	O
	ATOM	3158	CB	LEU A 419	9.846	72.783	193.157	1.00	70.27	C
	ATOM	3159	CG	LEU A 419	8.670	73.106	194.081	1.00	59.59	C
	ATOM	3160	CD1	LEU A 419	8.880	74.447	194.755	1.00	82.02	C
	ATOM	3161	CD2	LEU A 419	7.423	73.140	193.298	1.00	65.39	C
15	ATOM	3162	N	CYS A 420	12.392	70.836	192.149	1.00	67.99	N
	ATOM	3163	CA	CYS A 420	13.431	70.470	191.169	1.00	63.87	C
	ATOM	3164	C	CYS A 420	13.301	69.002	190.860	1.00	70.76	C
	ATOM	3165	O	CYS A 420	14.172	68.214	191.203	1.00	77.49	O
	ATOM	3166	CB	CYS A 420	14.855	70.702	191.679	1.00	62.35	C
20	ATOM	3167	SG	CYS A 420	15.302	72.373	192.002	1.00	84.98	S
	ATOM	3168	N	ASN A 421	12.212	68.625	190.214	1.00	70.91	N
	ATOM	3169	CA	ASN A 421	11.939	67.223	190.018	1.00	64.16	C
	ATOM	3170	C	ASN A 421	11.069	67.126	188.803	1.00	67.19	C
	ATOM	3171	O	ASN A 421	10.135	67.910	188.659	1.00	74.09	O
25	ATOM	3172	CB	ASN A 421	11.213	66.688	191.248	1.00	61.55	C
	ATOM	3173	CG	ASN A 421	11.342	65.194	191.404	1.00	66.96	C
	ATOM	3174	OD1	ASN A 421	11.169	64.432	190.450	1.00	64.29	O
	ATOM	3175	ND2	ASN A 421	11.668	64.761	192.620	1.00	71.96	N
	ATOM	3176	N	ASP A 422	11.388	66.188	187.916	1.00	76.31	N
30	ATOM	3177	CA	ASP A 422	10.619	65.986	186.690	1.00	85.81	C
	ATOM	3178	C	ASP A 422	10.020	64.589	186.684	1.00	87.77	C
	ATOM	3179	O	ASP A 422	9.622	64.073	185.638	1.00	101.46	O
	ATOM	3180	CB	ASP A 422	11.502	66.170	185.457	1.00	89.46	C
	ATOM	3181	CG	ASP A 422	12.101	67.559	185.369	1.00	100.60	C
35	ATOM	3182	OD1	ASP A 422	11.398	68.533	185.735	1.00	99.94	O
	ATOM	3183	OD2	ASP A 422	13.279	67.670	184.937	1.00	105.30	O
	ATOM	3184	N	SER A 423	9.947	63.987	187.864	1.00	75.44	N
	ATOM	3185	CA	SER A 423	9.610	62.578	187.974	1.00	80.98	C
	ATOM	3186	C	SER A 423	8.512	62.409	189.005	1.00	73.49	C
40	ATOM	3187	O	SER A 423	8.078	63.402	189.573	1.00	71.46	O

	ATOM	3188	CB	SER A 423	10.860	61.751	188.309	1.00	91.22	C
	ATOM	3189	OG	SER A 423	11.821	61.817	187.248	1.00	92.23	O
	ATOM	3190	N	SER A 424	8.050	61.175	189.221	1.00	66.02	N
	ATOM	3191	CA	SER A 424	6.843	60.919	190.031	1.00	76.29	C
5	ATOM	3192	C	SER A 424	6.671	59.460	190.457	1.00	75.07	C
	ATOM	3193	O	SER A 424	7.267	58.558	189.874	1.00	84.68	O
	ATOM	3194	CB	SER A 424	5.578	61.396	189.300	1.00	81.01	C
	ATOM	3195	OG	SER A 424	5.646	61.161	187.894	1.00	82.03	O
	ATOM	3196	N	LEU A 425	5.862	59.240	191.489	1.00	70.47	N
10	ATOM	3197	CA	LEU A 425	5.563	57.890	191.981	1.00	73.91	C
	ATOM	3198	C	LEU A 425	4.204	57.386	191.503	1.00	82.63	C
	ATOM	3199	O	LEU A 425	3.218	58.124	191.481	1.00	83.08	O
	ATOM	3200	CB	LEU A 425	5.571	57.858	193.507	1.00	68.46	C
	ATOM	3201	CG	LEU A 425	6.837	57.502	194.269	1.00	67.02	C
15	ATOM	3202	CD1	LEU A 425	6.539	57.557	195.747	1.00	96.08	C
	ATOM	3203	CD2	LEU A 425	7.310	56.129	193.893	1.00	79.49	C
	ATOM	3204	N	ASP A 426	4.142	56.117	191.140	1.00	86.80	N
	ATOM	3205	CA	ASP A 426	2.886	55.555	190.688	1.00	94.10	C
	ATOM	3206	C	ASP A 426	2.686	54.164	191.277	1.00	95.10	C
20	ATOM	3207	O	ASP A 426	3.640	53.398	191.430	1.00	89.28	O
	ATOM	3208	CB	ASP A 426	2.836	55.537	189.162	1.00	101.22	C
	ATOM	3209	CG	ASP A 426	1.788	54.604	188.633	1.00	114.10	C
	ATOM	3210	OD1	ASP A 426	0.602	54.994	188.604	1.00	122.48	O
	ATOM	3211	OD2	ASP A 426	2.154	53.475	188.251	1.00	117.99	O
25	ATOM	3212	N	PHE A 427	1.446	53.848	191.639	1.00	95.74	N
	ATOM	3213	CA	PHE A 427	1.189	52.580	192.299	1.00	90.79	C
	ATOM	3214	C	PHE A 427	0.686	51.548	191.329	1.00	94.84	C
	ATOM	3215	O	PHE A 427	-0.277	51.774	190.605	1.00	106.17	O
	ATOM	3216	CB	PHE A 427	0.230	52.720	193.479	1.00	87.96	C
30	ATOM	3217	CG	PHE A 427	0.086	51.456	194.275	1.00	87.79	C
	ATOM	3218	CD1	PHE A 427	1.113	51.020	195.101	1.00	91.01	C
	ATOM	3219	CD2	PHE A 427	-1.062	50.689	194.185	1.00	86.97	C
	ATOM	3220	CE1	PHE A 427	0.992	49.848	195.828	1.00	84.21	C
	ATOM	3221	CE2	PHE A 427	-1.186	49.517	194.908	1.00	88.72	C
35	ATOM	3222	CZ	PHE A 427	-0.157	49.099	195.731	1.00	87.33	C
	ATOM	3223	N	ASN A 428	1.353	50.406	191.339	1.00	85.44	N
	ATOM	3224	CA	ASN A 428	1.079	49.331	190.404	1.00	106.22	C
	ATOM	3225	C	ASN A 428	0.157	48.312	191.035	1.00	105.65	C
	ATOM	3226	O	ASN A 428	0.619	47.379	191.684	1.00	103.20	O
40	ATOM	3227	CB	ASN A 428	2.395	48.662	190.010	1.00	101.91	C

	ATOM	3228	CG	ASN A 428	2.238	47.627	188.915	1.00100.79	C
	ATOM	3229	OD1	ASN A 428	1.276	46.859	188.884	1.00100.87	O
	ATOM	3230	ND2	ASN A 428	3.206	47.591	188.017	1.00 98.82	N
	ATOM	3231	N	GLU A 429	-1.144	48.470	190.823	1.00110.89	N
5	ATOM	3232	CA	GLU A 429	-2.120	47.657	191.545	1.00118.20	C
	ATOM	3233	C	GLU A 429	-2.070	46.178	191.173	1.00119.57	C
	ATOM	3234	O	GLU A 429	-2.649	45.339	191.868	1.00116.60	O
	ATOM	3235	CB	GLU A 429	-3.534	48.222	191.386	1.00116.16	C
	ATOM	3236	CG	GLU A 429	-3.769	49.483	192.193	1.00113.41	C
10	ATOM	3237	CD	GLU A 429	-5.048	50.182	191.817	1.00121.91	C
	ATOM	3238	OE1	GLU A 429	-6.045	50.025	192.553	1.00127.94	O
	ATOM	3239	OE2	GLU A 429	-5.056	50.892	190.786	1.00124.41	O
	ATOM	3240	N	THR A 430	-1.360	45.858	190.095	1.00119.80	N
	ATOM	3241	CA	THR A 430	-1.246	44.468	189.668	1.00122.24	C
15	ATOM	3242	C	THR A 430	-0.047	43.762	190.311	1.00121.02	C
	ATOM	3243	O	THR A 430	-0.191	42.680	190.876	1.00123.28	O
	ATOM	3244	CB	THR A 430	-1.210	44.342	188.140	1.00119.46	C
	ATOM	3245	OG1	THR A 430	-2.260	45.138	187.578	1.00115.69	O
	ATOM	3246	CG2	THR A 430	-1.403	42.893	187.730	1.00122.24	C
20	ATOM	3247	N	LYS A 431	1.131	44.373	190.238	1.00118.38	N
	ATOM	3248	CA	LYS A 431	2.289	43.845	190.958	1.00117.08	C
	ATOM	3249	C	LYS A 431	2.180	44.190	192.444	1.00116.82	C
	ATOM	3250	O	LYS A 431	2.889	43.625	193.277	1.00115.77	O
	ATOM	3251	CB	LYS A 431	3.603	44.397	190.387	1.00109.46	C
25	ATOM	3252	CG	LYS A 431	3.941	43.935	188.981	1.00107.11	C
	ATOM	3253	CD	LYS A 431	5.235	44.568	188.515	1.00107.54	C
	ATOM	3254	CE	LYS A 431	5.299	44.673	186.993	1.00114.31	C
	ATOM	3255	NZ	LYS A 431	6.426	45.553	186.527	1.00108.44	N
	ATOM	3256	N	GLY A 432	1.288	45.126	192.763	1.00115.66	N
30	ATOM	3257	CA	GLY A 432	1.064	45.552	194.132	1.00112.57	C
	ATOM	3258	C	GLY A 432	2.257	46.267	194.734	1.00112.92	C
	ATOM	3259	O	GLY A 432	2.487	46.179	195.936	1.00120.66	O
	ATOM	3260	N	VAL A 433	3.023	46.972	193.904	1.00106.43	N
	ATOM	3261	CA	VAL A 433	4.246	47.631	194.358	1.00101.50	C
35	ATOM	3262	C	VAL A 433	4.304	49.082	193.880	1.00 93.87	C
	ATOM	3263	O	VAL A 433	3.760	49.412	192.835	1.00 92.90	O
	ATOM	3264	CB	VAL A 433	5.498	46.884	193.845	1.00105.86	C
	ATOM	3265	CG1	VAL A 433	6.758	47.379	194.551	1.00107.68	C
	ATOM	3266	CG2	VAL A 433	5.348	45.387	194.041	1.00107.48	C
40	ATOM	3267	N	TYR A 434	4.958	49.947	194.651	1.00 90.67	N

	ATOM	3268	CA	TYR A 434	5.178	51.334	194.247	1.00	86.83	C
	ATOM	3269	C	TYR A 434	6.299	51.430	193.220	1.00	86.81	C
	ATOM	3270	O	TYR A 434	7.444	51.075	193.527	1.00	90.88	O
	ATOM	3271	CB	TYR A 434	5.547	52.178	195.462	1.00	79.81	C
5	ATOM	3272	CG	TYR A 434	4.358	52.618	196.275	1.00	86.35	C
	ATOM	3273	CD2	TYR A 434	3.978	51.928	197.420	1.00	86.37	C
	ATOM	3274	CD1	TYR A 434	3.615	53.730	195.903	1.00	92.09	C
	ATOM	3275	CE2	TYR A 434	2.884	52.333	198.176	1.00	86.62	C
	ATOM	3276	CE1	TYR A 434	2.525	54.144	196.655	1.00	95.75	C
10	ATOM	3277	CZ	TYR A 434	2.161	53.442	197.790	1.00	87.82	C
	ATOM	3278	OH	TYR A 434	1.075	53.852	198.532	1.00	83.23	O
	ATOM	3279	N	GLU A 435	5.984	51.916	192.014	1.00	80.93	N
	ATOM	3280	CA	GLU A 435	6.978	51.997	190.933	1.00	82.42	C
	ATOM	3281	C	GLU A 435	7.319	53.423	190.500	1.00	73.96	C
15	ATOM	3282	O	GLU A 435	6.546	54.350	190.696	1.00	99.59	O
	ATOM	3283	CB	GLU A 435	6.520	51.189	189.716	1.00	78.81	C
	ATOM	3284	CG	GLU A 435	6.389	49.676	189.921	1.00	81.29	C
	ATOM	3285	CD	GLU A 435	5.840	48.971	188.675	1.00	98.47	C
	ATOM	3286	OE1	GLU A 435	4.816	49.437	188.121	1.00	92.41	O
20	ATOM	3287	OE2	GLU A 435	6.437	47.958	188.240	1.00	101.20	O
	ATOM	3288	N	LYS A 436	8.488	53.586	189.895	1.00	78.50	N
	ATOM	3289	CA	LYS A 436	8.971	54.915	189.499	1.00	76.71	C
	ATOM	3290	C	LYS A 436	8.540	55.350	188.102	1.00	78.55	C
	ATOM	3291	O	LYS A 436	8.275	54.534	187.212	1.00	74.61	O
25	ATOM	3292	CB	LYS A 436	10.500	55.012	189.594	1.00	69.79	C
	ATOM	3293	CG	LYS A 436	11.234	54.239	188.531	1.00	71.25	C
	ATOM	3294	CD	LYS A 436	12.563	54.914	188.219	1.00	69.82	C
	ATOM	3295	CE	LYS A 436	13.362	54.209	187.118	1.00	71.44	C
	ATOM	3296	NZ	LYS A 436	12.848	54.483	185.743	1.00	80.24	N
30	ATOM	3297	N	VAL A 437	8.485	56.661	187.935	1.00	71.05	N
	ATOM	3298	CA	VAL A 437	8.150	57.287	186.675	1.00	86.85	C
	ATOM	3299	C	VAL A 437	9.198	58.370	186.470	1.00	79.80	C
	ATOM	3300	O	VAL A 437	9.181	59.386	187.160	1.00	81.57	O
	ATOM	3301	CB	VAL A 437	6.743	57.891	186.735	1.00	72.78	C
35	ATOM	3302	CG1	VAL A 437	6.544	58.918	185.660	1.00	73.24	C
	ATOM	3303	CG2	VAL A 437	5.735	56.804	186.626	1.00	75.22	C
	ATOM	3304	N	GLY A 438	10.143	58.140	185.563	1.00	71.20	N
	ATOM	3305	CA	GLY A 438	11.243	59.077	185.398	1.00	70.71	C
	ATOM	3306	C	GLY A 438	12.571	58.600	185.966	1.00	71.57	C
40	ATOM	3307	O	GLY A 438	12.757	57.419	186.233	1.00	75.27	O

	ATOM	3308	N	GLU A 439	13.503	59.525	186.142	1.00	66.37	N
	ATOM	3309	CA	GLU A 439	14.846	59.155	186.563	1.00	93.93	C
	ATOM	3310	C	GLU A 439	14.843	58.623	187.984	1.00	78.94	C
	ATOM	3311	O	GLU A 439	14.248	59.231	188.873	1.00	69.29	O
5	ATOM	3312	CB	GLU A 439	15.816	60.340	186.446	1.00	103.14	C
	ATOM	3313	CG	GLU A 439	16.010	60.845	185.027	1.00	109.38	C
	ATOM	3314	CD	GLU A 439	16.272	59.720	184.034	1.00	110.16	C
	ATOM	3315	OE1	GLU A 439	15.346	59.377	183.258	1.00	109.78	O
	ATOM	3316	OE2	GLU A 439	17.404	59.185	184.034	1.00	109.58	O
10	ATOM	3317	N	ALA A 440	15.519	57.497	188.193	1.00	65.44	N
	ATOM	3318	CA	ALA A 440	15.629	56.906	189.518	1.00	69.88	C
	ATOM	3319	C	ALA A 440	16.136	57.897	190.568	1.00	67.31	C
	ATOM	3320	O	ALA A 440	15.626	57.924	191.700	1.00	62.16	O
	ATOM	3321	CB	ALA A 440	16.493	55.681	189.479	1.00	66.15	C
15	ATOM	3322	N	THR A 441	17.119	58.720	190.204	1.00	67.19	N
	ATOM	3323	CA	THR A 441	17.672	59.681	191.168	1.00	69.04	C
	ATOM	3324	C	THR A 441	16.664	60.748	191.516	1.00	68.76	C
	ATOM	3325	O	THR A 441	16.735	61.345	192.577	1.00	66.55	O
	ATOM	3326	CB	THR A 441	18.971	60.369	190.695	1.00	64.74	C
20	ATOM	3327	OG1	THR A 441	19.069	60.294	189.263	1.00	73.12	O
	ATOM	3328	CG2	THR A 441	20.166	59.695	191.338	1.00	64.82	C
	ATOM	3329	N	GLU A 442	15.732	61.002	190.614	1.00	60.07	N
	ATOM	3330	CA	GLU A 442	14.710	61.967	190.917	1.00	69.82	C
	ATOM	3331	C	GLU A 442	13.590	61.351	191.764	1.00	76.14	C
25	ATOM	3332	O	GLU A 442	13.227	61.901	192.820	1.00	75.58	O
	ATOM	3333	CB	GLU A 442	14.189	62.586	189.640	1.00	65.22	C
	ATOM	3334	CG	GLU A 442	14.691	63.974	189.453	1.00	69.43	C
	ATOM	3335	CD	GLU A 442	14.470	64.463	188.062	1.00	86.67	C
	ATOM	3336	OE1	GLU A 442	13.894	63.705	187.248	1.00	89.27	O
30	ATOM	3337	OE2	GLU A 442	14.884	65.608	187.787	1.00	97.89	O
	ATOM	3338	N	THR A 443	13.070	60.202	191.320	1.00	71.04	N
	ATOM	3339	CA	THR A 443	12.025	59.496	192.061	1.00	71.75	C
	ATOM	3340	C	THR A 443	12.469	59.156	193.493	1.00	71.31	C
	ATOM	3341	O	THR A 443	11.638	58.926	194.369	1.00	77.34	O
35	ATOM	3342	CB	THR A 443	11.563	58.210	191.344	1.00	70.09	C
	ATOM	3343	OG1	THR A 443	11.369	58.481	189.962	1.00	72.67	O
	ATOM	3344	CG2	THR A 443	10.242	57.730	191.905	1.00	73.60	C
	ATOM	3345	N	ALA A 444	13.772	59.132	193.737	1.00	61.31	N
	ATOM	3346	CA	ALA A 444	14.255	58.940	195.095	1.00	66.25	C
40	ATOM	3347	C	ALA A 444	14.005	60.177	195.958	1.00	68.03	C

	ATOM	3348	O	ALA A 444	13.712	60.055	197.165	1.00	73.24	O
	ATOM	3349	CB	ALA A 444	15.716	58.566	195.102	1.00	63.65	C
	ATOM	3350	N	LEU A 445	14.121	61.355	195.343	1.00	60.49	N
	ATOM	3351	CA	LEU A 445	13.731	62.603	196.002	1.00	65.90	C
5	ATOM	3352	C	LEU A 445	12.227	62.638	196.224	1.00	78.49	C
	ATOM	3353	O	LEU A 445	11.752	63.156	197.234	1.00	82.32	O
	ATOM	3354	CB	LEU A 445	14.098	63.818	195.154	1.00	71.82	C
	ATOM	3355	CG	LEU A 445	15.554	64.032	194.775	1.00	70.06	C
	ATOM	3356	CD1	LEU A 445	15.695	65.376	194.074	1.00	65.06	C
10	ATOM	3357	CD2	LEU A 445	16.425	63.952	195.998	1.00	55.30	C
	ATOM	3358	N	THR A 446	11.480	62.114	195.262	1.00	58.75	N
	ATOM	3359	CA	THR A 446	10.037	62.095	195.377	1.00	59.75	C
	ATOM	3360	C	THR A 446	9.595	61.273	196.595	1.00	70.27	C
	ATOM	3361	O	THR A 446	8.769	61.727	197.389	1.00	78.57	O
15	ATOM	3362	CB	THR A 446	9.360	61.589	194.066	1.00	73.69	C
	ATOM	3363	OG1	THR A 446	9.453	62.601	193.048	1.00	74.46	O
	ATOM	3364	CG2	THR A 446	7.887	61.239	194.303	1.00	69.19	C
	ATOM	3365	N	THR A 447	10.164	60.081	196.760	1.00	63.59	N
	ATOM	3366	CA	THR A 447	9.809	59.227	197.884	1.00	61.47	C
20	ATOM	3367	C	THR A 447	10.225	59.852	199.210	1.00	63.44	C
	ATOM	3368	O	THR A 447	9.658	59.549	200.243	1.00	61.15	O
	ATOM	3369	CB	THR A 447	10.436	57.834	197.760	1.00	65.75	C
	ATOM	3370	OG1	THR A 447	9.980	57.210	196.556	1.00	63.61	O
	ATOM	3371	CG2	THR A 447	10.048	56.961	198.941	1.00	63.40	C
25	ATOM	3372	N	LEU A 448	11.221	60.732	199.185	1.00	62.38	N
	ATOM	3373	CA	LEU A 448	11.726	61.332	200.421	1.00	62.89	C
	ATOM	3374	C	LEU A 448	10.757	62.379	200.865	1.00	67.60	C
	ATOM	3375	O	LEU A 448	10.522	62.545	202.062	1.00	72.32	O
	ATOM	3376	CB	LEU A 448	13.113	61.966	200.243	1.00	57.17	C
30	ATOM	3377	CG	LEU A 448	13.551	62.907	201.368	1.00	64.64	C
	ATOM	3378	CD1	LEU A 448	13.920	62.121	202.606	1.00	81.60	C
	ATOM	3379	CD2	LEU A 448	14.685	63.797	200.936	1.00	64.25	C
	ATOM	3380	N	VAL A 449	10.180	63.091	199.906	1.00	58.26	N
	ATOM	3381	CA	VAL A 449	9.215	64.103	200.276	1.00	74.96	C
35	ATOM	3382	C	VAL A 449	7.942	63.457	200.845	1.00	70.36	C
	ATOM	3383	O	VAL A 449	7.377	63.944	201.852	1.00	61.96	O
	ATOM	3384	CB	VAL A 449	8.954	65.070	199.141	1.00	58.34	C
	ATOM	3385	CG1	VAL A 449	7.820	66.028	199.508	1.00	63.69	C
	ATOM	3386	CG2	VAL A 449	10.240	65.842	198.861	1.00	64.82	C
40	ATOM	3387	N	GLU A 450	7.534	62.338	200.237	1.00	67.67	N

	ATOM	3388	CA	GLU A 450	6.478	61.503	200.811	1.00	73.51	C
	ATOM	3389	C	GLU A 450	6.795	61.046	202.229	1.00	62.76	C
	ATOM	3390	O	GLU A 450	5.963	61.186	203.119	1.00	67.91	O
	ATOM	3391	CB	GLU A 450	6.147	60.290	199.938	1.00	76.08	C
5	ATOM	3392	CG	GLU A 450	5.451	60.607	198.608	1.00	78.80	C
	ATOM	3393	CD	GLU A 450	4.418	61.730	198.692	1.00	74.89	C
	ATOM	3394	OE2	GLU A 450	4.393	62.569	197.771	1.00	74.20	O
	ATOM	3395	OE1	GLU A 450	3.627	61.782	199.655	1.00	69.96	O
	ATOM	3396	N	LYS A 451	7.983	60.502	202.440	1.00	62.32	N
10	ATOM	3397	CA	LYS A 451	8.367	60.039	203.758	1.00	62.42	C
	ATOM	3398	C	LYS A 451	8.499	61.183	204.742	1.00	61.81	C
	ATOM	3399	O	LYS A 451	8.185	61.021	205.915	1.00	62.72	O
	ATOM	3400	CB	LYS A 451	9.666	59.246	203.717	1.00	62.02	C
	ATOM	3401	CG	LYS A 451	9.539	57.832	203.245	1.00	75.05	C
15	ATOM	3402	CD	LYS A 451	10.923	57.262	203.043	1.00	80.48	C
	ATOM	3403	CE	LYS A 451	10.896	55.971	202.262	1.00	80.95	C
	ATOM	3404	NZ	LYS A 451	12.277	55.497	202.077	1.00	63.86	N
	ATOM	3405	N	MET A 452	8.964	62.343	204.296	1.00	60.50	N
	ATOM	3406	CA	MET A 452	9.123	63.450	205.247	1.00	66.56	C
20	ATOM	3407	C	MET A 452	7.780	64.024	205.676	1.00	67.52	C
	ATOM	3408	O	MET A 452	7.491	64.086	206.848	1.00	69.25	O
	ATOM	3409	CB	MET A 452	10.011	64.561	204.697	1.00	68.52	C
	ATOM	3410	CG	MET A 452	11.456	64.176	204.492	1.00	69.51	C
	ATOM	3411	SD	MET A 452	12.391	65.548	203.806	1.00	56.51	S
25	ATOM	3412	CE	MET A 452	12.291	66.772	205.110	1.00	143.08	C
	ATOM	3413	N	ASN A 453	6.961	64.441	204.722	1.00	76.18	N
	ATOM	3414	CA	ASN A 453	5.627	64.951	205.042	1.00	74.90	C
	ATOM	3415	C	ASN A 453	5.689	66.195	205.923	1.00	67.85	C
	ATOM	3416	O	ASN A 453	5.005	66.293	206.911	1.00	64.02	O
30	ATOM	3417	CB	ASN A 453	4.749	63.852	205.663	1.00	74.67	C
	ATOM	3418	CG	ASN A 453	3.295	64.264	205.809	1.00	75.77	C
	ATOM	3419	OD1	ASN A 453	2.881	65.316	205.316	1.00	70.33	O
	ATOM	3420	ND2	ASN A 453	2.511	63.425	206.488	1.00	67.98	N
	ATOM	3421	N	VAL A 454	6.503	67.156	205.512	1.00	67.31	N
35	ATOM	3422	CA	VAL A 454	6.785	68.362	206.289	1.00	69.28	C
	ATOM	3423	C	VAL A 454	5.584	69.221	206.743	1.00	75.17	C
	ATOM	3424	O	VAL A 454	5.711	70.051	207.653	1.00	63.41	O
	ATOM	3425	CB	VAL A 454	7.813	69.240	205.534	1.00	66.12	C
	ATOM	3426	CG1	VAL A 454	8.943	68.368	205.071	1.00	60.78	C
40	ATOM	3427	CG2	VAL A 454	7.180	69.907	204.345	1.00	60.12	C

	ATOM	3428	N	PHE A 455	4.425	69.034	206.123	1.00	63.97	N
	ATOM	3429	CA	PHE A 455	3.278	69.853	206.478	1.00	74.16	C
	ATOM	3430	C	PHE A 455	2.253	69.042	207.281	1.00	84.77	C
	ATOM	3431	O	PHE A 455	1.225	69.557	207.738	1.00	88.84	O
5	ATOM	3432	CB	PHE A 455	2.669	70.458	205.224	1.00	65.95	C
	ATOM	3433	CG	PHE A 455	3.515	71.516	204.608	1.00	74.70	C
	ATOM	3434	CD1	PHE A 455	3.710	72.712	205.251	1.00	65.07	C
	ATOM	3435	CD2	PHE A 455	4.130	71.315	203.391	1.00	80.81	C
	ATOM	3436	CE1	PHE A 455	4.489	73.692	204.698	1.00	64.19	C
10	ATOM	3437	CE2	PHE A 455	4.927	72.302	202.834	1.00	77.71	C
	ATOM	3438	CZ	PHE A 455	5.102	73.488	203.496	1.00	74.87	C
	ATOM	3439	N	ASN A 456	2.570	67.764	207.448	1.00	86.48	N
	ATOM	3440	CA	ASN A 456	1.779	66.837	208.237	1.00	86.04	C
	ATOM	3441	C	ASN A 456	0.401	66.615	207.663	1.00	86.26	C
15	ATOM	3442	O	ASN A 456	-0.553	66.406	208.402	1.00	94.54	O
	ATOM	3443	CB	ASN A 456	1.712	67.273	209.703	1.00	97.52	C
	ATOM	3444	CG	ASN A 456	3.069	67.212	210.388	1.00	111.98	C
	ATOM	3445	OD1	ASN A 456	3.627	68.233	210.812	1.00	108.25	O
	ATOM	3446	ND2	ASN A 456	3.616	66.006	210.489	1.00	123.40	N
20	ATOM	3447	N	THR A 457	0.295	66.632	206.340	1.00	75.19	N
	ATOM	3448	CA	THR A 457	-1.001	66.395	205.726	1.00	82.74	C
	ATOM	3449	C	THR A 457	-1.419	64.934	205.921	1.00	87.49	C
	ATOM	3450	O	THR A 457	-0.577	64.068	206.168	1.00	73.83	O
	ATOM	3451	CB	THR A 457	-1.068	66.828	204.244	1.00	77.41	C
25	ATOM	3452	OG1	THR A 457	-0.327	65.912	203.447	1.00	73.85	O
	ATOM	3453	CG2	THR A 457	-0.545	68.256	204.059	1.00	70.37	C
	ATOM	3454	N	GLU A 458	-2.724	64.686	205.809	1.00	97.13	N
	ATOM	3455	CA	GLU A 458	-3.352	63.480	206.338	1.00	93.54	C
	ATOM	3456	C	GLU A 458	-3.259	62.318	205.378	1.00	92.96	C
30	ATOM	3457	O	GLU A 458	-4.164	62.102	204.590	1.00	98.45	O
	ATOM	3458	CB	GLU A 458	-4.819	63.785	206.653	1.00	94.46	C
	ATOM	3459	CG	GLU A 458	-5.582	62.704	207.411	1.00	110.51	C
	ATOM	3460	CD	GLU A 458	-6.983	63.188	207.792	1.00	119.36	C
	ATOM	3461	OE1	GLU A 458	-7.191	64.418	207.647	1.00	121.48	O
35	ATOM	3462	OE2	GLU A 458	-7.853	62.369	208.219	1.00	110.56	O
	ATOM	3463	N	VAL A 459	-2.181	61.549	205.453	1.00	75.95	N
	ATOM	3464	CA	VAL A 459	-1.961	60.509	204.458	1.00	75.90	C
	ATOM	3465	C	VAL A 459	-2.279	59.093	204.922	1.00	86.77	C
	ATOM	3466	O	VAL A 459	-2.489	58.201	204.102	1.00	88.04	O
40	ATOM	3467	CB	VAL A 459	-0.537	60.546	203.909	1.00	73.27	C

	ATOM	3468	CG1 VAL A 459	-0.163	61.966	203.542	1.00	89.00	C
	ATOM	3469	CG2 VAL A 459	0.437	59.969	204.912	1.00	72.47	C
	ATOM	3470	N ARG A 460	-2.321	58.884	206.230	1.00	78.49	N
	ATOM	3471	CA ARG A 460	-2.574	57.557	206.775	1.00	101.40	C
5	ATOM	3472	C ARG A 460	-3.859	56.927	206.237	1.00	94.03	C
	ATOM	3473	O ARG A 460	-3.962	55.708	206.128	1.00	89.62	O
	ATOM	3474	CB ARG A 460	-2.584	57.602	208.310	1.00	117.91	C
	ATOM	3475	CG ARG A 460	-3.447	58.704	208.907	1.00	129.74	C
	ATOM	3476	CD ARG A 460	-3.197	58.866	210.403	1.00	136.60	C
10	ATOM	3477	NE ARG A 460	-4.357	59.453	211.074	1.00	144.34	N
	ATOM	3478	CZ ARG A 460	-4.617	60.756	211.128	1.00	143.02	C
	ATOM	3479	NH1 ARG A 460	-3.792	61.622	210.550	1.00	135.39	N
	ATOM	3480	NH2 ARG A 460	-5.704	61.192	211.760	1.00	143.74	N
	ATOM	3481	N ASN A 461	-4.825	57.757	205.868	1.00	98.88	N
15	ATOM	3482	CA ASN A 461	-6.127	57.233	205.469	1.00	113.16	C
	ATOM	3483	C ASN A 461	-6.400	57.156	203.970	1.00	117.92	C
	ATOM	3484	O ASN A 461	-7.465	56.702	203.552	1.00	90.03	O
	ATOM	3485	CB ASN A 461	-7.236	58.007	206.167	1.00	116.17	C
	ATOM	3486	CG ASN A 461	-7.353	57.640	207.615	1.00	116.21	C
20	ATOM	3487	OD1 ASN A 461	-7.137	58.470	208.501	1.00	115.77	O
	ATOM	3488	ND2 ASN A 461	-7.680	56.380	207.872	1.00	118.14	N
	ATOM	3489	N LEU A 462	-5.442	57.596	203.164	1.00	113.92	N
	ATOM	3490	CA LEU A 462	-5.596	57.542	201.723	1.00	109.04	C
	ATOM	3491	C LEU A 462	-5.302	56.135	201.230	1.00	85.73	C
25	ATOM	3492	O LEU A 462	-4.874	55.282	201.991	1.00	124.86	O
	ATOM	3493	CB LEU A 462	-4.672	58.553	201.065	1.00	82.05	C
	ATOM	3494	CG LEU A 462	-4.855	60.003	201.502	1.00	81.25	C
	ATOM	3495	CD1 LEU A 462	-3.640	60.827	201.192	1.00	78.22	C
	ATOM	3496	CD2 LEU A 462	-6.016	60.588	200.800	1.00	83.24	C
30	ATOM	3497	N SER A 463	-5.556	55.890	199.954	1.00	98.88	N
	ATOM	3498	CA SER A 463	-5.275	54.593	199.359	1.00	98.35	C
	ATOM	3499	C SER A 463	-3.881	54.622	198.754	1.00	99.98	C
	ATOM	3500	O SER A 463	-3.334	55.696	198.508	1.00	100.89	O
	ATOM	3501	CB SER A 463	-6.289	54.285	198.260	1.00	97.63	C
35	ATOM	3502	OG SER A 463	-6.012	55.048	197.098	1.00	94.88	O
	ATOM	3503	N LYS A 464	-3.320	53.443	198.497	1.00	100.40	N
	ATOM	3504	CA LYS A 464	-1.999	53.330	197.889	1.00	96.25	C
	ATOM	3505	C LYS A 464	-1.830	54.280	196.707	1.00	92.99	C
	ATOM	3506	O LYS A 464	-0.861	55.039	196.661	1.00	87.02	O
40	ATOM	3507	CB LYS A 464	-1.712	51.888	197.456	1.00	84.85	C

	ATOM	3508	CG	LYS A 464	-1.641	50.876	198.603	1.00	96.46	C
	ATOM	3509	CD	LYS A 464	-0.781	51.373	199.778	1.00	94.32	C
	ATOM	3510	CE	LYS A 464	0.164	50.288	200.294	1.00	92.00	C
	ATOM	3511	NZ	LYS A 464	-0.493	48.943	200.334	1.00	92.58	N
5	ATOM	3512	N	VAL A 465	-2.794	54.261	195.785	1.00	91.46	N
	ATOM	3513	CA	VAL A 465	-2.739	55.089	194.575	1.00	90.30	C
	ATOM	3514	C	VAL A 465	-2.662	56.585	194.862	1.00	92.56	C
	ATOM	3515	O	VAL A 465	-1.776	57.274	194.349	1.00	91.91	O
	ATOM	3516	CB	VAL A 465	-3.953	54.853	193.663	1.00	88.30	C
10	ATOM	3517	CG1	VAL A 465	-3.866	55.739	192.447	1.00	86.32	C
	ATOM	3518	CG2	VAL A 465	-4.035	53.400	193.259	1.00	91.87	C
	ATOM	3519	N	GLU A 466	-3.591	57.091	195.670	1.00	95.82	N
	ATOM	3520	CA	GLU A 466	-3.611	58.520	195.967	1.00	96.13	C
	ATOM	3521	C	GLU A 466	-2.507	58.923	196.952	1.00	96.61	C
15	ATOM	3522	O	GLU A 466	-1.988	60.044	196.882	1.00	96.70	O
	ATOM	3523	CB	GLU A 466	-5.000	58.997	196.415	1.00	92.45	C
	ATOM	3524	CG	GLU A 466	-5.706	58.089	197.380	1.00	106.51	C
	ATOM	3525	CD	GLU A 466	-7.069	58.632	197.769	1.00	129.64	C
	ATOM	3526	OE1	GLU A 466	-7.416	59.726	197.268	1.00	139.81	O
20	ATOM	3527	OE2	GLU A 466	-7.791	57.979	198.566	1.00	133.23	O
	ATOM	3528	N	ARG A 467	-2.137	57.997	197.837	1.00	90.41	N
	ATOM	3529	CA	ARG A 467	-1.011	58.188	198.754	1.00	89.19	C
	ATOM	3530	C	ARG A 467	0.330	58.423	198.024	1.00	88.06	C
	ATOM	3531	O	ARG A 467	1.216	59.098	198.550	1.00	85.08	O
25	ATOM	3532	CB	ARG A 467	-0.896	56.990	199.711	1.00	89.44	C
	ATOM	3533	CG	ARG A 467	0.372	56.940	200.566	1.00	74.53	C
	ATOM	3534	CD	ARG A 467	0.459	58.151	201.477	1.00	92.59	C
	ATOM	3535	NE	ARG A 467	1.670	58.213	202.297	1.00	87.38	N
	ATOM	3536	CZ	ARG A 467	2.566	59.197	202.234	1.00	88.62	C
30	ATOM	3537	NH1	ARG A 467	2.392	60.202	201.388	1.00	68.60	N
	ATOM	3538	NH2	ARG A 467	3.636	59.185	203.022	1.00	88.56	N
	ATOM	3539	N	ALA A 468	0.462	57.890	196.809	1.00	84.25	N
	ATOM	3540	CA	ALA A 468	1.751	57.853	196.113	1.00	79.43	C
	ATOM	3541	C	ALA A 468	2.431	59.203	195.840	1.00	80.94	C
35	ATOM	3542	O	ALA A 468	3.639	59.263	195.695	1.00	68.52	O
	ATOM	3543	CB	ALA A 468	1.633	57.060	194.836	1.00	83.80	C
	ATOM	3544	N	ASN A 469	1.670	60.285	195.769	1.00	82.01	N
	ATOM	3545	CA	ASN A 469	2.276	61.593	195.547	1.00	75.44	C
	ATOM	3546	C	ASN A 469	1.666	62.669	196.423	1.00	71.33	C
40	ATOM	3547	O	ASN A 469	1.857	63.859	196.169	1.00	69.36	O

	ATOM	3548	CB	ASN A 469	2.110	62.011	194.092	1.00	78.49	C
	ATOM	3549	CG	ASN A 469	2.897	61.146	193.144	1.00	85.47	C
	ATOM	3550	OD1	ASN A 469	4.063	61.435	192.842	1.00	91.41	O
	ATOM	3551	ND2	ASN A 469	2.261	60.084	192.648	1.00	85.48	N
5	ATOM	3552	N	ALA A 470	0.931	62.242	197.449	1.00	71.15	N
	ATOM	3553	CA	ALA A 470	0.164	63.149	198.305	1.00	70.24	C
	ATOM	3554	C	ALA A 470	0.949	64.358	198.831	1.00	75.64	C
	ATOM	3555	O	ALA A 470	0.552	65.493	198.611	1.00	72.28	O
	ATOM	3556	CB	ALA A 470	-0.462	62.384	199.440	1.00	71.54	C
10	ATOM	3557	N	CYS A 471	2.063	64.120	199.513	1.00	66.70	N
	ATOM	3558	CA	CYS A 471	2.803	65.211	200.131	1.00	69.09	C
	ATOM	3559	C	CYS A 471	3.549	66.088	199.123	1.00	75.95	C
	ATOM	3560	O	CYS A 471	3.787	67.273	199.367	1.00	74.34	O
	ATOM	3561	CB	CYS A 471	3.773	64.657	201.152	1.00	66.29	C
15	ATOM	3562	SG	CYS A 471	3.055	63.393	202.193	1.00	83.28	S
	ATOM	3563	N	ASN A 472	3.932	65.500	197.996	1.00	78.34	N
	ATOM	3564	CA	ASN A 472	4.542	66.262	196.918	1.00	69.38	C
	ATOM	3565	C	ASN A 472	3.560	67.282	196.344	1.00	74.04	C
	ATOM	3566	O	ASN A 472	3.929	68.423	196.064	1.00	73.99	O
20	ATOM	3567	CB	ASN A 472	5.052	65.327	195.825	1.00	65.00	C
	ATOM	3568	CG	ASN A 472	6.478	64.855	196.072	1.00	72.49	C
	ATOM	3569	OD1	ASN A 472	7.434	65.626	195.920	1.00	71.88	O
	ATOM	3570	ND2	ASN A 472	6.632	63.575	196.430	1.00	68.13	N
	ATOM	3571	N	SER A 473	2.305	66.870	196.185	1.00	74.27	N
25	ATOM	3572	CA	SER A 473	1.274	67.742	195.629	1.00	73.17	C
	ATOM	3573	C	SER A 473	1.016	68.965	196.495	1.00	78.63	C
	ATOM	3574	O	SER A 473	0.727	70.043	195.982	1.00	85.23	O
	ATOM	3575	CB	SER A 473	-0.029	66.984	195.440	1.00	70.07	C
	ATOM	3576	OG	SER A 473	0.213	65.715	194.874	1.00	110.89	O
30	ATOM	3577	N	VAL A 474	1.112	68.796	197.810	1.00	73.93	N
	ATOM	3578	CA	VAL A 474	0.892	69.901	198.733	1.00	74.73	C
	ATOM	3579	C	VAL A 474	1.947	70.976	198.503	1.00	78.45	C
	ATOM	3580	O	VAL A 474	1.654	72.171	198.625	1.00	88.79	O
	ATOM	3581	CB	VAL A 474	0.948	69.452	200.203	1.00	67.33	C
35	ATOM	3582	CG1	VAL A 474	0.651	70.606	201.107	1.00	74.88	C
	ATOM	3583	CG2	VAL A 474	0.009	68.318	200.460	1.00	68.86	C
	ATOM	3584	N	ILE A 475	3.167	70.555	198.165	1.00	73.27	N
	ATOM	3585	CA	ILE A 475	4.237	71.515	197.933	1.00	71.71	C
	ATOM	3586	C	ILE A 475	3.948	72.291	196.654	1.00	72.31	C
40	ATOM	3587	O	ILE A 475	4.218	73.486	196.588	1.00	80.57	O

	ATOM	3588	CB	ILE A 475	5.653	70.863	197.854	1.00	74.91	C
	ATOM	3589	CG1	ILE A 475	5.801	69.708	198.851	1.00	78.86	C
	ATOM	3590	CG2	ILE A 475	6.755	71.893	198.100	1.00	67.85	C
	ATOM	3591	CD1	ILE A 475	5.867	70.120	200.305	1.00	76.27	C
5	ATOM	3592	N	ARG A 476	3.382	71.620	195.650	1.00	68.36	N
	ATOM	3593	CA	ARG A 476	3.054	72.277	194.386	1.00	65.91	C
	ATOM	3594	C	ARG A 476	1.879	73.218	194.547	1.00	72.42	C
	ATOM	3595	O	ARG A 476	1.886	74.321	194.039	1.00	76.25	O
	ATOM	3596	CB	ARG A 476	2.780	71.254	193.303	1.00	69.06	C
10	ATOM	3597	CG	ARG A 476	3.884	70.246	193.169	1.00	75.28	C
	ATOM	3598	CD	ARG A 476	3.728	69.379	191.939	1.00	76.03	C
	ATOM	3599	NE	ARG A 476	4.072	67.997	192.243	1.00	83.99	N
	ATOM	3600	CZ	ARG A 476	3.173	67.053	192.502	1.00	93.11	C
	ATOM	3601	NH1	ARG A 476	1.884	67.359	192.466	1.00	97.16	N
15	ATOM	3602	NH2	ARG A 476	3.554	65.806	192.780	1.00	93.19	N
	ATOM	3603	N	GLN A 477	0.877	72.796	195.296	1.00	83.47	N
	ATOM	3604	CA	GLN A 477	-0.224	73.672	195.677	1.00	94.59	C
	ATOM	3605	C	GLN A 477	0.270	74.945	196.401	1.00	88.03	C
	ATOM	3606	O	GLN A 477	-0.482	75.894	196.613	1.00	90.33	O
20	ATOM	3607	CB	GLN A 477	-1.212	72.872	196.543	1.00	107.62	C
	ATOM	3608	CG	GLN A 477	-2.485	73.599	196.931	1.00	122.67	C
	ATOM	3609	CD	GLN A 477	-3.250	74.123	195.735	1.00	134.05	C
	ATOM	3610	OE1	GLN A 477	-3.071	73.650	194.610	1.00	137.47	O
	ATOM	3611	NE2	GLN A 477	-4.110	75.112	195.971	1.00	138.25	N
25	ATOM	3612	N	LEU A 478	1.551	74.959	196.752	1.00	79.89	N
	ATOM	3613	CA	LEU A 478	2.156	76.055	197.493	1.00	78.08	C
	ATOM	3614	C	LEU A 478	2.979	76.939	196.607	1.00	75.04	C
	ATOM	3615	O	LEU A 478	2.960	78.161	196.748	1.00	74.06	O
	ATOM	3616	CB	LEU A 478	3.098	75.511	198.553	1.00	76.84	C
30	ATOM	3617	CG	LEU A 478	2.933	76.167	199.902	1.00	73.39	C
	ATOM	3618	CD1	LEU A 478	1.515	75.871	200.391	1.00	70.65	C
	ATOM	3619	CD2	LEU A 478	3.981	75.597	200.818	1.00	72.16	C
	ATOM	3620	N	MET A 479	3.751	76.303	195.732	1.00	78.71	N
	ATOM	3621	CA	MET A 479	4.594	77.012	194.772	1.00	80.83	C
35	ATOM	3622	C	MET A 479	4.298	76.579	193.331	1.00	79.15	C
	ATOM	3623	O	MET A 479	4.298	75.384	193.004	1.00	72.24	O
	ATOM	3624	CB	MET A 479	6.085	76.820	195.107	1.00	77.87	C
	ATOM	3625	CG	MET A 479	6.559	77.484	196.422	1.00	73.66	C
	ATOM	3626	SD	MET A 479	6.597	79.301	196.449	1.00	81.46	S
40	ATOM	3627	CE	MET A 479	8.050	79.702	195.491	1.00	66.49	C

	ATOM	3628	N	LYS A 480	4.031	77.564	192.481	1.00	68.11	N
	ATOM	3629	CA	LYS A 480	3.819	77.324	191.057	1.00	86.86	C
	ATOM	3630	C	LYS A 480	5.180	77.281	190.370	1.00	67.82	C
	ATOM	3631	O	LYS A 480	5.861	78.293	190.319	1.00	74.31	O
5	ATOM	3632	CB	LYS A 480	2.961	78.446	190.451	1.00	71.70	C
	ATOM	3633	CG	LYS A 480	2.561	78.231	189.015	1.00	103.82	C
	ATOM	3634	CD	LYS A 480	1.930	79.490	188.410	1.00	111.54	C
	ATOM	3635	CE	LYS A 480	1.693	79.336	186.891	1.00	114.70	C
	ATOM	3636	NZ	LYS A 480	1.706	80.625	186.124	1.00	111.11	N
10	ATOM	3637	N	LYS A 481	5.595	76.121	189.862	1.00	78.22	N
	ATOM	3638	CA	LYS A 481	6.774	76.072	188.990	1.00	73.89	C
	ATOM	3639	C	LYS A 481	6.491	76.679	187.613	1.00	70.66	C
	ATOM	3640	O	LYS A 481	5.608	76.218	186.894	1.00	69.79	O
	ATOM	3641	CB	LYS A 481	7.251	74.647	188.787	1.00	65.19	C
15	ATOM	3642	CG	LYS A 481	8.546	74.595	188.044	1.00	103.32	C
	ATOM	3643	CD	LYS A 481	8.775	73.246	187.461	1.00	64.34	C
	ATOM	3644	CE	LYS A 481	8.802	72.208	188.488	1.00	63.06	C
	ATOM	3645	NZ	LYS A 481	9.286	70.975	187.898	1.00	62.96	N
	ATOM	3646	N	GLU A 482	7.248	77.706	187.247	1.00	70.68	N
20	ATOM	3647	CA	GLU A 482	6.995	78.429	186.013	1.00	70.53	C
	ATOM	3648	C	GLU A 482	7.803	77.861	184.852	1.00	70.55	C
	ATOM	3649	O	GLU A 482	7.259	77.591	183.781	1.00	77.67	O
	ATOM	3650	CB	GLU A 482	7.270	79.916	186.196	1.00	71.22	C
	ATOM	3651	CG	GLU A 482	6.302	80.602	187.144	1.00	71.99	C
25	ATOM	3652	CD	GLU A 482	6.451	82.104	187.099	1.00	89.03	C
	ATOM	3653	OE1	GLU A 482	5.948	82.791	187.996	1.00	73.88	O
	ATOM	3654	OE2	GLU A 482	7.074	82.610	186.154	1.00	85.74	O
	ATOM	3655	N	PHE A 483	9.096	77.672	185.068	1.00	69.11	N
	ATOM	3656	CA	PHE A 483	9.946	77.009	184.100	1.00	68.77	C
30	ATOM	3657	C	PHE A 483	11.109	76.282	184.766	1.00	66.53	C
	ATOM	3658	O	PHE A 483	11.320	76.379	185.975	1.00	65.02	O
	ATOM	3659	CB	PHE A 483	10.455	78.008	183.058	1.00	78.84	C
	ATOM	3660	CG	PHE A 483	10.932	79.309	183.632	1.00	76.74	C
	ATOM	3661	CD1	PHE A 483	10.043	80.345	183.872	1.00	78.01	C
35	ATOM	3662	CD2	PHE A 483	12.273	79.508	183.906	1.00	73.29	C
	ATOM	3663	CE1	PHE A 483	10.483	81.552	184.397	1.00	79.71	C
	ATOM	3664	CE2	PHE A 483	12.725	80.712	184.421	1.00	73.30	C
	ATOM	3665	CZ	PHE A 483	11.831	81.737	184.669	1.00	70.35	C
	ATOM	3666	N	THR A 484	11.877	75.558	183.970	1.00	66.55	N
40	ATOM	3667	CA	THR A 484	13.032	74.833	184.480	1.00	64.80	C

	ATOM	3668	C	THR A 484	14.314	75.245	183.755	1.00	76.59	C
	ATOM	3669	O	THR A 484	14.342	75.319	182.531	1.00	66.77	O
	ATOM	3670	CB	THR A 484	12.820	73.315	184.336	1.00	64.58	C
	ATOM	3671	OG1	THR A 484	11.872	72.864	185.314	1.00	72.00	O
5	ATOM	3672	CG2	THR A 484	14.120	72.559	184.512	1.00	63.41	C
	ATOM	3673	N	LEU A 485	15.374	75.529	184.509	1.00	73.54	N
	ATOM	3674	CA	LEU A 485	16.692	75.720	183.901	1.00	76.64	C
	ATOM	3675	C	LEU A 485	17.410	74.362	183.819	1.00	70.83	C
	ATOM	3676	O	LEU A 485	18.094	73.944	184.749	1.00	66.50	O
10	ATOM	3677	CB	LEU A 485	17.527	76.783	184.650	1.00	63.59	C
	ATOM	3678	CG	LEU A 485	16.865	78.159	184.860	1.00	68.16	C
	ATOM	3679	CD1	LEU A 485	17.848	79.290	185.136	1.00	64.65	C
	ATOM	3680	CD2	LEU A 485	15.971	78.513	183.698	1.00	66.35	C
	ATOM	3681	N	GLU A 486	17.207	73.672	182.703	1.00	69.25	N
15	ATOM	3682	CA	GLU A 486	17.743	72.333	182.474	1.00	72.13	C
	ATOM	3683	C	GLU A 486	19.216	72.224	182.814	1.00	74.82	C
	ATOM	3684	O	GLU A 486	19.983	73.157	182.570	1.00	82.42	O
	ATOM	3685	CB	GLU A 486	17.545	71.948	180.999	1.00	80.71	C
	ATOM	3686	CG	GLU A 486	17.814	73.083	180.009	1.00	92.43	C
20	ATOM	3687	CD	GLU A 486	18.161	72.588	178.609	1.00	104.06	C
	ATOM	3688	OE1	GLU A 486	17.866	71.410	178.300	1.00	110.98	O
	ATOM	3689	OE2	GLU A 486	18.733	73.375	177.817	1.00	101.84	O
	ATOM	3690	N	PHE A 487	19.606	71.079	183.366	1.00	70.73	N
	ATOM	3691	CA	PHE A 487	21.018	70.766	183.648	1.00	67.30	C
25	ATOM	3692	C	PHE A 487	22.018	71.091	182.545	1.00	68.28	C
	ATOM	3693	O	PHE A 487	21.734	70.899	181.369	1.00	78.90	O
	ATOM	3694	CB	PHE A 487	21.157	69.276	183.929	1.00	70.11	C
	ATOM	3695	CG	PHE A 487	22.531	68.873	184.351	1.00	62.22	C
	ATOM	3696	CD1	PHE A 487	23.471	68.482	183.416	1.00	63.68	C
30	ATOM	3697	CD2	PHE A 487	22.888	68.893	185.692	1.00	65.81	C
	ATOM	3698	CE1	PHE A 487	24.743	68.129	183.807	1.00	74.94	C
	ATOM	3699	CE2	PHE A 487	24.158	68.538	186.092	1.00	60.83	C
	ATOM	3700	CZ	PHE A 487	25.084	68.152	185.160	1.00	71.84	C
	ATOM	3701	N	SER A 488	23.203	71.543	182.945	1.00	67.32	N
35	ATOM	3702	CA	SER A 488	24.359	71.701	182.050	1.00	69.17	C
	ATOM	3703	C	SER A 488	25.662	71.316	182.760	1.00	72.33	C
	ATOM	3704	O	SER A 488	25.784	71.511	183.968	1.00	80.68	O
	ATOM	3705	CB	SER A 488	24.458	73.144	181.569	1.00	73.26	C
	ATOM	3706	OG	SER A 488	24.809	74.018	182.619	1.00	65.48	O
40	ATOM	3707	N	ARG A 489	26.644	70.787	182.030	1.00	74.29	N

	ATOM	3708	CA	ARG A 489	27.941	70.455	182.654	1.00	71.27	C
	ATOM	3709	C	ARG A 489	28.734	71.651	183.167	1.00	68.58	C
	ATOM	3710	O	ARG A 489	29.373	71.549	184.209	1.00	65.86	O
	ATOM	3711	CB	ARG A 489	28.830	69.621	181.746	1.00	72.91	C
5	ATOM	3712	CG	ARG A 489	28.545	68.140	181.813	1.00	92.22	C
	ATOM	3713	CD	ARG A 489	29.624	67.390	181.060	1.00	117.70	C
	ATOM	3714	NE	ARG A 489	29.262	66.011	180.739	1.00	130.69	N
	ATOM	3715	CZ	ARG A 489	30.071	65.168	180.102	1.00	137.41	C
	ATOM	3716	NH1	ARG A 489	31.284	65.569	179.733	1.00	137.80	N
10	ATOM	3717	NH2	ARG A 489	29.675	63.926	179.836	1.00	138.01	N
	ATOM	3718	N	ASP A 490	28.673	72.785	182.476	1.00	67.58	N
	ATOM	3719	CA	ASP A 490	29.373	73.978	182.942	1.00	67.79	C
	ATOM	3720	C	ASP A 490	29.111	74.405	184.410	1.00	90.64	C
	ATOM	3721	O	ASP A 490	29.818	75.270	184.933	1.00	96.14	O
15	ATOM	3722	CB	ASP A 490	29.114	75.145	182.006	1.00	69.17	C
	ATOM	3723	CG	ASP A 490	27.838	75.855	182.307	1.00	100.10	C
	ATOM	3724	OD2	ASP A 490	27.903	77.054	182.622	1.00	106.48	O
	ATOM	3725	OD1	ASP A 490	26.767	75.230	182.189	1.00	95.00	O
	ATOM	3726	N	ARG A 491	28.127	73.796	185.078	1.00	75.66	N
20	ATOM	3727	CA	ARG A 491	27.734	74.246	186.408	1.00	67.20	C
	ATOM	3728	C	ARG A 491	27.284	73.105	187.317	1.00	67.07	C
	ATOM	3729	O	ARG A 491	27.157	73.269	188.529	1.00	60.28	O
	ATOM	3730	CB	ARG A 491	26.634	75.296	186.292	1.00	68.47	C
	ATOM	3731	CG	ARG A 491	25.294	74.759	185.886	1.00	75.79	C
25	ATOM	3732	CD	ARG A 491	24.209	75.845	185.861	1.00	78.85	C
	ATOM	3733	NE	ARG A 491	23.320	75.590	184.736	1.00	82.20	N
	ATOM	3734	CZ	ARG A 491	22.097	75.105	184.829	1.00	62.40	C
	ATOM	3735	NH1	ARG A 491	21.559	74.863	186.007	1.00	75.87	N
	ATOM	3736	NH2	ARG A 491	21.416	74.879	183.725	1.00	77.74	N
30	ATOM	3737	N	LYS A 492	27.053	71.950	186.704	1.00	71.46	N
	ATOM	3738	CA	LYS A 492	26.629	70.730	187.398	1.00	68.62	C
	ATOM	3739	C	LYS A 492	25.423	70.904	188.324	1.00	70.95	C
	ATOM	3740	O	LYS A 492	25.430	70.435	189.453	1.00	83.89	O
	ATOM	3741	CB	LYS A 492	27.820	70.076	188.115	1.00	67.96	C
35	ATOM	3742	CG	LYS A 492	28.824	69.432	187.134	1.00	75.53	C
	ATOM	3743	CD	LYS A 492	30.233	69.299	187.711	1.00	90.69	C
	ATOM	3744	CE	LYS A 492	31.062	70.581	187.508	1.00	103.28	C
	ATOM	3745	NZ	LYS A 492	32.362	70.614	188.265	1.00	104.90	N
	ATOM	3746	N	SER A 493	24.383	71.574	187.835	1.00	68.24	N
40	ATOM	3747	CA	SER A 493	23.139	71.731	188.586	1.00	75.42	C

	ATOM	3748	C	SER A 493	21.985	72.045	187.628	1.00	85.58	C
	ATOM	3749	O	SER A 493	22.192	72.229	186.422	1.00	95.39	O
	ATOM	3750	CB	SER A 493	23.260	72.850	189.617	1.00	57.50	C
	ATOM	3751	OG	SER A 493	23.158	74.118	188.989	1.00	60.91	O
5	ATOM	3752	N	MET A 494	20.770	72.093	188.168	1.00	76.05	N
	ATOM	3753	CA	MET A 494	19.595	72.518	187.419	1.00	68.19	C
	ATOM	3754	C	MET A 494	18.773	73.289	188.401	1.00	73.34	C
	ATOM	3755	O	MET A 494	18.993	73.189	189.593	1.00	87.76	O
	ATOM	3756	CB	MET A 494	18.788	71.314	186.970	1.00	59.06	C
10	ATOM	3757	CG	MET A 494	18.169	70.558	188.118	1.00	59.83	C
	ATOM	3758	SD	MET A 494	16.527	69.918	187.784	1.00	92.85	S
	ATOM	3759	CE	MET A 494	15.633	71.460	187.700	1.00	90.16	C
	ATOM	3760	N	SER A 495	17.811	74.057	187.930	1.00	68.11	N
	ATOM	3761	CA	SER A 495	16.983	74.810	188.858	1.00	66.96	C
15	ATOM	3762	C	SER A 495	15.599	75.025	188.276	1.00	73.34	C
	ATOM	3763	O	SER A 495	15.395	74.872	187.067	1.00	72.02	O
	ATOM	3764	CB	SER A 495	17.626	76.156	189.189	1.00	66.91	C
	ATOM	3765	OG	SER A 495	17.077	77.187	188.401	1.00	75.56	O
	ATOM	3766	N	VAL A 496	14.652	75.366	189.146	1.00	59.38	N
20	ATOM	3767	CA	VAL A 496	13.292	75.676	188.729	1.00	60.60	C
	ATOM	3768	C	VAL A 496	12.937	77.074	189.215	1.00	73.02	C
	ATOM	3769	O	VAL A 496	13.320	77.459	190.317	1.00	72.23	O
	ATOM	3770	CB	VAL A 496	12.269	74.652	189.280	1.00	62.45	C
	ATOM	3771	CG1	VAL A 496	12.349	73.364	188.526	1.00	61.56	C
25	ATOM	3772	CG2	VAL A 496	12.512	74.386	190.741	1.00	60.63	C
	ATOM	3773	N	TYR A 497	12.234	77.851	188.401	1.00	62.85	N
	ATOM	3774	CA	TYR A 497	11.843	79.184	188.837	1.00	68.96	C
	ATOM	3775	C	TYR A 497	10.389	79.140	189.309	1.00	69.26	C
	ATOM	3776	O	TYR A 497	9.472	79.028	188.508	1.00	75.79	O
30	ATOM	3777	CB	TYR A 497	12.021	80.177	187.698	1.00	65.48	C
	ATOM	3778	CG	TYR A 497	11.739	81.625	188.041	1.00	75.70	C
	ATOM	3779	CD1	TYR A 497	10.437	82.090	188.154	1.00	75.05	C
	ATOM	3780	CD2	TYR A 497	12.778	82.543	188.209	1.00	75.25	C
	ATOM	3781	CE1	TYR A 497	10.172	83.407	188.455	1.00	78.83	C
35	ATOM	3782	CE2	TYR A 497	12.518	83.877	188.510	1.00	68.29	C
	ATOM	3783	CZ	TYR A 497	11.208	84.293	188.634	1.00	69.68	C
	ATOM	3784	OH	TYR A 497	10.911	85.597	188.923	1.00	104.60	O
	ATOM	3785	N	CYS A 498	10.171	79.223	190.612	1.00	63.71	N
	ATOM	3786	CA	CYS A 498	8.827	79.118	191.135	1.00	64.50	C
40	ATOM	3787	C	CYS A 498	8.311	80.441	191.680	1.00	76.26	C

