ISOPRENE SYNTHASE VARIANTS FOR IMPROVED MICROBIAL PRODUCTION OF ISOPRENE

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. provisional application serial no. 61/125,336 filed April 23, 2008, which is hereby incorporated by reference in its entirety.

FIELD OF THE INVENTION

[0002] The present invention provides methods and compositions comprising at least one isoprene synthase enzyme with improved catalytic activity and/or solubility. In particular, the present invention provides variant plant isoprene synthases for increased isoprene production in microbial host cells. Biosynthetically produced isoprene of the present invention finds use in the manufacture of rubber and elastomers.

BACKGROUND OF THE INVENTION

[0003] Isoprenoids are isoprene polymers that find use in pharmaceuticals, neutraceuticals, flavors, fragrances, and rubber products. Natural isoprenoid supplies, however, are limited due to ecological concerns. For this reason, and to provide isoprenoid compositions having fewer impurities and greater uniformity, isoprenoids such as rubber are often produced synthetically.

[0004] Isoprene (2-methyl-1,3-butadiene) is a volatile hydrocarbon that is insoluble in water and soluble in alcohol. Commercially viable quantities of isoprene can be obtained by direct isolation from petroleum C5 cracking fractions or by dehydration of C5 isoalkanes or isoalkenes (Weissermel and Arpe, Industrial Organic Chemistry, 4th ed., Wiley-VCH, pp. 117-122, 2003). The C5 skeleton can also be synthesized from smaller subunits. It would be desirable, however, to have a commercially viable method of producing isoprene that was independent of nonrenewable resources.

[0005] Biosynthetic production of isoprene occurs by two distinct metabolic pathways (Julsing et al., Appl Microbiol Biotechnol, 75:1377-1384, 2007). In eukaryotes and archae, isoprene is formed via the mevalonate (MVA) pathway, while some eubacteria and higher plants produce isoprene via the methylerythritol phosphate (MEP) pathway. Isoprene emissions from plants are light and temperature-dependent with increases linked to leaf development. An isoprene-producing enzyme, isoprene synthase, has been identified in Aspen trees (Silver and Fall, Plant Physiol, 97:1588-1591, 1991; and Silver and Fall, J Biol

Chem, 270:13010-13016, 1995) and is believed to be responsible for the *in vivo* production of isoprene from whole leaves. Bacterial production of isoprene has also been described (Kuzma et al., Curr Microbiol, 30:97-103, 1995; and Wilkins, Chemosphere, 32:1427-1434, 1996), and varies in amount with the phase of bacterial growth and the nutrient content of the culture medium (U.S. Patent No. 5,849,970 to Fall et al.; and Wagner et al., J Bacteriol, 181:4700-4703, 1999, both herein incorporated by reference in their entirety). The levels of isoprene obtainable through bacterial systems of the prior art, however, are insufficient for commercial uses.

[0006] Thus what the art needs is an efficient, large scale, bacterial isoprene production process to provide feedstock for the manufacture of isoprenoids.

[0007] All patents, patent applications, articles and publications mentioned herein are hereby expressly incorporated herein by reference.

SUMMARY OF THE INVENTION

[0008] The present invention provides methods and compositions comprising at least one isoprene synthase enzyme with improved catalytic activity and/or solubility. In particular, the present invention provides variant plant isoprene synthases for increased isoprene production in microbial host cells. Biosynthetically produced isoprene of the present invention finds use in the manufacture of rubber and elastomers.

[0009] Specifically, the present invention provides isolated isoprene synthase variants, wherein the variant comprises a substitution at a position corresponding to one or more residues (one, two, three, four, five, six, seven, eight, nine or ten) of a kudzu isoprene synthase comprising the amino acid sequence set forth in SEQ ID NO: 2. In some embodiments, the isoprene synthase variant is a kudzu (*Pueraria sp.*) isoprene synthase variant or a poplar (*Populus sp.*) isoprene synthase variant. In some embodiments, the one or more residues are selected from but not limited to the group consisting of L26, E30, F31, Q33, L35, E36, N37, L39, K40, V41, K43, L44, R61, V62, D63, Q65, K87, E94, N95, L99, D100, N105, K137, E138, G143, E144, N182, L184, K185, G187, N189, T190, P225, H226, K247, T257, E258, M259, D266, N334, D353, S357, I358I, E361, N389, I392, I393, K398, E401, C421, Q423, Q424, E425, D426, H430, L432, R433, S434, D437, R443, L462, E463, H476, N478, D479, Q485, D508, P513, A515, Q532, Y533, L537, G538, R539, Y542, A543, and P557. In some embodiments, the one or more residues are selected from but not limited to the group consisting of P24, N25, Y309, D310, L377, F381, E384, Y399, N402, A403, S406, S407, G409, A411, L413, F449, A456, T457, S458, A459, A460, E461, L462, E463,

R464, G465, E466, T467, T468, N469, M523, S527, and Y531. In some embodiments, the one or more residues are selected from but not limited to the group consisting of A20, N21, Y22, Q23, R271, W278, F299, V302, and S408. The present invention also provides an isolated isoprene synthase variant having an A20G substitution in a kudzu isoprene synthase having the amino acid sequence set forth in SEQ ID NO: 2. In a subset of these embodiments, the variant comprises at least two substitutions (two, three, four, five, six, seven, eight, nine or ten), wherein one of the substitutions is an A20G substitution in a kudzu isoprene synthase having the amino acid sequence set forth in SEQ ID NO: 2. The present invention also provides an isolated isoprene synthase variant having an S408D substitution in a kudzu isoprene synthase having the amino acid sequence set forth in SEQ ID NO: 2. In a subset of these embodiments, the variant comprises at least two substitutions (two, three, four, five, six, seven, eight, nine or ten), wherein one of the substitutions is an S408D substitution in a kudzu isoprene synthase having the amino acid sequence set forth in SEQ ID NO: 2. In some preferred embodiments, the isoprene synthase variant has at least one improved property as compared to wild-type isoprene synthase. In some particularly preferred embodiments, the at least one improved property is selected from but not limited to the group consisting of specific activity (production of isoprene from dimethylallyl diphosphate), and solubility.

[0010] In addition, the present invention further provides a polynucleotide sequence encoding the isoprene synthase variant. Also provided is an expression vector comprising a polynucleotide sequence encoding the isoprene synthase variant in operable combination with a promoter. In further embodiments, the present invention provides a host cell comprising the expression vector. Also provided is a lysate of the host cell, wherein the lysate further comprises lysozyme. In some embodiments, the lysate has a neutral pH (6.5 to 7.5), while in other embodiments the lysate has a basic pH (above 7.5 and below 9.5). The present invention also provides methods of producing isoprene, comprising: (a) providing host cells comprising the expression vector; and (b) culturing the host cells under conditions suitable for producing isoprene. In some embodiments, the methods further comprise (c) recovering the isoprene. In still further embodiments, the methods further comprise (d) polymerizing the isoprene. The present invention further provides methods of detecting isoprene synthase activity, comprising: (a) culturing host cells comprising the expression vector under conditions suitable for producing the isoprene synthase variant; (b) lysing the host cells with a lysis buffer comprising lysozyme to produce a cell lysate; and (c) detecting isoprene synthase activity in the cell lysate by measuring isoprene production from dimethylallyl diphosphate (DMAPP). In some embodiments, the host is selected from but not limited to the

group consisting of gram-positive bacterial cells, gram-negative bacterial cells, filamentous fungal cells, and yeast cells. In some preferred embodiments, the host is selected from but not limited to the group consisting of *Escherichia sp. (E. coli), Panteoa sp. (P. citrea), Bacillus sp. (B. subtilis), Yarrowia sp. (Y. lipolytica),* and *Trichoderma (T. reesei).* In some embodiments, the host cells are cultured in a medium that includes a carbon source selected from but not limited to the group consisting of glucose, glycerol, glycerine, dihydroxyacetone, yeast extract, biomass, molasses, sucrose, and oil.

[0011] Moreover, the present invention provides methods of detecting isoprene in a plurality of samples (high-throughput screening), comprising: (a) providing: i) a plurality of samples each comprising isoprene synthase; ii) a glass plate comprising a plurality of wells; and iii) a seal for the glass plate; (b) placing the plurality of samples in the plurality of wells of the glass plate; (c) sealing the glass plate with the seal to produce a sealed glass plate having a headspace associated with the sample in each of the plurality of wells; (d) incubating the glass plate under conditions in which the isoprene synthase is active; and (e) detecting isoprene in the headspace. In some embodiments, the isoprene is detected by gas chromatography-mass spectrometry (GC-MS). In some embodiments, the plurality of samples comprise host cells comprising an expression vector comprising a polynucleotide sequence encoding an isoprene synthase variant in operable combination with a promoter. In some embodiments, the plurality of samples comprise a lysate of the host cells, lysozyme, and dimethylallyl diphosphate (DMAPP). In some preferred embodiments, the glass plate is a deep-well glass block. In some preferred embodiments, the plurality of wells comprises at least 24 wells (preferably at least 48 wells, more preferably at least 96 wells, still more preferably at least 192 wells, and most preferably at least 384 wells). In particularly preferred embodiments, the plurality of wells each comprise a volume of 2 ml or less (preferably 2 ml to 0.2 ml).

[0012] Additionally the present invention provides a host cell comprising a heterologous polynucleotide sequence encoding an isoprene synthase variant in operable combination with a promoter, wherein the isoprene synthase variant comprises a substitution at a position corresponding to one or more residues (one, two, three, four, five, six, seven, eight, nine or ten) of a kudzu isoprene synthase comprising the amino acid sequence set forth in SEQ ID NO: 2. In some embodiments, the one or more residues are selected from but not limited to the group consisting of L26, E30, F31, Q33, L35, E36, N37, L39, K40, V41, K43, L44, R61, V62, D63, Q65, K87, E94, N95, L99, D100, N105, K137, E138, G143, E144, N182, L184, K185, G187, N189, T190, P225, H226, K247, T257, E258, M259, D266, N334, D353, S357,

I358I, E361, N389, I392, I393, K398, E401, C421, Q423, Q424, E425, D426, H430, L432, R433, S434, D437, R443, L462, E463, H476, N478, D479, Q485, D508, P513, A515, Q532, Y533, L537, G538, R539, Y542, A543, and P557. In some embodiments, the one or more residues are selected from but not limited to the group consisting of P24, N25, Y309, D310, L377, F381, E384, Y399, N402, A403, S406, S407, G409, A411, L413, F449, A456, T457, S458, A459, A460, E461, L462, E463, R464, G465, E466, T467, T468, N469, M523, S527, and Y531. In some embodiments, the one or more residues are selected from but not limited to the group consisting of A20, N21, Y22, Q23, R271, W278, F299, V302, and S408. The present invention also provides an isolated isoprene synthase variant having an A20G substitution and/or an S408D substitution in a kudzu isoprene synthase having the amino acid sequence set forth in SEQ ID NO: 2. In some preferred embodiments, the isoprene synthase variant has at least one improved property as compared to wild-type isoprene synthase. In some particularly preferred embodiments, the at least one improved property is selected from but not limited to the group consisting of specific activity (production of isoprene from dimethylallyl diphosphate), and solubility. In some preferred embodiments, the polynucleotide sequence is contained within a plasmid. In other preferred embodiments, the polynucleotide sequence is integrated into a chromosome of the host cell. In some embodiments, the host is selected from but not limited to the group consisting of gram-positive bacterial cells, gram-negative bacterial cells, filamentous fungal cells, and yeast cells. In some preferred embodiments, the host is selected from but not limited to the group consisting of *Escherichia sp. (E. coli), Panteoa sp. (P. citrea), Bacillus sp. (B. subtilis), Yarrowia sp. (Y. lipolytica),* and *Trichoderma (T. reesei).* In some embodiments, the host cells are cultured in a medium that includes a carbon source selected from but not limited to the group consisting of glucose, glycerol, glycerine, dihydroxyacetone, yeast extract, biomass, molasses, sucrose, and oil. In some embodiments, the host cell further comprises a heterologous or native nucleic acid encoding an IDI polypeptide and/or a heterologous or native nucleic acid encoding a DXS polypeptide, sometimes in combination with the native DXP pathway (for example, expression of *dxs* and *idi* in *E. coli* in addition to the native DXP pathway). Alternatively the entire DXP pathway (Figure 15) maybe expressed on a plasmid or integrated on the chromosome as an operon, with a single promoter controlling expression, or promoters of varying strengths (example GI 1.20, GI 1.5, or GI 1.6) controlling one or more of the individual genes. In some embodiments, the host cell further comprises one or more nucleic acids encoding an IDI polypeptide and a DXS polypeptide, while in some preferred embodiments, one vector encodes the isoprene synthase variant, the IDI

polypeptide, and the DXS polypeptide. In some embodiments, the host cell further comprises a heterologous nucleic acid encoding an MVA pathway polypeptide (e.g., an MVA pathway polypeptide from *Saccharomyces cerevisia* or *Enterococcus faecalis*). In some embodiments, the host cell further comprises one or more nucleic acids encoding an MVA pathway polypeptide and a DXS polypeptide, while in some preferred embodiments, one vector encodes the isoprene synthase variant, the MVA pathway polypeptide, and the DXS polypeptide. In some preferred embodiments, the host cell further comprises one or more nucleic acids encoding a DXS polypeptide, an IDI polypeptide, or one or more of the rest of the DXP pathway polypeptides, and a MVA pathway polypeptide. In some embodiments, the vector further comprises a selectable marker (e.g., antibiotic resistance nucleic acid). Also provided are methods of producing isoprene, comprising: (a) culturing the host cells under suitable culture conditions for production of isoprene; and (b) producing the isoprene. In some embodiments, the methods further comprise (c) recovering the isoprene. In some preferred embodiments, the methods further comprise (d) polymerizing isoprene. The present invention also provides methods of producing isoprene synthase, comprising: (a) providing: (i) a host cell; and (ii) a nucleic acid encoding an isoprene synthase variant in operable combination with a promoter, wherein the isoprene synthase variant comprises a substitution at a position corresponding to one or more residues (one, two, three, four, five, six, seven, eight, nine or ten) of a kudzu isoprene synthase comprising the amino acid sequence set forth in SEQ ID NO: 2;

(b) contacting the host cell with the nucleic acid to produce a transformed host cell; and (c) culturing the transformed host cells under suitable culture conditions for production of isoprene synthase.

[0013] In another aspect, the invention provides for isolated poplar isoprene synthase variants. In one embodiment, the variant comprises a truncation in the N-terminal portion of isoprene synthase. In another embodiment, the isoprene synthase variant has an increased specific activity compared to a full length isoprene synthase. In another embodiment, the isoprene synthase is *P. alba* isoprene synthase of SEQ ID NO:120. In another embodiment, wherein the variant is selected from the group consisting of: an MEA variant (SEQ ID NO:122), an MSV variant (SEQ ID NO:124), an MVS variant (SEQ ID NO:126), an MTE variant (SEQ ID NO:128), an MNV variant (SEQ ID NO:130). In another embodiment, the variant is an MEA variant (SEQ ID NO:122). In another embodiment, the variant is selected from the group consisting of: a TRC (-3) variant (SEQ ID NO:136), a TRC (-4) variant (SEQ ID NO:138), a TRC (-5) variant (SEQ ID NO:140), a TRC (-6) variant (SEQ ID NO:142) and

a TRC (-7) variant (SEQ ID NO:144). In another embodiment, the variant is a MET variant of *P. tremuloides* isoprene synthase (SEQ ID NO:146). In another embodiment, the variant is a MET variant of *P. trichocharpa* isoprene synthase (SEQ ID NO:148).

[0014] In another aspect, the invention provides for isolated poplar isoprene synthase variants, wherein the variant comprises a substitution of one or more amino acid residues of a wild type isoprene synthase; and wherein the isoprene synthase variant has increased isoprene synthase activity compared to a wild type isoprene synthase. In one embodiment, the increased isoprene synthase activity is indicated by a host cell comprising the isoprene variant growing at a faster rate in the presence of dimethylallyl pyrophosphate (DMAPP) compared to a host cell comprising a parent isoprene synthase. In another embodiment, the isoprene synthase is the *P. alba* isoprene synthase of SEQ ID NO:120. In another embodiment, the variant comprises one of more amino acid substitutions selected from the group consisting of V10M, F12S, T15A, E18G, V58I, V58F, L70Q, L70V, L70T, T71P, V79L, E89D, G94A, S119F, F120L, G127R, E175V, T212I, S257A, R262G, A266G, F280L, N297K, F305L, L319M, E323K, A328T, D342E, A359T, K366N, E368D, L374M, S396T, V418S, K438N, H440R, T442I, T442A, I449V, A469S, K500R, K505Q, G507S, S509N, F511Y, and N532K. In another embodiment, at least one amino acid substitution is a L70R substitution. In another embodiment, the variant comprises one of more amino acid substitutions selected from the group consisting of G127R/F511Y, L70Q/G94A/R262G/F305L, F12S/ T15A/E18G/N297K, S396T/T442I, V10M/E323K, F120L/A266G, K438N/K500R, V79L/S509N, E175V/S257A/E368D/A469S, T71P/L374M, F280L/H440R, E89D/H440R, V58F/A328T/N532K, S119F/D342E/I449V, and K366N/G507S.

[0015] In another aspect, the invention provides for a crystalline form of a polypeptide comprising the amino acid residues of SEQ ID NO:120 (Figure 19).

[0016] In another aspect, the invention provides for methods of producing isoprene, comprising: (a) providing a host cell comprising an expression vector comprising a polynucleotide sequence encoding an isoprene synthase variant; and (b) culturing the host cell under conditions suitable for producing isoprene. In one embodiment, the method further comprises (c) recovering the isoprene. In another embodiment, the method further comprises (d) polymerizing the isoprene.

[0017] In another aspect, the invention provides for methods of detecting isoprene synthase activity, comprising: (a) culturing a host cell comprising the expression vector under conditions suitable for producing an isoprene synthase variant; (b) lysing the host cells with a

lysis buffer comprising lysozyme to produce a cell lysate; and (c) detecting isoprene synthase activity in the cell lysate by measuring isoprene production from dimethylallyl diphosphate (DMAPP). In one embodiment, the host cell is selected from the group consisting of gram-positive bacterial cells, gram-negative bacterial cells, filamentous fungal cells, and yeast cells. In another embodiment,

the host cell is selected from the group consisting of *Escherichia sp. (E. coli), Panteoa sp. (P. citrea), Bacillus sp. (B. subtilis), Yarrowia sp. (Y. lipolytica),* and *Trichoderma (T. reesei).* In another embodiment, the host cell is cultured in a medium that includes a carbon source selected from the group consisting of glucose, glycerol, glycerine, dihydroxyacetone, yeast extract, biomass, molasses, sucrose, and oil.

[0018] In another aspect, the invention provides for host cells comprising a heterologous polynucleotide sequence encoding an isoprene synthase variant in operable combination with a promoter, wherein the isoprene synthase variant comprises a substitution at a position corresponding to one or more residues (one, two, three, four, five, six, seven, eight, nine or ten) of a poplar isoprene synthase. In one embodiment, the isoprene synthase is the *P. alba* isoprene synthase of SEQ ID NO:120. In another embodiment, the variant is selected from the group consisting of: an MEA variant (SEQ ID NO:122), an MSV variant (SEQ ID NO:124), an MVS variant (SEQ ID NO:126), an MTE variant (SEQ ID NO:128), an MNV variant (SEQ ID NO:130). In another embodiment, the variant is selected from the group consisting of: a TRC (-3) variant (SEQ ID NO:136), a TRC (-4) variant (SEQ ID NO:138), a TRC (-5) variant (SEQ ID NO:140), a TRC (-6) variant (SEQ ID NO:142) and a TRC (-7) variant (SEQ ID NO:144). In another embodiment, the variant is a MET variant of *P. tremuloides* isoprene synthase (SEQ ID NO:146). In another embodiment, the variant is a MET variant of *P. trichocharpa* isoprene synthase (SEQ ID NO:148). In another embodiment, the variant comprises one of more amino acid substitutions selected from the group consisting of V10M, F12S, T15A, E18G, V58I, V58F, L70Q, L70V, L70T, T71P, V79L, E89D, G94A, S119F, F120L, G127R, E175V, T212I, S257A, R262G, A266G, F280L, N297K, F305L, L319M, E323K, A328T, D342E, A359T, K366N, E368D, L374M, S396T, V418S, K438N, H440R, T442I, T442A, I449V, A469S, K500R, K505Q, G507S, S509N, F511Y, and N532K. In another embodiment, at least one amino acid substitution is a L70R substitution. In another embodiment, the variant comprises one of more amino acid substitutions selected from the group consisting of G127R/F511Y, L70Q/G94A/R262G/F305L, F12S/ T15A/E18G/N297K, S396T/T442I, V10M/E323K, F120L/A266G, K438N/K500R, V79L/S509N, E175V/S257A/E368D/A469S, T71P/L374M,

F280L/H440R, E89D/H440R, V58F/A328T/N532K, S119F/D342E/I449V, and K366N/G507S. In another embodiment, the polynucleotide sequence is contained within a plasmid. In another embodiment, the polynucleotide sequence is integrated into a chromosome of the host cell.

In another embodiment, the host is selected from the group consisting of gram-positive bacterial cells, gram-negative bacterial cells, filamentous fungal cells, and yeast cells. In another embodiment, the host is selected from the group consisting of *Escherichia sp. (E. coli), Panteoa sp. (P. citrea), Bacillus sp. (B. subtilis), Yarrowia sp. (Y. lipolytica),* and *Trichoderma (T. reesei).* In another embodiment, the host cell is cultured in a medium comprising a carbon source selected from the group consisting of glucose, glycerol, glycerine, dihydroxyacetone, yeast extract, biomass, molasses, sucrose, and oil. In another embodiment, the host cell further comprises a heterologous or native nucleic acid encoding an IDI polypeptide and/or a heterologous or native nucleic acid encoding a DXS polypeptide, optionally in combination with the native DXP pathway. In another embodiment, the host cell further comprises one or more nucleic acids encoding an IDI polypeptide and a DXS polypeptide. In another embodiment, the host cell comprises one vector encoding the isoprene synthase variant, the IDI polypeptide, and the DXS polypeptide. In another embodiment, the host cell further comprises a heterologous nucleic acid encoding an MVA pathway polypeptide selected from the group consisting of an MVA pathway polypeptide from *Saccharomyces cerevisia* and *Enterococcus faecalis*. In another embodiment, the host cell further comprises one or more nucleic acids encoding an MVA pathway polypeptide and a DXS polypeptide and wherein one vector encodes the isoprene synthase variant, the MVA pathway polypeptide, and the DXS polypeptide. In another embodiment, the host cell further comprises one or more nucleic acids encoding a DXS polypeptide, an IDI polypeptide, or one or more of the rest of the DXP pathway polypeptides, and a MVA pathway polypeptide.

[0019] In another aspect, the invention provides for methods of producing isoprene, comprising: (a) culturing the host cells comprising a heterologous polynucleotide sequence encoding an isoprene synthase variant in operable combination with a promoter, wherein the isoprene synthase variant comprises a substitution at a position corresponding to one or more residues (one, two, three, four, five, six, seven, eight, nine or ten) of a poplar isoprene synthase under suitable culture conditions for production of isoprene; and (b) producing the isoprene. In one embodiment, the method further comprises (c) recovering the isoprene. In another embodiment, the method further comprises (d) polymerizing isoprene.

[0020] In another aspect, the invention provides for methods of producing isoprene synthase, comprising: (a) providing: (i) a host cell; and (ii) a nucleic acid encoding an isoprene synthase variant in operable combination with a promoter, wherein the isoprene synthase variant comprises a substitution at a position corresponding to one or more residues (one, two, three, four, five, six, seven, eight, nine or ten) of a *P. alba* isoprene synthase of SEQ ID NO:120; (b) contacting the host cell with the nucleic acid to produce a transformed host cell; and (c) culturing the transformed host cells under suitable culture conditions for production of isoprene synthase.

BRIEF DESCRIPTION OF THE DRAWINGS

[0021] Figure 1 provides the coding sequence (SEQ ID NO:1) of kudzu (*Pueraria montana*) isoprene synthase, codon-optimized for expression in *Escherichia coli*.

[0022] Figure 2 provides the amino acid sequence (SEQ ID NO:2) of kudzu isoprene synthase.

[0023] Figure 3 provides the coding sequence (SEQ ID NO:6) of poplar (*Populus alba x tremula*) isoprene synthase, codon-optimized for expression in *Escherichia coli*.

[0024] Figure 4 provides the amino acid sequence (SEQ ID NO:7) of poplar (*Populus alba x tremula*) isoprene synthase.

[0025] Figure 5 provides a kudzu isoprene synthase homology model with the cysteine residues highlighted as space filling molecules.

[0026] Figure 6 provides a poplar isoprene synthase homology model with the cysteine residues highlighted as space filling molecules (dark grey). In addition, the cysteine residues from the kudzu model of Figure 5 are superimposed on the poplar model as space filling molecules (light grey).

[0027] Figure 7 provides a graph showing the growth curves of the kudzu IspS cysteine mutants of Example 5.

[0028] Figure 8 shows an SDS-PAGE analysis of kudzu IspS cysteine mutants from lysed cells. Pellet and supernatant fractions were prepared by centrifugation.

[0029] Figure 9 provides a map of plasmid MCM93 (pCR2.1-Kudzu).

[0030] Figure 10 provides the nucleotide sequence of plasmid MCM93 (SEQ ID NO:22).

[0031] Figure 11 provides a map of pET24D-Kudzu.

[0032] Figure 12 provides the nucleotide sequence of pET24D-Kudzu (SEQ ID NO:23).

[0033] Figure 13 shows an SDS-PAGE analysis of kudzu isoprene synthase-containing inclusion bodies. Lane M contains molecular weight markers, while the other lanes contain

increasing amounts of the purified inclusion body preparation. The kudzu isoprene synthase was estimated to have a purity of >90%.

[0034] Figure 14 provides graphs showing isoprene synthase activity of kudzu site evaluation library (SEL) members for positions Y22, A20 and S408. Most members show highly decreased activity, while conservative substitutions show a lesser decrease in activity. Panel A shows assay results for the Y22 library members in comparison with independent wild type samples (circled WT). Panel B shows assay results for the A20 library members in comparison to wild type samples (circled WT). Panel C shows assay results for the S408 library members, indicating that member S408D has 1.5 to 2-fold higher activity than the average of the wild type controls.

[0035] Figure 15 shows the MVA and DXP metabolic pathways for isoprene (based on F. Bouvier et al., Progress in Lipid Res. 44: 357-429, 2005). The following description includes alternative names for each polypeptide in the pathways and a reference that discloses an assay for measuring the activity of the indicated polypeptide (each of these references are each hereby incorporated by reference in their entireties, particularly with respect to assays for polypeptide activity for polypeptides in the MVA and DXP pathways). **Mevalonate Pathway: AACT**; Acetyl-CoA acetyltransferase, MvaE, EC 2.3.1.9. Assay: J. Bacteriol., 184: 2116–2122, 2002; **HMGS**; Hydroxymethylglutaryl-CoA synthase, MvaS, EC 2.3.3.10. Assay: J. Bacteriol., 184: 4065–4070, 2002; **HMGR**; 3-Hydroxy-3-methylglutaryl-CoA reductase, MvaE, EC 1.1.1.34. Assay: J. Bacteriol., 184: 2116–2122, 2002; **MVK**; Mevalonate kinase, ERG12, EC 2.7.1.36. Assay: Curr Genet 19:9-14, 1991. **PMK**; Phosphomevalonate kinase, ERG8, EC 2.7.4.2, Assay: Mol Cell Biol., 11:620–631, 1991; **DPMDC**; Diphosphomevalonate decarboxylase, MVD1, EC 4.1.1.33. Assay: Biochemistry, 33:13355-13362, 1994; **IDI**; Isopentenyl-diphosphate delta-isomerase, IDI1, EC 5.3.3.2. Assay: J. Biol. Chem. 264:19169-19175, 1989. **DXP Pathway: DXS**; 1-Deoxyxylulose-5-phosphate synthase, dxs, EC 2.2.1.7. Assay: PNAS, 94:12857-62, 1997; **DXR**; 1-Deoxy-D-xylulose 5-phosphate reductoisomerase, dxr, EC 2.2.1.7. Assay: Eur. J. Biochem. 269:4446–4457, 2002; **MCT**; 4-Diphosphocytidyl-2C-methyl-D-erythritol synthase, IspD, EC 2.7.7.60. Assay: PNAS, 97: 6451–6456, 2000; **CMK**; 4-Diphosphocytidyl-2-C-methyl-D-erythritol kinase, IspE, EC 2.7.1.148. Assay: PNAS, 97:1062-1067, 2000; **MCS**; 2C-Methyl-D-erythritol 2,4-cyclodiphosphate synthase, IspF, EC 4.6.1.12. Assay: PNAS, 96:11758-11763, 1999; **HDS**; 1-Hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase, ispG, EC 1.17.4.3. Assay: J. Org. Chem., 70:9168 -9174, 2005; **HDR**; 1-Hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate reductase, IspH, EC 1.17.1.2. Assay: JACS, 126:12847-12855, 2004.

[0036] Figure 16 provides a map of pDu27.

[0037] Figure 17 provides the amino acid sequence (SEQ ID NO:118) of 6Xhis N-terminally tagged *P. alba* IspS in pDu27.

[0038] Figure 18 provides the nucleotide sequence (SEQ ID NO:119) of plasmid pDu27.

[0039] Figure 19 provides the amino acid sequence (SEQ ID NO:120) of full length *P. alba* IspS in pET24a. Underlined residues indicate the locations of N-terminal truncations in IspS in plasmids pDu39 through pDu43.

[0040] Figure 20 provides the nucleotide sequence (SEQ ID NO:121) of plasmid P. alba pET24a.

[0041] Figure 21 shows purified IspS displays a lower molecular weight "doublet" by SDS-PAGE analysis.

[0042] Figure 22 shows tryptic peptides identified by mass spectrometry.

[0043] Figure 23 provides maps of pDu40, pDu41, pDu42 and pDu43 harboring N-terminal truncations of *P. alba* IspS.

[0044] Figure 24 provides a map of Pdu39 which is pET24a-*P. alba* MEA untagged (in strain MD09-173).

[0045] Figure 25 provides the amino acid sequence (SEQ ID NO:122) of truncated "MEA" variant of *P. alba* IspS in pDu39.

[0046] Figure 26 provides the nucleotide sequence (SEQ ID NO:123) of plasmid pDu39.

[0047] Figure 27 provides the amino acid sequence (SEQ ID NO:124) of truncated "MSV" variant *P. alba* IspS in pDu41.

[0048] Figure 28 provides the nucleotide sequence (SEQ ID NO:125) of plasmid pDu41 (pET24a-P.alba(MSV) Untagged).

[0049] Figure 29 provides the amino acid sequence (SEQ ID NO:126) of truncated "MVS" variant *P. alba* IspS in pDu43.

[0050] Figure 30 provides the nucleotide sequence (SEQ ID NO:127) of plasmid pDu43 (pET24a-P.alba(MVS) Untagged).

[0051] Figure 31 provides the amino acid sequence (SEQ ID NO:128) of truncated "MTE" variant of *P. alba* IspS in pDu42.

[0052] Figure 32 provides the nucleotide sequence (SEQ ID NO:129) of plasmid pDu42 (pET24a-P.alba(MTE) Untagged).

[0053] Figure 33 provides the amino acid sequence (SEQ ID NO:130) of truncated "MNV" P. alba IspS in pDu40.

[0054] Figure 34 provides the nucleotide sequence (SEQ ID NO:131) of plasmid pDu40 (pET24a-P.alba(MNV) Untagged).

[0055] Figure 35 provides maps of MD09-161 and MD09-163, C-terminally TEV, 6XHis-tagged IspS variants.

[0056] Figure 36 provides the amino acid sequence (SEQ ID NO:132) of P. alba MEA(+)TEV in MD09-163.

[0057] Figure 37 provides the nucleotide sequence (SEQ ID NO:133) of plasmid MD09-163 (pET24a-P.alba MEA(+)TEV. CDS is underlined, TEV protease site is bold.

[0058] Figure 38 provides the amino acid sequence (SEQ ID NO:134) of P. alba FL(+)TEV in MD09-161.

[0059] Figure 39 provides the nucleotide sequence (SEQ ID NO:135) of plasmid MD09-161 (pET24a-P.alba FL(+)TEV. CDS is underlined, TEV protease site is bold.

[0060] Figure 40 shows a graph representing specific activities of MD09-167, Full length (FL), MD09-165, and Truncated isoprene synthase (MD09-173). Reactions were run at 30 °C for 15 minutes in a solution containing 100 mM Tris, 100 mM NaCl, 50 mM $MgCl_2$, 5 mM DMAPP, and 2.5-4.5 µg isoprene synthase in the supernatant of whole cell lysate.

[0061] Figure 41 shows graphs demonstrating Rate/[E] vs. [DMAPP]. X's represent MD09-173, circles represent MD09-167, diamonds represent MD09-165 and squares represent full length IspS.