	ATOM	3788	O	CYS A 498	9.082	81.342	191.990	1.00	71.88	O
	ATOM	3789	CB	CYS A 498	8.794	78.047	192.208	1.00	63.01	C
	ATOM	3790	SG	CYS A 498	9.597	76.531	191.659	1.00	97.55	S
	ATOM	3791	N	SER A 499	6.988	80.538	191.774	1.00	88.49	N
5	ATOM	3792	CA	SER A 499	6.287	81.717	192.271	1.00	90.01	C
	ATOM	3793	C	SER A 499	5.200	81.254	193.244	1.00	89.82	C
	ATOM	3794	O	SER A 499	4.823	80.076	193.245	1.00	81.85	O
	ATOM	3795	CB	SER A 499	5.654	82.460	191.114	1.00	71.32	C
	ATOM	3796	OG	SER A 499	4.790	81.585	190.419	1.00	79.72	O
10	ATOM	3797	N	PRO A 500	4.696	82.172	194.088	1.00	92.54	N
	ATOM	3798	CA	PRO A 500	3.791	81.689	195.131	1.00	90.34	C
	ATOM	3799	C	PRO A 500	2.366	81.423	194.637	1.00	91.27	C
	ATOM	3800	O	PRO A 500	1.872	82.108	193.740	1.00	84.30	O
	ATOM	3801	CB	PRO A 500	3.845	82.805	196.176	1.00	89.90	C
15	ATOM	3802	CG	PRO A 500	4.192	84.026	195.416	1.00	88.93	C
	ATOM	3803	CD	PRO A 500	5.038	83.597	194.265	1.00	92.16	C
	ATOM	3804	N	ALA A 501	1.740	80.416	195.248	1.00	98.08	N
	ATOM	3805	CA	ALA A 501	0.423	79.892	194.880	1.00	98.59	C
	ATOM	3806	C	ALA A 501	-0.603	80.936	194.463	1.00	108.63	C
20	ATOM	3807	O	ALA A 501	-1.008	80.967	193.311	1.00	110.81	O
	ATOM	3808	CB	ALA A 501	-0.135	79.043	196.024	1.00	93.84	C
	ATOM	3809	N	LYS A 502	-1.020	81.779	195.404	1.00	123.99	N
	ATOM	3810	CA	LYS A 502	-2.097	82.746	195.172	1.00	140.42	C
	ATOM	3811	C	LYS A 502	-1.556	84.119	194.760	1.00	149.42	C
25	ATOM	3812	O	LYS A 502	-0.584	84.606	195.339	1.00	149.99	O
	ATOM	3813	CB	LYS A 502	-2.956	82.893	196.438	1.00	145.77	C
	ATOM	3814	CG	LYS A 502	-3.373	81.573	197.093	1.00	147.99	C
	ATOM	3815	CD	LYS A 502	-3.772	81.779	198.555	1.00	152.72	C
	ATOM	3816	CE	LYS A 502	-4.134	80.459	199.242	1.00	154.57	C
30	ATOM	3817	NZ	LYS A 502	-4.594	80.632	200.660	1.00	151.39	N
	ATOM	3818	N	SER A 503	-2.188	84.742	193.766	1.00	159.55	N
	ATOM	3819	CA	SER A 503	-1.774	86.075	193.308	1.00	169.90	C
	ATOM	3820	C	SER A 503	-2.842	86.828	192.497	1.00	190.35	C
	ATOM	3821	O	SER A 503	-3.828	86.243	192.042	1.00	194.21	O
35	ATOM	3822	CB	SER A 503	-0.473	85.995	192.502	1.00	157.45	C
	ATOM	3823	OG	SER A 503	0.615	85.635	193.333	1.00	148.80	O
	ATOM	3824	N	SER A 504	-2.631	88.135	192.334	1.00	201.01	N
	ATOM	3825	CA	SER A 504	-3.466	88.976	191.476	1.00	207.98	C
	ATOM	3826	C	SER A 504	-2.620	90.052	190.786	1.00	216.39	C
40	ATOM	3827	O	SER A 504	-3.011	91.219	190.726	1.00	220.13	O

	ATOM	3828	CB	SER A 504	-4.616	89.615	192.268	1.00205.50	C
	ATOM	3829	OG	SER A 504	-4.140	90.469	193.294	1.00201.44	O
	ATOM	3830	N	ARG A 505	-1.459	89.637	190.275	1.00219.34	N
	ATOM	3831	CA	ARG A 505	-0.513	90.512	189.570	1.00222.28	C
5	ATOM	3832	C	ARG A 505	-0.043	91.724	190.395	1.00221.11	C
	ATOM	3833	O	ARG A 505	-0.557	92.825	190.196	1.00223.88	O
	ATOM	3834	CB	ARG A 505	-1.092	90.953	188.215	1.00228.20	C
	ATOM	3835	CG	ARG A 505	-0.181	91.835	187.358	1.00229.73	C
	ATOM	3836	CD	ARG A 505	1.096	91.126	186.938	1.00226.58	C
10	ATOM	3837	NE	ARG A 505	1.924	91.990	186.103	1.00227.97	N
	ATOM	3838	CZ	ARG A 505	2.783	92.885	186.579	1.00229.49	C
	ATOM	3839	NH1	ARG A 505	2.932	93.031	187.888	1.00228.68	N
	ATOM	3840	NH2	ARG A 505	3.495	93.633	185.749	1.00231.83	N
	ATOM	3841	N	ALA A 506	0.902	91.563	191.330	1.00217.12	N
15	ATOM	3842	CA	ALA A 506	1.503	90.299	191.806	1.00212.38	C
	ATOM	3843	C	ALA A 506	2.164	89.352	190.794	1.00212.03	C
	ATOM	3844	O	ALA A 506	1.667	88.254	190.543	1.00214.47	O
	ATOM	3845	CB	ALA A 506	0.542	89.534	192.740	1.00210.82	C
	ATOM	3846	N	ALA A 507	3.281	89.789	190.222	1.00208.27	N
20	ATOM	3847	CA	ALA A 507	4.142	88.909	189.442	1.00199.78	C
	ATOM	3848	C	ALA A 507	5.443	88.762	190.216	1.00194.23	C
	ATOM	3849	O	ALA A 507	6.512	88.609	189.630	1.00195.36	O
	ATOM	3850	CB	ALA A 507	4.403	89.498	188.064	1.00197.90	C
	ATOM	3851	N	VAL A 508	5.336	88.829	191.543	1.00189.50	N
25	ATOM	3852	CA	VAL A 508	6.493	88.973	192.427	1.00187.51	C
	ATOM	3853	C	VAL A 508	6.423	88.016	193.644	1.00138.55	C
	ATOM	3854	O	VAL A 508	5.445	87.282	193.805	1.00136.99	O
	ATOM	3855	CB	VAL A 508	6.636	90.453	192.902	1.00101.22	C
	ATOM	3856	CG1	VAL A 508	8.109	90.812	193.189	1.00101.62	C
30	ATOM	3857	CG2	VAL A 508	6.040	91.428	191.873	1.00 98.26	C
	ATOM	3858	N	GLY A 509	7.468	88.026	194.484	1.00134.16	N
	ATOM	3859	CA	GLY A 509	7.589	87.151	195.652	1.00115.64	C
	ATOM	3860	C	GLY A 509	8.435	85.899	195.418	1.00101.92	C
	ATOM	3861	O	GLY A 509	8.541	85.045	196.282	1.00 68.86	O
35	ATOM	3862	N	ASN A 510	9.064	85.813	194.248	1.00 90.36	N
	ATOM	3863	CA	ASN A 510	9.541	84.542	193.705	1.00 74.56	C
	ATOM	3864	C	ASN A 510	10.894	84.048	194.220	1.00 73.61	C
	ATOM	3865	O	ASN A 510	11.645	84.779	194.878	1.00 75.19	O
	ATOM	3866	CB	ASN A 510	9.591	84.596	192.170	1.00 74.09	C
40	ATOM	3867	CG	ASN A 510	8.400	85.339	191.549	1.00 81.62	C

	ATOM	3868	OD1 ASN A 510	7.228	84.972	191.740	1.00	72.11	O
	ATOM	3869	ND2 ASN A 510	8.707	86.377	190.773	1.00	82.25	N
	ATOM	3870	N LYS A 511	11.199	82.802	193.866	1.00	64.53	N
	ATOM	3871	CA LYS A 511	12.371	82.087	194.346	1.00	62.71	C
5	ATOM	3872	C LYS A 511	12.864	81.204	193.220	1.00	74.42	C
	ATOM	3873	O LYS A 511	12.106	80.902	192.296	1.00	62.65	O
	ATOM	3874	CB LYS A 511	12.018	81.172	195.525	1.00	61.60	C
	ATOM	3875	CG LYS A 511	11.519	81.860	196.767	1.00	62.37	C
	ATOM	3876	CD LYS A 511	12.417	82.961	197.194	1.00	62.91	C
10	ATOM	3877	CE LYS A 511	12.028	83.485	198.533	1.00	63.67	C
	ATOM	3878	NZ LYS A 511	12.473	84.886	198.677	1.00	96.38	N
	ATOM	3879	N MET A 512	14.134	80.800	193.292	1.00	70.76	N
	ATOM	3880	CA MET A 512	14.653	79.734	192.434	1.00	70.76	C
	ATOM	3881	C MET A 512	15.176	78.618	193.301	1.00	68.26	C
15	ATOM	3882	O MET A 512	15.930	78.857	194.229	1.00	75.40	O
	ATOM	3883	CB MET A 512	15.761	80.229	191.513	1.00	73.09	C
	ATOM	3884	CG MET A 512	15.266	81.104	190.380	1.00	77.54	C
	ATOM	3885	SD MET A 512	16.628	81.887	189.503	1.00	74.38	S
	ATOM	3886	CE MET A 512	17.658	80.456	189.240	1.00	61.76	C
20	ATOM	3887	N PHE A 513	14.765	77.395	193.011	1.00	64.53	N
	ATOM	3888	CA PHE A 513	15.251	76.265	193.774	1.00	63.76	C
	ATOM	3889	C PHE A 513	16.231	75.504	192.909	1.00	66.49	C
	ATOM	3890	O PHE A 513	15.908	75.139	191.779	1.00	66.50	O
	ATOM	3891	CB PHE A 513	14.098	75.392	194.256	1.00	61.85	C
25	ATOM	3892	CG PHE A 513	13.104	76.137	195.117	1.00	64.68	C
	ATOM	3893	CD1 PHE A 513	13.433	76.511	196.414	1.00	58.16	C
	ATOM	3894	CD2 PHE A 513	11.841	76.478	194.617	1.00	70.72	C
	ATOM	3895	CE1 PHE A 513	12.526	77.203	197.190	1.00	62.22	C
	ATOM	3896	CE2 PHE A 513	10.925	77.172	195.384	1.00	62.60	C
30	ATOM	3897	CZ PHE A 513	11.262	77.536	196.667	1.00	64.49	C
	ATOM	3898	N VAL A 514	17.438	75.315	193.444	1.00	65.56	N
	ATOM	3899	CA VAL A 514	18.584	74.812	192.713	1.00	55.70	C
	ATOM	3900	C VAL A 514	19.041	73.515	193.318	1.00	54.92	C
	ATOM	3901	O VAL A 514	19.202	73.412	194.530	1.00	54.40	O
35	ATOM	3902	CB VAL A 514	19.746	75.780	192.871	1.00	64.59	C
	ATOM	3903	CG1 VAL A 514	20.976	75.235	192.205	1.00	61.97	C
	ATOM	3904	CG2 VAL A 514	19.388	77.128	192.318	1.00	68.81	C
	ATOM	3905	N LYS A 515	19.267	72.517	192.486	1.00	55.08	N
	ATOM	3906	CA LYS A 515	19.816	71.262	192.975	1.00	59.57	C
40	ATOM	3907	C LYS A 515	20.901	70.733	192.034	1.00	66.11	C

	ATOM	3908	O	LYS A 515	20.764	70.784	190.802	1.00	69.84	O
	ATOM	3909	CB	LYS A 515	18.707	70.218	193.169	1.00	54.48	C
	ATOM	3910	CG	LYS A 515	18.915	68.918	192.389	1.00	59.20	C
	ATOM	3911	CD	LYS A 515	17.716	68.009	192.471	1.00	55.11	C
5	ATOM	3912	CE	LYS A 515	17.138	67.783	191.109	1.00	61.61	C
	ATOM	3913	NZ	LYS A 515	17.325	66.392	190.623	1.00	67.60	N
	ATOM	3914	N	GLY A 516	21.985	70.228	192.613	1.00	65.44	N
	ATOM	3915	CA	GLY A 516	23.006	69.586	191.810	1.00	65.98	C
	ATOM	3916	C	GLY A 516	24.142	69.017	192.630	1.00	65.21	C
10	ATOM	3917	O	GLY A 516	23.947	68.598	193.764	1.00	74.35	O
	ATOM	3918	N	ALA A 517	25.337	69.011	192.050	1.00	59.81	N
	ATOM	3919	CA	ALA A 517	26.508	68.486	192.711	1.00	57.05	C
	ATOM	3920	C	ALA A 517	27.159	69.599	193.501	1.00	83.33	C
	ATOM	3921	O	ALA A 517	27.086	70.768	193.114	1.00	88.56	O
15	ATOM	3922	CB	ALA A 517	27.469	67.933	191.699	1.00	60.65	C
	ATOM	3923	N	PRO A 518	27.791	69.239	194.623	1.00	74.58	N
	ATOM	3924	CA	PRO A 518	28.479	70.191	195.487	1.00	75.94	C
	ATOM	3925	C	PRO A 518	29.589	70.919	194.749	1.00	76.34	C
	ATOM	3926	O	PRO A 518	29.803	72.104	195.031	1.00	82.15	O
20	ATOM	3927	CB	PRO A 518	29.055	69.297	196.579	1.00	78.22	C
	ATOM	3928	CG	PRO A 518	28.146	68.139	196.614	1.00	57.11	C
	ATOM	3929	CD	PRO A 518	27.727	67.902	195.229	1.00	57.10	C
	ATOM	3930	N	GLU A 519	30.271	70.226	193.832	1.00	73.83	N
	ATOM	3931	CA	GLU A 519	31.339	70.836	193.035	1.00	76.25	C
25	ATOM	3932	C	GLU A 519	30.786	72.098	192.413	1.00	66.73	C
	ATOM	3933	O	GLU A 519	31.406	73.168	192.468	1.00	64.40	O
	ATOM	3934	CB	GLU A 519	31.835	69.916	191.904	1.00	77.51	C
	ATOM	3935	CG	GLU A 519	32.459	68.604	192.335	1.00	85.07	C
	ATOM	3936	CD	GLU A 519	31.423	67.539	192.685	1.00	99.57	C
30	ATOM	3937	OE1	GLU A 519	30.582	67.771	193.586	1.00	99.28	O
	ATOM	3938	OE2	GLU A 519	31.453	66.462	192.057	1.00	105.78	O
	ATOM	3939	N	GLY A 520	29.593	71.965	191.847	1.00	65.47	N
	ATOM	3940	CA	GLY A 520	28.995	73.045	191.106	1.00	59.80	C
	ATOM	3941	C	GLY A 520	28.312	74.042	191.999	1.00	69.80	C
35	ATOM	3942	O	GLY A 520	28.478	75.248	191.805	1.00	65.64	O
	ATOM	3943	N	VAL A 521	27.556	73.540	192.976	1.00	57.89	N
	ATOM	3944	CA	VAL A 521	26.612	74.369	193.709	1.00	57.23	C
	ATOM	3945	C	VAL A 521	27.260	75.264	194.755	1.00	70.89	C
	ATOM	3946	O	VAL A 521	26.919	76.443	194.876	1.00	70.76	O
40	ATOM	3947	CB	VAL A 521	25.544	73.513	194.393	1.00	56.11	C

	ATOM	3948	CG1 VAL A 521	24.692	74.358	195.332	1.00	55.68	C
	ATOM	3949	CG2 VAL A 521	24.686	72.864	193.354	1.00	55.90	C
	ATOM	3950	N ILE A 522	28.204	74.712	195.506	1.00	70.84	N
	ATOM	3951	CA ILE A 522	28.700	75.404	196.682	1.00	71.54	C
5	ATOM	3952	C ILE A 522	29.444	76.706	196.401	1.00	67.06	C
	ATOM	3953	O ILE A 522	29.184	77.697	197.067	1.00	60.04	O
	ATOM	3954	CB ILE A 522	29.472	74.457	197.593	1.00	76.30	C
	ATOM	3955	CG1 ILE A 522	28.487	73.478	198.233	1.00	74.63	C
	ATOM	3956	CG2 ILE A 522	30.226	75.225	198.669	1.00	73.10	C
10	ATOM	3957	CD1 ILE A 522	29.077	72.703	199.381	1.00	81.32	C
	ATOM	3958	N ASP A 523	30.330	76.735	195.408	1.00	60.72	N
	ATOM	3959	CA ASP A 523	30.971	78.002	195.052	1.00	62.18	C
	ATOM	3960	C ASP A 523	29.953	79.126	194.818	1.00	79.57	C
	ATOM	3961	O ASP A 523	30.242	80.302	195.020	1.00	90.64	O
15	ATOM	3962	CB ASP A 523	31.848	77.835	193.822	1.00	71.35	C
	ATOM	3963	CG ASP A 523	32.318	79.181	193.236	1.00	77.99	C
	ATOM	3964	OD2 ASP A 523	31.792	79.589	192.170	1.00	84.17	O
	ATOM	3965	OD1 ASP A 523	33.227	79.819	193.823	1.00	70.52	O
	ATOM	3966	N ARG A 524	28.745	78.755	194.419	1.00	64.38	N
20	ATOM	3967	CA ARG A 524	27.754	79.735	194.034	1.00	61.64	C
	ATOM	3968	C ARG A 524	26.819	80.124	195.182	1.00	68.59	C
	ATOM	3969	O ARG A 524	25.814	80.805	194.958	1.00	71.57	O
	ATOM	3970	CB ARG A 524	26.953	79.205	192.856	1.00	60.46	C
	ATOM	3971	CG ARG A 524	27.694	79.201	191.567	1.00	61.56	C
25	ATOM	3972	CD ARG A 524	26.782	78.889	190.395	1.00	61.42	C
	ATOM	3973	NE ARG A 524	26.748	77.470	190.080	1.00	60.66	N
	ATOM	3974	CZ ARG A 524	25.637	76.757	189.964	1.00	66.21	C
	ATOM	3975	NH1 ARG A 524	24.466	77.339	190.137	1.00	59.40	N
	ATOM	3976	NH2 ARG A 524	25.699	75.464	189.669	1.00	61.86	N
30	ATOM	3977	N CYS A 525	27.142	79.693	196.404	1.00	69.57	N
	ATOM	3978	CA CYS A 525	26.347	80.043	197.589	1.00	69.77	C
	ATOM	3979	C CYS A 525	27.008	81.133	198.422	1.00	72.14	C
	ATOM	3980	O CYS A 525	28.106	80.938	198.937	1.00	80.97	O
	ATOM	3981	CB CYS A 525	26.156	78.834	198.491	1.00	58.61	C
35	ATOM	3982	SG CYS A 525	25.193	77.534	197.799	1.00	78.74	S
	ATOM	3983	N ASN A 526	26.337	82.271	198.575	1.00	63.73	N
	ATOM	3984	CA ASN A 526	26.842	83.332	199.435	1.00	63.37	C
	ATOM	3985	C ASN A 526	26.303	83.246	200.835	1.00	68.83	C
	ATOM	3986	O ASN A 526	26.852	83.828	201.761	1.00	75.92	O
40	ATOM	3987	CB ASN A 526	26.490	84.694	198.876	1.00	67.16	C

	ATOM	3988	CG	ASN A 526	27.225	84.991	197.623	1.00	71.33	C
	ATOM	3989	OD1	ASN A 526	28.147	84.267	197.265	1.00	78.26	O
	ATOM	3990	ND2	ASN A 526	26.826	86.051	196.929	1.00	71.97	N
	ATOM	3991	N	TYR A 527	25.209	82.525	200.990	1.00	72.25	N
5	ATOM	3992	CA	TYR A 527	24.572	82.447	202.279	1.00	66.68	C
	ATOM	3993	C	TYR A 527	24.304	81.019	202.664	1.00	62.87	C
	ATOM	3994	O	TYR A 527	24.374	80.102	201.863	1.00	59.31	O
	ATOM	3995	CB	TYR A 527	23.260	83.202	202.261	1.00	70.13	C
	ATOM	3996	CG	TYR A 527	23.361	84.636	201.804	1.00	78.98	C
10	ATOM	3997	CD1	TYR A 527	23.832	85.629	202.664	1.00	77.11	C
	ATOM	3998	CD2	TYR A 527	22.941	85.007	200.521	1.00	73.55	C
	ATOM	3999	CE1	TYR A 527	23.892	86.946	202.256	1.00	77.78	C
	ATOM	4000	CE2	TYR A 527	23.005	86.317	200.102	1.00	69.93	C
	ATOM	4001	CZ	TYR A 527	23.477	87.281	200.973	1.00	82.21	C
15	ATOM	4002	OH	TYR A 527	23.537	88.587	200.561	1.00	95.17	O
	ATOM	4003	N	VAL A 528	23.978	80.852	203.926	1.00	68.63	N
	ATOM	4004	CA	VAL A 528	23.636	79.563	204.456	1.00	67.39	C
	ATOM	4005	C	VAL A 528	22.279	79.729	205.148	1.00	70.23	C
	ATOM	4006	O	VAL A 528	22.036	80.737	205.815	1.00	65.40	O
20	ATOM	4007	CB	VAL A 528	24.753	79.128	205.392	1.00	60.30	C
	ATOM	4008	CG1	VAL A 528	24.237	78.249	206.477	1.00	85.86	C
	ATOM	4009	CG2	VAL A 528	25.841	78.456	204.580	1.00	79.77	C
	ATOM	4010	N	ARG A 529	21.361	78.790	204.938	1.00	73.71	N
	ATOM	4011	CA	ARG A 529	20.108	78.843	205.685	1.00	68.66	C
25	ATOM	4012	C	ARG A 529	20.190	78.073	207.012	1.00	62.80	C
	ATOM	4013	O	ARG A 529	20.430	76.854	207.049	1.00	59.84	O
	ATOM	4014	CB	ARG A 529	18.889	78.413	204.850	1.00	63.64	C
	ATOM	4015	CG	ARG A 529	17.571	78.587	205.628	1.00	61.49	C
	ATOM	4016	CD	ARG A 529	16.448	79.224	204.817	1.00	60.13	C
30	ATOM	4017	NE	ARG A 529	16.835	80.445	204.114	1.00	65.00	N
	ATOM	4018	CZ	ARG A 529	16.865	80.566	202.787	1.00	69.10	C
	ATOM	4019	NH1	ARG A 529	16.528	79.549	202.002	1.00	58.01	N
	ATOM	4020	NH2	ARG A 529	17.242	81.706	202.234	1.00	72.99	N
	ATOM	4021	N	VAL A 530	20.010	78.831	208.087	1.00	62.45	N
35	ATOM	4022	CA	VAL A 530	19.937	78.312	209.442	1.00	66.88	C
	ATOM	4023	C	VAL A 530	18.507	78.472	209.908	1.00	73.15	C
	ATOM	4024	O	VAL A 530	18.157	79.532	210.433	1.00	63.11	O
	ATOM	4025	CB	VAL A 530	20.796	79.156	210.412	1.00	63.91	C
	ATOM	4026	CG1	VAL A 530	20.986	78.429	211.693	1.00	65.19	C
40	ATOM	4027	CG2	VAL A 530	22.146	79.462	209.806	1.00	72.08	C

	ATOM	4028	N	GLY A 531	17.680	77.445	209.700	1.00	70.53	N
	ATOM	4029	CA	GLY A 531	16.280	77.498	210.105	1.00	68.70	C
	ATOM	4030	C	GLY A 531	15.373	78.251	209.143	1.00	71.83	C
	ATOM	4031	O	GLY A 531	14.819	77.663	208.218	1.00	76.87	O
5	ATOM	4032	N	THR A 532	15.181	79.546	209.375	1.00	75.19	N
	ATOM	4033	CA	THR A 532	14.529	80.402	208.379	1.00	75.98	C
	ATOM	4034	C	THR A 532	15.365	81.659	208.210	1.00	79.23	C
	ATOM	4035	O	THR A 532	15.067	82.514	207.378	1.00	83.50	O
	ATOM	4036	CB	THR A 532	13.093	80.850	208.760	1.00	68.17	C
10	ATOM	4037	OG1	THR A 532	13.141	82.122	209.422	1.00	66.08	O
	ATOM	4038	CG2	THR A 532	12.389	79.820	209.623	1.00	64.31	C
	ATOM	4039	N	THR A 533	16.404	81.783	209.024	1.00	78.72	N
	ATOM	4040	CA	THR A 533	17.252	82.950	208.957	1.00	65.31	C
	ATOM	4041	C	THR A 533	18.349	82.628	207.971	1.00	82.69	C
15	ATOM	4042	O	THR A 533	18.455	81.487	207.517	1.00	78.20	O
	ATOM	4043	CB	THR A 533	17.851	83.225	210.311	1.00	78.23	C
	ATOM	4044	OG1	THR A 533	18.483	82.030	210.804	1.00	80.03	O
	ATOM	4045	CG2	THR A 533	16.761	83.642	211.271	1.00	81.13	C
	ATOM	4046	N	ARG A 534	19.165	83.614	207.619	1.00	64.88	N
20	ATOM	4047	CA	ARG A 534	20.325	83.312	206.783	1.00	66.87	C
	ATOM	4048	C	ARG A 534	21.541	84.095	207.228	1.00	68.37	C
	ATOM	4049	O	ARG A 534	21.447	85.202	207.742	1.00	75.16	O
	ATOM	4050	CB	ARG A 534	20.055	83.517	205.280	1.00	65.96	C
	ATOM	4051	CG	ARG A 534	20.383	84.909	204.739	1.00	64.70	C
25	ATOM	4052	CD	ARG A 534	19.983	85.021	203.297	1.00	64.12	C
	ATOM	4053	NE	ARG A 534	20.305	86.325	202.732	1.00	77.13	N
	ATOM	4054	CZ	ARG A 534	19.838	86.771	201.566	1.00	77.94	C
	ATOM	4055	NH1	ARG A 534	19.009	86.024	200.846	1.00	79.06	N
	ATOM	4056	NH2	ARG A 534	20.183	87.972	201.119	1.00	78.07	N
30	ATOM	4057	N	VAL A 535	22.697	83.489	207.040	1.00	67.22	N
	ATOM	4058	CA	VAL A 535	23.931	84.098	207.446	1.00	68.83	C
	ATOM	4059	C	VAL A 535	24.958	83.818	206.370	1.00	75.01	C
	ATOM	4060	O	VAL A 535	24.854	82.819	205.650	1.00	72.74	O
	ATOM	4061	CB	VAL A 535	24.392	83.519	208.771	1.00	70.15	C
35	ATOM	4062	CG1	VAL A 535	23.523	84.049	209.876	1.00	70.72	C
	ATOM	4063	CG2	VAL A 535	24.345	82.003	208.724	1.00	66.45	C
	ATOM	4064	N	PRO A 536	25.929	84.726	206.230	1.00	76.36	N
	ATOM	4065	CA	PRO A 536	27.006	84.637	205.252	1.00	73.47	C
	ATOM	4066	C	PRO A 536	27.719	83.297	205.236	1.00	75.03	C
40	ATOM	4067	O	PRO A 536	28.133	82.812	206.288	1.00	79.98	O

	ATOM	4068	CB	PRO A 536	27.945	85.733	205.719	1.00	72.67	C
	ATOM	4069	CG	PRO A 536	27.024	86.773	206.217	1.00	71.46	C
	ATOM	4070	CD	PRO A 536	25.876	86.063	206.842	1.00	69.54	C
	ATOM	4071	N	MET A 537	27.837	82.703	204.051	1.00	72.32	N
5	ATOM	4072	CA	MET A 537	28.689	81.536	203.872	1.00	74.04	C
	ATOM	4073	C	MET A 537	30.130	81.975	204.119	1.00	74.54	C
	ATOM	4074	O	MET A 537	30.493	83.123	203.852	1.00	76.54	O
	ATOM	4075	CB	MET A 537	28.517	80.926	202.471	1.00	69.75	C
	ATOM	4076	CG	MET A 537	29.467	79.773	202.155	1.00	62.58	C
10	ATOM	4077	SD	MET A 537	29.046	78.205	202.934	1.00	81.92	S
	ATOM	4078	CE	MET A 537	27.960	77.496	201.712	1.00	59.50	C
	ATOM	4079	N	THR A 538	30.935	81.078	204.672	1.00	72.29	N
	ATOM	4080	CA	THR A 538	32.319	81.382	204.976	1.00	80.79	C
	ATOM	4081	C	THR A 538	33.180	80.160	204.748	1.00	83.19	C
15	ATOM	4082	O	THR A 538	32.668	79.067	204.506	1.00	85.31	O
	ATOM	4083	CB	THR A 538	32.502	81.822	206.433	1.00	82.52	C
	ATOM	4084	OG1	THR A 538	32.015	80.800	207.308	1.00	77.92	O
	ATOM	4085	CG2	THR A 538	31.775	83.128	206.702	1.00	70.79	C
	ATOM	4086	N	GLY A 539	34.490	80.359	204.834	1.00	80.50	N
20	ATOM	4087	CA	GLY A 539	35.438	79.296	204.600	1.00	70.42	C
	ATOM	4088	C	GLY A 539	35.155	78.020	205.364	1.00	83.09	C
	ATOM	4089	O	GLY A 539	34.864	77.002	204.752	1.00	68.15	O
	ATOM	4090	N	PRO A 540	35.253	78.063	206.707	1.00	82.89	N
	ATOM	4091	CA	PRO A 540	35.142	76.848	207.515	1.00	70.47	C
25	ATOM	4092	C	PRO A 540	33.771	76.215	207.427	1.00	80.95	C
	ATOM	4093	O	PRO A 540	33.674	75.017	207.665	1.00	82.47	O
	ATOM	4094	CB	PRO A 540	35.393	77.351	208.927	1.00	97.13	C
	ATOM	4095	CG	PRO A 540	36.183	78.565	208.748	1.00	74.23	C
	ATOM	4096	CD	PRO A 540	35.671	79.209	207.528	1.00	72.83	C
30	ATOM	4097	N	VAL A 541	32.738	76.996	207.104	1.00	78.70	N
	ATOM	4098	CA	VAL A 541	31.404	76.442	206.895	1.00	75.81	C
	ATOM	4099	C	VAL A 541	31.431	75.615	205.624	1.00	70.77	C
	ATOM	4100	O	VAL A 541	31.026	74.457	205.624	1.00	68.28	O
	ATOM	4101	CB	VAL A 541	30.317	77.527	206.745	1.00	72.96	C
35	ATOM	4102	CG1	VAL A 541	28.994	76.884	206.412	1.00	71.92	C
	ATOM	4103	CG2	VAL A 541	30.179	78.334	207.989	1.00	65.73	C
	ATOM	4104	N	LYS A 542	31.903	76.228	204.542	1.00	72.37	N
	ATOM	4105	CA	LYS A 542	32.133	75.528	203.280	1.00	79.26	C
	ATOM	4106	C	LYS A 542	32.915	74.232	203.475	1.00	79.37	C
40	ATOM	4107	O	LYS A 542	32.459	73.156	203.087	1.00	62.56	O

	ATOM	4108	CB	LYS A 542	32.884	76.438	202.313	1.00	79.26	C
	ATOM	4109	CG	LYS A 542	32.781	76.010	200.889	1.00	80.62	C
	ATOM	4110	CD	LYS A 542	33.262	77.086	199.943	1.00	80.62	C
	ATOM	4111	CE	LYS A 542	32.597	78.412	200.207	1.00	73.53	C
5	ATOM	4112	NZ	LYS A 542	33.402	79.480	199.559	1.00	73.86	N
	ATOM	4113	N	GLU A 543	34.086	74.345	204.099	1.00	77.39	N
	ATOM	4114	CA	GLU A 543	34.937	73.188	204.382	1.00	75.96	C
	ATOM	4115	C	GLU A 543	34.194	72.093	205.165	1.00	70.49	C
	ATOM	4116	O	GLU A 543	34.459	70.901	204.960	1.00	68.55	O
10	ATOM	4117	CB	GLU A 543	36.217	73.607	205.122	1.00	68.93	C
	ATOM	4118	CG	GLU A 543	37.127	74.581	204.376	1.00	119.98	C
	ATOM	4119	CD	GLU A 543	38.057	73.895	203.368	1.00	123.85	C
	ATOM	4120	OE1	GLU A 543	37.849	72.689	203.089	1.00	126.26	O
	ATOM	4121	OE2	GLU A 543	38.998	74.558	202.853	1.00	122.90	O
15	ATOM	4122	N	LYS A 544	33.261	72.499	206.036	1.00	71.28	N
	ATOM	4123	CA	LYS A 544	32.548	71.577	206.929	1.00	64.71	C
	ATOM	4124	C	LYS A 544	31.556	70.751	206.159	1.00	69.98	C
	ATOM	4125	O	LYS A 544	31.513	69.535	206.286	1.00	74.79	O
	ATOM	4126	CB	LYS A 544	31.805	72.335	208.031	1.00	65.21	C
20	ATOM	4127	CG	LYS A 544	30.837	71.475	208.859	1.00	64.32	C
	ATOM	4128	CD	LYS A 544	31.513	70.224	209.387	1.00	83.47	C
	ATOM	4129	CE	LYS A 544	30.647	69.411	210.337	1.00	86.10	C
	ATOM	4130	NZ	LYS A 544	31.320	68.123	210.720	1.00	66.79	N
	ATOM	4131	N	ILE A 545	30.725	71.435	205.389	1.00	61.53	N
25	ATOM	4132	CA	ILE A 545	29.825	70.788	204.466	1.00	60.01	C
	ATOM	4133	C	ILE A 545	30.602	69.814	203.583	1.00	80.94	C
	ATOM	4134	O	ILE A 545	30.224	68.646	203.479	1.00	77.04	O
	ATOM	4135	CB	ILE A 545	29.135	71.833	203.592	1.00	59.02	C
	ATOM	4136	CG1	ILE A 545	28.337	72.793	204.467	1.00	68.86	C
30	ATOM	4137	CG2	ILE A 545	28.251	71.165	202.547	1.00	57.74	C
	ATOM	4138	CD1	ILE A 545	28.009	74.112	203.800	1.00	72.77	C
	ATOM	4139	N	LEU A 546	31.696	70.273	202.972	1.00	61.27	N
	ATOM	4140	CA	LEU A 546	32.410	69.420	202.021	1.00	83.88	C
	ATOM	4141	C	LEU A 546	32.941	68.155	202.689	1.00	79.66	C
35	ATOM	4142	O	LEU A 546	32.891	67.059	202.116	1.00	72.62	O
	ATOM	4143	CB	LEU A 546	33.523	70.184	201.294	1.00	62.89	C
	ATOM	4144	CG	LEU A 546	33.050	71.314	200.384	1.00	78.43	C
	ATOM	4145	CD1	LEU A 546	34.147	72.310	200.082	1.00	63.55	C
	ATOM	4146	CD2	LEU A 546	32.418	70.777	199.104	1.00	61.09	C
40	ATOM	4147	N	SER A 547	33.416	68.307	203.917	1.00	64.00	N

	ATOM	4148	CA	SER A 547	34.049	67.206	204.600	1.00	75.62	C
	ATOM	4149	C	SER A 547	33.053	66.108	204.961	1.00	75.64	C
	ATOM	4150	O	SER A 547	33.421	64.932	205.006	1.00	80.22	O
	ATOM	4151	CB	SER A 547	34.781	67.708	205.823	1.00	67.12	C
5	ATOM	4152	OG	SER A 547	33.885	68.370	206.688	1.00	89.68	O
	ATOM	4153	N	VAL A 548	31.796	66.480	205.207	1.00	72.69	N
	ATOM	4154	CA	VAL A 548	30.756	65.488	205.493	1.00	79.97	C
	ATOM	4155	C	VAL A 548	30.362	64.772	204.208	1.00	87.94	C
	ATOM	4156	O	VAL A 548	30.158	63.554	204.204	1.00	95.75	O
10	ATOM	4157	CB	VAL A 548	29.482	66.113	206.108	1.00	81.17	C
	ATOM	4158	CG1	VAL A 548	28.410	65.042	206.363	1.00	60.93	C
	ATOM	4159	CG2	VAL A 548	29.811	66.840	207.367	1.00	62.35	C
	ATOM	4160	N	ILE A 549	30.248	65.528	203.117	1.00	79.77	N
	ATOM	4161	CA	ILE A 549	29.946	64.917	201.833	1.00	71.75	C
15	ATOM	4162	C	ILE A 549	31.028	63.891	201.513	1.00	69.97	C
	ATOM	4163	O	ILE A 549	30.730	62.814	201.005	1.00	76.07	O
	ATOM	4164	CB	ILE A 549	29.822	65.954	200.695	1.00	70.27	C
	ATOM	4165	CG1	ILE A 549	28.856	67.068	201.079	1.00	70.23	C
	ATOM	4166	CG2	ILE A 549	29.296	65.319	199.457	1.00	58.94	C
20	ATOM	4167	CD1	ILE A 549	28.715	68.130	200.030	1.00	67.64	C
	ATOM	4168	N	LYS A 550	32.278	64.194	201.851	1.00	65.78	N
	ATOM	4169	CA	LYS A 550	33.332	63.225	201.606	1.00	64.99	C
	ATOM	4170	C	LYS A 550	33.144	61.936	202.386	1.00	69.04	C
	ATOM	4171	O	LYS A 550	33.252	60.851	201.821	1.00	70.71	O
25	ATOM	4172	CB	LYS A 550	34.717	63.795	201.890	1.00	66.63	C
	ATOM	4173	CG	LYS A 550	35.817	62.778	201.557	1.00	68.78	C
	ATOM	4174	CD	LYS A 550	37.209	63.279	201.838	1.00	70.76	C
	ATOM	4175	CE	LYS A 550	37.461	64.557	201.107	1.00	93.11	C
	ATOM	4176	NZ	LYS A 550	38.830	65.002	201.433	1.00	104.53	N
30	ATOM	4177	N	GLU A 551	32.857	62.067	203.681	1.00	74.15	N
	ATOM	4178	CA	GLU A 551	32.758	60.926	204.590	1.00	74.72	C
	ATOM	4179	C	GLU A 551	31.627	59.986	204.199	1.00	75.29	C
	ATOM	4180	O	GLU A 551	31.721	58.768	204.377	1.00	73.93	O
	ATOM	4181	CB	GLU A 551	32.537	61.415	206.012	1.00	79.72	C
35	ATOM	4182	CG	GLU A 551	32.630	60.310	207.046	1.00	99.10	C
	ATOM	4183	CD	GLU A 551	32.387	60.804	208.465	1.00	114.16	C
	ATOM	4184	OE1	GLU A 551	33.248	60.542	209.344	1.00	119.64	O
	ATOM	4185	OE2	GLU A 551	31.332	61.445	208.695	1.00	114.63	O
	ATOM	4186	N	TRP A 552	30.560	60.572	203.666	1.00	64.39	N
40	ATOM	4187	CA	TRP A 552	29.416	59.819	203.185	1.00	72.20	C

	ATOM	4188	C	TRP A 552	29.757	59.051	201.917	1.00	79.82	C
	ATOM	4189	O	TRP A 552	29.247	57.951	201.695	1.00	85.59	O
	ATOM	4190	CB	TRP A 552	28.234	60.755	202.923	1.00	68.59	C
	ATOM	4191	CG	TRP A 552	27.533	61.196	204.174	1.00	61.24	C
5	ATOM	4192	CD1	TRP A 552	27.913	60.936	205.446	1.00	67.12	C
	ATOM	4193	CD2	TRP A 552	26.325	61.966	204.265	1.00	59.80	C
	ATOM	4194	NE1	TRP A 552	27.032	61.500	206.332	1.00	62.33	N
	ATOM	4195	CE2	TRP A 552	26.054	62.138	205.633	1.00	64.97	C
	ATOM	4196	CE3	TRP A 552	25.460	62.521	203.329	1.00	58.43	C
10	ATOM	4197	CZ2	TRP A 552	24.938	62.844	206.081	1.00	73.29	C
	ATOM	4198	CZ3	TRP A 552	24.376	63.227	203.770	1.00	70.01	C
	ATOM	4199	CH2	TRP A 552	24.113	63.380	205.134	1.00	69.30	C
	ATOM	4200	N	GLY A 553	30.621	59.636	201.091	1.00	80.36	N
	ATOM	4201	CA	GLY A 553	31.057	58.999	199.864	1.00	84.27	C
15	ATOM	4202	C	GLY A 553	31.930	57.779	200.104	1.00	95.03	C
	ATOM	4203	O	GLY A 553	31.738	56.734	199.485	1.00	100.79	O
	ATOM	4204	N	THR A 554	32.880	57.903	201.023	1.00	96.54	N
	ATOM	4205	CA	THR A 554	33.944	56.914	201.166	1.00	94.57	C
	ATOM	4206	C	THR A 554	33.644	55.789	202.148	1.00	92.90	C
20	ATOM	4207	O	THR A 554	34.493	54.907	202.361	1.00	75.04	O
	ATOM	4208	CB	THR A 554	35.237	57.588	201.627	1.00	93.10	C
	ATOM	4209	OG1	THR A 554	35.022	58.162	202.920	1.00	91.30	O
	ATOM	4210	CG2	THR A 554	35.648	58.689	200.642	1.00	90.81	C
	ATOM	4211	N	GLY A 555	32.450	55.807	202.738	1.00	85.75	N
25	ATOM	4212	CA	GLY A 555	32.148	54.880	203.812	1.00	83.98	C
	ATOM	4213	C	GLY A 555	30.848	54.109	203.757	1.00	86.76	C
	ATOM	4214	O	GLY A 555	29.773	54.701	203.701	1.00	88.41	O
	ATOM	4215	N	ARG A 556	30.963	52.780	203.763	1.00	97.20	N
	ATOM	4216	CA	ARG A 556	29.858	51.864	204.110	1.00	108.94	C
30	ATOM	4217	C	ARG A 556	28.741	51.719	203.076	1.00	103.86	C
	ATOM	4218	O	ARG A 556	28.479	50.626	202.562	1.00	95.32	O
	ATOM	4219	CB	ARG A 556	29.237	52.238	205.469	1.00	115.25	C
	ATOM	4220	CG	ARG A 556	30.210	52.211	206.635	1.00	125.78	C
	ATOM	4221	CD	ARG A 556	29.563	52.704	207.916	1.00	132.51	C
35	ATOM	4222	NE	ARG A 556	30.444	52.488	209.059	1.00	148.65	N
	ATOM	4223	CZ	ARG A 556	30.097	52.678	210.328	1.00	157.45	C
	ATOM	4224	NH1	ARG A 556	28.875	53.096	210.628	1.00	159.23	N
	ATOM	4225	NH2	ARG A 556	30.974	52.450	211.301	1.00	159.03	N
	ATOM	4226	N	ASP A 557	28.058	52.821	202.808	1.00	105.63	N
40	ATOM	4227	CA	ASP A 557	26.953	52.803	201.873	1.00	107.37	C

	ATOM	4228	C	ASP A 557	27.286	53.642	200.653	1.00109.22	C
	ATOM	4229	O	ASP A 557	26.611	53.548	199.619	1.00117.02	O
	ATOM	4230	CB	ASP A 557	25.675	53.278	202.554	1.00109.06	C
	ATOM	4231	CG	ASP A 557	25.032	52.193	203.376	1.00116.29	C
5	ATOM	4232	OD1	ASP A 557	25.656	51.117	203.511	1.00121.57	O
	ATOM	4233	OD2	ASP A 557	23.914	52.413	203.889	1.00117.88	O
	ATOM	4234	N	THR A 558	28.343	54.442	200.781	1.00 97.88	N
	ATOM	4235	CA	THR A 558	28.897	55.192	199.663	1.00 84.80	C
	ATOM	4236	C	THR A 558	27.809	55.932	198.906	1.00 73.24	C
10	ATOM	4237	O	THR A 558	27.279	55.460	197.912	1.00 69.60	O
	ATOM	4238	CB	THR A 558	29.708	54.274	198.744	1.00 79.98	C
	ATOM	4239	OG1	THR A 558	28.858	53.269	198.173	1.00 80.55	O
	ATOM	4240	CG2	THR A 558	30.751	53.591	199.564	1.00 79.54	C
	ATOM	4241	N	LEU A 559	27.470	57.098	199.418	1.00 71.23	N
15	ATOM	4242	CA	LEU A 559	26.311	57.827	198.955	1.00 78.56	C
	ATOM	4243	C	LEU A 559	26.718	58.907	197.977	1.00 61.32	C
	ATOM	4244	O	LEU A 559	27.636	59.677	198.247	1.00 80.52	O
	ATOM	4245	CB	LEU A 559	25.637	58.507	200.150	1.00 86.63	C
	ATOM	4246	CG	LEU A 559	24.738	57.795	201.148	1.00 61.41	C
20	ATOM	4247	CD2	LEU A 559	25.007	58.400	202.492	1.00 75.05	C
	ATOM	4248	CD1	LEU A 559	24.981	56.327	201.180	1.00 72.23	C
	ATOM	4249	N	ARG A 560	26.023	58.989	196.856	1.00 64.53	N
	ATOM	4250	CA	ARG A 560	26.174	60.154	196.000	1.00 65.46	C
	ATOM	4251	C	ARG A 560	25.299	61.253	196.610	1.00 68.13	C
25	ATOM	4252	O	ARG A 560	24.161	60.981	197.006	1.00 63.74	O
	ATOM	4253	CB	ARG A 560	25.786	59.831	194.553	1.00 65.39	C
	ATOM	4254	CG	ARG A 560	25.603	61.047	193.676	1.00 90.14	C
	ATOM	4255	CD	ARG A 560	24.873	60.716	192.357	1.00114.85	C
	ATOM	4256	NE	ARG A 560	25.746	60.020	191.409	1.00130.04	N
30	ATOM	4257	CZ	ARG A 560	25.643	58.730	191.102	1.00138.71	C
	ATOM	4258	NH1	ARG A 560	24.684	57.985	191.651	1.00142.21	N
	ATOM	4259	NH2	ARG A 560	26.495	58.186	190.238	1.00136.72	N
	ATOM	4260	N	CYS A 561	25.833	62.474	196.707	1.00 67.31	N
	ATOM	4261	CA	CYS A 561	25.147	63.571	197.392	1.00 56.73	C
35	ATOM	4262	C	CYS A 561	24.697	64.703	196.476	1.00 58.11	C
	ATOM	4263	O	CYS A 561	25.403	65.043	195.543	1.00 56.75	O
	ATOM	4264	CB	CYS A 561	26.041	64.168	198.478	1.00 60.96	C
	ATOM	4265	SG	CYS A 561	26.691	63.031	199.750	1.00 63.76	S
	ATOM	4266	N	LEU A 562	23.534	65.295	196.758	1.00 56.90	N
40	ATOM	4267	CA	LEU A 562	23.064	66.502	196.060	1.00 54.68	C

	ATOM	4268	C	LEU A 562	23.099	67.707	196.980	1.00	61.67	C
	ATOM	4269	O	LEU A 562	22.645	67.627	198.113	1.00	65.86	O
	ATOM	4270	CB	LEU A 562	21.611	66.356	195.584	1.00	58.45	C
	ATOM	4271	CG	LEU A 562	21.252	65.517	194.374	1.00	55.12	C
5	ATOM	4272	CD1	LEU A 562	22.103	66.022	193.244	1.00	57.96	C
	ATOM	4273	CD2	LEU A 562	21.514	64.051	194.671	1.00	57.80	C
	ATOM	4274	N	ALA A 563	23.604	68.830	196.491	1.00	63.31	N
	ATOM	4275	CA	ALA A 563	23.563	70.069	197.260	1.00	71.09	C
	ATOM	4276	C	ALA A 563	22.305	70.833	196.906	1.00	72.98	C
10	ATOM	4277	O	ALA A 563	22.059	71.091	195.734	1.00	86.02	O
	ATOM	4278	CB	ALA A 563	24.777	70.909	196.959	1.00	71.11	C
	ATOM	4279	N	LEU A 564	21.510	71.207	197.899	1.00	64.33	N
	ATOM	4280	CA	LEU A 564	20.262	71.911	197.607	1.00	65.12	C
	ATOM	4281	C	LEU A 564	20.323	73.364	198.064	1.00	68.99	C
15	ATOM	4282	O	LEU A 564	20.698	73.654	199.209	1.00	68.07	O
	ATOM	4283	CB	LEU A 564	19.073	71.189	198.250	1.00	59.80	C
	ATOM	4284	CG	LEU A 564	19.119	69.678	198.015	1.00	60.35	C
	ATOM	4285	CD1	LEU A 564	18.535	68.902	199.156	1.00	55.87	C
	ATOM	4286	CD2	LEU A 564	18.392	69.332	196.738	1.00	61.94	C
20	ATOM	4287	N	ALA A 565	19.952	74.278	197.173	1.00	67.99	N
	ATOM	4288	CA	ALA A 565	19.994	75.701	197.511	1.00	70.96	C
	ATOM	4289	C	ALA A 565	18.809	76.495	196.942	1.00	74.32	C
	ATOM	4290	O	ALA A 565	18.040	75.986	196.139	1.00	67.73	O
	ATOM	4291	CB	ALA A 565	21.337	76.317	197.081	1.00	64.01	C
25	ATOM	4292	N	THR A 566	18.673	77.746	197.365	1.00	55.89	N
	ATOM	4293	CA	THR A 566	17.590	78.599	196.906	1.00	64.12	C
	ATOM	4294	C	THR A 566	18.152	79.958	196.536	1.00	70.63	C
	ATOM	4295	O	THR A 566	19.022	80.479	197.219	1.00	79.95	O
	ATOM	4296	CB	THR A 566	16.518	78.828	198.033	1.00	61.02	C
30	ATOM	4297	OG1	THR A 566	16.025	77.575	198.531	1.00	63.56	O
	ATOM	4298	CG2	THR A 566	15.344	79.650	197.521	1.00	65.08	C
	ATOM	4299	N	ARG A 567	17.668	80.554	195.463	1.00	58.61	N
	ATOM	4300	CA	ARG A 567	18.003	81.951	195.235	1.00	74.82	C
	ATOM	4301	C	ARG A 567	16.857	82.839	195.724	1.00	78.25	C
35	ATOM	4302	O	ARG A 567	15.842	82.990	195.046	1.00	85.24	O
	ATOM	4303	CB	ARG A 567	18.385	82.249	193.777	1.00	69.08	C
	ATOM	4304	CG	ARG A 567	18.890	83.670	193.595	1.00	62.35	C
	ATOM	4305	CD	ARG A 567	19.292	83.992	192.179	1.00	85.25	C
	ATOM	4306	NE	ARG A 567	19.854	85.338	192.075	1.00	65.07	N
40	ATOM	4307	CZ	ARG A 567	20.557	85.771	191.034	1.00	83.92	C

	ATOM	4308	NH1 ARG A 567	20.782	84.964	190.007	1.00	80.16	N
	ATOM	4309	NH2 ARG A 567	21.042	87.006	191.017	1.00	68.00	N
	ATOM	4310	N ASP A 568	17.052	83.413	196.910	1.00	74.03	N
	ATOM	4311	CA ASP A 568	16.054	84.214	197.611	1.00	78.29	C
5	ATOM	4312	C ASP A 568	15.595	85.485	196.894	1.00	84.65	C
	ATOM	4313	O ASP A 568	14.507	85.998	197.172	1.00	65.66	O
	ATOM	4314	CB ASP A 568	16.585	84.586	198.990	1.00	80.95	C
	ATOM	4315	CG ASP A 568	16.823	83.377	199.863	1.00	79.65	C
	ATOM	4316	OD1 ASP A 568	16.129	82.350	199.659	1.00	84.39	O
10	ATOM	4317	OD2 ASP A 568	17.702	83.450	200.760	1.00	66.44	O
	ATOM	4318	N THR A 569	16.428	86.018	196.008	1.00	85.94	N
	ATOM	4319	CA THR A 569	16.012	87.135	195.166	1.00	67.11	C
	ATOM	4320	C THR A 569	16.427	86.865	193.722	1.00	84.61	C
	ATOM	4321	O THR A 569	17.399	87.430	193.223	1.00	90.86	O
15	ATOM	4322	CB THR A 569	16.582	88.479	195.656	1.00	68.89	C
	ATOM	4323	OG1 THR A 569	16.294	88.635	197.042	1.00	68.99	O
	ATOM	4324	CG2 THR A 569	15.983	89.637	194.913	1.00	71.21	C
	ATOM	4325	N PRO A 570	15.684	85.990	193.034	1.00	81.80	N
	ATOM	4326	CA PRO A 570	16.037	85.684	191.649	1.00	78.97	C
20	ATOM	4327	C PRO A 570	15.787	86.899	190.784	1.00	80.72	C
	ATOM	4328	O PRO A 570	15.146	87.842	191.247	1.00	87.61	O
	ATOM	4329	CB PRO A 570	15.058	84.569	191.291	1.00	71.53	C
	ATOM	4330	CG PRO A 570	13.877	84.851	192.135	1.00	72.12	C
	ATOM	4331	CD PRO A 570	14.410	85.367	193.425	1.00	77.56	C
25	ATOM	4332	N PRO A 571	16.298	86.889	189.546	1.00	74.93	N
	ATOM	4333	CA PRO A 571	15.984	87.964	188.596	1.00	74.30	C
	ATOM	4334	C PRO A 571	14.517	87.939	188.159	1.00	78.03	C
	ATOM	4335	O PRO A 571	13.811	86.948	188.361	1.00	83.15	O
	ATOM	4336	CB PRO A 571	16.907	87.664	187.412	1.00	80.14	C
30	ATOM	4337	CG PRO A 571	17.256	86.209	187.544	1.00	69.89	C
	ATOM	4338	CD PRO A 571	17.268	85.919	189.001	1.00	71.79	C
	ATOM	4339	N LYS A 572	14.058	89.032	187.565	1.00	82.30	N
	ATOM	4340	CA LYS A 572	12.689	89.101	187.074	1.00	82.86	C
	ATOM	4341	C LYS A 572	12.465	88.111	185.935	1.00	92.87	C
35	ATOM	4342	O LYS A 572	13.365	87.834	185.142	1.00	101.86	O
	ATOM	4343	CB LYS A 572	12.369	90.508	186.584	1.00	83.90	C
	ATOM	4344	CG LYS A 572	12.181	91.553	187.656	1.00	85.05	C
	ATOM	4345	CD LYS A 572	12.071	92.931	187.016	1.00	97.05	C
	ATOM	4346	CE LYS A 572	11.967	94.033	188.062	1.00	108.16	C
40	ATOM	4347	NZ LYS A 572	13.169	94.083	188.951	1.00	110.75	N

	ATOM	4348	N	ARG A 573	11.248	87.592	185.866	1.00	90.80	N
	ATOM	4349	CA	ARG A 573	10.794	86.712	184.803	1.00	85.30	C
	ATOM	4350	C	ARG A 573	11.101	87.295	183.404	1.00	93.23	C
	ATOM	4351	O	ARG A 573	11.466	86.576	182.458	1.00	95.95	O
5	ATOM	4352	CB	ARG A 573	9.288	86.546	184.990	1.00	82.74	C
	ATOM	4353	CG	ARG A 573	8.686	85.342	184.341	1.00	93.20	C
	ATOM	4354	CD	ARG A 573	7.192	85.313	184.561	1.00	93.86	C
	ATOM	4355	NE	ARG A 573	6.838	85.191	185.968	1.00	77.85	N
	ATOM	4356	CZ	ARG A 573	6.312	86.174	186.693	1.00	95.37	C
10	ATOM	4357	NH1	ARG A 573	6.084	87.365	186.148	1.00	94.83	N
	ATOM	4358	NH2	ARG A 573	6.011	85.966	187.965	1.00	89.15	N
	ATOM	4359	N	GLU A 574	10.945	88.612	183.296	1.00	91.86	N
	ATOM	4360	CA	GLU A 574	11.165	89.358	182.064	1.00	93.19	C
	ATOM	4361	C	GLU A 574	12.632	89.378	181.611	1.00	93.42	C
15	ATOM	4362	O	GLU A 574	12.924	89.645	180.437	1.00	88.11	O
	ATOM	4363	CB	GLU A 574	10.678	90.795	182.251	1.00	87.21	C
	ATOM	4364	CG	GLU A 574	9.218	90.914	182.603	1.00	123.07	C
	ATOM	4365	CD	GLU A 574	8.951	90.689	184.075	1.00	130.24	C
	ATOM	4366	OE1	GLU A 574	9.846	90.979	184.892	1.00	125.39	O
20	ATOM	4367	OE2	GLU A 574	7.845	90.219	184.424	1.00	142.87	O
	ATOM	4368	N	GLU A 575	13.545	89.091	182.540	1.00	94.01	N
	ATOM	4369	CA	GLU A 575	14.980	89.249	182.304	1.00	95.12	C
	ATOM	4370	C	GLU A 575	15.732	87.926	182.081	1.00	90.63	C
	ATOM	4371	O	GLU A 575	16.961	87.897	182.092	1.00	83.06	O
25	ATOM	4372	CB	GLU A 575	15.613	90.005	183.471	1.00	105.99	C
	ATOM	4373	CG	GLU A 575	14.984	91.355	183.777	1.00	120.59	C
	ATOM	4374	CD	GLU A 575	15.336	91.875	185.174	1.00	130.94	C
	ATOM	4375	OE1	GLU A 575	15.053	93.062	185.452	1.00	137.38	O
	ATOM	4376	OE2	GLU A 575	15.889	91.104	185.997	1.00	127.01	O
30	ATOM	4377	N	MET A 576	14.994	86.842	181.862	1.00	97.49	N
	ATOM	4378	CA	MET A 576	15.590	85.525	181.668	1.00	76.39	C
	ATOM	4379	C	MET A 576	15.221	84.870	180.337	1.00	87.74	C
	ATOM	4380	O	MET A 576	14.123	85.074	179.791	1.00	88.00	O
	ATOM	4381	CB	MET A 576	15.194	84.606	182.815	1.00	75.09	C
35	ATOM	4382	CG	MET A 576	15.603	85.125	184.178	1.00	72.58	C
	ATOM	4383	SD	MET A 576	15.209	83.933	185.457	1.00	79.66	S
	ATOM	4384	CE	MET A 576	16.441	82.664	185.209	1.00	76.02	C
	ATOM	4385	N	VAL A 577	16.148	84.058	179.832	1.00	89.56	N
	ATOM	4386	CA	VAL A 577	16.075	83.515	178.471	1.00	98.14	C
40	ATOM	4387	C	VAL A 577	16.633	82.089	178.429	1.00	93.08	C

	ATOM	4388	O	VAL A 577	17.724	81.840	178.932	1.00	87.36	O
	ATOM	4389	CB	VAL A 577	16.834	84.421	177.501	1.00	81.06	C
	ATOM	4390	CG1	VAL A 577	17.193	83.671	176.272	1.00	139.12	C
	ATOM	4391	CG2	VAL A 577	15.975	85.623	177.144	1.00	90.58	C
5	ATOM	4392	N	LEU A 578	15.890	81.145	177.853	1.00	77.32	N
	ATOM	4393	CA	LEU A 578	16.239	79.735	178.052	1.00	75.60	C
	ATOM	4394	C	LEU A 578	16.791	78.997	176.828	1.00	83.24	C
	ATOM	4395	O	LEU A 578	16.994	77.779	176.877	1.00	80.13	O
	ATOM	4396	CB	LEU A 578	15.066	78.961	178.661	1.00	74.49	C
10	ATOM	4397	CG	LEU A 578	14.391	79.617	179.872	1.00	106.99	C
	ATOM	4398	CD1	LEU A 578	13.479	78.646	180.592	1.00	72.06	C
	ATOM	4399	CD2	LEU A 578	15.421	80.183	180.817	1.00	71.88	C
	ATOM	4400	N	ASP A 579	17.053	79.733	175.745	1.00	85.88	N
	ATOM	4401	CA	ASP A 579	17.555	79.140	174.498	1.00	87.93	C
15	ATOM	4402	C	ASP A 579	18.981	78.626	174.656	1.00	94.63	C
	ATOM	4403	O	ASP A 579	19.272	77.483	174.303	1.00	96.65	O
	ATOM	4404	CB	ASP A 579	17.433	80.107	173.316	1.00	84.55	C
	ATOM	4405	CG	ASP A 579	17.993	81.484	173.615	1.00	105.15	C
	ATOM	4406	OD2	ASP A 579	17.385	82.495	173.227	1.00	110.69	O
20	ATOM	4407	OD1	ASP A 579	19.054	81.573	174.236	1.00	105.85	O
	ATOM	4408	N	ASP A 580	19.859	79.470	175.200	1.00	98.71	N
	ATOM	4409	CA	ASP A 580	21.246	79.082	175.449	1.00	92.31	C
	ATOM	4410	C	ASP A 580	21.446	78.752	176.909	1.00	83.96	C
	ATOM	4411	O	ASP A 580	21.325	79.612	177.792	1.00	75.77	O
25	ATOM	4412	CB	ASP A 580	22.243	80.153	174.998	1.00	95.78	C
	ATOM	4413	CG	ASP A 580	23.696	79.754	175.258	1.00	97.12	C
	ATOM	4414	OD2	ASP A 580	24.534	80.673	175.399	1.00	102.03	O
	ATOM	4415	OD1	ASP A 580	24.008	78.536	175.319	1.00	90.77	O
	ATOM	4416	N	SER A 581	21.769	77.478	177.108	1.00	84.17	N
30	ATOM	4417	CA	SER A 581	21.947	76.809	178.388	1.00	79.18	C
	ATOM	4418	C	SER A 581	23.029	77.430	179.253	1.00	74.30	C
	ATOM	4419	O	SER A 581	23.108	77.169	180.449	1.00	70.00	O
	ATOM	4420	CB	SER A 581	22.291	75.345	178.082	1.00	83.82	C
	ATOM	4421	OG	SER A 581	22.763	74.626	179.197	1.00	70.05	O
35	ATOM	4422	N	SER A 582	23.856	78.268	178.647	1.00	75.37	N
	ATOM	4423	CA	SER A 582	25.090	78.701	179.280	1.00	78.58	C
	ATOM	4424	C	SER A 582	24.965	79.932	180.159	1.00	72.22	C
	ATOM	4425	O	SER A 582	25.923	80.299	180.802	1.00	90.56	O
	ATOM	4426	CB	SER A 582	26.139	78.976	178.230	1.00	75.02	C
40	ATOM	4427	OG	SER A 582	26.088	80.340	177.867	1.00	76.65	O