[0062] Figure 42 shows a graph showing Isoprene synthase activity vs. [DMAPP]. X's represent data generated with MD09-173 truncated isoprene synthase. Circles represent data generated with MD09-167 isoprene synthase. Diamonds represent data generated with MD09-165 isoprene synthase. Squares represent data generated with full length isoprene synthase. Each data set was run in triplicate from independently grown cultures.

[0063] Figure 43 shows graphs demonstrating the effects of varying k_{cat} and K_M and K_i on reaction rate. In panel A, line 1 represents the rate equation of truncated isoprene synthase activity divided by the rate equation of full length isoprene synthase plotted at varying DMAPP concentrations. Line 2 represents the rate equation of full length isoprene synthase in which the k_{cat} has been substituted by the k_{cat} of the truncated isoprene synthase divided by the rate equation of the full length isoprene synthase. Line 3 represents the rate equation of full length isoprene synthase in which the K_M has been substituted by the K_M of the truncated isoprene synthase divided by the rate equation of the full length isoprene synthase. Line 4 represents the rate equation of full length isoprene synthase in which the K_i has been substituted by the K_i of the truncated isoprene synthase divided by the rate equation of the

full length isoprene synthase. Panel B shows a graph demonstrating data fit to the ratio of the rate equation of truncated isoprene synthase to full length isoprene synthase vs.[DMAPP].

[0064] Figure 44 shows a graph demonstrating growth inhibition of MCM531 by Mevalonic Acid (MVA). Cells were grown in TM3 medium in a microtiter plate with different concentrations of MVA. OD_{600} of quadruplicate wells was measured at the indicated times.

[0065] Figure 45 shows graphs demonstrating DMAPP assays of L70 SSL plate. Dark bars represent either the full length (P. alba pET24a) or pDU39 (truncated) controls. The variants in wells C3 (27), D3 (39), or E3 (51) were chosen for further analysis.

[0066] Figure 46 shows a graph demonstrating the average specific activity of all variants selected for DMAPP assay with protein determination. Error bars show one standard deviation. All 3 L70R variants display higher activity than the control (WT).

[0067] Figure 47 shows a graph demonstrating the average specific activity of all 3 L70R variants compared to the "MEA" truncated *P. alba* IspS enzyme. Error bars show one standard deviation.

[0068] Figure 48 provides maps of plasmids pDu47-3, pDu47-4, and pDu47-5.

[0069] Figure 49 provides maps of plasmids pDu47-6, pDu47-7, and pDu48.

[0070] Figure 50 provides maps of plasmids pDu49, pDu50 and pDu50-4.

[0071] Figure 51 provides the amino acid sequence (SEQ ID NO:136) of *P. alba* TRC (-3) in pDu47-3.

[0072] Figure 52 provides the nucleotide sequence (SEQ ID NO:137) of plasmid pDu47-3.

[0073] Figure 53 provides the amino acid sequence (SEQ ID NO:138) of *P. alba* TRC (-4) in pDu47-4.

[0074] Figure 54 provides the nucleotide sequence (SEQ ID NO:139) of plasmid pDu47-4.

[0075] Figure 55 provides the amino acid sequence (SEQ ID NO:140) of *P. alba* TRC (-5) in pDu47-5.

[0076] Figure 56 provides the nucleotide sequence (SEQ ID NO:141) of plasmid pDu47-5.

[0077] Figure 57 provides the amino acid sequence (SEQ ID NO:142) of *P. alba* TRC (-6) in pDu47-6.

[0078] Figure 58 provides the nucleotide sequence (SEQ ID NO:143) of plasmid pDu47-6.

[0079] Figure 59 provides the amino acid sequence (SEQ ID NO:144) of *P. alba* TRC (-7) in pDu47-7.

[0080] Figure 60 provides the nucleotide sequence (SEQ ID NO:145) of plasmid pDu47-7.

[0081] Figure 61 provides the amino acid sequence (SEQ ID NO:146) of *P. tremuloides* TRC (MET) in pDu48.

[0082] Figure 62 provides the nucleotide sequence (SEQ ID NO:147) of plasmid pDu48.

[0083] Figure 63 provides the amino acid sequence (SEQ ID NO:148) of *P. trichocarpa* (TRC) in pDu49.

[0084] Figure 64 provides the nucleotide sequence (SEQ ID NO:149) of plasmid pDu49.

[0085] Figure 65 provides the amino acid sequence (SEQ ID NO:150) of Kudzu TRC (MEA) in pDu50.

[0086] Figure 66 provides the nucleotide sequence (SEQ ID NO:151) of plasmid pDu50.

[0087] Figure 67 provides the amino acid sequence (SEQ ID NO:152) of KudzuTRC (-4) in pDu50-4.

[0088] Figure 68 provides the nucleotide sequence (SEQ ID NO:153) of plasmid pDu50-4.

[0089] Figure 69 shows graphs demonstrating raw and OD-normalized data from DMAPP assay of truncated variants of IspS.

[0090] Figure 70 shows a graph reprensenting the specific activity of IspS truncations. *P. alba*, *P. tremuloides* and *P. trichocharpa* truncations were compared for specific activity relative to the *P. alba* "full length" variant.

[0091] Figure 71 provides a map of plasmid p9795.

[0092] Figure 72 porvides the nucleotide sequence of plasmid p9795 (SEQ ID NO:154).

[0093] Figure 73 provides a map of plasmid pTrcKudzu.

[0094] Figure 74 provides the nucleotide sequence (SEQ ID NO:155) of plasmid pTrcKudzu.

[0095] Figure 75 provides a map of plasmid pMAL-C4X.

[0096] Figure 76 provides the nucleotide sequence (SEQ ID NO:156) of plasmid pMAL-C4X.

[0097] Figure 77 provides a map of plasmid pMAL-C4X-Kudzu.

[0098] Figure 78 provides the nucleotide sequence (SEQ ID NO:157) of plasmid pMAL-C4X-Kudzu.

[0099] Figure 79 provides maps of plasmids pET24 P. tremuloides pET24a and P. trichocharpa pET24a.

[0100] Figure 80 provides the amino acid sequence (SEQ ID NO:158) of *P. tremuloides* IspS in P. trichocharpa pET24a.

[0101] Figure 81 provides the nucleotide sequence (SEQ ID NO:159) of plasmid P. tremuloides pET24a.

[0102] Figure 82 provides the amino acid sequence (SEQ ID NO:160) of *P. trichocharpa* IspS in P. trichocharpa pET24a.

[0103] Figure 83 provides the nucleotide sequence (SEQ ID NO:161) of plasmid P. trichocharpa pET24a.

[0104] Figure 84 provides maps of plasmids pDu30, pDu31, and pDu32.

[0105] Figure 85 provides the amino acid sequence (SEQ ID NO:162) of IspS variant P.albaTRC-pET200 in pDu30.

[0106] Figure 86 provides the nucleotide sequence (SEQ ID NO:163) of pDu30.

[0107] Figure 87 provides the amino acid sequence (SEQ ID NO:164) of IspS variant P.tremTRC-pET200 in pDu31.

[0108] Figure 88 provides the nucleotide sequence (SEQ ID NO:165) of pDu31.

[00100] Figure 89 provides the amino acid sequence (SEQ ID NO:166) of IspS variant P.trichTRC-pET200 in pDu32.

[0109] Figure 90 provides the nucleotide sequence (SEQ ID NO:167) of pDu32.

[0110] Figure 91 provides the three-dimensional structure of *P. tremuloides* IspS shown as a dimer. Chain A is in dark gray, chain B is in medium gray and the single magnesium ion foung in each active site is light gray.

[0111] Figure 92 provides a monomer view of the structure of *P. tremuloides* IspS. The magnesium is shown as a light gray sphere and the N- and C-terminals are indicated.

[0112] Figure 93 shows the structural alignments between (A) BdpS and LS, (B) BdpS and poplar IspS, (C) LS and poplar IspS, and (D) TEAS and poplar IspS. In each case the first structure is in light gray and the second is in dark gray. Divalent cations are shown as spheres.

[0113] Figure 94 shows the three dimensional structure of loops in BdpS and LS. Panel A shows the N-terminal loop of Ls in light gray and the N-terminal loop of BdpS in dark gray. Panel B shows that Loop I and Loop II are structurally homologous.

[0114] Figure 95 shows the N-teminal loop of BdpS (dark gray) and poplar IspS (light gray) are structurally divergent. Panel A shows the N-terminal loop and panel B shows Loop I and Loop II.

[0115] Figure 96 shows the N-teminal loop of LS (light gray) and poplar IspS (dark gray) are structurally divergent. Panel A shows the N-terminal loop and panel B shows Loop I and Loop II.

[0116] Figure 97 shows the N-teminal loop of TEAS (light gray) and poplar IspS (dark gray) are structurally divergent. Panel A shows the N-terminal loop and panel B shows Loop I and Loop II. Loop I is disordered in TEAS.

GENERAL DESCRIPTION OF THE INVENTION

[0117] The present invention provides methods and compositions comprising at least one isoprene synthase enzyme with improved catalytic activity and/or solubility. In particular, the present invention provides variant plant isoprene synthases for increased isoprene production in microbial host cells. Biosynthetically produced isoprene of the present invention finds use in the manufacture of rubber and elastomers.

[0118] Unless otherwise indicated, the practice of the present invention involves conventional techniques commonly used in molecular biology, microbiology, and recombinant DNA, which are within the skill of the art. Such techniques are known to those of skill in the art and are described in numerous texts and reference works (See e.g., Sambrook et al., "Molecular Cloning: A Laboratory Manual," Second Edition, Cold Spring Harbor, 1989; and Ausubel et al., "Current Protocols in Molecular Biology," 1987).

[0119] Unless defined otherwise herein, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention pertains. For example, Singleton and Sainsbury, Dictionary of Microbiology and Molecular Biology, 2d Ed., John Wiley and Sons, NY (1994); and Hale and Marham, The Harper Collins Dictionary of Biology, Harper Perennial, NY (1991) provide those of skill in the art with a general dictionaries of many of the terms used in the invention. Although any methods and materials similar or equivalent to those described herein find use in the practice of the present invention, the preferred methods and materials are described herein. Accordingly, the terms defined immediately below are more fully described by reference to the Specification as a whole.

[0120] Furthermore, the headings provided herein are not limitations of the various aspects or embodiments of the invention, which can be had by reference to the specification as a whole. Accordingly, the terms defined immediately below are more fully defined by reference to the specification as a whole. Nonetheless, in order to facilitate understanding of the invention, a number of terms are defined below.

Definitions

[0121] Unless defined otherwise herein, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention pertains. Although any methods and materials similar or equivalent to those described herein find use in the practice of the present invention, the preferred methods and materials are described herein. Accordingly, the terms defined immediately below are more fully described by reference to the Specification as a whole.

[0122] As used herein, the singular terms "a," "an," and "the" include the plural reference unless the context clearly indicates otherwise. Unless otherwise indicated, nucleic acids are written left to right in 5' to 3' orientation; amino acid sequences are written left to right in amino to carboxy orientation, respectively. It is to be understood that this invention is not limited to the particular methodology, protocols, and reagents described, as these may vary, depending upon the context they are used by those of skill in the art.

[0123] It is intended that every maximum numerical limitation given throughout this specification includes every lower numerical limitation, as if such lower numerical limitations were expressly written herein. Every minimum numerical limitation given throughout this specification will include every higher numerical limitation, as if such higher numerical limitations were expressly written herein. Every numerical range given throughout this specification will include every narrower numerical range that falls within such broader numerical range, as if such narrower numerical ranges were all expressly written herein.

[0124] All documents cited are, in relevant part, incorporated herein by reference. However, the citation of any document is not to be construed as an admission that it is prior art with respect to the present invention.

[0125] As used herein, the term 2-methyl-1,3-butadiene (CAS# 78-79-5) ("isoprene") refers to the direct and final volatile C5 hydrocarbon product from the elimination of pyrophosphate from 3,3-dimethylallyl pyrophosphate (DMAPP), and does not involve the linking or polymerization of [an] IPP molecule(s) to [a] DMAPP molecule(s). As used herein, the terms "isoprene synthase," and "IspS," refer to the enzymes that catalyze the elimination or pyrophosphate from diemethylallyl diphosphate (DMAPP) to form isoprene. In some preferred embodiments, the IspS is an enzyme obtained from plants such as kudzu, poplar or red oak. In some embodiments, the term "IspS" refers to a naturally occurring mature enzyme or portion thereof.

[0126] Related (and derivative) proteins comprise "variant proteins." In some preferred embodiments, variant proteins differ from a parent protein (e.g., kudzu IspS set forth as SEQ ID NO:2 or poplar IspS) and one another by a small number of amino acid residues. The number of differing amino acid residues may be one or more, preferably 1, 2, 3, 4, 5, 10, 15, 20, 30, 40, 50, or more amino acid residues. In some preferred embodiments, the number of different amino acids between variants is between 1 and 10. In some particularly preferred embodiments, related proteins and particularly variant proteins comprise at least 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, or 99% amino acid sequence identity. Additionally, a related protein or a variant protein as used herein

refers to a protein that differs from another related protein or a parent protein in the number of prominent regions. For example, in some embodiments, variant proteins have 1, 2, 3, 4, 5, or 10 corresponding prominent regions that differ from the parent protein.

[0127] Several methods are known in the art that are suitable for generating variants of the enzymes of the present invention, including but not limited to site-saturation mutagenesis, scanning mutagenesis, insertional mutagenesis, random mutagenesis, site-directed mutagenesis, and directed-evolution, as well as various other recombinatorial approaches.

[0128] Characterization of wild-type and mutant proteins is accomplished via any means or "test" suitable and is preferably based on the assessment of properties of interest. For example one or more of the following properties are assessed in some embodiments of the present invention: pH stability; temperature stability; oxidative stability; proteolytic stability; solubility; Km and/or specific activity of the conversion of DMAPP to isoprene *in vitro;* Km and/or specific activity of the conversion of DMAPP to isoprene *in vivo* in the context of a host organism (e.g., *E. coli*); and expression of enzyme(s) of the DXP pathway and/or the MVA pathway. Indeed, it is contemplated that enzymes having various degrees of stability, solubility, activity, and/or expression level in one or more of test conditions will find use in the present invention.

[0129] As used herein the term "gene" refers to a polynucleotide (*e.g.,* a DNA segment) that encodes a polypeptide and includes regions preceding and following the coding regions as well as intervening sequences (introns) between individual coding segments (exons).

[0130] As used herein, "homologous genes" refers to a pair of genes from different, but usually related species, which correspond to each other and which are identical or very similar to each other. The term encompasses genes that are separated by speciation (*i.e.*, the development of new species) (*e.g.,* orthologous genes), as well as genes that have been separated by genetic duplication (*e.g.,* paralogous genes).

[0131] As used herein, "ortholog" and "orthologous genes" refer to genes in different species that have evolved from a common ancestral gene (*i.e.,* a homologous gene) by speciation. Typically, orthologs retain the same function during the course of evolution. Identification of orthologs finds use in the reliable prediction of gene function in newly sequenced genomes.

[0132] As used herein, "paralog" and "paralogous genes" refer to genes that are related by duplication within a genome. While orthologs retain the same function through the course of evolution, paralogs evolve new functions, even though some functions are often related to the original one.

[0133] As used herein, "homology" refers to sequence similarity or identity, with identity being preferred. This homology is determined using standard techniques known in the art (*See e.g.*, Smith and Waterman, Adv Appl Math, 2:482, 1981; Needleman and Wunsch, J Mol Biol, 48:443, 1970; Pearson and Lipman, Proc Natl Acad Sci USA, 85:2444, 1988; programs such as GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, Madison, WI; and Devereux *et al.*, Nucl Acid Res, 12:387-395, 1984).

[0134] As used herein, an "analogous sequence" is one wherein the function of the gene is essentially the same as the gene based on the kudzu isoprene synthase (IspS) or poplar IspS (IspS). Additionally, analogous genes include at least 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99% or 100% sequence identity with the sequence of the kudzu isoprene synthase. In additional embodiments more than one of the above properties applies to the sequence. Analogous sequences are determined by known methods of sequence alignment. A commonly used alignment method is BLAST, although as indicated above and below, there are other methods that also find use in aligning sequences.

[0135] One example of a useful algorithm is PILEUP. PILEUP creates a multiple sequence alignment from a group of related sequences using progressive, pair-wise alignments. It can also plot a tree showing the clustering relationships used to create the alignment. PILEUP uses a simplification of the progressive alignment method of Feng and Doolittle (Feng and Doolittle, J Mol Evol, 35:351-360, 1987). The method is similar to that described by Higgins and Sharp (Higgins and Sharp, CABIOS 5:151-153, 1989). Useful PILEUP parameters including a default gap weight of 3.00, a default gap length weight of 0.10, and weighted end gaps.

[0136] Another example of a useful algorithm is the BLAST algorithm, described by Altschul *et al.*, (Altschul *et al.*, J Mol Biol, 215:403-410, 1990; and Karlin *et al.*, Proc Natl Acad Sci USA, 90:5873-5787, 1993). A particularly useful BLAST program is the WU-BLAST-2 program (*See*, Altschul *et al.*, Meth Enzymol, 266:460-480, 1996). WU-BLAST-2 uses several search parameters, most of which are set to the default values. The adjustable parameters are set with the following values: overlap span =1, overlap fraction = 0.125, word threshold (T) = 11. The HSP S and HSP S2 parameters are dynamic values and are established by the program itself depending upon the composition of the particular sequence and composition of the particular database against which the sequence of interest is being searched. However, the values may be adjusted to increase sensitivity. A % amino acid sequence identity value is determined by the number of matching identical residues divided

by the total number of residues of the "longer" sequence in the aligned region. The "longer" sequence is the one having the most actual residues in the aligned region (gaps introduced by WU-Blast-2 to maximize the alignment score are ignored).

[0137] Thus, "percent (%) nucleic acid sequence identity" is defined as the percentage of nucleotide residues in a candidate sequence that are identical to the nucleotide residues of the starting sequence (*i.e.*, the sequence of interest). A preferred method utilizes the BLASTN module of WU-BLAST-2 set to the default parameters, with overlap span and overlap fraction set to 1 and 0.125, respectively.

[0138] As used herein, the term "hybridization" refers to the process by which a strand of nucleic acid joins with a complementary strand through base pairing, as known in the art.

[0139] A nucleic acid sequence is considered to be "selectively hybridizable" to a reference nucleic acid sequence if the two sequences specifically hybridize to one another under moderate to high stringency hybridization and wash conditions. Hybridization conditions are based on the melting temperature (Tm) of the nucleic acid binding complex or probe. For example, "maximum stringency" typically occurs at about Tm-5°C (5° below the Tm of the probe); "high stringency" at about 5-10°C below the Tm; "intermediate stringency" at about 10-20°C below the Tm of the probe; and "low stringency" at about 20-25°C below the Tm. Functionally, maximum stringency conditions may be used to identify sequences having strict identity or near-strict identity with the hybridization probe; while intermediate or low stringency hybridization can be used to identify or detect polynucleotide sequence homologs.

[0140] Moderate and high stringency hybridization conditions are well known in the art. An example of high stringency conditions includes hybridization at about 42°C in 50% formamide, 5X SSC, 5X Denhardt's solution, 0.5% SDS and 100 μg/ml denatured carrier DNA followed by washing two times in 2X SSC and 0.5% SDS at room temperature and two additional times in 0.1X SSC and 0.5% SDS at 42°C. An example of moderate stringent conditions include an overnight incubation at 37°C in a solution comprising 20% formamide, 5 x SSC (150mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1x SSC at about 37 - 50°C. Those of skill in the art know how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

[0141] As used herein, "recombinant" includes reference to a cell or vector, that has been modified by the introduction of a heterologous nucleic acid sequence or that the cell is

derived from a cell so modified. Thus, for example, recombinant cells express genes that are not found in identical form within the native (non-recombinant) form of the cell or express native genes that are otherwise abnormally expressed, under expressed or not expressed at all as a result of deliberate human intervention. "Recombination," "recombining," and generating a "recombined" nucleic acid are generally the assembly of two or more nucleic acid fragments wherein the assembly gives rise to a chimeric gene.

[0142] In a preferred embodiment, mutant DNA sequences are generated with site saturation mutagenesis in at least one codon. In another preferred embodiment, site saturation mutagenesis is performed for two or more codons. In a further embodiment, mutant DNA sequences have more than 50%, more than 55%, more than 60%, more than 65%, more than 70%, more than 75%, more than 80%, more than 85%, more than 90%, more than 95%, or more than 98% homology with the wild-type sequence. In alternative embodiments, mutant DNA is generated *in vivo* using any known mutagenic procedure such as, for example, radiation, nitrosoguanidine and the like. The desired DNA sequence is then isolated and used in the methods provided herein.

[0143] As used herein, the term "target sequence" refers to a DNA sequence in the host cell that encodes the sequence where it is desired for the incoming sequence to be inserted into the host cell genome. In some embodiments, the target sequence encodes a functional wild-type gene or operon, while in other embodiments the target sequence encodes a functional mutant gene or operon, or a non-functional gene or operon.

[0144] As used herein, a "flanking sequence" refers to any sequence that is either upstream or downstream of the sequence being discussed (*e.g.*, for genes A-B-C, gene B is flanked by the A and C gene sequences). In a preferred embodiment, the incoming sequence is flanked by a homology box on each side. In another embodiment, the incoming sequence and the homology boxes comprise a unit that is flanked by stuffer sequence on each side. In some embodiments, a flanking sequence is present on only a single side (either 3' or 5'), but in preferred embodiments, it is on each side of the sequence being flanked. In some embodiments, a flanking sequence is present on only a single side (either 3' or 5'), while in preferred embodiments, it is present on each side of the sequence being flanked.

[0145] As used herein, the term "stuffer sequence" refers to any extra DNA that flanks homology boxes (typically vector sequences). However, the term encompasses any non-homologous DNA sequence. Not to be limited by any theory, a stuffer sequence provides a noncritical target for a cell to initiate DNA uptake.

[0146] As used herein, the terms "amplification" and "gene amplification" refer to a process by which specific DNA sequences are disproportionately replicated such that the amplified gene becomes present in a higher copy number than was initially present in the genome. In some embodiments, selection of cells by growth in the presence of a drug (*e.g.*, an inhibitor of an inhibitable enzyme) results in the amplification of either the endogenous gene encoding the gene product required for growth in the presence of the drug or by amplification of exogenous (*i.e.*, input) sequences encoding this gene product, or both.

[0147] "Amplification" is a special case of nucleic acid replication involving template specificity. It is to be contrasted with non-specific template replication (*i.e.*, replication that is template-dependent but not dependent on a specific template). Template specificity is here distinguished from fidelity of replication (*i.e.*, synthesis of the proper polynucleotide sequence) and nucleotide (ribo- or deoxyribo-) specificity. Template specificity is frequently described in terms of "target" specificity. Target sequences are "targets" in the sense that they are sought to be sorted out from other nucleic acid. Amplification techniques have been designed primarily for this sorting out.

[0148] As used herein, the term "co-amplification" refers to the introduction into a single cell of an amplifiable marker in conjunction with other gene sequences (*i.e.*, comprising one or more non-selectable genes such as those contained within an expression vector) and the application of appropriate selective pressure such that the cell amplifies both the amplifiable marker and the other, non-selectable gene sequences. The amplifiable marker may be physically linked to the other gene sequences or alternatively two separate pieces of DNA, one containing the amplifiable marker and the other containing the non-selectable marker, may be introduced into the same cell.

[0149] As used herein, the terms "amplifiable marker," "amplifiable gene," and "amplification vector" refer to a gene or a vector encoding a gene, which permits the amplification of that gene under appropriate growth conditions.

[0150] "Template specificity" is achieved in most amplification techniques by the choice of enzyme. Amplification enzymes are enzymes that, under conditions they are used, will process only specific sequences of nucleic acid in a heterogeneous mixture of nucleic acid. For example, in the case of Qß replicase, MDV-1 RNA is the specific template for the replicase (*See e.g.*, Kacian *et al.*, Proc Natl Acad Sci USA 69:3038, 1972) and other nucleic acids are not replicated by this amplification enzyme. Similarly, in the case of T7 RNA polymerase, this amplification enzyme has a stringent specificity for its own promoters (*See*, Chamberlin *et al.*, Nature 228:227, 1970). In the case of T4 DNA ligase, the enzyme will not

ligate the two oligonucleotides or polynucleotides, where there is a mismatch between the oligonucleotide or polynucleotide substrate and the template at the ligation junction (*See*, Wu and Wallace, Genomics 4:560, 1989). Finally, *Taq* and *Pfu* polymerases, by virtue of their ability to function at high temperature, are found to display high specificity for the sequences bounded and thus defined by the primers; the high temperature results in thermodynamic conditions that favor primer hybridization with the target sequences and not hybridization with non-target sequences.

[0151] As used herein, the term "amplifiable nucleic acid" refers to nucleic acids, which may be amplified by any amplification method. It is contemplated that "amplifiable nucleic acid" will usually comprise "sample template."

[0152] As used herein, the term "sample template" refers to nucleic acid originating from a sample, which is analyzed for the presence of "target" (defined below). In contrast, "background template" is used in reference to nucleic acid other than sample template, which may or may not be present in a sample. Background template is most often inadvertent. It may be the result of carryover, or it may be due to the presence of nucleic acid contaminants sought to be purified away from the sample. For example, nucleic acids from organisms other than those to be detected may be present as background in a test sample.

[0153] As used herein, the term "primer" refers to an oligonucleotide, whether occurring naturally as in a purified restriction digest or produced synthetically, which is capable of acting as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product which is complementary to a nucleic acid strand is induced, (*i.e.*, in the presence of nucleotides and an inducing agent such as DNA polymerase and at a suitable temperature and pH). The primer is preferably single stranded for maximum efficiency in amplification, but may alternatively be double stranded. If double stranded, the primer is first treated to separate its strands before being used to prepare extension products. Preferably, the primer is an oligodeoxyribonucleotide. The primer must be sufficiently long to prime the synthesis of extension products in the presence of the inducing agent. The exact lengths of the primers will depend on many factors, including temperature, source of primer and the use of the method.

[0154] As used herein, the term "probe" refers to an oligonucleotide (*i.e.*, a sequence of nucleotides), whether occurring naturally as in a purified restriction digest or produced synthetically, recombinantly or by PCR amplification, which is capable of hybridizing to another oligonucleotide of interest. A probe may be single-stranded or double-stranded. Probes are useful in the detection, identification and isolation of particular gene sequences. It

is contemplated that any probe used in the present invention will be labeled with any "reporter molecule," so that is detectable in any detection system, including, but not limited to enzyme (*e.g.*, ELISA, as well as enzyme-based histochemical assays), fluorescent, radioactive, and luminescent systems. It is not intended that the present invention be limited to any particular detection system or label.

[0155] As used herein, the term "target," when used in reference to the polymerase chain reaction, refers to the region of nucleic acid bounded by the primers used for polymerase chain reaction. Thus, the "target" is sought to be sorted out from other nucleic acid sequences. A "segment" is defined as a region of nucleic acid within the target sequence.

[0156] As used herein, in one embodiment, the term "polymerase chain reaction" ("PCR") refers to the methods of U.S. Patent Nos. 4,683,195 4,683,202, and 4,965,188, hereby incorporated by reference, which include methods for increasing the concentration of a segment of a target sequence in a mixture of genomic DNA without cloning or purification. This process for amplifying the target sequence consists of introducing a large excess of two oligonucleotide primers to the DNA mixture containing the desired target sequence, followed by a precise sequence of thermal cycling in the presence of a DNA polymerase. The two primers are complementary to their respective strands of the double stranded target sequence. To effect amplification, the mixture is denatured and the primers then annealed to their complementary sequences within the target molecule. Following annealing, the primers are extended with a polymerase so as to form a new pair of complementary strands. The steps of denaturation, primer annealing and polymerase extension can be repeated many times (*i.e.*, denaturation, annealing and extension constitute one "cycle"; there can be numerous "cycles") to obtain a high concentration of an amplified segment of the desired target sequence. The length of the amplified segment of the desired target sequence is determined by the relative positions of the primers with respect to each other, and therefore, this length is a controllable parameter. By virtue of the repeating aspect of the process, the method is referred to as the "polymerase chain reaction" (hereinafter "PCR"). Because the desired amplified segments of the target sequence become the predominant sequences (in terms of concentration) in the mixture, they are said to be "PCR amplified".

[0157] As used herein, the term "amplification reagents" refers to those reagents (deoxyribonucleotide triphosphates, buffer, etc.), needed for amplification except for primers, nucleic acid template and the amplification enzyme. Typically, amplification reagents along with other reaction components are placed and contained in a reaction vessel (test tube, microwell, etc.).

[0158] With PCR, it is possible to amplify a single copy of a specific target sequence in genomic DNA to a level detectable by several different methodologies (*e.g.*, hybridization with a labeled probe; incorporation of biotinylated primers followed by avidin-enzyme conjugate detection; incorporation of ^{32}P-labeled deoxynucleotide triphosphates, such as dCTP or dATP, into the amplified segment). In addition to genomic DNA, any oligonucleotide or polynucleotide sequence can be amplified with the appropriate set of primer molecules. In particular, the amplified segments created by the PCR process itself are, themselves, efficient templates for subsequent PCR amplifications.

[0159] As used herein, the terms "PCR product," "PCR fragment," and "amplification product" refer to the resultant mixture of compounds after two or more cycles of the PCR steps of denaturation, annealing and extension are complete. These terms encompass the case where there has been amplification of one or more segments of one or more target sequences.

[0160] As used herein, the term "RT-PCR" refers to the replication and amplification of RNA sequences. In this method, reverse transcription is coupled to PCR, most often using a one enzyme procedure in which a thermostable polymerase is employed, as described in U.S. Patent No. 5,322,770, herein incorporated by reference. In RT-PCR, the RNA template is converted to cDNA due to the reverse transcriptase activity of the polymerase, and then amplified using the polymerizing activity of the polymerase (*i.e.*, as in other PCR methods).

[0161] As used herein, the terms "restriction endonucleases" and "restriction enzymes" refer to bacterial enzymes, each of which cut double-stranded DNA at or near a specific nucleotide sequence.

[0162] A "restriction site" refers to a nucleotide sequence recognized and cleaved by a given restriction endonuclease and is frequently the site for insertion of DNA fragments. In certain embodiments of the invention restriction sites are engineered into the selective marker and into 5' and 3' ends of the DNA construct.

[0163] As used herein, the term "chromosomal integration" refers to the process whereby an incoming sequence is introduced into the chromosome of a host cell. The homologous regions of the transforming DNA align with homologous regions of the chromosome. Subsequently, the sequence between the homology boxes is replaced by the incoming sequence in a double crossover (*i.e.*, homologous recombination). In some embodiments of the present invention, homologous sections of an inactivating chromosomal segment of a DNA construct align with the flanking homologous regions of the indigenous chromosomal region of the *Escherichia* chromosome. Subsequently, the indigenous chromosomal region is deleted by the DNA construct in a double crossover (*i.e.*, homologous recombination).

[0164] "Homologous recombination" means the exchange of DNA fragments between two DNA molecules or paired chromosomes at the site of identical or nearly identical nucleotide sequences. In a preferred embodiment, chromosomal integration is homologous recombination. "Homologous sequences" as used herein means a nucleic acid or polypeptide sequence having 100%, 99%, 98%, 97%, 96%, 95%, 94%, 93%, 92%, 91%, 90%, 88%, 85%, 80%, 75%, or 70% sequence identity to another nucleic acid or polypeptide sequence when optimally aligned for comparison. In some embodiments, homologous sequences have between 85% and 100% sequence identity, while in other embodiments there is between 90% and 100% sequence identity, and in more preferred embodiments, there is 95% and 100% sequence identity.

[0165] As used herein "amino acid" refers to peptide or protein sequences or portions thereof. The terms "protein," "peptide," and "polypeptide" are used interchangeably.

[0166] As used herein, the term "heterologous protein" refers to a protein or polypeptide that does not naturally occur in the host cell. Examples of heterologous proteins include enzymes such as isoprene synthases. In some embodiments, the genes encoding the proteins are naturally occurring genes, while in other embodiments mutated and/or synthetic genes are used.

[0167] As used herein, "homologous protein" refers to a protein or polypeptide native or naturally occurring in a cell. In preferred embodiments, the cell is a Gram-negative cell, while in particularly preferred embodiments the cell is an *Escherichia* host cell.

[0168] An enzyme is "overexpressed" in a host cell if the enzyme is expressed in the cell at a higher level that the level at which it is expressed in a corresponding wild-type cell.

[0169] The terms "protein" and "polypeptide" are used interchangeability herein. The 3-letter code for amino acids as defined in conformity with the IUPAC-IUB Joint Commission on Biochemical Nomenclature (JCBN) is used through out this disclosure. It is also understood that a polypeptide may be coded for by more than one nucleotide sequence due to the degeneracy of the genetic code.

[0170] The term "mature" form of a protein or peptide refers to the final functional form of the protein or peptide. To exemplify, a mature form of kudzu isoprene synthase includes the amino acid sequence of SEQ ID NO:2.