	ATOM	4428	N	ARG A 583	23.815	80.593	180.189	1.00	89.48	N
	ATOM	4429	CA	ARG A 583	23.643	81.676	181.165	1.00	82.42	C
	ATOM	4430	C	ARG A 583	23.013	81.211	182.468	1.00	86.37	C
	ATOM	4431	O	ARG A 583	22.796	82.019	183.363	1.00	92.72	O
5	ATOM	4432	CB	ARG A 583	22.780	82.819	180.634	1.00	77.27	C
	ATOM	4433	CG	ARG A 583	22.421	82.773	179.180	1.00	75.71	C
	ATOM	4434	CD	ARG A 583	21.785	84.105	178.836	1.00	81.37	C
	ATOM	4435	NE	ARG A 583	21.957	84.494	177.442	1.00	84.08	N
	ATOM	4436	CZ	ARG A 583	21.324	83.906	176.431	1.00	93.79	C
10	ATOM	4437	NH1	ARG A 583	20.498	82.880	176.680	1.00	89.78	N
	ATOM	4438	NH2	ARG A 583	21.520	84.331	175.179	1.00	84.39	N
	ATOM	4439	N	PHE A 584	22.687	79.929	182.573	1.00	68.19	N
	ATOM	4440	CA	PHE A 584	21.937	79.470	183.719	1.00	66.26	C
	ATOM	4441	C	PHE A 584	22.839	79.438	184.938	1.00	92.49	C
15	ATOM	4442	O	PHE A 584	22.364	79.537	186.063	1.00	96.48	O
	ATOM	4443	CB	PHE A 584	21.339	78.089	183.477	1.00	71.54	C
	ATOM	4444	CG	PHE A 584	20.367	78.027	182.330	1.00	74.56	C
	ATOM	4445	CD1	PHE A 584	19.949	79.177	181.680	1.00	76.71	C
	ATOM	4446	CD2	PHE A 584	19.867	76.806	181.906	1.00	66.77	C
20	ATOM	4447	CE1	PHE A 584	19.074	79.104	180.616	1.00	80.94	C
	ATOM	4448	CE2	PHE A 584	19.000	76.728	180.847	1.00	68.33	C
	ATOM	4449	CZ	PHE A 584	18.601	77.875	180.199	1.00	70.05	C
	ATOM	4450	N	MET A 585	24.147	79.311	184.723	1.00	91.29	N
	ATOM	4451	CA	MET A 585	25.076	79.294	185.848	1.00	86.91	C
25	ATOM	4452	C	MET A 585	25.156	80.667	186.513	1.00	83.13	C
	ATOM	4453	O	MET A 585	25.356	80.761	187.718	1.00	92.91	O
	ATOM	4454	CB	MET A 585	26.453	78.777	185.451	1.00	65.30	C
	ATOM	4455	CG	MET A 585	27.400	78.559	186.653	1.00	64.51	C
	ATOM	4456	SD	MET A 585	29.179	78.630	186.304	1.00	71.93	S
30	ATOM	4457	CE	MET A 585	29.330	80.411	186.186	1.00	67.74	C
	ATOM	4458	N	GLU A 586	24.968	81.729	185.739	1.00	71.69	N
	ATOM	4459	CA	GLU A 586	24.823	83.060	186.318	1.00	71.24	C
	ATOM	4460	C	GLU A 586	23.392	83.334	186.839	1.00	72.11	C
	ATOM	4461	O	GLU A 586	23.195	84.147	187.748	1.00	73.25	O
35	ATOM	4462	CB	GLU A 586	25.266	84.134	185.328	1.00	77.69	C
	ATOM	4463	CG	GLU A 586	25.128	85.551	185.844	1.00	97.36	C
	ATOM	4464	CD	GLU A 586	24.756	86.536	184.746	1.00	122.63	C
	ATOM	4465	OE1	GLU A 586	25.637	86.873	183.919	1.00	134.12	O
	ATOM	4466	OE2	GLU A 586	23.579	86.966	184.706	1.00	128.06	O
40	ATOM	4467	N	TYR A 587	22.386	82.662	186.289	1.00	71.12	N

	ATOM	4468	CA	TYR A 587	21.042	82.814	186.838	1.00	72.28	C
	ATOM	4469	C	TYR A 587	21.047	82.219	188.253	1.00	72.26	C
	ATOM	4470	O	TYR A 587	20.468	82.771	189.194	1.00	72.07	O
	ATOM	4471	CB	TYR A 587	19.985	82.150	185.940	1.00	66.09	C
5	ATOM	4472	CG	TYR A 587	19.723	82.898	184.651	1.00	82.62	C
	ATOM	4473	CD1	TYR A 587	19.803	84.283	184.607	1.00	85.63	C
	ATOM	4474	CD2	TYR A 587	19.413	82.222	183.468	1.00	80.23	C
	ATOM	4475	CE1	TYR A 587	19.575	84.974	183.434	1.00	88.76	C
	ATOM	4476	CE2	TYR A 587	19.184	82.914	182.282	1.00	71.33	C
10	ATOM	4477	CZ	TYR A 587	19.265	84.287	182.277	1.00	72.89	C
	ATOM	4478	OH	TYR A 587	19.046	84.994	181.118	1.00	75.41	O
	ATOM	4479	N	GLU A 588	21.745	81.101	188.396	1.00	70.28	N
	ATOM	4480	CA	GLU A 588	21.863	80.445	189.677	1.00	69.80	C
	ATOM	4481	C	GLU A 588	23.111	80.902	190.434	1.00	74.21	C
15	ATOM	4482	O	GLU A 588	23.959	80.084	190.780	1.00	77.52	O
	ATOM	4483	CB	GLU A 588	21.908	78.945	189.474	1.00	60.23	C
	ATOM	4484	CG	GLU A 588	20.782	78.405	188.650	1.00	74.10	C
	ATOM	4485	CD	GLU A 588	21.072	76.993	188.196	1.00	82.97	C
	ATOM	4486	OE1	GLU A 588	22.137	76.448	188.599	1.00	75.62	O
20	ATOM	4487	OE2	GLU A 588	20.242	76.438	187.431	1.00	86.76	O
	ATOM	4488	N	THR A 589	23.221	82.211	190.670	1.00	71.03	N
	ATOM	4489	CA	THR A 589	24.199	82.752	191.615	1.00	72.11	C
	ATOM	4490	C	THR A 589	23.541	83.416	192.838	1.00	62.88	C
	ATOM	4491	O	THR A 589	22.329	83.407	192.983	1.00	67.93	O
25	ATOM	4492	CB	THR A 589	25.209	83.711	190.942	1.00	82.43	C
	ATOM	4493	OG1	THR A 589	24.530	84.812	190.335	1.00	66.23	O
	ATOM	4494	CG2	THR A 589	25.986	82.985	189.889	1.00	88.04	C
	ATOM	4495	N	ASP A 590	24.358	83.962	193.730	1.00	79.75	N
	ATOM	4496	CA	ASP A 590	23.877	84.550	194.978	1.00	70.78	C
30	ATOM	4497	C	ASP A 590	22.969	83.579	195.741	1.00	65.66	C
	ATOM	4498	O	ASP A 590	21.947	83.976	196.295	1.00	68.94	O
	ATOM	4499	CB	ASP A 590	23.163	85.868	194.695	1.00	76.49	C
	ATOM	4500	CG	ASP A 590	23.233	86.829	195.861	1.00	87.51	C
	ATOM	4501	OD1	ASP A 590	24.084	86.624	196.745	1.00	66.14	O
35	ATOM	4502	OD2	ASP A 590	22.443	87.797	195.888	1.00	93.80	O
	ATOM	4503	N	LEU A 591	23.343	82.301	195.756	1.00	62.88	N
	ATOM	4504	CA	LEU A 591	22.482	81.261	196.309	1.00	66.77	C
	ATOM	4505	C	LEU A 591	22.564	81.214	197.820	1.00	70.44	C
	ATOM	4506	O	LEU A 591	23.470	81.782	198.417	1.00	71.01	O
40	ATOM	4507	CB	LEU A 591	22.830	79.884	195.736	1.00	66.78	C

	ATOM	4508	CG	LEU A 591	22.721	79.696	194.224	1.00	70.36	C
	ATOM	4509	CD1	LEU A 591	22.749	78.211	193.877	1.00	72.92	C
	ATOM	4510	CD2	LEU A 591	21.472	80.367	193.672	1.00	65.24	C
	ATOM	4511	N	THR A 592	21.604	80.532	198.428	1.00	68.41	N
5	ATOM	4512	CA	THR A 592	21.595	80.291	199.855	1.00	61.24	C
	ATOM	4513	C	THR A 592	21.588	78.798	200.053	1.00	67.84	C
	ATOM	4514	O	THR A 592	20.662	78.125	199.612	1.00	69.58	O
	ATOM	4515	CB	THR A 592	20.321	80.814	200.467	1.00	60.82	C
	ATOM	4516	OG1	THR A 592	20.200	82.213	200.172	1.00	74.26	O
10	ATOM	4517	CG2	THR A 592	20.321	80.576	201.976	1.00	58.66	C
	ATOM	4518	N	PHE A 593	22.622	78.275	200.704	1.00	71.58	N
	ATOM	4519	CA	PHE A 593	22.721	76.845	200.956	1.00	65.69	C
	ATOM	4520	C	PHE A 593	21.583	76.367	201.849	1.00	62.96	C
	ATOM	4521	O	PHE A 593	21.219	77.053	202.808	1.00	69.27	O
15	ATOM	4522	CB	PHE A 593	24.044	76.500	201.629	1.00	56.50	C
	ATOM	4523	CG	PHE A 593	24.199	75.036	201.884	1.00	72.77	C
	ATOM	4524	CD1	PHE A 593	24.591	74.184	200.861	1.00	61.18	C
	ATOM	4525	CD2	PHE A 593	23.910	74.498	203.131	1.00	55.99	C
	ATOM	4526	CE1	PHE A 593	24.701	72.831	201.083	1.00	59.35	C
20	ATOM	4527	CE2	PHE A 593	24.022	73.143	203.355	1.00	60.29	C
	ATOM	4528	CZ	PHE A 593	24.417	72.308	202.333	1.00	59.94	C
	ATOM	4529	N	VAL A 594	21.015	75.200	201.547	1.00	55.74	N
	ATOM	4530	CA	VAL A 594	19.990	74.647	202.431	1.00	61.18	C
	ATOM	4531	C	VAL A 594	20.431	73.350	203.089	1.00	62.83	C
25	ATOM	4532	O	VAL A 594	20.571	73.288	204.316	1.00	64.77	O
	ATOM	4533	CB	VAL A 594	18.597	74.489	201.755	1.00	54.93	C
	ATOM	4534	CG1	VAL A 594	17.685	73.648	202.600	1.00	54.44	C
	ATOM	4535	CG2	VAL A 594	17.972	75.829	201.546	1.00	55.07	C
	ATOM	4536	N	GLY A 595	20.641	72.317	202.288	1.00	54.05	N
30	ATOM	4537	CA	GLY A 595	20.972	71.025	202.845	1.00	55.07	C
	ATOM	4538	C	GLY A 595	21.630	70.124	201.839	1.00	56.19	C
	ATOM	4539	O	GLY A 595	22.042	70.574	200.782	1.00	53.75	O
	ATOM	4540	N	VAL A 596	21.735	68.847	202.162	1.00	54.03	N
	ATOM	4541	CA	VAL A 596	22.309	67.893	201.230	1.00	64.47	C
35	ATOM	4542	C	VAL A 596	21.508	66.619	201.346	1.00	64.82	C
	ATOM	4543	O	VAL A 596	21.194	66.201	202.446	1.00	61.20	O
	ATOM	4544	CB	VAL A 596	23.812	67.599	201.552	1.00	54.79	C
	ATOM	4545	CG1	VAL A 596	24.298	66.323	200.860	1.00	55.21	C
	ATOM	4546	CG2	VAL A 596	24.692	68.783	201.191	1.00	55.99	C
40	ATOM	4547	N	VAL A 597	21.125	66.018	200.231	1.00	54.09	N

	ATOM	4548	CA	VAL A 597	20.574	64.674	200.313	1.00	70.76	C
	ATOM	4549	C	VAL A 597	21.689	63.747	199.890	1.00	66.07	C
	ATOM	4550	O	VAL A 597	22.370	64.041	198.927	1.00	67.86	O
	ATOM	4551	CB	VAL A 597	19.280	64.447	199.425	1.00	63.44	C
5	ATOM	4552	CG1	VAL A 597	18.052	65.119	200.024	1.00	54.16	C
	ATOM	4553	CG2	VAL A 597	19.481	64.909	198.006	1.00	54.25	C
	ATOM	4554	N	GLY A 598	21.916	62.667	200.628	1.00	55.97	N
	ATOM	4555	CA	GLY A 598	22.819	61.612	200.184	1.00	65.63	C
	ATOM	4556	C	GLY A 598	22.065	60.332	199.823	1.00	65.07	C
10	ATOM	4557	O	GLY A 598	21.288	59.815	200.627	1.00	76.03	O
	ATOM	4558	N	MET A 599	22.263	59.794	198.626	1.00	59.63	N
	ATOM	4559	CA	MET A 599	21.475	58.612	198.285	1.00	65.00	C
	ATOM	4560	C	MET A 599	22.242	57.357	197.907	1.00	68.45	C
	ATOM	4561	O	MET A 599	23.380	57.402	197.433	1.00	61.03	O
15	ATOM	4562	CB	MET A 599	20.369	58.914	197.257	1.00	62.33	C
	ATOM	4563	CG	MET A 599	20.864	59.492	195.968	1.00	58.42	C
	ATOM	4564	SD	MET A 599	19.534	60.029	194.901	1.00	106.44	S
	ATOM	4565	CE	MET A 599	19.143	61.600	195.652	1.00	56.59	C
	ATOM	4566	N	LEU A 600	21.551	56.241	198.110	1.00	67.23	N
20	ATOM	4567	CA	LEU A 600	22.126	54.917	198.076	1.00	68.66	C
	ATOM	4568	C	LEU A 600	21.733	54.271	196.766	1.00	73.00	C
	ATOM	4569	O	LEU A 600	20.662	54.549	196.245	1.00	84.05	O
	ATOM	4570	CB	LEU A 600	21.581	54.120	199.260	1.00	64.34	C
	ATOM	4571	CG	LEU A 600	21.850	52.631	199.397	1.00	81.83	C
25	ATOM	4572	CD1	LEU A 600	23.342	52.355	199.427	1.00	86.81	C
	ATOM	4573	CD2	LEU A 600	21.198	52.150	200.658	1.00	67.19	C
	ATOM	4574	N	ASP A 601	22.619	53.440	196.224	1.00	72.64	N
	ATOM	4575	CA	ASP A 601	22.388	52.735	194.972	1.00	78.15	C
	ATOM	4576	C	ASP A 601	23.070	51.398	195.169	1.00	84.36	C
30	ATOM	4577	O	ASP A 601	24.245	51.239	194.869	1.00	89.74	O
	ATOM	4578	CB	ASP A 601	22.992	53.530	193.800	1.00	84.20	C
	ATOM	4579	CG	ASP A 601	22.878	52.813	192.437	1.00	87.07	C
	ATOM	4580	OD1	ASP A 601	22.204	51.762	192.346	1.00	85.29	O
	ATOM	4581	OD2	ASP A 601	23.469	53.323	191.449	1.00	87.52	O
35	ATOM	4582	N	PRO A 602	22.327	50.429	195.699	1.00	70.78	N
	ATOM	4583	CA	PRO A 602	22.835	49.154	196.210	1.00	101.45	C
	ATOM	4584	C	PRO A 602	23.431	48.256	195.153	1.00	75.32	C
	ATOM	4585	O	PRO A 602	22.841	48.108	194.105	1.00	122.48	O
	ATOM	4586	CB	PRO A 602	21.579	48.486	196.771	1.00	73.74	C
40	ATOM	4587	CG	PRO A 602	20.477	49.080	195.997	1.00	94.56	C

	ATOM	4588	CD	PRO A 602	20.867	50.511	195.802	1.00	90.76	C
	ATOM	4589	N	PRO A 603	24.591	47.662	195.427	1.00	76.96	N
	ATOM	4590	CA	PRO A 603	25.123	46.588	194.599	1.00	94.66	C
	ATOM	4591	C	PRO A 603	24.078	45.545	194.248	1.00	81.46	C
5	ATOM	4592	O	PRO A 603	23.138	45.302	194.987	1.00	81.24	O
	ATOM	4593	CB	PRO A 603	26.190	45.982	195.492	1.00	81.37	C
	ATOM	4594	CG	PRO A 603	26.726	47.154	196.214	1.00	86.00	C
	ATOM	4595	CD	PRO A 603	25.592	48.130	196.392	1.00	76.41	C
	ATOM	4596	N	ARG A 604	24.259	44.960	193.076	1.00	67.53	N
10	ATOM	4597	CA	ARG A 604	23.432	43.895	192.554	1.00	72.77	C
	ATOM	4598	C	ARG A 604	23.669	42.727	193.503	1.00	84.48	C
	ATOM	4599	O	ARG A 604	24.689	42.700	194.189	1.00	89.30	O
	ATOM	4600	CB	ARG A 604	23.919	43.605	191.135	1.00	70.23	C
	ATOM	4601	CG	ARG A 604	23.007	42.832	190.236	1.00	82.11	C
15	ATOM	4602	CD	ARG A 604	21.721	43.570	189.900	1.00	84.44	C
	ATOM	4603	NE	ARG A 604	21.855	44.674	188.955	1.00	72.53	N
	ATOM	4604	CZ	ARG A 604	21.005	44.900	187.951	1.00	72.26	C
	ATOM	4605	NH1	ARG A 604	19.980	44.090	187.724	1.00	65.27	N
	ATOM	4606	NH2	ARG A 604	21.186	45.938	187.156	1.00	75.16	N
20	ATOM	4607	N	LYS A 605	22.740	41.783	193.594	1.00	91.46	N
	ATOM	4608	CA	LYS A 605	22.887	40.726	194.597	1.00	99.65	C
	ATOM	4609	C	LYS A 605	23.834	39.631	194.138	1.00	100.81	C
	ATOM	4610	O	LYS A 605	24.410	38.913	194.948	1.00	105.76	O
	ATOM	4611	CB	LYS A 605	21.534	40.119	194.976	1.00	111.36	C
25	ATOM	4612	CG	LYS A 605	20.497	41.131	195.426	1.00	121.87	C
	ATOM	4613	CD	LYS A 605	21.039	42.066	196.514	1.00	125.48	C
	ATOM	4614	CE	LYS A 605	21.241	41.361	197.849	1.00	119.62	C
	ATOM	4615	NZ	LYS A 605	21.606	42.341	198.907	1.00	111.25	N
	ATOM	4616	N	GLU A 606	24.003	39.511	192.831	1.00	97.53	N
30	ATOM	4617	CA	GLU A 606	24.804	38.429	192.288	1.00	97.83	C
	ATOM	4618	C	GLU A 606	26.158	38.883	191.726	1.00	99.02	C
	ATOM	4619	O	GLU A 606	26.961	38.041	191.321	1.00	106.15	O
	ATOM	4620	CB	GLU A 606	24.008	37.680	191.223	1.00	96.34	C
	ATOM	4621	CG	GLU A 606	22.512	37.636	191.498	1.00	103.81	C
35	ATOM	4622	CD	GLU A 606	21.770	38.851	190.954	1.00	107.12	C
	ATOM	4623	OE1	GLU A 606	22.333	39.560	190.102	1.00	105.07	O
	ATOM	4624	OE2	GLU A 606	20.623	39.101	191.376	1.00	115.29	O
	ATOM	4625	N	VAL A 607	26.416	40.194	191.703	1.00	86.99	N
	ATOM	4626	CA	VAL A 607	27.677	40.710	191.167	1.00	75.20	C
40	ATOM	4627	C	VAL A 607	28.900	40.209	191.898	1.00	77.36	C

	ATOM	4628	O	VAL A 607	29.887	39.860	191.265	1.00	78.62	O
	ATOM	4629	CB	VAL A 607	27.772	42.239	191.181	1.00	71.42	C
	ATOM	4630	CG1	VAL A 607	27.146	42.813	189.961	1.00	76.69	C
	ATOM	4631	CG2	VAL A 607	27.137	42.796	192.416	1.00	82.87	C
5	ATOM	4632	N	MET A 608	28.852	40.191	193.226	1.00	80.77	N
	ATOM	4633	CA	MET A 608	30.045	39.865	193.992	1.00	80.87	C
	ATOM	4634	C	MET A 608	30.513	38.454	193.660	1.00	84.28	C
	ATOM	4635	O	MET A 608	31.699	38.220	193.402	1.00	87.49	O
	ATOM	4636	CB	MET A 608	29.808	40.026	195.488	1.00	88.16	C
10	ATOM	4637	CG	MET A 608	31.074	39.793	196.300	1.00	96.10	C
	ATOM	4638	SD	MET A 608	30.824	39.963	198.061	1.00	136.52	S
	ATOM	4639	CE	MET A 608	29.577	38.698	198.329	1.00	112.21	C
	ATOM	4640	N	GLY A 609	29.565	37.523	193.643	1.00	85.26	N
	ATOM	4641	CA	GLY A 609	29.845	36.160	193.235	1.00	84.59	C
15	ATOM	4642	C	GLY A 609	30.131	36.030	191.748	1.00	81.12	C
	ATOM	4643	O	GLY A 609	30.840	35.122	191.329	1.00	88.40	O
	ATOM	4644	N	SER A 610	29.572	36.922	190.942	1.00	76.47	N
	ATOM	4645	CA	SER A 610	29.845	36.889	189.512	1.00	85.13	C
	ATOM	4646	C	SER A 610	31.289	37.271	189.208	1.00	89.43	C
20	ATOM	4647	O	SER A 610	31.941	36.620	188.399	1.00	95.08	O
	ATOM	4648	CB	SER A 610	28.883	37.790	188.733	1.00	84.15	C
	ATOM	4649	OG	SER A 610	27.630	37.158	188.550	1.00	86.61	O
	ATOM	4650	N	ILE A 611	31.780	38.326	189.856	1.00	84.30	N
	ATOM	4651	CA	ILE A 611	33.153	38.786	189.657	1.00	77.87	C
25	ATOM	4652	C	ILE A 611	34.139	37.707	190.092	1.00	83.45	C
	ATOM	4653	O	ILE A 611	35.212	37.544	189.509	1.00	89.47	O
	ATOM	4654	CB	ILE A 611	33.412	40.117	190.388	1.00	72.02	C
	ATOM	4655	CG1	ILE A 611	32.736	41.262	189.628	1.00	72.32	C
	ATOM	4656	CG2	ILE A 611	34.896	40.393	190.513	1.00	66.56	C
30	ATOM	4657	CD1	ILE A 611	32.595	42.546	190.438	1.00	74.14	C
	ATOM	4658	N	GLN A 612	33.750	36.931	191.092	1.00	84.99	N
	ATOM	4659	CA	GLN A 612	34.578	35.813	191.510	1.00	84.99	C
	ATOM	4660	C	GLN A 612	34.633	34.736	190.437	1.00	79.67	C
	ATOM	4661	O	GLN A 612	35.598	33.988	190.342	1.00	85.53	O
35	ATOM	4662	CB	GLN A 612	34.077	35.212	192.816	1.00	86.64	C
	ATOM	4663	CG	GLN A 612	34.972	34.105	193.325	1.00	93.97	C
	ATOM	4664	CD	GLN A 612	36.412	34.559	193.477	1.00	98.71	C
	ATOM	4665	OE1	GLN A 612	36.686	35.740	193.722	1.00	97.73	O
	ATOM	4666	NE2	GLN A 612	37.344	33.624	193.322	1.00	104.29	N
40	ATOM	4667	N	LEU A 613	33.593	34.646	189.626	1.00	74.64	N

	ATOM	4668	CA	LEU A 613	33.567	33.602	188.623	1.00	76.46	C
	ATOM	4669	C	LEU A 613	34.487	34.011	187.486	1.00	75.38	C
	ATOM	4670	O	LEU A 613	35.103	33.160	186.842	1.00	77.93	O
	ATOM	4671	CB	LEU A 613	32.145	33.352	188.132	1.00	73.01	C
5	ATOM	4672	CG	LEU A 613	31.911	31.971	187.515	1.00	76.34	C
	ATOM	4673	CD1	LEU A 613	32.031	30.872	188.557	1.00	79.15	C
	ATOM	4674	CD2	LEU A 613	30.562	31.918	186.808	1.00	74.82	C
	ATOM	4675	N	CYS A 614	34.583	35.321	187.262	1.00	72.33	N
	ATOM	4676	CA	CYS A 614	35.473	35.883	186.253	1.00	71.46	C
10	ATOM	4677	C	CYS A 614	36.923	35.656	186.627	1.00	79.88	C
	ATOM	4678	O	CYS A 614	37.754	35.422	185.749	1.00	86.31	O
	ATOM	4679	CB	CYS A 614	35.239	37.380	186.086	1.00	64.58	C
	ATOM	4680	SG	CYS A 614	33.746	37.791	185.228	1.00	75.42	S
	ATOM	4681	N	ARG A 615	37.226	35.746	187.923	1.00	74.45	N
15	ATOM	4682	CA	ARG A 615	38.559	35.411	188.422	1.00	77.44	C
	ATOM	4683	C	ARG A 615	38.893	33.963	188.117	1.00	83.00	C
	ATOM	4684	O	ARG A 615	39.906	33.681	187.495	1.00	92.86	O
	ATOM	4685	CB	ARG A 615	38.659	35.639	189.925	1.00	89.45	C
	ATOM	4686	CG	ARG A 615	38.959	37.063	190.311	1.00	97.73	C
20	ATOM	4687	CD	ARG A 615	39.328	37.174	191.780	1.00	98.85	C
	ATOM	4688	NE	ARG A 615	40.003	38.439	192.038	1.00	96.13	N
	ATOM	4689	CZ	ARG A 615	39.382	39.541	192.432	1.00	94.41	C
	ATOM	4690	NH1	ARG A 615	38.068	39.519	192.637	1.00	93.84	N
	ATOM	4691	NH2	ARG A 615	40.076	40.656	192.628	1.00	90.82	N
25	ATOM	4692	N	ASP A 616	38.032	33.051	188.556	1.00	88.57	N
	ATOM	4693	CA	ASP A 616	38.242	31.625	188.341	1.00	99.76	C
	ATOM	4694	C	ASP A 616	38.439	31.323	186.866	1.00	100.09	C
	ATOM	4695	O	ASP A 616	39.105	30.353	186.505	1.00	106.00	O
	ATOM	4696	CB	ASP A 616	37.054	30.813	188.864	1.00	108.74	C
30	ATOM	4697	CG	ASP A 616	36.878	30.927	190.367	1.00	116.18	C
	ATOM	4698	OD1	ASP A 616	37.882	31.178	191.072	1.00	117.50	O
	ATOM	4699	OD2	ASP A 616	35.733	30.758	190.842	1.00	117.91	O
	ATOM	4700	N	ALA A 617	37.855	32.163	186.018	1.00	96.64	N
	ATOM	4701	CA	ALA A 617	37.875	31.952	184.574	1.00	100.14	C
35	ATOM	4702	C	ALA A 617	38.835	32.908	183.866	1.00	101.33	C
	ATOM	4703	O	ALA A 617	38.762	33.088	182.649	1.00	91.02	O
	ATOM	4704	CB	ALA A 617	36.473	32.089	184.005	1.00	92.88	C
	ATOM	4705	N	GLY A 618	39.728	33.515	184.640	1.00	105.94	N
	ATOM	4706	CA	GLY A 618	40.745	34.395	184.100	1.00	74.60	C
40	ATOM	4707	C	GLY A 618	40.203	35.542	183.281	1.00	78.73	C

	ATOM	4708	O	GLY A 618	40.712	35.839	182.210	1.00	83.72	O
	ATOM	4709	N	ILE A 619	39.172	36.202	183.777	1.00	68.29	N
	ATOM	4710	CA	ILE A 619	38.594	37.323	183.051	1.00	75.64	C
	ATOM	4711	C	ILE A 619	38.664	38.605	183.866	1.00	70.93	C
5	ATOM	4712	O	ILE A 619	38.033	38.707	184.911	1.00	70.48	O
	ATOM	4713	CB	ILE A 619	37.120	37.047	182.715	1.00	76.59	C
	ATOM	4714	CG1	ILE A 619	36.991	35.760	181.900	1.00	64.31	C
	ATOM	4715	CG2	ILE A 619	36.489	38.239	181.996	1.00	71.90	C
	ATOM	4716	CD1	ILE A 619	35.580	35.428	181.546	1.00	63.95	C
10	ATOM	4717	N	ARG A 620	39.428	39.579	183.391	1.00	62.94	N
	ATOM	4718	CA	ARG A 620	39.547	40.843	184.094	1.00	62.14	C
	ATOM	4719	C	ARG A 620	38.262	41.631	183.978	1.00	74.08	C
	ATOM	4720	O	ARG A 620	37.587	41.577	182.958	1.00	75.58	O
	ATOM	4721	CB	ARG A 620	40.703	41.650	183.535	1.00	79.39	C
15	ATOM	4722	CG	ARG A 620	41.052	42.853	184.368	1.00	79.24	C
	ATOM	4723	CD	ARG A 620	42.552	43.010	184.441	1.00	78.01	C
	ATOM	4724	NE	ARG A 620	43.113	43.300	183.132	1.00	74.77	N
	ATOM	4725	CZ	ARG A 620	43.363	44.526	182.698	1.00	80.86	C
	ATOM	4726	NH1	ARG A 620	43.873	44.703	181.491	1.00	87.14	N
20	ATOM	4727	NH2	ARG A 620	43.112	45.569	183.474	1.00	62.54	N
	ATOM	4728	N	VAL A 621	37.919	42.359	185.033	1.00	71.01	N
	ATOM	4729	CA	VAL A 621	36.675	43.116	185.078	1.00	63.99	C
	ATOM	4730	C	VAL A 621	37.026	44.543	185.454	1.00	65.00	C
	ATOM	4731	O	VAL A 621	37.763	44.773	186.410	1.00	76.87	O
25	ATOM	4732	CB	VAL A 621	35.710	42.528	186.126	1.00	69.09	C
	ATOM	4733	CG1	VAL A 621	34.522	43.456	186.355	1.00	56.69	C
	ATOM	4734	CG2	VAL A 621	35.258	41.125	185.720	1.00	58.90	C
	ATOM	4735	N	ILE A 622	36.528	45.505	184.693	1.00	58.66	N
	ATOM	4736	CA	ILE A 622	36.907	46.897	184.912	1.00	62.29	C
30	ATOM	4737	C	ILE A 622	35.668	47.744	185.109	1.00	61.86	C
	ATOM	4738	O	ILE A 622	34.859	47.890	184.201	1.00	68.21	O
	ATOM	4739	CB	ILE A 622	37.734	47.480	183.710	1.00	69.79	C
	ATOM	4740	CG1	ILE A 622	38.999	46.653	183.455	1.00	65.53	C
	ATOM	4741	CG2	ILE A 622	38.107	48.948	183.944	1.00	53.84	C
35	ATOM	4742	CD1	ILE A 622	39.930	47.274	182.440	1.00	61.92	C
	ATOM	4743	N	MET A 623	35.512	48.304	186.296	1.00	55.22	N
	ATOM	4744	CA	MET A 623	34.396	49.203	186.535	1.00	57.33	C
	ATOM	4745	C	MET A 623	34.618	50.550	185.874	1.00	67.38	C
	ATOM	4746	O	MET A 623	35.675	51.153	186.026	1.00	75.83	O
40	ATOM	4747	CB	MET A 623	34.190	49.425	188.026	1.00	68.00	C

	ATOM	4748	CG	MET A 623	33.072	50.404	188.300	1.00	77.27	C
	ATOM	4749	SD	MET A 623	32.585	50.512	190.019	1.00	71.29	S
	ATOM	4750	CE	MET A 623	33.726	51.784	190.560	1.00	75.84	C
	ATOM	4751	N	ILE A 624	33.619	51.029	185.142	1.00	69.65	N
5	ATOM	4752	CA	ILE A 624	33.651	52.402	184.653	1.00	66.18	C
	ATOM	4753	C	ILE A 624	32.438	53.141	185.177	1.00	66.18	C
	ATOM	4754	O	ILE A 624	31.339	52.961	184.670	1.00	71.72	O
	ATOM	4755	CB	ILE A 624	33.669	52.465	183.139	1.00	63.10	C
	ATOM	4756	CG1	ILE A 624	34.831	51.633	182.613	1.00	73.07	C
10	ATOM	4757	CG2	ILE A 624	33.809	53.890	182.688	1.00	56.57	C
	ATOM	4758	CD1	ILE A 624	34.784	51.394	181.127	1.00	80.06	C
	ATOM	4759	N	THR A 625	32.655	53.956	186.206	1.00	65.72	N
	ATOM	4760	CA	THR A 625	31.592	54.658	186.912	1.00	64.99	C
	ATOM	4761	C	THR A 625	31.780	56.160	186.758	1.00	66.64	C
15	ATOM	4762	O	THR A 625	32.759	56.618	186.159	1.00	77.38	O
	ATOM	4763	CB	THR A 625	31.615	54.335	188.419	1.00	75.10	C
	ATOM	4764	OG1	THR A 625	30.529	54.997	189.080	1.00	83.41	O
	ATOM	4765	CG2	THR A 625	32.913	54.813	189.042	1.00	75.29	C
	ATOM	4766	N	GLY A 626	30.842	56.922	187.307	1.00	58.86	N
20	ATOM	4767	CA	GLY A 626	30.877	58.366	187.204	1.00	59.41	C
	ATOM	4768	C	GLY A 626	30.894	59.002	188.577	1.00	74.69	C
	ATOM	4769	O	GLY A 626	30.834	60.229	188.702	1.00	80.04	O
	ATOM	4770	N	ASP A 627	30.947	58.164	189.613	1.00	76.40	N
	ATOM	4771	CA	ASP A 627	31.157	58.640	190.973	1.00	84.98	C
25	ATOM	4772	C	ASP A 627	32.539	59.260	191.004	1.00	82.44	C
	ATOM	4773	O	ASP A 627	33.382	58.905	190.184	1.00	88.26	O
	ATOM	4774	CB	ASP A 627	31.170	57.468	191.957	1.00	96.55	C
	ATOM	4775	CG	ASP A 627	29.828	56.773	192.084	1.00	95.54	C
	ATOM	4776	OD2	ASP A 627	29.032	57.182	192.971	1.00	95.08	O
30	ATOM	4777	OD1	ASP A 627	29.601	55.801	191.321	1.00	85.59	O
	ATOM	4778	N	ASN A 628	32.801	60.155	191.953	1.00	76.03	N
	ATOM	4779	CA	ASN A 628	34.175	60.567	192.198	1.00	73.63	C
	ATOM	4780	C	ASN A 628	35.009	59.334	192.522	1.00	77.11	C
	ATOM	4781	O	ASN A 628	34.461	58.256	192.758	1.00	76.04	O
35	ATOM	4782	CB	ASN A 628	34.286	61.641	193.297	1.00	83.44	C
	ATOM	4783	CG	ASN A 628	33.810	61.162	194.678	1.00	87.24	C
	ATOM	4784	OD1	ASN A 628	33.645	59.964	194.926	1.00	85.13	O
	ATOM	4785	ND2	ASN A 628	33.605	62.118	195.591	1.00	87.38	N
	ATOM	4786	N	LYS A 629	36.326	59.487	192.538	1.00	80.78	N
40	ATOM	4787	CA	LYS A 629	37.207	58.335	192.647	1.00	72.26	C

	ATOM	4788	C	LYS A 629	37.054	57.576	193.953	1.00	74.96	C
	ATOM	4789	O	LYS A 629	37.042	56.347	193.953	1.00	74.03	O
	ATOM	4790	CB	LYS A 629	38.652	58.769	192.488	1.00	69.31	C
	ATOM	4791	CG	LYS A 629	39.625	57.626	192.415	1.00	65.15	C
5	ATOM	4792	CD	LYS A 629	41.008	58.216	192.427	1.00	84.96	C
	ATOM	4793	CE	LYS A 629	42.071	57.166	192.367	1.00	83.21	C
	ATOM	4794	NZ	LYS A 629	43.375	57.852	192.378	1.00	85.54	N
	ATOM	4795	N	GLY A 630	36.943	58.313	195.058	1.00	80.11	N
	ATOM	4796	CA	GLY A 630	36.948	57.723	196.388	1.00	87.65	C
10	ATOM	4797	C	GLY A 630	35.805	56.750	196.577	1.00	88.30	C
	ATOM	4798	O	GLY A 630	35.996	55.622	197.040	1.00	89.17	O
	ATOM	4799	N	THR A 631	34.615	57.199	196.194	1.00	82.62	N
	ATOM	4800	CA	THR A 631	33.419	56.384	196.255	1.00	77.31	C
	ATOM	4801	C	THR A 631	33.552	55.161	195.363	1.00	71.16	C
15	ATOM	4802	O	THR A 631	33.286	54.049	195.800	1.00	76.97	O
	ATOM	4803	CB	THR A 631	32.204	57.183	195.812	1.00	83.15	C
	ATOM	4804	OG1	THR A 631	32.203	58.450	196.478	1.00	86.93	O
	ATOM	4805	CG2	THR A 631	30.940	56.438	196.148	1.00	89.84	C
	ATOM	4806	N	ALA A 632	33.974	55.382	194.121	1.00	65.86	N
20	ATOM	4807	CA	ALA A 632	34.235	54.319	193.149	1.00	61.62	C
	ATOM	4808	C	ALA A 632	35.046	53.166	193.715	1.00	76.19	C
	ATOM	4809	O	ALA A 632	34.704	51.998	193.511	1.00	68.61	O
	ATOM	4810	CB	ALA A 632	34.946	54.887	191.955	1.00	60.13	C
	ATOM	4811	N	ILE A 633	36.121	53.504	194.427	1.00	80.89	N
25	ATOM	4812	CA	ILE A 633	37.020	52.506	195.006	1.00	75.37	C
	ATOM	4813	C	ILE A 633	36.357	51.770	196.156	1.00	76.26	C
	ATOM	4814	O	ILE A 633	36.525	50.562	196.296	1.00	75.62	O
	ATOM	4815	CB	ILE A 633	38.324	53.141	195.493	1.00	77.52	C
	ATOM	4816	CG1	ILE A 633	38.977	53.924	194.364	1.00	82.01	C
30	ATOM	4817	CG2	ILE A 633	39.301	52.081	195.944	1.00	70.82	C
	ATOM	4818	CD1	ILE A 633	40.269	54.531	194.752	1.00	69.24	C
	ATOM	4819	N	ALA A 634	35.598	52.504	196.967	1.00	80.53	N
	ATOM	4820	CA	ALA A 634	34.778	51.911	198.028	1.00	82.48	C
	ATOM	4821	C	ALA A 634	33.787	50.891	197.475	1.00	80.89	C
35	ATOM	4822	O	ALA A 634	33.599	49.813	198.040	1.00	85.23	O
	ATOM	4823	CB	ALA A 634	34.038	52.988	198.759	1.00	72.59	C
	ATOM	4824	N	ILE A 635	33.159	51.243	196.361	1.00	73.60	N
	ATOM	4825	CA	ILE A 635	32.253	50.344	195.663	1.00	75.60	C
	ATOM	4826	C	ILE A 635	32.952	49.087	195.108	1.00	80.12	C
40	ATOM	4827	O	ILE A 635	32.423	47.980	195.240	1.00	85.11	O

	ATOM	4828	CB	ILE A 635	31.476	51.099	194.547	1.00	81.48	C
	ATOM	4829	CG1	ILE A 635	30.738	52.301	195.149	1.00	80.31	C
	ATOM	4830	CG2	ILE A 635	30.502	50.163	193.839	1.00	62.82	C
	ATOM	4831	CD1	ILE A 635	30.582	53.490	194.231	1.00	63.11	C
5	ATOM	4832	N	CYS A 636	34.130	49.253	194.500	1.00	72.52	N
	ATOM	4833	CA	CYS A 636	34.920	48.110	194.027	1.00	72.54	C
	ATOM	4834	C	CYS A 636	35.304	47.129	195.149	1.00	82.26	C
	ATOM	4835	O	CYS A 636	35.383	45.913	194.933	1.00	68.94	O
	ATOM	4836	CB	CYS A 636	36.179	48.585	193.306	1.00	64.36	C
10	ATOM	4837	SG	CYS A 636	35.880	49.174	191.624	1.00	89.90	S
	ATOM	4838	N	ARG A 637	35.551	47.658	196.343	1.00	70.58	N
	ATOM	4839	CA	ARG A 637	35.943	46.822	197.455	1.00	74.07	C
	ATOM	4840	C	ARG A 637	34.741	46.028	197.909	1.00	86.70	C
	ATOM	4841	O	ARG A 637	34.828	44.828	198.163	1.00	88.85	O
15	ATOM	4842	CB	ARG A 637	36.463	47.680	198.589	1.00	76.44	C
	ATOM	4843	CG	ARG A 637	37.701	48.453	198.247	1.00	76.14	C
	ATOM	4844	CD	ARG A 637	38.472	48.836	199.486	1.00	79.69	C
	ATOM	4845	NE	ARG A 637	39.470	49.858	199.198	1.00	92.48	N
	ATOM	4846	CZ	ARG A 637	40.777	49.671	199.316	1.00	94.93	C
20	ATOM	4847	NH1	ARG A 637	41.230	48.497	199.729	1.00	99.95	N
	ATOM	4848	NH2	ARG A 637	41.628	50.655	199.035	1.00	92.81	N
	ATOM	4849	N	ARG A 638	33.612	46.720	197.989	1.00	86.89	N
	ATOM	4850	CA	ARG A 638	32.348	46.130	198.400	1.00	88.30	C
	ATOM	4851	C	ARG A 638	31.912	44.976	197.492	1.00	86.50	C
25	ATOM	4852	O	ARG A 638	31.381	43.980	197.964	1.00	87.59	O
	ATOM	4853	CB	ARG A 638	31.280	47.219	198.427	1.00	91.37	C
	ATOM	4854	CG	ARG A 638	29.999	46.835	199.128	1.00	101.09	C
	ATOM	4855	CD	ARG A 638	29.066	48.028	199.214	1.00	105.37	C
	ATOM	4856	NE	ARG A 638	27.760	47.662	199.751	1.00	113.39	N
30	ATOM	4857	CZ	ARG A 638	26.687	48.439	199.664	1.00	118.51	C
	ATOM	4858	NH1	ARG A 638	26.776	49.618	199.052	1.00	118.61	N
	ATOM	4859	NH2	ARG A 638	25.527	48.039	200.177	1.00	118.06	N
	ATOM	4860	N	ILE A 639	32.155	45.101	196.192	1.00	81.91	N
	ATOM	4861	CA	ILE A 639	31.725	44.075	195.245	1.00	78.44	C
35	ATOM	4862	C	ILE A 639	32.819	43.086	194.842	1.00	81.21	C
	ATOM	4863	O	ILE A 639	32.608	42.248	193.954	1.00	80.77	O
	ATOM	4864	CB	ILE A 639	31.124	44.688	193.973	1.00	75.56	C
	ATOM	4865	CG1	ILE A 639	32.133	45.591	193.276	1.00	71.88	C
	ATOM	4866	CG2	ILE A 639	29.883	45.493	194.304	1.00	79.96	C
40	ATOM	4867	CD1	ILE A 639	31.825	45.799	191.804	1.00	73.80	C

	ATOM	4868	N	GLY A 640	33.987	43.191	195.475	1.00	80.74	N
	ATOM	4869	CA	GLY A 640	35.052	42.224	195.259	1.00	81.98	C
	ATOM	4870	C	GLY A 640	36.029	42.447	194.110	1.00	79.16	C
	ATOM	4871	O	GLY A 640	36.811	41.558	193.782	1.00	83.26	O
5	ATOM	4872	N	ILE A 641	35.993	43.617	193.487	1.00	71.54	N
	ATOM	4873	CA	ILE A 641	37.007	43.967	192.508	1.00	74.89	C
	ATOM	4874	C	ILE A 641	38.351	44.086	193.233	1.00	90.39	C
	ATOM	4875	O	ILE A 641	39.376	43.570	192.767	1.00	93.72	O
	ATOM	4876	CB	ILE A 641	36.703	45.314	191.844	1.00	74.04	C
10	ATOM	4877	CG1	ILE A 641	35.335	45.292	191.173	1.00	62.43	C
	ATOM	4878	CG2	ILE A 641	37.763	45.644	190.819	1.00	80.68	C
	ATOM	4879	CD1	ILE A 641	35.357	44.960	189.726	1.00	60.43	C
	ATOM	4880	N	PHE A 642	38.323	44.771	194.381	1.00	91.27	N
	ATOM	4881	CA	PHE A 642	39.491	44.966	195.239	1.00	84.92	C
15	ATOM	4882	C	PHE A 642	39.355	44.198	196.543	1.00	86.89	C
	ATOM	4883	O	PHE A 642	38.290	43.694	196.862	1.00	94.33	O
	ATOM	4884	CB	PHE A 642	39.694	46.452	195.538	1.00	81.83	C
	ATOM	4885	CG	PHE A 642	40.117	47.256	194.340	1.00	83.25	C
	ATOM	4886	CD1	PHE A 642	40.822	46.665	193.311	1.00	81.88	C
20	ATOM	4887	CD2	PHE A 642	39.813	48.601	194.242	1.00	80.50	C
	ATOM	4888	CE1	PHE A 642	41.212	47.399	192.219	1.00	78.47	C
	ATOM	4889	CE2	PHE A 642	40.208	49.339	193.148	1.00	69.14	C
	ATOM	4890	CZ	PHE A 642	40.903	48.739	192.140	1.00	71.79	C
	ATOM	4891	N	GLY A 643	40.443	44.101	197.294	1.00	86.15	N
25	ATOM	4892	CA	GLY A 643	40.406	43.434	198.577	1.00	92.85	C
	ATOM	4893	C	GLY A 643	39.927	44.400	199.637	1.00	108.75	C
	ATOM	4894	O	GLY A 643	39.813	45.599	199.384	1.00	110.39	O
	ATOM	4895	N	GLU A 644	39.634	43.885	200.825	1.00	119.15	N
	ATOM	4896	CA	GLU A 644	39.220	44.747	201.921	1.00	126.67	C
30	ATOM	4897	C	GLU A 644	40.326	45.759	202.236	1.00	121.89	C
	ATOM	4898	O	GLU A 644	40.054	46.931	202.505	1.00	119.96	O
	ATOM	4899	CB	GLU A 644	38.847	43.913	203.154	1.00	143.72	C
	ATOM	4900	CG	GLU A 644	37.533	43.137	203.008	1.00	151.31	C
	ATOM	4901	CD	GLU A 644	37.368	42.026	204.046	1.00	162.12	C
35	ATOM	4902	OE1	GLU A 644	38.104	41.018	203.964	1.00	166.90	O
	ATOM	4903	OE2	GLU A 644	36.500	42.155	204.939	1.00	163.42	O
	ATOM	4904	N	ASN A 645	41.576	45.308	202.168	1.00	119.30	N
	ATOM	4905	CA	ASN A 645	42.710	46.186	202.438	1.00	118.08	C
	ATOM	4906	C	ASN A 645	43.739	46.222	201.302	1.00	115.22	C
40	ATOM	4907	O	ASN A 645	44.879	46.640	201.498	1.00	116.33	O

	ATOM	4908	CB	ASN A 645	43.375	45.802	203.760	1.00122.37	C
	ATOM	4909	CG	ASN A 645	42.375	45.651	204.887	1.00120.79	C
	ATOM	4910	OD1	ASN A 645	42.057	46.616	205.584	1.00121.92	O
	ATOM	4911	ND2	ASN A 645	41.866	44.436	205.068	1.00117.49	N
5	ATOM	4912	N	GLU A 646	43.323	45.795	200.113	1.00109.29	N
	ATOM	4913	CA	GLU A 646	44.185	45.834	198.938	1.00100.23	C
	ATOM	4914	C	GLU A 646	44.695	47.253	198.719	1.00102.89	C
	ATOM	4915	O	GLU A 646	44.086	48.222	199.163	1.00 99.93	O
	ATOM	4916	CB	GLU A 646	43.447	45.320	197.692	1.00 89.79	C
10	ATOM	4917	CG	GLU A 646	44.352	45.079	196.488	1.00 95.34	C
	ATOM	4918	CD	GLU A 646	43.662	44.388	195.311	1.00100.95	C
	ATOM	4919	OE1	GLU A 646	43.887	44.819	194.156	1.00101.93	O
	ATOM	4920	OE2	GLU A 646	42.921	43.404	195.530	1.00101.50	O
	ATOM	4921	N	GLU A 647	45.834	47.363	198.054	1.00113.20	N
15	ATOM	4922	CA	GLU A 647	46.422	48.651	197.737	1.00119.60	C
	ATOM	4923	C	GLU A 647	46.103	48.953	196.281	1.00117.80	C
	ATOM	4924	O	GLU A 647	46.346	48.115	195.409	1.00120.76	O
	ATOM	4925	CB	GLU A 647	47.931	48.570	197.946	1.00127.58	C
	ATOM	4926	CG	GLU A 647	48.566	49.844	198.437	1.00137.21	C
20	ATOM	4927	CD	GLU A 647	48.689	50.879	197.349	1.00143.62	C
	ATOM	4928	OE1	GLU A 647	49.229	50.546	196.267	1.00143.24	O
	ATOM	4929	OE2	GLU A 647	48.242	52.024	197.579	1.00148.03	O
	ATOM	4930	N	VAL A 648	45.532	50.123	195.999	1.00112.54	N
	ATOM	4931	CA	VAL A 648	45.129	50.418	194.617	1.00108.65	C
25	ATOM	4932	C	VAL A 648	45.451	51.829	194.120	1.00103.27	C
	ATOM	4933	O	VAL A 648	44.745	52.368	193.261	1.00 97.88	O
	ATOM	4934	CB	VAL A 648	43.612	50.134	194.365	1.00 86.77	C
	ATOM	4935	CG1	VAL A 648	43.260	48.716	194.742	1.00 88.65	C
	ATOM	4936	CG2	VAL A 648	42.731	51.104	195.127	1.00 74.55	C
30	ATOM	4937	N	ALA A 649	46.521	52.429	194.624	1.00101.14	N
	ATOM	4938	CA	ALA A 649	46.827	53.789	194.201	1.00103.59	C
	ATOM	4939	C	ALA A 649	47.424	53.790	192.801	1.00107.73	C
	ATOM	4940	O	ALA A 649	47.882	54.821	192.309	1.00116.29	O
	ATOM	4941	CB	ALA A 649	47.741	54.464	195.174	1.00107.92	C
35	ATOM	4942	N	ASP A 650	47.403	52.625	192.163	1.00 99.57	N
	ATOM	4943	CA	ASP A 650	47.883	52.479	190.805	1.00 96.08	C
	ATOM	4944	C	ASP A 650	46.970	51.569	189.999	1.00 97.88	C
	ATOM	4945	O	ASP A 650	47.324	51.158	188.897	1.00 99.69	O
	ATOM	4946	CB	ASP A 650	49.293	51.898	190.811	1.00110.76	C
40	ATOM	4947	CG	ASP A 650	49.352	50.505	191.417	1.00124.61	C

	ATOM	4948	OD2 ASP A 650	49.760	50.382	192.595	1.00137.78	O
	ATOM	4949	OD1 ASP A 650	49.008	49.529	190.714	1.00121.13	O
	ATOM	4950	N ARG A 651	45.803	51.239	190.552	1.00100.73	N
	ATOM	4951	CA ARG A 651	44.847	50.357	189.871	1.00 91.87	C
5	ATOM	4952	C ARG A 651	43.501	51.040	189.668	1.00 83.73	C
	ATOM	4953	O ARG A 651	42.560	50.432	189.167	1.00 90.63	O
	ATOM	4954	CB ARG A 651	44.657	49.037	190.632	1.00 98.30	C
	ATOM	4955	CG ARG A 651	45.814	48.045	190.502	1.00115.54	C
	ATOM	4956	CD ARG A 651	45.600	46.786	191.354	1.00130.62	C
10	ATOM	4957	NE ARG A 651	44.351	46.094	191.022	1.00141.77	N
	ATOM	4958	CZ ARG A 651	44.255	45.036	190.218	1.00143.17	C
	ATOM	4959	NH1 ARG A 651	45.342	44.528	189.652	1.00147.22	N
	ATOM	4960	NH2 ARG A 651	43.069	44.484	189.984	1.00135.54	N
	ATOM	4961	N ALA A 652	43.407	52.305	190.057	1.00 72.25	N
15	ATOM	4962	CA ALA A 652	42.190	53.064	189.825	1.00 69.66	C
	ATOM	4963	C ALA A 652	42.479	54.509	189.466	1.00 71.33	C
	ATOM	4964	O ALA A 652	43.222	55.193	190.158	1.00 82.39	O
	ATOM	4965	CB ALA A 652	41.265	52.989	191.027	1.00 70.13	C
	ATOM	4966	N TYR A 653	41.874	54.971	188.381	1.00 62.17	N
20	ATOM	4967	CA TYR A 653	42.153	56.300	187.848	1.00 76.13	C
	ATOM	4968	C TYR A 653	40.897	57.154	187.627	1.00 70.51	C
	ATOM	4969	O TYR A 653	39.877	56.665	187.170	1.00 58.83	O
	ATOM	4970	CB TYR A 653	42.973	56.190	186.539	1.00 73.12	C
	ATOM	4971	CG TYR A 653	44.370	55.650	186.743	1.00 64.79	C
25	ATOM	4972	CD1 TYR A 653	44.631	54.280	186.694	1.00 69.96	C
	ATOM	4973	CD2 TYR A 653	45.414	56.500	187.013	1.00 67.24	C
	ATOM	4974	CE1 TYR A 653	45.899	53.780	186.905	1.00 67.79	C
	ATOM	4975	CE2 TYR A 653	46.677	56.014	187.231	1.00 80.56	C
	ATOM	4976	CZ TYR A 653	46.922	54.658	187.179	1.00 77.74	C
30	ATOM	4977	OH TYR A 653	48.213	54.213	187.401	1.00 78.34	O
	ATOM	4978	N THR A 654	40.990	58.422	188.013	1.00 67.94	N
	ATOM	4979	CA THR A 654	40.125	59.488	187.543	1.00 65.55	C
	ATOM	4980	C THR A 654	40.417	59.608	186.055	1.00 75.12	C
	ATOM	4981	O THR A 654	41.536	59.332	185.636	1.00 77.22	O
35	ATOM	4982	CB THR A 654	40.540	60.829	188.182	1.00 74.35	C
	ATOM	4983	OG1 THR A 654	40.230	60.828	189.570	1.00 81.93	O
	ATOM	4984	CG2 THR A 654	39.830	61.986	187.566	1.00 81.73	C
	ATOM	4985	N GLY A 655	39.430	60.011	185.251	1.00 77.45	N
	ATOM	4986	CA GLY A 655	39.643	60.236	183.832	1.00 66.41	C
40	ATOM	4987	C GLY A 655	40.605	61.388	183.614	1.00 67.86	C

	ATOM	4988	O	GLY A 655	41.228	61.490	182.569	1.00	74.70	O
	ATOM	4989	N	ARG A 656	40.727	62.252	184.616	1.00	66.92	N
	ATOM	4990	CA	ARG A 656	41.607	63.412	184.555	1.00	64.61	C
	ATOM	4991	C	ARG A 656	43.026	63.013	184.911	1.00	68.77	C
5	ATOM	4992	O	ARG A 656	43.992	63.493	184.311	1.00	72.45	O
	ATOM	4993	CB	ARG A 656	41.130	64.480	185.531	1.00	65.85	C
	ATOM	4994	CG	ARG A 656	41.933	65.740	185.484	1.00	73.34	C
	ATOM	4995	CD	ARG A 656	41.286	66.837	186.298	1.00	75.78	C
	ATOM	4996	NE	ARG A 656	41.362	66.574	187.729	1.00	82.07	N
10	ATOM	4997	CZ	ARG A 656	42.467	66.698	188.463	1.00	95.96	C
	ATOM	4998	NH1	ARG A 656	43.620	67.079	187.915	1.00	104.02	N
	ATOM	4999	NH2	ARG A 656	42.418	66.429	189.754	1.00	99.26	N
	ATOM	5000	N	GLU A 657	43.135	62.151	185.916	1.00	66.93	N
	ATOM	5001	CA	GLU A 657	44.404	61.581	186.312	1.00	70.84	C
15	ATOM	5002	C	GLU A 657	44.936	60.809	185.130	1.00	70.17	C
	ATOM	5003	O	GLU A 657	46.105	60.933	184.774	1.00	80.82	O
	ATOM	5004	CB	GLU A 657	44.222	60.631	187.500	1.00	78.96	C
	ATOM	5005	CG	GLU A 657	43.913	61.306	188.831	1.00	89.56	C
	ATOM	5006	CD	GLU A 657	43.574	60.311	189.938	1.00	103.49	C
20	ATOM	5007	OE1	GLU A 657	43.367	59.118	189.625	1.00	101.05	O
	ATOM	5008	OE2	GLU A 657	43.514	60.723	191.122	1.00	114.23	O
	ATOM	5009	N	PHE A 658	44.060	60.029	184.507	1.00	70.36	N
	ATOM	5010	CA	PHE A 658	44.437	59.166	183.391	1.00	77.88	C
	ATOM	5011	C	PHE A 658	44.922	59.960	182.180	1.00	82.26	C
25	ATOM	5012	O	PHE A 658	45.691	59.466	181.356	1.00	87.04	O
	ATOM	5013	CB	PHE A 658	43.261	58.273	182.986	1.00	74.32	C
	ATOM	5014	CG	PHE A 658	43.572	57.354	181.846	1.00	72.06	C
	ATOM	5015	CD1	PHE A 658	44.265	56.175	182.063	1.00	68.02	C
	ATOM	5016	CD2	PHE A 658	43.187	57.676	180.552	1.00	72.68	C
30	ATOM	5017	CE1	PHE A 658	44.553	55.331	181.023	1.00	66.27	C
	ATOM	5018	CE2	PHE A 658	43.480	56.837	179.502	1.00	68.82	C
	ATOM	5019	CZ	PHE A 658	44.155	55.660	179.737	1.00	69.30	C
	ATOM	5020	N	ASP A 659	44.464	61.200	182.089	1.00	79.80	N
	ATOM	5021	CA	ASP A 659	44.791	62.062	180.973	1.00	78.34	C
35	ATOM	5022	C	ASP A 659	46.113	62.798	181.166	1.00	82.84	C
	ATOM	5023	O	ASP A 659	46.536	63.567	180.305	1.00	82.82	O
	ATOM	5024	CB	ASP A 659	43.653	63.057	180.763	1.00	78.16	C
	ATOM	5025	CG	ASP A 659	42.553	62.502	179.873	1.00	78.98	C
	ATOM	5026	OD1	ASP A 659	42.607	61.294	179.532	1.00	78.03	O
40	ATOM	5027	OD2	ASP A 659	41.637	63.275	179.518	1.00	78.16	O

	ATOM	5028	N	ASP A 660	46.769	62.571	182.295	1.00	86.30	N
	ATOM	5029	CA	ASP A 660	48.041	63.233	182.538	1.00	94.09	C
	ATOM	5030	C	ASP A 660	49.219	62.273	182.492	1.00	90.54	C
	ATOM	5031	O	ASP A 660	50.376	62.696	182.495	1.00	89.32	O
5	ATOM	5032	CB	ASP A 660	48.018	64.031	183.838	1.00	105.44	C
	ATOM	5033	CG	ASP A 660	47.403	65.400	183.653	1.00	121.61	C
	ATOM	5034	OD1	ASP A 660	48.164	66.340	183.338	1.00	127.03	O
	ATOM	5035	OD2	ASP A 660	46.162	65.536	183.798	1.00	127.17	O
	ATOM	5036	N	LEU A 661	48.925	60.980	182.445	1.00	84.24	N
10	ATOM	5037	CA	LEU A 661	49.973	60.010	182.236	1.00	76.49	C
	ATOM	5038	C	LEU A 661	50.369	60.162	180.769	1.00	92.98	C
	ATOM	5039	O	LEU A 661	49.504	60.322	179.903	1.00	96.65	O
	ATOM	5040	CB	LEU A 661	49.466	58.585	182.507	1.00	102.21	C
	ATOM	5041	CG	LEU A 661	48.538	58.234	183.679	1.00	72.41	C
15	ATOM	5042	CD1	LEU A 661	48.214	56.762	183.669	1.00	115.06	C
	ATOM	5043	CD2	LEU A 661	49.141	58.599	185.000	1.00	91.60	C
	ATOM	5044	N	PRO A 662	51.678	60.129	180.473	1.00	87.91	N
	ATOM	5045	CA	PRO A 662	52.072	60.024	179.071	1.00	94.25	C
	ATOM	5046	C	PRO A 662	51.409	58.814	178.443	1.00	88.34	C
20	ATOM	5047	O	PRO A 662	50.878	57.974	179.156	1.00	83.94	O
	ATOM	5048	CB	PRO A 662	53.587	59.827	179.158	1.00	110.85	C
	ATOM	5049	CG	PRO A 662	53.870	59.528	180.609	1.00	87.04	C
	ATOM	5050	CD	PRO A 662	52.849	60.252	181.353	1.00	84.49	C
	ATOM	5051	N	LEU A 663	51.417	58.712	177.126	1.00	92.57	N
25	ATOM	5052	CA	LEU A 663	50.611	57.664	176.521	1.00	95.94	C
	ATOM	5053	C	LEU A 663	51.187	56.313	176.916	1.00	93.03	C
	ATOM	5054	O	LEU A 663	50.446	55.357	177.163	1.00	74.92	O
	ATOM	5055	CB	LEU A 663	50.535	57.842	175.004	1.00	99.86	C
	ATOM	5056	CG	LEU A 663	50.119	59.254	174.610	1.00	77.18	C
30	ATOM	5057	CD1	LEU A 663	50.391	59.502	173.161	1.00	79.00	C
	ATOM	5058	CD2	LEU A 663	48.671	59.477	174.931	1.00	73.61	C
	ATOM	5059	N	ALA A 664	52.517	56.282	177.030	1.00	92.86	N
	ATOM	5060	CA	ALA A 664	53.276	55.079	177.344	1.00	83.20	C
	ATOM	5061	C	ALA A 664	52.727	54.416	178.588	1.00	81.33	C
35	ATOM	5062	O	ALA A 664	52.602	53.194	178.670	1.00	80.87	O
	ATOM	5063	CB	ALA A 664	54.690	55.447	177.557	1.00	87.90	C
	ATOM	5064	N	GLU A 665	52.372	55.271	179.542	1.00	80.48	N
	ATOM	5065	CA	GLU A 665	51.923	54.887	180.866	1.00	89.90	C
	ATOM	5066	C	GLU A 665	50.404	54.733	180.966	1.00	84.41	C
40	ATOM	5067	O	GLU A 665	49.903	54.151	181.931	1.00	84.82	O