[0171] The term "precursor" form of a protein or peptide refers to a mature form of the protein having a prosequence operably linked to the amino or carbonyl terminus of the protein. The precursor may also have a "signal" sequence operably linked, to the amino terminus of the prosequence. The precursor may also have additional polynucleotides that are

involved in post-translational activity (*e.g.*, polynucleotides cleaved therefrom to leave the mature form of a protein or peptide).

[0172] "Naturally occurring enzyme" refers to an enzyme having the unmodified amino acid sequence identical to that found in nature. Naturally occurring enzymes include native enzymes, those enzymes naturally expressed or found in the particular microorganism.

[0173] The term "identical" in the context of two nucleic acids or polypeptide sequences refers to the residues in the two sequences that are the same when aligned for maximum correspondence, as measured using one of the following sequence comparison or analysis algorithms.

[0174] The term "optimal alignment" refers to the alignment giving the highest percent identity score.

[0175] "Percent sequence identity," "percent amino acid sequence identity," "percent gene sequence identity," and/or "percent nucleic acid/polynucloetide sequence identity," with respect to two amino acid, polynucleotide and/or gene sequences (as appropriate), refer to the percentage of residues that are identical in the two sequences when the sequences are optimally aligned. Thus, 80% amino acid sequence identity means that 80% of the amino acids in two optimally aligned polypeptide sequences are identical.

[0176] The phrase "substantially identical" in the context of two nucleic acids or polypeptides thus refers to a polynucleotide or polypeptide that comprising at least 70% sequence identity, preferably at least 75%, preferably at least 80%, preferably at least 85%, preferably at least 90%, preferably at least 95%, preferably at least 97% , preferably at least 98% and preferably at least 99% sequence identity as compared to a reference sequence using the programs or algorithms (*e.g.*, BLAST, ALIGN, CLUSTAL) using standard parameters. One indication that two polypeptides are substantially identical is that the first polypeptide is immunologically cross-reactive with the second polypeptide. Typically, polypeptides that differ by conservative amino acid substitutions are immunologically cross-reactive. Thus, a polypeptide is substantially identical to a second polypeptide, for example, where the two peptides differ only by a conservative substitution. Another indication that two nucleic acid sequences are substantially identical is that the two molecules hybridize to each other under stringent conditions (*e.g.*, within a range of medium to high stringency).

[0177] The term "isolated" or "purified" refers to a material that is removed from its original environment (*e.g.*, the natural environment if it is naturally occurring). For example, the material is said to be "purified" when it is present in a particular composition in a higher or lower concentration than exists in a naturally occurring or wild type organism (e.g., kudzu)

or in combination with components not normally present upon expression from a naturally occurring or wild type organism. For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or polypeptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotides could be part of a vector, and/or such polynucleotides or polypeptides could be part of a composition, and still be isolated in that such vector or composition is not part of its natural environment. In preferred embodiments, a nucleic acid or protein is said to be purified, for example, if it gives rise to essentially one band in an electrophoretic gel or blot.

[0178] The term "isolated", when used in reference to a DNA sequence, refers to a DNA sequence that has been removed from its natural genetic milieu and is thus free of other extraneous or unwanted coding sequences, and is in a form suitable for use within genetically engineered protein production systems. Similarly, the term "isolated", when used in reference to a recombinant DNA sequence, refers to a DNA sequence that has been removed from the genetic milieu of the host organism and is thus free of other extraneous or unwanted coding sequences (e.g., kudzu IspS expression vector propagated in *E. coli*). Such isolated molecules are those that are separated from their natural environment and include cDNA and genomic clones. Isolated DNA molecules of the present invention are free of other genes with which they are ordinarily associated, but may include naturally occurring 5' and 3' untranslated regions such as promoters and terminators. The identification of associated regions will be evident to one of ordinary skill in the art (*See e.g.*, Dynan and Tijan, Nature 316:774-78, 1985). The term "an isolated DNA sequence" is alternatively referred to as "a cloned DNA sequence".

[0179] The term "isolated," when used in reference to a protein, refers to a protein that is found in a condition other than its native environment. In a preferred form, the isolated protein is substantially free of other proteins, particularly other homologous proteins. Similarly, the term "isolated", when used in reference to a recombinantly produced protein, refers to a protein that has been removed from the proteinaceous milieu of the host organism and is thus free of other extraneous or unwanted proteins (e.g., recombinant kudzu IspS produced in *E. coli*). An isolated protein is more than 10% pure, preferably more than 20% pure, and even more preferably more than 30% pure, as determined by SDS-PAGE. Further aspects of the invention encompass the protein in a highly purified form (*i.e.*, more than 40% pure, more than 60% pure, more than 80% pure, more than 90% pure, more than 95% pure, more than 97% pure, and even more than 99% pure), as determined by SDS-PAGE.

[0180] The following cassette mutagenesis method may be used to facilitate the construction of the enzyme variants of the present invention, although other methods may be used. First, as described herein, a naturally-occurring gene encoding the enzyme is obtained and sequenced in whole or in part. Then, the sequence is scanned for a point at which it is desired to make a mutation (deletion, insertion or substitution) of one or more amino acids in the encoded enzyme. The sequences flanking this point are evaluated for the presence of restriction sites for replacing a short segment of the gene with an oligonucleotide pool which when expressed will encode various mutants. Such restriction sites are preferably unique sites within the protein gene so as to facilitate the replacement of the gene segment. However, any convenient restriction site that is not overly redundant in the enzyme gene may be used, provided the gene fragments generated by restriction digestion can be reassembled in proper sequence. If restriction sites are not present at locations within a convenient distance from the selected point (from 10 to 15 nucleotides), such sites are generated by substituting nucleotides in the gene in such a fashion that neither the reading frame nor the amino acids encoded are changed in the final construction. Mutation of the gene in order to change its sequence to conform to the desired sequence is accomplished by M13 primer extension in accord with generally known methods. The task of locating suitable flanking regions and evaluating the needed changes to arrive at two convenient restriction site sequences is made routine by the redundancy of the genetic code, a restriction enzyme map of the gene and the large number of different restriction enzymes. Note that if a convenient flanking restriction site is available, the above method need be used only in connection with the flanking region that does not contain a site.

[0181] Once the naturally-occurring DNA and/or synthetic DNA is cloned, the restriction sites flanking the positions to be mutated are digested with the cognate restriction enzymes and a plurality of end termini-complementary oligonucleotide cassettes are ligated into the gene. The mutagenesis is simplified by this method because all of the oligonucleotides can be synthesized so as to have the same restriction sites, and no synthetic linkers are necessary to create the restriction sites.

[0182] As used herein, "corresponding to," refers to a residue at the enumerated position in a protein or peptide, or a residue that is analogous, homologous, or equivalent to an enumerated residue in a protein or peptide. As used herein, "corresponding region," generally refers to an analogous position along related proteins or a parent protein.

[0183] As used herein, the term, "combinatorial mutagenesis" refers to methods in which libraries of variants of a starting sequence are generated. In these libraries, the variants

contain one or several mutations chosen from a predefined set of mutations. In addition, the methods provide means to introduce random mutations, which were not members of the predefined set of mutations. In some embodiments, the methods include those set forth in U.S. Application No. 09/699,250, hereby incorporated by reference. In alternative embodiments, combinatorial mutagenesis methods encompass commercially available kits (*e.g.,* QUIKCHANGE Multisite mutagenesis kit, Stratagene, San Diego, CA).

[0184] As used herein, the term "library of mutants" refers to a population of cells which are identical in most of their genome but include different homologues of one or more genes. Such libraries can be used, for example, to identify genes or operons with improved traits.

[0185] As used herein, the terms "starting gene" and "parent gene" refer to a gene of interest that encodes a protein of interest that is to be improved and/or changed using the present invention.

[0186] As used herein, the terms "multiple sequence alignment" and "MSA" refer to the sequences of multiple homologs of a starting gene that are aligned using an algorithm (*e.g.*, Clustal W).

[0187] As used herein, the terms "consensus sequence" and "canonical sequence" refer to an archetypical amino acid sequence against which all variants of a particular protein or sequence of interest are compared. The terms also refer to a sequence that sets forth the nucleotides that are most often present in a DNA sequence of interest. For each position of a gene, the consensus sequence gives the amino acid that is most abundant in that position in the MSA.

[0188] As used herein, the term "consensus mutation" refers to a difference in the sequence of a starting gene and a consensus sequence. Consensus mutations are identified by comparing the sequences of the starting gene and the consensus sequence obtained from a MSA. In some embodiments, consensus mutations are introduced into the starting gene such that it becomes more similar to the consensus sequence. Consensus mutations also include amino acid changes that change an amino acid in a starting gene to an amino acid that is more frequently found in an MSA at that position relative to the frequency of that amino acid in the starting gene. Thus, the term consensus mutation comprises all single amino acid changes that replace an amino acid of the starting gene with an amino acid that is more abundant than the amino acid in the MSA.

[0189] The terms "modified sequence" and "modified genes" are used interchangeably herein to refer to a sequence that includes a deletion, insertion or interruption of naturally occurring nucleic acid sequence. In some preferred embodiments, the expression product of

the modified sequence is a truncated protein (*e.g.*, if the modification is a deletion or interruption of the sequence). In some particularly preferred embodiments, the truncated protein retains biological activity. In alternative embodiments, the expression product of the modified sequence is an elongated protein (*e.g.*, modifications comprising an insertion into the nucleic acid sequence). In some embodiments, an insertion leads to a truncated protein (*e.g.*, when the insertion results in the formation of a stop codon). Thus, an insertion may result in either a truncated protein or an elongated protein as an expression product.

[0190] As used herein, the terms "mutant sequence" and "mutant gene" are used interchangeably and refer to a sequence that has an alteration in at least one codon occurring in a host cell's wild-type sequence. The expression product of the mutant sequence is a protein with an altered amino acid sequence relative to the wild-type. The expression product may have an altered functional capacity (*e.g.*, enhanced enzymatic activity).

[0191] The terms "mutagenic primer" or "mutagenic oligonucleotide" (used interchangeably herein) are intended to refer to oligonucleotide compositions which correspond to a portion of the template sequence and which are capable of hybridizing thereto. With respect to mutagenic primers, the primer will not precisely match the template nucleic acid, the mismatch or mismatches in the primer being used to introduce the desired mutation into the nucleic acid library. As used herein, "non-mutagenic primer" or "non-mutagenic oligonucleotide" refers to oligonucleotide compositions that match precisely to the template nucleic acid. In one embodiment of the invention, only mutagenic primers are used. In another preferred embodiment of the invention, the primers are designed so that for at least one region at which a mutagenic primer has been included, there is also non-mutagenic primer included in the oligonucleotide mixture. By adding a mixture of mutagenic primers and non-mutagenic primers corresponding to at least one of the mutagenic primers, it is possible to produce a resulting nucleic acid library in which a variety of combinatorial mutational patterns are presented. For example, if it is desired that some of the members of the mutant nucleic acid library retain their parent sequence at certain positions while other members are mutant at such sites, the non-mutagenic primers provide the ability to obtain a specific level of non-mutant members within the nucleic acid library for a given residue. The methods of the invention employ mutagenic and non-mutagenic oligonucleotides which are generally between 10-50 bases in length, more preferably about 15-45 bases in length. However, it may be necessary to use primers that are either shorter than 10 bases or longer than 50 bases to obtain the mutagenesis result desired. With respect to corresponding mutagenic and non-mutagenic primers, it is not necessary that the corresponding

oligonucleotides be of identical length, but only that there is overlap in the region corresponding to the mutation to be added.

[0192] Primers may be added in a pre-defined ratio according to the present invention. For example, if it is desired that the resulting library have a significant level of a certain specific mutation and a lesser amount of a different mutation at the same or different site, by adjusting the amount of primer added, it is possible to produce the desired biased library. Alternatively, by adding lesser or greater amounts of non-mutagenic primers, it is possible to adjust the frequency with which the corresponding mutation(s) are produced in the mutant nucleic acid library.

[0193] The terms "wild-type sequence" or "wild-type gene" are used interchangeably herein, to refer to a sequence that is native or naturally occurring in a host cell. In some embodiments, the wild-type sequence refers to a sequence of interest that is the starting point of a protein-engineering project. The wild-type sequence may encode either a homologous or heterologous protein. A homologous protein is one the host cell would produce without intervention. A heterologous protein is one that the host cell would not produce but for the intervention.

[0194] As used herein the term "lysate" refers to a solution containing the contents of lysed cells. In some embodiments, the lysate is a bacterial cell lysate (e.g., *E. coli* cells lysed using READYLYSE™ lysozyme solution from Epicentre; or *E. coli* cells lysed using a French Pressure cell).

[0195] As used herein the term "lysozyme" refers to a glycosidase that hydrolyzes the bond between N-acetyl muramic acid and N-acetul glucosamine, thus cleaving an important polymer in the cell wall of many bacteria. Suitable lysozymes for use with the present invention include but are not limited to hen egg white lysozyme (Sigma), T4 lysozyme, recombinant non-mammalian, non-avian lysozyme (READYLYSE™), or a fungal lysozyme.

[0196] As used herein, the term "headspace" refers to the vapor/air mixture trapped above a solid or liquid sample in a sealed vessel.

[0197] As used herein, the terms "high throughput screening" and "HTS" refer to measuring isoprene in at least 96 samples in 4 hours or less. In preferred embodiments, the sample volume is less than 2 mL.

[0198] Unless otherwise noted, all component or composition levels are in reference to the active level of that component or composition, and are exclusive of impurities, for example, residual solvents or by-products, which may be present in commercially available sources.

[0199] Enzyme components weights are based on total active protein. All percentages and ratios are calculated by weight unless otherwise indicated. All percentages and ratios are calculated based on the total composition unless otherwise.

DETAILED DESCRIPTION OF THE INVENTION

[0200] Isoprene monomer is employed in the manufacture of polyisoprene and various copolymers (with isobutylene, butadiene, styrene, or other monomers). To build a strain (prokaryotic or eukaryotic) capable of producing commercially viable levels of isoprene requires optimization of the entire pathway, either MVA to isoprene or DXP to isoprene. A key enzyme in the pathway is isoprene synthase (IspS), which converts the precursor DMAPP to isoprene. The only isoprene synthases (IspS) identified to date are those from plants such as poplar, English oak and kudzu vine. Although some bacteria, such as *Bacillus subtilis*, also produce isoprene, a prokaryotic IspS has yet to be identified and the native IspS activity in *Bacillus* is not sufficient for a commercial process. The plant IspS enzymes identified to date have been partially characterized in part by expression in *E. coli* and some of the kinetic parameters of these enzymes have been determined *in vitro* with purified protein. However, the kinetic parameters (Km, rate etc) of the native IspS enzymes are insufficient for commercial production of isoprene in a biological host.

[0201] To solve this problem as described herein, a plant IspS is expressed in a bacterial host. In addition the IspS is engineered for a change in a property of interest. Characterization of wild-type and mutant IspS is accomplished via any means or "test" suitable and is preferably based on the assessment of properties of interest. Properties of interest include but are not limited to: pH optima, temperature stability (e.g., T_m value), intracellular and extracellular solubility, K_m value, k_{cat} value, or specific activity, as well as sensitivity to potential inhibitors including substrate or product inhibition. Oxidative and proteolytic stability are also of interest. Furthermore, activation or inhibition due to metal ion effects and ionic strength is of interest. These properties and parameters can be assessed by the conversion of DMAPP to isoprene *in vitro* with purified or partially purified isoprene synthase or *in vivo* in the context of a host organism such as *E. coli* expressing the DXP pathway, the MVA pathway, or both. It is contemplated that enzymes having various degrees of stability, solubility, activity, and/or expression level in one or more of test conditions will find use in the present invention for the production of isoprene in a diversity of hosts. High throughput methods such as those described in Example 10 are required to investigate these properties in an economical manner.

[0202] The invention features compositions and methods for the production of increased amounts of isoprene. In particular, these compositions and methods increase the rate of isoprene production and increase the total amount of isoprene that is produced. The biosynthetic processes for isoprene production described herein are a desirable alternative to using natural rubber. As discussed further below, the amount of isoprene produced by cells can be greatly increased by introducing a heterologous nucleic acid encoding an isoprene synthase (IspS) polypeptide into the cells. Isoprene synthase polypeptides convert dimethylallyl diphosphate (DMAPP) into isoprene. As shown in the examples, a heterologous *Pueraria montana* (kudzu) isoprene synthase polypeptide and variants thereof was expressed in Gram-negative bacterial cells (e.g., *Escherichia coli*). Also shown in the examples and contemplated within the scope of the invention are poplar isoprene synthase polypeptide and variants thereof was expressed in Gram-negative bacterial cells (e.g., *Escherichia coli*).

[0203] Heterologous expression of a plant IspS in bacterial host cells resulted in the production of more isoprene than the corresponding cells lacking the plant IspS.

[0204] It has been shown that mutating amino-acid residues on the surface of protease enzymes can improve their activity, expression, and stability (WO2008/153925, WO2008/153934, WO2008/153935). Surprisingly, we have found that mutating amino-acid residues on the surface of a completely different enzyme, isoprene synthase, can enhance its expression, solubility, and activity. L70R is an example of such a beneficial surface mutation.

[0205] Elucidation of the three-dimensional structure of an enzyme is essential for accurately identifying amino-acid residues on its surface. Homology modeling using structures with sequences approximately 40% identical to isoprene synthase (e.g., bornyl synthase and limonene synthase, the enzymes of known structure with closest identity to isoprene synthase) can reveal gross aspects of the modeled enzyme structure, but is insufficient to precisely identify surface-exposed residues and quantify their degree of surface exposure. Surface exposure of an amino-acid residue is quantified by the percentage of solvent-accessible surface area of its side chain.

[0206] The following classes of mutations in isoprene synthase may improve solubility of the enzyme by targeting amino-acid residues that are >50% solvent-exposed, preferably >65% solvent-exposed, and most preferably >85% solvent-exposed:

Hydrophobic → positively charged, and vice versa

Hydrophobic → negatively charged, and vice versa

Hydrophobic → neutral polar, and vice versa

Neutral polar → positively charged, and vice versa

Neutral polar → negatively charged, and vice versa

Positively charged → negatively charged, and vice versa

[0207] Additionally isoprene production by cells containing a heterologous isoprene synthase nucleic acid can be enhanced by increasing the amount of a 1-deoxy-D-xylulose-5-phosphate synthase (DXS) polypeptide, and/or an isopentenyl diphosphate isomerase (IDI) polypeptide, expressed by the cells. For example, a DXS nucleic acid and/or an IDI nucleic acid can be introduced into the cells. The DXS nucleic acid may be a heterologous nucleic acid or a duplicate copy of an endogenous nucleic acid. Similarly, the IDI nucleic acid may be a heterologous nucleic acid or a duplicate copy of an endogenous nucleic acid. In some embodiments, the amount of DXS and/or IDI polypeptide is increased by replacing the endogenous DXS and/or IDI promoters or regulatory regions with other promoters and/or regulatory regions that result in greater transcription of the DXS and/or IDI nucleic acids. In some embodiments, the cells contain both a heterologous nucleic acid encoding an isoprene synthase polypeptide (*e.g.*, a plant isoprene synthase nucleic acid) and a duplicate copy of an endogenous nucleic acid encoding an isoprene synthase polypeptide.

[0208] The encoded DXS and IDI polypeptides are part of the DXP pathway for the biosynthesis of isoprene (Figure 15). DXS polypeptides convert pyruvate and D-glyceraldehyde-3-phosphate into 1-deoxy-D-xylulose-5-phosphate. While not intending to be bound by any particular theory, it is believed that increasing the amount of DXS polypeptide increases the flow of carbon through the DXP pathway, leading to greater isoprene production. IDI polypeptides catalyze the interconversion of isopentenyl diphosphate (IPP) and dimethylallyl diphosphate (DMAPP). While not intending to be bound by any particular theory, it is believed that increasing the amount of IDI polypeptide in cells increases the amount of IPP that is converted into DMAPP, which in turn is converted into isoprene.

[0209] In some embodiments the production of isoprene by cells containing a heterologous isoprene synthase nucleic acid can be augmented by increasing expression of a MVA polypeptide in the cells (Figure 15). Exemplary MVA pathways polypeptides include any of the following polypeptides: acetyl-CoA acetyltransferase (AA-CoA thiolase) polypeptides, 3-hydroxy-3-methylglutaryl-CoA synthase (HMG-CoA synthase) polypeptides, 3-hydroxy-3-methylglutaryl-CoA reductase (HMG-CoA reductase) polypeptides, mevalonate kinase (MVK) polypeptides, phosphomevalonate kinase (PMK) polypeptides, diphosphomevalonte decarboxylase (MVD) polypeptides, IDI polypeptides, and polypeptides (*e.g.*, fusion polypeptides) having an activity of two or more MVA pathway polypeptides. For example,

one or more MVA pathway nucleic acids can be introduced into the cells. In some embodiments, the cells contain the upper MVA pathway, which includes AA-CoA thiolase, HMG-CoA synthase, and HMG-CoA reductase nucleic acids. In some embodiments, the cells contain the lower MVA pathway, which includes MVK, PMK, MVD, and IDI nucleic acids. In some embodiments, the cells contain the entire MVA pathway, which includes AA-CoA thiolase, HMG-CoA synthase, HMG-CoA reductase, MVK, PMK, MVD, and IDI nucleic acids. The MVA pathway nucleic acids may be heterologous nucleic acids or duplicate copies of endogenous nucleic acids. In some embodiments, the amount of one or more MVA pathway polypeptides is increased by replacing the endogenous promoters or regulatory regions for the MVA pathway nucleic acids with other promoters and/or regulatory regions that result in greater transcription of the MVA pathway nucleic acids. In some embodiments, the cells contain both a heterologous nucleic acid encoding an isoprene synthase polypeptide (*e.g.*, a plant isoprene synthase nucleic acid) and a duplicate copy of an endogenous nucleic acid encoding an isoprene synthase polypeptide.

[0210] In some embodiments, at least a portion of the cells maintain the heterologous isoprene synthase, DXS, IDI, and/or MVA pathway nucleic acid for at least about 5, 10, 20, 50, 75, 100, 200, 300, or more cell divisions in a continuous culture (such as a continuous culture without dilution). In some embodiments of any of the aspects of the invention, the nucleic acid comprising the heterologous or duplicate copy of an endogenous isoprene synthase, DXS, IDI, and/or MVA pathway nucleic acid also comprises a selective marker, such as a kanamycin, ampicillin, carbenicillin, gentamicin, hygromycin, phleomycin, bleomycin, neomycin, or chloramphenicol antibiotic resistance nucleic acid.

I. Exemplary Polypeptides and Nucleic Acids

[0211] Various isoprene synthase, DXS, IDI, and/or MVA pathway polypeptides and nucleic acids can be used in the compositions and methods of the invention.

[0212] As used herein, "polypeptides" includes polypeptides, proteins, peptides, fragments of polypeptides, and fusion polypeptides that include part or all of a first polypeptide (*e.g.*, an isoprene synthase, DXS, IDI, or MVA pathway polypeptide) and part or all of a second polypeptide (*e.g.*, a peptide that facilitates purification or detection of the fusion polypeptide, such as a His-tag). In some embodiments, the fusion polypeptide has an activity of two or more MVA pathway polypeptides (such as AA-CoA thiolase and HMG-CoA reductase polypeptides). In some embodiments, the polypeptide is a naturally-occurring polypeptide

(such as the polypeptide encoded by an *Enterococcus faecalis mvaE* nucleic acid) that has an activity of two or more MVA pathway polypeptides.

[0213] In various embodiments, a polypeptide has at least or about 50, 100, 150, 175, 200, 250, 300, 350, 400, or more amino acids. In some embodiments, the polypeptide fragment contains at least or about 25, 50, 75, 100, 150, 200, 300, or more contiguous amino acids from a full-length polypeptide and has at least or about 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, or 100% of an activity of a corresponding full-length polypeptide. In particular embodiments the polypeptide includes a segment of or the entire amino acid sequence of any naturally-occurring isoprene synthase, DXS, IDI, or MVA pathway polypeptide. In some embodiments, the polypeptide has one or more mutations compared to the sequence of a wild-type (*i.e.*, a sequence occurring in nature) isoprene synthase, DXS, IDI, or MVA pathway polypeptide.

[0214] In some embodiments, the polypeptide is an isolated polypeptide. As used herein, an "isolated polypeptide" is not part of a library of polypeptides, such as a library of 2, 5, 10, 20, 50 or more different polypeptides and is separated from at least one component with which it occurs in nature. An isolated polypeptide can be obtained, for example, by expression of a recombinant nucleic acid encoding the polypeptide.

[0215] In some embodiments, the polypeptide is a heterologous polypeptide. By "heterologous polypeptide" is meant a polypeptide whose amino acid sequence is not identical to that of another polypeptide naturally expressed in the same host cell.

[0216] As used herein, a "nucleic acid" refers to two or more deoxyribonucleotides and/or ribonucleotides in either single or double-stranded form. In some embodiments, the nucleic acid is a recombinant nucleic acid. By "recombinant nucleic acid" means a nucleic acid of interest that is free of one or more nucleic acids (*e.g.*, genes), which in the genome occurring in nature of the organism from which the nucleic acid of interest is derived, flank the nucleic acid of interest. The term therefore includes, for example, a recombinant DNA which is incorporated into a vector, into an autonomously replicating plasmid or virus, or into the genomic DNA of a prokaryote or eukaryote, or which exists as a separate molecule (*e.g.*, a cDNA, a genomic DNA fragment, or a cDNA fragment produced by PCR or restriction endonuclease digestion) independent of other sequences.

[0217] In various embodiments, the nucleic acid is a recombinant nucleic acid. For instance, in some embodiments, an isoprene synthase, DXS, IDI, or MVA pathway nucleic acid is operably linked to another nucleic acid encoding all or a portion of another polypeptide such that the recombinant nucleic acid encodes a fusion polypeptide that includes

an isoprene synthase, DXS, IDI, or MVA pathway polypeptide and all or part of another polypeptide (*e.g.*, a peptide that facilitates purification or detection of the fusion polypeptide, such as a His-tag). In some embodiments, part or all of a recombinant nucleic acid is chemically synthesized. In some embodiments, the nucleic acid is a heterologous nucleic acid. By "heterologous nucleic acid" is meant a nucleic acid whose nucleic acid sequence is not identical to that of another nucleic acid naturally found in the same host cell.

[0218] In particular embodiments the nucleic acid includes a segment of or the entire nucleic acid sequence of any naturally-occurring isoprene synthase, DXS, IDI, or MVA pathway nucleic acid. In some embodiments, the nucleic acid includes at least or about 50, 100, 150, 200, 300, 400, 500, 600, 700, 800, or more contiguous nucleotides from a naturally-occurring isoprene synthase nucleic acid DXS, IDI, or MVA pathway nucleic acid. In some embodiments, the nucleic acid has one or more mutations compared to the sequence of a wild-type (*i.e.*, a sequence occurring in nature) isoprene synthase, DXS, IDI, or MVA pathway nucleic acid. In some embodiments, the nucleic acid has one or more mutations (*e.g.*, a silent mutation) that increase the transcription or translation of isoprene synthase, DXS, IDI, or MVA pathway nucleic acid. In some embodiments, the nucleic acid is a degenerate variant of any nucleic acid encoding an isoprene synthase, DXS, IDI, or MVA pathway polypeptide.

[0219] "Codon degeneracy" refers to divergence in the genetic code permitting variation of the nucleotide sequence without affecting the amino acid sequence of an encoded polypeptide. The skilled artisan is well aware of the "codon-bias" exhibited by a specific host cell in usage of nucleotide codons to specify a given amino acid. Therefore, when synthesizing a nucleic acid for improved expression in a host cell, it is desirable in some embodiments to design the nucleic acid such that its frequency of codon usage approaches the frequency of preferred codon usage of the host cell.

[0220] The accession numbers of exemplary isoprene synthase, DXS, IDI, and/or MVA pathway polypeptides and nucleic acids are listed in Appendix 1 of U.S. Application No. 61/013,574, herein incorporated by reference in its entirety, particularly with respect to the amino acid and nucleic acid sequences of isoprene synthase, DXS, IDI, and/or MVA pathway polypeptides and nucleic acids). The Kegg database also contains the amino acid and nucleic acid sequences of numerous exemplary isoprene synthase, DXS, IDI, and/or MVA pathway polypeptides and nucleic acids (*See, e.g.*, the world-wide web at "genome.jp/kegg/pathway/map/map00100.html" and the sequences therein, which are each hereby incorporated by reference in their entireties, particularly with respect to the amino

acid and nucleic acid sequences of isoprene synthase, DXS, IDI, and/or MVA pathway polypeptides and nucleic acids). In some embodiments, one or more of the isoprene synthase, DXS, IDI, and/or MVA pathway polypeptides and/or nucleic acids have a sequence identical to a sequence publicly available on December 12, 2007, such as any of the sequences that correspond to any of the accession numbers in Appendix 1 of U.S. Application No. 61/013,574, or any of the sequences present in the Kegg database as of the date of this filing. Additional exemplary isoprene synthase, DXS, IDI, and/or MVA pathway polypeptides and nucleic acids are described further below.

Exemplary Isoprene Synthase Polypeptides and Nucleic Acids

[0221] As noted above, isoprene synthase polypeptides convert dimethylallyl diphosphate (DMAPP) into isoprene. Exemplary isoprene synthase polypeptides include polypeptides, fragments of polypeptides, peptides, and fusions polypeptides that have at least one activity of an isoprene synthase polypeptide. Standard methods can be used to determine whether a polypeptide has isoprene synthase polypeptide activity by measuring the ability of the polypeptide to convert DMAPP into isoprene *in vitro*, in a cell extract, or *in vivo*. Isoprene synthase polypeptide activity in the cell extract can be measured, for example, as described in Silver *et al.*, J. Biol. Chem. 270:13010-13016, 1995 and references therein, which are each hereby incorporated by reference in their entireties, particularly with respect to assays for isoprene synthase polypeptide activity. DMAPP (Sigma) is evaporated to dryness under a stream of nitrogen and rehydrated to a concentration of 100 mM in 100 mM potassium phosphate buffer pH 8.2 and stored at -20 °C. To perform the assay, a solution of 5 µl of 1M $MgCl_2$, 1 mM (250 µg/ml) DMAPP, 65 µl of Plant Extract Buffer (PEB) (50 mM Tris-HCl, pH 8.0, 20 mM $MgCl_2$, 5% glycerol, and 2 mM DTT) is added to 25 µl of cell extract in a 20 ml Headspace vial with a metal screw cap and teflon coated silicon septum (Agilent Technologies) and cultured at 37 °C for 15 minutes with shaking. The reaction is quenched by adding 200 µl of 250 mM EDTA or by heat inactivation, and isoprene is quantified by GC/MS.

[0222] Exemplary isoprene synthase nucleic acids include nucleic acids that encode a polypeptide, fragment of a polypeptide, peptide, or fusion polypeptide that has at least one activity of an isoprene synthase polypeptide. Exemplary isoprene synthase polypeptides and nucleic acids include naturally-occurring polypeptides and nucleic acids from any of the

source organisms described herein as well as mutant polypeptides and nucleic acids derived from any of the source organisms described herein.

[0223] In some embodiments, the isoprene synthase polypeptide or nucleic acid is from the family Fabaceae, the family Salicaceae, or the family Fagaceae. In some embodiments, the isoprene synthase polypeptide or nucleic acid is a naturally-occurring polypeptide or nucleic acid from *Pueraria montana* (kudzu) (Sharkey *et al.*, Plant Physiology 137: 700-712, 2005), poplar (such as *Populus alba x tremula* CAC35696) Miller *et al.*, Planta 213: 483-487, 2001) aspen (such as *Populus tremuloides*) Silver *et al.*, JBC 270(22): 13010-1316, 1995), or English Oak (*Quercus robur*) (Zimmer *et al.*, WO 98/02550), which are each hereby incorporated by reference in their entireties, particularly with respect to isoprene synthase nucleic acids and the expression of isoprene synthase polypeptides. Suitable isoprene synthases include, but are not limited to, those identified by GenBank Accession Nos. AY341431, AY316691, AY279379, AJ457070, and AY182241, which are each hereby incorporated by reference in their entireties, particularly with respect to sequences of isoprene synthase nucleic acids and polypeptides. In some embodiments, the isoprene synthase polypeptide or nucleic acid is not a naturally-occurring polypeptide or nucleic acid from *Quercus robur* (*i.e.*, the isoprene synthase polypeptide or nucleic acid is an isoprene synthase polypeptide or nucleic acid other than a naturally-occurring polypeptide or nucleic acid from *Quercus robur*). In some embodiments, the isoprene synthase nucleic acid or polypeptide is not a naturally-occurring polypeptide or nucleic acid from poplar (such as *Populus alba x tremula* CAC35696).