	ATOM	5068	CB	GLU A 665	52.404	55.924	181.872	1.00	81.31	C
	ATOM	5069	CG	GLU A 665	53.589	55.491	182.651	1.00	85.29	C
	ATOM	5070	CD	GLU A 665	54.071	56.585	183.570	1.00	110.25	C
	ATOM	5071	OE1	GLU A 665	55.174	56.458	184.166	1.00	114.88	O
5	ATOM	5072	OE2	GLU A 665	53.334	57.586	183.684	1.00	107.62	O
	ATOM	5073	N	GLN A 666	49.666	55.270	179.996	1.00	78.49	N
	ATOM	5074	CA	GLN A 666	48.227	55.024	179.939	1.00	73.44	C
	ATOM	5075	C	GLN A 666	48.007	53.589	179.470	1.00	77.35	C
	ATOM	5076	O	GLN A 666	47.118	52.892	179.965	1.00	66.24	O
10	ATOM	5077	CB	GLN A 666	47.541	55.999	178.984	1.00	68.77	C
	ATOM	5078	CG	GLN A 666	47.742	57.464	179.320	1.00	75.28	C
	ATOM	5079	CD	GLN A 666	47.080	58.387	178.310	1.00	77.32	C
	ATOM	5080	OE1	GLN A 666	46.514	57.932	177.311	1.00	66.73	O
	ATOM	5081	NE2	GLN A 666	47.149	59.693	178.567	1.00	69.23	N
15	ATOM	5082	N	ARG A 667	48.846	53.155	178.524	1.00	82.50	N
	ATOM	5083	CA	ARG A 667	48.775	51.800	177.985	1.00	69.98	C
	ATOM	5084	C	ARG A 667	49.070	50.858	179.128	1.00	93.60	C
	ATOM	5085	O	ARG A 667	48.445	49.802	179.270	1.00	85.84	O
	ATOM	5086	CB	ARG A 667	49.774	51.606	176.841	1.00	74.27	C
20	ATOM	5087	CG	ARG A 667	49.615	50.298	176.064	1.00	72.45	C
	ATOM	5088	CD	ARG A 667	50.678	50.120	174.964	1.00	78.94	C
	ATOM	5089	NE	ARG A 667	50.738	51.237	174.013	1.00	88.92	N
	ATOM	5090	CZ	ARG A 667	51.670	52.194	174.025	1.00	108.73	C
	ATOM	5091	NH1	ARG A 667	52.630	52.173	174.944	1.00	116.87	N
25	ATOM	5092	NH2	ARG A 667	51.651	53.177	173.120	1.00	110.99	N
	ATOM	5093	N	GLU A 668	50.018	51.281	179.960	1.00	99.46	N
	ATOM	5094	CA	GLU A 668	50.399	50.549	181.157	1.00	101.90	C
	ATOM	5095	C	GLU A 668	49.234	50.413	182.129	1.00	93.06	C
	ATOM	5096	O	GLU A 668	48.810	49.302	182.439	1.00	90.25	O
30	ATOM	5097	CB	GLU A 668	51.560	51.254	181.851	1.00	107.50	C
	ATOM	5098	CG	GLU A 668	52.465	50.325	182.609	1.00	111.04	C
	ATOM	5099	CD	GLU A 668	53.150	49.346	181.686	1.00	117.45	C
	ATOM	5100	OE1	GLU A 668	52.484	48.380	181.254	1.00	105.43	O
	ATOM	5101	OE2	GLU A 668	54.353	49.551	181.383	1.00	131.56	O
35	ATOM	5102	N	ALA A 669	48.735	51.553	182.606	1.00	85.21	N
	ATOM	5103	CA	ALA A 669	47.619	51.601	183.541	1.00	84.04	C
	ATOM	5104	C	ALA A 669	46.494	50.646	183.138	1.00	90.52	C
	ATOM	5105	O	ALA A 669	46.008	49.883	183.964	1.00	91.70	O
	ATOM	5106	CB	ALA A 669	47.098	53.028	183.663	1.00	76.36	C
40	ATOM	5107	N	CYS A 670	46.116	50.660	181.859	1.00	87.25	N

	ATOM	5108	CA	CYS A 670	45.053	49.789	181.353	1.00	80.35	C
	ATOM	5109	C	CYS A 670	45.316	48.298	181.570	1.00	80.98	C
	ATOM	5110	O	CYS A 670	44.403	47.486	181.490	1.00	79.77	O
	ATOM	5111	CB	CYS A 670	44.791	50.057	179.871	1.00	61.47	C
5	ATOM	5112	SG	CYS A 670	44.079	51.680	179.568	1.00	75.50	S
	ATOM	5113	N	ARG A 671	46.560	47.936	181.848	1.00	86.79	N
	ATOM	5114	CA	ARG A 671	46.914	46.534	182.030	1.00	90.25	C
	ATOM	5115	C	ARG A 671	46.609	46.075	183.462	1.00	83.97	C
	ATOM	5116	O	ARG A 671	46.343	44.901	183.711	1.00	80.40	O
10	ATOM	5117	CB	ARG A 671	48.398	46.320	181.681	1.00	98.58	C
	ATOM	5118	CG	ARG A 671	48.822	44.872	181.546	1.00	103.68	C
	ATOM	5119	CD	ARG A 671	49.939	44.543	182.511	1.00	111.36	C
	ATOM	5120	NE	ARG A 671	51.171	45.249	182.179	1.00	121.22	N
	ATOM	5121	CZ	ARG A 671	52.009	44.877	181.213	1.00	126.41	C
15	ATOM	5122	NH1	ARG A 671	51.732	43.812	180.471	1.00	126.91	N
	ATOM	5123	NH2	ARG A 671	53.119	45.573	180.980	1.00	124.57	N
	ATOM	5124	N	ARG A 672	46.643	47.012	184.401	1.00	81.70	N
	ATOM	5125	CA	ARG A 672	46.509	46.671	185.810	1.00	89.02	C
	ATOM	5126	C	ARG A 672	45.255	47.294	186.430	1.00	98.33	C
20	ATOM	5127	O	ARG A 672	44.767	46.832	187.464	1.00	108.92	O
	ATOM	5128	CB	ARG A 672	47.764	47.105	186.582	1.00	81.08	C
	ATOM	5129	CG	ARG A 672	48.185	48.539	186.294	1.00	80.70	C
	ATOM	5130	CD	ARG A 672	49.341	49.026	187.162	1.00	89.91	C
	ATOM	5131	NE	ARG A 672	50.182	49.961	186.417	1.00	95.49	N
25	ATOM	5132	CZ	ARG A 672	50.017	51.283	186.397	1.00	95.15	C
	ATOM	5133	NH1	ARG A 672	49.053	51.849	187.102	1.00	88.01	N
	ATOM	5134	NH2	ARG A 672	50.827	52.045	185.671	1.00	103.34	N
	ATOM	5135	N	ALA A 673	44.742	48.344	185.796	1.00	91.79	N
	ATOM	5136	CA	ALA A 673	43.604	49.086	186.321	1.00	87.61	C
30	ATOM	5137	C	ALA A 673	42.335	48.258	186.269	1.00	87.43	C
	ATOM	5138	O	ALA A 673	42.092	47.542	185.299	1.00	87.36	O
	ATOM	5139	CB	ALA A 673	43.410	50.373	185.540	1.00	92.92	C
	ATOM	5140	N	CYS A 674	41.526	48.363	187.320	1.00	88.89	N
	ATOM	5141	CA	CYS A 674	40.213	47.727	187.348	1.00	75.31	C
35	ATOM	5142	C	CYS A 674	39.125	48.715	187.709	1.00	70.39	C
	ATOM	5143	O	CYS A 674	37.987	48.325	187.867	1.00	67.65	O
	ATOM	5144	CB	CYS A 674	40.190	46.568	188.327	1.00	66.80	C
	ATOM	5145	SG	CYS A 674	41.234	45.228	187.811	1.00	109.68	S
	ATOM	5146	N	CYS A 675	39.468	49.994	187.823	1.00	75.18	N
40	ATOM	5147	CA	CYS A 675	38.474	50.999	188.188	1.00	76.33	C

	ATOM	5148	C	CYS A 675	38.732	52.379	187.588	1.00	70.93	C
	ATOM	5149	O	CYS A 675	39.656	53.070	187.977	1.00	68.19	O
	ATOM	5150	CB	CYS A 675	38.371	51.097	189.712	1.00	84.55	C
	ATOM	5151	SG	CYS A 675	37.373	52.463	190.344	1.00	67.53	S
5	ATOM	5152	N	PHE A 676	37.907	52.775	186.631	1.00	68.53	N
	ATOM	5153	CA	PHE A 676	38.004	54.113	186.065	1.00	67.03	C
	ATOM	5154	C	PHE A 676	36.821	54.965	186.526	1.00	65.35	C
	ATOM	5155	O	PHE A 676	35.655	54.590	186.343	1.00	63.08	O
	ATOM	5156	CB	PHE A 676	38.062	54.069	184.530	1.00	61.70	C
10	ATOM	5157	CG	PHE A 676	39.352	53.553	183.992	1.00	59.69	C
	ATOM	5158	CD1	PHE A 676	40.458	54.387	183.899	1.00	65.95	C
	ATOM	5159	CD2	PHE A 676	39.469	52.234	183.586	1.00	61.58	C
	ATOM	5160	CE1	PHE A 676	41.669	53.922	183.414	1.00	69.62	C
	ATOM	5161	CE2	PHE A 676	40.675	51.752	183.097	1.00	73.68	C
15	ATOM	5162	CZ	PHE A 676	41.783	52.602	183.011	1.00	75.74	C
	ATOM	5163	N	ALA A 677	37.120	56.118	187.111	1.00	58.39	N
	ATOM	5164	CA	ALA A 677	36.065	56.977	187.614	1.00	64.08	C
	ATOM	5165	C	ALA A 677	36.060	58.331	186.934	1.00	63.94	C
	ATOM	5166	O	ALA A 677	37.096	58.804	186.505	1.00	57.01	O
20	ATOM	5167	CB	ALA A 677	36.186	57.134	189.130	1.00	74.33	C
	ATOM	5168	N	ARG A 678	34.873	58.937	186.861	1.00	63.65	N
	ATOM	5169	CA	ARG A 678	34.657	60.267	186.282	1.00	62.33	C
	ATOM	5170	C	ARG A 678	35.353	60.456	184.954	1.00	66.00	C
	ATOM	5171	O	ARG A 678	36.233	61.328	184.844	1.00	57.76	O
25	ATOM	5172	CB	ARG A 678	35.116	61.360	187.241	1.00	66.12	C
	ATOM	5173	CG	ARG A 678	34.288	61.444	188.500	1.00	81.60	C
	ATOM	5174	CD	ARG A 678	33.396	62.676	188.543	1.00	88.44	C
	ATOM	5175	NE	ARG A 678	32.408	62.566	189.615	1.00	96.50	N
	ATOM	5176	CZ	ARG A 678	32.432	63.280	190.734	1.00	105.39	C
30	ATOM	5177	NH1	ARG A 678	33.392	64.177	190.926	1.00	110.99	N
	ATOM	5178	NH2	ARG A 678	31.487	63.106	191.653	1.00	106.50	N
	ATOM	5179	N	VAL A 679	34.954	59.651	183.960	1.00	64.16	N
	ATOM	5180	CA	VAL A 679	35.622	59.644	182.661	1.00	70.08	C
	ATOM	5181	C	VAL A 679	34.722	60.123	181.536	1.00	74.91	C
35	ATOM	5182	O	VAL A 679	33.510	60.179	181.700	1.00	85.88	O
	ATOM	5183	CB	VAL A 679	36.136	58.242	182.289	1.00	71.10	C
	ATOM	5184	CG1	VAL A 679	36.865	57.582	183.468	1.00	67.92	C
	ATOM	5185	CG2	VAL A 679	35.014	57.393	181.797	1.00	52.44	C
	ATOM	5186	N	GLU A 680	35.334	60.465	180.399	1.00	84.01	N
40	ATOM	5187	CA	GLU A 680	34.649	60.937	179.178	1.00	88.30	C

	ATOM	5188	C	GLU A 680	34.270	59.791	178.260	1.00	87.41	C
	ATOM	5189	O	GLU A 680	34.851	58.710	178.342	1.00	90.28	O
	ATOM	5190	CB	GLU A 680	35.562	61.864	178.377	1.00	95.28	C
	ATOM	5191	CG	GLU A 680	36.005	63.094	179.115	1.00	107.23	C
5	ATOM	5192	CD	GLU A 680	34.902	64.108	179.228	1.00	114.05	C
	ATOM	5193	OE1	GLU A 680	33.968	64.074	178.389	1.00	107.08	O
	ATOM	5194	OE2	GLU A 680	34.975	64.934	180.162	1.00	122.96	O
	ATOM	5195	N	PRO A 681	33.301	60.019	177.361	1.00	85.90	N
	ATOM	5196	CA	PRO A 681	32.998	58.899	176.462	1.00	78.75	C
10	ATOM	5197	C	PRO A 681	34.179	58.582	175.536	1.00	71.90	C
	ATOM	5198	O	PRO A 681	34.362	57.411	175.171	1.00	69.61	O
	ATOM	5199	CB	PRO A 681	31.744	59.368	175.699	1.00	79.18	C
	ATOM	5200	CG	PRO A 681	31.704	60.854	175.878	1.00	85.83	C
	ATOM	5201	CD	PRO A 681	32.348	61.133	177.214	1.00	87.31	C
15	ATOM	5202	N	SER A 682	34.977	59.591	175.189	1.00	55.40	N
	ATOM	5203	CA	SER A 682	36.228	59.331	174.476	1.00	64.27	C
	ATOM	5204	C	SER A 682	37.047	58.212	175.142	1.00	63.86	C
	ATOM	5205	O	SER A 682	37.577	57.329	174.456	1.00	64.63	O
	ATOM	5206	CB	SER A 682	37.076	60.585	174.397	1.00	65.92	C
20	ATOM	5207	OG	SER A 682	37.843	60.724	175.585	1.00	81.31	O
	ATOM	5208	N	HIS A 683	37.116	58.243	176.476	1.00	55.54	N
	ATOM	5209	CA	HIS A 683	37.913	57.288	177.256	1.00	61.20	C
	ATOM	5210	C	HIS A 683	37.549	55.821	177.020	1.00	66.22	C
	ATOM	5211	O	HIS A 683	38.373	54.932	177.239	1.00	70.16	O
25	ATOM	5212	CB	HIS A 683	37.850	57.590	178.764	1.00	61.65	C
	ATOM	5213	CG	HIS A 683	38.563	58.842	179.167	1.00	65.83	C
	ATOM	5214	ND1	HIS A 683	38.071	59.712	180.120	1.00	68.44	N
	ATOM	5215	CD2	HIS A 683	39.742	59.377	178.764	1.00	74.36	C
	ATOM	5216	CE1	HIS A 683	38.899	60.723	180.278	1.00	68.89	C
30	ATOM	5217	NE2	HIS A 683	39.929	60.542	179.464	1.00	73.07	N
	ATOM	5218	N	LYS A 684	36.324	55.553	176.585	1.00	70.02	N
	ATOM	5219	CA	LYS A 684	35.941	54.161	176.390	1.00	72.37	C
	ATOM	5220	C	LYS A 684	36.728	53.554	175.237	1.00	69.87	C
	ATOM	5221	O	LYS A 684	37.267	52.444	175.352	1.00	62.05	O
35	ATOM	5222	CB	LYS A 684	34.425	53.989	176.221	1.00	63.28	C
	ATOM	5223	CG	LYS A 684	33.732	53.534	177.500	1.00	53.74	C
	ATOM	5224	CD	LYS A 684	32.380	52.923	177.230	1.00	60.57	C
	ATOM	5225	CE	LYS A 684	31.647	52.606	178.527	1.00	66.89	C
	ATOM	5226	NZ	LYS A 684	30.166	52.525	178.310	1.00	65.33	N
40	ATOM	5227	N	SER A 685	36.822	54.305	174.144	1.00	68.47	N

	ATOM	5228	CA	SER A 685	37.574	53.854	172.983	1.00	68.50	C
	ATOM	5229	C	SER A 685	39.077	53.804	173.298	1.00	73.23	C
	ATOM	5230	O	SER A 685	39.761	52.825	172.969	1.00	67.50	O
	ATOM	5231	CB	SER A 685	37.303	54.771	171.798	1.00	62.92	C
5	ATOM	5232	OG	SER A 685	35.933	55.099	171.718	1.00	64.62	O
	ATOM	5233	N	LYS A 686	39.575	54.861	173.940	1.00	73.45	N
	ATOM	5234	CA	LYS A 686	40.959	54.905	174.397	1.00	69.40	C
	ATOM	5235	C	LYS A 686	41.338	53.609	175.122	1.00	75.38	C
	ATOM	5236	O	LYS A 686	42.307	52.943	174.762	1.00	86.49	O
10	ATOM	5237	CB	LYS A 686	41.197	56.118	175.304	1.00	58.91	C
	ATOM	5238	CG	LYS A 686	41.928	57.264	174.625	1.00	68.62	C
	ATOM	5239	CD	LYS A 686	42.431	58.292	175.651	1.00	82.17	C
	ATOM	5240	CE	LYS A 686	43.729	59.005	175.182	1.00	101.52	C
	ATOM	5241	NZ	LYS A 686	44.341	59.949	176.186	1.00	92.42	N
15	ATOM	5242	N	ILE A 687	40.556	53.241	176.125	1.00	66.74	N
	ATOM	5243	CA	ILE A 687	40.813	52.011	176.860	1.00	67.14	C
	ATOM	5244	C	ILE A 687	40.839	50.766	175.956	1.00	70.42	C
	ATOM	5245	O	ILE A 687	41.787	49.992	176.003	1.00	71.59	O
	ATOM	5246	CB	ILE A 687	39.811	51.844	178.026	1.00	62.06	C
20	ATOM	5247	CG1	ILE A 687	40.016	52.962	179.044	1.00	60.50	C
	ATOM	5248	CG2	ILE A 687	39.969	50.489	178.696	1.00	53.29	C
	ATOM	5249	CD1	ILE A 687	39.050	52.926	180.182	1.00	60.14	C
	ATOM	5250	N	VAL A 688	39.810	50.587	175.130	1.00	68.77	N
	ATOM	5251	CA	VAL A 688	39.739	49.440	174.227	1.00	64.57	C
25	ATOM	5252	C	VAL A 688	40.973	49.382	173.359	1.00	68.59	C
	ATOM	5253	O	VAL A 688	41.539	48.306	173.162	1.00	68.58	O
	ATOM	5254	CB	VAL A 688	38.480	49.484	173.327	1.00	65.04	C
	ATOM	5255	CG1	VAL A 688	38.669	48.686	172.055	1.00	53.16	C
	ATOM	5256	CG2	VAL A 688	37.299	48.950	174.073	1.00	65.35	C
30	ATOM	5257	N	GLU A 689	41.399	50.543	172.860	1.00	72.37	N
	ATOM	5258	CA	GLU A 689	42.621	50.634	172.054	1.00	71.22	C
	ATOM	5259	C	GLU A 689	43.827	50.047	172.783	1.00	71.70	C
	ATOM	5260	O	GLU A 689	44.519	49.185	172.240	1.00	73.04	O
	ATOM	5261	CB	GLU A 689	42.907	52.076	171.633	1.00	65.64	C
35	ATOM	5262	CG	GLU A 689	41.994	52.586	170.541	1.00	74.41	C
	ATOM	5263	CD	GLU A 689	42.215	54.060	170.235	1.00	94.86	C
	ATOM	5264	OE1	GLU A 689	41.434	54.636	169.440	1.00	97.48	O
	ATOM	5265	OE2	GLU A 689	43.170	54.646	170.797	1.00	106.90	O
	ATOM	5266	N	TYR A 690	44.066	50.499	174.012	1.00	68.83	N
40	ATOM	5267	CA	TYR A 690	45.219	50.038	174.769	1.00	62.24	C

	ATOM	5268	C	TYR A 690	45.131	48.548	175.062	1.00	62.25	C
	ATOM	5269	O	TYR A 690	46.108	47.825	174.930	1.00	72.94	O
	ATOM	5270	CB	TYR A 690	45.375	50.834	176.055	1.00	79.38	C
	ATOM	5271	CG	TYR A 690	45.866	52.239	175.849	1.00	63.36	C
5	ATOM	5272	CD1	TYR A 690	46.951	52.493	175.057	1.00	65.96	C
	ATOM	5273	CD2	TYR A 690	45.239	53.309	176.453	1.00	75.05	C
	ATOM	5274	CE1	TYR A 690	47.410	53.770	174.872	1.00	67.34	C
	ATOM	5275	CE2	TYR A 690	45.690	54.595	176.275	1.00	63.48	C
	ATOM	5276	CZ	TYR A 690	46.773	54.819	175.479	1.00	67.08	C
10	ATOM	5277	OH	TYR A 690	47.238	56.099	175.284	1.00	67.75	O
	ATOM	5278	N	LEU A 691	43.955	48.081	175.445	1.00	59.98	N
	ATOM	5279	CA	LEU A 691	43.781	46.671	175.744	1.00	60.15	C
	ATOM	5280	C	LEU A 691	44.055	45.868	174.499	1.00	74.32	C
	ATOM	5281	O	LEU A 691	44.615	44.771	174.549	1.00	77.82	O
15	ATOM	5282	CB	LEU A 691	42.360	46.402	176.214	1.00	57.70	C
	ATOM	5283	CG	LEU A 691	41.956	47.144	177.479	1.00	71.47	C
	ATOM	5284	CD1	LEU A 691	40.442	47.021	177.713	1.00	69.01	C
	ATOM	5285	CD2	LEU A 691	42.767	46.620	178.662	1.00	58.61	C
	ATOM	5286	N	GLN A 692	43.651	46.433	173.371	1.00	72.36	N
20	ATOM	5287	CA	GLN A 692	43.806	45.753	172.105	1.00	70.35	C
	ATOM	5288	C	GLN A 692	45.286	45.520	171.826	1.00	76.03	C
	ATOM	5289	O	GLN A 692	45.663	44.507	171.236	1.00	77.91	O
	ATOM	5290	CB	GLN A 692	43.111	46.535	170.983	1.00	60.90	C
	ATOM	5291	CG	GLN A 692	41.744	45.977	170.652	1.00	58.59	C
25	ATOM	5292	CD	GLN A 692	40.832	46.964	169.937	1.00	74.55	C
	ATOM	5293	OE1	GLN A 692	41.252	48.053	169.526	1.00	79.52	O
	ATOM	5294	NE2	GLN A 692	39.561	46.585	169.796	1.00	68.35	N
	ATOM	5295	N	SER A 693	46.129	46.435	172.291	1.00	76.64	N
	ATOM	5296	CA	SER A 693	47.542	46.343	171.973	1.00	79.19	C
30	ATOM	5297	C	SER A 693	48.187	45.188	172.723	1.00	84.66	C
	ATOM	5298	O	SER A 693	49.276	44.747	172.354	1.00	99.68	O
	ATOM	5299	CB	SER A 693	48.271	47.664	172.229	1.00	80.57	C
	ATOM	5300	OG	SER A 693	48.556	47.838	173.600	1.00	83.33	O
	ATOM	5301	N	TYR A 694	47.518	44.690	173.763	1.00	77.39	N
35	ATOM	5302	CA	TYR A 694	47.981	43.474	174.433	1.00	80.87	C
	ATOM	5303	C	TYR A 694	47.207	42.257	173.966	1.00	84.13	C
	ATOM	5304	O	TYR A 694	47.155	41.256	174.682	1.00	87.65	O
	ATOM	5305	CB	TYR A 694	47.806	43.534	175.943	1.00	80.24	C
	ATOM	5306	CG	TYR A 694	48.502	44.650	176.653	1.00	83.20	C
40	ATOM	5307	CD1	TYR A 694	49.887	44.624	176.854	1.00	79.21	C

	ATOM	5308	CD2 TYR A 694	47.769	45.711	177.181	1.00	81.51	C
	ATOM	5309	CE1 TYR A 694	50.523	45.645	177.532	1.00	79.23	C
	ATOM	5310	CE2 TYR A 694	48.395	46.736	177.856	1.00	86.40	C
	ATOM	5311	CZ TYR A 694	49.770	46.698	178.029	1.00	85.82	C
5	ATOM	5312	OH TYR A 694	50.377	47.724	178.702	1.00	95.88	O
	ATOM	5313	N ASP A 695	46.595	42.347	172.792	1.00	79.61	N
	ATOM	5314	CA ASP A 695	45.847	41.229	172.231	1.00	83.97	C
	ATOM	5315	C ASP A 695	44.795	40.712	173.200	1.00	76.98	C
	ATOM	5316	O ASP A 695	44.615	39.502	173.331	1.00	79.65	O
10	ATOM	5317	CB ASP A 695	46.769	40.065	171.835	1.00	93.58	C
	ATOM	5318	CG ASP A 695	47.798	40.448	170.794	1.00	108.57	C
	ATOM	5319	OD2 ASP A 695	48.704	39.625	170.539	1.00	119.22	O
	ATOM	5320	OD1 ASP A 695	47.704	41.556	170.225	1.00	111.79	O
	ATOM	5321	N GLU A 696	44.110	41.611	173.892	1.00	74.97	N
15	ATOM	5322	CA GLU A 696	43.056	41.165	174.802	1.00	82.39	C
	ATOM	5323	C GLU A 696	41.668	41.298	174.187	1.00	84.82	C
	ATOM	5324	O GLU A 696	41.337	42.337	173.609	1.00	93.70	O
	ATOM	5325	CB GLU A 696	43.151	41.867	176.166	1.00	79.89	C
	ATOM	5326	CG GLU A 696	43.741	40.952	177.242	1.00	88.10	C
20	ATOM	5327	CD GLU A 696	44.088	41.665	178.529	1.00	93.30	C
	ATOM	5328	OE1 GLU A 696	44.537	42.834	178.470	1.00	94.88	O
	ATOM	5329	OE2 GLU A 696	43.917	41.045	179.603	1.00	92.53	O
	ATOM	5330	N ILE A 697	40.865	40.241	174.293	1.00	75.90	N
	ATOM	5331	CA ILE A 697	39.486	40.286	173.795	1.00	75.01	C
25	ATOM	5332	C ILE A 697	38.535	41.005	174.767	1.00	73.45	C
	ATOM	5333	O ILE A 697	38.167	40.462	175.813	1.00	73.32	O
	ATOM	5334	CB ILE A 697	38.946	38.889	173.492	1.00	73.90	C
	ATOM	5335	CG1 ILE A 697	39.850	38.197	172.495	1.00	78.58	C
	ATOM	5336	CG2 ILE A 697	37.593	38.993	172.862	1.00	74.74	C
30	ATOM	5337	CD1 ILE A 697	39.824	38.870	171.169	1.00	81.56	C
	ATOM	5338	N THR A 698	38.130	42.220	174.398	1.00	65.24	N
	ATOM	5339	CA THR A 698	37.397	43.105	175.299	1.00	64.76	C
	ATOM	5340	C THR A 698	35.885	43.182	175.042	1.00	69.39	C
	ATOM	5341	O THR A 698	35.435	43.386	173.918	1.00	78.24	O
35	ATOM	5342	CB THR A 698	37.951	44.531	175.199	1.00	67.93	C
	ATOM	5343	OG1 THR A 698	39.334	44.534	175.560	1.00	74.71	O
	ATOM	5344	CG2 THR A 698	37.193	45.464	176.112	1.00	68.16	C
	ATOM	5345	N ALA A 699	35.100	43.036	176.097	1.00	59.18	N
	ATOM	5346	CA ALA A 699	33.679	43.281	176.008	1.00	53.51	C
40	ATOM	5347	C ALA A 699	33.384	44.577	176.732	1.00	63.89	C

	ATOM	5348	O	ALA A 699	33.580	44.682	177.935	1.00	79.12	O
	ATOM	5349	CB	ALA A 699	32.906	42.141	176.635	1.00	57.02	C
	ATOM	5350	N	MET A 700	32.917	45.570	175.997	1.00	63.51	N
	ATOM	5351	CA	MET A 700	32.560	46.853	176.576	1.00	56.13	C
5	ATOM	5352	C	MET A 700	31.031	46.990	176.630	1.00	65.75	C
	ATOM	5353	O	MET A 700	30.329	46.578	175.708	1.00	79.26	O
	ATOM	5354	CB	MET A 700	33.173	47.954	175.720	1.00	50.87	C
	ATOM	5355	CG	MET A 700	32.856	49.348	176.145	1.00	51.74	C
	ATOM	5356	SD	MET A 700	33.910	49.839	177.491	1.00	73.48	S
10	ATOM	5357	CE	MET A 700	35.466	50.145	176.689	1.00	121.23	C
	ATOM	5358	N	THR A 701	30.518	47.549	177.722	1.00	62.95	N
	ATOM	5359	CA	THR A 701	29.096	47.869	177.847	1.00	54.88	C
	ATOM	5360	C	THR A 701	28.837	49.296	177.373	1.00	57.42	C
	ATOM	5361	O	THR A 701	29.765	50.083	177.217	1.00	61.49	O
15	ATOM	5362	CB	THR A 701	28.596	47.747	179.318	1.00	62.45	C
	ATOM	5363	OG1	THR A 701	29.159	48.794	180.123	1.00	61.27	O
	ATOM	5364	CG2	THR A 701	28.930	46.382	179.927	1.00	49.17	C
	ATOM	5365	N	GLY A 702	27.571	49.629	177.156	1.00	61.26	N
	ATOM	5366	CA	GLY A 702	27.175	50.978	176.783	1.00	60.30	C
20	ATOM	5367	C	GLY A 702	25.671	51.097	176.603	1.00	64.67	C
	ATOM	5368	O	GLY A 702	24.968	50.089	176.456	1.00	69.47	O
	ATOM	5369	N	ASP A 703	25.170	52.329	176.607	1.00	60.03	N
	ATOM	5370	CA	ASP A 703	23.726	52.554	176.550	1.00	58.14	C
	ATOM	5371	C	ASP A 703	23.327	53.812	175.797	1.00	59.53	C
25	ATOM	5372	O	ASP A 703	22.260	53.857	175.193	1.00	67.39	O
	ATOM	5373	CB	ASP A 703	23.120	52.575	177.958	1.00	57.53	C
	ATOM	5374	CG	ASP A 703	23.873	53.489	178.908	1.00	75.95	C
	ATOM	5375	OD1	ASP A 703	24.901	53.033	179.467	1.00	89.08	O
	ATOM	5376	OD2	ASP A 703	23.439	54.649	179.114	1.00	73.99	O
30	ATOM	5377	N	GLY A 704	24.172	54.834	175.834	1.00	60.21	N
	ATOM	5378	CA	GLY A 704	23.847	56.099	175.197	1.00	69.21	C
	ATOM	5379	C	GLY A 704	24.367	56.177	173.785	1.00	71.76	C
	ATOM	5380	O	GLY A 704	25.147	55.325	173.366	1.00	74.36	O
	ATOM	5381	N	VAL A 705	23.937	57.193	173.041	1.00	75.10	N
35	ATOM	5382	CA	VAL A 705	24.413	57.370	171.669	1.00	68.83	C
	ATOM	5383	C	VAL A 705	25.932	57.510	171.656	1.00	68.01	C
	ATOM	5384	O	VAL A 705	26.602	56.968	170.784	1.00	78.44	O
	ATOM	5385	CB	VAL A 705	23.749	58.564	170.959	1.00	63.60	C
	ATOM	5386	CG1	VAL A 705	22.295	58.296	170.765	1.00	75.71	C
40	ATOM	5387	CG2	VAL A 705	23.938	59.835	171.719	1.00	64.51	C

	ATOM	5388	N	ASN A 706	26.479	58.191	172.657	1.00	60.95	N
	ATOM	5389	CA	ASN A 706	27.912	58.376	172.745	1.00	61.82	C
	ATOM	5390	C	ASN A 706	28.693	57.108	173.081	1.00	70.29	C
	ATOM	5391	O	ASN A 706	29.931	57.118	173.089	1.00	77.70	O
5	ATOM	5392	CB	ASN A 706	28.224	59.459	173.760	1.00	65.48	C
	ATOM	5393	CG	ASN A 706	27.757	60.815	173.313	1.00	74.26	C
	ATOM	5394	OD1	ASN A 706	27.539	61.064	172.113	1.00	67.93	O
	ATOM	5395	ND2	ASN A 706	27.598	61.716	174.272	1.00	83.96	N
	ATOM	5396	N	ASP A 707	27.987	56.019	173.369	1.00	66.91	N
10	ATOM	5397	CA	ASP A 707	28.669	54.758	173.623	1.00	69.21	C
	ATOM	5398	C	ASP A 707	28.879	54.017	172.315	1.00	75.38	C
	ATOM	5399	O	ASP A 707	29.614	53.028	172.265	1.00	74.16	O
	ATOM	5400	CB	ASP A 707	27.899	53.891	174.613	1.00	68.63	C
	ATOM	5401	CG	ASP A 707	27.840	54.506	175.998	1.00	74.68	C
15	ATOM	5402	OD1	ASP A 707	28.890	54.950	176.511	1.00	72.65	O
	ATOM	5403	OD2	ASP A 707	26.733	54.564	176.567	1.00	79.34	O
	ATOM	5404	N	ALA A 708	28.249	54.524	171.255	1.00	73.63	N
	ATOM	5405	CA	ALA A 708	28.263	53.863	169.952	1.00	65.26	C
	ATOM	5406	C	ALA A 708	29.656	53.564	169.389	1.00	71.31	C
20	ATOM	5407	O	ALA A 708	29.908	52.421	169.001	1.00	76.06	O
	ATOM	5408	CB	ALA A 708	27.427	54.623	168.955	1.00	61.32	C
	ATOM	5409	N	PRO A 709	30.566	54.569	169.349	1.00	69.75	N
	ATOM	5410	CA	PRO A 709	31.918	54.323	168.839	1.00	67.33	C
	ATOM	5411	C	PRO A 709	32.675	53.218	169.571	1.00	66.67	C
25	ATOM	5412	O	PRO A 709	33.190	52.313	168.913	1.00	75.49	O
	ATOM	5413	CB	PRO A 709	32.619	55.648	169.088	1.00	55.72	C
	ATOM	5414	CG	PRO A 709	31.584	56.615	169.080	1.00	56.84	C
	ATOM	5415	CD	PRO A 709	30.420	55.979	169.738	1.00	68.69	C
	ATOM	5416	N	ALA A 710	32.748	53.291	170.898	1.00	64.87	N
30	ATOM	5417	CA	ALA A 710	33.466	52.285	171.680	1.00	68.85	C
	ATOM	5418	C	ALA A 710	32.799	50.919	171.609	1.00	62.58	C
	ATOM	5419	O	ALA A 710	33.482	49.899	171.667	1.00	60.16	O
	ATOM	5420	CB	ALA A 710	33.620	52.731	173.133	1.00	68.31	C
	ATOM	5421	N	LEU A 711	31.472	50.905	171.493	1.00	58.05	N
35	ATOM	5422	CA	LEU A 711	30.735	49.652	171.363	1.00	59.26	C
	ATOM	5423	C	LEU A 711	31.084	48.981	170.043	1.00	60.18	C
	ATOM	5424	O	LEU A 711	31.140	47.752	169.958	1.00	60.02	O
	ATOM	5425	CB	LEU A 711	29.224	49.880	171.439	1.00	63.15	C
	ATOM	5426	CG	LEU A 711	28.540	50.098	172.798	1.00	59.66	C
40	ATOM	5427	CD1	LEU A 711	27.149	50.670	172.586	1.00	51.39	C

	ATOM	5428	CD2 LEU A 711	28.466	48.806	173.602	1.00	55.81	C
	ATOM	5429	N LYS A 712	31.323	49.796	169.020	1.00	59.31	N
	ATOM	5430	CA LYS A 712	31.719	49.288	167.707	1.00	63.36	C
	ATOM	5431	C LYS A 712	33.164	48.798	167.758	1.00	65.13	C
5	ATOM	5432	O LYS A 712	33.481	47.685	167.334	1.00	64.51	O
	ATOM	5433	CB LYS A 712	31.537	50.368	166.628	1.00	56.81	C
	ATOM	5434	CG LYS A 712	30.065	50.646	166.248	1.00	55.62	C
	ATOM	5435	CD LYS A 712	29.944	51.817	165.265	1.00	71.87	C
	ATOM	5436	CE LYS A 712	28.506	52.099	164.820	1.00	83.28	C
10	ATOM	5437	NZ LYS A 712	27.831	50.953	164.120	1.00	90.69	N
	ATOM	5438	N LYS A 713	34.027	49.643	168.312	1.00	67.79	N
	ATOM	5439	CA LYS A 713	35.453	49.375	168.440	1.00	57.63	C
	ATOM	5440	C LYS A 713	35.766	48.150	169.304	1.00	58.03	C
	ATOM	5441	O LYS A 713	36.663	47.386	168.973	1.00	63.99	O
15	ATOM	5442	CB LYS A 713	36.143	50.618	168.989	1.00	55.47	C
	ATOM	5443	CG LYS A 713	37.618	50.689	168.743	1.00	69.34	C
	ATOM	5444	CD LYS A 713	38.153	52.093	169.017	1.00	79.25	C
	ATOM	5445	CE LYS A 713	39.393	52.366	168.171	1.00	92.55	C
	ATOM	5446	NZ LYS A 713	40.255	51.144	168.001	1.00	98.52	N
20	ATOM	5447	N ALA A 714	35.028	47.949	170.398	1.00	54.66	N
	ATOM	5448	CA ALA A 714	35.228	46.764	171.250	1.00	59.36	C
	ATOM	5449	C ALA A 714	35.082	45.453	170.476	1.00	66.18	C
	ATOM	5450	O ALA A 714	34.381	45.406	169.473	1.00	75.03	O
	ATOM	5451	CB ALA A 714	34.278	46.778	172.427	1.00	49.78	C
25	ATOM	5452	N GLU A 715	35.753	44.400	170.935	1.00	52.06	N
	ATOM	5453	CA GLU A 715	35.582	43.077	170.345	1.00	61.01	C
	ATOM	5454	C GLU A 715	34.138	42.654	170.500	1.00	56.72	C
	ATOM	5455	O GLU A 715	33.525	42.189	169.548	1.00	52.68	O
	ATOM	5456	CB GLU A 715	36.493	42.022	170.985	1.00	68.39	C
30	ATOM	5457	CG GLU A 715	37.940	42.031	170.504	1.00	67.15	C
	ATOM	5458	CD GLU A 715	38.660	43.312	170.878	1.00	75.68	C
	ATOM	5459	OE1 GLU A 715	38.777	43.603	172.098	1.00	73.65	O
	ATOM	5460	OE2 GLU A 715	39.098	44.030	169.951	1.00	77.46	O
	ATOM	5461	N ILE A 716	33.594	42.826	171.702	1.00	61.55	N
35	ATOM	5462	CA ILE A 716	32.161	42.603	171.939	1.00	66.74	C
	ATOM	5463	C ILE A 716	31.422	43.808	172.554	1.00	70.40	C
	ATOM	5464	O ILE A 716	31.641	44.165	173.697	1.00	67.57	O
	ATOM	5465	CB ILE A 716	31.921	41.381	172.811	1.00	58.15	C
	ATOM	5466	CG1 ILE A 716	32.372	40.123	172.082	1.00	61.70	C
40	ATOM	5467	CG2 ILE A 716	30.465	41.270	173.108	1.00	59.42	C

	ATOM	5468	CD1 ILE A 716	33.105	39.161	172.957	1.00	69.94	C
	ATOM	5469	N GLY A 717	30.551	44.444	171.783	1.00	77.18	N
	ATOM	5470	CA GLY A 717	29.802	45.580	172.287	1.00	74.08	C
	ATOM	5471	C GLY A 717	28.548	45.059	172.949	1.00	72.61	C
5	ATOM	5472	O GLY A 717	27.835	44.249	172.377	1.00	87.31	O
	ATOM	5473	N ILE A 718	28.277	45.504	174.163	1.00	62.30	N
	ATOM	5474	CA ILE A 718	27.151	44.974	174.904	1.00	54.05	C
	ATOM	5475	C ILE A 718	26.215	46.088	175.356	1.00	55.15	C
	ATOM	5476	O ILE A 718	26.539	46.862	176.259	1.00	58.05	O
10	ATOM	5477	CB ILE A 718	27.631	44.192	176.108	1.00	55.17	C
	ATOM	5478	CG1 ILE A 718	28.341	42.922	175.661	1.00	56.76	C
	ATOM	5479	CG2 ILE A 718	26.462	43.787	176.959	1.00	70.04	C
	ATOM	5480	CD1 ILE A 718	28.909	42.106	176.818	1.00	60.56	C
	ATOM	5481	N ALA A 719	25.045	46.161	174.728	1.00	54.00	N
15	ATOM	5482	CA ALA A 719	24.099	47.236	174.991	1.00	52.18	C
	ATOM	5483	C ALA A 719	23.112	46.894	176.095	1.00	60.18	C
	ATOM	5484	O ALA A 719	22.719	45.735	176.254	1.00	56.27	O
	ATOM	5485	CB ALA A 719	23.347	47.573	173.726	1.00	67.80	C
	ATOM	5486	N MET A 720	22.705	47.916	176.845	1.00	62.09	N
20	ATOM	5487	CA MET A 720	21.637	47.768	177.830	1.00	65.64	C
	ATOM	5488	C MET A 720	20.301	47.809	177.106	1.00	70.83	C
	ATOM	5489	O MET A 720	20.087	48.655	176.231	1.00	69.25	O
	ATOM	5490	CB MET A 720	21.686	48.879	178.890	1.00	60.51	C
	ATOM	5491	CG MET A 720	23.031	49.026	179.580	1.00	53.74	C
25	ATOM	5492	SD MET A 720	23.525	47.503	180.407	1.00	75.36	S
	ATOM	5493	CE MET A 720	25.066	47.170	179.570	1.00	156.72	C
	ATOM	5494	N GLY A 721	19.416	46.887	177.475	1.00	73.47	N
	ATOM	5495	CA GLY A 721	18.071	46.841	176.938	1.00	77.12	C
	ATOM	5496	C GLY A 721	17.233	48.045	177.320	1.00	77.45	C
30	ATOM	5497	O GLY A 721	16.391	48.495	176.546	1.00	83.81	O
	ATOM	5498	N SER A 722	17.456	48.575	178.518	1.00	75.02	N
	ATOM	5499	CA SER A 722	16.770	49.790	178.949	1.00	72.98	C
	ATOM	5500	C SER A 722	17.373	51.003	178.254	1.00	74.54	C
	ATOM	5501	O SER A 722	16.907	52.131	178.465	1.00	74.89	O
35	ATOM	5502	CB SER A 722	16.890	49.968	180.457	1.00	72.29	C
	ATOM	5503	OG SER A 722	18.215	50.339	180.836	1.00	70.81	O
	ATOM	5504	N GLY A 723	18.400	50.751	177.432	1.00	69.91	N
	ATOM	5505	CA GLY A 723	19.184	51.775	176.757	1.00	70.04	C
	ATOM	5506	C GLY A 723	18.589	52.371	175.491	1.00	68.57	C
40	ATOM	5507	O GLY A 723	17.372	52.480	175.377	1.00	75.62	O

	ATOM	5508	N	THR A 724	19.444	52.777	174.550	1.00	65.48	N
	ATOM	5509	CA	THR A 724	18.976	53.393	173.298	1.00	76.01	C
	ATOM	5510	C	THR A 724	19.117	52.483	172.075	1.00	75.63	C
	ATOM	5511	O	THR A 724	20.032	51.661	172.004	1.00	77.27	O
5	ATOM	5512	CB	THR A 724	19.654	54.766	172.996	1.00	75.08	C
	ATOM	5513	OG1	THR A 724	21.069	54.685	173.190	1.00	62.90	O
	ATOM	5514	CG2	THR A 724	19.093	55.849	173.885	1.00	65.77	C
	ATOM	5515	N	ALA A 725	18.203	52.646	171.119	1.00	71.88	N
	ATOM	5516	CA	ALA A 725	18.205	51.854	169.893	1.00	66.71	C
10	ATOM	5517	C	ALA A 725	19.534	52.022	169.206	1.00	70.77	C
	ATOM	5518	O	ALA A 725	20.125	51.052	168.735	1.00	66.64	O
	ATOM	5519	CB	ALA A 725	17.098	52.298	168.972	1.00	70.48	C
	ATOM	5520	N	VAL A 726	19.992	53.271	169.166	1.00	73.24	N
	ATOM	5521	CA	VAL A 726	21.289	53.639	168.616	1.00	63.84	C
15	ATOM	5522	C	VAL A 726	22.432	52.832	169.235	1.00	67.63	C
	ATOM	5523	O	VAL A 726	23.340	52.373	168.536	1.00	65.10	O
	ATOM	5524	CB	VAL A 726	21.555	55.131	168.837	1.00	69.40	C
	ATOM	5525	CG1	VAL A 726	22.980	55.463	168.481	1.00	66.38	C
	ATOM	5526	CG2	VAL A 726	20.581	55.975	168.032	1.00	68.51	C
20	ATOM	5527	N	ALA A 727	22.390	52.637	170.542	1.00	59.23	N
	ATOM	5528	CA	ALA A 727	23.493	51.941	171.182	1.00	63.75	C
	ATOM	5529	C	ALA A 727	23.384	50.438	170.997	1.00	68.40	C
	ATOM	5530	O	ALA A 727	24.339	49.717	171.256	1.00	73.16	O
	ATOM	5531	CB	ALA A 727	23.596	52.299	172.660	1.00	59.47	C
25	ATOM	5532	N	LYS A 728	22.230	49.956	170.555	1.00	65.63	N
	ATOM	5533	CA	LYS A 728	22.076	48.519	170.410	1.00	67.72	C
	ATOM	5534	C	LYS A 728	22.516	48.069	169.035	1.00	77.99	C
	ATOM	5535	O	LYS A 728	22.935	46.923	168.875	1.00	86.39	O
	ATOM	5536	CB	LYS A 728	20.636	48.068	170.657	1.00	63.45	C
30	ATOM	5537	CG	LYS A 728	20.008	48.610	171.906	1.00	61.96	C
	ATOM	5538	CD	LYS A 728	18.792	47.817	172.281	1.00	61.39	C
	ATOM	5539	CE	LYS A 728	17.938	48.603	173.262	1.00	62.87	C
	ATOM	5540	NZ	LYS A 728	16.736	47.861	173.751	1.00	64.98	N
	ATOM	5541	N	THR A 729	22.399	48.952	168.040	1.00	76.61	N
35	ATOM	5542	CA	THR A 729	22.781	48.600	166.670	1.00	75.68	C
	ATOM	5543	C	THR A 729	24.291	48.455	166.662	1.00	78.91	C
	ATOM	5544	O	THR A 729	24.841	47.589	165.970	1.00	83.70	O
	ATOM	5545	CB	THR A 729	22.388	49.663	165.613	1.00	101.61	C
	ATOM	5546	OG1	THR A 729	23.140	50.864	165.840	1.00	108.28	O
40	ATOM	5547	CG2	THR A 729	20.892	49.969	165.625	1.00	65.06	C

	ATOM	5548	N	ALA A 730	24.953	49.307	167.446	1.00	71.39	N
	ATOM	5549	CA	ALA A 730	26.403	49.221	167.633	1.00	65.70	C
	ATOM	5550	C	ALA A 730	26.850	47.870	168.211	1.00	68.65	C
	ATOM	5551	O	ALA A 730	28.020	47.494	168.108	1.00	72.03	O
5	ATOM	5552	CB	ALA A 730	26.903	50.370	168.522	1.00	57.65	C
	ATOM	5553	N	SER A 731	25.907	47.127	168.772	1.00	53.93	N
	ATOM	5554	CA	SER A 731	26.230	46.010	169.633	1.00	52.83	C
	ATOM	5555	C	SER A 731	26.062	44.653	169.017	1.00	72.80	C
	ATOM	5556	O	SER A 731	25.437	44.485	167.972	1.00	81.96	O
10	ATOM	5557	CB	SER A 731	25.361	46.075	170.870	1.00	71.40	C
	ATOM	5558	OG	SER A 731	25.385	47.393	171.371	1.00	76.00	O
	ATOM	5559	N	GLU A 732	26.627	43.682	169.717	1.00	69.19	N
	ATOM	5560	CA	GLU A 732	26.585	42.290	169.325	1.00	72.74	C
	ATOM	5561	C	GLU A 732	25.659	41.532	170.275	1.00	78.04	C
15	ATOM	5562	O	GLU A 732	25.111	40.491	169.903	1.00	86.26	O
	ATOM	5563	CB	GLU A 732	28.004	41.687	169.312	1.00	68.15	C
	ATOM	5564	CG	GLU A 732	28.864	42.101	168.108	1.00	68.11	C
	ATOM	5565	CD	GLU A 732	29.426	43.514	168.209	1.00	73.53	C
	ATOM	5566	OE1	GLU A 732	30.156	43.776	169.185	1.00	75.40	O
20	ATOM	5567	OE2	GLU A 732	29.158	44.359	167.317	1.00	74.72	O
	ATOM	5568	N	MET A 733	25.483	42.070	171.489	1.00	71.08	N
	ATOM	5569	CA	MET A 733	24.543	41.535	172.489	1.00	65.90	C
	ATOM	5570	C	MET A 733	23.756	42.648	173.141	1.00	64.32	C
	ATOM	5571	O	MET A 733	24.289	43.733	173.367	1.00	68.71	O
25	ATOM	5572	CB	MET A 733	25.282	40.841	173.627	1.00	71.29	C
	ATOM	5573	CG	MET A 733	26.022	39.577	173.269	1.00	81.03	C
	ATOM	5574	SD	MET A 733	26.075	38.502	174.715	1.00	115.30	S
	ATOM	5575	CE	MET A 733	26.198	39.728	175.996	1.00	53.36	C
	ATOM	5576	N	VAL A 734	22.500	42.375	173.477	1.00	64.64	N
30	ATOM	5577	CA	VAL A 734	21.751	43.264	174.365	1.00	55.74	C
	ATOM	5578	C	VAL A 734	21.359	42.539	175.656	1.00	60.25	C
	ATOM	5579	O	VAL A 734	20.859	41.417	175.616	1.00	70.09	O
	ATOM	5580	CB	VAL A 734	20.487	43.780	173.708	1.00	57.62	C
	ATOM	5581	CG1	VAL A 734	19.843	44.817	174.600	1.00	72.04	C
35	ATOM	5582	CG2	VAL A 734	20.810	44.370	172.379	1.00	59.59	C
	ATOM	5583	N	LEU A 735	21.601	43.165	176.799	1.00	58.08	N
	ATOM	5584	CA	LEU A 735	21.240	42.560	178.078	1.00	62.99	C
	ATOM	5585	C	LEU A 735	19.822	42.971	178.427	1.00	68.48	C
	ATOM	5586	O	LEU A 735	19.545	44.158	178.639	1.00	66.64	O
40	ATOM	5587	CB	LEU A 735	22.183	43.019	179.189	1.00	64.48	C

	ATOM	5588	CG	LEU A 735	23.693	42.945	178.970	1.00	63.95	C
	ATOM	5589	CD1	LEU A 735	24.374	43.684	180.088	1.00	64.54	C
	ATOM	5590	CD2	LEU A 735	24.160	41.509	178.930	1.00	64.18	C
	ATOM	5591	N	ALA A 736	18.932	41.984	178.481	1.00	69.05	N
5	ATOM	5592	CA	ALA A 736	17.515	42.220	178.711	1.00	70.21	C
	ATOM	5593	C	ALA A 736	17.279	42.891	180.075	1.00	80.02	C
	ATOM	5594	O	ALA A 736	16.467	43.812	180.212	1.00	85.18	O
	ATOM	5595	CB	ALA A 736	16.790	40.923	178.628	1.00	65.67	C
	ATOM	5596	N	ASP A 737	18.027	42.436	181.074	1.00	82.21	N
10	ATOM	5597	CA	ASP A 737	17.865	42.895	182.438	1.00	64.43	C
	ATOM	5598	C	ASP A 737	18.996	43.834	182.898	1.00	71.30	C
	ATOM	5599	O	ASP A 737	19.132	44.120	184.087	1.00	74.41	O
	ATOM	5600	CB	ASP A 737	17.764	41.679	183.355	1.00	68.63	C
	ATOM	5601	CG	ASP A 737	18.990	40.778	183.277	1.00	68.15	C
15	ATOM	5602	OD1	ASP A 737	19.976	41.157	182.618	1.00	61.97	O
	ATOM	5603	OD2	ASP A 737	18.976	39.694	183.897	1.00	65.96	O
	ATOM	5604	N	ASP A 738	19.815	44.287	181.955	1.00	59.98	N
	ATOM	5605	CA	ASP A 738	20.866	45.273	182.213	1.00	61.21	C
	ATOM	5606	C	ASP A 738	21.912	44.758	183.179	1.00	67.73	C
20	ATOM	5607	O	ASP A 738	22.792	45.511	183.592	1.00	63.33	O
	ATOM	5608	CB	ASP A 738	20.290	46.586	182.749	1.00	63.41	C
	ATOM	5609	CG	ASP A 738	19.359	47.279	181.759	1.00	81.47	C
	ATOM	5610	OD1	ASP A 738	18.850	46.627	180.818	1.00	89.41	O
	ATOM	5611	OD2	ASP A 738	19.122	48.490	181.937	1.00	86.06	O
25	ATOM	5612	N	ASN A 739	21.822	43.475	183.527	1.00	75.71	N
	ATOM	5613	CA	ASN A 739	22.646	42.899	184.589	1.00	74.31	C
	ATOM	5614	C	ASN A 739	24.072	42.526	184.181	1.00	75.14	C
	ATOM	5615	O	ASN A 739	24.294	41.972	183.103	1.00	78.94	O
	ATOM	5616	CB	ASN A 739	21.952	41.685	185.208	1.00	65.41	C
30	ATOM	5617	CG	ASN A 739	22.353	41.467	186.660	1.00	72.93	C
	ATOM	5618	OD1	ASN A 739	23.175	42.205	187.208	1.00	67.52	O
	ATOM	5619	ND2	ASN A 739	21.753	40.468	187.298	1.00	82.81	N
	ATOM	5620	N	PHE A 740	25.031	42.844	185.051	1.00	67.16	N
	ATOM	5621	CA	PHE A 740	26.404	42.404	184.866	1.00	66.50	C
35	ATOM	5622	C	PHE A 740	26.450	40.888	184.817	1.00	68.70	C
	ATOM	5623	O	PHE A 740	27.160	40.293	184.009	1.00	74.58	O
	ATOM	5624	CB	PHE A 740	27.312	42.900	186.000	1.00	64.54	C
	ATOM	5625	CG	PHE A 740	28.757	42.496	185.833	1.00	64.90	C
	ATOM	5626	CD2	PHE A 740	29.625	43.267	185.067	1.00	64.72	C
40	ATOM	5627	CD1	PHE A 740	29.235	41.333	186.405	1.00	60.71	C

	ATOM	5628	CE2 PHE A 740	30.939	42.893	184.897	1.00	63.24	C
	ATOM	5629	CE1 PHE A 740	30.555	40.954	186.232	1.00	57.78	C
	ATOM	5630	CZ PHE A 740	31.405	41.732	185.481	1.00	61.07	C
	ATOM	5631	N SER A 741	25.680	40.266	185.692	1.00	61.95	N
5	ATOM	5632	CA SER A 741	25.706	38.826	185.831	1.00	72.70	C
	ATOM	5633	C SER A 741	25.266	38.164	184.536	1.00	72.30	C
	ATOM	5634	O SER A 741	25.660	37.033	184.228	1.00	69.04	O
	ATOM	5635	CB SER A 741	24.807	38.419	186.988	1.00	86.37	C
	ATOM	5636	OG SER A 741	25.048	39.279	188.093	1.00	95.23	O
10	ATOM	5637	N THR A 742	24.465	38.891	183.767	1.00	71.49	N
	ATOM	5638	CA THR A 742	24.020	38.400	182.475	1.00	77.60	C
	ATOM	5639	C THR A 742	25.195	38.273	181.509	1.00	81.50	C
	ATOM	5640	O THR A 742	25.268	37.313	180.739	1.00	84.33	O
	ATOM	5641	CB THR A 742	22.970	39.321	181.860	1.00	76.79	C
15	ATOM	5642	OG1 THR A 742	21.939	39.582	182.821	1.00	78.85	O
	ATOM	5643	CG2 THR A 742	22.371	38.669	180.635	1.00	77.09	C
	ATOM	5644	N ILE A 743	26.106	39.246	181.562	1.00	73.71	N
	ATOM	5645	CA ILE A 743	27.309	39.227	180.743	1.00	66.80	C
	ATOM	5646	C ILE A 743	28.148	37.973	181.002	1.00	72.51	C
20	ATOM	5647	O ILE A 743	28.635	37.326	180.069	1.00	77.10	O
	ATOM	5648	CB ILE A 743	28.183	40.465	181.000	1.00	59.63	C
	ATOM	5649	CG1 ILE A 743	27.399	41.739	180.680	1.00	61.39	C
	ATOM	5650	CG2 ILE A 743	29.485	40.384	180.187	1.00	56.73	C
	ATOM	5651	CD1 ILE A 743	28.215	43.033	180.764	1.00	54.78	C
25	ATOM	5652	N VAL A 744	28.318	37.630	182.273	1.00	64.32	N
	ATOM	5653	CA VAL A 744	29.155	36.499	182.627	1.00	58.25	C
	ATOM	5654	C VAL A 744	28.477	35.213	182.202	1.00	70.41	C
	ATOM	5655	O VAL A 744	29.128	34.283	181.740	1.00	74.48	O
	ATOM	5656	CB VAL A 744	29.449	36.459	184.123	1.00	60.85	C
30	ATOM	5657	CG1 VAL A 744	30.221	35.185	184.481	1.00	66.40	C
	ATOM	5658	CG2 VAL A 744	30.218	37.707	184.543	1.00	53.08	C
	ATOM	5659	N ALA A 745	27.157	35.165	182.343	1.00	79.45	N
	ATOM	5660	CA ALA A 745	26.412	33.987	181.911	1.00	78.45	C
	ATOM	5661	C ALA A 745	26.492	33.868	180.391	1.00	78.40	C
35	ATOM	5662	O ALA A 745	26.470	32.764	179.834	1.00	78.08	O
	ATOM	5663	CB ALA A 745	24.975	34.059	182.374	1.00	69.44	C
	ATOM	5664	N ALA A 746	26.597	35.010	179.720	1.00	71.78	N
	ATOM	5665	CA ALA A 746	26.746	34.993	178.280	1.00	70.73	C
	ATOM	5666	C ALA A 746	28.099	34.376	177.945	1.00	77.14	C
40	ATOM	5667	O ALA A 746	28.190	33.469	177.100	1.00	83.59	O

	ATOM	5668	CB	ALA A 746	26.604	36.392	177.694	1.00	61.17	C
	ATOM	5669	N	VAL A 747	29.140	34.839	178.636	1.00	63.34	N
	ATOM	5670	CA	VAL A 747	30.488	34.356	178.371	1.00	56.98	C
	ATOM	5671	C	VAL A 747	30.620	32.860	178.647	1.00	60.21	C
5	ATOM	5672	O	VAL A 747	31.304	32.142	177.929	1.00	60.60	O
	ATOM	5673	CB	VAL A 747	31.542	35.185	179.118	1.00	55.09	C
	ATOM	5674	CG1	VAL A 747	32.808	34.399	179.323	1.00	52.12	C
	ATOM	5675	CG2	VAL A 747	31.848	36.442	178.333	1.00	57.01	C
	ATOM	5676	N	GLU A 748	29.917	32.380	179.659	1.00	74.14	N
10	ATOM	5677	CA	GLU A 748	29.980	30.966	179.997	1.00	83.28	C
	ATOM	5678	C	GLU A 748	29.354	30.145	178.901	1.00	83.00	C
	ATOM	5679	O	GLU A 748	29.862	29.092	178.537	1.00	81.84	O
	ATOM	5680	CB	GLU A 748	29.250	30.677	181.308	1.00	88.84	C
	ATOM	5681	CG	GLU A 748	29.343	29.221	181.737	1.00	87.74	C
15	ATOM	5682	CD	GLU A 748	28.932	29.008	183.182	1.00	85.75	C
	ATOM	5683	OE1	GLU A 748	28.705	30.009	183.905	1.00	80.02	O
	ATOM	5684	OE2	GLU A 748	28.839	27.828	183.584	1.00	88.64	O
	ATOM	5685	N	GLU A 749	28.234	30.628	178.380	1.00	88.31	N
	ATOM	5686	CA	GLU A 749	27.512	29.865	177.385	1.00	87.13	C
20	ATOM	5687	C	GLU A 749	28.346	29.870	176.132	1.00	84.01	C
	ATOM	5688	O	GLU A 749	28.308	28.914	175.359	1.00	85.84	O
	ATOM	5689	CB	GLU A 749	26.127	30.445	177.117	1.00	84.54	C
	ATOM	5690	CG	GLU A 749	25.165	29.420	176.547	1.00	92.64	C
	ATOM	5691	CD	GLU A 749	24.578	28.511	177.620	1.00	100.00	C
25	ATOM	5692	OE1	GLU A 749	24.290	29.019	178.733	1.00	101.40	O
	ATOM	5693	OE2	GLU A 749	24.407	27.296	177.348	1.00	98.19	O
	ATOM	5694	N	GLY A 750	29.111	30.945	175.950	1.00	74.20	N
	ATOM	5695	CA	GLY A 750	30.009	31.044	174.819	1.00	73.12	C
	ATOM	5696	C	GLY A 750	30.924	29.837	174.834	1.00	74.63	C
30	ATOM	5697	O	GLY A 750	31.034	29.100	173.847	1.00	74.08	O
	ATOM	5698	N	ARG A 751	31.555	29.621	175.983	1.00	70.97	N
	ATOM	5699	CA	ARG A 751	32.479	28.513	176.154	1.00	69.27	C
	ATOM	5700	C	ARG A 751	31.770	27.168	175.993	1.00	82.29	C
	ATOM	5701	O	ARG A 751	32.341	26.212	175.471	1.00	91.02	O
35	ATOM	5702	CB	ARG A 751	33.166	28.599	177.519	1.00	60.49	C
	ATOM	5703	CG	ARG A 751	33.950	29.890	177.758	1.00	61.19	C
	ATOM	5704	CD	ARG A 751	34.933	29.683	178.905	1.00	69.44	C
	ATOM	5705	NE	ARG A 751	35.604	30.915	179.328	1.00	78.08	N
	ATOM	5706	CZ	ARG A 751	36.448	30.987	180.360	1.00	82.51	C
40	ATOM	5707	NH1	ARG A 751	36.735	29.898	181.071	1.00	77.63	N