Exemplary DXS Polypeptides and Nucleic Acids

[0224] As noted above, 1-deoxy-D-xylulose-5-phosphate synthase (DXS) polypeptides convert pyruvate and D-glyceraldehyde-3-phosphate into 1-deoxy-D-xylulose-5-phosphate. Exemplary DXS polypeptides include polypeptides, fragments of polypeptides, peptides, and fusions polypeptides that have at least one activity of a DXS polypeptide. Standard methods (such as those described herein) can be used to determine whether a polypeptide has DXS polypeptide activity by measuring the ability of the polypeptide to convert pyruvate and D-glyceraldehyde-3-phosphate into 1-deoxy-D-xylulose-5-phosphate *in vitro*, in a cell extract, or *in vivo*. Exemplary DXS nucleic acids include nucleic acids that encode a polypeptide, fragment of a polypeptide, peptide, or fusion polypeptide that has at least one activity of a DXS polypeptide. Exemplary DXS polypeptides and nucleic acids include naturally-occurring polypeptides and nucleic acids from any of the source organisms described herein

as well as mutant polypeptides and nucleic acids derived from any of the source organisms described herein.

Exemplary IDI Polypeptides and Nucleic Acids

[0225] Isopentenyl diphosphate isomerase polypeptides (isopentenyl-diphosphate delta-isomerase or IDI) catalzyes the interconversion of isopentenyl diphosphate (IPP) and dimethylallyl diphosphate (DMAPP) (*e.g.*, converting IPP into DMAPP and/or converting DMAPP into IPP). Exemplary IDI polypeptides include polypeptides, fragments of polypeptides, peptides, and fusions polypeptides that have at least one activity of an IDI polypeptide. Standard methods (such as those described herein) can be used to determine whether a polypeptide has IDI polypeptide activity by measuring the ability of the polypeptide to interconvert IPP and DMAPP *in vitro*, in a cell extract, or *in vivo*. Exemplary IDI nucleic acids include nucleic acids that encode a polypeptide, fragment of a polypeptide, peptide, or fusion polypeptide that has at least one activity of an IDI polypeptide. Exemplary IDI polypeptides and nucleic acids include naturally-occurring polypeptides and nucleic acids from any of the source organisms described herein as well as mutant polypeptides and nucleic acids derived from any of the source organisms described herein.

Exemplary MVA Pathway Polypeptides and Nucleic Acids

[0226] Exemplary MVA pathway polypeptides include acetyl-CoA acetyltransferase (AA-CoA thiolase) polypeptides, 3-hydroxy-3-methylglutaryl-CoA synthase (HMG-CoA synthase) polypeptides, 3-hydroxy-3-methylglutaryl-CoA reductase (HMG-CoA reductase) polypeptides, mevalonate kinase (MVK) polypeptides, phosphomevalonate kinase (PMK) polypeptides, diphosphomevalonte decarboxylase (MVD) polypeptides, IDI polypeptides, and polypeptides (*e.g.*, fusion polypeptides) having an activity of two or more MVA pathway polypeptides. In particular, MVA pathway polypeptides include polypeptides, fragments of polypeptides, peptides, and fusions polypeptides that have at least one activity of an MVA pathway polypeptide. Exemplary MVA pathway nucleic acids include nucleic acids that encode a polypeptide, fragment of a polypeptide, peptide, or fusion polypeptide that has at least one activity of an MVA pathway polypeptide. Exemplary MVA pathway polypeptides and nucleic acids include naturally-occurring polypeptides and nucleic acids from any of the source organisms described herein as well as mutant polypeptides and nucleic acids derived from any of the source organisms described herein.

[0227] In particular, acetyl-CoA acetyltransferase polypeptides (AA-CoA thiolase or AACT) convert two molecules of acetyl-CoA into acetoacetyl-CoA. Standard methods (such as those described herein) can be used to determine whether a polypeptide has AA-CoA thiolase polypeptide activity by measuring the ability of the polypeptide to convert two molecules of acetyl-CoA into acetoacetyl-CoA *in vitro*, in a cell extract, or *in vivo*.

[0228] 3-hydroxy-3-methylglutaryl-CoA synthase (HMG-CoA synthase or HMGS) polypeptides convert acetoacetyl-CoA into 3-hydroxy-3-methylglutaryl-CoA. Standard methods (such as those described herein) can be used to determine whether a polypeptide has HMG-CoA synthase polypeptide activity by measuring the ability of the polypeptide to convert acetoacetyl-CoA into 3-hydroxy-3-methylglutaryl-CoA *in vitro*, in a cell extract, or *in vivo*.

[0229] 3-hydroxy-3-methylglutaryl-CoA reductase (HMG-CoA reductase or HMGR) polypeptides convert 3-hydroxy-3-methylglutaryl-CoA into mevalonate. Standard methods (such as those described herein) can be used to determine whether a polypeptide has HMG-CoA reductase polypeptide activity by measuring the ability of the polypeptide to convert 3-hydroxy-3-methylglutaryl-CoA into mevalonate *in vitro*, in a cell extract, or *in vivo*.

[0230] Mevalonate kinase (MVK) polypeptides phosphorylates mevalonate to form mevalonate-5-phosphate. Standard methods (such as those described herein) can be used to determine whether a polypeptide has MVK polypeptide activity by measuring the ability of the polypeptide to convert mevalonate into mevalonate-5-phosphate *in vitro*, in a cell extract, or *in vivo*.

[0231] Phosphomevalonate kinase (PMK) polypeptides phosphorylates mevalonate-5-phosphate to form mevalonate-5-diphosphate. Standard methods (such as those described herein) can be used to determine whether a polypeptide has PMK polypeptide activity by measuring the ability of the polypeptide to convert mevalonate-5-phosphate into mevalonate-5-diphosphate *in vitro*, in a cell extract, or *in vivo*.

[0232] Diphosphomevalonte decarboxylase (MVD or DPMDC) polypeptides convert mevalonate-5-diphosphate into isopentenyl diphosphate polypeptides (IPP). Standard methods (such as those described herein) can be used to determine whether a polypeptide has MVD polypeptide activity by measuring the ability of the polypeptide to convert mevalonate-5-diphosphate into IPP *in vitro*, in a cell extract, or *in vivo*.

Exemplary Methods for Isolating Nucleic Acids

[0233] Isoprene synthase, DXS, IDI, and/or MVA pathway nucleic acids can be isolated using standard methods. Methods of obtaining desired nucleic acids from a source organism of interest (such as a bacterial genome) are common and well known in the art of molecular biology (*see*, for example, WO 2004/033646 and references cited therein, which are each hereby incorporated by reference in their entireties, particularly with respect to the isolation of nucleic acids of interest). For example, if the sequence of the nucleic acid is known (such as any of the known nucleic acids described herein), suitable genomic libraries may be created by restriction endonuclease digestion and may be screened with probes complementary to the desired nucleic acid sequence. Once the sequence is isolated, the DNA may be amplified using standard primer directed amplification methods such as polymerase chain reaction (PCR) (U.S. Patent No. 4,683,202, which is incorporated by reference in its entirety, particularly with respect to PCR methods) to obtain amounts of DNA suitable for transformation using appropriate vectors. Alternatively, isoprene synthase, DXS, IDI, and/or MVA pathway nucleic acids (such as any isoprene synthase, DXS, IDI, and/or MVA pathway nucleic acids with a known nucleic acid sequence) can be chemically synthesized using standard methods.

[0234] Additional isoprene synthase, DXS, IDI, or MVA pathway polypeptides and nucleic acids that may be suitable for use in the compositions and methods described herein can be identified using standard methods. For example, cosmid libraries of the chromosomal DNA of organisms known to produce isoprene naturally can be constructed in organisms such as *E. coli*, and then screened for isoprene production. Additional methods for obtaining isoprene synthase, DXS, IDI, and/or MVA pathway nucleic acids include screening a metagenomic library by assay (such as the headspace assay described herein) or by PCR using primers directed against nucleotides encoding for a length of conserved amino acids (for example, at least 3 conserved amino acids). Conserved amino acids can be identified by aligning amino acid sequences of known isoprene synthase, DXS, IDI, and/or MVA pathway polypeptides. Conserved amino acids for isoprene synthase polypeptides can be identified based on aligned sequences of known isoprene synthase polypeptides. An organism found to produce isoprene naturally can be subjected to standard protein purification methods (which are well known in the art) and the resulting purified polypeptide can be sequenced using standard methods. Other methods are found in the literature (See, e.g., Julsing et al., Applied. Microbiol. Biotechnol. 75: 1377-84, 2007; and Withers et al., Appl Environ Microbiol. 73:6277-83, 2007, which are each hereby incorporated by reference in their entireties, particularly with respect to identification of nucleic acids involved in the synthesis of isoprene).

[0235] Additionally, standard sequence alignment and/or structure prediction programs can be used to identify additional DXS, IDI, or MVA pathway polypeptides and nucleic acids based on the similarity of their primary and/or predicted polypeptide secondary structure with that of known DXS, IDI, or MVA pathway polypeptides and nucleic acids. Standard databases such as the swissprot-trembl database (world-wide web at "expasy.org", Swiss Institute of Bioinformatics Swiss-Prot group CMU - 1 rue Michel Servet CH-1211 Geneva 4, Switzerland) can also be used to identify isoprene synthase, DXS, IDI, or MVA pathway polypeptides and nucleic acids. The secondary and/or tertiary structure of an isoprene synthase, DXS, IDI, or MVA pathway polypeptide can be predicted using the default settings of standard structure prediction programs, such as PredictProtein (Rost et al., The PredictProtein Server. Nucleic Acids Research 32(Web Server issue):W321-W326, 2004). Alternatively, the actual secondary and/or tertiary structure of an isoprene synthase, DXS, IDI, or MVA pathway polypeptide can be determined using standard methods. Additional isoprene synthase, DXS, IDI, or MVA pathway nucleic acids can also be identified by hybridization to probes generated from known isoprene synthase, DXS, IDI, or MVA pathway nucleic acids.

Exemplary Promoters and Vectors

[0236] Any of the isoprene synthase, DXS, IDI, or MVA pathway nucleic acid described herein can be included in one or more vectors. Accordingly, the invention also features vectors with one more nucleic acids encoding any of the isoprene synthase, DXS, IDI, or MVA pathway polypeptides that are described herein. As used herein, a "vector" means a construct that is capable of delivering, and desirably expressing one or more nucleic acids of interest in a host cell. Examples of vectors include, but are not limited to, plasmids, viral vectors, DNA or RNA expression vectors, cosmids, and phage vectors. In some embodiments, the vector contains a nucleic acid under the control of an expression control sequence.

[0237] As used herein, an "expression control sequence" means a nucleic acid sequence that directs transcription of a nucleic acid of interest. An expression control sequence can be a promoter, such as a constitutive or an inducible promoter, or an enhancer. An "inducible promoter" is a promoter that is active under environmental or developmental regulation. The expression control sequence is operably linked to the nucleic acid segment to be transcribed.

[0238] In some embodiments, the vector contains a selective marker. The term "selective marker" refers to a nucleic acid capable of expression in a host cell that allows for ease of

selection of those host cells containing an introduced nucleic acid or vector. Examples of selectable markers include, but are not limited to, antibiotic resistance nucleic acids (*e.g.*, kanamycin, ampicillin, carbenicillin, gentamicin, hygromycin, phleomycin, bleomycin, neomycin, or chloramphenicol) and/or nucleic acids that confer a metabolic advantage, such as a nutritional advantage on the host cell. In some embodiments, an isoprene synthase, DXS, IDI, or MVA pathway nucleic acid integrates into a chromosome of the cells without a selective marker.

[0239] Suitable vectors are those that are compatible with the host cell employed. Suitable vectors can be derived, for example, from a bacterium, a virus (such as bacteriophage T7 or a M-13 derived phage), a cosmid, a yeast, or a plant. Protocols for obtaining and using such vectors are known in the art (*See, e.g.,* Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor, 1989, which is hereby incorporated by reference in its entirety, particularly with respect to the use of vectors).

[0240] Promoters are well known in the art. Any promoter that functions in the host cell can be used for expression of an isoprene synthase, DXS, IDI, or MVA pathway nucleic acid in the host cell. Initiation control regions or promoters, which are useful to drive expression of isoprene synthase, DXS, IDI, or MVA pathway nucleic acids in various host cells are numerous and familiar to those skilled in the art (*see*, for example, WO 2004/033646 and references cited therein, which are each hereby incorporated by reference in their entireties, particularly with respect to vectors for the expression of nucleic acids of interest). Virtually any promoter capable of driving these nucleic acids is suitable for the present invention including, but not limited to lac, trp, λP_L, λP_R, T7, tac, and trc (useful for expression in *E. coli*).

[0241] In some embodiments, a glucose isomerase promoter is used (*see*, for example, U.S. Patent No. 7,132,527 and references cited therein, which are each hereby incorporated by reference in their entireties, particularly with respect promoters and plasmid systems for expressing polypeptides of interest). Reported glucose isomerase promoter mutants can be used to vary the level of expression of the polypeptide encoded by a nucleic acid operably linked to the glucose isomerase promoter (U.S. Patent No. 7,132,527). In various embodiments, the glucose isomerase promoter is contained in a low, medium, or high copy plasmid (U.S. Patent No. 7,132,527).

[0242] In various embodiments, an isoprene synthase, DXS, IDI, and/or MVA pathway nucleic acid is contained in a low copy plasmid (*e.g.*, a plasmid that is maintained at about 1

to about 4 copies per cell), medium copy plasmid (*e.g.*, a plasmid that is maintained at about 10 to about 15 copies per cell), or high copy plasmid (*e.g.*, a plasmid that is maintained at about 50 or more copies per cell). In some embodiments, the heterologous or extra endogenous isoprene synthase, DXS, IDI, or MVA pathway nucleic acid is operably linked to a T7 promoter. In some embodiments, the heterologous or extra endogenous isoprene synthase, DXS, IDI, or MVA pathway nucleic acid operably linked to a T7 promoter is contained in a medium or high copy plasmid. In some embodiments, the heterologous or extra endogenous isoprene synthase, DXS, IDI, or MVA pathway nucleic acid is operably linked to a Trc promoter. In some embodiments, the heterologous or extra endogenous isoprene synthase, DXS, IDI, or MVA pathway nucleic acid operably linked to a Trc promoter is contained in a medium or high copy plasmid. In some embodiments, the heterologous or extra endogenous isoprene synthase, DXS, IDI, or MVA pathway nucleic acid is operably linked to a Lac promoter. In some embodiments, the heterologous or extra endogenous isoprene synthase, DXS, IDI, or MVA pathway nucleic acid operably linked to a Lac promoter is contained in a low copy plasmid. In some embodiments, the heterologous or extra endogenous isoprene synthase, DXS, IDI, or MVA pathway nucleic acid is operably linked to an endogenous promoter, such as an endogenous *Escherichia, Panteoa, Bacillus, Yarrowia, Streptomyces,* or *Trichoderma* promoter or an endogenous alkaline serine protease, isoprene synthase, DXS, IDI, or MVA pathway promoter. In some embodiments, the heterologous or extra endogenous isoprene synthase, DXS, IDI, or MVA pathway nucleic acid operably linked to an endogenous promoter is contained in a high copy plasmid. In some embodiments, the vector is a replicating plasmid that does not integrate into a chromosome in the cells. In some embodiments part or all of the vector integrates into a chromosome in the cells.

[0243] In some embodiments, the expression vector also includes a termination sequence. Termination control regions may also be derived from various genes native to the host cell. In some embodiments, the termination sequence and the promoter sequence are derived from the same source. In another embodiment, the termination sequence is endogenous to the host cell.

[0244] In some embodiments, the promoter, coding, region, and terminator all originate from the isoprene synthase, DXS, IDI, or MVA pathway nucleic acid to be expressed. In some embodiments, the coding region for an isoprene synthase, DXS, IDI, or MVA pathway nucleic acid is inserted into a general-purpose expression vector such that it is under the transcriptional control of the expression construct promoter and terminator sequences. In

some embodiments, genes or part thereof are inserted downstream of the strong *cbh*1 promoter.

[0245] An isoprene synthase, DXS, IDI, or MVA pathway nucleic acid can be incorporated into a vector, such as an expression vector, using standard techniques (Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, Cold Spring Harbor, 1982, which is hereby incorporated by reference in its entirety, particularly with respect to the screening of appropriate DNA sequences and the construction of vectors). Methods used to ligate the DNA construct comprising a nucleic acid of interest (such as an isoprene synthase, DXS, IDI, or MVA pathway nucleic acid), a promoter, a terminator, and other sequences and to insert them into a suitable vector are well known in the art. For example, restriction enzymes can be used to cleave the isoprene synthase, DXS, IDI, or MVA pathway nucleic acid and the vector. Then, the compatible ends of the cleaved isoprene synthase, DXS, IDI, or MVA pathway nucleic acid and the cleaved vector can be ligated. Linking is generally accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide linkers are used in accordance with conventional practice (*see*, Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor, 1989, and Bennett and Lasure, More Gene Manipulations in Fungi, Academic Press, San Diego, pp 70–76, 1991, which are each hereby incorporated by reference in their entireties, particularly with respect to oligonucleotide linkers). Additionally, vectors can be constructed using known recombination techniques (*e.g.*, Invitrogen Life Technologies, Gateway Technology).

[0246] In some embodiments, it may be desirable to over-express isoprene synthase, DXS, IDI, or MVA pathway nucleic acids at levels far higher than currently found in naturally-occurring cells. This result may be accomplished by the selective cloning of the nucleic acids encoding those polypeptides into multicopy plasmids or placing those nucleic acids under a strong inducible or constitutive promoter. Methods for over-expressing desired polypeptides are common and well known in the art of molecular biology and examples may be found in Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor, 1989, which is hereby incorporated by reference in its entirety, particularly with respect to cloning techniques.

[0247] The following resources include descriptions of additional general methodology useful in accordance with the invention: Kreigler, Gene Transfer and Expression; A Laboratory Manual, 1990; and Ausubel *et al.*, Eds. Current Protocols in Molecular Biology,

1994, which are each hereby incorporated by reference in their entireties, particularly with respect to molecular biology and cloning techniques.

Exemplary Source Organisms

[0248] Isoprene synthase, DXS, IDI, or MVA pathway nucleic acids (and their encoded polypeptides) can be obtained from any organism that naturally contains isoprene synthase, DXS, IDI, and/or MVA pathway nucleic acids. As noted above, isoprene is formed naturally by a variety of organisms, such as bacteria, yeast, plants, and animals. Organisms contain the MVA pathway, DXP pathway, or both the MVA and DXP pathways for producing isoprene (Figure 15). Thus, DXS nucleic acids can be obtained, *e.g.*, from any organism that contains the DXP pathway or contains both the MVA and DXP pathways. IDI and isoprene synthase nucleic acids can be obtained, *e.g.*, from any organism that contains the MVA pathway, DXP pathway, or both the MVA and DXP pathways. MVA pathway nucleic acids can be obtained, *e.g.*, from any organism that contains the MVA pathway or contains both the MVA and DXP pathways.

[0249] In some embodiments, the nucleic acid sequence of the isoprene synthase, DXS, IDI, or MVA pathway nucleic is identical to the sequence of a nucleic acid that is produced by any of the following organisms in nature. In some embodiments, the amino acid sequence of the isoprene synthase, DXS, IDI, or MVA pathway polypeptide is identical to the sequence of a polypeptide that is produced by any of the following organisms in nature. In some embodiments, the isoprene synthase, DXS, IDI, or MVA pathway nucleic acid or polypeptide is a mutant nucleic acid or polypeptide derived from any of the organisms described herein. As used herein, "derived from" refers to the source of the nucleic acid or polypeptide into which one or more mutations is introduced. For example, a polypeptide that is "derived from a plant polypeptide" refers to polypeptide of interest that results from introducing one or more mutations into the sequence of a wild-type (*i.e.*, a sequence occurring in nature) plant polypeptide.

[0250] In some embodiments, the source organism is a bacterium, such as strains of *Escherichia* (e.g., *E. coli*), or strains of *Bacillus* (e.g., *B. subtilis*).

[0251] As used herein, "the genus *Escherichia*" includes all species within the genus "*Escherichia*," as known to those of skill in the art, including but not limited to *E. coli, E. adecarboxylata, E. albertii, E. blattae, E. fergusonii, E. hermannii, E. senegalensis, and E. vulneris.* The genus "*Escherichia*" is defined as Gram-negative, non-spore forming,

facultatively anaerobic, rod-shaped bacteria are classified as members of the Family *Enterobacteriaceae*, Order *Enterobacteriales*, Class *Gamma Proteobacteria*.

[0252] As used herein, "the genus *Bacillus*" includes all species within the genus "*Bacillus*," as known to those of skill in the art, including but not limited to *B. subtilis*, *B. licheniformis*, *B. lentus*, *B. brevis*, *B. stearothermophilus*, *B. alkalophilus*, *B. amyloliquefaciens*, *B. clausii*, *B. halodurans*, *B. megaterium*, *B. coagulans*, *B. circulans*, *B. lautus*, and *B. thuringiensis*. It is recognized that the genus *Bacillus* continues to undergo taxonomical reorganization. Thus, it is intended that the genus include species that have been reclassified, including but not limited to such organisms as *B. stearothermophilus*, which is now named "*Geobacillus stearothermophilus*." The production of resistant endospores in the presence of oxygen is considered the defining feature of the genus *Bacillus*, although this characteristic also applies to the recently named *Alicyclobacillus*, *Amphibacillus*, *Aneurinibacillus*, *Anoxybacillus*, *Brevibacillus*, *Filobacillus*, *Gracilibacillus*, *Halobacillus*, *Paenibacillus*, *Salibacillus*, *Thermobacillus*, *Ureibacillus*, and *Virgibacillus*.

Exemplary Host Cells

[0253] A variety of host cells can be used to express isoprene synthase, DXS, IDI, and/or MVA pathway polypeptides and to produce isoprene in the methods of the claimed invention. Exemplary host cells include cells from any of the organisms listed in the prior section under the heading "*Exemplary Source Organisms*." The host cell may be a cell that naturally produces isoprene or a cell that does not naturally produce isoprene. In some embodiments, the host cell naturally produces isoprene using the DXP pathway, and an isoprene synthase, DXS, and/or IDI nucleic acid is added to enhance production of isoprene using this pathway. In some embodiments, the host cell naturally produces isoprene using the MVA pathway, and an isoprene synthase and/or one or more MVA pathway nucleic acids are added to enhance production of isoprene using this pathway. In some embodiments, the host cell naturally produces isoprene using the DXP pathway and one or more MVA pathway nucleic acids are added to produce isoprene using part or all of the MVA pathway as well as the DXP pathway. In some embodiments, the host cell naturally produces isoprene using both the DXP and MVA pathways and one or more isoprene synthase, DXS, IDI, or MVA pathway nucleic acids are added to enhance production of isoprene by one or both of these pathways.

Exemplary Transformation Methods

[0254] Isoprene synthase, DXS, IDI, and/or MVA pathway nucleic acids or vectors containing them can be inserted into a host cell (*e.g.*, a bacterial cell) using standard techniques for expression of the encoded isoprene synthase, DXS, IDI, and/or MVA pathway polypeptide. Introduction of a DNA construct or vector into a host cell can be performed using techniques such as transformation, electroporation, nuclear microinjection, transduction, transfection (*e.g.*, lipofection mediated or DEAE-Dextrin mediated transfection or transfection using a recombinant phage virus), incubation with calcium phosphate DNA precipitate, high velocity bombardment with DNA-coated microprojectiles, and protoplast fusion. General transformation techniques are known in the art (*see, e.g.*, Current Protocols in Molecular Biology (F. M. Ausubel *et al.* (eds) Chapter 9, 1987; Sambrook *et al.*, Molecular Cloning: A Laboratory Manual, 2nd ed., Cold Spring Harbor, 1989; and Campbell *et al.*, *Curr Genet,* 16:53-56, 1989, which are each hereby incorporated by reference in their entireties, particularly with respect to transformation methods). The introduced nucleic acids may be integrated into chromosomal DNA or maintained as extrachromosomal replicating sequences.

Exemplary Cell Culture Media

[0255] The invention also includes a cell or a population of cells in culture that produce isoprene. By "cells in culture" is meant two or more cells in a solution (*e.g.*, a cell medium) that allows the cells to undergo one or more cell divisions. "Cells in culture" do not include plant cells that are part of a living, multicellular plant containing cells that have differentiated into plant tissues. In various embodiments, the cell culture includes at least or about 10, 20, 50, 100, 200, 500, 1,000, 5,000, 10,000 or more cells.

[0256] Any carbon source can be used to cultivate the host cells. The term "carbon source" refers to one or more carbon-containing compounds capable of being metabolized by a host cell or organism. For example, the cell medium used to cultivate the host cells may include any carbon source suitable for maintaining the viability or growing the host cells.

[0257] In some embodiments, the carbon source is a carbohydrate (such as monosaccharide, disaccharide, oligosaccharide, or polysaccharides), invert sugar (*e.g.*, enzymatically treated sucrose syrup), glycerol, glycerine (*e.g.*, a glycerine byproduct of a biodiesel or soap-making process), dihydroxyacetone, one-carbon source, fatty acid (*e.g.*, a saturated fatty acid, unsaturated fatty acid, or polyunsaturated fatty acid), lipid, phospholipid, glycerolipid, monoglyceride, diglyceride, triglyceride, polypeptide (*e.g.*, a microbial or plant protein or peptide), renewable carbon source (*e.g.*, a biomass carbon source such as a hydrolyzed biomass carbon source; beet sugar or cane sugar molasses), yeast extract,

component from a yeast extract, polymer, acid, alcohol, aldehyde, ketone, amino acid, succinate, lactate, acetate, ethanol, or any combination of two or more of the foregoing. In some embodiments, the carbon source is a product of photosynthesis, including, but not limited to, glucose.

[0258] Exemplary monosaccharides include glucose and fructose; exemplary oligosaccharides include lactose and sucrose, and exemplary polysaccharides include starch and cellulose. Exemplary carbohydrates include C6 sugars (*e.g.*, fructose, mannose, galactose, or glucose) and C5 sugars (*e.g.*, xylose or arabinose). In some embodiments, the cell medium includes a carbohydrate as well as a carbon source other than a carbohydrate (*e.g.*, glycerol, glycerine, dihydroxyacetone, one-carbon source, fatty acid, lipid, phospholipid, glycerolipid, monoglyceride, diglyceride, triglyceride, renewable carbon source, or a component from a yeast extract). In some embodiments, the cell medium includes a carbohydrate as well as a polypeptide (*e.g.*, a microbial or plant protein or peptide). In some embodiments, the microbial polypeptide is a polypeptide from yeast or bacteria. In some embodiments, the plant polypeptide is a polypeptide from soy, corn, canola, jatropha, palm, peanut, sunflower, coconut, mustard, rapeseed, cottonseed, palm kernel, olive, safflower, sesame, or linseed.

[0259] In some embodiments, the concentration of the carbohydrate is at least or about 5 grams per liter of broth (g/L, wherein the volume of broth includes both the volume of the cell medium and the volume of the cells), such as at least or about 10, 15, 20, 30, 40, 50, 60, 80, 100, 150, 200, 300, 400, or more g/L. In some embodiments, the concentration of the carbohydrate is between about 50 and about 400 g/L, such as between about 100 and about 360 g/L, between about 120 and about 360 g/L, or between about 200 and about 300 g/L. In some embodiments, this concentration of carbohydrate includes the total amount of carbohydrate that is added before and/or during the culturing of the host cells.

[0260] Exemplary lipids are any substance containing one or more fatty acids that are C4 and above fatty acids that are saturated, unsaturated, or branched.

[0261] Exemplary fatty acids include compounds of the formula R-COOH, where "R" is a hydrocarbon. Exemplary unsaturated fatty acids include compounds where "R" includes at least one carbon-carbon double bond. Exemplary unsaturated fatty acids include, but are not limited to, oleic acid, vaccenic acid, linoleic acid, palmitelaidic acid, and arachidonic acid. Exemplary polyunsaturated fatty acids include compounds where "R" includes a plurality of carbon-carbon double bonds. Exemplary saturated fatty acids include compounds where "R" is a saturated aliphatic group. In some embodiments, the carbon source includes one or

more C_{12}-C_{22} fatty acids, such as a C_{12} saturated fatty acid, a C_{14} saturated fatty acid, a C_{16} saturated fatty acid, a C_{18} saturated fatty acid, a C_{20} saturated fatty acid, or a C_{22} saturated fatty acid. In an exemplary embodiment, the fatty acid is palmitic acid. In some embodiments, the carbon source is a salt of a fatty acid (*e.g.*, an unsaturated fatty acid), a derivative of a fatty acid (*e.g.*, an unsaturated fatty acid), or a salt of a derivative of fatty acid (*e.g.*, an unsaturated fatty acid). Suitable salts include, but are not limited to, lithium salts, potassium salts, sodium salts, and the like. Di- and triglycerols are fatty acid esters of glycerol.

[0262] In some embodiments, the concentration of the lipid, fatty acid, monoglyceride, diglyceride, or triglyceride is at least or about 1 gram per liter of broth (g/L, wherein the volume of broth includes both the volume of the cell medium and the volume of the cells), such as at least or about 5, 10, 15, 20, 30, 40, 50, 60, 80, 100, 150, 200, 300, 400, or more g/L. In some embodiments, the concentration of the lipid, fatty acid, monoglyceride, diglyceride, or triglyceride is between about 10 and about 400 g/L, such as between about 25 and about 300 g/L, between about 60 and about 180 g/L, or between about 75 and about 150 g/L. In some embodiments, the concentration includes the total amount of the lipid, fatty acid, monoglyceride, diglyceride, or triglyceride that is added before and/or during the culturing of the host cells. In some embodiments, the carbon source includes both (i) a lipid, fatty acid, monoglyceride, diglyceride, or triglyceride and (ii) a carbohydrate, such as glucose. In some embodiments, the ratio of the lipid, fatty acid, monoglyceride, diglyceride, or triglyceride to the carbohydrate is about 1:1 on a carbon basis (*i.e.*, one carbon in the lipid, fatty acid, monoglyceride, diglyceride, or triglyceride per carbohydrate carbon). In particular embodiments, the amount of the lipid, fatty acid, monoglyceride, diglyceride, or triglyceride is between about 60 and 180 g/L, and the amount of the carbohydrate is between about 120 and 360 g/L.

[0263] Exemplary microbial polypeptide carbon sources include one or more polypeptides from yeast or bacteria. Exemplary plant polypeptide carbon sources include one or more polypeptides from soy, corn, canola, jatropha, palm, peanut, sunflower, coconut, mustard, rapeseed, cottonseed, palm kernel, olive, safflower, sesame, or linseed.

[0264] Exemplary renewable carbon sources include cheese whey permeate, cornsteep liquor, sugar beet molasses, barley malt, and components from any of the foregoing. Exemplary renewable carbon sources also include glucose, hexose, pentose and xylose present in biomass, such as corn, switchgrass, sugar cane, cell waste of fermentation processes, and protein by-product from the milling of soy, corn, or wheat. In some embodiments, the biomass carbon source is a lignocellulosic, hemicellulosic, or cellulosic

material such as, but are not limited to, a grass, wheat, wheat straw, bagasse, sugar cane bagasse, soft wood pulp, corn, corn cob or husk, corn kernel, fiber from corn kernels, corn stover, switch grass, rice hull product, or a by-product from wet or dry milling of grains (*e.g.*, corn, sorghum, rye, triticate, barley, wheat, and/or distillers grains). Exemplary cellulosic materials include wood, paper and pulp waste, herbaceous plants, and fruit pulp. In some embodiments, the carbon source includes any plant part, such as stems, grains, roots, or tubers. In some embodiments, all or part of any of the following plants are used as a carbon source: corn, wheat, rye, sorghum, triticate, rice, millet, barley, cassava, legumes, such as beans and peas, potatoes, sweet potatoes, bananas, sugarcane, and/or tapioca. In some embodiments, the carbon source is a biomass hydrolysate, such as a biomass hydrolysate that includes both xylose and glucose or that includes both sucrose and glucose.

[0265] In some embodiments, the renewable carbon source (such as biomass) is pretreated before it is added to the cell culture medium. In some embodiments, the pretreatment includes enzymatic pretreatment, chemical pretreatment, or a combination of both enzymatic and chemical pretreatment (*see*, for example, Farzaneh *et al.*, *Bioresource Technology* 96 (18): 2014-2018, 2005; U.S. Patent No. 6,176,176; U.S. Patent No. 6,106,888; which are each hereby incorporated by reference in their entireties, particularly with respect to the pretreatment of renewable carbon sources). In some embodiments, the renewable carbon source is partially or completely hydrolyzed before it is added to the cell culture medium.