	ATOM	5708	NH2 ARG A 751	37.010	32.147	180.682	1.00	82.82	N
	ATOM	5709	N ALA A 752	30.520	27.104	176.432	1.00	87.02	N
	ATOM	5710	CA ALA A 752	29.762	25.862	176.388	1.00	87.40	C
	ATOM	5711	C ALA A 752	29.445	25.484	174.953	1.00	87.85	C
5	ATOM	5712	O ALA A 752	29.562	24.320	174.567	1.00	90.32	O
	ATOM	5713	CB ALA A 752	28.480	25.993	177.201	1.00	86.12	C
	ATOM	5714	N ILE A 753	29.044	26.478	174.170	1.00	81.63	N
	ATOM	5715	CA ILE A 753	28.629	26.241	172.801	1.00	78.22	C
	ATOM	5716	C ILE A 753	29.811	25.738	172.021	1.00	81.70	C
10	ATOM	5717	O ILE A 753	29.690	24.801	171.224	1.00	87.93	O
	ATOM	5718	CB ILE A 753	28.121	27.528	172.141	1.00	74.68	C
	ATOM	5719	CG1 ILE A 753	26.795	27.937	172.766	1.00	82.45	C
	ATOM	5720	CG2 ILE A 753	27.961	27.346	170.637	1.00	66.21	C
	ATOM	5721	CD1 ILE A 753	26.385	29.325	172.406	1.00	86.44	C
15	ATOM	5722	N TYR A 754	30.961	26.360	172.267	1.00	80.22	N
	ATOM	5723	CA TYR A 754	32.164	26.065	171.496	1.00	80.99	C
	ATOM	5724	C TYR A 754	32.568	24.614	171.697	1.00	76.50	C
	ATOM	5725	O TYR A 754	32.864	23.897	170.750	1.00	72.64	O
	ATOM	5726	CB TYR A 754	33.298	27.004	171.893	1.00	79.99	C
20	ATOM	5727	CG TYR A 754	34.535	26.805	171.070	1.00	82.20	C
	ATOM	5728	CD2 TYR A 754	34.737	27.515	169.900	1.00	87.39	C
	ATOM	5729	CD1 TYR A 754	35.495	25.900	171.455	1.00	82.22	C
	ATOM	5730	CE2 TYR A 754	35.874	27.326	169.147	1.00	88.30	C
	ATOM	5731	CE1 TYR A 754	36.623	25.706	170.711	1.00	84.77	C
25	ATOM	5732	CZ TYR A 754	36.816	26.416	169.563	1.00	88.82	C
	ATOM	5733	OH TYR A 754	37.968	26.201	168.836	1.00	98.10	O
	ATOM	5734	N ASN A 755	32.558	24.186	172.947	1.00	75.18	N
	ATOM	5735	CA ASN A 755	32.773	22.791	173.264	1.00	82.75	C
	ATOM	5736	C ASN A 755	31.699	21.877	172.689	1.00	78.42	C
30	ATOM	5737	O ASN A 755	31.918	20.685	172.517	1.00	77.58	O
	ATOM	5738	CB ASN A 755	32.839	22.609	174.777	1.00	95.62	C
	ATOM	5739	CG ASN A 755	34.250	22.573	175.286	1.00	102.36	C
	ATOM	5740	OD1 ASN A 755	34.719	21.531	175.742	1.00	107.26	O
	ATOM	5741	ND2 ASN A 755	34.954	23.706	175.190	1.00	99.82	N
35	ATOM	5742	N ASN A 756	30.523	22.415	172.415	1.00	80.73	N
	ATOM	5743	CA ASN A 756	29.482	21.567	171.878	1.00	88.83	C
	ATOM	5744	C ASN A 756	29.655	21.422	170.384	1.00	90.06	C
	ATOM	5745	O ASN A 756	29.324	20.384	169.809	1.00	88.73	O
	ATOM	5746	CB ASN A 756	28.093	22.092	172.204	1.00	93.08	C
40	ATOM	5747	CG ASN A 756	27.034	21.026	172.040	1.00	95.47	C

	ATOM	5748	OD1 ASN A 756	26.939	20.122	172.859	1.00102.41	O
	ATOM	5749	ND2 ASN A 756	26.242	21.117	170.981	1.00 89.69	N
	ATOM	5750	N MET A 757	30.174	22.473	169.762	1.00 87.83	N
	ATOM	5751	CA MET A 757	30.550	22.397	168.366	1.00 86.95	C
5	ATOM	5752	C MET A 757	31.624	21.330	168.262	1.00 86.83	C
	ATOM	5753	O MET A 757	31.562	20.456	167.410	1.00 90.40	O
	ATOM	5754	CB MET A 757	31.118	23.731	167.877	1.00 89.60	C
	ATOM	5755	CG MET A 757	30.200	24.939	168.029	1.00 90.37	C
	ATOM	5756	SD MET A 757	31.092	26.449	167.612	1.00138.98	S
10	ATOM	5757	CE MET A 757	29.768	27.535	167.092	1.00 56.31	C
	ATOM	5758	N LYS A 758	32.605	21.400	169.154	1.00 89.00	N
	ATOM	5759	CA LYS A 758	33.773	20.531	169.060	1.00 94.12	C
	ATOM	5760	C LYS A 758	33.418	19.062	169.224	1.00 96.86	C
	ATOM	5761	O LYS A 758	34.049	18.194	168.626	1.00102.88	O
15	ATOM	5762	CB LYS A 758	34.862	20.948	170.061	1.00 97.00	C
	ATOM	5763	CG LYS A 758	35.868	21.952	169.492	1.00100.13	C
	ATOM	5764	CD LYS A 758	37.036	22.209	170.438	1.00102.33	C
	ATOM	5765	CE LYS A 758	38.191	22.852	169.686	1.00106.14	C
	ATOM	5766	NZ LYS A 758	39.112	23.659	170.543	1.00109.23	N
20	ATOM	5767	N GLN A 759	32.402	18.781	170.026	1.00 96.31	N
	ATOM	5768	CA GLN A 759	32.024	17.398	170.266	1.00101.96	C
	ATOM	5769	C GLN A 759	31.023	16.913	169.224	1.00104.43	C
	ATOM	5770	O GLN A 759	30.822	15.715	169.045	1.00105.71	O
	ATOM	5771	CB GLN A 759	31.506	17.200	171.699	1.00104.10	C
25	ATOM	5772	CG GLN A 759	30.340	18.080	172.096	1.00105.35	C
	ATOM	5773	CD GLN A 759	30.139	18.117	173.598	1.00111.05	C
	ATOM	5774	OE1 GLN A 759	30.794	17.384	174.338	1.00116.62	O
	ATOM	5775	NE2 GLN A 759	29.236	18.976	174.057	1.00112.82	N
	ATOM	5776	N PHE A 760	30.396	17.851	168.531	1.00108.13	N
30	ATOM	5777	CA PHE A 760	29.506	17.487	167.444	1.00114.47	C
	ATOM	5778	C PHE A 760	30.350	16.925	166.318	1.00111.54	C
	ATOM	5779	O PHE A 760	30.139	15.796	165.871	1.00116.77	O
	ATOM	5780	CB PHE A 760	28.731	18.708	166.946	1.00121.09	C
	ATOM	5781	CG PHE A 760	27.253	18.650	167.219	1.00122.88	C
35	ATOM	5782	CD1 PHE A 760	26.399	17.991	166.349	1.00125.02	C
	ATOM	5783	CD2 PHE A 760	26.717	19.266	168.336	1.00123.02	C
	ATOM	5784	CE1 PHE A 760	25.043	17.940	166.592	1.00127.38	C
	ATOM	5785	CE2 PHE A 760	25.362	19.222	168.582	1.00126.63	C
	ATOM	5786	CZ PHE A 760	24.524	18.557	167.709	1.00129.01	C
40	ATOM	5787	N ILE A 761	31.326	17.716	165.881	1.00104.22	N

	ATOM	5788	CA	ILE A 761	32.132	17.363	164.720	1.00	97.59	C
	ATOM	5789	C	ILE A 761	33.062	16.179	164.978	1.00	98.04	C
	ATOM	5790	O	ILE A 761	33.343	15.412	164.058	1.00	108.72	O
	ATOM	5791	CB	ILE A 761	32.927	18.568	164.164	1.00	87.17	C
5	ATOM	5792	CG1	ILE A 761	34.125	18.895	165.036	1.00	86.27	C
	ATOM	5793	CG2	ILE A 761	32.052	19.787	164.085	1.00	85.13	C
	ATOM	5794	CD1	ILE A 761	34.755	20.201	164.655	1.00	92.94	C
	ATOM	5795	N	ARG A 762	33.525	16.014	166.215	1.00	85.68	N
	ATOM	5796	CA	ARG A 762	34.350	14.857	166.540	1.00	87.81	C
10	ATOM	5797	C	ARG A 762	33.563	13.581	166.274	1.00	93.09	C
	ATOM	5798	O	ARG A 762	34.123	12.553	165.891	1.00	95.00	O
	ATOM	5799	CB	ARG A 762	34.818	14.894	167.992	1.00	92.21	C
	ATOM	5800	CG	ARG A 762	35.524	13.622	168.423	1.00	98.50	C
	ATOM	5801	CD	ARG A 762	36.322	13.818	169.692	1.00	109.17	C
15	ATOM	5802	NE	ARG A 762	35.476	14.152	170.837	1.00	115.94	N
	ATOM	5803	CZ	ARG A 762	34.760	13.264	171.522	1.00	120.79	C
	ATOM	5804	NH1	ARG A 762	34.770	11.978	171.177	1.00	121.25	N
	ATOM	5805	NH2	ARG A 762	34.026	13.666	172.550	1.00	120.80	N
	ATOM	5806	N	TYR A 763	32.251	13.669	166.455	1.00	96.66	N
20	ATOM	5807	CA	TYR A 763	31.362	12.540	166.230	1.00	96.13	C
	ATOM	5808	C	TYR A 763	31.115	12.299	164.744	1.00	98.79	C
	ATOM	5809	O	TYR A 763	31.057	11.146	164.295	1.00	96.96	O
	ATOM	5810	CB	TYR A 763	30.031	12.759	166.946	1.00	91.90	C
	ATOM	5811	CG	TYR A 763	29.141	11.548	166.891	1.00	93.93	C
25	ATOM	5812	CD1	TYR A 763	29.477	10.393	167.583	1.00	95.46	C
	ATOM	5813	CD2	TYR A 763	27.967	11.552	166.145	1.00	91.08	C
	ATOM	5814	CE1	TYR A 763	28.670	9.279	167.537	1.00	97.06	C
	ATOM	5815	CE2	TYR A 763	27.154	10.439	166.091	1.00	89.89	C
	ATOM	5816	CZ	TYR A 763	27.514	9.306	166.787	1.00	97.27	C
30	ATOM	5817	OH	TYR A 763	26.718	8.188	166.742	1.00	107.28	O
	ATOM	5818	N	LEU A 764	30.965	13.384	163.985	1.00	96.27	N
	ATOM	5819	CA	LEU A 764	30.694	13.271	162.556	1.00	97.08	C
	ATOM	5820	C	LEU A 764	31.893	12.729	161.813	1.00	99.11	C
	ATOM	5821	O	LEU A 764	31.784	11.783	161.029	1.00	101.30	O
35	ATOM	5822	CB	LEU A 764	30.277	14.610	161.964	1.00	98.42	C
	ATOM	5823	CG	LEU A 764	28.784	14.625	161.635	1.00	117.97	C
	ATOM	5824	CD1	LEU A 764	27.920	14.420	162.901	1.00	121.81	C
	ATOM	5825	CD2	LEU A 764	28.397	15.900	160.885	1.00	124.49	C
	ATOM	5826	N	ILE A 765	33.043	13.328	162.079	1.00	94.01	N
40	ATOM	5827	CA	ILE A 765	34.273	12.931	161.423	1.00	93.22	C

	ATOM	5828	C	ILE A 765	34.682	11.478	161.724	1.00101.07	C
	ATOM	5829	O	ILE A 765	34.968	10.707	160.801	1.00106.02	O
	ATOM	5830	CB	ILE A 765	35.400	13.911	161.759	1.00 85.48	C
	ATOM	5831	CG1	ILE A 765	35.121	15.249	161.090	1.00 84.16	C
5	ATOM	5832	CG2	ILE A 765	36.733	13.378	161.293	1.00 90.53	C
	ATOM	5833	CD1	ILE A 765	36.059	16.338	161.522	1.00 89.80	C
	ATOM	5834	N	SER A 766	34.692	11.092	162.997	1.00 97.05	N
	ATOM	5835	CA	SER A 766	35.133	9.744	163.342	1.00103.16	C
	ATOM	5836	C	SER A 766	34.169	8.682	162.821	1.00109.59	C
10	ATOM	5837	O	SER A 766	34.584	7.583	162.462	1.00109.71	O
	ATOM	5838	CB	SER A 766	35.353	9.590	164.847	1.00108.66	C
	ATOM	5839	OG	SER A 766	34.147	9.778	165.559	1.00118.52	O
	ATOM	5840	N	SER A 767	32.884	9.016	162.766	1.00117.90	N
	ATOM	5841	CA	SER A 767	31.892	8.078	162.245	1.00121.63	C
15	ATOM	5842	C	SER A 767	32.061	7.918	160.731	1.00122.02	C
	ATOM	5843	O	SER A 767	31.977	6.807	160.203	1.00126.45	O
	ATOM	5844	CB	SER A 767	30.460	8.507	162.610	1.00117.53	C
	ATOM	5845	OG	SER A 767	29.931	9.455	161.697	1.00116.63	O
	ATOM	5846	N	ASN A 768	32.318	9.025	160.040	1.00114.23	N
20	ATOM	5847	CA	ASN A 768	32.526	8.979	158.596	1.00107.80	C
	ATOM	5848	C	ASN A 768	33.832	8.289	158.214	1.00101.79	C
	ATOM	5849	O	ASN A 768	33.876	7.514	157.260	1.00105.64	O
	ATOM	5850	CB	ASN A 768	32.447	10.377	157.982	1.00105.99	C
	ATOM	5851	CG	ASN A 768	31.016	10.841	157.770	1.00109.65	C
25	ATOM	5852	OD1	ASN A 768	30.080	10.295	158.358	1.00111.41	O
	ATOM	5853	ND2	ASN A 768	30.839	11.851	156.922	1.00110.42	N
	ATOM	5854	N	VAL A 769	34.889	8.559	158.970	1.00 93.37	N
	ATOM	5855	CA	VAL A 769	36.178	7.909	158.739	1.00 94.25	C
	ATOM	5856	C	VAL A 769	36.122	6.370	158.820	1.00 95.63	C
30	ATOM	5857	O	VAL A 769	36.666	5.677	157.954	1.00 97.84	O
	ATOM	5858	CB	VAL A 769	37.258	8.467	159.692	1.00 90.35	C
	ATOM	5859	CG1	VAL A 769	38.374	7.471	159.898	1.00 86.98	C
	ATOM	5860	CG2	VAL A 769	37.801	9.776	159.156	1.00 87.55	C
	ATOM	5861	N	GLY A 770	35.464	5.844	159.848	1.00 90.49	N
35	ATOM	5862	CA	GLY A 770	35.284	4.409	159.975	1.00 90.63	C
	ATOM	5863	C	GLY A 770	34.596	3.805	158.763	1.00 96.37	C
	ATOM	5864	O	GLY A 770	35.004	2.752	158.253	1.00 98.06	O
	ATOM	5865	N	GLU A 771	33.545	4.474	158.298	1.00 99.13	N
	ATOM	5866	CA	GLU A 771	32.827	4.030	157.112	1.00106.93	C
40	ATOM	5867	C	GLU A 771	33.797	3.888	155.943	1.00114.92	C

	ATOM	5868	O	GLU A 771	33.853	2.840	155.300	1.00121.89	O
	ATOM	5869	CB	GLU A 771	31.694	5.002	156.772	1.00111.71	C
	ATOM	5870	CG	GLU A 771	30.550	5.006	157.786	1.00121.10	C
	ATOM	5871	CD	GLU A 771	29.370	5.870	157.354	1.00131.03	C
5	ATOM	5872	OE1	GLU A 771	29.566	6.750	156.489	1.00135.19	O
	ATOM	5873	OE2	GLU A 771	28.246	5.665	157.872	1.00132.60	O
	ATOM	5874	N	VAL A 772	34.582	4.935	155.697	1.00111.22	N
	ATOM	5875	CA	VAL A 772	35.621	4.908	154.666	1.00105.31	C
	ATOM	5876	C	VAL A 772	36.618	3.761	154.867	1.00110.24	C
10	ATOM	5877	O	VAL A 772	36.976	3.064	153.914	1.00117.43	O
	ATOM	5878	CB	VAL A 772	36.384	6.253	154.592	1.00 94.66	C
	ATOM	5879	CG1	VAL A 772	37.657	6.116	153.777	1.00 90.65	C
	ATOM	5880	CG2	VAL A 772	35.495	7.329	154.001	1.00 95.85	C
	ATOM	5881	N	VAL A 773	37.053	3.559	156.105	1.00104.99	N
15	ATOM	5882	CA	VAL A 773	38.030	2.518	156.392	1.00104.51	C
	ATOM	5883	C	VAL A 773	37.520	1.123	156.032	1.00113.52	C
	ATOM	5884	O	VAL A 773	38.126	0.433	155.210	1.00116.53	O
	ATOM	5885	CB	VAL A 773	38.486	2.545	157.864	1.00 95.59	C
	ATOM	5886	CG1	VAL A 773	39.302	1.293	158.194	1.00 93.99	C
20	ATOM	5887	CG2	VAL A 773	39.281	3.814	158.148	1.00 85.35	C
	ATOM	5888	N	CYS A 774	36.406	0.720	156.638	1.00118.63	N
	ATOM	5889	CA	CYS A 774	35.893	-0.638	156.461	1.00121.86	C
	ATOM	5890	C	CYS A 774	35.674	-0.963	154.991	1.00125.46	C
	ATOM	5891	O	CYS A 774	36.059	-2.029	154.516	1.00133.05	O
25	ATOM	5892	CB	CYS A 774	34.590	-0.835	157.229	1.00117.34	C
	ATOM	5893	SG	CYS A 774	33.172	-0.016	156.494	1.00158.94	S
	ATOM	5894	N	ILE A 775	35.065	-0.028	154.276	1.00121.57	N
	ATOM	5895	CA	ILE A 775	34.824	-0.198	152.853	1.00124.80	C
	ATOM	5896	C	ILE A 775	36.146	-0.278	152.090	1.00129.99	C
30	ATOM	5897	O	ILE A 775	36.262	-0.984	151.084	1.00133.10	O
	ATOM	5898	CB	ILE A 775	33.924	0.928	152.317	1.00122.17	C
	ATOM	5899	CG1	ILE A 775	32.479	0.644	152.707	1.00117.55	C
	ATOM	5900	CG2	ILE A 775	34.022	1.039	150.812	1.00126.76	C
	ATOM	5901	CD1	ILE A 775	32.060	-0.782	152.393	1.00117.07	C
35	ATOM	5902	N	PHE A 776	37.156	0.422	152.590	1.00126.51	N
	ATOM	5903	CA	PHE A 776	38.462	0.365	151.960	1.00122.32	C
	ATOM	5904	C	PHE A 776	39.184	-0.952	152.245	1.00127.37	C
	ATOM	5905	O	PHE A 776	39.661	-1.609	151.322	1.00135.58	O
	ATOM	5906	CB	PHE A 776	39.331	1.541	152.379	1.00116.74	C
40	ATOM	5907	CG	PHE A 776	40.637	1.582	151.666	1.00118.43	C

	ATOM	5908	CD1 PHE A 776	40.708	2.059	150.369	1.00120.72	C
	ATOM	5909	CD2 PHE A 776	41.787	1.117	152.274	1.00119.49	C
	ATOM	5910	CE1 PHE A 776	41.908	2.087	149.692	1.00123.66	C
	ATOM	5911	CE2 PHE A 776	42.991	1.141	151.605	1.00123.35	C
5	ATOM	5912	CZ PHE A 776	43.053	1.626	150.309	1.00124.99	C
	ATOM	5913	N LEU A 777	39.271	-1.330	153.517	1.00123.65	N
	ATOM	5914	CA LEU A 777	39.930	-2.575	153.893	1.00123.40	C
	ATOM	5915	C LEU A 777	39.302	-3.756	153.181	1.00130.70	C
	ATOM	5916	O LEU A 777	40.001	-4.650	152.700	1.00135.53	O
10	ATOM	5917	CB LEU A 777	39.833	-2.806	155.397	1.00117.05	C
	ATOM	5918	CG LEU A 777	40.614	-1.828	156.261	1.00117.34	C
	ATOM	5919	CD1 LEU A 777	40.486	-2.225	157.711	1.00120.24	C
	ATOM	5920	CD2 LEU A 777	42.070	-1.786	155.834	1.00116.47	C
	ATOM	5921	N THR A 778	37.976	-3.746	153.111	1.00131.80	N
15	ATOM	5922	CA THR A 778	37.234	-4.870	152.558	1.00136.29	C
	ATOM	5923	C THR A 778	37.626	-5.130	151.096	1.00138.38	C
	ATOM	5924	O THR A 778	37.537	-6.259	150.612	1.00143.61	O
	ATOM	5925	CB THR A 778	35.697	-4.692	152.746	1.00135.45	C
	ATOM	5926	OG1 THR A 778	35.044	-5.968	152.703	1.00136.83	O
20	ATOM	5927	CG2 THR A 778	35.105	-3.772	151.689	1.00134.14	C
	ATOM	5928	N ALA A 779	38.097	-4.095	150.410	1.00132.84	N
	ATOM	5929	CA ALA A 779	38.571	-4.258	149.039	1.00130.12	C
	ATOM	5930	C ALA A 779	40.098	-4.291	148.947	1.00133.31	C
	ATOM	5931	O ALA A 779	40.653	-5.074	148.180	1.00141.38	O
25	ATOM	5932	CB ALA A 779	38.009	-3.176	148.149	1.00124.98	C
	ATOM	5933	N ALA A 780	40.771	-3.451	149.729	1.00128.43	N
	ATOM	5934	CA ALA A 780	42.234	-3.378	149.706	1.00129.85	C
	ATOM	5935	C ALA A 780	42.909	-4.682	150.144	1.00135.09	C
	ATOM	5936	O ALA A 780	44.006	-5.013	149.690	1.00136.50	O
30	ATOM	5937	CB ALA A 780	42.721	-2.223	150.560	1.00126.45	C
	ATOM	5938	N LEU A 781	42.250	-5.417	151.031	1.00136.15	N
	ATOM	5939	CA LEU A 781	42.786	-6.684	151.506	1.00135.64	C
	ATOM	5940	C LEU A 781	42.272	-7.853	150.671	1.00140.42	C
	ATOM	5941	O LEU A 781	42.805	-8.959	150.746	1.00139.44	O
35	ATOM	5942	CB LEU A 781	42.442	-6.890	152.981	1.00127.53	C
	ATOM	5943	CG LEU A 781	43.154	-5.988	153.988	1.00119.53	C
	ATOM	5944	CD1 LEU A 781	42.533	-6.156	155.359	1.00115.48	C
	ATOM	5945	CD2 LEU A 781	44.648	-6.283	154.029	1.00116.26	C
	ATOM	5946	N GLY A 782	41.235	-7.600	149.879	1.00146.33	N
40	ATOM	5947	CA GLY A 782	40.668	-8.616	149.007	1.00150.91	C

	ATOM	5948	C	GLY A 782	39.601	-9.442	149.700	1.00151.44	C
	ATOM	5949	O	GLY A 782	39.487	-10.648	149.465	1.00152.88	O
	ATOM	5950	N	LEU A 783	38.821	-8.785	150.555	1.00148.17	N
	ATOM	5951	CA	LEU A 783	37.778	-9.451	151.333	1.00143.43	C
5	ATOM	5952	C	LEU A 783	36.425	-9.370	150.641	1.00142.84	C
	ATOM	5953	O	LEU A 783	36.244	-8.568	149.720	1.00139.75	O
	ATOM	5954	CB	LEU A 783	37.666	-8.816	152.722	1.00136.46	C
	ATOM	5955	CG	LEU A 783	38.440	-9.486	153.854	1.00129.91	C
	ATOM	5956	CD1	LEU A 783	39.920	-9.255	153.687	1.00132.56	C
10	ATOM	5957	CD2	LEU A 783	37.969	-8.957	155.186	1.00125.02	C
	ATOM	5958	N	PRO A 784	35.469	-10.215	151.073	1.00144.25	N
	ATOM	5959	CA	PRO A 784	34.078	-10.027	150.652	1.00146.21	C
	ATOM	5960	C	PRO A 784	33.540	-8.723	151.229	1.00150.78	C
	ATOM	5961	O	PRO A 784	34.022	-8.278	152.276	1.00152.13	O
15	ATOM	5962	CB	PRO A 784	33.352	-11.217	151.291	1.00139.92	C
	ATOM	5963	CG	PRO A 784	34.406	-12.228	151.528	1.00138.37	C
	ATOM	5964	CD	PRO A 784	35.640	-11.451	151.857	1.00139.22	C
	ATOM	5965	N	GLU A 785	32.568	-8.117	150.555	1.00151.24	N
	ATOM	5966	CA	GLU A 785	31.981	-6.873	151.031	1.00150.43	C
20	ATOM	5967	C	GLU A 785	31.373	-7.088	152.406	1.00146.53	C
	ATOM	5968	O	GLU A 785	30.488	-7.928	152.581	1.00144.78	O
	ATOM	5969	CB	GLU A 785	30.910	-6.383	150.062	1.00158.10	C
	ATOM	5970	CG	GLU A 785	31.342	-6.424	148.612	1.00171.14	C
	ATOM	5971	CD	GLU A 785	30.426	-5.624	147.709	1.00182.46	C
25	ATOM	5972	OE1	GLU A 785	29.203	-5.595	147.969	1.00185.94	O
	ATOM	5973	OE2	GLU A 785	30.935	-5.011	146.745	1.00186.33	O
	ATOM	5974	N	ALA A 786	31.867	-6.342	153.388	1.00143.03	N
	ATOM	5975	CA	ALA A 786	31.321	-6.423	154.733	1.00139.68	C
	ATOM	5976	C	ALA A 786	29.969	-5.713	154.799	1.00142.27	C
30	ATOM	5977	O	ALA A 786	29.133	-6.035	155.644	1.00145.74	O
	ATOM	5978	CB	ALA A 786	32.293	-5.833	155.741	1.00132.98	C
	ATOM	5979	N	LEU A 787	29.755	-4.755	153.897	1.00137.11	N
	ATOM	5980	CA	LEU A 787	28.522	-3.970	153.886	1.00131.79	C
	ATOM	5981	C	LEU A 787	27.997	-3.665	152.477	1.00130.71	C
35	ATOM	5982	O	LEU A 787	28.679	-3.039	151.664	1.00127.54	O
	ATOM	5983	CB	LEU A 787	28.718	-2.662	154.661	1.00128.56	C
	ATOM	5984	CG	LEU A 787	29.164	-2.746	156.124	1.00124.03	C
	ATOM	5985	CD1	LEU A 787	29.607	-1.380	156.628	1.00119.41	C
	ATOM	5986	CD2	LEU A 787	28.057	-3.322	157.005	1.00124.54	C
40	ATOM	5987	N	ILE A 788	26.777	-4.116	152.204	1.00133.27	N

	ATOM	5988	CA	ILE A 788	26.050	-3.759	150.990	1.00136.61	C
	ATOM	5989	C	ILE A 788	25.692	-2.278	151.075	1.00141.21	C
	ATOM	5990	O	ILE A 788	25.371	-1.796	152.158	1.00146.67	O
	ATOM	5991	CB	ILE A 788	24.770	-4.636	150.868	1.00119.38	C
5	ATOM	5992	CG1	ILE A 788	25.124	-6.011	150.300	1.00123.34	C
	ATOM	5993	CG2	ILE A 788	23.689	-3.977	150.017	1.00120.03	C
	ATOM	5994	CD1	ILE A 788	23.973	-6.991	150.296	1.00126.26	C
	ATOM	5995	N	PRO A 789	25.769	-1.546	149.945	1.00142.52	N
	ATOM	5996	CA	PRO A 789	25.443	-0.113	149.887	1.00143.53	C
10	ATOM	5997	C	PRO A 789	24.167	0.233	150.651	1.00145.55	C
	ATOM	5998	O	PRO A 789	24.103	1.248	151.346	1.00142.18	O
	ATOM	5999	CB	PRO A 789	25.221	0.126	148.394	1.00147.30	C
	ATOM	6000	CG	PRO A 789	26.116	-0.852	147.734	1.00149.83	C
	ATOM	6001	CD	PRO A 789	26.152	-2.071	148.621	1.00147.08	C
15	ATOM	6002	N	VAL A 790	23.166	-0.631	150.514	1.00150.48	N
	ATOM	6003	CA	VAL A 790	21.886	-0.479	151.195	1.00150.24	C
	ATOM	6004	C	VAL A 790	22.052	-0.483	152.710	1.00141.84	C
	ATOM	6005	O	VAL A 790	21.437	0.317	153.414	1.00140.80	O
	ATOM	6006	CB	VAL A 790	20.926	-1.615	150.799	1.00156.50	C
20	ATOM	6007	CG1	VAL A 790	19.640	-1.533	151.599	1.00160.32	C
	ATOM	6008	CG2	VAL A 790	20.645	-1.569	149.310	1.00158.98	C
	ATOM	6009	N	GLN A 791	22.884	-1.392	153.204	1.00136.25	N
	ATOM	6010	CA	GLN A 791	23.135	-1.498	154.634	1.00133.41	C
	ATOM	6011	C	GLN A 791	23.789	-0.235	155.178	1.00133.97	C
25	ATOM	6012	O	GLN A 791	23.554	0.150	156.324	1.00137.99	O
	ATOM	6013	CB	GLN A 791	24.014	-2.712	154.933	1.00130.23	C
	ATOM	6014	CG	GLN A 791	23.352	-4.034	154.609	1.00134.49	C
	ATOM	6015	CD	GLN A 791	24.319	-5.195	154.672	1.00138.63	C
	ATOM	6016	OE1	GLN A 791	25.527	-5.021	154.505	1.00138.73	O
30	ATOM	6017	NE2	GLN A 791	23.794	-6.389	154.917	1.00141.43	N
	ATOM	6018	N	LEU A 792	24.600	0.414	154.348	1.00129.81	N
	ATOM	6019	CA	LEU A 792	25.360	1.579	154.782	1.00125.86	C
	ATOM	6020	C	LEU A 792	24.439	2.754	155.049	1.00122.63	C
	ATOM	6021	O	LEU A 792	24.423	3.304	156.148	1.00123.72	O
35	ATOM	6022	CB	LEU A 792	26.401	1.962	153.732	1.00129.43	C
	ATOM	6023	CG	LEU A 792	27.547	2.872	154.183	1.00126.06	C
	ATOM	6024	CD1	LEU A 792	28.312	2.248	155.345	1.00121.65	C
	ATOM	6025	CD2	LEU A 792	28.482	3.160	153.014	1.00126.16	C
	ATOM	6026	N	LEU A 793	23.663	3.125	154.039	1.00123.84	N
40	ATOM	6027	CA	LEU A 793	22.731	4.242	154.155	1.00131.25	C

	ATOM	6028	C	LEU A 793	21.748	4.089	155.321	1.00134.17	C
	ATOM	6029	O	LEU A 793	21.230	5.080	155.832	1.00135.13	O
	ATOM	6030	CB	LEU A 793	21.964	4.430	152.843	1.00137.49	C
	ATOM	6031	CG	LEU A 793	22.807	4.668	151.589	1.00136.07	C
5	ATOM	6032	CD1	LEU A 793	21.909	4.924	150.387	1.00137.21	C
	ATOM	6033	CD2	LEU A 793	23.775	5.826	151.805	1.00133.30	C
	ATOM	6034	N	TRP A 794	21.493	2.849	155.734	1.00136.26	N
	ATOM	6035	CA	TRP A 794	20.606	2.586	156.863	1.00134.37	C
	ATOM	6036	C	TRP A 794	21.236	3.065	158.156	1.00133.49	C
10	ATOM	6037	O	TRP A 794	20.656	3.882	158.874	1.00134.15	O
	ATOM	6038	CB	TRP A 794	20.295	1.096	156.979	1.00132.12	C
	ATOM	6039	CG	TRP A 794	19.769	0.711	158.330	1.00131.04	C
	ATOM	6040	CD1	TRP A 794	20.417	-0.015	159.287	1.00130.64	C
	ATOM	6041	CD2	TRP A 794	18.491	1.046	158.878	1.00130.27	C
15	ATOM	6042	NE1	TRP A 794	19.617	-0.160	160.394	1.00130.20	N
	ATOM	6043	CE2	TRP A 794	18.429	0.482	160.168	1.00130.84	C
	ATOM	6044	CE3	TRP A 794	17.391	1.764	158.405	1.00132.88	C
	ATOM	6045	CZ2	TRP A 794	17.315	0.617	160.987	1.00136.20	C
	ATOM	6046	CZ3	TRP A 794	16.287	1.898	159.218	1.00137.90	C
20	ATOM	6047	CH2	TRP A 794	16.256	1.327	160.496	1.00140.10	C
	ATOM	6048	N	VAL A 795	22.418	2.531	158.450	1.00129.97	N
	ATOM	6049	CA	VAL A 795	23.202	2.965	159.596	1.00126.81	C
	ATOM	6050	C	VAL A 795	23.347	4.473	159.554	1.00127.36	C
	ATOM	6051	O	VAL A 795	23.116	5.162	160.546	1.00126.55	O
25	ATOM	6052	CB	VAL A 795	24.604	2.342	159.573	1.00123.46	C
	ATOM	6053	CG1	VAL A 795	25.499	2.981	160.630	1.00119.27	C
	ATOM	6054	CG2	VAL A 795	24.513	0.847	159.775	1.00127.25	C
	ATOM	6055	N	ASN A 796	23.708	4.981	158.382	1.00129.94	N
	ATOM	6056	CA	ASN A 796	23.875	6.411	158.197	1.00131.04	C
30	ATOM	6057	C	ASN A 796	22.587	7.196	158.453	1.00130.13	C
	ATOM	6058	O	ASN A 796	22.638	8.367	158.815	1.00134.95	O
	ATOM	6059	CB	ASN A 796	24.415	6.717	156.803	1.00134.26	C
	ATOM	6060	CG	ASN A 796	25.001	8.100	156.712	1.00139.42	C
	ATOM	6061	OD1	ASN A 796	24.352	9.042	156.246	1.00140.90	O
35	ATOM	6062	ND2	ASN A 796	26.234	8.242	157.184	1.00142.27	N
	ATOM	6063	N	LEU A 797	21.437	6.555	158.267	1.00123.95	N
	ATOM	6064	CA	LEU A 797	20.158	7.197	158.560	1.00112.97	C
	ATOM	6065	C	LEU A 797	19.925	7.239	160.059	1.00111.41	C
	ATOM	6066	O	LEU A 797	19.655	8.298	160.625	1.00109.35	O
40	ATOM	6067	CB	LEU A 797	19.008	6.455	157.887	1.00107.09	C

	ATOM	6068	CG	LEU A 797	17.600	6.827	158.347	1.00106.56	C
	ATOM	6069	CD1	LEU A 797	17.353	8.306	158.211	1.00 86.07	C
	ATOM	6070	CD2	LEU A 797	16.573	6.061	157.542	1.00114.13	C
	ATOM	6071	N	VAL A 798	20.032	6.076	160.692	1.00112.40	N
5	ATOM	6072	CA	VAL A 798	19.810	5.951	162.128	1.00117.30	C
	ATOM	6073	C	VAL A 798	20.691	6.890	162.953	1.00120.10	C
	ATOM	6074	O	VAL A 798	20.187	7.629	163.799	1.00123.78	O
	ATOM	6075	CB	VAL A 798	20.022	4.500	162.609	1.00120.02	C
	ATOM	6076	CG1	VAL A 798	19.679	4.370	164.082	1.00116.16	C
10	ATOM	6077	CG2	VAL A 798	19.178	3.542	161.785	1.00128.57	C
	ATOM	6078	N	THR A 799	21.997	6.874	162.706	1.00118.44	N
	ATOM	6079	CA	THR A 799	22.912	7.690	163.501	1.00119.12	C
	ATOM	6080	C	THR A 799	22.659	9.195	163.358	1.00121.69	C
	ATOM	6081	O	THR A 799	22.636	9.906	164.357	1.00124.44	O
15	ATOM	6082	CB	THR A 799	24.402	7.368	163.226	1.00117.67	C
	ATOM	6083	OG1	THR A 799	24.762	7.806	161.908	1.00127.73	O
	ATOM	6084	CG2	THR A 799	24.670	5.877	163.373	1.00104.98	C
	ATOM	6085	N	ASP A 800	22.464	9.675	162.130	1.00123.04	N
	ATOM	6086	CA	ASP A 800	22.196	11.099	161.896	1.00125.25	C
20	ATOM	6087	C	ASP A 800	20.849	11.522	162.496	1.00128.13	C
	ATOM	6088	O	ASP A 800	20.644	12.692	162.832	1.00123.45	O
	ATOM	6089	CB	ASP A 800	22.217	11.431	160.395	1.00126.29	C
	ATOM	6090	CG	ASP A 800	23.610	11.329	159.781	1.00124.78	C
	ATOM	6091	OD1	ASP A 800	24.550	10.894	160.486	1.00125.99	O
25	ATOM	6092	OD2	ASP A 800	23.757	11.671	158.584	1.00119.06	O
	ATOM	6093	N	GLY A 801	19.939	10.560	162.631	1.00130.73	N
	ATOM	6094	CA	GLY A 801	18.590	10.841	163.090	1.00130.93	C
	ATOM	6095	C	GLY A 801	18.388	10.801	164.595	1.00127.92	C
	ATOM	6096	O	GLY A 801	17.629	11.609	165.146	1.00122.57	O
30	ATOM	6097	N	LEU A 802	19.048	9.857	165.266	1.00126.05	N
	ATOM	6098	CA	LEU A 802	18.878	9.711	166.714	1.00116.93	C
	ATOM	6099	C	LEU A 802	20.112	10.143	167.538	1.00101.56	C
	ATOM	6100	O	LEU A 802	20.082	11.214	168.141	1.00 97.24	O
	ATOM	6101	CB	LEU A 802	18.343	8.313	167.094	1.00116.47	C
35	ATOM	6102	CG	LEU A 802	17.090	7.814	166.367	1.00118.70	C
	ATOM	6103	CD1	LEU A 802	16.717	6.419	166.836	1.00122.97	C
	ATOM	6104	CD2	LEU A 802	15.918	8.769	166.556	1.00118.98	C
	ATOM	6105	N	PRO A 803	21.200	9.344	167.552	1.00 95.38	N
	ATOM	6106	CA	PRO A 803	22.302	9.748	168.434	1.00 95.30	C
40	ATOM	6107	C	PRO A 803	22.915	11.097	168.057	1.00102.35	C

	ATOM	6108	O	PRO A 803	23.259	11.875	168.948	1.00104.29	O
	ATOM	6109	CB	PRO A 803	23.338	8.634	168.238	1.00 89.52	C
	ATOM	6110	CG	PRO A 803	22.582	7.501	167.674	1.00 93.91	C
	ATOM	6111	CD	PRO A 803	21.547	8.124	166.805	1.00 96.61	C
5	ATOM	6112	N	ALA A 804	23.046	11.372	166.763	1.00102.37	N
	ATOM	6113	CA	ALA A 804	23.605	12.644	166.322	1.00 98.06	C
	ATOM	6114	C	ALA A 804	22.757	13.831	166.783	1.00 98.73	C
	ATOM	6115	O	ALA A 804	23.297	14.840	167.242	1.00 96.62	O
	ATOM	6116	CB	ALA A 804	23.781	12.667	164.810	1.00 94.99	C
10	ATOM	6117	N	THR A 805	21.436	13.715	166.661	1.00101.44	N
	ATOM	6118	CA	THR A 805	20.552	14.788	167.108	1.00103.61	C
	ATOM	6119	C	THR A 805	20.670	14.924	168.613	1.00101.74	C
	ATOM	6120	O	THR A 805	20.834	16.026	169.141	1.00103.13	O
	ATOM	6121	CB	THR A 805	19.077	14.534	166.728	1.00108.21	C
15	ATOM	6122	OG1	THR A 805	18.947	14.504	165.301	1.00118.05	O
	ATOM	6123	CG2	THR A 805	18.179	15.635	167.281	1.00 99.75	C
	ATOM	6124	N	ALA A 806	20.636	13.782	169.292	1.00100.30	N
	ATOM	6125	CA	ALA A 806	20.680	13.730	170.749	1.00102.83	C
	ATOM	6126	C	ALA A 806	21.887	14.449	171.354	1.00106.19	C
20	ATOM	6127	O	ALA A 806	21.906	14.730	172.552	1.00109.50	O
	ATOM	6128	CB	ALA A 806	20.630	12.283	171.225	1.00 99.94	C
	ATOM	6129	N	LEU A 807	22.887	14.748	170.530	1.00103.10	N
	ATOM	6130	CA	LEU A 807	24.092	15.420	171.001	1.00 96.75	C
	ATOM	6131	C	LEU A 807	23.849	16.893	171.289	1.00102.49	C
25	ATOM	6132	O	LEU A 807	24.572	17.505	172.084	1.00 99.92	O
	ATOM	6133	CB	LEU A 807	25.219	15.272	169.983	1.00 89.02	C
	ATOM	6134	CG	LEU A 807	25.817	13.872	169.927	1.00 89.96	C
	ATOM	6135	CD1	LEU A 807	26.996	13.836	168.976	1.00 85.58	C
	ATOM	6136	CD2	LEU A 807	26.227	13.419	171.326	1.00 93.35	C
30	ATOM	6137	N	GLY A 808	22.831	17.460	170.645	1.00106.53	N
	ATOM	6138	CA	GLY A 808	22.513	18.866	170.825	1.00112.45	C
	ATOM	6139	C	GLY A 808	22.053	19.179	172.237	1.00115.05	C
	ATOM	6140	O	GLY A 808	22.063	20.333	172.683	1.00111.21	O
	ATOM	6141	N	PHE A 809	21.662	18.125	172.943	1.00119.29	N
35	ATOM	6142	CA	PHE A 809	21.063	18.243	174.260	1.00122.64	C
	ATOM	6143	C	PHE A 809	22.038	17.739	175.314	1.00123.74	C
	ATOM	6144	O	PHE A 809	21.653	17.102	176.293	1.00129.06	O
	ATOM	6145	CB	PHE A 809	19.746	17.466	174.285	1.00127.71	C
	ATOM	6146	CG	PHE A 809	18.872	17.750	173.098	1.00132.62	C
40	ATOM	6147	CD1	PHE A 809	18.750	19.048	172.609	1.00136.22	C

	ATOM	6148	CD2 PHE A 809	18.201	16.730	172.451	1.00135.19	C
	ATOM	6149	CE1 PHE A 809	17.967	19.323	171.506	1.00138.99	C
	ATOM	6150	CE2 PHE A 809	17.410	16.997	171.348	1.00140.62	C
	ATOM	6151	CZ PHE A 809	17.293	18.296	170.874	1.00141.84	C
5	ATOM	6152	N ASN A 810	23.315	18.024	175.087	1.00120.04	N
	ATOM	6153	CA ASN A 810	24.357	17.752	176.064	1.00114.61	C
	ATOM	6154	C ASN A 810	24.360	18.847	177.138	1.00109.10	C
	ATOM	6155	O ASN A 810	23.748	19.901	176.956	1.00112.27	O
	ATOM	6156	CB ASN A 810	25.722	17.666	175.365	1.00108.74	C
10	ATOM	6157	CG ASN A 810	25.926	16.345	174.626	1.00105.58	C
	ATOM	6158	OD1 ASN A 810	24.970	15.693	174.211	1.00107.61	O
	ATOM	6159	ND2 ASN A 810	27.182	15.946	174.469	1.00101.69	N
	ATOM	6160	N PRO A 811	25.017	18.596	178.275	1.00 95.84	N
	ATOM	6161	CA PRO A 811	25.172	19.671	179.252	1.00 94.60	C
15	ATOM	6162	C PRO A 811	26.444	20.445	178.974	1.00 99.18	C
	ATOM	6163	O PRO A 811	27.302	19.945	178.242	1.00100.58	O
	ATOM	6164	CB PRO A 811	25.365	18.901	180.546	1.00 94.47	C
	ATOM	6165	CG PRO A 811	26.129	17.725	180.100	1.00 90.71	C
	ATOM	6166	CD PRO A 811	25.467	17.309	178.825	1.00 89.61	C
20	ATOM	6167	N PRO A 812	26.571	21.652	179.549	1.00101.91	N
	ATOM	6168	CA PRO A 812	27.859	22.346	179.549	1.00100.18	C
	ATOM	6169	C PRO A 812	28.939	21.431	180.094	1.00104.79	C
	ATOM	6170	O PRO A 812	28.709	20.753	181.091	1.00114.72	O
	ATOM	6171	CB PRO A 812	27.617	23.501	180.514	1.00 98.28	C
25	ATOM	6172	CG PRO A 812	26.190	23.833	180.293	1.00101.85	C
	ATOM	6173	CD PRO A 812	25.498	22.502	180.087	1.00104.47	C
	ATOM	6174	N ASP A 813	30.088	21.399	179.432	1.00103.80	N
	ATOM	6175	CA ASP A 813	31.209	20.584	179.873	1.00106.89	C
	ATOM	6176	C ASP A 813	31.581	20.964	181.299	1.00107.48	C
30	ATOM	6177	O ASP A 813	31.202	22.026	181.786	1.00106.34	O
	ATOM	6178	CB ASP A 813	32.401	20.788	178.939	1.00108.82	C
	ATOM	6179	CG ASP A 813	33.067	19.485	178.555	1.00112.22	C
	ATOM	6180	OD2 ASP A 813	33.479	19.343	177.384	1.00111.67	O
	ATOM	6181	OD1 ASP A 813	33.175	18.601	179.427	1.00116.41	O
35	ATOM	6182	N LEU A 814	32.306	20.095	181.985	1.00112.09	N
	ATOM	6183	CA LEU A 814	32.632	20.369	183.379	1.00119.16	C
	ATOM	6184	C LEU A 814	33.836	21.293	183.500	1.00117.00	C
	ATOM	6185	O LEU A 814	34.645	21.395	182.574	1.00114.81	O
	ATOM	6186	CB LEU A 814	32.868	19.067	184.151	1.00123.90	C
40	ATOM	6187	CG LEU A 814	31.627	18.228	184.460	1.00123.18	C

	ATOM	6188	CD1 LEU A 814	32.021	17.034	185.304	1.00131.39	C
	ATOM	6189	CD2 LEU A 814	30.552	19.059	185.161	1.00117.04	C
	ATOM	6190	N ASP A 815	33.933	21.969	184.645	1.00118.49	N
	ATOM	6191	CA ASP A 815	35.093	22.789	184.978	1.00123.49	C
5	ATOM	6192	C ASP A 815	35.425	23.699	183.812	1.00112.50	C
	ATOM	6193	O ASP A 815	36.577	23.845	183.424	1.00116.95	O
	ATOM	6194	CB ASP A 815	36.287	21.895	185.326	1.00137.23	C
	ATOM	6195	CG ASP A 815	35.978	20.918	186.457	1.00145.27	C
	ATOM	6196	OD1 ASP A 815	35.541	21.375	187.541	1.00146.56	O
10	ATOM	6197	OD2 ASP A 815	36.158	19.693	186.252	1.00145.15	O
	ATOM	6198	N ILE A 816	34.380	24.286	183.250	1.00104.00	N
	ATOM	6199	CA ILE A 816	34.465	25.026	182.003	1.00 93.92	C
	ATOM	6200	C ILE A 816	34.949	26.442	182.262	1.00 97.04	C
	ATOM	6201	O ILE A 816	35.440	27.123	181.359	1.00101.24	O
15	ATOM	6202	CB ILE A 816	33.084	25.071	181.322	1.00 82.93	C
	ATOM	6203	CG1 ILE A 816	33.204	25.250	179.816	1.00 77.12	C
	ATOM	6204	CG2 ILE A 816	32.206	26.146	181.937	1.00 80.58	C
	ATOM	6205	CD1 ILE A 816	31.871	25.307	179.146	1.00 75.18	C
	ATOM	6206	N MET A 817	34.818	26.886	183.504	1.00 98.22	N
20	ATOM	6207	CA MET A 817	35.276	28.219	183.855	1.00 94.45	C
	ATOM	6208	C MET A 817	36.283	28.225	184.986	1.00101.03	C
	ATOM	6209	O MET A 817	36.433	29.224	185.686	1.00 97.26	O
	ATOM	6210	CB MET A 817	34.102	29.137	184.140	1.00 80.93	C
	ATOM	6211	CG MET A 817	33.263	29.307	182.910	1.00 68.59	C
25	ATOM	6212	SD MET A 817	32.355	30.838	182.916	1.00 98.26	S
	ATOM	6213	CE MET A 817	33.477	31.966	182.133	1.00 55.83	C
	ATOM	6214	N ASP A 818	36.960	27.092	185.152	1.00110.54	N
	ATOM	6215	CA ASP A 818	38.176	27.021	185.945	1.00118.00	C
	ATOM	6216	C ASP A 818	39.330	26.947	184.961	1.00117.57	C
30	ATOM	6217	O ASP A 818	40.480	26.709	185.337	1.00126.76	O
	ATOM	6218	CB ASP A 818	38.158	25.800	186.851	1.00125.99	C
	ATOM	6219	CG ASP A 818	36.958	25.787	187.761	1.00132.93	C
	ATOM	6220	OD2 ASP A 818	35.974	25.097	187.416	1.00137.54	O
	ATOM	6221	OD1 ASP A 818	36.994	26.477	188.808	1.00130.54	O
35	ATOM	6222	N ARG A 819	38.992	27.141	183.690	1.00107.94	N
	ATOM	6223	CA ARG A 819	39.967	27.280	182.625	1.00101.14	C
	ATOM	6224	C ARG A 819	40.063	28.760	182.268	1.00 96.77	C
	ATOM	6225	O ARG A 819	39.169	29.541	182.598	1.00 99.42	O
	ATOM	6226	CB ARG A 819	39.533	26.463	181.406	1.00 99.72	C
40	ATOM	6227	CG ARG A 819	39.347	24.983	181.685	1.00104.42	C

	ATOM	6228	CD	ARG A 819	39.024	24.219	180.417	1.00110.31	C
	ATOM	6229	NE	ARG A 819	40.116	24.264	179.445	1.00119.97	N
	ATOM	6230	CZ	ARG A 819	41.071	23.342	179.339	1.00132.19	C
	ATOM	6231	NH1	ARG A 819	41.086	22.289	180.150	1.00135.63	N
5	ATOM	6232	NH2	ARG A 819	42.016	23.471	178.417	1.00137.17	N
	ATOM	6233	N	PRO A 820	41.157	29.162	181.614	1.00 88.65	N
	ATOM	6234	CA	PRO A 820	41.328	30.547	181.171	1.00 90.13	C
	ATOM	6235	C	PRO A 820	40.687	30.745	179.800	1.00 90.12	C
	ATOM	6236	O	PRO A 820	40.292	29.744	179.193	1.00 92.42	O
10	ATOM	6237	CB	PRO A 820	42.852	30.696	181.077	1.00 88.39	C
	ATOM	6238	CG	PRO A 820	43.405	29.511	181.769	1.00 94.86	C
	ATOM	6239	CD	PRO A 820	42.417	28.427	181.527	1.00 90.61	C
	ATOM	6240	N	PRO A 821	40.577	32.006	179.325	1.00 79.70	N
	ATOM	6241	CA	PRO A 821	39.930	32.227	178.033	1.00 75.66	C
15	ATOM	6242	C	PRO A 821	40.633	31.463	176.935	1.00 86.00	C
	ATOM	6243	O	PRO A 821	41.858	31.368	176.941	1.00 89.58	O
	ATOM	6244	CB	PRO A 821	40.114	33.731	177.798	1.00 73.79	C
	ATOM	6245	CG	PRO A 821	40.259	34.316	179.137	1.00 71.98	C
	ATOM	6246	CD	PRO A 821	40.996	33.277	179.946	1.00 76.70	C
20	ATOM	6247	N	ARG A 822	39.853	30.911	176.013	1.00 92.68	N
	ATOM	6248	CA	ARG A 822	40.392	30.303	174.806	1.00 84.40	C
	ATOM	6249	C	ARG A 822	41.239	31.338	174.108	1.00 86.00	C
	ATOM	6250	O	ARG A 822	40.995	32.547	174.214	1.00 82.58	O
	ATOM	6251	CB	ARG A 822	39.259	29.865	173.875	1.00 78.61	C
25	ATOM	6252	CG	ARG A 822	39.669	28.850	172.833	1.00 78.83	C
	ATOM	6253	CD	ARG A 822	38.464	28.264	172.103	1.00 78.83	C
	ATOM	6254	NE	ARG A 822	37.997	29.099	170.999	1.00 79.92	N
	ATOM	6255	CZ	ARG A 822	36.938	29.903	171.053	1.00 83.20	C
	ATOM	6256	NH1	ARG A 822	36.598	30.619	169.985	1.00 85.36	N
30	ATOM	6257	NH2	ARG A 822	36.214	29.990	172.167	1.00 81.67	N
	ATOM	6258	N	SER A 823	42.258	30.868	173.410	1.00 96.65	N
	ATOM	6259	CA	SER A 823	43.037	31.768	172.600	1.00103.20	C
	ATOM	6260	C	SER A 823	42.251	32.067	171.343	1.00111.73	C
	ATOM	6261	O	SER A 823	41.661	31.163	170.745	1.00117.04	O
35	ATOM	6262	CB	SER A 823	44.371	31.149	172.230	1.00103.25	C
	ATOM	6263	OG	SER A 823	45.070	32.029	171.375	1.00107.72	O
	ATOM	6264	N	PRO A 824	42.214	33.343	170.945	1.00114.14	N
	ATOM	6265	CA	PRO A 824	41.744	33.586	169.587	1.00116.25	C
	ATOM	6266	C	PRO A 824	42.821	32.995	168.703	1.00124.54	C
40	ATOM	6267	O	PRO A 824	43.968	32.907	169.149	1.00135.24	O

	ATOM	6268	CB	PRO A 824	41.740	35.109	169.493	1.00120.12	C
	ATOM	6269	CG	PRO A 824	42.794	35.552	170.474	1.00119.31	C
	ATOM	6270	CD	PRO A 824	42.725	34.563	171.596	1.00117.91	C
	ATOM	6271	N	LYS A 825	42.468	32.548	167.506	1.00124.39	N
5	ATOM	6272	CA	LYS A 825	43.454	31.994	166.574	1.00134.81	C
	ATOM	6273	C	LYS A 825	43.992	30.598	166.939	1.00132.70	C
	ATOM	6274	O	LYS A 825	44.625	29.952	166.106	1.00142.93	O
	ATOM	6275	CB	LYS A 825	44.603	32.985	166.312	1.00146.95	C
	ATOM	6276	CG	LYS A 825	44.138	34.352	165.817	1.00154.97	C
10	ATOM	6277	CD	LYS A 825	45.291	35.334	165.681	1.00164.31	C
	ATOM	6278	CE	LYS A 825	44.800	36.686	165.179	1.00168.95	C
	ATOM	6279	NZ	LYS A 825	45.908	37.664	164.989	1.00174.75	N
	ATOM	6280	N	GLU A 826	43.755	30.132	168.164	1.00122.20	N
	ATOM	6281	CA	GLU A 826	43.946	28.714	168.468	1.00116.81	C
15	ATOM	6282	C	GLU A 826	43.090	27.923	167.482	1.00116.28	C
	ATOM	6283	O	GLU A 826	41.873	28.097	167.447	1.00120.13	O
	ATOM	6284	CB	GLU A 826	43.513	28.389	169.898	1.00114.09	C
	ATOM	6285	CG	GLU A 826	43.227	26.902	170.125	1.00120.34	C
	ATOM	6286	CD	GLU A 826	42.383	26.636	171.366	1.00123.77	C
20	ATOM	6287	OE1	GLU A 826	41.515	25.730	171.323	1.00121.90	O
	ATOM	6288	OE2	GLU A 826	42.592	27.330	172.386	1.00126.08	O
	ATOM	6289	N	PRO A 827	43.723	27.060	166.671	1.00111.70	N
	ATOM	6290	CA	PRO A 827	43.032	26.394	165.566	1.00108.54	C
	ATOM	6291	C	PRO A 827	41.880	25.556	166.084	1.00111.32	C
25	ATOM	6292	O	PRO A 827	41.983	24.986	167.171	1.00112.66	O
	ATOM	6293	CB	PRO A 827	44.112	25.487	164.984	1.00112.20	C
	ATOM	6294	CG	PRO A 827	45.003	25.202	166.129	1.00112.63	C
	ATOM	6295	CD	PRO A 827	45.059	26.487	166.896	1.00114.44	C
	ATOM	6296	N	LEU A 828	40.792	25.497	165.323	1.00113.77	N
30	ATOM	6297	CA	LEU A 828	39.605	24.761	165.740	1.00112.27	C
	ATOM	6298	C	LEU A 828	39.909	23.282	165.925	1.00113.23	C
	ATOM	6299	O	LEU A 828	39.485	22.660	166.896	1.00113.60	O
	ATOM	6300	CB	LEU A 828	38.499	24.939	164.715	1.00115.06	C
	ATOM	6301	CG	LEU A 828	37.251	24.095	164.938	1.00122.40	C
35	ATOM	6302	CD1	LEU A 828	36.646	24.320	166.321	1.00124.15	C
	ATOM	6303	CD2	LEU A 828	36.257	24.439	163.867	1.00126.94	C
	ATOM	6304	N	ILE A 829	40.645	22.723	164.977	1.00116.67	N
	ATOM	6305	CA	ILE A 829	41.125	21.359	165.107	1.00115.25	C
	ATOM	6306	C	ILE A 829	42.628	21.341	165.345	1.00120.44	C
40	ATOM	6307	O	ILE A 829	43.423	21.635	164.447	1.00120.92	O

	ATOM	6308	CB	ILE A 829	40.783	20.522	163.884	1.00110.04	C
	ATOM	6309	CG1	ILE A 829	39.264	20.379	163.772	1.00109.80	C
	ATOM	6310	CG2	ILE A 829	41.454	19.165	163.983	1.00108.30	C
	ATOM	6311	CD1	ILE A 829	38.801	19.586	162.566	1.00112.06	C
5	ATOM	6312	N	SER A 830	43.001	21.021	166.578	1.00123.21	N
	ATOM	6313	CA	SER A 830	44.393	20.878	166.950	1.00123.18	C
	ATOM	6314	C	SER A 830	44.967	19.735	166.151	1.00113.77	C
	ATOM	6315	O	SER A 830	44.240	18.806	165.793	1.00101.95	O
	ATOM	6316	CB	SER A 830	44.506	20.567	168.442	1.00136.00	C
10	ATOM	6317	OG	SER A 830	45.786	20.047	168.762	1.00148.23	O
	ATOM	6318	N	GLY A 831	46.266	19.818	165.864	1.00118.81	N
	ATOM	6319	CA	GLY A 831	46.970	18.755	165.172	1.00118.16	C
	ATOM	6320	C	GLY A 831	46.746	17.459	165.915	1.00116.71	C
	ATOM	6321	O	GLY A 831	46.403	16.436	165.323	1.0075.48	O
15	ATOM	6322	N	TRP A 832	46.914	17.530	167.232	1.00118.93	N
	ATOM	6323	CA	TRP A 832	46.642	16.407	168.122	1.00121.88	C
	ATOM	6324	C	TRP A 832	45.219	15.875	167.969	1.00122.25	C
	ATOM	6325	O	TRP A 832	45.000	14.665	167.919	1.00117.98	O
	ATOM	6326	CB	TRP A 832	46.871	16.811	169.584	1.00116.17	C
20	ATOM	6327	CG	TRP A 832	46.096	15.954	170.528	1.00106.22	C
	ATOM	6328	CD1	TRP A 832	44.922	16.270	171.141	1.00101.92	C
	ATOM	6329	CD2	TRP A 832	46.415	14.618	170.934	1.00102.37	C
	ATOM	6330	NE1	TRP A 832	44.496	15.218	171.911	1.00101.71	N
	ATOM	6331	CE2	TRP A 832	45.396	14.192	171.802	1.00100.26	C
25	ATOM	6332	CE3	TRP A 832	47.467	13.745	170.648	1.00108.46	C
	ATOM	6333	CZ2	TRP A 832	45.397	12.931	172.394	1.00102.96	C
	ATOM	6334	CZ3	TRP A 832	47.467	12.494	171.235	1.00112.35	C
	ATOM	6335	CH2	TRP A 832	46.439	12.099	172.100	1.00110.58	C
	ATOM	6336	N	LEU A 833	44.254	16.787	167.916	1.00123.25	N
30	ATOM	6337	CA	LEU A 833	42.850	16.404	167.849	1.00119.12	C
	ATOM	6338	C	LEU A 833	42.584	15.534	166.620	1.00112.13	C
	ATOM	6339	O	LEU A 833	41.941	14.488	166.716	1.00105.02	O
	ATOM	6340	CB	LEU A 833	41.962	17.651	167.849	1.00116.65	C
	ATOM	6341	CG	LEU A 833	40.465	17.434	168.055	1.00112.36	C
35	ATOM	6342	CD1	LEU A 833	40.239	16.360	169.103	1.00109.73	C
	ATOM	6343	CD2	LEU A 833	39.793	18.746	168.457	1.00111.85	C
	ATOM	6344	N	PHE A 834	43.116	15.962	165.477	1.00110.51	N
	ATOM	6345	CA	PHE A 834	42.996	15.215	164.228	1.00107.79	C
	ATOM	6346	C	PHE A 834	43.449	13.767	164.382	1.00109.06	C
40	ATOM	6347	O	PHE A 834	42.967	12.877	163.680	1.00110.85	O

	ATOM	6348	CB	PHE A 834	43.810	15.890	163.125	1.00104.15	C
	ATOM	6349	CG	PHE A 834	43.590	15.298	161.766	1.00105.66	C
	ATOM	6350	CD2	PHE A 834	44.416	14.291	161.288	1.00110.74	C
	ATOM	6351	CD1	PHE A 834	42.558	15.748	160.964	1.00104.32	C
5	ATOM	6352	CE2	PHE A 834	44.214	13.742	160.034	1.00107.38	C
	ATOM	6353	CE1	PHE A 834	42.350	15.208	159.715	1.00104.24	C
	ATOM	6354	CZ	PHE A 834	43.183	14.205	159.247	1.00105.27	C
	ATOM	6355	N	PHE A 835	44.385	13.538	165.295	1.00102.20	N
	ATOM	6356	CA	PHE A 835	44.827	12.193	165.580	1.00 98.74	C
10	ATOM	6357	C	PHE A 835	43.653	11.369	166.104	1.00101.98	C
	ATOM	6358	O	PHE A 835	43.415	10.252	165.643	1.00 99.91	O
	ATOM	6359	CB	PHE A 835	45.965	12.210	166.596	1.00102.77	C
	ATOM	6360	CG	PHE A 835	46.568	10.868	166.845	1.00111.49	C
	ATOM	6361	CD1	PHE A 835	45.968	9.975	167.714	1.00111.23	C
15	ATOM	6362	CD2	PHE A 835	47.737	10.496	166.204	1.00121.20	C
	ATOM	6363	CE1	PHE A 835	46.514	8.735	167.931	1.00119.07	C
	ATOM	6364	CE2	PHE A 835	48.294	9.254	166.424	1.00127.36	C
	ATOM	6365	CZ	PHE A 835	47.680	8.371	167.291	1.00124.80	C
	ATOM	6366	N	ARG A 836	42.920	11.920	167.068	1.00106.32	N
20	ATOM	6367	CA	ARG A 836	41.796	11.198	167.664	1.00113.02	C
	ATOM	6368	C	ARG A 836	40.729	10.886	166.627	1.00114.52	C
	ATOM	6369	O	ARG A 836	40.115	9.818	166.656	1.00113.89	O
	ATOM	6370	CB	ARG A 836	41.165	11.998	168.798	1.00115.58	C
	ATOM	6371	CG	ARG A 836	42.057	12.208	169.990	1.00121.56	C
25	ATOM	6372	CD	ARG A 836	41.354	13.094	170.990	1.00123.12	C
	ATOM	6373	NE	ARG A 836	40.037	12.568	171.328	1.00123.70	N
	ATOM	6374	CZ	ARG A 836	39.230	13.114	172.231	1.00123.76	C
	ATOM	6375	NH1	ARG A 836	39.610	14.208	172.882	1.00121.13	N
	ATOM	6376	NH2	ARG A 836	38.047	12.566	172.483	1.00123.44	N
30	ATOM	6377	N	TYR A 837	40.511	11.831	165.717	1.00112.61	N
	ATOM	6378	CA	TYR A 837	39.516	11.663	164.667	1.00105.78	C
	ATOM	6379	C	TYR A 837	39.909	10.463	163.833	1.00103.85	C
	ATOM	6380	O	TYR A 837	39.071	9.635	163.479	1.00104.69	O
	ATOM	6381	CB	TYR A 837	39.411	12.917	163.795	1.00101.50	C
35	ATOM	6382	CG	TYR A 837	38.871	14.127	164.529	1.00102.17	C
	ATOM	6383	CD1	TYR A 837	38.425	14.024	165.837	1.00105.07	C
	ATOM	6384	CD2	TYR A 837	38.798	15.368	163.911	1.00100.43	C
	ATOM	6385	CE1	TYR A 837	37.937	15.118	166.512	1.00105.09	C
	ATOM	6386	CE2	TYR A 837	38.304	16.471	164.581	1.00 99.46	C
40	ATOM	6387	CZ	TYR A 837	37.873	16.335	165.882	1.00104.46	C