[0266] In some embodiments, the renewable carbon source (such as corn stover) undergoes ammonia fiber expansion (AFEX) pretreatment before it is added to the cell culture medium (*see*, for example, Farzaneh *et al.*, *Bioresource Technology* 96 (18): 2014-2018, 2005). During AFEX pretreatment, a renewable carbon source is treated with liquid anhydrous ammonia at moderate temperatures (such as about 60 to about 100 °C) and high pressure (such as about 250 to about 300 psi) for about 5 minutes. Then, the pressure is rapidly released. In this process, the combined chemical and physical effects of lignin solubilization, hemicellulose hydrolysis, cellulose decrystallization, and increased surface area enables near complete enzymatic conversion of cellulose and hemicellulose to fermentable sugars. AFEX pretreatment has the advantage that nearly all of the ammonia can be recovered and reused, while the remaining serves as nitrogen source for microbes in downstream processes. Also, a wash stream is not required for AFEX pretreatment. Thus, dry matter recovery following the AFEX treatment is essentially 100%. AFEX is basically a dry-to-dry process. The treated renewable carbon source is stable for long periods and can be fed at very high solid loadings in enzymatic hydrolysis or fermentation processes. Cellulose and hemicellulose are well preserved in the AFEX process,

with little or no degradation. There is no need for neutralization prior to the enzymatic hydrolysis of a renewable carbon source that has undergone AFEX pretreatment. Enzymatic hydrolysis of AFEX-treated carbon sources produces clean sugar streams for subsequent fermentation use.

[0267] In some embodiments, the concentration of the carbon source (*e.g.*, a renewable carbon source) is equivalent to at least or about 0.1, 0.5, 1, 1.5 2, 3, 4, 5, 10, 15, 20, 30, 40, or 50% glucose (w/v). The equivalent amount of glucose can be determined by using standard HPLC methods with glucose as a reference to measure the amount of glucose generated from the carbon source. In some embodiments, the concentration of the carbon source (*e.g.*, a renewable carbon source) is equivalent to between about 0.1 and about 20% glucose, such as between about 0.1 and about 10% glucose, between about 0.5 and about 10% glucose, between about 1 and about 10% glucose, between about 1 and about 5% glucose, or between about 1 and about 2% glucose.

[0268] In some embodiments, the carbon source includes yeast extract or one or more components of yeast extract. In some embodiments, the concentration of yeast extract is at least 1 gram of yeast extract per liter of broth (g/L, wherein the volume of broth includes both the volume of the cell medium and the volume of the cells), such at least or about 5, 10, 15, 20, 30, 40, 50, 60, 80, 100, 150, 200, 300, or more g/L. In some embodiments, the concentration of yeast extract is between about 1 and about 300 g/L, such as between about 1 and about 200 g/L, between about 5 and about 200 g/L, between about 5 and about 100 g/L, or between about 5 and about 60 g/L. In some embodiments, the concentration includes the total amount of yeast extract that is added before and/or during the culturing of the host cells. In some embodiments, the carbon source includes both yeast extract (or one or more components thereof) and another carbon source, such as glucose. In some embodiments, the ratio of yeast extract to the other carbon source is about 1:5, about 1:10, or about 1:20 (w/w).

[0269] Additionally the carbon source may also be one-carbon substrates such as carbon dioxide, or methanol. Glycerol production from single carbon sources (*e.g.*, methanol, formaldehyde, or formate) has been reported in methylotrophic yeasts (Yamada *et al.*, *Agric. Biol. Chem.*, 53(2) 541-543, 1989, which is hereby incorporated by reference in its entirety, particularly with respect to carbon sources) and in bacteria (Hunter *et. al.*, *Biochemistry*, 24, 4148-4155, 1985, which is hereby incorporated by reference in its entirety, particularly with respect to carbon sources). These organisms can assimilate single carbon compounds, ranging in oxidation state from methane to formate, and produce glycerol. The pathway of carbon assimilation can be through ribulose monophosphate, through serine, or through xylulose-

momophosphate (Gottschalk, Bacterial Metabolism. Second Edition, Springer-Verlag: New York, 1986, which is hereby incorporated by reference in its entirety, particularly with respect to carbon sources). The ribulose monophosphate pathway involves the condensation of formate with ribulose-5-phosphate to form a six carbon sugar that becomes fructose and eventually the three carbon product glyceraldehyde-3-phosphate. Likewise, the serine pathway assimilates the one-carbon compound into the glycolytic pathway via methylenetetrahydrofolate.

[0270] In addition to one and two carbon substrates, methylotrophic organisms are also known to utilize a number of other carbon containing compounds such as methylamine, glucosamine and a variety of amino acids for metabolic activity. For example, methylotrophic yeast are known to utilize the carbon from methylamine to form trehalose or glycerol (Bellion *et al.*, *Microb. Growth Cl Compd.*, [Int. Symp.], 7th ed., 415-32. Editors: Murrell *et al.*, Publisher: Intercept, Andover, UK, 1993, which is hereby incorporated by reference in its entirety, particularly with respect to carbon sources). Similarly, various species of *Candida* metabolize alanine or oleic acid (Sulter *et al.*, *Arch. Microbiol.* 153(5), 485-9, 1990, which is hereby incorporated by reference in its entirety, particularly with respect to carbon sources).

[0271] In some embodiments, cells are cultured in a standard medium containing physiological salts and nutrients (*see*, *e.g.*, Pourquie, J. *et al.*, Biochemistry and Genetics of Cellulose Degradation, *eds.* Aubert *et al.*, Academic Press, pp. 71-86, 1988; and Ilmen *et al.*, *Appl. Environ. Microbiol.* 63:1298-1306, 1997, hereby incorporated by reference, particularly with respect to cell media). Exemplary growth media are common commercially prepared media such as Luria Bertani (LB) broth, Sabouraud Dextrose (SD) broth, or Yeast medium (YM) broth. Other defined or synthetic growth media may also be used, and the appropriate medium for growth of particular host cells are known by someone skilled in the art of microbiology or fermentation science.

[0272] In addition to an appropriate carbon source, the cell medium desirably contains suitable minerals, salts, cofactors, buffers, and other components known to those skilled in the art suitable for the growth of the cultures or the enhancement of isoprene production (*see*, for example, WO 2004/033646 and references cited therein and WO 96/35796 and references cited therein, which are each hereby incorporated by reference in their entireties, particularly with respect cell medias and cell culture conditions). In some embodiments where an isoprene synthase, DXS, IDI, and/or MVA pathway nucleic acid is under the control of an inducible promoter, the inducing agent (*e.g.*, a sugar, metal salt or antimicrobial), is desirably added to the medium at a concentration effective to induce expression of an isoprene

synthase, DXS, IDI, and/or MVA pathway polypeptide. In some embodiments, cell medium has an antibiotic (such as kanamycin) that corresponds to the antibiotic resistance nucleic acid (such as a kanamycin resistance nucleic acid) on a vector that has one or more DXS, IDI, or MVA pathway nucleic acids.

Exemplary Production of Isoprene

[0273] In some embodiments, the cells are cultured in a culture medium under conditions permitting the production of isoprene by the cells. In some embodiments, the cells in culture produce isoprene at greater than or about 1, 10, 25, 50, 100, 150, 200, 250, 300, 400, 500, 600, 700, 800, 900, 1,000, 1,250, 1,500, 1,750, 2,000, 2,500, 3,000, 4,000, 5,000, or more nmole of isoprene/gram of cells for the wet weight of the cells/hour (nmole/g_{wcm}/hr). In some embodiments, the amount of isoprene is between about 2 to about 5,000 nmole/g_{wcm}/hr, such as between about 2 to about 100 nmole/g_{wcm}/hr, about 100 to about 500 nmole/g_{wcm}/hr, about 150 to about 500 nmole/g_{wcm} /hr, about 500 to about 1,000 nmole/g_{wcm}/hr, about 1,000 to about 2,000 nmole/g_{wcm}/hr, or about 2,000 to about 5,000 nmole/g_{wcm}/hr. The amount of isoprene in units of nmole/g_{wcm}/hr can be measured as disclosed in U.S. Patent No. 5,849,970, which is hereby incorporated by reference in its entirety, particularly with respect to the measurement of isoprene production. For example, two mL of headspace (*e.g.*, headspace from a culture such as 2 mL of culture cultured in sealed vials at 32 °C with shaking at 200 rpm for approximately 3 hours) are analyzed for isoprene using a standard gas chromatography system, such as a system operated isothermally (85 °C) with an n-octane/porasil C column (Alltech Associates, Inc., Deerfield, IL) and coupled to a RGD2 mercuric oxide reduction gas detector (Trace Analytical, Menlo Park, CA) (*see*, for example, Greenberg et al, *Atmos. Environ.* 27A: 2689-2692, 1993; Silver *et al.*, *Plant Physiol.* 97:1588-1591, 1991, which are each hereby incorporated by reference in their entireties, particularly with respect to the measurement of isoprene production). The gas chromatography area units are converted to nmol isoprene via a standard isoprene concentration calibration curve. In some embodiments, the value for the grams of cells for the wet weight of the cells is calculated by obtaining the A_{600} value for a sample of the cell culture, and then converting the A_{600} value to grams of cells based on a calibration curve of wet weights for cell cultures with a known A_{600} value. In some embodiments, the grams of the cells is estimated by assuming that one liter of broth (including cell medium and cells) with an A_{600} value of 1 has a wet cell weight of 1 gram. The value is also divided by the number of hours the culture has been incubating for, such as three hours.

[0274] In some embodiments, the cells in culture produce isoprene at greater than or about 1, 10, 25, 50, 100, 150, 200, 250, 300, 400, 500, 600, 700, 800, 900, 1,000, 1,250, 1,500, 1,750, 2,000, 2,500, 3,000, 4,000, 5,000, 10,000, 100,000, or more ng of isoprene/gram of cells for the wet weight of the cells/hr ($ng/g_{wcm}/h$). In some embodiments, the amount of isoprene is between about 2 to about 5,000 $ng/g_{wcm}/h$, such as between about 2 to about 100 $ng/g_{wcm}/h$, about 100 to about 500 $ng/g_{wcm}/h$, about 500 to about 1,000 $ng/g_{wcm}/h$, about 1,000 to about 2,000 $ng/g_{wcm}/h$, or about 2,000 to about 5,000 $ng/g_{wcm}/h$. The amount of isoprene in $ng/g_{wcm}/h$ can be calculated by multiplying the value for isoprene production in the units of $nmole/g_{wcm}/hr$ discussed above by 68.1 (as described in Equation 5 below).

[0275] In some embodiments, the cells in culture produce a cumulative titer (total amount) of isoprene at greater than or about 1, 10, 25, 50, 100, 150, 200, 250, 300, 400, 500, 600, 700, 800, 900, 1,000, 1,250, 1,500, 1,750, 2,000, 2,500, 3,000, 4,000, 5,000, 10,000, 50,000, 100,000, or more mg of isoprene/L of broth (mg/L_{broth}, wherein the volume of broth includes the volume of the cells and the cell medium). In some embodiments, the amount of isoprene is between about 2 to about 5,000 mg/L_{broth}, such as between about 2 to about 100 mg/L_{broth}, about 100 to about 500 mg/L_{broth}, about 500 to about 1,000 mg/L_{broth}, about 1,000 to about 2,000 mg/L_{broth}, or about 2,000 to about 5,000 mg/L_{broth}. The specific productivity of isoprene in mg of isoprene/L of headspace from shake flask or similar cultures can be measured by taking a 1 ml sample from the cell culture at an OD_{600} value of approximately 1.0, putting it in a 20 mL vial, incubating for 30 minutes, and then measuring the amount of isoprene in the headspace. If the OD_{600} value is not 1.0, then the measurement can be normalized to an OD_{600} value of 1.0 by dividing by the OD_{600} value. The value of mg isoprene/L headspace can be converted to $mg/L_{broth}/hr/OD_{600}$ of culture broth by multiplying by a factor of 38. The value in units of $mg/L_{broth}/hr/OD_{600}$ can be multiplied by the number of hours and the OD_{600} value to obtain the cumulative titer in units of mg of isoprene/L of broth.

[0276] The instantaneous isoprene production rate in $mg/L_{broth}/hr$ in a fermentor can be measured by taking a sample of the fermentor off-gas, analyzing it for the amount of isoprene (in units such as mg of isoprene per L_{gas}), and multiplying this value by the rate at which off-gas is passed though each liter of broth (*e.g.*, at 1 vvm (volume of air/volume of broth/minute) this is 60 L_{gas} per hour). Thus, an off-gas level of 1 mg/L_{gas} corresponds to an instantaneous production rate of 60 $mg/L_{broth}/hr$ at air flow of 1 vvm. If desired, the value in the units $mg/L_{broth}/hr$ can be divided by the OD_{600} value to obtain the specific rate in units of $mg/L_{broth}/hr/OD$. The average value of mg isoprene/L_{gas} can be converted to the total product productivity (grams of isoprene per liter of fermentation broth, mg/L_{broth}) by multiplying this

average off-gas isoprene concentration by the total amount of off-gas sparged per liter of fermentation broth during the fermentation. Thus, an average off-gas isoprene concentration of 0.5 mg/L_{broth}/hr over 10 hours at 1 vvm corresponds to a total product concentration of 300 mg isoprene/L_{broth}.

[0277] In some embodiments, the cells in culture convert greater than or about 0.0015, 0.002, 0.005, 0.01, 0.02, 0.05, 0.1, 0.12, 0.14, 0.16, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9, 1.0, 1.2, 1.4, or 1.6% of the carbon in the cell culture medium into isoprene. In some embodiments, the percent conversion of carbon into isoprene is between about 0.002 to about 1.6%, such as about 0.002 to about 0.005%, about 0.005 to about 0.01%, about 0.01 to about 0.05%, about 0.05 to about 0.15%, 0.15 to about 0.2%, about 0.2 to about 0.3%, about 0.3 to about 0.5%, about 0.5 to about 0.8%, about 0.8 to about 1.0%, or about 1.0 to about 1.6%. The percent conversion of carbon into isoprene (also referred to as "% carbon yield") can be measured by dividing the moles carbon in the isoprene produced by the moles carbon in the carbon source (such as the moles of carbon in batched and fed glucose and yeast extract). This number is multiplied by 100% to give a percentage value (as indicated in Equation 1).

Equation 1

[0278] % Carbon Yield = (moles carbon in isoprene produced)/(moles carbon in carbon source) * 100

[0279] For this calculation, yeast extract can be assumed to contain 50% w/w carbon.

Equation 2

[0280] % Carbon Yield = (39.1 g isoprene * 1/68.1mol/g * 5 C/mol)/[(181221 g glucose * 1/180 mol/g * 6 C/mol) + (17780 g yeast extract * 0.5 * 1/12 mol/g)] * 100 = 0.042%

[0281] One skilled in the art can readily convert the rates of isoprene production or amount of isoprene produced into any other units. Exemplary equations are listed below for interconverting between units.

Units for Rate of Isoprene production (total and specific)

Equation 3

[0282] 1 g isoprene/L_{broth}/hr = 14.7 mmol isoprene/L_{broth}/hr (total volumetric rate)

Equation 4

[0283] 1 nmol isoprene /g_{wcm}/hr = 1 nmol isoprene /L_{broth}/hr/OD_{600} (This conversion assumes that one liter of broth with an OD_{600} value of 1 has a wet cell weight of 1 gram.)

Equation 5

[0284] 1 nmol isoprene/g_{wcm}/hr = 68.1 ng isoprene/g_{wcm}/hr (given the molecular weight of isoprene)

Equation 6

[0285] 1 nmol isoprene/L_{gas} O_2/hr = 90 nmol isoprene/L_{broth}/hr (at an O_2 flow rate of 90 L/hr per L of culture broth)

Equation 7

[0286] 1 μg isoprene/L_{gas} isoprene in off-gas = 60 μg isoprene/L_{broth}/hr at a flow rate of 60 L_{gas} per L_{broth} (1 vvm)

Units for Titer (total and specific)

Equation 8

[0287] 1 nmol isoprene/mg cell protein = 150 nmol isoprene/L_{broth}/OD_{600} (This conversion assumes that one liter of broth with an OD_{600} value of 1 has a total cell protein of approximately 150 mg) (specific productivity)

Equation 9

[0288] 1 g isoprene/L_{broth} = 14.7 mmol isoprene/L_{broth} (total titer)

[0289] If desired, Equation 10 can be used to convert any of the units that include the wet weight of the cells into the corresponding units that include the dry weight of the cells.

Equation 10

[0290] Dry weight of cells = (wet weight of cells)/3.3

[0291] In some embodiments encompassed by the invention, a cell comprising a heterologous nucleic acid encoding an isoprene synthase polypeptide produces an amount of isoprene that is at least or about 2-fold, 3-fold, 5-fold, 10-fold, 25-fold, 50-fold, 100-fold, 150-fold, 200-fold, 400-fold, or greater than the amount of isoprene produced from a

corresponding cell grown under essentially the same conditions without the heterologous nucleic acid encoding the isoprene synthase polypeptide.

[0292] In some embodiments encompassed by the invention, a cell comprising a heterologous nucleic acid encoding an isoprene synthase polypeptide and one or more heterologous nucleic acids encoding a DXS, IDI, and/or MVA pathway polypeptide produces an amount of isoprene that is at least or about 2-fold, 3-fold, 5-fold, 10-fold, 25-fold, 50-fold, 100-fold, 150-fold, 200-fold, 400-fold, or greater than the amount of isoprene produced from a corresponding cell grown under essentially the same conditions without the heterologous nucleic acids.

Exemplary Isoprene Purification Methods

[0293] In some embodiments, any of the methods described herein further include recovering the isoprene. For example, the isoprene produced using the compositions and methods of the invention can be recovered using standard techniques. such as gas stripping, fractionation, adsorption/desorption, pervaporation, thermal or vacuum desorption of isoprene from a solid phase, or extraction of isoprene immobilized or absorbed to a solid phase with a solvent (see, for example, U.S. Patent Nos. 4,703,007 and 4,570,029, which are each hereby incorporated by reference in their entireties, particularly with respect to isoprene recovery and purification methods). In some embodiments, the recovery of isoprene involves the isolation of isoprene in a liquid form (such as a neat solution of isoprene or a solution of isoprene in a solvent). Gas stripping involves the removal of isoprene vapor from the fermentation off-gas stream in a continuous manner. Such removal can be achieved in several different ways including, but not limited to, adsorption to a solid phase, partition into a liquid phase, or direct condensation. In some embodiments, membrane enrichment of a dilute isoprene vapor stream above the dew point of the vapor resulting in the condensation of liquid isoprene.

[0294] The recovery of isoprene may involve one step or multiple steps. In some embodiments, the removal of isoprene vapor from the fermentation off-gas and the conversion of isoprene to a liquid phase are performed simultaneously. For example, isoprene can be directly condensed from the off-gas stream to form a liquid. In some embodiments, the removal of isoprene vapor from the fermentation off-gas and the conversion of isoprene to a liquid phase are performed sequentially. For example, isoprene may be adsorbed to a solid phase and then extracted from the solid phase with a solvent.

[0295] In some embodiments, any of the methods described herein further include purifying the isoprene. For example, the isoprene produced using the compositions and methods of the invention can be purified using standard techniques. Purification refers to a process through which isoprene is separated from one or more components that are present when the isoprene is produced. In some embodiments, the isoprene is obtained as a substantially pure liquid. Examples of purification methods include (i) distillation from a solution in a liquid extractant and (ii) chromatography. As used herein, "purified isoprene" means isoprene that has been separated from one or more components that are present when the isoprene is produced. In some embodiments, the isoprene is at least about 20%, by weight, free from other components that are present when the isoprene is produced. In various embodiments, the isoprene is at least or about 25%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 90%, 95%, or 99%, by weight, pure. Purity can be assayed by any appropriate method, *e.g.*, by column chromatography, HPLC analysis, or GC-MS analysis.

[0296]

[0297] Crystal Structure of Isoprene Synthase

[0298] The invention also contemplates crystalline forms of plant isoprene synthase (e.g., poplar and kudzu) and its variants as described *supra* and in the Examples. In one embodiment, the invention comprises any polypeptide which has the crystal structure of poplar isoprene synthase as disclosed in Table 16-7.

EXPERIMENTAL

[0299] The following examples are provided in order to demonstrate and further illustrate certain preferred embodiments and aspects of the present invention and are not to be construed as limiting the scope thereof.

[0300] In the experimental disclosure which follows, the following abbreviations apply: °C (degrees Centigrade); rpm (revolutions per minute); H_2O (water); diH_2O (deionized water); aa and AA (amino acid); bp (base pair); kb (kilobase pair); kD (kilodaltons); gm (grams); µg and ug (micrograms); mg (milligrams); ng (nanograms); µl and ul (microliters); ml (milliliters); mm (millimeters); qs (quantity sufficient); nm (nanometers); µm and um (micrometer); M (molar); mM (millimolar); µM and uM (micromolar); pM (picomolar); U (units); MW (molecular weight); sec (seconds); min (minute/minutes); hr (hour/hours); OD_{600} (optical density at 600 nm); BSA (bovine serum albumin); DMAPP (dimethylallyl diphosphate); DTT (dithiothreitol); EtOH (ethanol); IPTG (isopropyl-beta-D-

thiogalactopyranoside); isoprene (2-methyl-1,3-butadiene); IspS (isoprene synthase); PAGE (polyacrylamide gel electrophoresis); PBS (phosphate buffered saline [150 mM NaCl, 10 mM sodium phosphate buffer, pH 7.2]); and SDS (sodium dodecyl sulfate).

[0301] The following abbreviations apply to companies whose products or services may have been referred to in the experimental examples: Agilent (Agilent Technologies, Santa Clara, CA); Becton Coulter (Becton Coulter, Inc., Fullerton, CA); Bio-Rad (Bio-Rad Laboratories, Hercules, CA); Cayman Chemical (Cayman Chemical Co., Ann Arbor, MI); CTC Analytics (CTC Analytics A.G., Zwingen, Switzerland); EMS (Electron Microscopy Supply, Hatfield, PA); Epicentre (Epicentre Biotechnologies, Madison, WI); Integrated DNA Technologies (Integrated DNA Technologies, Coralville, IA); Invitrogen (Invitrogen Corp., Carlsbad, CA); Molecular Dynamics (Molecular Dynamics, Sunnyvale, CA); Novagen (Novagen, Inc., Madison, WI); Perkin Elmer (Perkin Elmer, Waltham, MA); Roche (Roche Applied Science, Indianopolis, IN); Sigma (Sigma-Aldrich, St. Louis, MO); Stratagene (Stratagene Cloning Systems, La Jolla, CA); Qiagen (Qiagen, Inc., Valencia, CA); Takara (Takara Bio USA, Madison, WI); Thomson Instrument (Thomson Instrument Co., Oceanside, CA); V&P Scientific (V&P Scientific, Inc., San Diego, CA); and Zinsser (Zinsser North America, Northridge, CA).

EXAMPLE 1

Cloning of Kudzu Isoprene Synthase for Expression in Recombinant Bacteria

[0302] In this example, methods used to produce kudzu isoprene synthase (IspS) in *E. coli* are described. The protein sequence for the kudzu (*Pueraria montana*) isoprene synthase gene (IspS) was obtained from GenBank (AAQ84170). A kudzu isoprene synthase gene, optimized for *E. coli* codon usage, was purchased from DNA2.0 (Menlo Park, CA), and is set forth as SEQ ID NO:1 (Figure 1). The isoprene synthase gene was removed from the supplied plasmid by restriction endonuclease digestion with *Bsp*LU11I/*Pst*I, gel-purified, and ligated into pTrcHis2B (Invitrogen) that had been digested with *Nco*I/*Pst*I. The construct was designed such that the stop codon in the isoprene synthase gene was 5' to the *Pst*I site. As a result, when the construct was expressed the His-Tag is not attached to the isoprene synthase protein. The resulting plasmid, pTrcKudzu, was verified by sequencing.

[0303] The isoprene synthase gene was also cloned into pET16b (Novagen). In this case, the isoprene synthase gene was inserted into pET16b such that the recombinant isoprene synthase protein contained the N-terminal His tag. The isoprene synthase gene was amplified

from pTrcKudzu by PCR using the primer set pET-His-Kudzu-2F: 5'-CGTGAGATCA TATGTGTGCG ACCTCTTCTC AATTTAC (SEQ ID NO:3) and pET-His-Kudzu-R: 5'-CGGTCGACGG ATCCCTGCAG TTAGACATAC ATCAGCTG (SEQ ID NO:4). These primers added an *Nde*I site at the 5'-end and a *Bam*H1 site at the 3' end of the gene respectively. The plasmid pTrcKudzu, described above, was used as template DNA, HERCULASE DNA polymerase (Stratagene) was used according to manufacturer's directions, and primers were added at a concentration of 10 pM. The PCR was carried out in a total volume of 25 µl. The PCR product was digested with *Nde*I/*Bam*H1 and cloned into pET16b digested with the same enzymes. The ligation mix was transformed into *E. coli* Top10 (Invitrogen) and the correct clone selected by sequencing. The resulting plasmid designated pETNHisKudzu is then transformed into BL21(λDE3)pLysS (Novagen) cells for expression from the T7 promoter.

[0304] The kudzu isoprene synthase gene was also cloned into the low copy number plasmid pCL1920 (Lerner and Inouye, Nucl Acids Res, 18:4631, 1990). Primers were used to amplify the kudzu isoprene synthase gene from pTrcKudzu described above. The forward primer added a *Hin*dIII site and an *E. coli* consensus RBS to the 5' end. The *Pst*I cloning site was already present in pTrcKudzu just 3' of the stop codon so the reverse primer was constructed such that the final PCR product includes the *Pst*I site. The sequences of the primers were: HindIII-rbs-Kudzu F: 5'-CATATGAAAG CTTGTATCGA TTAAATAAGG AGGAATAAAC C (SEQ ID NO:5) and BamH1-Kudzu R: 5'-CGGTCGACGG ATCCCTGCAG TTAGACATAC ATCAGCTG (SEQ ID NO:4). The PCR product was amplified using HERCULASE DNA polymerase (Stratagene) with primers at a concentration of 10 pM and with 1 ng of template DNA (pTrcKudzu). The amplification protocol included 30 cycles of (95° C for 1 minute, 60° C for 1 minute, 72° C for 2 minutes). The product was digested with *Hin*dIII and *Pst*I and ligated into pCL1920, which had also been digested with *Hin*dIII and *Pst*I. The ligation mix was transformed into *E. coli* Top10. Several transformants were verified by sequence analysis. The resulting plasmid was designated pCL-lac-Kudzu.

[0305] In order to remove the beta-lactamase gene, pTrcKudzu was digested with *Bsp*HI, treated with shrimp alkaline phosphatase (SAP), incubated at 65°C for 10 min to heat kill the SAP, then end-filled by incubating with 2 units of Klenow fragment (New England BioLabs)and dNTPS. The 5 kb fragment was purified from an agarose gel and ligated to the Kan(R) gene. The Kan(R) gene was prepared by PCR amplification from pCR-Blunt-II-TOPO (Invitrogen) using primers MCM22 and MCM23 and Taq DNA polymerase according

to the Manufacturer's instructions. The PCR fragment was digested with *Hin*dIII and *Pvu*I, and end-filled using Klenow Fragment and dNTPs. The ligation mixture was transformed into *E. coli* Top 10 chemically competent cells and a transformant carrying a plasmid conferring kanamycin resistance, pTrcKudzu(kan), was selected on Luria Agar containing kanamycin (50μg/ml). The sequences of the primers were: MCM22 5'- gatcaagctt AACCGGAATTGCCAGCTG (SEQ ID NO:15); and MCM23 5'- gatccgatcgTCAGAAGAACTCGTCAAGAAGGC (SEQ ID NO:16).

EXAMPLE 2

Cloning of Poplar Isoprene Synthase for Expression in Recombinant Bacteria

[0306] In this example, methods used to produce poplar isoprene synthase (IspS) in *E. coli* are described. The protein sequence for the poplar (*Populus alba x Populus tremula*) isoprene synthase (Schnitzler et al., Planta 222:777-786, 2005) was obtained from GenBank (CAC35696). A gene, codon optimized for *E. coli*, was purchased from DNA2.0 and is set forth as SEQ ID NO:6 (Figure 3). The isoprene synthase gene was removed from the supplied plasmid (p9796-poplar) by restriction endonuclease digestion with *Bsp*LU11I/*Pst*I, gel-purified, and ligated into pTrcHis2B that had been digested with *Nco*I/*Pst*I. The construct is cloned such that the stop codon in the insert is before the *Pst*I site, which results in a construct in which the His-Tag is not attached to the isoprene synthase protein. The resulting plasmid, pTrcPoplar, was verified by sequencing using commercially available primers that hybridize within the vector sequence (Forward and Reverse), as well as the primer Poplar InSeq 5'-GAGAAAATCG GTAAGGAACT GG (SEQ ID NO:8).

EXAMPLE 3

Isoprene Production in Recombinant Bacteria

[0307] In this example, methods used to produce and measure isoprene in recombinant *E. coli* are described.

I. Determination of isoprene production

[0308] For the shake flask cultures, one ml of a culture was transferred from shake flasks to 20 ml CTC headspace vials (Agilent vial Catalog No. 5188 2753, and cap Catalog No. 5188 2759). The cap was screwed on tightly and the vials incubated at the equivalent temperature

with shaking at 250 rpm. After 30 minutes, the vials were removed from the incubator and analyzed as described below. In cases where isoprene production in fermentors was determined, samples were taken from the off-gas of the fermentor and analyzed directly.

[0309] The analysis was performed using an Agilent 6890 GC/MS system interfaced with a CTC Analytics CombiPAL autosampler operating in headspace mode. An Agilent HP-5MS GC/MS column (30 m x 0.25 mm; 0.25 μm film thickness) was used for separation of analytes. The sampler was set up to inject 500 μL of headspace gas. The GC/MS method utilized helium as the carrier gas at a flow of 1 ml/min. The injection port was held at 250° C with a split ratio of 50:1. The oven temperature was held at 37° C for the 2 min duration of the analysis. The Agilent 5793N mass selective detector was run in single ion monitoring (SIM) mode on m/z 67. The detector was switched off from 1.4 to 1.7 minutes to allow the elution of permanent gases. Under these conditions, isoprene (2-methyl-1,3-butadiene) was observed to elute at 1.78 minutes. A calibration table was used to quantify the absolute amount of isoprene and was found to be linear from 1 μg/L to 200 μg/L. The limit of detection was estimated to be 50 to 100 ng/L using this method.

II. Production of isoprene in shake flasks

[0310] The vectors described above were introduced into *E. coli* strain BL21(λDE3)pLysS (Novagen) to produce strains BL21/ptrcKudzu, BL21/pCL-lac-Kudzu and BL21/pETHisKudzu. The strains were spread for isolation onto LA (Luria agar) containing the appropriate antibiotic (50 μg/ml carbenicillin for BL21/ptrcKudzu and BL21/pETHisKudzu or 50 μg/ml spectinomycin for BL21/pCL-lac-Kudzu) and incubated overnight at 37° C. Single colonies were inoculated into 250 ml baffled shake flasks containing 20 ml Luria Bertani broth (LB) and the appropriate antibiotic. Cultures were grown overnight at 20° C with shaking at 200 rpm. The OD_{600} of the overnight cultures was measured and the cultures were diluted into a 250 ml baffled shake flask containing 30 ml MAGICMEDIA expression medium (Invitrogen) containing the appropriate antibiotic to an OD_{600} ~ 0.05. The culture was incubated at 30° C with shaking at 200 rpm. When the OD_{600} ~ 0.5 - 0.8, 400 μM IPTG was added and the cells were incubated for a further 6 hours at 30° C with shaking at 200 rpm. At 0, 2, 4 and 6 hours after induction with IPTG, 1 ml aliquots of the cultures were collected, the OD_{600} was determined and the amount of isoprene produced was measured as described above.

III. Production of Isoprene from BL21/ptrcKudzu in 14 liter fermentation

[0311] Large-scale production of isoprene from *E. coli* containing the recombinant kudzu isoprene synthase gene was determined from a fed-batch culture. The recipe for the fermentation media (TM2) per liter of fermentation medium was as follows: K_2HPO_4 13.6 g, KH_2PO_4 13.6 g, $MgSO_4$ * $7H_2O$ 2 g, citric acid monohydrate 2 g, ferric ammonium citrate 0.3 g, $(NH_4)_2SO_4$ 3.2 g, yeast extract 5 g, 1000X Modified Trace Metal Solution 1 ml. All of the components were added together and dissolved in diH_2O. The pH was adjusted to 6.8 with potassium hydroxide (KOH) and qs to volume. The final product was filter sterilized with 0.22 μM filter, but not autoclaved. The recipe for 1000X Modified Trace Metal Solution was as follows: Citric Acids * H_2O 40 g, $MnSO_4$ * H_2O 30 g, NaCl 10 g, $FeSO_4$ * $7H_2O$ 1 g, $CoCl_2$ * $6H_2O$ 1 g, ZnSO * $7H_2O$ 1 g, $CuSO_4$ * $5H_2O$ 100 mg, H_3BO_3 100 mg, $NaMoO_4$ * $2H_2O$ 100 mg. Each component was dissolved one at a time in diH_2O, the pH was adjusted to 3.0 with HCl/NaOH, then qs to volume and filter sterilized with a 0.22 μ filter.

[0312] This experiment was carried out in 14 L bioreactor to monitor isoprene formation from glucose at the desired fermentation, pH 6.7 and temperature 34° C. An inoculum of *E. coli* strain BL21/ptrcKudzu taken from a frozen vial was prepared in soytone-yeast extract-glucose medium in two 600 ml flasks.. After the inoculum grew to OD_{550} = 0.6, two 600 ml flasks were centrifuged and the contents resuspended in 70 ml supernatant to transfer the cell pellet (70 ml of OD 3.1 material) to the bioreactor. At various times after inoculation, samples were removed and the amount of isoprene produced was determined as described above.