	ATOM	6388	OH	TYR A 837	37.375	17.414	166.573	1.00109.54	O
	ATOM	6389	N	MET A 838	41.200	10.353	163.552	1.00100.67	N
	ATOM	6390	CA	MET A 838	41.701	9.217	162.799	1.00101.96	C
	ATOM	6391	C	MET A 838	41.764	7.952	163.661	1.00105.17	C
5	ATOM	6392	O	MET A 838	41.206	6.917	163.287	1.00108.20	O
	ATOM	6393	CB	MET A 838	43.061	9.536	162.171	1.00103.50	C
	ATOM	6394	CG	MET A 838	42.993	10.558	161.046	1.00100.67	C
	ATOM	6395	SD	MET A 838	41.532	10.276	160.030	1.00132.63	S
	ATOM	6396	CE	MET A 838	41.959	11.144	158.525	1.00168.74	C
10	ATOM	6397	N	ALA A 839	42.420	8.044	164.817	1.00101.88	N
	ATOM	6398	CA	ALA A 839	42.631	6.875	165.667	1.00103.68	C
	ATOM	6399	C	ALA A 839	41.324	6.151	166.014	1.00110.74	C
	ATOM	6400	O	ALA A 839	41.215	4.935	165.845	1.00108.62	O
	ATOM	6401	CB	ALA A 839	43.390	7.259	166.924	1.00 99.86	C
15	ATOM	6402	N	ILE A 840	40.334	6.909	166.478	1.00117.26	N
	ATOM	6403	CA	ILE A 840	39.016	6.359	166.791	1.00118.11	C
	ATOM	6404	C	ILE A 840	38.331	5.842	165.530	1.00127.22	C
	ATOM	6405	O	ILE A 840	37.744	4.752	165.524	1.00130.21	O
	ATOM	6406	CB	ILE A 840	38.111	7.418	167.456	1.00104.73	C
20	ATOM	6407	CG1	ILE A 840	38.675	7.812	168.824	1.00103.74	C
	ATOM	6408	CG2	ILE A 840	36.687	6.909	167.587	1.00 98.04	C
	ATOM	6409	CD1	ILE A 840	38.799	6.660	169.794	1.00102.48	C
	ATOM	6410	N	GLY A 841	38.425	6.633	164.463	1.00126.95	N
	ATOM	6411	CA	GLY A 841	37.770	6.318	163.207	1.00120.55	C
25	ATOM	6412	C	GLY A 841	38.287	5.029	162.619	1.00115.36	C
	ATOM	6413	O	GLY A 841	37.512	4.182	162.176	1.00114.68	O
	ATOM	6414	N	GLY A 842	39.608	4.886	162.628	1.00111.17	N
	ATOM	6415	CA	GLY A 842	40.248	3.689	162.128	1.00108.94	C
	ATOM	6416	C	GLY A 842	39.731	2.475	162.863	1.00112.41	C
30	ATOM	6417	O	GLY A 842	39.392	1.467	162.241	1.00113.80	O
	ATOM	6418	N	TYR A 843	39.651	2.584	164.188	1.00113.66	N
	ATOM	6419	CA	TYR A 843	39.189	1.478	165.017	1.00111.61	C
	ATOM	6420	C	TYR A 843	37.824	0.993	164.565	1.00112.51	C
	ATOM	6421	O	TYR A 843	37.591	-0.212	164.465	1.00112.13	O
35	ATOM	6422	CB	TYR A 843	39.130	1.857	166.496	1.00107.29	C
	ATOM	6423	CG	TYR A 843	38.803	0.667	167.365	1.00112.11	C
	ATOM	6424	CD1	TYR A 843	39.797	-0.220	167.758	1.00112.88	C
	ATOM	6425	CD2	TYR A 843	37.499	0.410	167.768	1.00119.15	C
	ATOM	6426	CE1	TYR A 843	39.506	-1.321	168.541	1.00116.27	C
40	ATOM	6427	CE2	TYR A 843	37.197	-0.692	168.552	1.00124.16	C

	ATOM	6428	CZ	TYR A 843	38.208	-1.553	168.935	1.00122.19	C
	ATOM	6429	OH	TYR A 843	37.916	-2.648	169.711	1.00125.91	O
	ATOM	6430	N	VAL A 844	36.931	1.941	164.291	1.00113.16	N
	ATOM	6431	CA	VAL A 844	35.586	1.620	163.827	1.00115.27	C
5	ATOM	6432	C	VAL A 844	35.652	0.715	162.605	1.00112.80	C
	ATOM	6433	O	VAL A 844	35.141	-0.401	162.623	1.00107.62	O
	ATOM	6434	CB	VAL A 844	34.802	2.891	163.469	1.00115.22	C
	ATOM	6435	CG1	VAL A 844	33.400	2.530	163.000	1.00114.20	C
	ATOM	6436	CG2	VAL A 844	34.752	3.838	164.659	1.00115.91	C
10	ATOM	6437	N	GLY A 845	36.312	1.202	161.558	1.00115.54	N
	ATOM	6438	CA	GLY A 845	36.488	0.450	160.329	1.00116.24	C
	ATOM	6439	C	GLY A 845	37.239	-0.849	160.539	1.00119.23	C
	ATOM	6440	O	GLY A 845	36.843	-1.888	160.009	1.00124.72	O
	ATOM	6441	N	ALA A 846	38.321	-0.794	161.312	1.00114.76	N
15	ATOM	6442	CA	ALA A 846	39.079	-1.994	161.654	1.00108.52	C
	ATOM	6443	C	ALA A 846	38.182	-3.028	162.345	1.00112.89	C
	ATOM	6444	O	ALA A 846	38.206	-4.212	162.009	1.00111.36	O
	ATOM	6445	CB	ALA A 846	40.270	-1.641	162.532	1.00 97.51	C
	ATOM	6446	N	ALA A 847	37.374	-2.567	163.293	1.00116.76	N
20	ATOM	6447	CA	ALA A 847	36.501	-3.460	164.044	1.00119.59	C
	ATOM	6448	C	ALA A 847	35.383	-4.037	163.188	1.00118.87	C
	ATOM	6449	O	ALA A 847	35.115	-5.234	163.252	1.00122.12	O
	ATOM	6450	CB	ALA A 847	35.922	-2.754	165.267	1.00119.46	C
	ATOM	6451	N	THR A 848	34.731	-3.193	162.392	1.00115.94	N
25	ATOM	6452	CA	THR A 848	33.549	-3.629	161.651	1.00115.60	C
	ATOM	6453	C	THR A 848	33.895	-4.717	160.657	1.00114.28	C
	ATOM	6454	O	THR A 848	33.124	-5.658	160.488	1.00115.64	O
	ATOM	6455	CB	THR A 848	32.832	-2.481	160.912	1.00117.51	C
	ATOM	6456	OG1	THR A 848	33.732	-1.875	159.985	1.00123.06	O
30	ATOM	6457	CG2	THR A 848	32.336	-1.429	161.887	1.00117.40	C
	ATOM	6458	N	VAL A 849	35.051	-4.594	160.006	1.00116.98	N
	ATOM	6459	CA	VAL A 849	35.538	-5.665	159.132	1.00122.07	C
	ATOM	6460	C	VAL A 849	36.216	-6.768	159.940	1.00123.17	C
	ATOM	6461	O	VAL A 849	36.182	-7.929	159.552	1.00126.63	O
35	ATOM	6462	CB	VAL A 849	36.495	-5.173	158.010	1.00122.01	C
	ATOM	6463	CG1	VAL A 849	35.791	-4.183	157.093	1.00121.15	C
	ATOM	6464	CG2	VAL A 849	37.773	-4.583	158.589	1.00122.57	C
	ATOM	6465	N	GLY A 850	36.814	-6.407	161.073	1.00120.88	N
	ATOM	6466	CA	GLY A 850	37.390	-7.390	161.969	1.00120.93	C
40	ATOM	6467	C	GLY A 850	36.306	-8.271	162.559	1.00130.89	C

	ATOM	6468	O	GLY A 850	36.590	-9.316	163.141	1.00137.29	O
	ATOM	6469	N	ALA A 851	35.057	-7.837	162.414	1.00133.35	N
	ATOM	6470	CA	ALA A 851	33.903	-8.604	162.866	1.00136.80	C
	ATOM	6471	C	ALA A 851	33.442	-9.556	161.771	1.00140.65	C
5	ATOM	6472	O	ALA A 851	33.076	-10.699	162.040	1.00144.06	O
	ATOM	6473	CB	ALA A 851	32.776	-7.676	163.262	1.00136.04	C
	ATOM	6474	N	ALA A 852	33.451	-9.079	160.532	1.00140.14	N
	ATOM	6475	CA	ALA A 852	33.120	-9.931	159.400	1.00142.47	C
	ATOM	6476	C	ALA A 852	34.205	-10.984	159.229	1.00150.98	C
10	ATOM	6477	O	ALA A 852	33.924	-12.131	158.883	1.00158.75	O
	ATOM	6478	CB	ALA A 852	32.971	-9.108	158.132	1.00137.03	C
	ATOM	6479	N	ALA A 853	35.448	-10.589	159.488	1.00150.62	N
	ATOM	6480	CA	ALA A 853	36.589	-11.488	159.348	1.00150.56	C
	ATOM	6481	C	ALA A 853	36.558	-12.578	160.401	1.00151.56	C
15	ATOM	6482	O	ALA A 853	37.103	-13.660	160.203	1.00155.26	O
	ATOM	6483	CB	ALA A 853	37.891	-10.715	159.442	1.00150.29	C
	ATOM	6484	N	TRP A 854	35.915	-12.285	161.522	1.00149.86	N
	ATOM	6485	CA	TRP A 854	35.879	-13.217	162.638	1.00154.30	C
	ATOM	6486	C	TRP A 854	34.903	-14.373	162.417	1.00157.42	C
20	ATOM	6487	O	TRP A 854	35.221	-15.520	162.732	1.00157.89	O
	ATOM	6488	CB	TRP A 854	35.564	-12.474	163.935	1.00155.93	C
	ATOM	6489	CG	TRP A 854	35.382	-13.365	165.115	1.00158.48	C
	ATOM	6490	CD1	TRP A 854	36.362	-13.963	165.855	1.00159.06	C
	ATOM	6491	CD2	TRP A 854	34.139	-13.750	165.707	1.00159.83	C
25	ATOM	6492	NE1	TRP A 854	35.802	-14.702	166.868	1.00161.65	N
	ATOM	6493	CE2	TRP A 854	34.438	-14.587	166.800	1.00162.60	C
	ATOM	6494	CE3	TRP A 854	32.799	-13.469	165.418	1.00158.50	C
	ATOM	6495	CZ2	TRP A 854	33.448	-15.145	167.602	1.00166.86	C
	ATOM	6496	CZ3	TRP A 854	31.819	-14.021	166.215	1.00161.72	C
30	ATOM	6497	CH2	TRP A 854	32.147	-14.851	167.295	1.00166.40	C
	ATOM	6498	N	TRP A 855	33.723	-14.078	161.876	1.00161.36	N
	ATOM	6499	CA	TRP A 855	32.756	-15.132	161.586	1.00169.85	C
	ATOM	6500	C	TRP A 855	33.307	-16.054	160.512	1.00173.49	C
	ATOM	6501	O	TRP A 855	33.030	-17.255	160.500	1.00178.88	O
35	ATOM	6502	CB	TRP A 855	31.411	-14.563	161.130	1.00173.87	C
	ATOM	6503	CG	TRP A 855	30.389	-15.639	160.871	1.00182.32	C
	ATOM	6504	CD1	TRP A 855	29.513	-16.171	161.773	1.00185.47	C
	ATOM	6505	CD2	TRP A 855	30.151	-16.326	159.633	1.00189.25	C
	ATOM	6506	NE1	TRP A 855	28.741	-17.137	161.174	1.00189.32	N
40	ATOM	6507	CE2	TRP A 855	29.117	-17.255	159.862	1.00191.90	C

	ATOM	6508	CE3 TRP A 855	30.713 -16.244 158.354	1.00192.52	C
	ATOM	6509	CZ2 TRP A 855	28.626 -18.092 158.858	1.00196.13	C
	ATOM	6510	CZ3 TRP A 855	30.227 -17.079 157.359	1.00195.29	C
	ATOM	6511	CH2 TRP A 855	29.194 -17.990 157.617	1.00196.67	C
5	ATOM	6512	N PHE A 856	34.096 -15.477 159.612	1.00170.19	N
	ATOM	6513	CA PHE A 856	34.686 -16.221 158.508	1.00166.85	C
	ATOM	6514	C PHE A 856	35.858 -17.109 158.935	1.00162.11	C
	ATOM	6515	O PHE A 856	36.390 -17.855 158.120	1.00159.88	O
	ATOM	6516	CB PHE A 856	35.124 -15.258 157.400	1.00164.66	C
10	ATOM	6517	CG PHE A 856	34.085 -15.042 156.334	1.00164.02	C
	ATOM	6518	CD1 PHE A 856	33.376 -16.111 155.809	1.00165.81	C
	ATOM	6519	CD2 PHE A 856	33.816 -13.772 155.856	1.00162.31	C
	ATOM	6520	CE1 PHE A 856	32.422 -15.916 154.824	1.00164.89	C
	ATOM	6521	CE2 PHE A 856	32.864 -13.572 154.872	1.00162.92	C
15	ATOM	6522	CZ PHE A 856	32.166 -14.646 154.357	1.00163.94	C
	ATOM	6523	N MET A 857	36.252 -17.039 160.205	1.00161.30	N
	ATOM	6524	CA MET A 857	37.397 -17.815 160.687	1.00162.42	C
	ATOM	6525	C MET A 857	37.158 -18.592 161.989	1.00166.93	C
	ATOM	6526	O MET A 857	37.106 -19.824 161.977	1.00172.08	O
20	ATOM	6527	CB MET A 857	38.636 -16.924 160.827	1.00161.50	C
	ATOM	6528	CG MET A 857	39.277 -16.526 159.502	1.00160.56	C
	ATOM	6529	SD MET A 857	40.824 -15.611 159.698	1.00178.07	S
	ATOM	6530	CE MET A 857	40.328 -13.983 159.144	1.00 94.25	C
	ATOM	6531	N TYR A 858	37.022 -17.878 163.105	1.00164.01	N
25	ATOM	6532	CA TYR A 858	36.979 -18.525 164.422	1.00164.27	C
	ATOM	6533	C TYR A 858	35.573 -18.928 164.876	1.00161.96	C
	ATOM	6534	O TYR A 858	35.414 -19.549 165.930	1.00160.14	O
	ATOM	6535	CB TYR A 858	37.619 -17.635 165.496	1.00164.89	C
	ATOM	6536	CG TYR A 858	39.039 -17.192 165.206	1.00163.86	C
30	ATOM	6537	CD2 TYR A 858	39.557 -16.042 165.793	1.00163.92	C
	ATOM	6538	CD1 TYR A 858	39.862 -17.917 164.354	1.00162.94	C
	ATOM	6539	CE2 TYR A 858	40.851 -15.624 165.537	1.00162.20	C
	ATOM	6540	CE1 TYR A 858	41.158 -17.506 164.090	1.00163.19	C
	ATOM	6541	CZ TYR A 858	41.648 -16.358 164.685	1.00161.30	C
35	ATOM	6542	OH TYR A 858	42.937 -15.944 164.429	1.00159.09	O
	ATOM	6543	N ALA A 859	34.560 -18.570 164.092	1.00161.41	N
	ATOM	6544	CA ALA A 859	33.175 -18.880 164.442	1.00162.77	C
	ATOM	6545	C ALA A 859	32.904 -20.383 164.382	1.00166.84	C
	ATOM	6546	O ALA A 859	33.219 -21.036 163.387	1.00168.98	O
40	ATOM	6547	CB ALA A 859	32.218 -18.130 163.532	1.00158.61	C

	ATOM	6548	N	GLU A 860	32.317 -20.927 165.445	1.00168.18	N
	ATOM	6549	CA	GLU A 860	32.072 -22.366 165.522	1.00170.87	C
	ATOM	6550	C	GLU A 860	31.007 -22.841 164.533	1.00173.54	C
	ATOM	6551	O	GLU A 860	31.113 -23.940 163.981	1.00174.71	O
5	ATOM	6552	CB	GLU A 860	31.716 -22.797 166.952	1.00169.62	C
	ATOM	6553	CG	GLU A 860	32.887 -22.771 167.932	1.00167.27	C
	ATOM	6554	CD	GLU A 860	33.886 -23.896 167.703	1.00169.52	C
	ATOM	6555	OE1	GLU A 860	33.675 -24.721 166.791	1.00170.28	O
	ATOM	6556	OE2	GLU A 860	34.889 -23.960 168.443	1.00171.45	O
10	ATOM	6557	N	ASP A 861	29.985 -22.018 164.308	1.00173.18	N
	ATOM	6558	CA	ASP A 861	28.968 -22.340 163.309	1.00172.19	C
	ATOM	6559	C	ASP A 861	29.332 -21.758 161.942	1.00168.17	C
	ATOM	6560	O	ASP A 861	28.541 -21.811 161.001	1.00167.12	O
	ATOM	6561	CB	ASP A 861	27.577 -21.875 163.755	1.00169.38	C
15	ATOM	6562	CG	ASP A 861	27.490 -20.372 163.939	1.00164.60	C
	ATOM	6563	OD1	ASP A 861	28.506 -19.676 163.740	1.00158.24	O
	ATOM	6564	OD2	ASP A 861	26.395 -19.882 164.286	1.00169.85	O
	ATOM	6565	N	GLY A 862	30.533 -21.199 161.846	1.00166.02	N
	ATOM	6566	CA	GLY A 862	31.031 -20.670 160.592	1.00165.16	C
20	ATOM	6567	C	GLY A 862	32.023 -21.611 159.932	1.00170.73	C
	ATOM	6568	O	GLY A 862	32.358 -22.659 160.488	1.00174.99	O
	ATOM	6569	N	PRO A 863	32.497 -21.243 158.733	1.00171.12	N
	ATOM	6570	CA	PRO A 863	33.489 -22.031 157.991	1.00172.09	C
	ATOM	6571	C	PRO A 863	34.916 -21.784 158.491	1.00173.44	C
25	ATOM	6572	O	PRO A 863	35.381 -20.645 158.473	1.00175.63	O
	ATOM	6573	CB	PRO A 863	33.336 -21.510 156.560	1.00168.61	C
	ATOM	6574	CG	PRO A 863	32.886 -20.093 156.726	1.00165.98	C
	ATOM	6575	CD	PRO A 863	32.050 -20.055 157.981	1.00167.41	C
	ATOM	6576	N	GLY A 864	35.598 -22.836 158.934	1.00171.97	N
30	ATOM	6577	CA	GLY A 864	36.958 -22.703 159.427	1.00170.70	C
	ATOM	6578	C	GLY A 864	37.930 -22.294 158.336	1.00171.07	C
	ATOM	6579	O	GLY A 864	38.258 -23.091 157.462	1.00175.19	O
	ATOM	6580	N	VAL A 865	38.384 -21.045 158.381	1.00169.82	N
	ATOM	6581	CA	VAL A 865	39.286 -20.501 157.364	1.00173.01	C
35	ATOM	6582	C	VAL A 865	40.488 -19.822 158.057	1.00179.82	C
	ATOM	6583	O	VAL A 865	41.015 -18.811 157.584	1.00176.93	O
	ATOM	6584	CB	VAL A 865	38.524 -19.514 156.417	1.00124.25	C
	ATOM	6585	CG1	VAL A 865	39.326 -19.165 155.174	1.00122.52	C
	ATOM	6586	CG2	VAL A 865	37.186 -20.100 155.990	1.00123.41	C
40	ATOM	6587	N	THR A 866	40.915 -20.405 159.180	1.00188.13	N

	ATOM	6588	CA	THR A 866	41.970 -19.842 160.042	1.00192.12	C
	ATOM	6589	C	THR A 866	43.300 -19.548 159.333	1.00192.81	C
	ATOM	6590	O	THR A 866	44.038 -20.464 158.964	1.00195.23	O
	ATOM	6591	CB	THR A 866	42.238 -20.744 161.274	1.00147.31	C
5	ATOM	6592	OG1	THR A 866	41.074 -20.775 162.108	1.00150.10	O
	ATOM	6593	CG2	THR A 866	43.414 -20.219 162.088	1.00147.42	C
	ATOM	6594	N	TYR A 867	43.588 -18.258 159.158	1.00189.53	N
	ATOM	6595	CA	TYR A 867	44.786 -17.786 158.458	1.00188.64	C
	ATOM	6596	C	TYR A 867	44.835 -18.206 156.987	1.00192.24	C
10	ATOM	6597	O	TYR A 867	45.834 -17.997 156.296	1.00196.43	O
	ATOM	6598	CB	TYR A 867	46.063 -18.175 159.214	1.00188.61	C
	ATOM	6599	CG	TYR A 867	46.290 -17.315 160.433	1.00189.58	C
	ATOM	6600	CD2	TYR A 867	47.121 -17.730 161.467	1.00193.64	C
	ATOM	6601	CD1	TYR A 867	45.663 -16.078 160.549	1.00186.69	C
15	ATOM	6602	CE2	TYR A 867	47.319 -16.929 162.586	1.00194.49	C
	ATOM	6603	CE1	TYR A 867	45.854 -15.275 161.657	1.00185.95	C
	ATOM	6604	CZ	TYR A 867	46.680 -15.701 162.672	1.00188.79	C
	ATOM	6605	OH	TYR A 867	46.864 -14.892 163.770	1.00184.90	O
	ATOM	6606	N	HIS A 868	43.733 -18.786 156.524	1.00189.19	N
20	ATOM	6607	CA	HIS A 868	43.559 -19.178 155.133	1.00183.17	C
	ATOM	6608	C	HIS A 868	43.086 -17.931 154.384	1.00174.88	C
	ATOM	6609	O	HIS A 868	42.478 -17.029 154.975	1.00168.97	O
	ATOM	6610	CB	HIS A 868	42.540 -20.331 155.072	1.00176.44	C
	ATOM	6611	CG	HIS A 868	42.212 -20.819 153.692	1.00169.72	C
25	ATOM	6612	ND1	HIS A 868	41.517 -20.062 152.774	1.00165.24	N
	ATOM	6613	CD2	HIS A 868	42.429 -22.018 153.100	1.00169.92	C
	ATOM	6614	CE1	HIS A 868	41.350 -20.760 151.665	1.00165.96	C
	ATOM	6615	NE2	HIS A 868	41.893 -21.951 151.838	1.00169.12	N
	ATOM	6616	N	GLN A 869	43.398 -17.859 153.095	1.00167.05	N
30	ATOM	6617	CA	GLN A 869	42.989 -16.713 152.305	1.00157.92	C
	ATOM	6618	C	GLN A 869	41.479 -16.639 152.164	1.00153.84	C
	ATOM	6619	O	GLN A 869	40.879 -17.362 151.372	1.00150.61	O
	ATOM	6620	CB	GLN A 869	43.633 -16.724 150.916	1.00157.03	C
	ATOM	6621	CG	GLN A 869	45.065 -16.224 150.874	1.00155.28	C
35	ATOM	6622	CD	GLN A 869	46.064 -17.289 151.271	1.00154.77	C
	ATOM	6623	OE1	GLN A 869	46.355 -18.207 150.497	1.00153.27	O
	ATOM	6624	NE2	GLN A 869	46.597 -17.174 152.484	1.00153.71	N
	ATOM	6625	N	LEU A 870	40.872 -15.770 152.963	1.00154.60	N
	ATOM	6626	CA	LEU A 870	39.564 -15.234 152.636	1.00155.73	C
40	ATOM	6627	C	LEU A 870	39.862 -14.198 151.563	1.00163.90	C

	ATOM	6628	O	LEU A 870	38.981 -13.753 150.828	1.00166.70	O
	ATOM	6629	CB	LEU A 870	38.931 -14.576 153.857	1.00148.19	C
	ATOM	6630	CG	LEU A 870	37.582 -13.879 153.667	1.00140.17	C
	ATOM	6631	CD2	LEU A 870	37.159 -13.210 154.953	1.00132.86	C
5	ATOM	6632	CD1	LEU A 870	36.521 -14.863 153.193	1.00141.85	C
	ATOM	6633	N	THR A 871	41.138 -13.823 151.500	1.00167.55	N
	ATOM	6634	CA	THR A 871	41.694 -13.038 150.412	1.00171.03	C
	ATOM	6635	C	THR A 871	41.430 -13.724 149.072	1.00180.33	C
	ATOM	6636	O	THR A 871	41.261 -13.051 148.057	1.00182.72	O
10	ATOM	6637	CB	THR A 871	43.222 -12.862 150.592	1.00168.03	C
	ATOM	6638	OG1	THR A 871	43.504 -12.382 151.913	1.00159.65	O
	ATOM	6639	CG2	THR A 871	43.789 -11.887 149.566	1.00170.86	C
	ATOM	6640	N	HIS A 872	41.388 -15.058 149.075	1.00185.28	N
	ATOM	6641	CA	HIS A 872	41.167 -15.827 147.850	1.00191.49	C
15	ATOM	6642	C	HIS A 872	39.939 -15.388 147.063	1.00192.09	C
	ATOM	6643	O	HIS A 872	38.863 -15.167 147.620	1.00183.62	O
	ATOM	6644	CB	HIS A 872	41.068 -17.328 148.127	1.00202.04	C
	ATOM	6645	CG	HIS A 872	40.664 -18.136 146.926	1.00211.41	C
	ATOM	6646	ND1	HIS A 872	41.296 -18.022 145.702	1.00213.91	N
20	ATOM	6647	CD2	HIS A 872	39.692 -19.062 146.760	1.00212.74	C
	ATOM	6648	CE1	HIS A 872	40.728 -18.844 144.839	1.00213.24	C
	ATOM	6649	NE2	HIS A 872	39.753 -19.488 145.451	1.00212.55	N
	ATOM	6650	N	PHE A 873	40.129 -15.299 145.752	1.00205.97	N
	ATOM	6651	CA	PHE A 873	39.133 -14.792 144.820	1.00217.73	C
25	ATOM	6652	C	PHE A 873	37.807 -15.538 144.903	1.00213.97	C
	ATOM	6653	O	PHE A 873	37.765 -16.763 145.006	1.00212.84	O
	ATOM	6654	CB	PHE A 873	39.709 -14.793 143.404	1.00233.11	C
	ATOM	6655	CG	PHE A 873	41.052 -14.116 143.312	1.00244.64	C
	ATOM	6656	CD1	PHE A 873	41.145 -12.733 143.291	1.00247.16	C
30	ATOM	6657	CD2	PHE A 873	42.218 -14.862 143.277	1.00250.59	C
	ATOM	6658	CE1	PHE A 873	42.374 -12.104 143.223	1.00249.37	C
	ATOM	6659	CE2	PHE A 873	43.454 -14.241 143.208	1.00253.35	C
	ATOM	6660	CZ	PHE A 873	43.533 -12.858 143.181	1.00252.29	C
	ATOM	6661	N	MET A 874	36.727 -14.768 144.851	1.00213.28	N
35	ATOM	6662	CA	MET A 874	35.403 -15.237 145.238	1.00213.90	C
	ATOM	6663	C	MET A 874	34.793 -16.290 144.319	1.00211.86	C
	ATOM	6664	O	MET A 874	33.778 -16.897 144.665	1.00208.65	O
	ATOM	6665	CB	MET A 874	34.460 -14.041 145.367	1.00217.62	C
	ATOM	6666	CG	MET A 874	35.043 -12.911 146.194	1.00217.14	C
40	ATOM	6667	SD	MET A 874	35.725 -13.502 147.760	1.00239.09	S

	ATOM	6668	CE	MET A 874	36.395	-11.977	148.407	1.00	95.09	C
	ATOM	6669	N	GLN A 875	35.395	-16.495	143.151	1.00	213.88	N
	ATOM	6670	CA	GLN A 875	34.924	-17.534	142.242	1.00	216.04	C
	ATOM	6671	C	GLN A 875	35.032	-18.890	142.939	1.00	215.37	C
5	ATOM	6672	O	GLN A 875	34.018	-19.517	143.242	1.00	216.91	O
	ATOM	6673	CB	GLN A 875	35.715	-17.518	140.933	1.00	216.65	C
	ATOM	6674	CG	GLN A 875	35.083	-18.351	139.826	1.00	216.64	C
	ATOM	6675	CD	GLN A 875	35.671	-18.062	138.458	1.00	214.73	C
	ATOM	6676	OE1	GLN A 875	36.219	-16.985	138.218	1.00	212.17	O
10	ATOM	6677	NE2	GLN A 875	35.561	-19.027	137.552	1.00	215.23	N
	ATOM	6678	N	CYS A 876	36.264	-19.324	143.193	1.00	210.80	N
	ATOM	6679	CA	CYS A 876	36.541	-20.434	144.106	1.00	206.00	C
	ATOM	6680	C	CYS A 876	35.653	-21.671	143.934	1.00	203.65	C
	ATOM	6681	O	CYS A 876	34.799	-21.958	144.773	1.00	200.52	O
15	ATOM	6682	CB	CYS A 876	36.462	-19.940	145.552	1.00	205.02	C
	ATOM	6683	SG	CYS A 876	37.066	-21.112	146.769	1.00	134.70	S
	ATOM	6684	N	THR A 877	35.854	-22.384	142.832	1.00	204.48	N
	ATOM	6685	CA	THR A 877	35.214	-23.676	142.609	1.00	202.91	C
	ATOM	6686	C	THR A 877	36.307	-24.652	142.196	1.00	204.06	C
20	ATOM	6687	O	THR A 877	36.063	-25.841	141.964	1.00	205.10	O
	ATOM	6688	CB	THR A 877	34.144	-23.596	141.507	1.00	200.52	C
	ATOM	6689	OG1	THR A 877	34.683	-22.925	140.361	1.00	198.08	O
	ATOM	6690	CG2	THR A 877	32.932	-22.829	142.000	1.00	198.69	C
	ATOM	6691	N	GLU A 878	37.520	-24.113	142.126	1.00	201.95	N
25	ATOM	6692	CA	GLU A 878	38.702	-24.807	141.626	1.00	199.08	C
	ATOM	6693	C	GLU A 878	39.023	-26.060	142.416	1.00	194.09	C
	ATOM	6694	O	GLU A 878	39.540	-27.038	141.871	1.00	189.67	O
	ATOM	6695	CB	GLU A 878	39.898	-23.859	141.693	1.00	196.67	C
	ATOM	6696	CG	GLU A 878	39.617	-22.476	141.128	1.00	191.19	C
30	ATOM	6697	CD	GLU A 878	40.794	-21.537	141.283	1.00	186.50	C
	ATOM	6698	OE1	GLU A 878	41.576	-21.727	142.238	1.00	184.70	O
	ATOM	6699	OE2	GLU A 878	40.939	-20.615	140.451	1.00	185.39	O
	ATOM	6700	N	ASP A 879	38.729	-25.996	143.710	1.00	195.16	N
	ATOM	6701	CA	ASP A 879	38.985	-27.080	144.648	1.00	200.12	C
35	ATOM	6702	C	ASP A 879	40.471	-27.322	144.923	1.00	199.51	C
	ATOM	6703	O	ASP A 879	40.843	-28.406	145.362	1.00	202.22	O
	ATOM	6704	CB	ASP A 879	38.303	-28.383	144.202	1.00	204.86	C
	ATOM	6705	CG	ASP A 879	36.796	-28.252	144.116	1.00	204.12	C
	ATOM	6706	OD2	ASP A 879	36.171	-29.074	143.412	1.00	206.00	O
40	ATOM	6707	OD1	ASP A 879	36.236	-27.335	144.758	1.00	201.34	O

	ATOM	6708	N	HIS A 880	41.319	-26.326	144.685	1.00194.19	N
	ATOM	6709	CA	HIS A 880	42.729	-26.475	145.055	1.00190.13	C
	ATOM	6710	C	HIS A 880	43.002	-26.385	146.569	1.00190.64	C
	ATOM	6711	O	HIS A 880	43.900	-27.069	147.059	1.00191.04	O
5	ATOM	6712	CB	HIS A 880	43.656	-25.550	144.249	1.00185.70	C
	ATOM	6713	CG	HIS A 880	43.790	-24.174	144.820	1.00182.34	C
	ATOM	6714	ND1	HIS A 880	42.999	-23.122	144.413	1.00181.79	N
	ATOM	6715	CD2	HIS A 880	44.612	-23.679	145.777	1.00181.40	C
	ATOM	6716	CE1	HIS A 880	43.330	-22.037	145.091	1.00182.56	C
10	ATOM	6717	NE2	HIS A 880	44.306	-22.349	145.926	1.00182.10	N
	ATOM	6718	N	PRO A 881	42.242	-25.548	147.318	1.00190.95	N
	ATOM	6719	CA	PRO A 881	42.418	-25.617	148.770	1.00193.51	C
	ATOM	6720	C	PRO A 881	41.181	-26.164	149.493	1.00198.51	C
	ATOM	6721	O	PRO A 881	41.167	-26.216	150.725	1.00197.77	O
15	ATOM	6722	CB	PRO A 881	42.622	-24.148	149.147	1.00186.90	C
	ATOM	6723	CG	PRO A 881	41.871	-23.366	148.076	1.00184.77	C
	ATOM	6724	CD	PRO A 881	41.483	-24.336	146.968	1.00187.93	C
	ATOM	6725	N	HIS A 882	40.162	-26.563	148.734	1.00202.52	N
	ATOM	6726	CA	HIS A 882	38.915	-27.061	149.302	1.00205.61	C
20	ATOM	6727	C	HIS A 882	38.546	-28.399	148.679	1.00211.89	C
	ATOM	6728	O	HIS A 882	38.203	-28.459	147.501	1.00214.60	O
	ATOM	6729	CB	HIS A 882	37.774	-26.083	149.028	1.00204.91	C
	ATOM	6730	CG	HIS A 882	38.196	-24.649	148.960	1.00205.65	C
	ATOM	6731	ND1	HIS A 882	38.473	-23.898	150.082	1.00205.49	N
25	ATOM	6732	CD2	HIS A 882	38.363	-23.822	147.903	1.00204.44	C
	ATOM	6733	CE1	HIS A 882	38.807	-22.672	149.717	1.00201.89	C
	ATOM	6734	NE2	HIS A 882	38.746	-22.598	148.400	1.00201.25	N
	ATOM	6735	N	PHE A 883	38.605	-29.468	149.464	1.00215.89	N
	ATOM	6736	CA	PHE A 883	38.202	-30.784	148.976	1.00220.14	C
30	ATOM	6737	C	PHE A 883	37.090	-31.364	149.849	1.00223.91	C
	ATOM	6738	O	PHE A 883	36.112	-31.918	149.345	1.00226.28	O
	ATOM	6739	CB	PHE A 883	39.394	-31.748	148.931	1.00219.96	C
	ATOM	6740	CG	PHE A 883	40.398	-31.443	147.846	1.00216.77	C
	ATOM	6741	CD2	PHE A 883	41.570	-30.762	148.140	1.00216.29	C
35	ATOM	6742	CD1	PHE A 883	40.183	-31.861	146.541	1.00214.68	C
	ATOM	6743	CE2	PHE A 883	42.502	-30.491	147.150	1.00216.07	C
	ATOM	6744	CE1	PHE A 883	41.110	-31.593	145.546	1.00214.15	C
	ATOM	6745	CZ	PHE A 883	42.273	-30.914	145.852	1.00215.11	C
	ATOM	6746	N	ASP A 887	34.296	-24.882	150.836	1.00164.65	N
40	ATOM	6747	CA	ASP A 887	33.222	-25.530	150.091	1.00170.75	C

	ATOM	6748	C	ASP A 887	31.900 -24.765 150.188	1.00173.26	C
	ATOM	6749	O	ASP A 887	31.220 -24.834 151.213	1.00175.97	O
	ATOM	6750	CB	ASP A 887	33.011 -26.966 150.587	1.00174.92	C
	ATOM	6751	CG	ASP A 887	34.197 -27.866 150.300	1.00179.31	C
5	ATOM	6752	OD2	ASP A 887	34.258 -28.975 150.873	1.00179.53	O
	ATOM	6753	OD1	ASP A 887	35.062 -27.471 149.491	1.00182.44	O
	ATOM	6754	N	CYS A 888	31.525 -24.038 149.138	1.00172.51	N
	ATOM	6755	CA	CYS A 888	32.344 -23.842 147.948	1.00175.20	C
	ATOM	6756	C	CYS A 888	32.230 -22.375 147.563	1.00177.38	C
10	ATOM	6757	O	CYS A 888	33.189 -21.763 147.085	1.00179.04	O
	ATOM	6758	CB	CYS A 888	31.851 -24.713 146.786	1.00176.99	C
	ATOM	6759	SG	CYS A 888	32.285 -26.476 146.869	1.00226.19	S
	ATOM	6760	N	GLU A 889	31.038 -21.823 147.775	1.00175.82	N
	ATOM	6761	CA	GLU A 889	30.756 -20.414 147.523	1.00170.95	C
15	ATOM	6762	C	GLU A 889	29.715 -19.923 148.516	1.00161.18	C
	ATOM	6763	O	GLU A 889	28.819 -19.160 148.162	1.00158.37	O
	ATOM	6764	CB	GLU A 889	30.227 -20.201 146.101	1.00178.94	C
	ATOM	6765	CG	GLU A 889	31.264 -20.283 144.987	1.00185.63	C
	ATOM	6766	CD	GLU A 889	30.673 -19.944 143.625	1.00192.19	C
20	ATOM	6767	OE1	GLU A 889	29.482 -19.568 143.569	1.00193.25	O
	ATOM	6768	OE2	GLU A 889	31.393 -20.052 142.611	1.00195.69	O
	ATOM	6769	N	ILE A 890	29.827 -20.368 149.761	1.00158.53	N
	ATOM	6770	CA	ILE A 890	28.889 -19.962 150.804	1.00159.52	C
	ATOM	6771	C	ILE A 890	29.348 -18.630 151.421	1.00159.68	C
25	ATOM	6772	O	ILE A 890	28.818 -18.169 152.434	1.00158.13	O
	ATOM	6773	CB	ILE A 890	28.718 -21.090 151.862	1.00165.37	C
	ATOM	6774	CG1	ILE A 890	28.512 -22.443 151.160	1.00162.80	C
	ATOM	6775	CG2	ILE A 890	27.556 -20.800 152.812	1.00167.75	C
	ATOM	6776	CD1	ILE A 890	28.212 -23.611 152.093	1.00158.67	C
30	ATOM	6777	N	PHE A 891	30.325 -18.005 150.765	1.00161.83	N
	ATOM	6778	CA	PHE A 891	30.892 -16.719 151.186	1.00160.30	C
	ATOM	6779	C	PHE A 891	29.892 -15.557 151.194	1.00156.32	C
	ATOM	6780	O	PHE A 891	30.159 -14.514 151.791	1.00152.79	O
	ATOM	6781	CB	PHE A 891	32.071 -16.330 150.281	1.00159.81	C
35	ATOM	6782	CG	PHE A 891	33.351 -17.059 150.581	1.00158.09	C
	ATOM	6783	CD1	PHE A 891	33.447 -17.912 151.667	1.00156.09	C
	ATOM	6784	CD2	PHE A 891	34.468 -16.875 149.778	1.00159.94	C
	ATOM	6785	CE1	PHE A 891	34.631 -18.576 151.942	1.00155.47	C
	ATOM	6786	CE2	PHE A 891	35.653 -17.534 150.047	1.00160.27	C
40	ATOM	6787	CZ	PHE A 891	35.735 -18.386 151.132	1.00157.12	C

	ATOM	6788	N	GLU A 892	28.761 -15.722 150.514	1.00156.09	N
	ATOM	6789	CA	GLU A 892	27.753 -14.665 150.445	1.00157.04	C
	ATOM	6790	C	GLU A 892	26.789 -14.720 151.626	1.00156.65	C
	ATOM	6791	O	GLU A 892	25.650 -14.262 151.534	1.00154.34	O
5	ATOM	6792	CB	GLU A 892	26.972 -14.744 149.133	1.00162.27	C
	ATOM	6793	CG	GLU A 892	27.379 -13.704 148.104	1.00165.32	C
	ATOM	6794	CD	GLU A 892	26.549 -13.785 146.836	1.00170.44	C
	ATOM	6795	OE1	GLU A 892	26.127 -14.905 146.472	1.00173.29	O
	ATOM	6796	OE2	GLU A 892	26.314 -12.729 146.208	1.00170.15	O
10	ATOM	6797	N	ALA A 893	27.260 -15.283 152.734	1.00157.32	N
	ATOM	6798	CA	ALA A 893	26.444 -15.444 153.929	1.00157.27	C
	ATOM	6799	C	ALA A 893	26.043 -14.100 154.529	1.00154.87	C
	ATOM	6800	O	ALA A 893	26.788 -13.122 154.438	1.00151.76	O
	ATOM	6801	CB	ALA A 893	27.185 -16.295 154.959	1.00158.96	C
15	ATOM	6802	N	PRO A 894	24.845 -14.044 155.131	1.00157.30	N
	ATOM	6803	CA	PRO A 894	24.372 -12.847 155.833	1.00157.51	C
	ATOM	6804	C	PRO A 894	25.010 -12.710 157.216	1.00160.43	C
	ATOM	6805	O	PRO A 894	24.996 -11.620 157.792	1.00162.87	O
	ATOM	6806	CB	PRO A 894	22.869 -13.102 155.972	1.00157.82	C
20	ATOM	6807	CG	PRO A 894	22.751 -14.585 156.007	1.00159.57	C
	ATOM	6808	CD	PRO A 894	23.808 -15.089 155.063	1.00159.31	C
	ATOM	6809	N	GLU A 895	25.557 -13.805 157.736	1.00159.45	N
	ATOM	6810	CA	GLU A 895	26.191 -13.799 159.056	1.00156.75	C
	ATOM	6811	C	GLU A 895	27.383 -12.829 159.224	1.00154.13	C
25	ATOM	6812	O	GLU A 895	27.422 -12.078 160.198	1.00153.56	O
	ATOM	6813	CB	GLU A 895	26.571 -15.220 159.496	1.00158.06	C
	ATOM	6814	CG	GLU A 895	25.393 -16.139 159.817	1.00163.18	C
	ATOM	6815	CD	GLU A 895	24.987 -17.020 158.645	1.00165.44	C
	ATOM	6816	OE1	GLU A 895	25.168 -16.587 157.491	1.00164.18	O
30	ATOM	6817	OE2	GLU A 895	24.493 -18.147 158.879	1.00167.42	O
	ATOM	6818	N	PRO A 896	28.359 -12.839 158.292	1.00153.42	N
	ATOM	6819	CA	PRO A 896	29.492 -11.920 158.474	1.00152.24	C
	ATOM	6820	C	PRO A 896	29.081 -10.450 158.474	1.00152.22	C
	ATOM	6821	O	PRO A 896	29.593 -9.665 159.273	1.00151.60	O
35	ATOM	6822	CB	PRO A 896	30.376 -12.210 157.252	1.00151.61	C
	ATOM	6823	CG	PRO A 896	29.468 -12.837 156.255	1.00151.06	C
	ATOM	6824	CD	PRO A 896	28.523 -13.653 157.075	1.00153.87	C
	ATOM	6825	N	MET A 897	28.164 -10.091 157.583	1.00153.13	N
	ATOM	6826	CA	MET A 897	27.694 -8.719 157.473	1.00151.37	C
40	ATOM	6827	C	MET A 897	26.914 -8.299 158.716	1.00155.03	C

	ATOM	6828	O	MET A 897	26.975	-7.145	159.137	1.00159.05	O
	ATOM	6829	CB	MET A 897	26.837	-8.554	156.217	1.00150.02	C
	ATOM	6830	CG	MET A 897	27.560	-8.936	154.934	1.00150.12	C
	ATOM	6831	SD	MET A 897	26.539	-8.754	153.459	1.00142.25	S
5	ATOM	6832	CE	MET A 897	25.200	-9.876	153.848	1.00138.55	C
	ATOM	6833	N	THR A 898	26.192	-9.241	159.314	1.00154.69	N
	ATOM	6834	CA	THR A 898	25.410	-8.946	160.513	1.00156.04	C
	ATOM	6835	C	THR A 898	26.250	-8.909	161.782	1.00151.90	C
	ATOM	6836	O	THR A 898	25.718	-8.948	162.887	1.00153.00	O
10	ATOM	6837	CB	THR A 898	24.271	-9.947	160.721	1.00161.43	C
	ATOM	6838	OG1	THR A 898	24.748	-11.271	160.463	1.00169.57	O
	ATOM	6839	CG2	THR A 898	23.153	-9.648	159.785	1.00157.25	C
	ATOM	6840	N	MET A 899	27.563	-8.865	161.617	1.00145.09	N
	ATOM	6841	CA	MET A 899	28.450	-8.559	162.719	1.00139.22	C
15	ATOM	6842	C	MET A 899	29.061	-7.225	162.358	1.00135.82	C
	ATOM	6843	O	MET A 899	29.209	-6.339	163.198	1.00133.06	O
	ATOM	6844	CB	MET A 899	29.522	-9.634	162.860	1.00136.21	C
	ATOM	6845	CG	MET A 899	28.961	-11.003	163.197	1.00135.75	C
	ATOM	6846	SD	MET A 899	28.248	-11.059	164.851	1.00236.78	S
20	ATOM	6847	CE	MET A 899	29.722	-10.865	165.850	1.00103.50	C
	ATOM	6848	N	ALA A 900	29.392	-7.093	161.079	1.00137.92	N
	ATOM	6849	CA	ALA A 900	29.878	-5.843	160.529	1.00143.20	C
	ATOM	6850	C	ALA A 900	28.837	-4.748	160.733	1.00152.19	C
	ATOM	6851	O	ALA A 900	29.155	-3.673	161.240	1.00158.37	O
25	ATOM	6852	CB	ALA A 900	30.200	-6.008	159.053	1.00142.35	C
	ATOM	6853	N	LEU A 901	27.591	-5.024	160.350	1.00151.45	N
	ATOM	6854	CA	LEU A 901	26.506	-4.066	160.549	1.00145.98	C
	ATOM	6855	C	LEU A 901	26.231	-3.893	162.038	1.00138.62	C
	ATOM	6856	O	LEU A 901	25.863	-2.812	162.500	1.00128.87	O
30	ATOM	6857	CB	LEU A 901	25.231	-4.530	159.844	1.00147.01	C
	ATOM	6858	CG	LEU A 901	24.139	-3.463	159.735	1.00146.15	C
	ATOM	6859	CD1	LEU A 901	24.422	-2.551	158.553	1.00144.45	C
	ATOM	6860	CD2	LEU A 901	22.756	-4.083	159.626	1.00147.33	C
	ATOM	6861	N	SER A 902	26.423	-4.976	162.781	1.00139.57	N
35	ATOM	6862	CA	SER A 902	26.173	-4.980	164.211	1.00143.43	C
	ATOM	6863	C	SER A 902	27.214	-4.167	164.971	1.00143.68	C
	ATOM	6864	O	SER A 902	26.865	-3.286	165.755	1.00146.88	O
	ATOM	6865	CB	SER A 902	26.149	-6.413	164.734	1.00149.50	C
	ATOM	6866	OG	SER A 902	25.934	-6.439	166.131	1.00155.04	O
40	ATOM	6867	N	VAL A 903	28.488	-4.469	164.744	1.00141.08	N

	ATOM	6868	CA	VAL A 903	29.573	-3.757	165.415	1.00135.53	C
	ATOM	6869	C	VAL A 903	29.547	-2.276	165.066	1.00130.99	C
	ATOM	6870	O	VAL A 903	29.777	-1.421	165.923	1.00131.97	O
	ATOM	6871	CB	VAL A 903	30.948	-4.368	165.076	1.00130.95	C
5	ATOM	6872	CG1	VAL A 903	32.078	-3.372	165.323	1.00121.89	C
	ATOM	6873	CG2	VAL A 903	31.157	-5.646	165.878	1.00135.85	C
	ATOM	6874	N	LEU A 904	29.235	-1.978	163.811	1.00125.04	N
	ATOM	6875	CA	LEU A 904	29.151	-0.596	163.356	1.00122.10	C
	ATOM	6876	C	LEU A 904	28.068	0.173	164.107	1.00130.32	C
10	ATOM	6877	O	LEU A 904	28.332	1.234	164.679	1.00127.66	O
	ATOM	6878	CB	LEU A 904	28.880	-0.552	161.854	1.00112.82	C
	ATOM	6879	CG	LEU A 904	28.840	0.833	161.220	1.00100.38	C
	ATOM	6880	CD1	LEU A 904	30.035	1.640	161.688	1.00 98.97	C
	ATOM	6881	CD2	LEU A 904	28.821	0.704	159.707	1.00 91.03	C
15	ATOM	6882	N	VAL A 905	26.851	-0.371	164.095	1.00134.61	N
	ATOM	6883	CA	VAL A 905	25.715	0.237	164.784	1.00127.84	C
	ATOM	6884	C	VAL A 905	25.998	0.367	166.276	1.00125.34	C
	ATOM	6885	O	VAL A 905	25.703	1.394	166.886	1.00130.31	O
	ATOM	6886	CB	VAL A 905	24.418	-0.578	164.565	1.00123.74	C
20	ATOM	6887	CG1	VAL A 905	23.353	-0.187	165.570	1.00121.68	C
	ATOM	6888	CG2	VAL A 905	23.905	-0.382	163.155	1.00122.76	C
	ATOM	6889	N	THR A 906	26.594	-0.671	166.851	1.00116.18	N
	ATOM	6890	CA	THR A 906	26.922	-0.670	168.267	1.00115.81	C
	ATOM	6891	C	THR A 906	28.031	0.344	168.597	1.00115.12	C
25	ATOM	6892	O	THR A 906	27.913	1.107	169.558	1.00110.72	O
	ATOM	6893	CB	THR A 906	27.321	-2.083	168.743	1.00120.49	C
	ATOM	6894	OG1	THR A 906	26.349	-3.033	168.292	1.00122.29	O
	ATOM	6895	CG2	THR A 906	27.408	-2.139	170.256	1.00122.51	C
	ATOM	6896	N	ILE A 907	29.100	0.357	167.800	1.00115.37	N
30	ATOM	6897	CA	ILE A 907	30.215	1.266	168.059	1.00108.96	C
	ATOM	6898	C	ILE A 907	29.748	2.706	167.946	1.00107.09	C
	ATOM	6899	O	ILE A 907	30.131	3.552	168.750	1.00111.41	O
	ATOM	6900	CB	ILE A 907	31.417	1.027	167.118	1.00105.00	C
	ATOM	6901	CG1	ILE A 907	32.217	-0.187	167.575	1.00105.75	C
35	ATOM	6902	CG2	ILE A 907	32.337	2.231	167.104	1.00107.83	C
	ATOM	6903	CD1	ILE A 907	33.667	-0.184	167.128	1.00106.05	C
	ATOM	6904	N	GLU A 908	28.901	2.969	166.956	1.00105.68	N
	ATOM	6905	CA	GLU A 908	28.342	4.300	166.745	1.00112.99	C
	ATOM	6906	C	GLU A 908	27.639	4.819	167.996	1.00118.18	C
40	ATOM	6907	O	GLU A 908	27.627	6.025	168.261	1.00116.38	O

	ATOM	6908	CB	GLU A 908	27.366	4.294	165.566	1.00121.69	C
	ATOM	6909	CG	GLU A 908	28.020	4.459	164.203	1.00129.50	C
	ATOM	6910	CD	GLU A 908	28.634	5.838	164.009	1.00134.84	C
	ATOM	6911	OE1	GLU A 908	27.942	6.727	163.469	1.00135.26	O
5	ATOM	6912	OE2	GLU A 908	29.809	6.036	164.394	1.00137.55	O
	ATOM	6913	N	MET A 909	27.055	3.903	168.763	1.00120.11	N
	ATOM	6914	CA	MET A 909	26.406	4.260	170.017	1.00117.13	C
	ATOM	6915	C	MET A 909	27.445	4.512	171.101	1.00114.13	C
	ATOM	6916	O	MET A 909	27.366	5.502	171.820	1.00112.51	O
10	ATOM	6917	CB	MET A 909	25.435	3.163	170.454	1.00119.98	C
	ATOM	6918	CG	MET A 909	24.366	2.864	169.425	1.00120.61	C
	ATOM	6919	SD	MET A 909	23.575	4.373	168.842	1.00140.93	S
	ATOM	6920	CE	MET A 909	23.080	3.874	167.198	1.00101.12	C
	ATOM	6921	N	CYS A 910	28.420	3.614	171.211	1.00115.19	N
15	ATOM	6922	CA	CYS A 910	29.504	3.771	172.177	1.00117.33	C
	ATOM	6923	C	CYS A 910	30.287	5.060	171.943	1.00119.23	C
	ATOM	6924	O	CYS A 910	30.491	5.857	172.860	1.00121.31	O
	ATOM	6925	CB	CYS A 910	30.448	2.578	172.106	1.00116.60	C
	ATOM	6926	SG	CYS A 910	29.679	1.033	172.560	1.00138.04	S
20	ATOM	6927	N	ASN A 911	30.715	5.260	170.703	1.00117.75	N
	ATOM	6928	CA	ASN A 911	31.424	6.469	170.316	1.00115.16	C
	ATOM	6929	C	ASN A 911	30.543	7.717	170.451	1.00116.04	C
	ATOM	6930	O	ASN A 911	31.023	8.841	170.320	1.00118.94	O
	ATOM	6931	CB	ASN A 911	31.942	6.322	168.882	1.00113.74	C
25	ATOM	6932	CG	ASN A 911	32.874	7.446	168.471	1.00110.50	C
	ATOM	6933	OD1	ASN A 911	33.688	7.924	169.263	1.00108.41	O
	ATOM	6934	ND2	ASN A 911	32.756	7.875	167.219	1.00109.31	N
	ATOM	6935	N	ALA A 912	29.253	7.521	170.707	1.00115.29	N
	ATOM	6936	CA	ALA A 912	28.359	8.640	170.979	1.00113.04	C
30	ATOM	6937	C	ALA A 912	28.407	8.989	172.464	1.00114.75	C
	ATOM	6938	O	ALA A 912	28.305	10.160	172.838	1.00112.19	O
	ATOM	6939	CB	ALA A 912	26.935	8.322	170.537	1.00111.52	C
	ATOM	6940	N	LEU A 913	28.571	7.966	173.302	1.00117.82	N
	ATOM	6941	CA	LEU A 913	28.784	8.163	174.733	1.00116.63	C
35	ATOM	6942	C	LEU A 913	30.095	8.901	174.926	1.00117.35	C
	ATOM	6943	O	LEU A 913	30.249	9.701	175.849	1.00116.97	O
	ATOM	6944	CB	LEU A 913	28.858	6.823	175.468	1.00112.50	C
	ATOM	6945	CG	LEU A 913	27.644	5.897	175.403	1.00110.97	C
	ATOM	6946	CD1	LEU A 913	27.842	4.689	176.317	1.00108.80	C
40	ATOM	6947	CD2	LEU A 913	26.366	6.648	175.751	1.00108.96	C

	ATOM	6948	N	ASN A 914	31.042	8.616	174.039	1.00115.84	N
	ATOM	6949	CA	ASN A 914	32.341	9.258	174.080	1.00114.45	C
	ATOM	6950	C	ASN A 914	32.242	10.733	173.753	1.00118.25	C
	ATOM	6951	O	ASN A 914	33.136	11.508	174.081	1.00124.91	O
5	ATOM	6952	CB	ASN A 914	33.308	8.581	173.113	1.00109.98	C
	ATOM	6953	CG	ASN A 914	34.123	7.504	173.777	1.00110.68	C
	ATOM	6954	OD1	ASN A 914	34.347	6.439	173.203	1.00111.72	O
	ATOM	6955	ND2	ASN A 914	34.572	7.773	175.003	1.00111.20	N
	ATOM	6956	N	SER A 915	31.149	11.119	173.107	1.00114.97	N
10	ATOM	6957	CA	SER A 915	30.981	12.500	172.680	1.00111.96	C
	ATOM	6958	C	SER A 915	30.132	13.291	173.656	1.00106.35	C
	ATOM	6959	O	SER A 915	29.490	14.267	173.271	1.00104.86	O
	ATOM	6960	CB	SER A 915	30.383	12.564	171.278	1.00117.42	C
	ATOM	6961	OG	SER A 915	31.268	11.986	170.331	1.00123.19	O
15	ATOM	6962	N	LEU A 916	30.140	12.863	174.918	1.00105.27	N
	ATOM	6963	CA	LEU A 916	29.446	13.574	175.988	1.00100.48	C
	ATOM	6964	C	LEU A 916	30.268	14.758	176.461	1.00101.31	C
	ATOM	6965	O	LEU A 916	29.728	15.808	176.810	1.00104.10	O
	ATOM	6966	CB	LEU A 916	29.155	12.641	177.157	1.00 96.82	C
20	ATOM	6967	CG	LEU A 916	27.933	11.752	176.944	1.00 99.45	C
	ATOM	6968	CD1	LEU A 916	27.656	10.915	178.178	1.00104.81	C
	ATOM	6969	CD2	LEU A 916	26.726	12.601	176.583	1.00 96.86	C
	ATOM	6970	N	SER A 917	31.581	14.579	176.472	1.00 99.71	N
	ATOM	6971	CA	SER A 917	32.492	15.664	176.778	1.00104.38	C
25	ATOM	6972	C	SER A 917	33.582	15.630	175.732	1.00115.72	C
	ATOM	6973	O	SER A 917	33.698	14.653	174.994	1.00123.05	O
	ATOM	6974	CB	SER A 917	33.097	15.485	178.170	1.00105.02	C
	ATOM	6975	OG	SER A 917	33.992	16.541	178.471	1.00104.03	O
	ATOM	6976	N	GLU A 918	34.379	16.690	175.655	1.00116.63	N
30	ATOM	6977	CA	GLU A 918	35.543	16.678	174.783	1.00115.13	C
	ATOM	6978	C	GLU A 918	36.661	15.860	175.423	1.00116.68	C
	ATOM	6979	O	GLU A 918	37.108	14.855	174.868	1.00114.48	O
	ATOM	6980	CB	GLU A 918	36.009	18.100	174.490	1.00117.63	C
	ATOM	6981	CG	GLU A 918	35.644	18.590	173.096	1.00124.72	C
35	ATOM	6982	CD	GLU A 918	36.570	18.045	172.014	1.00133.69	C
	ATOM	6983	OE1	GLU A 918	37.778	17.862	172.289	1.00133.36	O
	ATOM	6984	OE2	GLU A 918	36.089	17.805	170.883	1.00137.67	O
	ATOM	6985	N	ASN A 919	37.095	16.282	176.605	1.00120.75	N
	ATOM	6986	CA	ASN A 919	38.178	15.599	177.306	1.00124.24	C
40	ATOM	6987	C	ASN A 919	37.734	14.776	178.522	1.00131.30	C

	ATOM	6988	O	ASN A 919	38.379	13.784	178.875	1.00137.32	O
	ATOM	6989	CB	ASN A 919	39.254	16.605	177.729	1.00117.51	C
	ATOM	6990	CG	ASN A 919	40.078	17.109	176.561	1.00109.13	C
	ATOM	6991	OD1	ASN A 919	40.262	16.412	175.560	1.00106.77	O
5	ATOM	6992	ND2	ASN A 919	40.591	18.325	176.689	1.00109.48	N
	ATOM	6993	N	GLN A 920	36.638	15.183	179.158	1.00124.21	N
	ATOM	6994	CA	GLN A 920	36.211	14.555	180.405	1.00114.86	C
	ATOM	6995	C	GLN A 920	35.725	13.112	180.278	1.00113.93	C
	ATOM	6996	O	GLN A 920	34.927	12.777	179.399	1.00106.95	O
10	ATOM	6997	CB	GLN A 920	35.177	15.420	181.114	1.00106.24	C
	ATOM	6998	CG	GLN A 920	35.726	16.771	181.520	1.00105.80	C
	ATOM	6999	CD	GLN A 920	36.823	16.668	182.562	1.00110.64	C
	ATOM	7000	OE1	GLN A 920	37.008	15.626	183.194	1.00113.70	O
	ATOM	7001	NE2	GLN A 920	37.558	17.757	182.749	1.00111.01	N
15	ATOM	7002	N	SER A 921	36.218	12.277	181.192	1.00118.35	N
	ATOM	7003	CA	SER A 921	35.956	10.839	181.203	1.00122.09	C
	ATOM	7004	C	SER A 921	34.484	10.477	181.386	1.00122.10	C
	ATOM	7005	O	SER A 921	33.635	11.347	181.580	1.00125.11	O
	ATOM	7006	CB	SER A 921	36.782	10.175	182.309	1.00124.74	C
20	ATOM	7007	OG	SER A 921	36.451	8.803	182.443	1.00124.17	O
	ATOM	7008	N	LEU A 922	34.185	9.184	181.321	1.00118.12	N
	ATOM	7009	CA	LEU A 922	32.837	8.718	181.618	1.00115.61	C
	ATOM	7010	C	LEU A 922	32.634	8.536	183.121	1.00119.82	C
	ATOM	7011	O	LEU A 922	31.522	8.682	183.619	1.00121.44	O
25	ATOM	7012	CB	LEU A 922	32.502	7.431	180.856	1.00109.81	C
	ATOM	7013	CG	LEU A 922	32.113	7.635	179.391	1.00103.86	C
	ATOM	7014	CD1	LEU A 922	31.517	6.377	178.814	1.00103.12	C
	ATOM	7015	CD2	LEU A 922	31.134	8.782	179.256	1.00105.22	C
	ATOM	7016	N	MET A 923	33.707	8.240	183.850	1.00119.24	N
30	ATOM	7017	CA	MET A 923	33.597	8.085	185.297	1.00117.85	C
	ATOM	7018	C	MET A 923	33.434	9.444	185.962	1.00118.58	C
	ATOM	7019	O	MET A 923	33.217	9.519	187.169	1.00124.91	O
	ATOM	7020	CB	MET A 923	34.798	7.340	185.893	1.00119.59	C
	ATOM	7021	CG	MET A 923	35.236	6.099	185.117	1.00120.57	C
35	ATOM	7022	SD	MET A 923	33.875	5.063	184.538	1.00212.63	S
	ATOM	7023	CE	MET A 923	34.425	4.628	182.871	1.00 98.69	C
	ATOM	7024	N	ARG A 924	33.538	10.515	185.175	1.00116.64	N
	ATOM	7025	CA	ARG A 924	33.297	11.866	185.684	1.00119.81	C
	ATOM	7026	C	ARG A 924	32.055	12.510	185.059	1.00124.32	C
40	ATOM	7027	O	ARG A 924	31.319	13.238	185.723	1.00130.84	O