EXAMPLE 4

Selection of Sites for Improvement of Plant Isoprene Synthases

[0313] The isoprene synthases of plants were expected to be homologous to the terpene synthases. The three-dimensional structures of two homologous terpene synthases have been determined from bornyl diphosphate synthase (pdb entry 1N1B) and 5-epi-aristolochene synthase (pdb entry 5EAU). These enzymes share only 32% homology but their tertiary structure is conserved. In addition, the structures of intermediate complexes with both enzymes have shown that not only tertiary folding, but also detailed interactions in the active sites of these enzymes are highly conserved.

[0314] The kudzu and poplar isoprene synthases have higher sequence identity than was seen between the bornyl diphosphate synthase and the 5-epi-aristolochene synthase as shown in Table 4-1 below.

Table 4-1. Percent Identity of Various Enzymes

	BDP-synthase	5EA-synthase	Kudzu IspS
Poplar IspS	40.1	32.9	54.4
Kudzu IspS	40.7	33.8	
5ES synthase	31.9		

[0315] A homology model of the poplar isoprene synthase has been made based on the bornyl diphosphate synthase (BDP-synthase) pdb entry 1N24 (~40% sequence identity). The homology model appears to be plausible based on the close similarity of 10 trial models created using the program MOE written and supported by The Chemical Computing Group, Inc. The plausibility is based on the conservation of common amino acid residues at sites found to be involved in catalysis in the BDP-synthase structure.

[0316] A comparison of the active site from the structure of BDP-synthase and the homology model of poplar IspS indicates that the active site involved in metal ion binding and phosphate recognition is conserved. In particular, Lys 272, Asp 309, Asp 313, Glu 387, Arg 450 and Asn 453 of poplar IspS were observed to overlap equivalent residues in BDP-synthase. In this example, amino acid residue positions for poplar IspS are derived from SEQ ID NO:7. The positioning of an intermediate of the BDP-synthase was also compared with the poplar IspS homology model. Based on this, it was possible to identify the analogous binding region and the approach direction that isopentenyl diphosphate would require in order to bind and react with the poplar IspS enzyme.

[0317] A homology model of the kudzu isoprene synthase has been made based on bornyl diphosphate synthase pdb entry 1N24 having (~40% sequence identity). A comparison of the active site from the structure of BDP-synthase with the homology model of kudzu IspS indicates that numerous active site residues involved in metal ion binding and phosphate recognition are conserved. In particular, Arg 269, Asp 306, Asp 310, Glu 384, Arg 450 and Asn 453 of kudzu IspS were observed to overlap equivalent residues in BDP-synthase.

[0318] A comparison of the active site residues identified in the homology models of poplar and kudzu IspS revealed that residues from one homology model are also quite homologous with similar residues, appearing with only minor shifts in the relative position numbers for some of the residues, in the other homology model. Based on the homology models, sites in poplar and kudzu IspS were identified as candidates for mutagenesis to produce variant IspS enzymes with improved performance. Briefly, sites were selected in the

IspS that might alter the interaction of the metal binding, the diphosphate recognition, the IPP chain binding and/or the approach to the active site.

I. Diphosphate/ Metal Binding Sites

[0319] The side chains of amino acid residues in the poplar IspS that are found in proximity to the metal and diphosphate (DPP) binding side chains were identified. These residues include Phe 384, Tyr 402, Ala 406, Ser 409, Ala 460 and Asn 469. The inventors note that Lys 272 is incorrect based on homology to other known poplar IspS sequences, which have an Arg at this position.

II. Substrate Access Loop

[0320] The substrate access loop of poplar IspS is in a region that deviates from the BDP-synthase structure. In the BDP-synthase structure the residues form a segment that creates a cover. Without being bound by theory, the inventors expect that this segment in the actual three-dimensional structure of poplar IspS will form a similar structure. As such the residues in this loop, including residues 455-466, will be in a position to alter the activity of the poplar IspS enzyme. In the poplar IspS enzyme residues 454-466 have the following sequence: LASASAEIARGET (SEQ ID NO:9).

III. Isoprenyl Binding Site

[0321] The complex of BDP-synthase and the product of the reaction, bornyl diphosphate (pdb entry 1N24), was used to identify residues in the poplar model that may modulate substrate specificity and/or reaction rate (altered on and off rates of substrate and product). These residues include Arg 274, Trp 281 Phe 302, Val 305, Ser 411, Gln 415, Phe 449, Ser 537 and Glu 540.

Table 4-2. Candidate Mutagenesis Sites

	Poplar Amino Acid	Kudzu Amino Acid / codon
DPP/metal sites	Phe 384	Phe 381 / 1141-1143
	Tyr 402	Tyr 399 / 1195-1197
	Ala 406	Ala 403 / 1207-1209
	Ser 409	Ser 406 / 1216-1218
	Asn 469	Asn 469 / 1405-1407

Extra DPP sites	Tyr 312	Tyr 309 / 925-927
	Asp 313	Asp 310 / 928-930
	Leu 380	Leu 377 / 1129-1131
	Glu 387	Glu 384 / 1150-1152
	Asn 404	Asn 402 / 1204-1206
	Ser 410	Ser 407 / 1219-1221
N_terminal access segment	22	20 / 58-60
	23	21 / 61-63
	24	22 / 64-66
	25	23 / 67-69
	26	24 / 70-72
	27	25 / 73-75
Substrate access loop	Leu 454	Ala 456 / 4102-4104
	Ala 455	Thr 457 / 4105-4107
	Ser 456	Ser 458 / 4108-4110
	Ala 457	Ala 459 / 4111-4113
	Ser 458	Ala 460 / 4114-4116
	Ala 459	Glu 461 / 4117-4119
	Glu 460	Leu 462 / 4120-4122
	Ile 461	Glu 463 / 4123-4125
	Ala 462	
	Arg 463	Arg 464 / 4126-4128
	Gly 464	Gly 465 / 4129-4131
	Glu 465	Glu 466 / 4132-4134
	Thr 466	Thr 467 / 4135-4137
		Thr 468 / 4138-4140
Isoprenyl binding site	Arg 274	Arg 271 / 811-813
	Trp 281	Trp 278 / 832-834
	Phe 302	Phe 299 / 895-897
	Val 305	Val 302 / 904-906
	Ser 411	Ser 408 / 1222-1224
	Gln 415	
	Phe 449	Phe 449 / 1345-1347
	Ser 537	Ser 458 / 1372-1374
	Glu 540	Tyr 531 / 1591-1593
Extra Isoprenyl sites	Gly 412	Gly 409 / 1225-1227

	Leu 414	Ala 411 / 1231-1233
	Leu 416	Leu 413 / 1237-1239
	Leu 521	Met 523 / 1567-1569
	Ser 525	Ser 527 / 1579-1581

EXAMPLE 5

Mutation of Non-Conserved Cysteines in Kudzu Isoprene Synthase

[0322] The kudzu and poplar isoprene synthase (IspS) homology models, based on the bornyl diphosphate synthase crystal structure, were compared with respect to the positions of the cysteine residues. Cysteines have the potential to form disulfide bonds and stabilize structures. The non-conserved cysteines, contemplated to affect solubility and/or activity, were altered by site-directed mutagenesis. The kudzu IspS amino acid sequence used for the modeling is shown in Figure 2 (SEQ ID NO:2). There are eight cysteines in kudzu IspS at positions 57, 291, 343, 378, 421, 446, 451 and 529 (relative to the mature form of the protein) as shown in the homology model of Figure 5. In contrast, there are five cysteines in poplar IspS amino acid sequence has five cysteines, as shown in the homology model of Figure 6 upon which the kudzu cysteines are superimposed. Several of the cysteines are apparently conserved between the poplar and kudzu IspS sequences indicating that these positions are important in stabilizing the structure, activity and/or other protein function. The remaining cysteines (nonconserved residues 57, 291, 421 and 446) in kudzu were mutated to serine as described herein.

I. Mutagenesis

[0323] The QUIKCHANGE® Multi-Site Directed Mutagenesis Kit (Stratagene) was used as per the manufacturer's directions. The following primers were utilized for mutagenesis:

C57S-F 5'- CTGGAGGAAGAAGTTCGC **TCC**
ATGATCAACCGTGTAGAC (SEQ ID NO:10);

C291S-F 5'- CGCCAGACCCGCAGTTTGGTGAA **TCT**
CGCAAAGCTGTTACTAAAATG (SEQ ID NO:11);

C421S-F 5'-CGCCGTCTTACTTTTCCGTA **TCC**
CAGCAGCAGGAAGACATC (SEQ ID NO:12);

C446S-F 5'-CATGGTCTGGTGCGTTCTAGC **TCC**
GTTATCTTCCGCCTGTGC (SEQ ID NO:13); and

C421S-R 5'-GATGTCTTCCTGCTGCTG **GGA**

TACGGAAAAGTAAGACGGCG (SEQ ID NO:14).

[0324] The plasmid pTrcKudzu(kan) described in Example 1 was used as template DNA. The primers C57S-F, C291S-F, C421S-F, and C446-F were combined in a single reaction (100 pmol). Template DNA was added (~200 nanograms) and 0.5 μl of Quiksolution was added to the recommended volumes of enzyme and buffer. The PCR reaction was carried out in an Eppendorf PCR machine using an annealing temperature of 55°C and an extension time of 12 minutes for 30 cycles. Other parameters of the cycle were as indicated in the instructions. The PCR mix was treated with *Dpn*I for 4 hours at 37°C (2 x 1 μl for 2 h each) and then 5 μl of the reaction were transformed into *E. coli* Top10 (Invitrogen) chemically competent cells and plated on Luria agar containing kanamycin (50 μg/ml). After overnight incubation at 37°C, several colonies were picked and inoculated into 5 ml of Luria Broth containing kanamycin (50 μg/ml). The plasmids were isolated using the QIAprep Spin Miniprep kit (Qiagen), and the IspS genes were sequenced in their entirety. Various single and combinations of mutations were made as indicated in the Table 5-1 below.

Table 5-1. BL21(λDE3) Cells Transformed with Mutated pTrcKudzu Plasmids*

Strain*	C57S	C291S	C421S	C446S
C1	+	+		
C2		+		+
C4	+	+		+
C6	+			+
C11				+
C20			+	
C6-4	+		+	+

[0325] All the variant plasmids were transformed into chemically competent BL21(λDE3) cells (Novagen). In a second reaction pTrcKudzu(kan) and plasmid DNA isolated from C6 were used as templates in a QUIKCHANGE® site directed mutagenesis kit (Stratagene) single site reaction with C421S-F and C421S-R primers. After confirmation by sequencing, two additional strains were obtained.

II. Cell Growth and Isoprene Production

[0326] Cells were grown in 5 ml tubes containing Luria Broth supplemented with 50 mg/L kanamycin at 30°C overnight with agitation. These cultures were diluted into TM3 broth supplemented with 10 g/L glucose and 50 mg/L kanamycin. The culture volume was 25 ml in a 250 ml baffled Bellco Delong flask in which cells were grown at 30°C with agitation (225 rpm). Samples were taken aseptically, as indicated, for optical density measurements at A_{600}. The results are shown in Figure 7. The cultures were induced at 3.33 hrs with 200 μM IPTG and allowed to continue growth until harvest at 7.8 hr. The cultures were centrifuged at 10,000 X g for 10 min, the supernatants decanted and the cell pellets frozen at -80°C overnight.

[0327] Frozen cell pellets were thawed and resuspended in 2 ml PEB (50 mM Tris-HCl, pH 8.0, 20 mM MgCl, 2 mM dithiothreitol, and 50% [v/v] glycerol). Cells were lysed by French pressure cell disruption, one pass, at 20,000 psi. The lysate was centrifuged for 15 min at 10,000 X g. The supernatants were decanted and the pellets resuspended in 2 ml PEB. The pellets and supernatants were analyzed by SDS-PAGE, 4-12% NuPage gels (Invitrogen), run in MES buffer under reducing conditions. The molecular weight standard was SeeBlue2 (Invitrogen). The results are shown in Figure 8. The IspS protein concentrations were estimated using the BCA assay (Pierce) using BSA as standard (Table 5-2).

III. Assays for Isoprene Synthase Activity and Solubility

[0328] Briefly the activity of the supernatants was measured by reaction with DMAPP, and the isoprene evolved was quantified by GC/MS.

[0329] Headspace Assay. A sample of 200 μl of the desired culture is inoculated into 2 ml CTC headspace vials (Agilent vial Catalog No. 5188 2753, and cap Catalog No. 5188 2759). The cap was screwed on tightly and the vials were incubated at 37°C with shaking at 250 rpm. After 30 minutes the vials were removed from the incubator and cooled briefly with ambient tap water. The vials were placed into the CombiPal Headspace auto sampler for analysis by GC-MS. The analysis was performed using an Agilent 6890 GC/MS system interfaced with a CTC Analytics CombiPAL autosampler operating in headspace mode. An Agilent HP-5MS GC/MS column (30 m x 0.25 mm; 0.25 μm film thickness) was used for separation of analytes. The sampler was set up to inject 500 μL of headspace gas. The GC/MS method utilized helium as the carrier gas at a flow of 1 ml/min. The injection port was held at 250°C with a split ratio of 50:1. The oven temperature was held at 37°C for the 2 min duration of the analysis. The Agilent 5793N mass selective detector was run in single ion

monitoring (SIM) mode on m/z 67. The detector was switched off from 1.4 to 1.7 minutes to allow the elution of permanent gases. Under these conditions isoprene (2-methyl-1,3-butadiene) was observed to elute at 1.78 minutes. A calibration table was used to quantify the absolute amount of isoprene and was found to be linear from 1 μg/L to 200 μg/L. The limit of detection was estimated to be 50-100 ng/L using this method.

[0330] DMAPP Assay. An aliquot of 95 μl of the supernatant fraction from the centrifuged French Pressure cell lysate was added to the headspace vials. A 5 μL aliquot of 8 mM DMAPP in 100 mM potassium phosphate buffer, pH 8.2 was added, the vials sealed and allowed to incubate at room temperature for 30 min. The amount of isoprene produced was measured by GC/MS as described above and reported in Table 5-2.

Table 5-2. Isoprene Synthase Activity from Crude Extracts of Cysteine Mutants

Supernatant	Activity (mU/ml)	Protein (mg/ml)	Specific Activity (mU/mgP)
Wt	59.0	2.48	23.79
C1	5.3	2.64	2.01
C2	0.2	3.52	0.06
C4	0.5	3.22	0.16
C6	9.0	3.32	2.71
C11	0.1	4.26	0.03

[0331] The values shown in Table 5-2 are averages of reactions with two different concentrations of extract. All proteins containing any of the cysteine mutations resulted in severe diminution of enzyme activity and an apparent decrease of soluble protein as judged by a relative increase in the proportion of protein in the insoluble (pellet) fraction.

EXAMPLE 6

Mutation of Residues in Poplar Isoprene Synthase

[0332] Alignment of the amino acid sequences of kudzu and poplar isoprene synthases with other synthases was done using Vector Nti (Invitrogen). The aligned sequences included: beta-ocimene synthase *Lotus corniculatus* (AAT86042); putative terpene synthetase *Medficago trunculata* (AAV36465); hypothetical protein *Vitis vinifera* (can65805); hypothetical protein *Vitis vinifera* (CAN62729); pinene synthase *Quercus ilex* (CAK55186); IspS *Pueraria montana* (kudzu) Sharkey (AAQ84170); monoterpene synthase *Eucaliptus globulus* (BAF02832); IspS *Populus nigra* Fortunati (CAL69918); IspS *Populus tremuloides*

Sharkey (AAQ16588); IspS *Populus alba* (BAD98243); and IspS *Populus alba x tremula* Zimmer (CAC35696). The sequence from the database of *Populus alba x tremula* (CAC35696) exhibited different amino acids at positions 272 and 497 that were otherwise highly conserved. Additionally based on analysis of the homology model of poplar IspS, position 453 was identified as a third candidate for mutagenesis.

I. Mutagenesis

[0333] The QUIKCHANGE® Multi-Site Directed Mutagenesis kit (Stratagene) was used as per the manufacturer's directions to introduce the following mutations singly and in combination into the *Populus alba x tremula* IspS sequence (SEQ ID NO:7): K272R; C497W; and N453D. The following primers were utilized for mutagenesis:
Poplar K272R 5'-ccaaactgcacttcg ctcgtgaccgcctgattgag (SEQ ID NO:17);
Poplar N453D 5'-atctttcgcctgtgcgacgacctggcaagc (SEQ ID NO:18); and
Poplar C497W 5'-tgaatctgatcgacgaaacctggaagaaaatgaacaaagaaaaac (SEQ ID NO:19).
The following primer, Poplar InSeq, 5'-gagaaaatcggtaaggaactgg (SEQ ID NO:8) was used for sequencing.

[0334] Mutagenesis was done according to the manufacturer's directions, with all three mutagenesis primers being added to a single reaction mix (100 ng each) with pTrcPoplar as the template DNA (100 ng). Addition of 0.5 µl of Quik Solution aided the mutagenesis reaction. The suggested PCR cycle was run with an annealing temperature of 55°C and an extension time of 12 min. Other parameters were as indicated in the instructions. The PCR mix was digested with *Dpn*I for 4 hrs at 37°C (1 µl each x 2 h) and then 5 µl of the reaction was transformed into *E. coli* Top10 chemically competent cells (Invitrogen). Several colonies were selected and grown up in 5 ml of Luria Broth (LB) containing carbenicillin (50 µg/ml). Plasmids were isolated using the Qiagen QIAprep spin mini-prep kit and sent for sequencing using forward and reverse primers that hybridized to the vector, as well as the Poplar InSeq primer.

[0335] The resulting variants of pTrcPoplar were obtained: pTrcPoplar K272R, pTrcPoplar K272R/N453D; pTrcPoplar K272R/N453D/C497W; and pTrcPoplar 272R/497W. These plasmids were transformed into BL21(λDE3)pLysS chemically competent cells (Novagen) for analysis. The variants were analyzed for headspace activity (production of isoprene from whole cells), solubility, and specific activity.

II. Cell Growth and Isoprene Production

[0336] The variants, the parent Poplar strain, and the strain containing pTrcKudzu were grown overnight at 37°C in 5 ml of Luria Bertani medium containing either carbenicillin (50 μg/ml-Poplar strains) or kanamycin (50 μg/ml-Kudzu strain). These cultures were diluted into TM3 broth to an OD_{600} of 0.05, supplemented with 10g/L glucose and either 50 μg/ml carbenicillin (Poplar mutants and wild type) or 50 mg/L kanamycin (BL21/pTrcKudzu). The recipe for TM3 broth is as follows: K_2HPO_4 (13.6 g/l) KH_2PO_4 (13.6 g/l), $MgSO_4$ * $7H_2O$ (2 g/l) Citric Acid Monohydrate (2 g/L) Ferric Ammonium Citrate (0.3 g/L) $(NH_4)_2SO_4$ (3.2 g/L) yeast extract (0.2 g/L) 1 ml of 1000x Trace Elements solution, pH adjusted to 6.8 with ammonium hydroxide qs to volume with sterile diH_2O and filter sterilized with a 0.22 micron filter. The recipe for 1000X Trace Elements solution is as follows: Citric Acids * H_2O (40 g/L), $MnSO_4$ * H_2O (30 g/L), NaCl (10 g/L), $FeSO_4$ * 7 H_2O (1 g/L), $CoCl_2$ * 6 H_2O (1 g/L), ZnSO * 7 H_2O (1 g/L), $CuSO_4$ * 5 H_2O (100 mg/L), H_3BO_3 (100 mg/L), $NaMoO_4$ * 2 H_2O (100 mg/L). Each component was dissolved one at a time in diH_2O, pH adjusted to 3.0 with HCl/NaOH, qs to volume and filter sterilized with a 0.22 micron filter.

[0337] The diluted culture volume was 25 ml in a 250 ml baffled Bellco Delong flask for growth at 30°C with agitation (225 rpm). Samples were taken aseptically, as indicated, for optical density measurements at A_{600}. Two sets of cultures were set up, one for induction with 0.2 mM IPTG and one that remained un-induced. After 3 hours of growth at 30°C with shaking at 200 rpm (OD_{600}~0.5), one set of the cultures was induced with 0.2 mM IPTG and incubated for a further 3 h at 30°C with shaking at 200 rpm, the un-induced set was further incubated for the same amount of time. The OD_{600} was determined for all cultures prior to the induction time (3 h post inoculation) and at the time of the measurement of isoprene by the Headspace assay (3 h post-induction, total of 6 h of growth). The cell cultures were centrifuged at 7000 x g for 15 minutes in a Sorvall superspeed centrifuge to pellet the cells. The supernatant was removed and the cell pellet frozen for use in an in vitro assay for isoprene synthase activity. Results of the growth and headspace assays are shown in the following tables.

Table 6-1. Growth of *E. coli* Strains Expressing Poplar IspS Variants (OD_{600} values)

Strain	Pre-induction (after 3h growth)	Post-induction (3h with IPTG)	Non-induced (after 6h growth)
pTrcPoplar	0.49	3.3	4.7

K272R			
pTrcPoplar K272R/N453D	0.48	3.7	4.8
pTrcPoplar K272R/N453D/C497W	0.41	3.1	5.1
pTrcPoplar K272R/497W H2	0.45	0.8	0.97
pTrcPoplar WT	0.49	3.5	4.7
pTrcKudzu WT	0.44	3.3	4.2

Table 6-2. Production of Isoprene by *E. coli* Strains Expressing Poplar IspS Variants (μg/L)

Strain	Pre-induction (after 3h growth)	Post-induction (3h with IPTG)	Non-induced (after 6h growth)
pTrcPoplar K272R	n/a	0	0
pTrcPoplar K272R/N453D	n/a	0	0
pTrcPoplar K272R/N453D/C497W	n/a	0	0
pTrcPoplar K272R/497W H2	n/a	0	0
pTrcPoplar WT	n/a	0	0
pTrcKudzu WT	n/a	1.3	0.29

[0338] Surprisingly, the strain expressing the kudzu IspS demonstrated any measurable isoprene production. This is unexpected given that kinetic properties of the poplar enzymes were reported in the literature to be superior to those of kudzu enzymes. In particular, the prior art describes the specific activity (U/mg) and K_m (μM) of recombinant kudzu IspS to be 0.075 and 7,700 respectively, native aspen IspS to be 0.5 and 8,000 respectively, and recombinant poplar IspS to be 0.16 and 9,000 respectively (Silver and Fall, J Biol Chem, 270:13010-1316, 1995; Miller et al., Planta, 213:483-487, 2001; and Sharkey et al., Plant Physiology, 137:700-712, 2005). The published K_m values for the three enzymes are all quite high and within range of each other, but the specific activity for kudzu isoprene synthase is significantly worse than that of the other two isoprene synthases.

III. Assays for Isoprene Synthase Activity and Solubility

[0339] By using the DMAPP assay, the activity of isoprene synthase can be measured directly as DMAPP is the direct substrate for the enzyme. The cell pellets of the poplar parent and mutant strains, as well as the wild type kudzu were thawed and resuspended in 2 ml PEB (50 mM Tris-HCl, pH 8.0, 20 mM MgCl, 2 mM dithiothreitol, and 50% [v/v] glycerol). Cells were lysed by French pressure cell disruption, one pass, at 20,000 psi. The lysate (1 ml) was then centrifuged in a microfuge for 20 min at 20,000 rpm at 4°C. The supernatant was removed and the pellet resuspended in 1 ml of PEB. The supernatant and pellet samples were analyzed by SDS-PAGE, and DMAPP assay, while the total protein content was determined by BCA.

Table 6-3. DMAPP Assay of Isoprene Production from the Supernatant of the Centrifuged Cell Lysate

Strain	OD600 (prior to lysis)	Total Protein (mg/ml)	Isoprene/ Total Protein
Induced			
pTrcPoplar K272R	3.3	1.70	0.03
pTrcPoplar K272R/N453D	3.6	1.3	0.08
pTrcPoplar K272R/N453D/C497W	3.1	1.10	0.08
pTrcPoplar K272R/497W H2	0.803	0.80	0.11
pTrcPoplar WT	3.5	1.30	0.06
pTrcKudzu WT	3.3	1.50	11.15
Uninduced			
pTrcPoplar K272R	4.7	1.7	0.26
pTrcPoplar K272R/N453D	4.8	1.8	0.07
pTrcPoplar K272R/N453D/C497W	5.2	1.9	0.02
pTrcPoplar K272R/497W H2	0.969	1.0	0.17
pTrcPoplar WT	4.6	1.7	0.05
pTrcKudzu WT	4.2	1.9	1.62

[0340] Production was normalized to total cell lysate supernatant protein.

Table 6-4. DMAPP Assay of Isoprene Production from the Pellet of the Centrifuged Cell Lysate

Strain	OD600 (prior to lysis)	Total Protein (mg/ml)	Isoprene/ Total Protein
Induced			
pTrcPoplar K272R	3.3	1.02	0.118
pTrcPoplar K272R/N453D	3.6	1.36	0.000
pTrcPoplar K272R/N453D/C497W	3.1	1.49	0.040
pTrcPoplar K272R/C497W H2	0.80	1.38	0.043
pTrcPoplar WT	3.5	1.57	0.050
pTrcKudzu WT	3.3	1.47	0.040
Uninduced			
pTrcPoplar K272R	4.7	1.40	0.170
pTrcPoplar K272R/N453D	4.8	1.53	0.120
pTrcPoplar K272R/N453D/C497W	5.2	1.42	0.131
pTrcPoplar K272R/C497W H2	0.97	1.55	0.080
pTrcPoplar WT	4.6	1.38	0.120
pTrcKudzu WT	4.2	1.55	0.120

[0341] Production was normalized to total cell lysate pellet protein.

[0342] The poplar variant K272R/C497W showed a 1.8x increase in activity as compared to the wild type in the supernatant fraction of the induced cultures. Likewise, the poplar variants K272R and K272R/C497W showed a 5.2x and 3.4x increase in activity as compared to the wild type in the supernatant fraction of the uninduced cultures. Moreover the poplar variant K272R showed a 2x increase in activity as compared to wild type in the pellet of the induced cultures. However, the most striking result was that the kudzu IspS is more active than the poplar IspS employed herein (185x). In the above tables, H2 is the name of the clone designated pTrcPoplar K272R/C497W H2.

EXAMPLE 7

Subcloning of Kudzu Isoprene Synthase

[0343] In this Example, methods used in the construction of kudzu isoprene synthase (IspS) SELs are described. To create an expression vector for construction of site evaluation libraries (SEL), the kudzu isoprene synthase gene was subcloned into the pET24d vector (Novagen) from the pCR2.1 vector (Invitrogen). The kudzu IspS gene was amplified from pTrcKudzu template DNA using primers MCM50 5'-GATCATGCAT TCGCCCTTAG GAGGTAAAAA AACATGTGTG CGACCTCTTC TCAATTTACT (SEQ ID NO:20); and MCM53 5'-CGGTCGACGG ATCCCTGCAG TTAGACATAC ATCAGCTG (SEQ ID NO:21). PCR reactions were carried out using Taq DNA Polymerase (Invitrogen), and the resulting PCR product was cloned into pCR2.1-TOPO TA cloning vector (Invitrogen), and transformed into *E. coli* Top10 chemically competent cells (Invitrogen). Transformants were plated on L agar containing carbenicillin (50 μg/ml) and incubated overnight at 37°C. Five ml Luria Broth cultures containing carbenicillin 50 μg/ml were inoculated with single transformants and grown overnight at 37°C. Five colonies were screened for the correct insert by sequencing of plasmid DNA isolated from 1 ml of liquid culture (Luria Broth) and purified using the QIAprep Spin Mini-prep Kit (Qiagen). The resulting plasmid, designated MCM93, contains the kudzu IspS coding sequence in a pCR2.1 backbone (Figure 9). The sequence of MCM93 (SEQ ID NO:22) is shown in Figure 10.

[0344] The kudzu coding sequence was removed by restriction endonuclease digestion with *Pci*I and *Bam*H1 (Roche) and gel purified using the QIAquick Gel Extraction kit (Qiagen). The pET24d vector DNA was digested with *Nco*I and *Bam*HI (Roche), treated with shrimp alkaline phosphatase (Roche), and purified using the QIAprep Spin Mini-prep Kit (Qiagen). The kudzu IspS fragment was ligated to the *Nco*I/*Bam*H1 digested pET24d using the Rapid DNA Ligation Kit (Roche) at a 5:1 fragment to vector ratio in a total volume of 20 μl. A portion of the ligation mixture (5 μl) was transformed into *E. coli* Top 10 chemically competent cells and plated on L agar containing kanamycin (50 μg/ml). The correct transformant was confirmed by sequencing and transformed into chemically competent BL21(λDE3)pLysS cells (Novagen). A single colony was selected after overnight growth at 37°C on L agar containing kanamycin (50 μg/ml). A map of the resulting plasmid designated as pET24D-Kudzu is shown in Figure 11. The sequence of pET24D-Kudzu (SEQ ID NO:23) is shown in Figure 12. IspS Activity was confirmed using the headspace assay as described in Example 5).

EXAMPLE 8

Construction of Isoprene Synthase Site Evaluation Libraries (SELs)

[0345] In order to improve the kinetic parameters of a plant IspS SELs are prepared at sites selected from homology models of both the kudzu and the poplar IspS enzymes. While it is predicted from the homology models that engineering at the indicated sites would improve both enzymes, in this embodiment, kudzu SELs are described. Kudzu IspS surface sites of interest include but are not limited to: 26 L, 30 E, 31 F, 33 Q, 35 L, 36 E, 37 N, 39 L, 40 K, 41 V, 43 K, 44 L, 61 R, 62 V, 63 D, 65 Q, 87 K, 94 E, 95 N, 99 L, 100 D, 105 N, 137 K, 138 E, 143 G, 144 E, 182 N, 184 L, 185 K, 187 G, 189 N, 190 T, 225 P, 226 H, 247 K, 257 T, 258 E, 259 M, 266 D, 334 N, 353 D, 357 S, 358 I, 361 E, 389 N, 392 I, 393 I, 398 K, 401 E, 421 C, 423 Q, 424 Q, 425 E, 426 D, 430 H, 432 L, 433 R, 434 S, 437 D, 443 R, 462 L, 463 E, 476 H, 478 N, 479 D, 485 Q, 508 D, 513 P, 515 A, 532 Q, 533 Y, 537 L, 538 G, 539 R, 542 Y, 543 A, and 557 P. Kudzu IspS active site positions of interest include but are not limited to: 24 P, 25 N, 309 Y, 310 D, 377 L, 381 F, 384 E, 399 Y, 402 N, 403 A, 406 S, 407 S, 409 G, 411 A, 413 L, 449 F, 456 A, 457 T, 458 S, 458 S, 459 A, 460 A, 461 E, 462 L, 463 E, 464 R, 465 G, 466 E, 467 T, 468 T, 469 N, 523 M, 527 S, and 531 Y. Additional kudzu IspS active site positions of interest include but are not limited to: 20 A, 21 N, 22 Y, 23 Q, 271 R, 278 W, 299 F, 302 V, and 408 S. Each library SEL contains clones, maximally including 20 different variants. For example, kudzu isoprene synthase SEL 531 contains variants in which the DNA triplet coding for tyrosine at position 531 of the mature kudzu enzyme is replaced by another DNA triplet encoding: alanine, aspartic acid, cysteine, glutamic acid, phenylalanine, glycine, histidine, isoleucine, lysine, leucine, methionine, asparagine, proline, glutamine, arginine, serine, threonine, valine, or tryptophan. Briefly, DNA triplets of specific positions in the DNA coding strand of the mature IspS are replaced. The mutated IspS nucleic acids are subsequently ligated to a suitable expression vector and used to transform suitable host cells.

[0346] Site evaluation libraries are created either by ordering synthetic constructs (e.g., DNA2.0) or by ordering primers with the "nns" sequence in place of the codon to be mutated. The primers are then be used to mutate the gene to produce an SEL at the indicated site using commercially available mutagenesis kits (e.g., Stratagene) as has been described (e.g., WO0507682A2). The mutated codons are identified by sequence analysis. The site libraries are arrayed in 96 well master plates, and frozen for later use. Cultures are grown from the master plates and prepared for screening.

[0347] The desired end products are IspS enzymes that function optimally in a host metabolically engineered to maximize carbon flow through IspS. To this end several stages of

screening are used to ensure that correct parameters are being addressed. Exemplary screens include but are not limited to: expression, DMAPP feeding for production of HG, microreactor, protein determination, and headspace assays. Expression screen: One example of a method to analyze the level of protein expression is as follows. Soluble and insoluble fractions of cell lysates (obtained from lysed cell cultures) are prepared by centrifugation. The resulting supernatants and pellets are analyzed by SDS-PAGE. The percent soluble protein is determined by densitometry analysis of the protein present in the supernatant versus the pellet.