	ATOM	7028	CB	ARG A 924	34.524	12.761	185.492	1.00116.46	C
	ATOM	7029	CG	ARG A 924	34.346	14.166	186.058	1.00118.71	C
	ATOM	7030	CD	ARG A 924	35.648	14.947	186.045	1.00126.40	C
	ATOM	7031	NE	ARG A 924	35.472	16.338	186.458	1.00133.53	N
5	ATOM	7032	CZ	ARG A 924	35.506	16.750	187.723	1.00143.25	C
	ATOM	7033	NH1	ARG A 924	35.701	15.875	188.705	1.00147.52	N
	ATOM	7034	NH2	ARG A 924	35.339	18.038	188.008	1.00144.24	N
	ATOM	7035	N	MET A 925	31.831	12.254	183.778	1.00120.71	N
	ATOM	7036	CA	MET A 925	30.574	12.638	183.150	1.00117.38	C
10	ATOM	7037	C	MET A 925	29.935	11.384	182.598	1.00120.14	C
	ATOM	7038	O	MET A 925	30.143	11.030	181.439	1.00122.98	O
	ATOM	7039	CB	MET A 925	30.785	13.678	182.051	1.00115.21	C
	ATOM	7040	CG	MET A 925	31.191	15.035	182.593	1.00118.14	C
	ATOM	7041	SD	MET A 925	31.114	16.383	181.399	1.00164.99	S
15	ATOM	7042	CE	MET A 925	29.438	16.203	180.799	1.00 85.94	C
	ATOM	7043	N	PRO A 926	29.166	10.694	183.448	1.00118.78	N
	ATOM	7044	CA	PRO A 926	28.549	9.391	183.184	1.00120.89	C
	ATOM	7045	C	PRO A 926	27.661	9.378	181.942	1.00114.23	C
	ATOM	7046	O	PRO A 926	27.274	10.436	181.461	1.00103.42	O
20	ATOM	7047	CB	PRO A 926	27.712	9.144	184.445	1.00125.44	C
	ATOM	7048	CG	PRO A 926	27.545	10.495	185.068	1.00122.50	C
	ATOM	7049	CD	PRO A 926	28.822	11.196	184.785	1.00117.25	C
	ATOM	7050	N	PRO A 927	27.356	8.182	181.416	1.00118.90	N
	ATOM	7051	CA	PRO A 927	26.422	8.055	180.294	1.00117.60	C
25	ATOM	7052	C	PRO A 927	25.099	8.784	180.537	1.00113.89	C
	ATOM	7053	O	PRO A 927	24.494	9.291	179.596	1.00105.85	O
	ATOM	7054	CB	PRO A 927	26.183	6.548	180.227	1.00119.75	C
	ATOM	7055	CG	PRO A 927	27.466	5.963	180.699	1.00120.45	C
	ATOM	7056	CD	PRO A 927	27.977	6.891	181.764	1.00120.88	C
30	ATOM	7057	N	TRP A 928	24.669	8.851	181.791	1.00120.37	N
	ATOM	7058	CA	TRP A 928	23.349	9.391	182.117	1.00122.31	C
	ATOM	7059	C	TRP A 928	23.296	10.911	182.306	1.00122.32	C
	ATOM	7060	O	TRP A 928	22.312	11.434	182.822	1.00126.06	O
	ATOM	7061	CB	TRP A 928	22.757	8.676	183.342	1.00120.74	C
35	ATOM	7062	CG	TRP A 928	23.559	8.839	184.601	1.00124.96	C
	ATOM	7063	CD1	TRP A 928	23.543	9.911	185.453	1.00128.26	C
	ATOM	7064	CD2	TRP A 928	24.483	7.896	185.162	1.00127.92	C
	ATOM	7065	NE1	TRP A 928	24.406	9.695	186.504	1.00132.28	N
	ATOM	7066	CE2	TRP A 928	24.993	8.466	186.351	1.00133.58	C
40	ATOM	7067	CE3	TRP A 928	24.930	6.630	184.777	1.00127.24	C

	ATOM	7068	CZ2 TRP A 928	25.929	7.810	187.151	1.00136.10	C
	ATOM	7069	CZ3 TRP A 928	25.857	5.984	185.573	1.00132.40	C
	ATOM	7070	CH2 TRP A 928	26.347	6.575	186.746	1.00136.32	C
	ATOM	7071	N VAL A 929	24.339	11.622	181.888	1.00120.91	N
5	ATOM	7072	CA VAL A 929	24.312	13.083	181.949	1.00123.09	C
	ATOM	7073	C VAL A 929	23.393	13.631	180.860	1.00122.03	C
	ATOM	7074	O VAL A 929	22.826	14.718	180.990	1.00118.04	O
	ATOM	7075	CB VAL A 929	25.710	13.698	181.801	1.00123.88	C
	ATOM	7076	CG1 VAL A 929	25.650	15.155	182.108	1.00121.45	C
10	ATOM	7077	CG2 VAL A 929	26.665	13.055	182.763	1.00130.43	C
	ATOM	7078	N ASN A 930	23.261	12.858	179.786	1.00124.51	N
	ATOM	7079	CA ASN A 930	22.298	13.130	178.725	1.00122.95	C
	ATOM	7080	C ASN A 930	21.358	11.940	178.573	1.00126.67	C
	ATOM	7081	O ASN A 930	21.738	10.915	178.002	1.00128.34	O
15	ATOM	7082	CB ASN A 930	23.025	13.389	177.402	1.00116.90	C
	ATOM	7083	CG ASN A 930	22.080	13.775	176.266	1.00114.36	C
	ATOM	7084	OD1 ASN A 930	20.950	13.288	176.170	1.00113.54	O
	ATOM	7085	ND2 ASN A 930	22.553	14.655	175.390	1.00111.08	N
	ATOM	7086	N ILE A 931	20.131	12.071	179.070	1.00127.12	N
20	ATOM	7087	CA ILE A 931	19.172	10.973	178.971	1.00126.64	C
	ATOM	7088	C ILE A 931	18.592	10.824	177.563	1.00126.66	C
	ATOM	7089	O ILE A 931	18.397	9.701	177.089	1.00128.65	O
	ATOM	7090	CB ILE A 931	18.034	11.081	180.010	1.00120.21	C
	ATOM	7091	CG1 ILE A 931	17.337	12.435	179.910	1.00118.78	C
25	ATOM	7092	CG2 ILE A 931	18.577	10.877	181.403	1.00118.03	C
	ATOM	7093	CD1 ILE A 931	15.985	12.461	180.583	1.00124.74	C
	ATOM	7094	N TRP A 932	18.325	11.949	176.901	1.00119.31	N
	ATOM	7095	CA TRP A 932	17.785	11.927	175.550	1.00116.17	C
	ATOM	7096	C TRP A 932	18.690	11.079	174.679	1.00118.16	C
30	ATOM	7097	O TRP A 932	18.221	10.339	173.816	1.00119.30	O
	ATOM	7098	CB TRP A 932	17.690	13.333	174.971	1.00117.22	C
	ATOM	7099	CG TRP A 932	16.781	14.247	175.726	1.00126.58	C
	ATOM	7100	CD1 TRP A 932	15.425	14.318	175.624	1.00129.16	C
	ATOM	7101	CD2 TRP A 932	17.167	15.245	176.684	1.00131.59	C
35	ATOM	7102	NE1 TRP A 932	14.937	15.291	176.467	1.00134.04	N
	ATOM	7103	CE2 TRP A 932	15.987	15.873	177.131	1.00133.16	C
	ATOM	7104	CE3 TRP A 932	18.395	15.665	177.211	1.00130.49	C
	ATOM	7105	CZ2 TRP A 932	15.997	16.896	178.077	1.00133.54	C
	ATOM	7106	CZ3 TRP A 932	18.404	16.681	178.151	1.00129.93	C
40	ATOM	7107	CH2 TRP A 932	17.213	17.287	178.573	1.00132.69	C

	ATOM	7108	N	LEU A 933	19.994	11.184	174.928	1.00119.21	N
	ATOM	7109	CA	LEU A 933	20.974	10.344	174.249	1.00116.28	C
	ATOM	7110	C	LEU A 933	20.733	8.881	174.586	1.00117.93	C
	ATOM	7111	O	LEU A 933	20.714	8.023	173.701	1.00119.66	O
5	ATOM	7112	CB	LEU A 933	22.403	10.734	174.629	1.00110.15	C
	ATOM	7113	CG	LEU A 933	23.455	9.828	173.983	1.00110.62	C
	ATOM	7114	CD1	LEU A 933	23.350	9.884	172.457	1.00109.69	C
	ATOM	7115	CD2	LEU A 933	24.866	10.172	174.455	1.00108.06	C
	ATOM	7116	N	LEU A 934	20.551	8.599	175.869	1.00114.01	N
10	ATOM	7117	CA	LEU A 934	20.263	7.240	176.290	1.00114.12	C
	ATOM	7118	C	LEU A 934	18.955	6.781	175.648	1.00114.77	C
	ATOM	7119	O	LEU A 934	18.848	5.639	175.192	1.00115.29	O
	ATOM	7120	CB	LEU A 934	20.193	7.137	177.817	1.00114.28	C
	ATOM	7121	CG	LEU A 934	21.447	7.444	178.646	1.00102.66	C
15	ATOM	7122	CD1	LEU A 934	21.249	6.973	180.077	1.00 96.81	C
	ATOM	7123	CD2	LEU A 934	22.697	6.819	178.045	1.00 96.76	C
	ATOM	7124	N	GLY A 935	17.974	7.681	175.592	1.00111.55	N
	ATOM	7125	CA	GLY A 935	16.701	7.377	174.960	1.00118.97	C
	ATOM	7126	C	GLY A 935	16.853	7.025	173.489	1.00122.89	C
20	ATOM	7127	O	GLY A 935	16.312	6.022	173.002	1.00118.25	O
	ATOM	7128	N	SER A 936	17.616	7.855	172.786	1.00123.87	N
	ATOM	7129	CA	SER A 936	17.837	7.692	171.357	1.00120.69	C
	ATOM	7130	C	SER A 936	18.579	6.405	171.032	1.00117.10	C
	ATOM	7131	O	SER A 936	18.295	5.769	170.021	1.00120.80	O
25	ATOM	7132	CB	SER A 936	18.623	8.879	170.813	1.00123.04	C
	ATOM	7133	OG	SER A 936	19.909	8.930	171.402	1.00126.88	O
	ATOM	7134	N	ILE A 937	19.537	6.035	171.879	1.00115.32	N
	ATOM	7135	CA	ILE A 937	20.294	4.798	171.687	1.00119.64	C
	ATOM	7136	C	ILE A 937	19.355	3.592	171.709	1.00135.56	C
30	ATOM	7137	O	ILE A 937	19.475	2.678	170.887	1.00142.16	O
	ATOM	7138	CB	ILE A 937	21.387	4.624	172.767	1.00112.34	C
	ATOM	7139	CG1	ILE A 937	22.453	5.707	172.633	1.00105.98	C
	ATOM	7140	CG2	ILE A 937	22.042	3.256	172.669	1.00111.06	C
	ATOM	7141	CD1	ILE A 937	23.488	5.686	173.743	1.00103.36	C
35	ATOM	7142	N	CYS A 938	18.408	3.604	172.642	1.00139.04	N
	ATOM	7143	CA	CYS A 938	17.440	2.523	172.757	1.00142.52	C
	ATOM	7144	C	CYS A 938	16.512	2.502	171.555	1.00141.06	C
	ATOM	7145	O	CYS A 938	16.237	1.443	170.988	1.00140.22	O
	ATOM	7146	CB	CYS A 938	16.629	2.681	174.037	1.00145.87	C
40	ATOM	7147	SG	CYS A 938	17.649	2.767	175.509	1.00149.12	S

	ATOM	7148	N	LEU A 939	16.032	3.684	171.178	1.00138.53	N
	ATOM	7149	CA	LEU A 939	15.187	3.841	170.000	1.00141.75	C
	ATOM	7150	C	LEU A 939	15.879	3.314	168.734	1.00146.44	C
	ATOM	7151	O	LEU A 939	15.248	2.680	167.883	1.00150.91	O
5	ATOM	7152	CB	LEU A 939	14.788	5.309	169.830	1.00135.45	C
	ATOM	7153	CG	LEU A 939	13.425	5.750	170.370	1.00133.64	C
	ATOM	7154	CD1	LEU A 939	13.141	5.156	171.736	1.00137.58	C
	ATOM	7155	CD2	LEU A 939	13.364	7.264	170.428	1.00126.32	C
	ATOM	7156	N	SER A 940	17.179	3.578	168.622	1.00141.95	N
10	ATOM	7157	CA	SER A 940	17.989	3.050	167.532	1.00134.50	C
	ATOM	7158	C	SER A 940	18.037	1.540	167.645	1.00135.66	C
	ATOM	7159	O	SER A 940	17.660	0.817	166.723	1.00140.51	O
	ATOM	7160	CB	SER A 940	19.414	3.589	167.627	1.00129.16	C
	ATOM	7161	OG	SER A 940	19.423	4.991	167.821	1.00129.35	O
15	ATOM	7162	N	MET A 941	18.500	1.078	168.799	1.00131.46	N
	ATOM	7163	CA	MET A 941	18.662	-0.341	169.067	1.00133.79	C
	ATOM	7164	C	MET A 941	17.385	-1.151	168.859	1.00138.40	C
	ATOM	7165	O	MET A 941	17.440	-2.347	168.567	1.00137.82	O
	ATOM	7166	CB	MET A 941	19.197	-0.543	170.483	1.00133.38	C
20	ATOM	7167	CG	MET A 941	20.665	-0.222	170.604	1.00127.80	C
	ATOM	7168	SD	MET A 941	21.539	-0.912	169.193	1.00135.00	S
	ATOM	7169	CE	MET A 941	23.237	-0.585	169.652	1.00190.13	C
	ATOM	7170	N	SER A 942	16.237	-0.499	169.007	1.00142.28	N
	ATOM	7171	CA	SER A 942	14.962	-1.175	168.801	1.00145.76	C
25	ATOM	7172	C	SER A 942	14.604	-1.278	167.314	1.00150.08	C
	ATOM	7173	O	SER A 942	13.733	-2.064	166.932	1.00158.30	O
	ATOM	7174	CB	SER A 942	13.839	-0.508	169.610	1.00137.55	C
	ATOM	7175	OG	SER A 942	13.798	0.889	169.392	1.00129.58	O
	ATOM	7176	N	LEU A 943	15.283	-0.493	166.480	1.00139.14	N
30	ATOM	7177	CA	LEU A 943	15.085	-0.574	165.037	1.00133.56	C
	ATOM	7178	C	LEU A 943	16.012	-1.607	164.428	1.00135.45	C
	ATOM	7179	O	LEU A 943	15.624	-2.359	163.535	1.00135.24	O
	ATOM	7180	CB	LEU A 943	15.331	0.776	164.384	1.00129.40	C
	ATOM	7181	CG	LEU A 943	14.292	1.831	164.732	1.00137.46	C
35	ATOM	7182	CD1	LEU A 943	14.769	3.176	164.239	1.00137.32	C
	ATOM	7183	CD2	LEU A 943	12.951	1.469	164.118	1.00142.50	C
	ATOM	7184	N	HIS A 944	17.249	-1.633	164.907	1.00137.85	N
	ATOM	7185	CA	HIS A 944	18.196	-2.631	164.448	1.00138.37	C
	ATOM	7186	C	HIS A 944	17.642	-4.006	164.790	1.00141.27	C
40	ATOM	7187	O	HIS A 944	17.668	-4.922	163.971	1.00142.70	O

	ATOM	7188	CB	HIS A 944	19.566	-2.425	165.090	1.00136.37	C
	ATOM	7189	CG	HIS A 944	20.658	-3.193	164.419	1.00139.32	C
	ATOM	7190	ND1	HIS A 944	21.117	-4.404	164.894	1.00144.82	N
	ATOM	7191	CD2	HIS A 944	21.366	-2.938	163.294	1.00140.49	C
5	ATOM	7192	CE1	HIS A 944	22.070	-4.855	164.096	1.00144.61	C
	ATOM	7193	NE2	HIS A 944	22.240	-3.984	163.117	1.00142.71	N
	ATOM	7194	N	PHE A 945	17.107	-4.134	165.998	1.00144.26	N
	ATOM	7195	CA	PHE A 945	16.465	-5.374	166.405	1.00154.94	C
	ATOM	7196	C	PHE A 945	15.176	-5.620	165.627	1.00160.82	C
10	ATOM	7197	O	PHE A 945	14.659	-6.738	165.600	1.00162.71	O
	ATOM	7198	CB	PHE A 945	16.194	-5.378	167.910	1.00159.35	C
	ATOM	7199	CG	PHE A 945	17.264	-6.057	168.707	1.00160.52	C
	ATOM	7200	CD1	PHE A 945	18.340	-5.340	169.200	1.00158.30	C
	ATOM	7201	CD2	PHE A 945	17.204	-7.420	168.946	1.00164.38	C
15	ATOM	7202	CE1	PHE A 945	19.331	-5.969	169.927	1.00158.81	C
	ATOM	7203	CE2	PHE A 945	18.193	-8.055	169.671	1.00164.86	C
	ATOM	7204	CZ	PHE A 945	19.258	-7.329	170.163	1.00161.50	C
	ATOM	7205	N	LEU A 946	14.664	-4.573	164.988	1.00159.75	N
	ATOM	7206	CA	LEU A 946	13.430	-4.684	164.224	1.00159.82	C
20	ATOM	7207	C	LEU A 946	13.710	-5.220	162.822	1.00161.34	C
	ATOM	7208	O	LEU A 946	13.075	-6.176	162.382	1.00167.05	O
	ATOM	7209	CB	LEU A 946	12.711	-3.333	164.165	1.00154.27	C
	ATOM	7210	CG	LEU A 946	11.242	-3.292	163.752	1.00154.39	C
	ATOM	7211	CD1	LEU A 946	10.601	-2.022	164.281	1.00153.92	C
25	ATOM	7212	CD2	LEU A 946	11.091	-3.365	162.242	1.00153.48	C
	ATOM	7213	N	ILE A 947	14.664	-4.613	162.123	1.00157.88	N
	ATOM	7214	CA	ILE A 947	14.976	-5.032	160.759	1.00158.50	C
	ATOM	7215	C	ILE A 947	15.687	-6.374	160.736	1.00155.67	C
	ATOM	7216	O	ILE A 947	15.895	-6.951	159.672	1.00158.21	O
30	ATOM	7217	CB	ILE A 947	15.864	-4.012	160.028	1.00158.34	C
	ATOM	7218	CG1	ILE A 947	17.282	-4.037	160.596	1.00156.14	C
	ATOM	7219	CG2	ILE A 947	15.263	-2.619	160.113	1.00158.98	C
	ATOM	7220	CD1	ILE A 947	18.232	-3.116	159.876	1.00153.19	C
	ATOM	7221	N	LEU A 948	16.063	-6.860	161.913	1.00152.63	N
35	ATOM	7222	CA	LEU A 948	16.732	-8.149	162.037	1.00150.91	C
	ATOM	7223	C	LEU A 948	15.762	-9.320	162.091	1.00157.06	C
	ATOM	7224	O	LEU A 948	15.981	-10.347	161.452	1.00159.52	O
	ATOM	7225	CB	LEU A 948	17.599	-8.178	163.293	1.00143.47	C
	ATOM	7226	CG	LEU A 948	19.042	-7.732	163.116	1.00133.10	C
40	ATOM	7227	CD1	LEU A 948	19.839	-8.111	164.344	1.00130.46	C

	ATOM	7228	CD2 LEU A 948	19.612	-8.380	161.874	1.00132.37	C
	ATOM	7229	N TYR A 949	14.692	-9.165	162.859	1.00160.88	N
	ATOM	7230	CA TYR A 949	13.842	-10.297	163.191	1.00170.86	C
	ATOM	7231	C TYR A 949	12.558	-10.407	162.374	1.00176.94	C
5	ATOM	7232	O TYR A 949	12.032	-11.509	162.203	1.00186.75	O
	ATOM	7233	CB TYR A 949	13.501	-10.278	164.681	1.00178.64	C
	ATOM	7234	CG TYR A 949	14.645	-10.676	165.584	1.00186.30	C
	ATOM	7235	CD1 TYR A 949	15.648	-11.524	165.137	1.00189.25	C
	ATOM	7236	CD2 TYR A 949	14.718	-10.207	166.890	1.00192.35	C
10	ATOM	7237	CE1 TYR A 949	16.694	-11.891	165.966	1.00191.67	C
	ATOM	7238	CE2 TYR A 949	15.759	-10.568	167.724	1.00194.84	C
	ATOM	7239	CZ TYR A 949	16.745	-11.411	167.256	1.00194.68	C
	ATOM	7240	OH TYR A 949	17.785	-11.775	168.080	1.00196.06	O
	ATOM	7241	N VAL A 950	12.060	-9.282	161.867	1.00171.62	N
15	ATOM	7242	CA VAL A 950	10.700	-9.231	161.319	1.00178.33	C
	ATOM	7243	C VAL A 950	10.388	-10.234	160.186	1.00192.28	C
	ATOM	7244	O VAL A 950	9.292	-10.803	160.160	1.00203.85	O
	ATOM	7245	CB VAL A 950	10.284	-7.791	160.937	1.00172.44	C
	ATOM	7246	CG1 VAL A 950	11.110	-7.287	159.772	1.00173.29	C
20	ATOM	7247	CG2 VAL A 950	8.794	-7.720	160.628	1.00171.53	C
	ATOM	7248	N ASP A 951	11.340	-10.426	159.265	1.00190.43	N
	ATOM	7249	CA ASP A 951	11.294	-11.428	158.162	1.00189.86	C
	ATOM	7250	C ASP A 951	10.884	-10.997	156.727	1.00185.30	C
	ATOM	7251	O ASP A 951	11.298	-11.644	155.766	1.00184.88	O
25	ATOM	7252	CB ASP A 951	10.628	-12.768	158.553	1.00188.48	C
	ATOM	7253	CG ASP A 951	11.505	-13.620	159.461	1.00182.36	C
	ATOM	7254	OD1 ASP A 951	12.545	-14.127	158.989	1.00177.56	O
	ATOM	7255	OD2 ASP A 951	11.142	-13.789	160.643	1.00182.99	O
	ATOM	7256	N PRO A 952	10.081	-9.926	156.561	1.00185.74	N
30	ATOM	7257	CA PRO A 952	9.953	-9.493	155.167	1.00187.43	C
	ATOM	7258	C PRO A 952	10.977	-8.411	154.849	1.00187.25	C
	ATOM	7259	O PRO A 952	10.906	-7.761	153.807	1.00190.68	O
	ATOM	7260	CB PRO A 952	8.534	-8.907	155.107	1.00188.99	C
	ATOM	7261	CG PRO A 952	7.995	-8.956	156.519	1.00189.40	C
35	ATOM	7262	CD PRO A 952	9.143	-9.196	157.425	1.00185.73	C
	ATOM	7263	N LEU A 953	11.920	-8.224	155.764	1.00180.86	N
	ATOM	7264	CA LEU A 953	12.915	-7.159	155.666	1.00166.15	C
	ATOM	7265	C LEU A 953	14.373	-7.648	155.653	1.00162.90	C
	ATOM	7266	O LEU A 953	15.179	-7.127	154.878	1.00160.77	O
40	ATOM	7267	CB LEU A 953	12.714	-6.122	156.781	1.00152.02	C

	ATOM	7268	CG	LEU A 953	11.689	-4.997	156.611	1.00140.63	C
	ATOM	7269	CD1	LEU A 953	10.293	-5.519	156.350	1.00145.03	C
	ATOM	7270	CD2	LEU A 953	11.698	-4.163	157.860	1.00130.44	C
	ATOM	7271	N	PRO A 954	14.724	-8.635	156.511	1.00160.49	N
5	ATOM	7272	CA	PRO A 954	16.104	-9.135	156.467	1.00158.04	C
	ATOM	7273	C	PRO A 954	16.520	-9.674	155.104	1.00162.94	C
	ATOM	7274	O	PRO A 954	17.716	-9.798	154.851	1.00161.90	O
	ATOM	7275	CB	PRO A 954	16.091	-10.272	157.488	1.00155.64	C
	ATOM	7276	CG	PRO A 954	15.070	-9.869	158.463	1.00157.40	C
10	ATOM	7277	CD	PRO A 954	14.000	-9.179	157.675	1.00160.23	C
	ATOM	7278	N	MET A 955	15.557	-9.988	154.243	1.00167.64	N
	ATOM	7279	CA	MET A 955	15.877	-10.448	152.898	1.00169.71	C
	ATOM	7280	C	MET A 955	16.291	-9.287	152.005	1.00169.09	C
	ATOM	7281	O	MET A 955	17.078	-9.461	151.074	1.00172.31	O
15	ATOM	7282	CB	MET A 955	14.702	-11.203	152.284	1.00174.27	C
	ATOM	7283	CG	MET A 955	14.438	-12.546	152.943	1.00177.23	C
	ATOM	7284	SD	MET A 955	15.882	-13.628	152.924	1.00234.37	S
	ATOM	7285	CE	MET A 955	16.039	-13.968	151.171	1.00197.31	C
	ATOM	7286	N	ILE A 956	15.759	-8.105	152.292	1.00164.57	N
20	ATOM	7287	CA	ILE A 956	16.140	-6.909	151.557	1.00160.34	C
	ATOM	7288	C	ILE A 956	17.462	-6.369	152.077	1.00158.13	C
	ATOM	7289	O	ILE A 956	18.330	-5.958	151.306	1.00161.01	O
	ATOM	7290	CB	ILE A 956	15.079	-5.812	151.680	1.00159.05	C
	ATOM	7291	CG1	ILE A 956	13.812	-6.216	150.932	1.00160.56	C
25	ATOM	7292	CG2	ILE A 956	15.612	-4.491	151.144	1.00159.13	C
	ATOM	7293	CD1	ILE A 956	12.890	-5.061	150.668	1.00160.94	C
	ATOM	7294	N	PHE A 957	17.609	-6.378	153.396	1.00153.88	N
	ATOM	7295	CA	PHE A 957	18.811	-5.864	154.034	1.00149.50	C
	ATOM	7296	C	PHE A 957	19.923	-6.902	154.069	1.00146.55	C
30	ATOM	7297	O	PHE A 957	21.035	-6.613	154.518	1.00143.30	O
	ATOM	7298	CB	PHE A 957	18.491	-5.390	155.448	1.00149.99	C
	ATOM	7299	CG	PHE A 957	17.931	-4.002	155.503	1.00146.76	C
	ATOM	7300	CD1	PHE A 957	18.484	-2.991	154.732	1.00140.21	C
	ATOM	7301	CD2	PHE A 957	16.851	-3.708	156.317	1.00146.55	C
35	ATOM	7302	CE1	PHE A 957	17.974	-1.715	154.776	1.00137.77	C
	ATOM	7303	CE2	PHE A 957	16.336	-2.431	156.365	1.00143.71	C
	ATOM	7304	CZ	PHE A 957	16.898	-1.432	155.592	1.00140.26	C
	ATOM	7305	N	LYS A 958	19.611	-8.099	153.580	1.00147.29	N
	ATOM	7306	CA	LYS A 958	20.538	-9.225	153.605	1.00150.29	C
40	ATOM	7307	C	LYS A 958	21.151	-9.422	154.990	1.00150.03	C

	ATOM	7308	O	LYS A 958	22.343	-9.188	155.194	1.00150.25	O
	ATOM	7309	CB	LYS A 958	21.615	-9.084	152.522	1.00150.83	C
	ATOM	7310	CG	LYS A 958	21.128	-9.477	151.125	1.00153.59	C
	ATOM	7311	CD	LYS A 958	22.148	-10.343	150.391	1.00152.74	C
5	ATOM	7312	CE	LYS A 958	21.473	-11.289	149.402	1.00155.49	C
	ATOM	7313	NZ	LYS A 958	22.452	-12.157	148.679	1.00154.10	N
	ATOM	7314	N	LEU A 959	20.316	-9.846	155.935	1.00149.50	N
	ATOM	7315	CA	LEU A 959	20.736	-10.022	157.319	1.00147.75	C
	ATOM	7316	C	LEU A 959	20.202	-11.332	157.909	1.00150.55	C
10	ATOM	7317	O	LEU A 959	19.106	-11.775	157.555	1.00153.54	O
	ATOM	7318	CB	LEU A 959	20.238	-8.849	158.171	1.00149.32	C
	ATOM	7319	CG	LEU A 959	20.519	-7.403	157.746	1.00149.16	C
	ATOM	7320	CD1	LEU A 959	19.881	-6.430	158.729	1.00148.91	C
	ATOM	7321	CD2	LEU A 959	22.005	-7.124	157.620	1.00148.47	C
15	ATOM	7322	N	LYS A 960	20.976	-11.945	158.805	1.00148.69	N
	ATOM	7323	CA	LYS A 960	20.495	-13.082	159.600	1.00151.11	C
	ATOM	7324	C	LYS A 960	20.513	-12.751	161.095	1.00160.63	C
	ATOM	7325	O	LYS A 960	21.351	-11.976	161.558	1.00161.84	O
	ATOM	7326	CB	LYS A 960	21.319	-14.350	159.333	1.00142.39	C
20	ATOM	7327	CG	LYS A 960	20.802	-15.602	160.055	1.00139.42	C
	ATOM	7328	CD	LYS A 960	21.756	-16.782	159.924	1.00138.20	C
	ATOM	7329	CE	LYS A 960	21.293	-17.985	160.745	1.00138.24	C
	ATOM	7330	NZ	LYS A 960	21.039	-19.190	159.902	1.00134.93	N
	ATOM	7331	N	ALA A 961	19.581	-13.339	161.840	1.00168.61	N
25	ATOM	7332	CA	ALA A 961	19.510	-13.179	163.289	1.00172.84	C
	ATOM	7333	C	ALA A 961	20.827	-13.541	163.981	1.00175.33	C
	ATOM	7334	O	ALA A 961	21.655	-14.267	163.431	1.00172.94	O
	ATOM	7335	CB	ALA A 961	18.371	-14.022	163.847	1.00177.48	C
	ATOM	7336	N	LEU A 962	21.013	-13.026	165.192	1.00180.94	N
30	ATOM	7337	CA	LEU A 962	22.207	-13.321	165.974	1.00183.31	C
	ATOM	7338	C	LEU A 962	21.835	-13.816	167.364	1.00187.22	C
	ATOM	7339	O	LEU A 962	21.150	-13.118	168.114	1.00188.24	O
	ATOM	7340	CB	LEU A 962	23.081	-12.078	166.118	1.00181.32	C
	ATOM	7341	CG	LEU A 962	23.325	-11.184	164.907	1.00178.61	C
35	ATOM	7342	CD1	LEU A 962	24.105	-9.960	165.346	1.00177.55	C
	ATOM	7343	CD2	LEU A 962	24.068	-11.939	163.826	1.00176.60	C
	ATOM	7344	N	ASP A 963	22.297	-15.013	167.710	1.00188.76	N
	ATOM	7345	CA	ASP A 963	22.063	-15.553	169.044	1.00191.36	C
	ATOM	7346	C	ASP A 963	22.889	-14.805	170.093	1.00191.04	C
40	ATOM	7347	O	ASP A 963	23.671	-13.906	169.765	1.00185.53	O

	ATOM	7348	CB	ASP A 963	22.359 -17.058 169.093	1.00188.01	C
	ATOM	7349	CG	ASP A 963	21.240 -17.896 168.494	1.00184.11	C
	ATOM	7350	OD2	ASP A 963	21.543 -18.946 167.894	1.00182.06	O
	ATOM	7351	OD1	ASP A 963	20.060 -17.508 168.627	1.00183.84	O
5	ATOM	7352	N	LEU A 964	22.710 -15.186 171.355	1.00192.97	N
	ATOM	7353	CA	LEU A 964	23.418 -14.554 172.463	1.00185.90	C
	ATOM	7354	C	LEU A 964	24.884 -14.986 172.500	1.00187.15	C
	ATOM	7355	O	LEU A 964	25.649 -14.552 173.360	1.00187.03	O
	ATOM	7356	CB	LEU A 964	22.723 -14.882 173.785	1.00181.11	C
10	ATOM	7357	CG	LEU A 964	21.205 -14.697 173.736	1.00175.71	C
	ATOM	7358	CD1	LEU A 964	20.534 -15.193 175.018	1.00180.62	C
	ATOM	7359	CD2	LEU A 964	20.855 -13.242 173.451	1.00163.78	C
	ATOM	7360	N	THR A 965	25.262 -15.846 171.559	1.00187.14	N
	ATOM	7361	CA	THR A 965	26.648 -16.251 171.376	1.00183.76	C
15	ATOM	7362	C	THR A 965	27.357 -15.217 170.511	1.00179.68	C
	ATOM	7363	O	THR A 965	28.566 -15.005 170.629	1.00176.20	O
	ATOM	7364	CB	THR A 965	26.724 -17.614 170.672	1.00183.22	C
	ATOM	7365	OG1	THR A 965	25.839 -18.535 171.319	1.00186.84	O
	ATOM	7366	CG2	THR A 965	28.145 -18.162 170.700	1.00183.48	C
20	ATOM	7367	N	GLN A 966	26.582 -14.563 169.652	1.00179.89	N
	ATOM	7368	CA	GLN A 966	27.124 -13.657 168.647	1.00177.28	C
	ATOM	7369	C	GLN A 966	27.134 -12.203 169.107	1.00174.45	C
	ATOM	7370	O	GLN A 966	28.136 -11.503 168.937	1.00172.48	O
	ATOM	7371	CB	GLN A 966	26.335 -13.801 167.345	1.00178.19	C
25	ATOM	7372	CG	GLN A 966	26.349 -15.224 166.806	1.00182.32	C
	ATOM	7373	CD	GLN A 966	25.057 -15.611 166.115	1.00184.38	C
	ATOM	7374	OE1	GLN A 966	24.323 -16.479 166.590	1.00187.20	O
	ATOM	7375	NE2	GLN A 966	24.779 -14.977 164.982	1.00181.63	N
	ATOM	7376	N	TRP A 967	26.025 -11.752 169.692	1.00172.52	N
30	ATOM	7377	CA	TRP A 967	25.928 -10.374 170.174	1.00166.61	C
	ATOM	7378	C	TRP A 967	26.951 -10.106 171.274	1.00159.63	C
	ATOM	7379	O	TRP A 967	27.327 -8.958 171.519	1.00154.14	O
	ATOM	7380	CB	TRP A 967	24.515 -10.056 170.676	1.00169.30	C
	ATOM	7381	CG	TRP A 967	23.522 -9.702 169.592	1.00169.35	C
35	ATOM	7382	CD1	TRP A 967	22.553 -10.513 169.067	1.00172.08	C
	ATOM	7383	CD2	TRP A 967	23.395 -8.441 168.915	1.00163.58	C
	ATOM	7384	NE1	TRP A 967	21.836 -9.837 168.105	1.00169.66	N
	ATOM	7385	CE2	TRP A 967	22.334 -8.564 167.994	1.00165.91	C
	ATOM	7386	CE3	TRP A 967	24.077 -7.222 168.998	1.00152.76	C
40	ATOM	7387	CZ2	TRP A 967	21.941 -7.515 167.161	1.00159.68	C

	ATOM	7388	CZ3 TRP A 967	23.681	-6.181	168.172	1.00145.99	C
	ATOM	7389	CH2 TRP A 967	22.627	-6.335	167.266	1.00148.92	C
	ATOM	7390	N LEU A 968	27.395	-11.177	171.926	1.00159.29	N
	ATOM	7391	CA LEU A 968	28.404	-11.095	172.975	1.00159.29	C
5	ATOM	7392	C LEU A 968	29.695	-10.501	172.426	1.00157.78	C
	ATOM	7393	O LEU A 968	30.224	-9.521	172.957	1.00153.93	O
	ATOM	7394	CB LEU A 968	28.681	-12.489	173.545	1.00160.39	C
	ATOM	7395	CG LEU A 968	29.588	-12.580	174.776	1.00158.46	C
	ATOM	7396	CD1 LEU A 968	28.877	-12.033	176.011	1.00156.53	C
10	ATOM	7397	CD2 LEU A 968	30.067	-14.011	175.002	1.00158.54	C
	ATOM	7398	N MET A 969	30.189	-11.105	171.351	1.00160.71	N
	ATOM	7399	CA MET A 969	31.435	-10.683	170.727	1.00161.78	C
	ATOM	7400	C MET A 969	31.381	-9.216	170.302	1.00156.85	C
	ATOM	7401	O MET A 969	32.384	-8.503	170.367	1.00154.61	O
15	ATOM	7402	CB MET A 969	31.745	-11.582	169.530	1.00163.78	C
	ATOM	7403	CG MET A 969	33.087	-11.313	168.871	1.00163.31	C
	ATOM	7404	SD MET A 969	34.452	-11.333	170.044	1.00241.86	S
	ATOM	7405	CE MET A 969	35.828	-11.628	168.939	1.00 98.09	C
	ATOM	7406	N VAL A 970	30.200	-8.772	169.884	1.00153.36	N
20	ATOM	7407	CA VAL A 970	29.997	-7.384	169.487	1.00150.53	C
	ATOM	7408	C VAL A 970	30.284	-6.429	170.647	1.00152.83	C
	ATOM	7409	O VAL A 970	30.633	-5.274	170.430	1.00152.38	O
	ATOM	7410	CB VAL A 970	28.570	-7.154	168.963	1.00148.57	C
	ATOM	7411	CG1 VAL A 970	28.462	-5.797	168.265	1.00142.62	C
25	ATOM	7412	CG2 VAL A 970	28.174	-8.276	168.019	1.00148.17	C
	ATOM	7413	N LEU A 971	30.141	-6.907	171.879	1.00152.40	N
	ATOM	7414	CA LEU A 971	30.573	-6.114	173.024	1.00149.44	C
	ATOM	7415	C LEU A 971	32.099	-6.049	173.066	1.00152.21	C
	ATOM	7416	O LEU A 971	32.681	-4.959	173.081	1.00152.68	O
30	ATOM	7417	CB LEU A 971	30.024	-6.679	174.332	1.00145.10	C
	ATOM	7418	CG LEU A 971	28.537	-6.430	174.579	1.00139.32	C
	ATOM	7419	CD1 LEU A 971	28.140	-6.903	175.970	1.00142.28	C
	ATOM	7420	CD2 LEU A 971	28.204	-4.962	174.393	1.00131.41	C
	ATOM	7421	N LYS A 972	32.735	-7.220	173.066	1.00148.30	N
35	ATOM	7422	CA LYS A 972	34.195	-7.321	173.085	1.00139.13	C
	ATOM	7423	C LYS A 972	34.862	-6.551	171.938	1.00134.63	C
	ATOM	7424	O LYS A 972	35.959	-6.018	172.095	1.00135.83	O
	ATOM	7425	CB LYS A 972	34.631	-8.790	173.069	1.00135.13	C
	ATOM	7426	CG LYS A 972	34.527	-9.489	174.418	1.00135.53	C
40	ATOM	7427	CD LYS A 972	34.956	-10.956	174.335	1.00137.10	C

	ATOM	7428	CE	LYS A 972	35.002	-11.612	175.722	1.00142.59	C
	ATOM	7429	NZ	LYS A 972	35.173	-13.101	175.681	1.00143.63	N
	ATOM	7430	N	ILE A 973	34.194	-6.487	170.792	1.00129.62	N
	ATOM	7431	CA	ILE A 973	34.728	-5.780	169.636	1.00127.50	C
5	ATOM	7432	C	ILE A 973	34.482	-4.279	169.721	1.00127.77	C
	ATOM	7433	O	ILE A 973	35.378	-3.475	169.457	1.00123.56	O
	ATOM	7434	CB	ILE A 973	34.095	-6.293	168.336	1.00131.30	C
	ATOM	7435	CG1	ILE A 973	34.478	-7.755	168.095	1.00137.59	C
	ATOM	7436	CG2	ILE A 973	34.526	-5.434	167.163	1.00130.88	C
10	ATOM	7437	CD1	ILE A 973	33.933	-8.325	166.796	1.00137.94	C
	ATOM	7438	N	SER A 974	33.258	-3.911	170.092	1.00133.54	N
	ATOM	7439	CA	SER A 974	32.833	-2.513	170.102	1.00135.22	C
	ATOM	7440	C	SER A 974	33.349	-1.739	171.303	1.00134.40	C
	ATOM	7441	O	SER A 974	34.055	-0.742	171.146	1.00137.40	O
15	ATOM	7442	CB	SER A 974	31.304	-2.409	170.079	1.00137.62	C
	ATOM	7443	OG	SER A 974	30.751	-3.172	169.022	1.00139.52	O
	ATOM	7444	N	LEU A 975	32.976	-2.206	172.493	1.00126.67	N
	ATOM	7445	CA	LEU A 975	33.227	-1.491	173.745	1.00118.98	C
	ATOM	7446	C	LEU A 975	34.605	-0.843	173.892	1.00118.01	C
20	ATOM	7447	O	LEU A 975	34.691	0.307	174.317	1.00116.20	O
	ATOM	7448	CB	LEU A 975	32.913	-2.379	174.956	1.00120.17	C
	ATOM	7449	CG	LEU A 975	31.431	-2.712	175.139	1.00118.41	C
	ATOM	7450	CD1	LEU A 975	31.248	-3.819	176.165	1.00121.13	C
	ATOM	7451	CD2	LEU A 975	30.647	-1.466	175.531	1.00111.49	C
25	ATOM	7452	N	PRO A 976	35.688	-1.560	173.533	1.00120.07	N
	ATOM	7453	CA	PRO A 976	36.993	-0.898	173.659	1.00120.86	C
	ATOM	7454	C	PRO A 976	37.145	0.413	172.882	1.00118.66	C
	ATOM	7455	O	PRO A 976	38.150	1.091	173.078	1.00123.13	O
	ATOM	7456	CB	PRO A 976	37.987	-1.954	173.152	1.00119.68	C
30	ATOM	7457	CG	PRO A 976	37.157	-3.072	172.603	1.00119.37	C
	ATOM	7458	CD	PRO A 976	35.837	-3.000	173.272	1.00119.47	C
	ATOM	7459	N	VAL A 977	36.177	0.776	172.041	1.00114.47	N
	ATOM	7460	CA	VAL A 977	36.208	2.090	171.406	1.00112.18	C
	ATOM	7461	C	VAL A 977	35.995	3.152	172.471	1.00119.90	C
35	ATOM	7462	O	VAL A 977	36.430	4.292	172.319	1.00124.37	O
	ATOM	7463	CB	VAL A 977	35.164	2.255	170.273	1.00102.54	C
	ATOM	7464	CG1	VAL A 977	33.775	2.500	170.833	1.00 98.17	C
	ATOM	7465	CG2	VAL A 977	35.557	3.413	169.367	1.00 98.58	C
	ATOM	7466	N	ILE A 978	35.326	2.765	173.552	1.00124.00	N
40	ATOM	7467	CA	ILE A 978	35.173	3.626	174.717	1.00124.10	C

	ATOM	7468	C	ILE A 978	36.460	3.555	175.517	1.00123.40	C
	ATOM	7469	O	ILE A 978	36.915	4.553	176.077	1.00118.89	O
	ATOM	7470	CB	ILE A 978	33.992	3.184	175.602	1.00120.58	C
	ATOM	7471	CG1	ILE A 978	32.679	3.349	174.839	1.00120.51	C
5	ATOM	7472	CG2	ILE A 978	33.953	3.986	176.887	1.00114.65	C
	ATOM	7473	CD1	ILE A 978	31.471	2.885	175.607	1.00123.48	C
	ATOM	7474	N	GLY A 979	37.045	2.361	175.558	1.00122.22	N
	ATOM	7475	CA	GLY A 979	38.348	2.186	176.160	1.00122.17	C
	ATOM	7476	C	GLY A 979	39.337	3.093	175.459	1.00118.68	C
10	ATOM	7477	O	GLY A 979	39.968	3.950	176.082	1.00118.23	O
	ATOM	7478	N	LEU A 980	39.440	2.920	174.148	1.00113.71	N
	ATOM	7479	CA	LEU A 980	40.402	3.658	173.349	1.00112.89	C
	ATOM	7480	C	LEU A 980	40.260	5.167	173.518	1.00117.09	C
	ATOM	7481	O	LEU A 980	41.247	5.867	173.736	1.00121.83	O
15	ATOM	7482	CB	LEU A 980	40.272	3.276	171.876	1.00110.23	C
	ATOM	7483	CG	LEU A 980	41.191	4.053	170.934	1.00111.46	C
	ATOM	7484	CD1	LEU A 980	42.648	3.888	171.350	1.00112.26	C
	ATOM	7485	CD2	LEU A 980	40.978	3.619	169.492	1.00111.42	C
	ATOM	7486	N	ASP A 981	39.036	5.669	173.426	1.00116.41	N
20	ATOM	7487	CA	ASP A 981	38.821	7.109	173.494	1.00115.75	C
	ATOM	7488	C	ASP A 981	39.091	7.612	174.904	1.00109.42	C
	ATOM	7489	O	ASP A 981	39.512	8.754	175.096	1.00101.48	O
	ATOM	7490	CB	ASP A 981	37.399	7.471	173.058	1.00123.12	C
	ATOM	7491	CG	ASP A 981	37.285	8.900	172.547	1.00128.57	C
25	ATOM	7492	OD1	ASP A 981	38.161	9.731	172.873	1.00128.55	O
	ATOM	7493	OD2	ASP A 981	36.316	9.193	171.814	1.00131.39	O
	ATOM	7494	N	GLU A 982	38.851	6.745	175.885	1.00112.26	N
	ATOM	7495	CA	GLU A 982	39.071	7.086	177.284	1.00109.22	C
	ATOM	7496	C	GLU A 982	40.558	7.292	177.512	1.00110.28	C
30	ATOM	7497	O	GLU A 982	40.973	8.221	178.211	1.00104.73	O
	ATOM	7498	CB	GLU A 982	38.556	5.974	178.189	1.00107.24	C
	ATOM	7499	CG	GLU A 982	38.085	6.454	179.540	1.00115.65	C
	ATOM	7500	CD	GLU A 982	36.735	7.132	179.474	1.00123.42	C
	ATOM	7501	OE2	GLU A 982	36.323	7.722	180.495	1.00126.18	O
35	ATOM	7502	OE1	GLU A 982	36.083	7.072	178.407	1.00125.79	O
	ATOM	7503	N	ILE A 983	41.346	6.407	176.904	1.00113.38	N
	ATOM	7504	CA	ILE A 983	42.802	6.511	176.878	1.00111.79	C
	ATOM	7505	C	ILE A 983	43.248	7.810	176.208	1.00113.33	C
	ATOM	7506	O	ILE A 983	44.041	8.566	176.769	1.00115.61	O
40	ATOM	7507	CB	ILE A 983	43.426	5.320	176.117	1.00103.33	C

	ATOM	7508	CG1 ILE A 983	43.107	4.003	176.825	1.00104.71	C
	ATOM	7509	CG2 ILE A 983	44.922	5.497	175.980	1.00 99.98	C
	ATOM	7510	CD1 ILE A 983	43.543	2.779	176.050	1.00104.72	C
	ATOM	7511	N LEU A 984	42.736	8.056	175.005	1.00111.10	N
5	ATOM	7512	CA LEU A 984	43.005	9.300	174.297	1.00112.84	C
	ATOM	7513	C LEU A 984	42.648	10.512	175.148	1.00114.60	C
	ATOM	7514	O LEU A 984	43.463	11.416	175.320	1.00114.75	O
	ATOM	7515	CB LEU A 984	42.240	9.337	172.979	1.00114.99	C
	ATOM	7516	CG LEU A 984	42.880	8.482	171.886	1.00122.60	C
10	ATOM	7517	CD1 LEU A 984	42.060	8.517	170.604	1.00123.70	C
	ATOM	7518	CD2 LEU A 984	44.298	8.965	171.635	1.00125.20	C
	ATOM	7519	N LYS A 985	41.433	10.518	175.689	1.00116.92	N
	ATOM	7520	CA LYS A 985	40.987	11.600	176.562	1.00116.14	C
	ATOM	7521	C LYS A 985	41.883	11.721	177.792	1.00116.56	C
15	ATOM	7522	O LYS A 985	42.115	12.820	178.293	1.00111.84	O
	ATOM	7523	CB LYS A 985	39.536	11.386	176.996	1.00115.59	C
	ATOM	7524	CG LYS A 985	38.480	11.888	176.024	1.00112.98	C
	ATOM	7525	CD LYS A 985	37.152	11.190	176.307	1.00119.51	C
	ATOM	7526	CE LYS A 985	35.953	12.083	176.024	1.00121.14	C
20	ATOM	7527	NZ LYS A 985	34.671	11.433	176.429	1.00122.20	N
	ATOM	7528	N PHE A 986	42.387	10.590	178.275	1.00120.35	N
	ATOM	7529	CA PHE A 986	43.270	10.598	179.437	1.00125.05	C
	ATOM	7530	C PHE A 986	44.548	11.376	179.154	1.00124.31	C
	ATOM	7531	O PHE A 986	44.906	12.288	179.902	1.00122.77	O
25	ATOM	7532	CB PHE A 986	43.619	9.176	179.873	1.00127.31	C
	ATOM	7533	CG PHE A 986	44.560	9.116	181.044	1.00130.59	C
	ATOM	7534	CD1 PHE A 986	44.095	9.299	182.334	1.00133.30	C
	ATOM	7535	CD2 PHE A 986	45.910	8.866	180.854	1.00132.99	C
	ATOM	7536	CE1 PHE A 986	44.959	9.239	183.409	1.00138.27	C
30	ATOM	7537	CE2 PHE A 986	46.778	8.804	181.928	1.00134.97	C
	ATOM	7538	CZ PHE A 986	46.303	8.991	183.205	1.00137.22	C
	ATOM	7539	N ILE A 987	45.225	11.001	178.070	1.00122.11	N
	ATOM	7540	CA ILE A 987	46.434	11.686	177.624	1.00118.68	C
	ATOM	7541	C ILE A 987	46.182	13.187	177.483	1.00119.98	C
35	ATOM	7542	O ILE A 987	47.024	14.004	177.850	1.00123.88	O
	ATOM	7543	CB ILE A 987	46.945	11.104	176.286	1.00110.85	C
	ATOM	7544	CG1 ILE A 987	47.095	9.582	176.393	1.00114.08	C
	ATOM	7545	CG2 ILE A 987	48.256	11.754	175.883	1.00105.48	C
	ATOM	7546	CD1 ILE A 987	47.687	8.914	175.163	1.00 88.87	C
40	ATOM	7547	N ALA A 988	45.003	13.542	176.980	1.00114.64	N

	ATOM	7548	CA	ALA A 988	44.618	14.940	176.824	1.00106.45	C
	ATOM	7549	C	ALA A 988	44.588	15.688	178.154	1.00112.67	C
	ATOM	7550	O	ALA A 988	45.367	16.619	178.357	1.00110.78	O
	ATOM	7551	CB	ALA A 988	43.269	15.042	176.126	1.00 95.31	C
5	ATOM	7552	N	ARG A 989	43.691	15.268	179.049	1.00121.32	N
	ATOM	7553	CA	ARG A 989	43.444	15.956	180.324	1.00126.54	C
	ATOM	7554	C	ARG A 989	44.731	16.224	181.097	1.00132.53	C
	ATOM	7555	O	ARG A 989	44.901	17.280	181.708	1.00127.68	O
	ATOM	7556	CB	ARG A 989	42.488	15.143	181.214	1.00125.78	C
10	ATOM	7557	CG	ARG A 989	41.181	14.709	180.554	1.00121.13	C
	ATOM	7558	CD	ARG A 989	40.199	14.115	181.565	1.00118.83	C
	ATOM	7559	NE	ARG A 989	40.874	13.330	182.593	1.00120.84	N
	ATOM	7560	CZ	ARG A 989	40.999	12.006	182.570	1.00120.56	C
	ATOM	7561	NH1	ARG A 989	40.483	11.303	181.567	1.00113.96	N
15	ATOM	7562	NH2	ARG A 989	41.638	11.387	183.557	1.00123.75	N
	ATOM	7563	N	ASN A 990	45.637	15.256	181.056	1.00143.68	N
	ATOM	7564	CA	ASN A 990	46.873	15.333	181.817	1.00151.56	C
	ATOM	7565	C	ASN A 990	48.024	15.972	181.035	1.00157.85	C
	ATOM	7566	O	ASN A 990	49.101	16.180	181.591	1.00164.09	O
20	ATOM	7567	CB	ASN A 990	47.267	13.943	182.325	1.00152.81	C
	ATOM	7568	CG	ASN A 990	46.139	13.258	183.089	1.00153.67	C
	ATOM	7569	OD1	ASN A 990	45.568	12.272	182.625	1.00153.61	O
	ATOM	7570	ND2	ASN A 990	45.816	13.782	184.267	1.00155.31	N
	ATOM	7571	O	TYR A 991	48.445	17.975	176.768	1.00135.76	O
25	ATOM	7572	N	TYR A 991	47.788	16.285	179.757	1.00153.59	N
	ATOM	7573	CA	TYR A 991	48.787	16.951	178.914	1.00143.91	C
	ATOM	7574	C	TYR A 991	48.173	17.998	177.968	1.00137.66	C
	ATOM	7575	CB	TYR A 991	49.561	15.929	178.063	1.00136.91	C
	ATOM	7576	CG	TYR A 991	50.302	14.825	178.804	1.00137.42	C
30	ATOM	7577	CD2	TYR A 991	50.167	13.491	178.417	1.00134.18	C
	ATOM	7578	CD1	TYR A 991	51.165	15.110	179.856	1.00142.89	C
	ATOM	7579	CE2	TYR A 991	50.853	12.470	179.075	1.00133.08	C
	ATOM	7580	CE1	TYR A 991	51.851	14.096	180.526	1.00143.31	C
	ATOM	7581	CZ	TYR A 991	51.690	12.781	180.128	1.00135.26	C
35	ATOM	7582	OH	TYR A 991	52.360	11.779	180.785	1.00131.07	O
	ATOM	7583	O	LEU A 992	47.638	21.621	179.234	1.00132.19	O
	ATOM	7584	N	LEU A 992	47.345	18.906	178.486	1.00132.66	N
	ATOM	7585	CA	LEU A 992	46.820	19.998	177.653	1.00125.68	C
	ATOM	7586	C	LEU A 992	47.383	21.363	178.058	1.00129.48	C
40	ATOM	7587	CB	LEU A 992	45.278	20.021	177.608	1.00115.91	C

	ATOM	7588	CG	LEU A	992	44.375	20.181	178.839	1.00105.54	C
	ATOM	7589	CD1	LEU A	992	44.448	21.571	179.438	1.00100.78	C
	ATOM	7590	CD2	LEU A	992	42.931	19.849	178.476	1.00 99.12	C
	HETATM	7591	PG	ACP A	1001	27.501	55.276	185.678	1.00259.59	P
5	HETATM	7592	O1G	ACP A	1001	27.926	53.948	186.414	1.00 71.63	O
	HETATM	7593	O2G	ACP A	1001	28.605	55.314	184.541	1.00 93.20	O
	HETATM	7594	O3G	ACP A	1001	26.208	55.252	184.951	1.00258.96	O
	HETATM	7595	PB	ACP A	1001	26.745	57.965	186.757	1.00116.64	P
	HETATM	7596	O1B	ACP A	1001	25.237	57.666	187.109	1.00178.37	O
10	HETATM	7597	O2B	ACP A	1001	26.885	58.919	185.633	1.00103.22	O
	HETATM	7598	C3B	ACP A	1001	27.659	56.571	186.674	1.00 40.16	C
	HETATM	7599	O3A	ACP A	1001	27.296	58.568	188.106	0.25182.50	O
	TER									
	ATOM	7600	O	MET B	1	13.003	21.802	175.465	1.00187.25	O
15	ATOM	7601	N	MET B	1	13.367	24.334	176.520	1.00186.63	N
	ATOM	7602	CA	MET B	1	12.070	23.951	175.978	1.00187.82	C
	ATOM	7603	C	MET B	1	11.997	22.434	175.791	1.00187.34	C
	ATOM	7604	CB	MET B	1	11.824	24.665	174.643	1.00184.83	C
	ATOM	7605	CG	MET B	1	11.929	26.189	174.709	1.00189.60	C
20	ATOM	7606	SD	MET B	1	11.524	27.002	173.146	1.00176.44	S
	ATOM	7607	CE	MET B	1	11.675	28.737	173.570	1.00139.24	C
	ATOM	7608	O	GLU B	2	9.954	19.116	173.816	1.00170.34	O
	ATOM	7609	N	GLU B	2	10.814	21.851	175.996	1.00185.35	N
	ATOM	7610	CA	GLU B	2	10.609	20.422	175.735	1.00178.25	C
25	ATOM	7611	C	GLU B	2	10.381	20.191	174.241	1.00173.66	C
	ATOM	7612	CB	GLU B	2	9.436	19.855	176.550	1.00177.20	C
	ATOM	7613	CG	GLU B	2	9.440	18.321	176.670	1.00172.69	C
	ATOM	7614	CD	GLU B	2	8.136	17.744	177.208	1.00174.60	C
	ATOM	7615	OE1	GLU B	2	7.341	18.499	177.812	1.00181.72	O
30	ATOM	7616	OE2	GLU B	2	7.910	16.527	177.024	1.00166.71	O
	ATOM	7617	O	ARG B	3	11.711	19.759	170.376	1.00144.11	O
	ATOM	7618	N	ARG B	3	10.673	21.216	173.447	1.00171.86	N
	ATOM	7619	CA	ARG B	3	10.594	21.118	172.000	1.00164.29	C
	ATOM	7620	C	ARG B	3	11.724	20.231	171.509	1.00149.73	C
35	ATOM	7621	CB	ARG B	3	10.694	22.509	171.365	1.00174.10	C
	ATOM	7622	CG	ARG B	3	9.591	23.471	171.805	1.00188.62	C
	ATOM	7623	CD	ARG B	3	9.699	24.827	171.114	1.00196.45	C
	ATOM	7624	NE	ARG B	3	8.665	25.757	171.567	1.00204.68	N
	ATOM	7625	CZ	ARG B	3	8.577	27.025	171.174	1.00208.92	C
40	ATOM	7626	NH1	ARG B	3	9.466	27.516	170.320	1.00207.97	N

	ATOM	7627	NH2 ARG B	3	7.605	27.802	171.635	1.00213.54	N
	ATOM	7628	O SER B	4	14.125	16.997	171.215	1.00124.46	O
	ATOM	7629	N SER B	4	12.696	20.001	172.386	1.00146.22	N
	ATOM	7630	CA SER B	4	13.890	19.231	172.058	1.00140.60	C
5	ATOM	7631	C SER B	4	13.598	17.740	172.040	1.00131.66	C
	ATOM	7632	CB SER B	4	14.978	19.506	173.091	1.00144.57	C
	ATOM	7633	OG SER B	4	14.718	18.793	174.286	1.00147.18	O
	ATOM	7634	O THR B	5	11.352	14.381	171.541	1.00124.18	O
	ATOM	7635	N THR B	5	12.762	17.307	172.973	1.00133.65	N
10	ATOM	7636	CA THR B	5	12.399	15.903	173.079	1.00131.63	C
	ATOM	7637	C THR B	5	11.399	15.527	171.992	1.00127.99	C
	ATOM	7638	CB THR B	5	11.806	15.598	174.460	1.00133.49	C
	ATOM	7639	OG1 THR B	5	12.713	16.052	175.474	1.00139.17	O
	ATOM	7640	CG2 THR B	5	11.566	14.104	174.623	1.00129.27	C
15	ATOM	7641	O ARG B	6	10.138	15.291	168.333	1.00106.04	O
	ATOM	7642	N ARG B	6	10.599	16.502	171.571	1.00129.19	N
	ATOM	7643	CA ARG B	6	9.679	16.295	170.462	1.00124.49	C
	ATOM	7644	C ARG B	6	10.479	16.119	169.177	1.00115.93	C
	ATOM	7645	CB ARG B	6	8.691	17.463	170.341	1.00131.05	C
20	ATOM	7646	CG ARG B	6	7.897	17.475	169.044	1.00136.24	C
	ATOM	7647	CD ARG B	6	6.853	18.581	169.017	1.00148.29	C
	ATOM	7648	NE ARG B	6	6.399	18.880	167.656	1.00158.44	N
	ATOM	7649	CZ ARG B	6	5.509	18.159	166.972	1.00163.27	C
	ATOM	7650	NH1 ARG B	6	4.966	17.070	167.507	1.00165.98	N
25	ATOM	7651	NH2 ARG B	6	5.166	18.525	165.742	1.00161.06	N
	ATOM	7652	O GLU B	7	12.949	14.913	166.521	1.00115.63	O
	ATOM	7653	N GLU B	7	11.557	16.887	169.047	1.00122.19	N
	ATOM	7654	CA GLU B	7	12.403	16.831	167.857	1.00126.02	C
	ATOM	7655	C GLU B	7	12.983	15.440	167.635	1.00121.86	C
30	ATOM	7656	CB GLU B	7	13.539	17.846	167.947	1.00135.52	C
	ATOM	7657	CG GLU B	7	14.539	17.725	166.812	1.00141.22	C
	ATOM	7658	CD GLU B	7	15.612	18.785	166.866	1.00149.14	C
	ATOM	7659	OE1 GLU B	7	15.668	19.520	167.879	1.00153.98	O
	ATOM	7660	OE2 GLU B	7	16.395	18.883	165.894	1.00149.50	O
35	ATOM	7661	N LEU B	8	13.510	14.852	168.703	1.00122.85	N
	ATOM	7662	CA LEU B	8	14.067	13.506	168.636	1.00121.79	C
	ATOM	7663	C LEU B	8	12.983	12.444	168.383	1.00126.32	C
	ATOM	7664	O LEU B	8	13.171	11.536	167.574	1.00122.47	O
	ATOM	7665	CB LEU B	8	14.875	13.198	169.902	1.00116.94	C
40	ATOM	7666	CG LEU B	8	15.794	11.977	169.864	1.00118.99	C