[0348] In an exemplary embodiment, kudzu site evaluation libraries are constructed in the pET24D expression vector. The pET24D-Kudzu vector, containing the kudzu isoprene synthase gene, serves as the template DNA.

Materials:

pET24D-Kudzu vector (~50 ng/μl)

Kudzu IS site-directed mutagenic primers (Integrated DNA Technologies)

QUIKCHANGE® Multi Site-Directed Mutagenesis Kit (Stratagene)

MJ Research PTC-200 Peltier Thermal Cylcer (Bio-Rad Laboratories)

One Shot TOP10 competent cells (Invitrogen)

QIAprep Spin Miniprep Kit (Qiagen)

BL21(λDE3) pLysS competent cells (Invitrogen)

Luria Broth (LB) agar plates

Methods:

[0349] The method of mutagenesis was based on the codon-specific mutation approach, in which the creation of all possible mutations in a specific DNA triplet was performed using a single forward primer with a length of 25 to 45 nucleotides, enclosing a specific designed triple DNA sequence NNS (N = A, C, T or G and S = C or G) corresponding with the sequence of the codon to be mutated. This method results in the random incorporation of nucleotides at a specific pET24D-kudzu codon of interest. Table 8-1 lists the oligonucleotide primers used for mutagenesis, with the number in the primer name corresponding with the codon position in the mature kudzu isoprene synthase enzyme sequence. All oligonucleotide primers were synthesized (Integrated DNA Technologies) on a 100 nmole scale and PAGE purified.

Table 8-1. Kudzu IspS Codon-Specific Mutation Primers

Name	SEQ ID	Primer Sequence
IS_A20	NO:24	CATAATTCCCGTCGTTCCNNSAACTATCAGCCAAACCTG
IS_N21	NO:25	CATAATTCCCGTCGTTCCGCANNSTATCAGCCAAACCTGTG
IS_Y22	NO:26	CCCGTCGTTCCGCAAACNNSCAGCCAAACCTGTGGAATTTC
IS_Q23	NO:27	GTCGTTCCGCAAACTATNNSCCAAACCTGTGGAATTTC
IS_R271	NO:28	CTGGATTTTGTACGCGACNNSCTGATGGAAGTTTATTTC
IS_W278	NO:29	CTGATGGAAGTTTATTTCNNSGCACTGGGTATGGCGCC
IS_F299	NO:30	CAAAGCTGTTACTAAAATGNNSGGTCTGGTGACGATCATC
IS_V302	NO:31	CTAAAATGTTTGGTCTGNNSACGATCATCGATGACGTG
IS_S408	NO:32	GAAAACGCCAGCGTTTCCTCCNNSGGTGTAGCGCTGCTGGC

[0350] A PCR reaction was set up in a 0.5ml thin-walled PCR tube following the manufacturer's protocol for the QUIKCHANGE® Multi Site-Directed Mutagenesis Kit (Stratagene): 1μl pET24 Kudzu vector (50ng/μl); 1μl Kudzu IS site-directed forward mutagenic primer (10μM); 2.5μl 10X QUIKCHANGE® Multi Reaction buffer; 1μl dNTP Mix, 1μl QUIKCHANGE® Multi enzyme blend (2.5U/μl); and 18.5μl distilled autoclaved water to provide a 25μl total reaction mix. The pET24 Kudzu SELs were amplified using the following conditions: 95°C, for 1 min (1st cycle only), followed by 95°C for 1 min, 55°C for 1 min, 65°C for 12 min, and repeat cycling 29 times. Then the reaction mixture was subjected to *Dpn*I digestion (supplied with QUIKCHANGE® Multi Site-Directed Mutagenesis Kit) by addition of 1.5μl *Dpn*I restriction enzyme to each tube, and incubated at 37°C for 2 hours to digest the parental pET24D-kudzu vector. The *DpnI*-treated PCR reaction was then transformed into One Shot TOP10 competent cells (Invitrogen), plated onto LB agar plates containing 50μg/ml kanamycin, and incubated overnight at 37°C. The next day, 96 random colonies were picked and sequenced to identify a minimum of 15 of the possible 19 amino acid variants. Upon identification of the site-directed variants, each variant clone was then inoculated in a 5ml tube of LB + 50μg/ml kanamycin and grown overnight at 37°C with shaking (250 rpm). The following day plasmid DNA was purified using the QIAprep Spin Miniprep Kit (Qiagen). The variants were then transformed into One Shot BL21(λDE3) pLysS competent cells (Invitrogen) for protein expression screening, plated on LB agar plates containing 50μg/ml kanamycin and 30μg/ml chloramphenicol and incubated overnight at 37°C.

[0351] An alternative method for producing pET24D-Kudzu SELs in *E. coli* BL21(λDE3) pLysS cells was also successfully employed. The TOP10 competent cell transformants obtained from the *DpnI*-treated PCR reaction described above were harvested by applying 3ml of LB media to the top of the agar and resuspending the cells by scraping with a sterile plate spreader. The 3ml of pooled, resuspended cells were then used to inoculate a 25ml shake flask containing LB + 50μg/ml kanamycin. The pooled culture was then grown overnight at 37°C with shaking (250rpm). The following day plasmid DNA was purified from the pooled cultures using the QIAprep Spin Miniprep Kit (Qiagen). The pooled plasmid DNA was then transformed into One Shot BL21(λDE3) pLysS competent cells for protein expression screening as described above.

[0352] To make a master plate, the correct constructs are arrayed in quadruplicate in 96 well plates. One colony of the correct sequence is used to inoculate 4 wells and the plates are grown for several hours to overnight at 37°C in LB containing 50 μg/ml kanamycin with shaking (200 rpm). Sterile glycerol is added to the cultures to a final concentration of 15% (for a final total volume of 150-200 μl/well). The plates are then sealed using BREATHE-EASIER (EMS Catalog No. 70536-20) membranes and stored at -80°C.

EXAMPLE 9

Production and Purification of Isoprene Synthase Inclusion Bodies

[0353] Inclusion bodies containing kudzu isoprene synthase were formed when the enzyme is overexpressed in the presence of the chaperone GroELS in the strain BL21(λDE3). Briefly pETNHisKudzu (U.S. Application No. 61/013,574, herein incorporated by reference) was subcloned into pGro7 (Takara Catalog No. 3340) according to the manufacturer's instructions. A 500 mL of culture was grown essentially as described (Whittington et al., Proc Natl Acad Sci USA, 99:15375-15380, 2002). Despite the presence of chaperone and low temperature of cultivation the culture yielded predominantly inclusion bodies and only low levels of soluble active protein. The inclusion bodies were harvested using the IFOLD Protein Refolding System (Novagen Catalog No. 71552-3) according to the manufacturer's instructions. This procedure led to a high yield (>50 mg) of recombinant kudzu isoprene synthase. The purity of the inclusion body is shown in Figure 13. This preparation was used for the production of rabbit polyclonal anti-isoprene synthase antisera (Invitrogen).

EXAMPLE 10

High Throughput Biochemical Screen of Isoprene Synthase Variants

[0354] This example describes high throughput methods for the determination of isoprene synthase activity. Libraries of BL21(λDE3)pLysS *E.coli* host cells capable of expressing isoprene synthase variants are arrayed in 96-well plates and stored frozen at -80°C as 15% glycerol stocks as described above in Example 8. To analyze a plate of up to 96 variants, a replica stamp of the glycerol stock master plate is made with a 96-pin MULTI-BLOT floating pin tool (V&P Scientific Catalog No. VP 408AF) onto Luria broth agar containing appropriate antibiotic(s) (e.g., 30 μg/mL chloramphenicol, 50 μg/mL kanamycin). The replica plate is incubated over night at 30°C to allow growth of bacterial patches. Using the same floating pin replicator a 96-square deep well plate containing 250 μL of TM3 medium supplemented with 0.08% Biospringer yeast extract and 1% glucose plus antibiotics (30 μg/mL chloramphenicol, 50 μg/mL kanamycin) is inoculated from the agar plate and incubated overnight at 30°C. The recipe for TM3 broth is as follows: K_2HPO_4 (13.6 g/l) KH_2PO_4 (13.6 g/l), $MgSO_4$ * $7H_2O$ (2 g/l) Citric Acid Monohydrate (2 g/L) Ferric Ammonium Citrate (0.3 g/L) $(NH_4)_2SO_4$ (3.2 g/L) yeast extract (0.2 g/L) 1 ml of 1000x Trace Elements solution, pH adjusted to 6.8 with ammonium hydroxide qs to volume with sterile diH_2O and filter sterilized with a 0.22 micron filter. The recipe for 1000X Trace Elements solution is as follows: Citric Acids * H_2O (40 g/L), $MnSO_4$ * H_2O (30 g/L), NaCl (10 g/L), $FeSO_4$ * 7 H_2O (1 g/L), $CoCl_2$ * 6 H_2O (1 g/L), ZnSO * 7 H_2O (1 g/L), $CuSO_4$ * 5 H_2O (100 mg/L), H_3BO_3 (100 mg/L), $NaMoO_4$ * 2 H_2O (100 mg/L). Each component was dissolved one at a time in diH_2O, pH adjusted to 3.0 with HCl/NaOH, qs to volume and filter sterilized with a 0.22 micron filter. The overnight cultures are diluted with the same medium to an OD_{600} of 0.05 and grown in another 96-square deep well plate (Thomson Instrument, Catalog No. 951652C), with each well containing 600 μL of the dilution. The dilutions are grown at 30°C with shaking to an OD_{600} of 0.8 and are then induced with IPTG added to a concentration of 400 μM. The plate is grown for 5 hours and OD_{600} is determined for quality control and normalization.

[0355] A volume of 400 μL of culture is transferred into a new 96-well plate (Perkin Elmer, Catalog No. 6008290) and cells are harvested by centrifugation in a Beckman Coulter Allegra 6R centrifuge at 2500 x g. The pellet is resuspended in 200 μL of hypotonic buffer (5mM $MgCL_2$, 5mM Tris HCl, 5mM DTT pH 8.0) and the plate is frozen at – 80°C for a minimum time of 60 min. Cell lysate is prepared by thawing the plate and adding 32 μL of isoprene synthase DMAPP assay buffer (57mM Tris HCl, 19 mM $MgCl_2$, 74 μg/mL DNase I

(Sigma Catalog No. DN-25), $2.63x10^5$ U/mL of READYLYSE lysozyme solution (Epicentre Catalog No. R1802M), and 5 mg/mL of molecular biology grade BSA. The plate is incubated with shaking at 25°C for 30 min and then placed on ice. For isoprene production, an 80 μL aliquot of lysate is transferred to a 96-deep well glass plate (Zinsser Catalog No. 3600600) and 20 μL of a 10 mM DMAPP solution in 100mM $KHPO_4$, pH 8.2 (Cayman Chemical Catalog No. 63180) is added. The plate is sealed with an aluminum plate seal (Beckman Coultor Catalog No. 538619) and incubated with shaking at 30°C of 60 minutes. The enzymatic reactions are terminated by heating the glass block (70°C for 5 min). The headspace of each well is quantitatively analyzed as described in Example 5.

[0356] To determine protein concentration 5μL or more of lysate is run on precast gels (Invitrogen Catalog No. NP0301BOX) for western blot analysis after transfer to a nitrocellulose membrane (Invitrogen Catalog No. LC2000). The primary antibody employed is an anti-isoprene synthase antibody of Example 9. Primary antibody binding is followed by development with a secondary antibody labeled with Alexa Fluor 488 (Invitrogen Catalog No. A-11008) to permit quantitative signal determination. The western blot procedure was carried out as described by Invitrogen. The fluorescence signal was recorded with a Molecular Dynamics STORM instrument using the blue filter setting and quantitatively analyzed with the Molecular Dynamics IMAGEQUANT image analysis software package. Specific activity of the library members was calculated from the ratio of the amount of isoprene produced divided by either the A_{600} of the induction cultures or the isoprene synthase protein concentration determined by western blot. Isoprene synthase protein standard was calibrated by standard gel densitometry with BSA stained with Coomassie brilliant blue R250 serving as primary standard. Increased, decreased, or no change in specific activity of the entire library was tabulated for further analysis. Figure 14 provides graphs showing isoprene synthase activity of kudzu site evaluation library (SEL) members for positions Y22, A20, and S408. Most members show highly decreased activity relative to wild type, while conservative substitutions show a lesser decrease in activity. . Activity of variant A20G approximates that of the wild type kudzu enzyme, indicating that it is a candidate partner for a combinatorial mutant. Interestingly, variant S408D of library S408 showed an increase in activity compared to wild type thus providing another candidate partner for a combinatorial mutant.

Example 11

Isoprene Synthase Truncations

[0357] This example describes the identification of the amino acid sequence of the protein in the lower band of the doublet seen in purified poplar IspS preparations (see Figure 21). A series of N-terminally truncated IspS molecules based on putative cleavage sites identified by mass spectrometry was also generated. A shorter N-terminal truncation of IspS (the "MEA" truncation in pDu39, see below) was also generated, to examine the effect of further truncation on IspS activity (Williams DC, McGarvey DJ, Katahira EJ, Croteau R (1998) Biochemistry 37:12213–12220).

I. Construction of an N-terminally 6XHis-tagged IspS (in pDu27) for protein purification:

[0358] The full length *P. alba* IspS from the template P. alba pET24a (Figures 19 and 20) was prepared by PCR. The following PCR reaction was prepared: 1µl (Template)-P. alba pET24a, 5 µl 10X PfuUltraII Fusion buffer, 1 µl dNTP's (10 mM), 1µl primer (50 µM) primer F-(MCM219), 1 µl primer (50 µM) primer R-(MCM182), 41 µl diH_2O and 1 µl of PfuUltra II Fusion DNA Polymerase (Stratagene). PCR cycling parameters were as follows: 95 °C 1 min., 95 °C 1 min, 55 °C 20 sec., 72 °C 27 sec. for 29 cycles followed by 72 °C 3 min and 4 °C until cool, using an Eppendorf Mastercycler. The PCR product was gel extracted and purified, using 0.8% E-gel (Invitrogen) and Qiagen QIAquick Gel Extraction and QIAprep Spin Miniprep kits, according to the manufacturer's recommended protocol. A 3 µl aliquot of purified product was ligated to the pET200D/TOPO vector (Invitrogen), according to the manufacturer's protocol. The reaction was incubated for 5 minutes at room temperature, and the 6 µl topoisomerase mixture was then transformed into *E. coli* Top10 chemically competent cells (Invitrogen) according to the manufacturer's protocol. Transformants were selected for on LB plates containing kanamycin (50 µg/ml) (Kan50), and incubated at 37 °C overnight. Five colonies were picked and screened using PuReTaq Ready-To-Go PCR Beads (Amersham) using the T7 Forward and MCM182 primers. Clones harboring inserts of the correct size were further verified by sequencing using the T7 Forward and T7 Reverse primers (Quintara Biosciences). One construct, pDu27 (Figures 16-18), was chosen for further study. A 1 µl aliquot of the plasmid preparation was transformed into BL21(λDE3)*pLysS* (Invitrogen) according to the manufacturer's protocol. Transformants were selected for on LB plates containing Kan50+ and chloramphenicol (35 µg/ml) (Cm35) and incubated at 37 °C overnight. The resulting strain was used for expression and purification of N-terminally 6XHis-tagged P. alba IspS.

[0359]

II. Purification of 6XHis-tagged IspS

Expression of 6XHis-tagged IspS

[0360] N-terminally 6XHis-tagged IspS was expressed and purified from strain MD08-99. The growth procedure is suitable for histidine tagged enzymes expressed in BL21(λDE3)*pLysS* cells. A 10 ml of overnight culture was prepared for each 1L of planned growth. The appropriate antibiotics (50 mg/ml kanamycin, 50 mg/ml chloramphenicol, and/or 50 mg/ml Carbenecillin) was added to 10 ml of LB medium in a 25 ml flask and was inoculated with 1 colony from a fresh plate of cells or directly from glycerol frozen cell stock. Cultures were grown at 30 °C overnight with shaking at ~220 rpm. Day cultures were prepared in 1 liter of LB medium with appropriate antibiotics for each culture. Each 1L day culture was inoculated with 10 ml of overnight culture and grown at 30-37 °C with shaking at ~220 rpm until the OD_{600} reached ~0.4-0.6. Day cultures were then induced with 400 μM IPTG and allowed to continue growing at 30°C with shaking at 220 rpm for ~5-6 hours. Cells were then harvested by centrifugation at 10,000 x g for 10 min, 4 °C. Following Harvest, cells were used directly or stored at -80°C until ready to process.

Purification of 6XHis-tagged IspS

[0361] For purification of histidine tagged enzymes from BL21(λDE3)pLysS cells, cells were gently resuspended in fresh Lysis buffer (Lysis buffer: Ni wash buffer + 0.5 mM PMSF, 0.01% Tween-20, 1 mg/ml lysozyme, 0.2 mg/ml DNaseI; Ni wash buffer: 50 mM NaH_2PO_4, 300 mM NaCl, 20 mM Imidazole, pH 8.0). Approximately 40-50 ml of lysis buffer was used per 1L of cell pellet. Cells were then incubated on ice for approximately 30 min. The cell suspension was then lysed fully by passing 2-3 times through a french pressure cell (large french press cell at 1200 psi/High setting) until lysate started to look clear. A sample of the lysate was saved for activity assay and gel analysis (~100 μl). The lysate was then clarified by centrifuging the lysate at 30,000xg for 30 min, 4°C in a Sorvall Discovery 90SE ultracentrifuge. The supernatant was removed and retained. A sample of the "clarified lysate" was saved for activity assay and gel analysis (~100 μl).

[0362] The clarified lysate was run over HisTrap HP columns (GE Healthcare) using a gradient from 0-100% Ni buffer B. Samples were then analyzed by SDS-PAGE gel (4-12% gel NUPAGE, Invitrogen) according to manufacturer's directions. Desired fractions were concentrated on spin filters (Vivaspin-20, Sartoris,) and then desalted over a HiPrep 26/10

Desalting column (GE heathcare) packed with Sephadex G25 resin. The G-25 buffer consisted of 50 mM HEPES, 50 mM NaCl, and 1 mM DTT, pH 7.4. The desired sample was then purified over a HiTrap Q HP column (GE) using a gradient elution from 0% Q seph buffer A to 100% Q seph buffer B (Q seph buffer A: 50 mM Tris, 0.05 M NaCl, 1 mM DTT, pH 7.6 and Q seph buffer B: 50 mM Tris, 1.0 M NaCl, 1 mM DTT, pH 7.6). Fractions containing the desired protein were analyzed and concentrated. Sample buffer was then exchanged into 50 mM HEPES, 50 mM NaCL, pH 7.4 with 1 mM DTT by passing the sample over a Hi Prep 26/10 Desalting column (GE heathcare) packed with Sephadex G25 resin. A final polishing step of Gel filtration was used when necessary. The sample was passed through a Hi Load 26/60 Superdex 200 prep grade (GE) in gel fitration buffer: (50 mM HEPES, 150 mM NaCl, 1mM DTT, pH 7.4). Fractions were then analyzed and concentrated. The samples were then stored at -80 °C. For preparation for analysis of the band, the sample is run on an SDS-PAGE gel (4-12% NUPAGE gel, Invitrogen), stained and the desired band excised and processed as described below.

III. Mass Spectrometry of Isoprene Synthase

Sample preparation

[0363] An In-Gel Digestion and LCQ-Deca Mass Spectrometry Procedure was utilized (Modified Rosenfeld in-gel Digest Protocol) (Rosenfeld *et al*, Anal. Biochem. (1992) 203, 173-179; Hellman *et al*, Anal Biochem, (1995) 224, 451-455). The purified sample of Isoprene synthase was run on a 4-12% SDS-PAGE (NUPAGE, Invitrogen) and stained with Coomassie Brilliant Blue R-250 (Thermo Scientific) or SimplyBlue Safe Stain (Invitrogen). Band(s) of interest were excised from the gel and destained. Each gel slice was diced into small pieces ~1 mm x 1mm and placed into 0.65 mL "slick" (siliconized) tubes from PGC Scientific. Approximately 100µL of 25mM NH_4HCO_3/50% ACN/H_2O was added to each tube and vortexed for 10 min. Supernatants were extracted and discarded. These steps were repeated twice. Then gel pieces were then run in a Savant SpeedVac to dryness (~ 20 to 30 min).

[0364] Samples were then reducted and alkylated. For reduction, 25 µL (or enough to cover) of 10 mM DTT in 25 mM NH_4HCO_3 (prepared fresh) were added to dried gels. Tubes were then vortexed and spun briefly. Reactions were incubated at 50 °C for 1 hour. For alkylation, supernatants were removed and 25 µL or more of 55 mM iodoacetamide (IAA) in 25 mM NH_4HCO_3 were added to the gel. Reaction tubes were vortexed and spun briefly

again. Reactions were allowed in dark for 1 hour at room temperature. Supernatants were removed and gels were washed with ~ 100 µL of 25mM NH_4HCO_3/50% ACN/H_2O, by vortexing for 10 min and briefly spinning. Supernatant were removed and the wash step was repeated once. Gel pieces were then dried in a SpeedVac (~ 15 -30 min).

[0365] Digestion buffer was prepared by adding 400 µL of 0.1% n-octyl B-D-glucopyranosidase water to 100 uL of 8M Urea. 400 uL of this digestion buffer was added to 20 ug of freshly prepared Trypsin. 0.05 µg/µL of sequencing-grade Trypsin was prepared from one vial of 20 µg sequencing grade trypsin (Promega) that was dissolved into 400 uL of 1.6 M Urea solution. Trypsin enzyme solution was added enough to cover gel pieces. Tubes were covered with parafilm and incubated at 37 °C overnight (16-20 hrs). It was ensured that there is a little extra buffer above the gel.

[0366] Peptides were extracted from gels by briefly vortexing and spinning the digest. The digest solution was transferred with gel loading tips into a 0.65 mL siliconized tube. 50 µL (enough to cover) of 50% ACN/0.1% FA/H_2O were added to the gel pieces and samples were vortexed for 10 min, spun, and then sonicated for five min. Extracted peptides were pooled together in one tube. Extraction steps were repeated two to three more times until the gel pieces became white in appearance and shrank in size. Extracted digests were vortexed, spun and dried in a Speed Vac to a volume of 55 µL. In cases where the volume was less than 55 µL, enough 0.1% FA was added to make up a final volume of 55 µL.

Mass Spectrometry

[0367] The sample was injected onto a Thermofinnigan (San Jose, CA) LCQ-Deca electrospray ionization (ESI) ion-trap mass spectrometer. A Vydac C18 column (5µ, 300A, 0.2 x 150 mm, Michrom Bioresources, Auburn, CA) was used with a flow rate of 200 µL/min. The injection volume was 50 uL, and was filtered through an on-line trapping cartridge (Peptide CapTrap, Michrom Bioresources, Auburn, CA) before loading onto the column. Separation of the in-gel digest was performed with the following gradient (Solvent A: 0.1% trifluoroacetic acid in H2O (J.T. Baker, Phillipsburg, NJ), Solvent B: 0.08% trifluoroacetic acid in acetonitrile (J.T. Baker, Phillipsburg, NJ)):

Table 11-1. Gradient Table

	min	A%	B%

0	0.00	100	0
1	10.00	86	14
2	16.00	81	19
3	20.00	78	22
4	21.00	77	23
5	22.00	75	25
6	24.00	73	27
7	32.00	69	31
8	34.00	66	34
9	37.00	64	36
10	47.00	60	40
11	50.00	30	70
12	55.00	100	0
13	60.00	100	0
14	65.00	100	0
15		100	0

Mass Spectrometry Results

[0368] An aliquot of 6.4 µg of protein was loaded into 5 lanes on a 4-12% bis-tris NUPAGE gel (Invitrogen), MOPS buffer, 50 min run. As described above, the gel was stained for 2 minutes, and then de-stained for 15 minutes. The gel was washed in H_2O, then all bands were excised, cut into small pieces, and destained. Gel pieces were reduced and alkyated with DTT/IAA for 1 hour each at 52 °C and RT, respectively. Trypsin was added for an overnight digestion. Extracted peptides were run on the LCQ-Deca. Figures 21 and 22 show the results for the mass spectrometry analysis. The lower doublet band (in Figure 21) is identified as IspS. Figure 22 shows that N-terminal truncations were observed after amino acids 39, 40, 42, and 44 (according to the peptide sequence of the N-terminally His-tagged IspS protein in pDu27). The C-terminus of IspS is intact.

IV. Construction of N-terminally truncated IspS variants:

[0369] All truncated constructs without affinity tags were generated using the QuickChange Site-directed Mutagenesis kit (Stratagene) using the template P. alba pET24a

for PCR amplification. Approximately 50 ng of template DNA was used for amplification (with an Eppendorf Mastercycler Gradient PCR Machine) of the mutagenized PCR product with the Forward (For) and Reverse (Rev) primer pairs that correspond to each relevant truncation (QC MSV For and QC MSV Rev, for example, see Table 11-2). The following PCR reaction mixtures were used: 1 µl P. alba pET24a, 5 µl 10X PfuUltra HF buffer, 1 µl dNTP's, 1 ul (50 µM) primer-For (*e.g.* QC MSV For), 1 µl (50 µM) primer-Rev (*e.g.* QC MSV Rev), 2 µl DMSO, 39 µl diH_2O, 1 µl PfuUltra HF Polymerase (Stratagene). The following PCR cycling parameters were used: 95 °C 1 min, 95 °C 30 sec., 55 °C 1 min., 68 °C 7.3 min. for one cycle followed by 95 °C 30 sec., 55 °C 1 min., 68 °C 7.3 min for a total of 18 cycles and then followed by 4 °C. The PCR products were treated with 1-2 µl of *Dpn*I (Roche) for 1-3 hour at 37 °C. A 5 µl aliquot of the *Dpn*I treated products was visualized on a 0.8% E-gel (Invitrogen). A 1 µl aliquot of each product was transformed into chemically competent *E. coli* Top10 cells (Invitrogen) according to the manufacturer's protocol. Transformants were selected for on LB medium containing kanamycin at a concentration of 50 µg/ml (Kan50), and incubated overnight at 37 °C. Five colonies of each transformation were selected and grown to stationary phase in 3 ml liquid LB Kan50. Plasmids were purified using a Qiagen miniprep kit according to the manufacturer's recommended protocol. Purified plasmids were sequenced (by Quintara Biosciences) with T7 Forward and Reverse primers, and confirmed for their respective truncation. The resulting plasmids (pDU39 through pDU43, see Table 11-4, Figures 23-34) were transformed into chemically competent *E. coli* BL21(λDE3) *pLysS* (Invitrogen) according to the manufacturer's recommended protocol. Table X describes the strains used for expression of truncated IspS enzymes.

[0370] Constructs with affinity (6XHis) and proteolysis (TEV, Tobacco Etch Virus) tags were generated using P. alba pET24a as a template for PCR reactions. PCR reaction mixtures were prepared as follows: 1ul (P. alba pET24a), 5ul 10X PfuUltraII Fusion buffer, 1ul dNTP's (10 mM), 1ul primer (50 µM) Alba FL-NdeI-For or Alba TRC (MEA)-NdeI-F, 1ul primer (50uM) Alba FLTRC (+) TEV-R, 41 ul diH_2O and 1ul of PfuUltra II Fusion DNA Polymerase from Stratagene. PCR cycling parameters were as follows: 95 °C 1 min., 95 °C 30 sec., 55 °C 20 sec., 72 °C 25 sec. for one cycle and then repeating 95°C 30 sec., 55 °C 20 sec., 72 °C 25 sec. for an additional 28 cycles, followed by 72°C 3min and then 4 °C. After amplification and verification of the correct molecular weight of the product by visualization on 0.8% E-gel (Invitrogen), PCR products were digested with restriction enzymes *Nde*I and *Xho*I (Roche) for 2 hours at 37 °C, and then gel purified using the Qiaquick Gel Purification system (Qiagen) according to the manufacturer's recommended protocol. 3 µl of purified

product was ligated to pET-24a (Invitrogen) that was digested with *Nde*I and *Xho*I (Roche), gel purified and dephosphorylated (using SAP, shrimp alkaline phosphatase) (Promega) according to the manufacturer's recommended protocols. T4 ligase (NEB) was used for the ligation reaction, which was incubated overnight at 16 °C. The ligation reaction was dialyzed into water for 30 min., and 2 µl of the reaction were used to electroporate MCM331 (see below) competent cells. Cells were allowed to recover at 30 °C for 2 hours, and then selected on Kan50 with 5 mM (R)-(-)-Mevalonolactone (MVA) (Sigma) spread onto the plate. Positive transformants were inoculated into 3 ml of liquid LB Kan50, and plasmids were isolated using the QIAPrep Spin miniprep kit (Qiagen). Inserts were verified by restriction digestion using *Nde*I and *Xho*I (Roche) and positive clones were sequenced (Quintara Biosciences) with T7 promoter and T7 terminator sequencing primers. 1 µl of each plasmid (see Table 11-4 for plasmid description and Figures 35-39) was transformed into chemically competent *E. coli* BL21(λDE3) pLysS (Invitrogen) according to the manufacturer's recommended protocol. Transformants were selected on LB Kan50 + Cm35 (Chloramphenicol 35 ug/ml) plates and incubated at 37 °C. See Table 11-5 for a description of all expression strains.

[0371] Strain MCM331 was prepared as follows. A synthetic operon containing mevalonate kinase, mevalonate phosphate kinase, mevalonate pyrophosphate decarboxylase, and the IPP isomerase was integrated into the chromosome of *E. coli*. If desired, expression may be altered by integrating different promoters 5' of the operon.

i) Target vector construction

[0372] The attTn7 site was selected for integration. Regions of homology upstream (attTn7 up) (primers MCM78 and MCM79) and downstream (attTn7 down) (primers MCM88 and MCM89) were amplified by PCR from MG1655 cells. A 50 µL reaction with 1 µL 10 µM primers, 3 µL ddH_2O, 45 µL Invitrogen Platinum PCR Supermix High Fidelity, and a scraped colony of MG1655 was denatured for 2:00 at 94 °C, cycled 25 times (2:00 at 94 °C, 0:30 at 50 °C, and 1:00 at 68 °C), extended for 7:00 at 72 °C, and cooled to 4 °C. This resulting DNA was cloned into pCR2.1 (Invitrogen) according to the manufacturer's instructions, resulting in plasmids MCM278 (attTn7 up) and MCM252 (attTn7 down). The 832 bp *Apa*I-*Pvu*I fragment digested and gel purified from MCM252 was cloned into *Apa*I-*Pvu*I digested and gel purified plasmid pR6K, creating plasmid MCM276. The 825bp *Pst*I-*Not*I fragment digested and gel purified from MCM278 was cloned into *Pst*I-*Not*I digested and gel purified MCM276, creating plasmid MCM281.

ii) Cloning of lower pathway and promoter

[0373] MVK-PMK-MVD-IDI genes were amplified from pTrcKKDyIkIS with primers MCM104 and MCM105 using Roche Expand Long PCR System according to the manufacturer's instructions. This product was digested with *Not*I and *Apa*I and cloned into MCM281 which had been digested with *Not*I and *Apa*I and gel purified. Primers MCM120 and MCM127 were used to amplify CMR cassette from the GeneBridges FRT-gb2-Cm-FRT template DNA using Stratagene Pfu Ultra II. A PCR program of denaturing at 95 °C for 4:00, 5 cycles of 95 °C for 0:20, 55 °C for 0:20, 72 °C for 2:00, 25 cycles of 95 °C for 0:20, 58 °C for 0:20, 72 °C for 2:00, 72 °C for 10:00, and then cooling to 4 °C was used with four 50 uL PCR reactions containing 1uL ~10ng/μL template, 1 μL each primer, 1.25 μL 10mM dNTPs, 5 μL 10x buffer, 1 μL enzyme, and 39.75 μL ddH_20. Reactions were pooled, purified on a Qiagen PCR cleanup column, and used to electroporate water-washed Pir1 cells containing plasmid MCM296. Electroporation was carried out in 2 mM cuvettes at 2.5V and 200 ohms. Electroporation reactions were recovered in LB for 3 hr at 30 °C. Transformant MCM330 was selected on LA with CMP5, Kan50.

iii) Integration into *E. coli* chromosome

[0374] Miniprepped DNA (Qiaquick Spin kit) from MCM330 was digested with SnaBI and used to electroporate BL21(DE3) (Novagen) or MG1655 containing GeneBridges plasmid pRedET Carb. Cells were grown at 30 °C to ~OD1 then induced with 0.4% L-arabinose at 37 °C for 1.5 hours. These cells were washed three times in 4 C ddH_2O before electroporation with 2 μL of DNA. Integrants were selected on L agar with containing chloramphenicol (5 μg/ml) and subsequently confirmed to not grow on L agar + Kanamycin (50 μg/ml). BL21 integrant MCM331 and MG1655 integrant MCM333 were frozen.