	ATOM	7667	CD1 LEU B	8	17.060	12.221	170.675	1.00106.25	C
	ATOM	7668	CD2 LEU B	8	15.059	10.744	170.378	1.00122.82	C
	ATOM	7669	N CYS B	9	11.849	12.560	169.067	1.00132.83	N
	ATOM	7670	CA CYS B	9	10.745	11.625	168.860	1.00135.42	C
5	ATOM	7671	C CYS B	9	10.239	11.634	167.413	1.00137.78	C
	ATOM	7672	O CYS B	9	9.956	10.577	166.846	1.00141.61	O
	ATOM	7673	CB CYS B	9	9.594	11.911	169.830	1.00135.64	C
	ATOM	7674	SG CYS B	9	8.129	10.876	169.564	1.00120.46	S
	ATOM	7675	N LEU B	10	10.131	12.822	166.819	1.00135.95	N
10	ATOM	7676	CA LEU B	10	9.674	12.944	165.434	1.00134.86	C
	ATOM	7677	C LEU B	10	10.690	12.386	164.443	1.00134.25	C
	ATOM	7678	O LEU B	10	10.327	11.940	163.354	1.00129.95	O
	ATOM	7679	CB LEU B	10	9.357	14.396	165.079	1.00134.78	C
	ATOM	7680	CG LEU B	10	8.074	14.991	165.653	1.00136.26	C
15	ATOM	7681	CD1 LEU B	10	7.804	16.355	165.030	1.00134.81	C
	ATOM	7682	CD2 LEU B	10	6.899	14.044	165.446	1.00134.94	C
	ATOM	7683	N ASN B	11	11.966	12.426	164.815	1.00136.04	N
	ATOM	7684	CA ASN B	11	13.003	11.812	163.996	1.00132.61	C
	ATOM	7685	C ASN B	11	12.853	10.295	164.006	1.00132.02	C
20	ATOM	7686	O ASN B	11	12.916	9.652	162.963	1.00131.17	O
	ATOM	7687	CB ASN B	11	14.403	12.227	164.465	1.00128.62	C
	ATOM	7688	CG ASN B	11	14.827	13.588	163.928	1.00122.26	C
	ATOM	7689	OD1 ASN B	11	14.032	14.315	163.326	1.00116.81	O
	ATOM	7690	ND2 ASN B	11	16.087	13.939	164.150	1.00122.99	N
25	ATOM	7691	N PHE B	12	12.636	9.731	165.191	1.00133.86	N
	ATOM	7692	CA PHE B	12	12.426	8.295	165.332	1.00136.04	C
	ATOM	7693	C PHE B	12	11.187	7.808	164.579	1.00133.50	C
	ATOM	7694	O PHE B	12	11.150	6.672	164.102	1.00136.15	O
	ATOM	7695	CB PHE B	12	12.324	7.908	166.811	1.00139.82	C
30	ATOM	7696	CG PHE B	12	11.673	6.573	167.043	1.00139.53	C
	ATOM	7697	CD1 PHE B	12	12.415	5.406	166.974	1.00142.15	C
	ATOM	7698	CD2 PHE B	12	10.317	6.488	167.320	1.00135.92	C
	ATOM	7699	CE1 PHE B	12	11.820	4.182	167.178	1.00144.77	C
	ATOM	7700	CE2 PHE B	12	9.717	5.268	167.521	1.00138.69	C
35	ATOM	7701	CZ PHE B	12	10.468	4.113	167.451	1.00144.35	C
	ATOM	7702	N THR B	13	10.170	8.661	164.487	1.00128.49	N
	ATOM	7703	CA THR B	13	8.928	8.298	163.805	1.00127.17	C
	ATOM	7704	C THR B	13	9.139	8.051	162.311	1.00127.17	C
	ATOM	7705	O THR B	13	8.662	7.055	161.759	1.00123.39	O
40	ATOM	7706	CB THR B	13	7.849	9.384	163.978	1.00121.33	C

	ATOM	7707	OG1 THR B	13	7.619	9.617	165.374	1.00120.65	O
	ATOM	7708	CG2 THR B	13	6.545	8.958	163.302	1.00116.59	C
	ATOM	7709	N VAL B	14	9.859	8.969	161.671	1.00128.54	N
	ATOM	7710	CA VAL B	14	10.137	8.910	160.237	1.00130.24	C
5	ATOM	7711	C VAL B	14	10.852	7.625	159.805	1.00140.68	C
	ATOM	7712	O VAL B	14	10.432	6.965	158.851	1.00143.99	O
	ATOM	7713	CB VAL B	14	10.947	10.143	159.789	1.00123.31	C
	ATOM	7714	CG1 VAL B	14	11.627	9.902	158.440	1.00123.34	C
	ATOM	7715	CG2 VAL B	14	10.047	11.364	159.744	1.00119.05	C
10	ATOM	7716	N VAL B	15	11.919	7.269	160.516	1.00143.36	N
	ATOM	7717	CA VAL B	15	12.689	6.070	160.198	1.00148.71	C
	ATOM	7718	C VAL B	15	11.958	4.803	160.630	1.00155.09	C
	ATOM	7719	O VAL B	15	12.368	3.695	160.285	1.00158.72	O
	ATOM	7720	CB VAL B	15	14.068	6.093	160.859	1.00153.16	C
15	ATOM	7721	CG1 VAL B	15	14.794	7.373	160.501	1.00152.26	C
	ATOM	7722	CG2 VAL B	15	13.921	5.979	162.356	1.00155.76	C
	ATOM	7723	N LEU B	16	10.885	4.972	161.399	1.00157.63	N
	ATOM	7724	CA LEU B	16	9.975	3.871	161.698	1.00157.91	C
	ATOM	7725	C LEU B	16	8.957	3.727	160.570	1.00151.19	C
20	ATOM	7726	O LEU B	16	8.728	2.625	160.072	1.00154.18	O
	ATOM	7727	CB LEU B	16	9.251	4.091	163.029	1.00157.44	C
	ATOM	7728	CG LEU B	16	8.202	3.022	163.348	1.00158.05	C
	ATOM	7729	CD1 LEU B	16	8.862	1.658	163.529	1.00162.27	C
	ATOM	7730	CD2 LEU B	16	7.382	3.400	164.571	1.00156.14	C
25	ATOM	7731	N ILE B	17	8.357	4.846	160.168	1.00141.65	N
	ATOM	7732	CA ILE B	17	7.413	4.855	159.057	1.00141.63	C
	ATOM	7733	C ILE B	17	8.101	4.421	157.762	1.00146.27	C
	ATOM	7734	O ILE B	17	7.475	3.831	156.883	1.00149.61	O
	ATOM	7735	CB ILE B	17	6.759	6.240	158.878	1.00140.13	C
30	ATOM	7736	CG1 ILE B	17	5.966	6.625	160.129	1.00144.25	C
	ATOM	7737	CG2 ILE B	17	5.838	6.251	157.673	1.00138.13	C
	ATOM	7738	CD1 ILE B	17	4.831	5.672	160.457	1.00148.44	C
	ATOM	7739	N THR B	18	9.398	4.702	157.660	1.00147.36	N
	ATOM	7740	CA THR B	18	10.210	4.252	156.526	1.00147.15	C
35	ATOM	7741	C THR B	18	10.358	2.731	156.507	1.00155.17	C
	ATOM	7742	O THR B	18	10.140	2.085	155.477	1.00161.68	O
	ATOM	7743	CB THR B	18	11.610	4.898	156.541	1.00137.15	C
	ATOM	7744	OG1 THR B	18	11.490	6.287	156.224	1.00135.57	O
	ATOM	7745	CG2 THR B	18	12.517	4.241	155.522	1.00134.14	C
40	ATOM	7746	N VAL B	19	10.731	2.167	157.650	1.00153.05	N

	ATOM	7747	CA	VAL B	19	10.842	0.720	157.796	1.00154.56	C
	ATOM	7748	C	VAL B	19	9.485	0.038	157.559	1.00158.74	C
	ATOM	7749	O	VAL B	19	9.416	-1.034	156.953	1.00164.41	O
	ATOM	7750	CB	VAL B	19	11.442	0.352	159.176	1.00148.35	C
5	ATOM	7751	CG1	VAL B	19	11.338	-1.130	159.443	1.00150.47	C
	ATOM	7752	CG2	VAL B	19	12.888	0.789	159.247	1.00145.97	C
	ATOM	7753	N	ILE B	20	8.412	0.679	158.018	1.00155.95	N
	ATOM	7754	CA	ILE B	20	7.049	0.197	157.780	1.00159.52	C
	ATOM	7755	C	ILE B	20	6.747	-0.002	156.287	1.00162.99	C
10	ATOM	7756	O	ILE B	20	6.286	-1.073	155.888	1.00170.84	O
	ATOM	7757	CB	ILE B	20	5.984	1.147	158.416	1.00120.09	C
	ATOM	7758	CG1	ILE B	20	5.847	0.884	159.920	1.00119.31	C
	ATOM	7759	CG2	ILE B	20	4.622	1.003	157.723	1.00118.95	C
	ATOM	7760	CD1	ILE B	20	4.943	1.883	160.646	1.00106.30	C
15	ATOM	7761	N	LEU B	21	7.019	1.018	155.471	1.00154.54	N
	ATOM	7762	CA	LEU B	21	6.694	0.984	154.042	1.00148.69	C
	ATOM	7763	C	LEU B	21	7.358	-0.186	153.321	1.00156.47	C
	ATOM	7764	O	LEU B	21	6.804	-0.747	152.372	1.00160.27	O
	ATOM	7765	CB	LEU B	21	7.085	2.297	153.362	1.00140.24	C
20	ATOM	7766	CG	LEU B	21	6.430	3.573	153.890	1.00135.41	C
	ATOM	7767	CD1	LEU B	21	6.833	4.779	153.051	1.00131.00	C
	ATOM	7768	CD2	LEU B	21	4.917	3.425	153.944	1.00137.13	C
	ATOM	7769	N	ILE B	22	8.548	-0.551	153.782	1.00158.48	N
	ATOM	7770	CA	ILE B	22	9.293	-1.648	153.184	1.00164.75	C
25	ATOM	7771	C	ILE B	22	8.655	-3.001	153.529	1.00179.13	C
	ATOM	7772	O	ILE B	22	8.686	-3.940	152.733	1.00186.99	O
	ATOM	7773	CB	ILE B	22	10.777	-1.570	153.587	1.00155.70	C
	ATOM	7774	CG1	ILE B	22	11.363	-0.246	153.084	1.00144.09	C
	ATOM	7775	CG2	ILE B	22	11.550	-2.746	153.036	1.00162.84	C
30	ATOM	7776	CD1	ILE B	22	12.826	-0.058	153.367	1.00139.35	C
	ATOM	7777	N	TRP B	23	8.055	-3.082	154.712	1.00182.93	N
	ATOM	7778	CA	TRP B	23	7.236	-4.230	155.087	1.00191.23	C
	ATOM	7779	C	TRP B	23	6.001	-4.257	154.190	1.00188.03	C
	ATOM	7780	O	TRP B	23	5.491	-5.326	153.843	1.00190.19	O
35	ATOM	7781	CB	TRP B	23	6.841	-4.116	156.566	1.00196.48	C
	ATOM	7782	CG	TRP B	23	5.960	-5.216	157.112	1.00204.42	C
	ATOM	7783	CD1	TRP B	23	5.785	-6.469	156.600	1.00209.23	C
	ATOM	7784	CD2	TRP B	23	5.133	-5.143	158.284	1.00204.90	C
	ATOM	7785	NE1	TRP B	23	4.904	-7.181	157.380	1.00211.11	N
40	ATOM	7786	CE2	TRP B	23	4.488	-6.390	158.419	1.00208.70	C

	ATOM	7787	CE3 TRP B	23	4.876	-4.143	159.231	1.00199.32	C
	ATOM	7788	CZ2 TRP B	23	3.603	-6.663	159.463	1.00209.29	C
	ATOM	7789	CZ3 TRP B	23	3.995	-4.417	160.267	1.00198.82	C
	ATOM	7790	CH2 TRP B	23	3.370	-5.666	160.374	1.00204.00	C
5	ATOM	7791	O LEU B	24	3.822	-3.447	150.670	1.00196.61	O
	ATOM	7792	N LEU B	24	5.542	-3.066	153.804	1.00182.10	N
	ATOM	7793	CA LEU B	24	4.373	-2.915	152.942	1.00181.57	C
	ATOM	7794	C LEU B	24	4.703	-3.126	151.466	1.00188.01	C
	ATOM	7795	CB LEU B	24	3.732	-1.538	153.129	1.00174.76	C
10	ATOM	7796	CG LEU B	24	3.070	-1.231	154.475	1.00174.17	C
	ATOM	7797	CD1 LEU B	24	2.593	0.217	154.534	1.00171.05	C
	ATOM	7798	CD2 LEU B	24	1.914	-2.180	154.735	1.00177.47	C
	ATOM	7799	O LEU B	25	6.480	-5.017	148.238	1.00191.09	O
	ATOM	7800	N LEU B	25	5.968	-2.946	151.099	1.00183.76	N
15	ATOM	7801	CA LEU B	25	6.373	-3.114	149.704	1.00181.04	C
	ATOM	7802	C LEU B	25	6.698	-4.573	149.365	1.00186.36	C
	ATOM	7803	CB LEU B	25	7.552	-2.192	149.363	1.00171.04	C
	ATOM	7804	CG LEU B	25	8.027	-2.140	147.906	1.00165.78	C
	ATOM	7805	CD2 LEU B	25	9.092	-1.069	147.734	1.00159.53	C
20	ATOM	7806	CD1 LEU B	25	6.867	-1.898	146.950	1.00162.10	C
	ATOM	7807	O VAL B	26	6.309	-8.477	149.152	1.00213.43	O
	ATOM	7808	N VAL B	26	7.207	-5.315	150.345	1.00186.72	N
	ATOM	7809	CA VAL B	26	7.602	-6.705	150.128	1.00196.17	C
	ATOM	7810	C VAL B	26	6.402	-7.639	150.053	1.00206.18	C
25	ATOM	7811	CB VAL B	26	8.540	-7.202	151.233	1.00193.22	C
	ATOM	7812	CG2 VAL B	26	9.813	-6.404	151.218	1.00188.82	C
	ATOM	7813	CG1 VAL B	26	8.834	-8.685	151.054	1.00201.21	C
	ATOM	7814	O ARG B	27	2.763	-8.801	149.194	1.00213.48	O
	ATOM	7815	N ARG B	27	5.493	-7.495	151.011	1.00206.05	N
30	ATOM	7816	CA ARG B	27	4.249	-8.254	151.012	1.00211.09	C
	ATOM	7817	C ARG B	27	3.454	-7.938	149.743	1.00209.43	C
	ATOM	7818	CB ARG B	27	3.428	-7.928	152.266	1.00210.12	C
	ATOM	7819	CG ARG B	27	2.192	-8.802	152.454	1.00217.08	C
	ATOM	7820	CD ARG B	27	1.451	-8.472	153.748	1.00214.82	C
35	ATOM	7821	NE ARG B	27	0.905	-7.116	153.757	1.00208.13	N
	ATOM	7822	CZ ARG B	27	-0.311	-6.793	153.323	1.00207.17	C
	ATOM	7823	NH1 ARG B	27	-1.117	-7.729	152.836	1.00212.99	N
	ATOM	7824	NH2 ARG B	27	-0.722	-5.532	153.375	1.00200.41	N
	ATOM	7825	O SER B	28	2.752	-7.465	145.967	1.00200.70	O
40	ATOM	7826	N SER B	28	3.571	-6.695	149.278	1.00201.55	N

	ATOM	7827	CA	SER	B	28	2.933	-6.259	148.039	1.00196.75	C	
	ATOM	7828	C	SER	B	28	3.501	-6.997	146.826	1.00199.17	C	
	ATOM	7829	CB	SER	B	28	3.096	-4.747	147.861	1.00187.03	C	
	ATOM	7830	OG	SER	B	28	2.464	-4.294	146.678	1.00187.52	O	
5	ATOM	7831	O	TYR	B	29	5.175	-10.015	144.767	1.00225.46	O	
	ATOM	7832	N	TYR	B	29	4.825	-7.098	146.761	1.00198.99	N	
	ATOM	7833	CA	TYR	B	29	5.476	-7.812	145.671	1.00206.58	C	
	ATOM	7834	C	TYR	B	29	5.269	-9.322	145.780	1.00216.54	C	
	ATOM	7835	CB	TYR	B	29	6.973	-7.495	145.609	1.00207.65	C	
10	ATOM	7836	CG	TYR	B	29	7.701	-8.382	144.626	1.00219.85	C	
	ATOM	7837	CD1	TYR	B	29	7.667	-8.111	143.266	1.00225.45	C	
	ATOM	7838	CD2	TYR	B	29	8.394	-9.511	145.053	1.00226.75	C	
	ATOM	7839	CE1	TYR	B	29	8.316	-8.931	142.354	1.00235.09	C	
	ATOM	7840	CE2	TYR	B	29	9.042	-10.338	144.148	1.00236.59	C	
15	ATOM	7841	CZ	TYR	B	29	9.000	-10.042	142.800	1.00239.13	C	
	ATOM	7842	OH	TYR	B	29	9.646	-10.851	141.893	1.00246.46	O	
	ATOM	7843	O	GLN	B	30	3.387	-12.781	146.284	1.00238.93	O	
	ATOM	7844	N	GLN	B	30	5.212	-9.835	147.005	1.00216.77	N	
	ATOM	7845	CA	GLN	B	30	5.004	-11.267	147.216	1.00226.27	C	
20	ATOM	7846	C	GLN	B	30	3.586	-11.694	146.831	1.00230.52	C	
	ATOM	7847	CB	GLN	B	30	5.309	-11.657	148.666	1.00223.69	C	
	ATOM	7848	CG	GLN	B	30	6.790	-11.660	149.012	1.00223.22	C	
	ATOM	7849	CD	GLN	B	30	7.042	-11.758	150.506	1.00219.91	C	
	ATOM	7850	OE1	GLN	B	30	6.155	-11.489	151.315	1.00217.88	O	
25	ATOM	7851	NE2	GLN	B	30	8.255	-12.145	150.877	1.00220.14	N	
	ATOM	7852	O	TYR	B	31	-0.516	-9.703	145.824	1.00219.37	O	
	ATOM	7853	N	TYR	B	31	2.611	-10.832	147.115	1.00222.74	N	
	ATOM	7854	CA	TYR	B	31	1.213	-11.086	146.761	1.00220.22	C	
	ATOM	7855	C	TYR	B	31	0.411	-9.792	146.633	1.00216.36	C	
30	ATOM	7856	CB	TYR	B	31	0.554	-12.018	147.781	1.00213.12	C	
	ATOM	7857	CG	TYR	B	31	0.723	-13.483	147.459	1.00214.51	C	
	ATOM	7858	CD2	TYR	B	31	1.132	-14.386	148.431	1.00214.22	C	
	ATOM	7859	CD1	TYR	B	31	0.488	-13.963	146.178	1.00217.32	C	
	ATOM	7860	CE2	TYR	B	31	1.292	-15.726	148.139	1.00220.69	C	
35	ATOM	7861	CE1	TYR	B	31	0.646	-15.302	145.876	1.00224.26	C	
	ATOM	7862	CZ	TYR	B	31	1.048	-16.178	146.860	1.00225.18	C	
	ATOM	7863	OH	TYR	B	31	1.206	-17.512	146.567	1.00233.44	O	
	TER											
	HETATM	7864	K	K	C	1	31.885	45.788	168.344	1.00	78.99	K+1
40	TER											

	HETATM 7865	O	HOH E	1	32.856	43.462	166.218	1.00	64.80	O
	HETATM 7866	O	HOH E	5	24.169	55.654	181.754	1.00	79.61	O
	TER									
	HETATM 7867	MG	MG G	1	25.053	54.107	183.246	1.00	70.63	MG2+
5	TER									
	HETATM 7868	MG	MG D	1	25.651	11.539	153.998	1.00	124.67	MG2+
	TER									
	HETATM 7869	MG	MG F	1	26.860	10.272	159.152	1.00	114.08	MG2+
	TER									
10	END									

CLAIMS

1. Use of a three-dimensional structural representation of at least part of the SERCA Ca^{2+} ATPase/SLN complex as defined by the coordinates listed in Table (i), optionally
5 varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof, in a method for selecting or designing one or more binding partners of a Ca^{2+} ATPase and/or SLN.
2. A method for identifying or selecting or designing one or more binding partners of
10 a Ca^{2+} ATPase and/or SLN, the method comprising using molecular modelling means to select or design one or more binding partners of a Ca^{2+} ATPase and/or SLN, wherein the three-dimensional structural representation of at least part of the SERCA Ca^{2+} ATPase/SLN complex as listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof, is
15 compared with a three-dimensional structural representation of one or more candidate binding partners, and one or more binding partners that are predicted to interact with the Ca^{2+} ATPase and/or SLN are identified or selected or designed.
3. A use according to Claim 1 or a method according to Claim 2 wherein the one or
20 more binding partners are one or more binding partners of a Ca^{2+} ATPase, or one or more binding partners of SLN, or one or more binding partners of both a Ca^{2+} ATPase and SLN.
4. A use according to Claim 1 or 3, or a method according to Claim 2 or 3, wherein
25 the one or more binding partners are modulators of Ca^{2+} ATPase activity and/or SLN activity.
5. A use according to any of Claims 1, 3 and 4, or a method according to any of Claims 2-4, wherein the one or more binding partners are modulators of the SERCA Ca^{2+}
30 ATPase/SLN interaction.
6. A use according to any of Claims 1 and 3-5, or a method according to any of Claims 2-5, wherein one or more binding partners are any of a polypeptide, an antibody, a small molecule, a natural product, a peptidomimetic, or a nucleic acid.

7. A use according to any of Claims 1 and 3-6, or a method according to any of Claims 2-6, wherein the binding partner is small molecule with a molecule weight less than 500 daltons.
- 5 8. A use according to any of Claims 1 and 3-7, or a method according to any of Claims 2-7, wherein the three-dimensional structure of at least part of the SERCA Ca^{2+} ATPase/SLN complex is a three dimensional structure of the SERCA Ca^{2+} ATPase/SLN interaction site, or part thereof.
- 10 9. A use according to any of Claims 1 and 3-8, or a method according to any of Claims 2-8, wherein the one or more binding partners are predicted to bind to at least one amino acid within the SERCA Ca^{2+} ATPase/SLN interaction site.
10. A method according to any of Claims 2-9, comprising:
- 15 providing a three-dimensional structural representation of at least part of the SERCA Ca^{2+} ATPase/SLN complex as listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof;
- providing a three-dimensional structural representation of one or more candidate
- 20 binding partners,
- selecting or designing of one or more binding partners that are structurally complementary to the three-dimensional structural representation of at least part of the SERCA Ca^{2+} ATPase/SLN complex.
- 25 11. A method for identifying or selecting or designing one or more binding partners of a Ca^{2+} ATPase having a binding pocket in the position structurally equivalent to the binding pocket of rabbit SERCA Ca^{2+} ATPase that is defined by residues including Phe88, Phe92, Val93, Leu96, Ile97, Ala100, Ile103, Val104, Trp107, Gln108, Asn111, Tyr122, Arg324, Lys328, Trp794, Leu797, Asp800, Gly801, Leu802, Thr805, Ala806,
- 30 Phe809, Trp932, Ser936, Leu939, Ser942, Leu943, Leu946, Ile947, Pro952, Leu953, Ile956, and Phe957 of rabbit SERCA Ca^{2+} ATPase, the method comprising the step of using molecular modelling means to select or design one or more binding partners that are predicted to interact with the said Ca^{2+} ATPase, wherein a three-dimensional structural representation of one or more candidate binding partners are compared with a
- 35 three-dimensional structural representation of the said binding pocket, and one or more candidate binding partners that are predicted to interact with the said binding pocket, are identified or selected or designed.

12. A method for identifying or selecting or designing one or more binding partners of a SLN having a binding pocket in the position structurally equivalent to the binding pocket of rabbit SLN that is defined by residues including Met1, Glu2, Arg3, Ser4, Thr5, Arg6, Glu7, Leu8, Cys9, Leu10, and Asn11 of rabbit SLN, the method comprising the step of using molecular modelling means to select or design one or more binding partners that are predicted to interact with the said SLN, wherein a three-dimensional structural representation of one or more candidate binding partners are compared with a three-dimensional structural representation of the said binding pocket, and one or more candidate binding partners that are predicted to interact with the said binding pocket, are identified or selected or designed.

13. A method according to Claim 11 or 12, wherein the three-dimensional structural representation is that defined by the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof.

14. A method according to any of Claims 11-13 wherein the one or more binding partners are as defined in any of Claims 3-7.

15. A method for the analysis of the interaction of one or more binding partners with a Ca^{2+} ATPase and/or SLN, comprising:

providing a three dimensional structural representation of the SERCA Ca^{2+} ATPase/SLN complex as defined by the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof;

providing a three dimensional structural representation of one or more binding partners to be fitted to the structural representation of the SERCA Ca^{2+} ATPase/SLN complex or selected coordinates thereof; and

fitting the one of more binding partners to said structural representation.

16. A method according to any of Claims 2-15, wherein the three-dimensional structural representation of the one or more candidate binding partners is obtained by:

providing structural representations of a plurality of molecular fragments;
fitting the structural representation of each of the molecular fragments to the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied

by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof; and

assembling the representations of the molecular fragments into one or more representations of single molecules to provide the three-dimensional structural representation of one or more candidate binding partners.

17. A method according to any of Claims 2-16 further comprising modifying the structural representation of the one or more binding partners so as to increase or decrease their interaction with Ca²⁺ ATPase and/or SLN.

18. A method according to any of Claims 15-17, wherein the binding partner or molecular fragment is fitted to at least 10 atoms.

19. A use according to any of Claims 1 and 3-9, or a method according to any of Claims 2-10 and 13-18 wherein the selected coordinates are of at least 500 atoms.

20. A method according to any of Claims 2-19, further comprising the steps of:
obtaining or synthesising the one or more binding partners; and
contacting the one or more binding partners with a Ca²⁺ ATPase and/or SLN to determine the ability of the one or more binding partners to interact with a Ca²⁺ ATPase and/or SLN.

21. A method according to Claim 20 wherein it is determined if the one or more binding partners are modulators of the SERCA Ca²⁺ ATPase/SLN interaction

22. A method according to any of Claims 2-21, further comprising the steps of:
obtaining or synthesising the one or more binding partners;
forming one or more complexes of a binding partner with a Ca²⁺ ATPase and/or SLN; and

analysing the one or more complexes by X-ray crystallography to determine the ability of the one or more binding partners to interact with a Ca²⁺ ATPase and/or SLN.

23. A method for the analysis of the interaction of one or more binding partners with a Ca²⁺ ATPase and/or SLN, comprising:

obtaining or synthesising one or more binding partners;
forming one or more crystallised complexes of a binding partner with a Ca²⁺ ATPase and/or SLN; and

analysing the one or more complexes by X-ray crystallography by employing the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof, to determine the ability of the one or more binding partners to
5 interact with the a Ca^{2+} ATPase and/or SLN.

24. A method according to Claim 23, wherein the one or more crystallised complexes are formed by either (a) providing a crystal of a Ca^{2+} ATPase and/or SLN and soaking the crystal with the binding partner to form a complex; or (b) mixing a Ca^{2+} ATPase
10 and/or SLN with the binding partner and crystallising a complex of the binding partner with the Ca^{2+} ATPase and/or SLN.

25. A method for producing a binding partner of a Ca^{2+} ATPase and/or SLN comprising:
15 identifying a binding partner according to the methods of any of Claims 2-24, and synthesising the binding partner.

26. A binding partner produced by the method of Claim 25.

20 27. A use according to any of Claims 1, 3-9 and 19, or a method according to any of Claims 2-10 and 13-25, wherein the Ca^{2+} ATPase is SERCA Ca^{2+} ATPase.

28. A method of predicting the three dimensional structure of a binding partner of unknown structure, or part thereof, which binds to a Ca^{2+} ATPase and/or SLN,
25 comprising:

providing the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof;

providing an X-ray diffraction pattern of a Ca^{2+} ATPase and/or SLN complexed
30 with the binding partner; and

using said coordinates to predict at least part of the structure coordinates of the binding partner.

29. A method according to Claim 28, wherein the X-ray diffraction pattern is obtained
35 from a crystal formed either by (a) soaking a crystal of a Ca^{2+} ATPase and/or SLN with the binding partner to form a complex, or (b) mixing a Ca^{2+} ATPase and/or SLN with the

binding partner and crystallising a complex of the binding partner with the Ca^{2+} ATPase and/or SLN.

5 30. A method according to any of Claims 2-25 and 27-29, wherein the method is computer-based.

10 31. A method for producing a medicament, pharmaceutical composition or drug, the process comprising: (a) providing a binding partner according to Claim 26 and (b) preparing a medicament, pharmaceutical composition or drug containing the binding partner.

32. A method of predicting a three dimensional structural representation of a target protein of unknown structure, or part thereof, comprising:
providing the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in
15 Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof; and
predicting the three-dimensional structural representation of the target protein, or part thereof, by modelling the structural representation on all or the selected coordinates.

20 33. A method according to Claim 32, further comprising aligning the amino acid sequence of the target protein of unknown structure with the amino acid sequence of SERCA Ca^{2+} ATPase or SLN as listed in Figure 8, to match homologous regions of the amino acid sequences prior to predicting the structural representation, and wherein modelling the structural representation comprises modelling the structural representation
25 of the matched homologous regions of the target protein on the corresponding regions of the SERCA Ca^{2+} ATPase or SLN to obtain a three dimensional structural representation for the target protein that substantially preserves the structural representation of the matched homologous regions.

30 34. A method of predicting the three dimensional structural representation of a target protein of unknown structure, or part thereof, comprising:
providing the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof; and either (a) positioning the coordinates in
35 the crystal unit cell of the protein so as to predict its structural representation, or (b) assigning NMR spectra peaks of the protein by manipulating the coordinates.

35. A method of predicting a three dimensional structural representation of a target protein of unknown structure, or part thereof, comprising:

providing the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof;

providing an X-ray diffraction pattern of the target protein; and

using the coordinates to predict at least part of the structure coordinates of the target protein.

36. A method according to any of Claims 32-35, wherein the target protein has at least 20% sequence identity to SERCA Ca^{2+} ATPase or SLN as listed in Figure 8.

37. A method according to any of Claims 32-36, wherein the target protein is an ATPase.

38. A method of providing data for generating three dimensional structural representations of SERCA Ca^{2+} ATPase and/or SLN, homologues or analogues of SERCA Ca^{2+} ATPase and/or SLN, or complexes of a binding partner with SERCA Ca^{2+} ATPase and/or SLN, or complexes of a binding partner with SERCA Ca^{2+} ATPase and/or SLN homologues or analogues, or for optimising binding of binding partners to said SERCA Ca^{2+} ATPase and/or SLN, or to homologues or analogues or complexes thereof, the method comprising:

(i) establishing communication with a remote device containing computer-readable data comprising at least one of:

(a) the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof;

(b) the coordinates of a target SERCA Ca^{2+} ATPase and/or SLN homologue or analogue generated by homology modelling of the target based on the data in (a);

(c) the coordinates of a binding partner generated by interpreting X-ray crystallographic data or NMR data by reference to the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof, and

(d) structure factor data derivable from the coordinates of (a), (b) or (c); and

(ii) receiving said computer-readable data from said remote device.

39. A method of obtaining a three dimensional structural representation of a crystal of a complex of SERCA Ca^{2+} ATPase and SLN, which method comprises providing the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied
5 by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof, and generating a three-dimensional structural representation of said coordinates.

40. A method according to Claim 39, wherein the three-dimensional structural
10 representation is a computer generated representation or a physical representation.

41. A method according to Claim 39 or 40, wherein the computer used to generate the representation comprises:

(i) a computer-readable data storage medium comprising a data storage material
15 encoded with computer-readable data, wherein said data comprise the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof; and

(ii) instructions for processing the computer-readable data into a three-
20 dimensional structural representation.

42. A method according to any of Claims 38-41, wherein the representation is any of a wire-frame model, a chicken-wire model, a ball-and-stick model, a space-filling model, a stick model, a ribbon model, a snake model, an arrow and cylinder model, an electron
25 density map or a molecular surface model.

43. A method of predicting one or more sites of interaction of SERCA Ca^{2+} ATPase and/or SLN, or homologues thereof, the method comprising:
providing the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in
30 Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof; and
analysing said coordinates to predict one or more sites of interaction.

44. A method of predicting the location of internal and/or external parts of the
35 structure of SERCA Ca^{2+} ATPase and/or SLN, or homologues thereof, the method comprising:

providing the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof; and

5 analysing said coordinates to predict the location of internal and/or external parts of the structure.

45. A computer system, intended to generate three dimensional structural representations of SERCA Ca^{2+} ATPase and/or SLN, homologues or analogues of SERCA Ca^{2+} ATPase and/or SLN, complexes of binding partners with SERCA Ca^{2+} ATPase and/or SLN, or complexes of binding partners with homologues or analogues of SERCA Ca^{2+} ATPase, or, to analyse or optimise binding of binding partners to SERCA Ca^{2+} ATPase and/or SLN, or homologues or analogues or complexes thereof, the system containing computer-readable data comprising one or more of:

15 (a) the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof;

(b) the coordinates of a target SERCA Ca^{2+} ATPase and/or SLN homologue or analogue generated by homology modelling of the target based on the data in (a);

20 (c) the coordinates of a binding partner generated by interpreting X-ray crystallographic data or NMR data by reference to the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof, and
(d) structure factor data derivable from the coordinates of (a), (b) or (c).

25 46. A computer system according to Claim 45, comprising:

(i) a computer-readable data storage medium comprising data storage material encoded with the computer-readable data;

(ii) a working memory for storing instructions for processing the computer-readable data; and

30 (iii) a central processing unit coupled to the working memory and to the computer-readable data storage medium for processing the computer-readable data to generate said structural representations or to analyse or optimise said binding.

47. A computer system according to Claim 46, further comprising a display coupled to the central-processing unit for displaying structural representations.

35

48. A computer-readable storage medium, comprising a data storage material encoded with computer readable data, wherein the data comprises one or more of

(a) the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof;

(b) the coordinates of a target SERCA Ca^{2+} ATPase and/or SLN homologue or analogue generated by homology modelling of the target based on the data in (a);

(c) the coordinates of a binding partner generated by interpreting X-ray crystallographic data or NMR data by reference to the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof, and

(d) structure factor data derivable from the coordinates of (a), (b) or (c).

49. A computer-readable storage medium comprising a data storage material encoded with a first set of computer-readable data comprising a Fourier transform of at least a portion of the structural coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof; which data, when combined with a second set of machine readable data comprising an X-ray diffraction pattern of a molecule or molecular complex of unknown structure (eg a target protein of unknown structure), using a machine programmed with the instructions for using said first set of data and said second set of data, can determine at least a portion of the structure coordinates corresponding to the second set of machine readable data.

50. A computer-readable storage medium comprising a data storage material encoded with the data generated by carrying out the methods of any one of Claims 2-25, 27-30 and 32-44.

51. A method of preparing the computer-readable storage medium of Claim 49 or 50, comprising encoding a data storage material with the computer-readable data.

52. A method of producing a protein with a binding region that has substrate specificity substantially identical to that of SERCA Ca^{2+} ATPase, the method comprising

a) aligning the amino acid sequence of a target protein with the amino acid sequence of SERCA Ca^{2+} ATPase;

b) identifying the amino acid residues in the target protein that correspond to any one or more of the following positions according to the numbering of the rabbit SERCA

Ca²⁺ ATPase as set out in Figure 8: Phe88, Phe92, Val93, Leu96, Ile97, Ala100, Ile103, Val104, Trp107, Gln108, Asn111, Tyr122, Arg324, Lys328, Trp794, Leu797, Asp800, Gly801, Leu802, Thr805, Ala806, Phe809, Trp932, Ser936, Leu939, Ser942, Leu943, Leu946, Ile947, Pro952, Leu953, Ile956, and Phe957; and

- 5 c) making one or more mutations in the amino acid sequence of the target protein to replace one or more identified amino acid residues with the corresponding residue in the rabbit SERCA Ca²⁺ ATPase.

53. A method of producing a protein with a binding region that has substrate
10 specificity substantially identical to that of SLN, the method comprising

 a) aligning the amino acid sequence of a target protein with the amino acid sequence of SLN;

 b) identifying the amino acid residues in the target protein that correspond to any one or more of the following positions according to the numbering of the rabbit SLN as
15 set out in Figure 8: Met1, Glu2, Arg3, Ser4, Thr5, Arg6, Glu7, Leu8, Cys9, Leu10, and Asn11; and

 c) making one or more mutations in the amino acid sequence of the target protein to replace one or more identified amino acid residues with the corresponding residue in the rabbit SLN.

20

54. A mutant SERCA Ca²⁺ ATPase or homologue thereof, wherein any one or more of amino acid residues Phe88, Phe92, Val93, Leu96, Ile97, Ala100, Ile103, Val104, Trp107, Gln108, Asn111, Tyr122, Arg324, Lys328, Trp794, Leu797, Asp800, Gly801, Leu802, Thr805, Ala806, Phe809, Trp932, Ser936, Leu939, Ser942, Leu943, Leu946,
25 Ile947, Pro952, Leu953, Ile956, and Phe957, according to the numbering of the rabbit SERCA Ca²⁺ ATPase in Figure 8, or any one or amino acids that correspond to said residues, are mutated.

55. A mutant SLN or homologue thereof, wherein any one or more of amino acid
30 residues Met1, Glu2, Arg3, Ser4, Thr5, Arg6, Glu7, Leu8, Cys9, Leu10, and Asn11, according to the numbering of the rabbit SLN in Figure 8, or any one or amino acids that correspond to said residues, are mutated.

56. A method of assessing the conformational state of a structure for SERCA Ca²⁺
35 ATPase, comprising:

providing the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof;

performing a statistical analysis and/or a topological analysis on the coordinates;

5 and

comparing the results of the analysis with the results of an analysis of coordinates of proteins of known conformational states.

57. A method according to Claim 56, wherein the statistical analysis is a multivariate analysis such as one performed using a technique selected from any of principal components analysis, hierarchical cluster analysis, genetic algorithms and neural networks.

58. A method according to Claim 56 or 57, wherein the conformational state is classified as any of E1, E1P, E2 and E2P.

59. A crystal comprising a Ca^{2+} ATPase/SLN complex.

60. A crystal according to Claim 59, wherein the crystal comprises SERCA Ca^{2+} ATPase/SLN.

61. A crystal according to Claim 59 or 60 wherein the complex has the structure defined by the coordinates of the SERCA Ca^{2+} ATPase/SLN complex listed in Table (i), optionally varied by a root mean square deviation of C alpha atoms of not more than 4.95 Å, or selected coordinates thereof.

62. A crystal according to any of Claims 59-61, having a resolution of 3.1 Å or better.

63. A crystal according to any of Claims 59-62, further comprising a binding partner of Ca^{2+} ATPase and/or SLN.

64. A method of making a crystal comprising a Ca^{2+} ATPase/SLN complex, the method comprising:

providing a purified Ca^{2+} ATPase/SLN complex;

and crystallising the complex by using the hanging drop vapour diffusion technique, using a precipitant solution comprising 15-25% (w/v) PEG6000, 100-200 mM magnesium sulphate, 4-6% glycerol and 5-7% 2-methyl-2,4-pentandiol (MPD).

65. A method according to Claim 62, wherein the precipitant solution comprises about 19.5% (w/v) PEG6000, about 150 mM magnesium sulphate, about 5% glycerol and about 6% 2-methyl-2,4-pentandiol (MPD).

5

66. A method according to Claim 64 or 65, wherein the crystal further comprises a Ca^{2+} ATPase and/or SLN binding partner.

67. A crystal obtainable by the method of any of Claims 64-66.

10

FIGURE 1



FIGURE 2

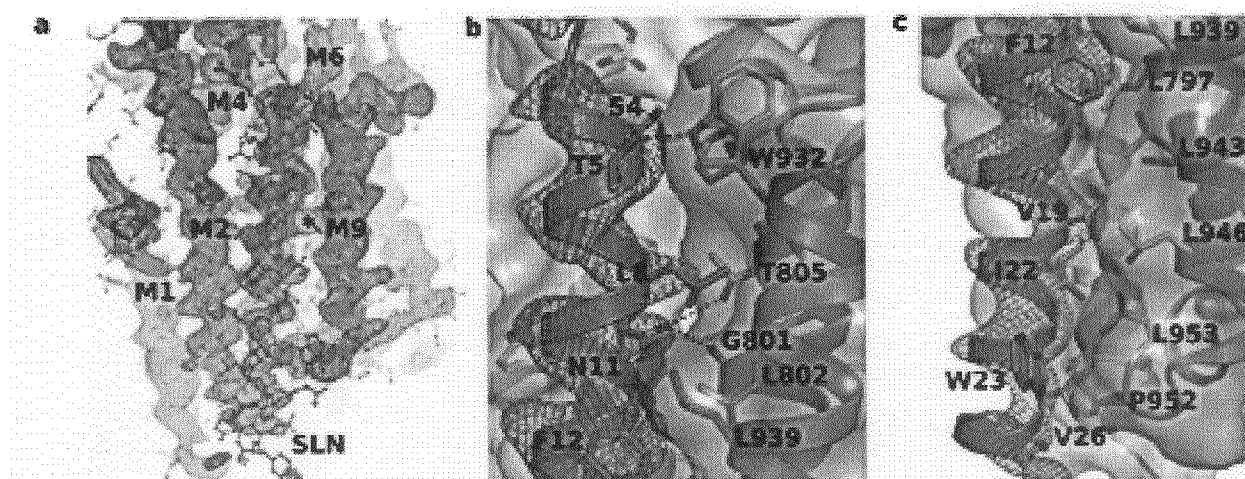


FIGURE 3

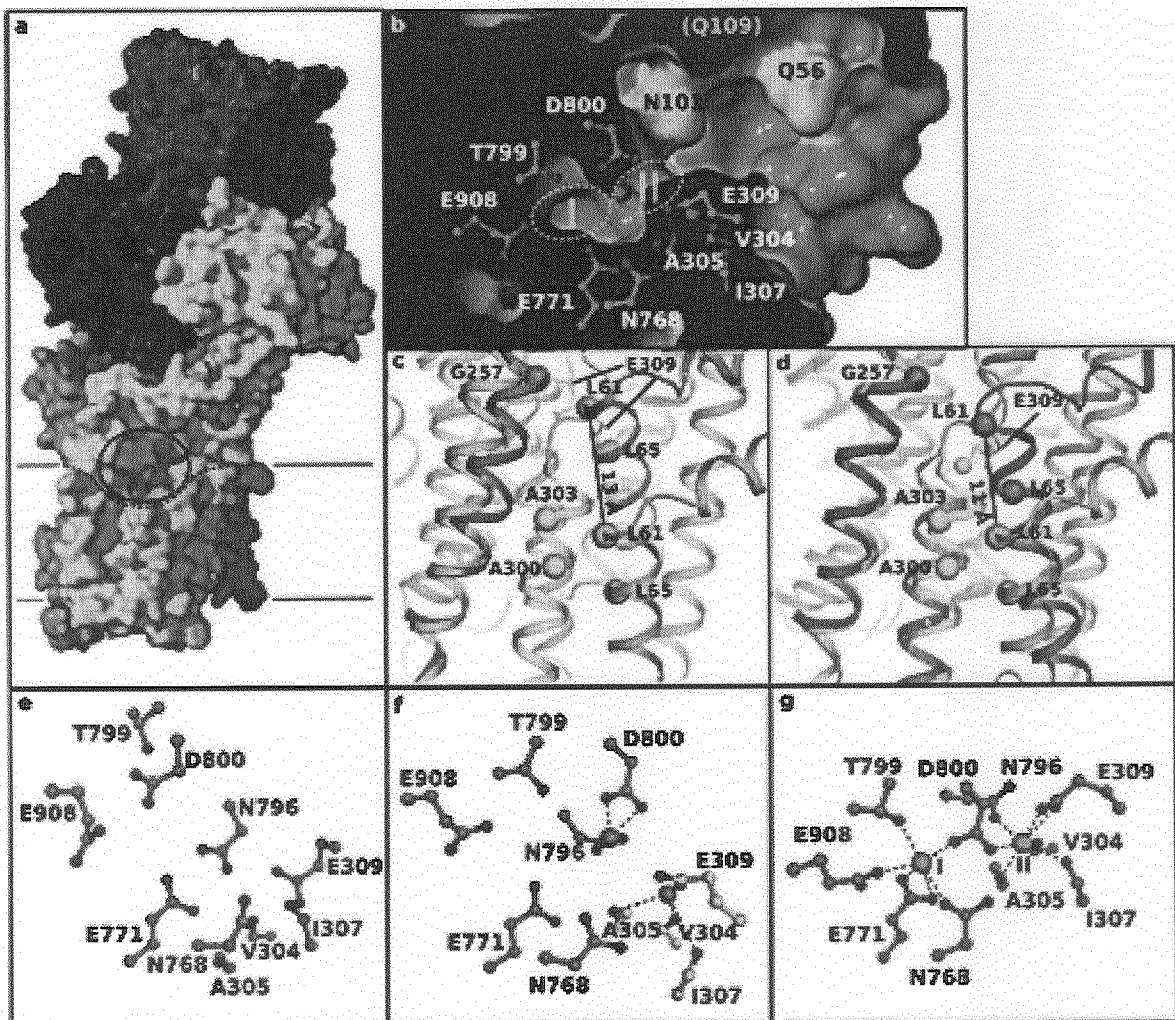


FIGURE 4

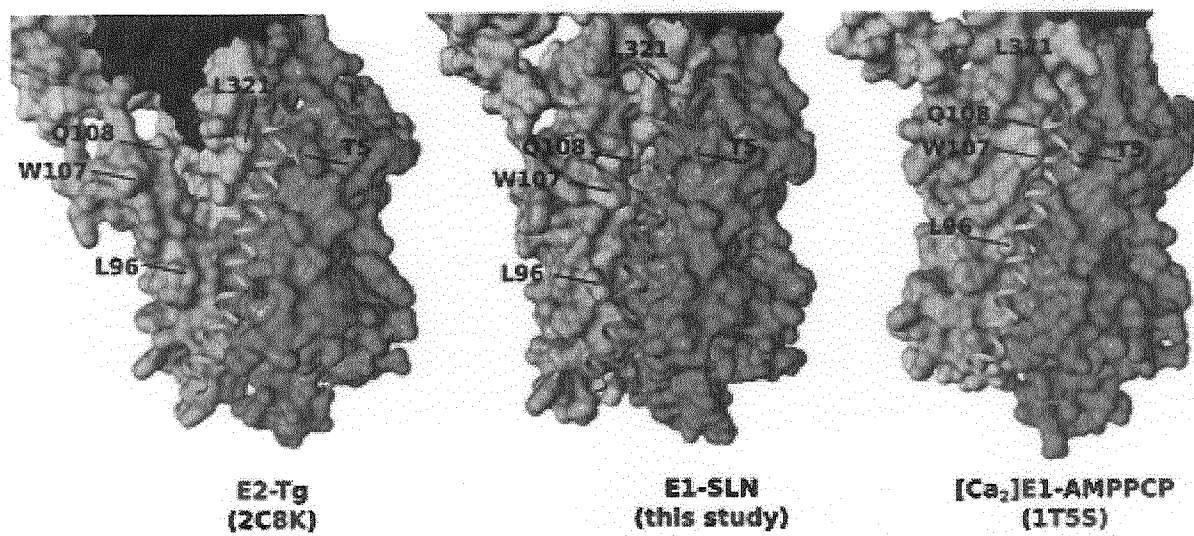


FIGURE 5

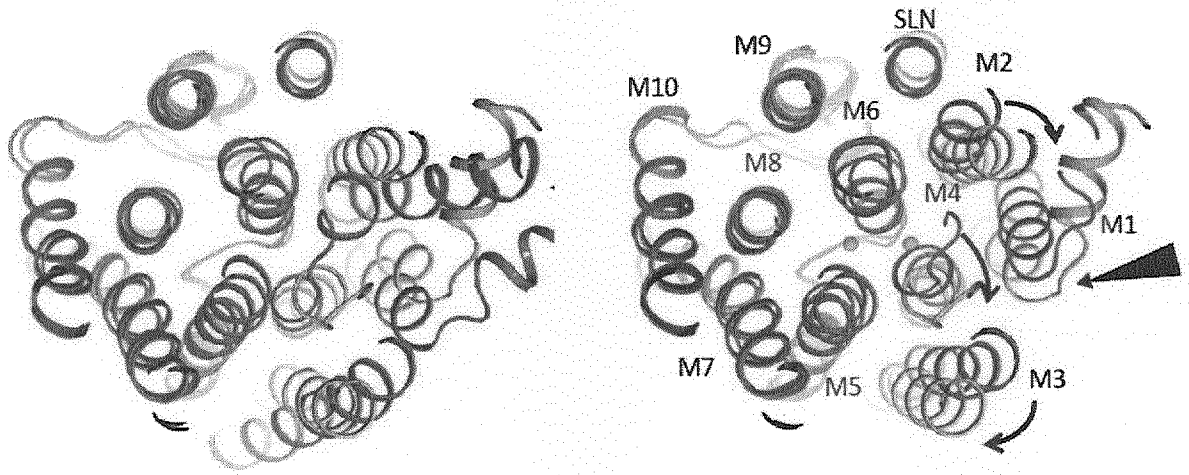


FIGURE 6

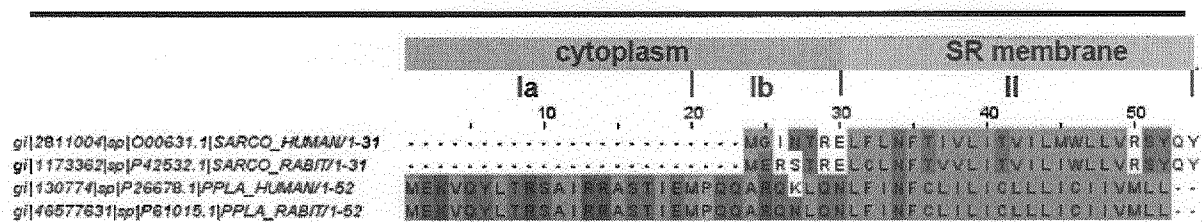


FIGURE 7

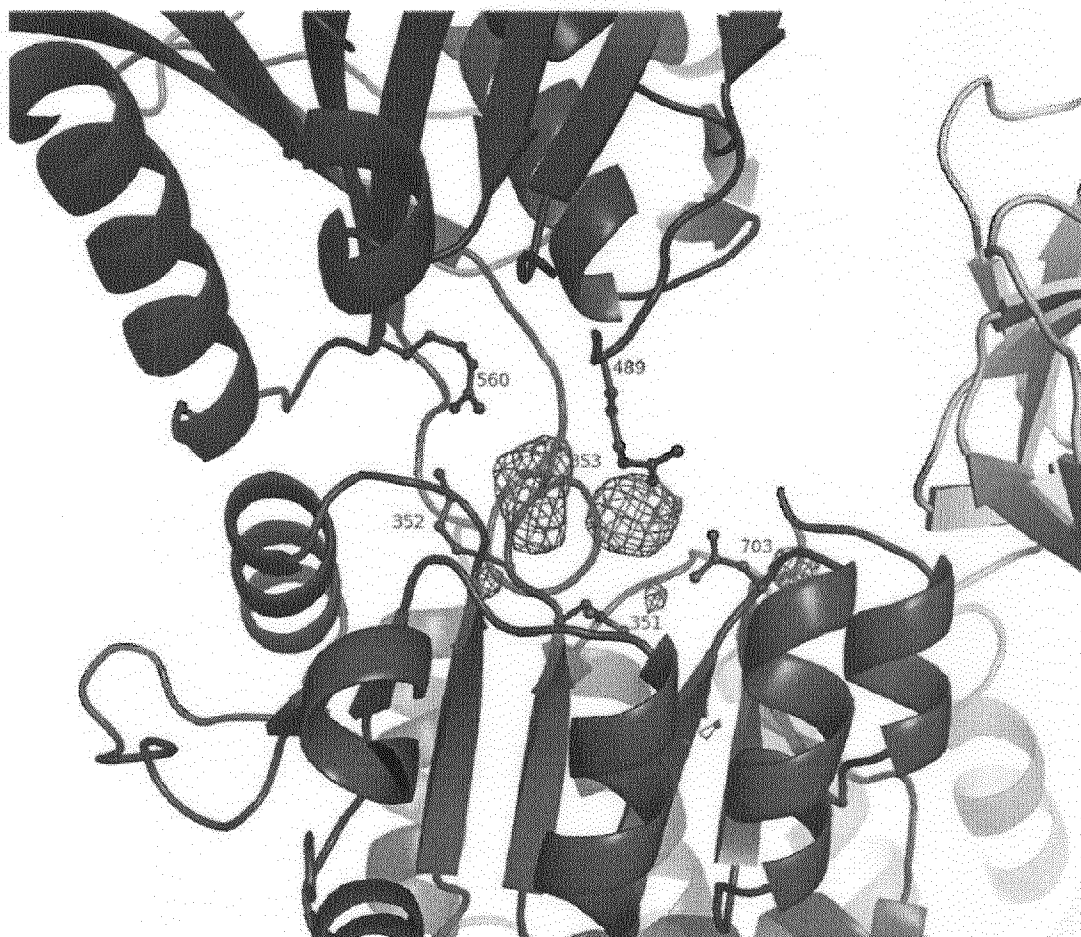


FIGURE 8

A

>SERCA|CHAIN|SEQUENCE
MEAAHSKSTEECLAYFGVSETTGLTPDQVKRHLEKYGHNELPAEEGKSLWELVIEQ
FEDLLVRILLLAACISFVLAWFE
TAFVEPFVILLILIANAIVGVWQERNAENAIEALKEYEPEMGKVYRADRKSVQRIKAR
DIVPGDIVEVAVGDKVP
ADIRILSIKSTTLRVDQSSILTGESVSVIKHTEPVPDPRAVNQDKKNMLFSGTNIAAGKA
LGIVATTGVSTEIGKIRDQMA
ATEQDKTPLQKQLDEFGEQLSKVISLICVAVWLINIGHFNDPVHGGSWIRGAIYYFKI
AVALAVAAIPEGLPAVITTCLA
LGTRRMAKKNAIVRSLPSVETLGCTSVICSDKTGTLTTNQMSVCKMFIIDKVDGDFC
SLNEFSITGSTYAPEGEVLKNDK
PIRSGQFDGLVELATICALCNDSSLDFFNETKGVYEKVGAEATETALTTLVEKMNVFNT
EVRNLSKVERANACNSVIRQLMK
KEFTLEFSRDRKSMSVYCSPAKSSRAAVGNKMFVKGAPEGVIDRCNYVRVGTTRV
PMTGPVKEKILSVIKEWGTGRDTLR
CLALATRDTPPKREEMVLDDSSRFMEYETDLTFVGVVGMLDPPRKEVMGSIQLCR
DAGIRVIMITGDNKGTAIAICRRIG
IFGENEEVADRAYTGREFDDLPLAEQREACRRACCFARVEPSHKSKIVEYLQSYDEI
TAMTGDGVNDAPALKKAEIGIAM
GSGTAVAKTASEMVLADDNFSTIVAAVEEGRAIYNNMKQFIRYLISNVGEVVCIFLT
AALGLPEALIPVQLLWVNLVTD
GLPATALGFNPPDLDIMDRPPRSPKEPLISGWLFFRYMAIGGYVGAATVGAAAWWF
MYAEDGPGVTYHQLTHFMQCTEDH
PHFDCEIFEAPEPMTMALSVLVTIEMCNALNSLSENQSLMRMPPWVNIWLLGSICLS
MSLHFLILYVDPLPMIFKLK
ALDLTQWLMVLKISLPVIGLDEILKFIARNYLEG

B

>SLN|CHAIN|SEQUENCE
MERSTRELCLNFTVVLITVILIWLLVRSYQY

FIGURE 9

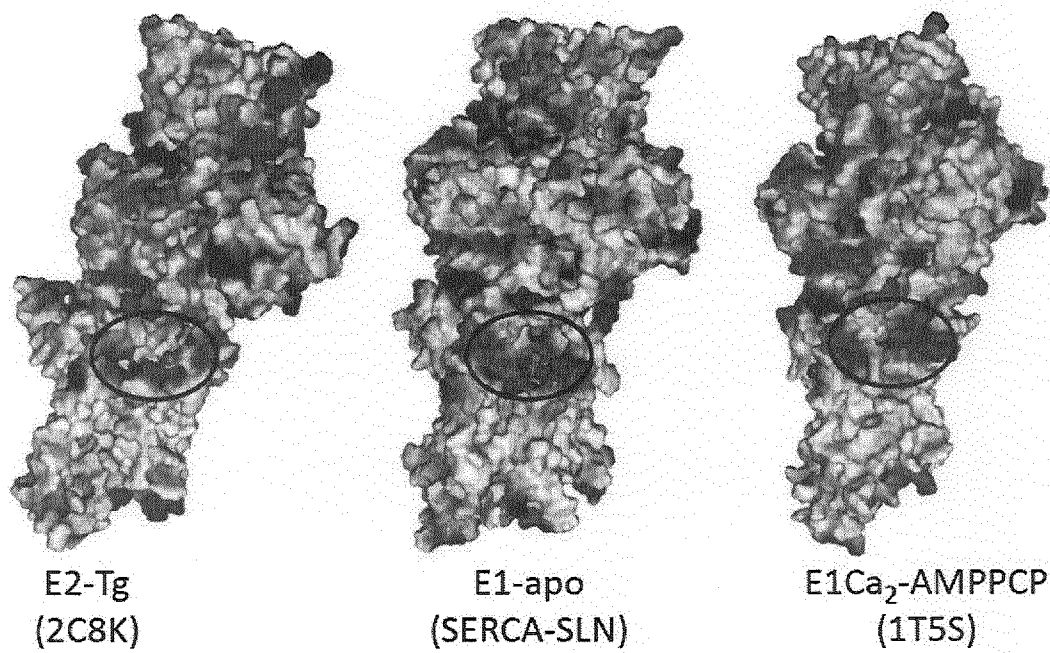


FIGURE 10

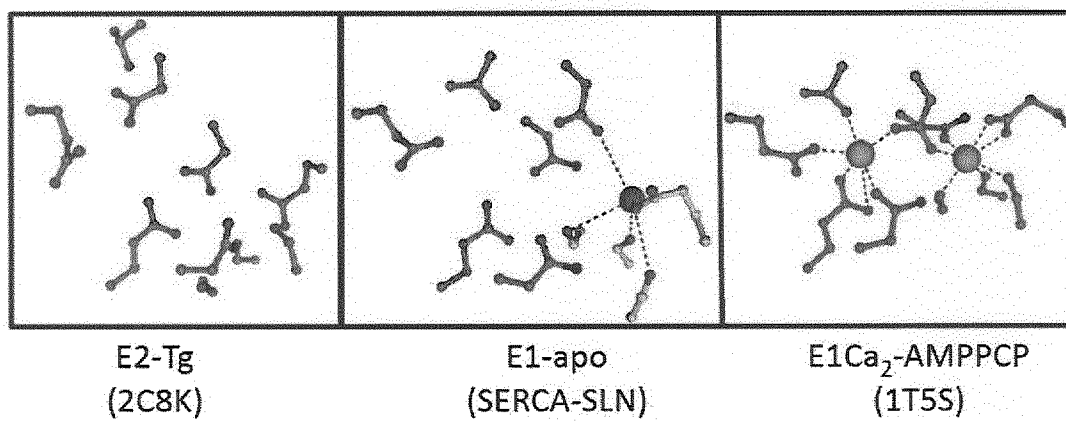


FIGURE 11

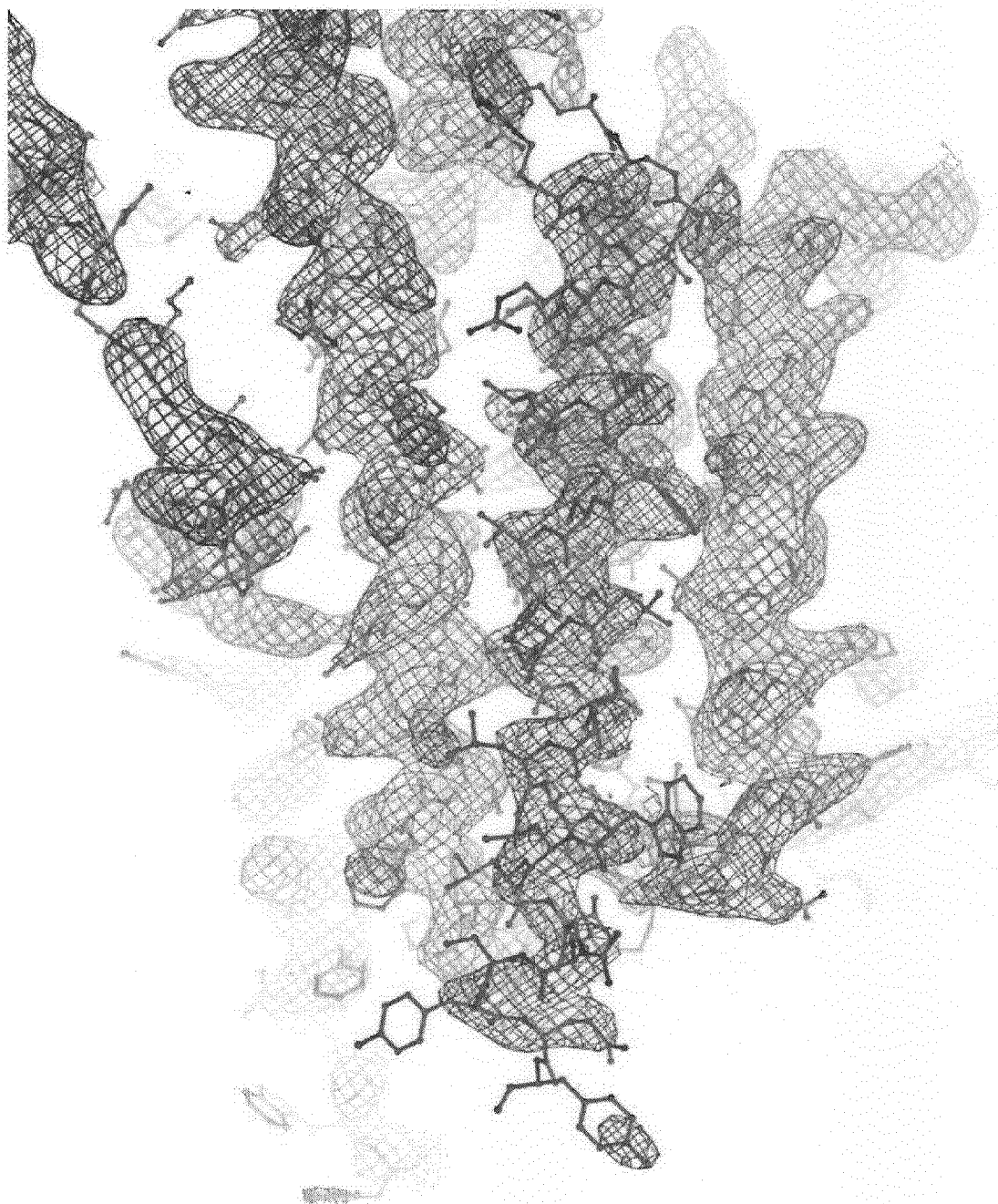


FIGURE 12