Table 11-2. Primers

MCM219	caccatgcgttgtagcgtgtcca (SEQ ID NO:33)
MCM182	gggcccgtttaaactttaactagactctgcagttagcgttcaaacggcagaa (SEQ ID NO:34)
QC MSV For	gaaggagatatacatatgagcgtgtccaccgaaaatg (SEQ ID NO:35)
QC MSV Rev	cattttcggtggacacgctcatatgtatatctccttc (SEQ ID NO:36)
QC MVS For	gaaggagatatacatatggtgtccaccgaaaatgtgtc (SEQ ID NO:37)
QC MVS Rev	gacacattttcggtggacaccatatgtatatctccttc (SEQ ID NO:38)
QC MTE For	gaaggagatatacatatgaccgaaaatgtgtctttcac (SEQ ID NO:39)
QC MTE Rev	gtgaaagacacattttcggtcatatgtatatctccttc (SEQ ID NO:40)
QC MNV For	gaaggagatatacatatgaatgtgtctttcaccgaaac (SEQ ID NO:41)
QC MNV Rev	gtttcggtgaaagacacattcatatgtatatctccttc (SEQ ID NO:42)
QC MEA For	gaaggagatatacatatggaagctcgtcgttctgcg (SEQ ID NO:43)
QC MEA Rev	cgcagaacgacgagcttccatatgtatatctccttc (SEQ ID NO:44)
Alba FL-NdeI-For	gaaggagatatacatatgcgttgtagcgtg (SEQ ID NO:45)

Alba FLTRC (+) TEV-R	cccgcgcttactcgaggccctgaaaatacaggttttcgcg ttcaaacggcagaatcggtt (SEQ ID NO:46)
Alba TRC (MEA)-NdeI-F	gaaactgaaacccatatggaagctcgtcgttctgc (SEQ ID NO:47)

Table 11-3. Primers for construction of strain MCM331

MCM78	attTn7 up rev for integration construct	gcatgctcgagcggccgcTTTTAATCAAACATCCTGCCAACTC (SEQ ID NO:48)
MCM79	attTn7 down rev for integration construct	gatcgaagggcgatcgTGTCACAGTCTGGCGAAACCG (SEQ ID NO:49)
MCM88	attTn7 up forw for integration construct	ctgaattctgcagatatcTGTTTTTCCACTCTTCGTTCACTTT (SEQ ID NO:50)
MCM89	attTn7 down forw for integration construct	tctagagggcccAAGAAAAATGCCCCGCTTACG (SEQ ID NO:51)
MCM104	GI1.2 promoter – MVK	Gatcgcggccgcgcccttgacgatgccacatcctgagcaa Ataattcaaccactaattgtgagcggataacacaaggagg Aaacagctatgtcattaccgttcttaacttc (SEQ ID NO:52)
MCM105	aspA terminator – yIDI	Gatcgggccccaagaaaaaaggcacgtcatctgacgtgcc Ttttttatttgtagacgcgttgttatagcattcta (SEQ ID NO:53)
MCM120	Forward of attTn7: attTn7 homology, GB marker homology	aaagtagccgaagatgacggtttgtcacatggagtt ggcaggatgtttgattaaaagcAATTAACCCTCACTA AAGGGCGG (SEQ ID NO:54)
MCM127	Rev complement of 1.2 GI: GB marker homology(extra long), promoter, RBS, ATG	AGAGTGTTCACCAAAAATAATAACCTTTCCCGGTGCAgaa Gttaagaacggtaatgacatagctgtttcctccttgtgtt Atccgctcacaattagtggttgaattatttgctcaggatg tggcatcgtcaagggcTAATACGACTCACTATAGGGCTCG (SEQ ID NO:55)

Table 11-4. Plasmids for expression of IspS variants

MD09-161	pET24a-P.alba FL C-Term (+) TEV, His tag/MCM331
MD09-163	pET24a-P.alba TRC (MEA) C-Term (+) TEV, His tag/MCM331
pDu27	Alba-FL-pET200/D-TOPO
pDu39	Mtg pET24a-P.alba-MEA /Top10 (Untagged)
pDu40	Mtg pET24a-P.alba-MNV/Top10 (Untagged)
pDu41	Mtg pET24a-P.alba-MSV/Top10 (Untagged)
pDu42	Mtg pET24a-P.alba-MTE/Top10 (Untagged)
pDu43	Mtg pET24a-P.alba-MVS/Top10 (Untagged)

Table 11-5. Strains for expression of IspS variants

MD08-99	Alba-FL-pET200/D-TOPO (pDu27) in BL21 (λDE3) pLysS
MD09-165	BL21(λDE3)pLysS, pET24a-P.alba FL C-Term (+) TEV, His tag
MD09-167	BL21(λDE3) pLysS, pET24a-P.alba TRC (MEA) C-Term (+) TEV, His tag
MD09-173	BL21(λDE3)pLysS, pET24a-P.alba (MEA) Untagged (pDu39)
MD09-174	BL21(λDE3)pLysS, pET24a-P.alba (MNV) Untagged (pDu40)
MD09-175	BL21(λDE3)pLysS, pET24a-P.alba (MSV) Untagged (pDu41)

MD09-176	BL21(λDE3)pLysS, pET24a-P.alba (MTE) Untagged (pDu42)
MD09-177	BL21(λDE3)pLysS, pET24a-P.alba (MVS) Untagged (pDu43)

V. Biochemical Analysis of IspS Truncations

[0375] The relative activity of the various N-terminally truncated IspS enzymes was determined by DMAPP assay. The strains described above were analyzed via DMAPP assay in a 96-well plate. All strains were assayed in quadruplicate. The "Full Length" variant refers to the IspS enzyme expressed in BL21(λDE3) pLysS (Invitrogen) from the P. alba pET24a plasmid.

Table 11-6. DMAPP Assay of N-terminal Truncations

Activity Data				Avg	OD
Variant	Average	Std Dev	%CV	OD_{600}	Normalized
MD09-173	1125.6	93.7	8.3	5.2	217.6
MD09-174	118.6	8.0	6.7	5.2	22.8
MD09-175	1064.6	71.7	6.7	4.9	219.0
MD09-176	1179.1	64.7	5.5	4.9	238.7
MD09-177	831.7	89.6	10.8	4.9	168.2
Full Length	805.8	65.1	8.1	5.0	161.3

[0376] Results: Table X shows that when normalized for OD_{600}, strains MD09-173 (with plasmid pDu39), MD09-175 (pDu41), MD09-176 (pDu42), and MD09-177 (pDu43) all displayed higher DMAPP activity than the "Full Length" wild type IspS enzyme (in strain BL21(λDE3) *pLysS* with P. alba pET24a).

VI. Detailed Kinetic Analysis of the "MEA" Truncation in IspS

[0377] The relative specific activity was determined and the kinetics of "N-terminally truncated" *P. alba* isoprene synthases were examined compared to "Full length" *P. alba* isoprene synthases. Four strains expressing four different constructs were used in this analysis: BL21(λDE3) *pLysS* with P. alba pET24a; MD09-173; MD09-165; and MD09-167 (Strains described above in detail). These strains express "full length" *P. alba* IspS, "truncated" P. alba IspS (the MEA truncation), "full length" C-terminally TEV and His-tagged *P. alba* IspS, and "truncated" C-terminally TEV and His-tagged *P. alba* IspS, respectively. In the experiments described below, "truncated" refers specifically to the MEA variant of *P. alba* IspS.

[0378] All strains were inoculated into LB containing 30 mg/L chloramphenicol(Cm) and 50 mg/L kanamycin and grown overnight in 2 mL culture tubes at 37 °C. The overnight cultures were diluted 1:100 in 25 mL of LB broth containing 30 mg/L chloramphenicol(Cm) and 50 mg/L kanamycin the following morning and grown at 37 °C until OD~0.5. Each strain was grown in triplicate. The cultures were then induced with 400 uM IPTG and incubated at 30 °C for 4 hours. 20 mL of each culture were centrifuged at 3000 x g for 20 min. and the supernatant was discarded. The pellets were frozen at -80 °C overnight. Pellets were resuspended in 2 mL of a buffer containing 100 mM Tris, 100 mM NaCl, 0.25 mg/mL lysozyme and 0.25 mg/mL DNAase, pH 8. Cell suspensions were french pressed at 20,000 psi twice and the lysate was then centrifuged at 14000 x g for 20 minutes to yield cell free extract that was used for kinetic studies and protein concentration determination.

[0379] To measure specific activity, 5 µL of cell free extract from each strain was incubated with 5 mM DMAPP, 50 mM $MgCl_2$ in a buffer containing 100 mM Tris and 100 mM NaCl (pH 8) to a final volume of 100 µL for 15 min. at 30 °C in gas tight 2 mL vials. Reactions were terminated with the addition of 100 µL of 500 uM EDTA, pH 8. Samples were analyzed by GC-MS to determine the concentration of isoprene in the headspace of the vials.

[0380] To determine k_{cat} and K_M, 5 uL of cell free extract from each strain was incubated with DMAPP at concentrations ranging from 0.625 to 40 mM DMAPP in a buffer containing 100 mM Tris, 50 mM $MgCl_2$ and 100 mM NaCl (pH 8) to a final volume of 100 µL for 15 min. at 30 °C in gas tight 2 mL vials. Reactions were terminated with the addition of 100 µL of 500 mM EDTA, pH 8. Samples were analyzed by GC-MS to determine the concentration of isoprene in the headspace of the vials. Data were analyzed using Kaleidagraph and fit to following equation for uncompetitive substrate inhibition: $rate/E = k_{cat}*S/(K_M+S*(1+S/K_i))$. All data were run in triplicate with the exception of MD09-167 with 2.5 mM DMAPP which was run in duplicate.

[0381] Cell free extract was run on a Caliper microfluidic electrophoresis instrument (Caliper Life Sciences, Hopkinton, MA, USA) in order to quantify the amount of isoprene synthase in each sample. The microfluidic chip and protein samples were prepared according to the manufacturer's instructions (LabChip® HT Protein Express, P/N 760301). Culture lysates were prepared in 96-well mictrotiter plates by adding 50 mM Tris pH 8.0 containing 0.1% Tween 20, 0.1 mg/ml lysozyme, 1.0 ug/ml DNAse at room temperature for 30 minutes, followed by centrifugation. Supernatants were then transferred to another 96 well plate and stored at -20 °C until use, when they were thawed at room temperature for 30 minutes. After

shaking briefly, the 2 µl of each culture sample was transferred to a 96-well PCR plate (Bio-Rad, Hercules, CA,USA) containing 7 µl samples buffer (Caliper) followed by heating the plate to 90 °C for 5 minutes on a thermostatically controlled plate heater. The plate was allowed to cool before adding 35 µl water to each sample. The plate was then placed in the instrument along with a protein standard supplied and calibrated by the manufacturer. The instrument functions by mixing the sample with a fluorescent dye that attaches non-covalently to the proteins, followed by electrophoresis through a gel matrix. As the proteins move past a focal point in the chip, the fluorescence signal is recorded and the protein concentration is determined by quantitating the signal relative to the signal generated by a calibrated set of protein standards.

Table 11-7. k_{cat} and K_M and specific activity values for isoprene synthases

Isoprene Synthase	k_{cat} ± S.D. (s^{-1})	K_M ± S.D.(mM)	K_i ± S.D.(mM)	S.A. (nmol/mg/min)
Full Length	0.72±0.09	2.4±0.3	15.7±0.2	420±60
Truncated	1.5±0.2	1.8±0.2	9.8±0.9	800±100
MD09-165	0.8±0.1	2.4±0.5	19±4	440±80
MD09-167	1.1±0.3	2±1	8.7±0.9	610±60

[0382] Parameters were determined by fitting the following uncompetitive substrate inhibition equation to data obtained for rate/[E] vs. [DMAPP]:

$$\frac{rate}{[E]} = \frac{k_{cat} * [S]}{K_M + [S] * \left(1 + \frac{[S]}{K_i}\right)}$$

[0383] The specific activities (S.A.) were calculated for reactions containing 5 mM DMAPP, 50 mM $MgCl_2$, 100 mM Tris, 100 mM NaCl, and 2.5-4.5 µg isoprene synthase from the supernatant of whole cell lysate. Reactions were performed at 30 °C for 15 minutes in triplicate using independently grown cultures.

Results/Discussion:

[0384] The specific activity of each protein was determined (Figure 40 and Table 11-7). The specific activity of truncated isoprene synthase was approximately 2-fold greater than the specific activity of full length isoprene synthase. The C-terminally His-tagged full length isoprene synthase yielded approximately the same specific activity as the full length isoprene

synthase. The C-terminally His-tagged truncated isoprene synthase gave a specific activity that was less than the non-tagged truncated isoprene synthase, but greater than the specific activity of both full length isoprene synthases.

[0385] The rate of conversion of DMAPP to isoprene was analyzed over a range of DMAPP concentrations in order to determine the k_{cat} and K_M parameters of the enzymes (Figures 41 and 42 and Table 11-7). The enzymes all exhibited rate profiles consistent with uncompetitive substrate inhibition by DMAPP. The K_i for the full length constructs was greater than the K_i for truncated constructs as determined by altering K_i and observing the best fit (R-value) to the data (data not shown). All data has been fit to a K_i of 10 mM in the figures in this document. The K_Ms of truncated isoprene synthase decreased relative to the full length isoprene synthases. Therefore, as the substrate concentration decreases the ratio between the isoprene synthase activity of the truncated isoprene synthase to the full length isoprene synthase will increase (Figure 43). The k_{cats} of truncated isoprene synthases increased relative to the full length isoprene synthases. This results in greater isoprene synthase activity for the truncated isoprene synthases than the full length isoprene synthases at all substrate concentrations (Figure 43). The ratio of the isoprene synthase activity of the truncated isoprene synthase to the full length isoprene synthase at varying DMAPP levels was determined (Figure 43).

[0386] Conclusions: "Truncated" isoprene synthases exhibit increased k_{cat} values and decreased K_M values with respect to the catalysis of the conversion of DMAPP to isoprene compared to "full length" isoprene synthases. The specific activity of "truncated" isoprene synthases is increased relative to the specific activity of "full length" isoprene synthases. The most active isoprene synthase was non-tagged truncated isoprene synthase "MEA" variant (in strain MD09-173). The truncated isoprene synthase may increase the isoprene synthase activity in organisms used for production of isoprene compared to the full length isoprene synthase.

Example 12

Isoprene Synthase Enrichment – Relief of DMAPP Toxicity

[0387] This example identifies residue changes within IspS that confer better activity to the enzyme through kinetic improvement, increased expression, increased solubility, or any other means by which DMAPP is more effectively converted to isoprene by Isoprene Synthase. This procedure allows for the relief of cytotoxic intracellular levels of DMAPP by expression of improved IspS variants. In a population of cells expressing a heterogeneous mixture of

IspS variants, the best enzymes should allow for better growth of their host strain, and should be enriched in the mixed population.

I. Strain Construction

[0388] Construction of Strains MCM518-521 and 528-531 in which Lambda promoters drive integrated mKKDyI was as follows. Primers MCM120 and MCM224 (Table 12-1) were used to amplify the resistance cassette from the GeneBridges FRT-gb2-Cm-FRT template using Stratagene Herculase II Fusion kit according to the manufacturer's protocol. Four 50 µL reactions were cycled as follows: 95°C, 2 min; (95 °C, 20 sec, 55 °C, 20 sec, 72 °C, 1 min) for 30 cycles; 72 °C, 3 min; and 4°C until cool. The four reactions were pooled and purified on a Qiagen PCR column according to the manufacturer's protocol and eluted with 60 µL EB at 55 °C.

[0389] Plasmid pRedET-carb (GeneBridges) was electroporated into MCM446. Transformants were recovered by shaking for one hour in SOC (Invitrogen) at 30 °C and then selected on LB containing carbenicillin (50 µg/ml) (carb50) plates at 30 °C overnight. A carbenicillin resistant colony was frozen as MCM508 (Table 12-2).

[0390] Strain MCM508 was grown from a fresh streak in 5mL LB/carb50 at 30 °C to an OD_{600} of ~0.5. 40mM L-arabinose was added and culture was incubated at 37 °C for 1.5 hrs. Cells were harvested and electroporated with 3 µL of purified amplicons as previously, and then recovered in 500 µL SOC at 37 °C for 1.5-3hrs. Transformants were selected on LB/kan10 plates at 37 °C.

[0391] Recombination of the amplicon at the target locus was confirmed by PCR with primers GB-DW and MCM208. The resulting amplicons were sequenced to identify four clones with the sequences below. Carbenicillin-sensitive clones were frozen as strains MCM518-521.

[0392] MCM518-521 were restreaked on LB kan10 plates and grown overnight at 37 °C.

[0393] Strains MCM518-521 were cultured in LB/kan10 at 37 °C and then electrotransformed with plasmid pCP20 (Datsenko KA, Wanner BL. One-step inactivation of chromosomal genes in *Escherichia coli* K-12 using PCR products. Proc Natl Acad Sci U S A. 2000 Jun 6;97(12):6640-5). Cells were recovered in 500 µL SOC, shaking at 30 °C for 1hour. Transformants were selected on LB/carb50 plates at 30 °C overnight. The following morning a colony from each transformation was grown at 30 °C in liquid LB/carb50 until visibly turbid. The culture was then shifted to 37 °C for at least 3 hrs. Cells were streaked from this culture onto LB plates and grown overnight at 37 °C.

[0394] The following day colonies were patched to LB, LB/carb50 and LB/kan10. Clones that grew on neither carb50 nor kan10 and were cultured in liquid LB from the patch on LB and frozen as MCM528-531.

DNA Sequences

[0395] These assemblies include the new promoters inserted on the chromosome in strains MCM518-521, as well as the very beginning of the mMVK ORF. Upstream of these assemblies is sequence from the GeneBridges FRT-gb2-Cm-FRT cassette. Downstream is the remainder of the mMVK ORF and then the rest of the lower MVA pathway integron from strain MCM508.

MCM518

aaagaccgaccaagcgacgtctgagagctccctggcgaattcggtaccaataaaagagcttt
attttcatgatctgtgtgttggttttgtgtgcggcgcggaagttcctattctctagaaagt
ataggaacttcctcgagccctatagtgagtcgtattaaattcatataaaaaacatacagata
accatctgcggtgataaattatctctggcggtgttgacataaataccactggcggtgatact
gagcacatcagcaggacgcactgaccaccatgaaggtgcaaaggaggtaaaaaaacatggta
tcctgttctgcgccgggtaagatttacctgttcggtgaacacgccgtagtttatggcgaaac
tgcaattgcgtgtgcggtggaactgcgtacccgtgttcgcgcggaactcaatgactctatca
ctattcagagc (SEQ ID NO:56)

MCM519

aaagaccgaccaagcgacgtctgagagctccctggcgaattcggtaccaataaaagagcttt
attttcatgatctgtgtgttggttttgtgtgcggcgcggaagttcctattctctagaaagt
ataggaacttcctcgagccctatagtgagtcgtattaaattcatataaaaaacatacagata
accatctgcggtgataaattatctctggcggtgttgacctaaataccactggcggtgatact
gagcacatcagcaggacgcactgaccaccatgaaggtgcaaaggaggtaaaaaaacatggta
tcctgttctgcgccgggtaagatttacctgttcggtgaacacgccgtagtttatggcgaaac
tgcaattgcgtgtgcggtggaactgcgtacccgtgttcgcgcggaactcaatgactctatca
ctattcagagc (SEQ ID NO:57)

MCM520

aaagaccgaccaagcgacgtctgagagctccctggcgaattcggtaccaataaaagagcttt
attttcatgatctgtgtgttggttttgtgtgcggcgcggaagttcctattctctagaaagt

ataggaacttcctcgagccctatagtgagtcgtattaaattcatataaaaaacatacagata
accatctgcggtgataaattatctctggcggtgttgacctaaataccactggcggtgatact
gagcacatcagcaggacgcactgaccaccatgaaggtgcaaaggtaaaaaaacatggtatcc
tgttctgcgccgggtaagatttacctgttcggtgaacacgccgtagtttatggcgaaactgc
aattgcgtgtgcggtggaactgcgtacccgtgttcgcgcggaactcaatgactctatcacta
ttcagagc (SEQ ID NO:58)

MCM521 (in strains MCM531 and MD09-171)

aaagaccgaccaagcgacgtctgagagctccctggcgaattcggtaccaataaaagagcttt
attttcatgatctgtgtgttggtttttgtgtgcggcgcggaagttcctattctctagaaagt
ataggaacttcctcgagccctatagtgagtcgtattaaattcatataaaaaacatacagata
accatctgcggtgataaattatctctggcggtgttgacgtaaataccactggcggtgatact
gagcacatcagcaggacgcactgaccaccatgaaggtgcaaaggaggtaaaaaaacatggta
tcctgttctgcgccgggtaagatttacctgttcggtgaacacgccgtagtttatggcgaaac
tgcaattgcgtgtgcggtggaactgcgtacccgtgttcgcgcggaactcaatgactctatca
ctattcagagc (SEQ ID NO:59)

[0396] The neo-PL.2-mKKDyI (from MCM521) was transduced into BL21(λDE3) to generate strain MD09-171. A P1 lysate of MCM521 was made and transduced into BL21(λDE3) according to standard molecular biology techniques (Miller, A Short Course in Bacterial Genetics). Transductants were selected on Kan20 LB medium plates. Positive colonies were further verified by PCR to confirm the presence of PL.2-mKKDyI in the BL21(λDE3) strain. 1 µl of pCP20 plasmid was then transformed into this strain and selected for on LB + Carb50 and incubated at 30 °C. Positive transformants were subsequently streaked on an LB plate and incubated at 37 °C for loss of the pCP20 plasmid. To confirm the loss of the neomycin (kanamycin) resistance marker, colonies that grew at 37 °C were patched onto LB Kan20, LB Carb50, and plain LB plates. The strains with integrated PL.2 mKKDyI without the kanamycin resistance marker that have lost pCP20 should be sensitive to kanamycin and carbenicillin. 4 KanS CarbS were used to check by PCR for the presence of mKKDyI in BL21(λDE3) with the parental BL21(λDE3) strain as a control. Once PCR confirmed the presence of mKKDyI, the resulting strain was transformed with 1 µl of the pLysS plasmid (Invitrogen). The resulting strain, MD09-171, was used for the enrichment experiments described below.

Table 12-1. Primers used for strain construction

MCM120	aaagtagccgaagatgacggtttgtcacatggagttggcaggatgtttgat taaaagcaattaaccctcactaaagggcgg (SEQ ID NO:60)
MCM208	gctctgaatagtgatagagtca (SEQ ID NO:61)
MCM224	taaatcttacccggcgcagaacaggataccatgtttttttacctcctttgc accttcatggtggtcagtgcgtcctgctgatgtgctcagtatcac cgccagtggtatttangtcaacaccgccagagataatttatcaccgcagat ggttatctgtatgtttttttatatgaatttaatacgactcactatag ggctcg (SEQ ID NO:62)
GB-DW	aaagaccgaccaagcgacgtctga (SEQ ID NO:63)
MCM161	caccatggtatcctgttctgcg (SEQ ID NO:64)
MCM162	ttaatctactttcagaccttgc (SEQ ID NO:65)
MCM143	aggaggtggtctcaaatgactgccgacaacaatagta (SEQ ID NO:66)
MCM144	aggaggtggtctcagcgctctgcagttatagcattctatgaatttgcctg (SEQ ID NO:67)

Table 12-2. Strains

Strain	Description	Parent
MCM508	BL21 gi1.6-mKKDyI + predet.-carb	MCM446
MCM518	BL21 neo-PL.6-mKKDyI, clone10	MCM508
MCM519	BL21 neo-PL.0-mKKDyI, clone11	MCM508
MCM520	BL21 neo-PL.0-mKKDyI (bad RBS in front of mMVK), clone13	MCM508
MCM521	BL21 neo-PL.2-mKKDyI, clone15	MCM508
MCM528	BL21 PL.6-mKKDyI, loopedout	MCM518
MCM529	BL21 PL.0-mKKDyI, loopedout	MCM519
MCM530	BL21 PL.0-mKKDyI (bad RBS in front of mMVK), loopedout	MCM520
MCM531	BL21 PL.2-mKKDyI, loopedout	MCM521
MD09-171	BL21 (λDE3) PL.2-mKKDyI, loopedout + pLysS	MCM521

II. Growth Inhibition of MCM531 by Mevalonic Acid

[0397] An overnight culture of MCM531 (see strain description) was back-diluted to an OD_{600} of 0.05 (this corresponds to an OD_{600} of approx 0.005 in a 96-well plate reader) (SpectraMax M2, Molecular Devices). The diluted culture was then aliquotted into separate wells in a 96-well deep-well plate into standard TM3 medium (13.6 g K_2PO_4, 13.6 g KH_2PO_4, 2.0 g $MgSO_4*7H_2O$) supplemented with 1% glucose and 0.8 g/L Biospringer yeast extract (1% Yeast extract final))with 0, 1, 5, 10, 15 or 20 mM MVA added. Figure 44 shows the growth curve of MCM531 in the various concentrations of MVA. Each MVA concentration was assayed in quadruplicate, error bars were negligible. Figure 44 shows that

MCM531 was severely inhibited for growth at concentrations of 5 mM MVA and higher.

III. Mutagenesis of IspS and Selection/Enrichment Assay

[0398] To generate a randomly mutagenized IspS open reading frame, the GeneMorph II EZ Clone domain mutagenesis kit (Stratagene) was used according to the manufacturer's recommended protocol. Specific primers to amplify the template (Pdu39 (pET24a-P. alba (MEA))) are described below (Table 12-3, pET24 Megaprime Forward and Reverse). To achieve the desired mutation frequency, the protocol outlined in the GeneMorph II kit was followed. To generate 2 to 3 residue changes per molecule, approximately 150 ng of starting template DNA was used for the initial PCR reaction. More or less template was used to generate IspS enzymes with either fewer or more residue changes, respectively. The resulting mutant "megaprimers" were then used to amplify the rest of the plasmid according to the manufacturer's recommended protocol.

[0399] The final PCR product from the GeneMorph II kit was treated with *Dpn*I according to the manufacturer's recommended protocol. Prior to transformation into *E. coli*, it was necessary to desalt the PCR reaction by microdialysis. Typically, approximately 20 µl of the PCR reaction was subjected to microdialysis and used for electroporation into strain MD09-171 (Table 12-2) by standard molecular biology procedures. After electroporation, cells were recovered for 2 hours at 30 °C, and then plated onto LB medium Kan50 Cm35. The entire transformation volume was plated to recover all mutations generated by the mutagenesis procedure.

[0400] For enrichment, all transformants were scraped and pooled together. An aliquot from each pool was frozen for storage in the -80. Prior to the enrichment, strains (control or experimental pools) were inoculated directly into LB with Kan50 and grown for a few hours, to minimize the loss of pool heterogeneity. After this recovery period, cells were diluted into liquid TM3 medium (described above) with Kan50, 5 mM MVA, and 200 µM IPTG. (The exact dilution was determined empirically for each pool/source of medium/control reaction). Cultures were then placed in the shaking incubator at 34°C until an OD_{600} of no more than 5. At this point, plasmids were purified from 1 ml of the "enriched" culture via miniprep protocol (Qiagen). This plasmid preparation was then transformed into electrocompetent MD09-171 cells as described above. The transformed cells were recovered for 2 hours in LB medium without antibiotics, and then subjected to a subsequent round of enrichment by dilution into TM3 with Kan50, 5 mM MVA and 200 µM IPTG as described above. This culture was placed into the shaking incubator at 34°C until it reached an OD_{600} of no more

than 5, as described above. Plasmids were then purified, retransformed and subjected to further rounds of "enrichment." The enrichment process continued for 5 or 6 rounds of selection, plasmid purification, and retransformation. The process continued until the culture was homogeneous, *i.e.* contained only one variant of IspS by sequencing analysis.

[0401] After the last round of enrichment, the plasmid pool was transformed into chemically competent *E. coli* Top10 cells (Invitrogen) per the manufacturer's recommended protocol, recovered, plated onto LB medium with Kan50, and sent for complete sequencing (Quintara Biosciences) for comparison to the wild type sequence of P. alba IspS. Primers used for sequencing are described below.

Table 12-3. Primers used for IspS mutagenesis and sequencing

pET24 Megaprime Forward	gtttaactttaagaaggagatatacat
pET24 Megaprime Reverse	gagctcgaattcggatcctta
alba sequencing reverse	ctcgtacaggctcaggatag
alba sequencing reverse2	ttacgtcccaacgctcaact
EWL1000	gcactgtctttccgtctgctgc
QB1493	cttcggcaacgcatggaaat

IV. Individual Residue Changes Identified by Enrichment/DMAPP Toxicity Relief:

[0402] Plasmids isolated from selection/enrichment were fully sequenced. The following residue changes were confirmed by sequencing (Quintara Biosciences). The residue numbering corresponds to the P. alba "Full Length" sequence (in P. alba pET24a; SEQ ID NO:120), where the starting methionine is amino acid number 1. Identified residue changes included: V10M, F12S, T15A, E18G, V58I, V58F, L70Q, L70V, L70T, T71P, V79L, E89D, G94A, S119F, F120L, G127R, E175V, T212I, S257A, R262G, A266G, F280L, N297K, F305L, L319M, E323K, A328T, D342E, A359T, K366N, E368D, L374M, S396T, V418S, K438N, H440R, T442I, T442A, I449V, A469S, K500R, K505Q, G507S, S509N, F511Y, and N532K.

[0403] Combinations of Residue Changes (in a single IspS enzyme) Identified by Enrichment/DMAPP Toxicity Relief: G127R/F511Y, L70Q/G94A/R262G/F305L, F12S/ T15A/E18G/N297K, S396T/T442I, V10M/E323K, F120L/A266G, K438N/K500R, V79L/S509N, E175V/S257A/E368D/A469S, T71P/L374M, F280L/H440R, E89D/H440R, V58F/A328T/N532K, S119F/D342E/I449V, and K366N/G507S.

Example 13

Construction of Site Saturation Libraries (SSLs) and Biochemical Analysis of the L70R Variant

[0404] This example includes an examination of possible amino acid substitutions at sites identified by the selection/enrichment procedure described above and other sites of potential interest (active site, conserved between Poplar species) for their effect on solubility, expression, and activity of IspS.

I. Strain Construction

[0405] Residues identified by the selection/enrichment procedure (L70, G94, R262, F305) described above were chosen for analysis. In addition, residues that are putatively involved in substrate binding (F303, V3065, F385, S412, Q416, F450), and residues that are different between the various Poplar species (*e.g.* V418, T442) were chosen for further analysis (numbering corresponds to the "full length" amino acid sequence of *P. alba* IspS). To generate a randomized pool of amino acid substitutions (the Site Saturation Library, SSL), pDu39 (see description above) was subjected to QuickChange (Stratagene) mutagenesis with the QC primers indicated below (Table 13-1), according to the manufacturer's recommended protocol. The PCR Reaction was prepared as follows:
1 µl pDu39, 5 µl 10X PfuUltra HF buffer, 1 µl dNTP's, 1 µl (50 µM) primer-For (e.g. QC L69 F), 1 µl (50uM) primer-Rev (e.g. QC L69 R), 2 µl DMSO, 39 µl diH2O, and1 µl PfuUltra HF Polymerase (Stratagene). The PCR cycling parameters for QuickChange were as follows: 95°C 1 min, 95°C 30 sec., 55°C 1 min., 68°C 7.3 min. for one cycle followed by 95°C 30 sec., 55°C 1 min., 68°C 7.3 min for 17 more cycles. The temperature was then reduced to 4°C. Incorporation of the bases NNK at the codon for the residues described above allows for the insertion of codons that represent all 20 possible amino acids at the given site. 1 µl of the resulting pools of mutagenized PCR products was *Dpn*I treated (described above), and transformed into chemically competent *E. coli* Top10 cells (Invitrogen) according to the manufacturer's recommended protocol. Entire transformation reactions were recovered in 1 ml LB medium without antibiotics at 37 °C for 1 hour and plated onto LB Kan50. The next day, all transformants were scraped off of the LB plates, mixed thoroughly, and plasmids were purified via miniprep (Qiagen). Pools of plasmids were then transformed into chemically competent BL21(λDE3)pLysS cells (Invitrogen) according to the manufacturer's protocol. The transformation reactions were recovered in 1 ml LB medium at 37 °C for 1 hour and then plated onto LB Kan50 Cm35 at dilutions sufficient to generate separation of positive colonies. After overnight incubation at 37 °C,

individual colonies were inoculated into individual wells in a 96-well deep-well microtiter plate (VWR) containing 500 ul of liquid LB Kan50 Cm35 each. In eight wells (typically column 12, A through H) strain MD09-173 (see above) or BL21(λDE3)pLysS with P. alba pET24a (Full Length) was inoculated as a control for the DMAPP assay. The microtiter plates were then sealed with a semi-permeable membrane (Breathe-Easier, Diversified Biotech), and incubated overnight at 30 °C in a shaking incubator (Vertiga). The next day, 100 µl samples from each well within a 96-well plate were mixed with 50 µl of 50% glycerol in a new 200 ul 96-well plate, and frozen at -80 °C until further analysis. This plate was then used for the DMAPP assay described below.

Table 13-1. Primers used for mutagenesis

QC L70 F	gaaaaagcagaatttnnkaccctgctggaactg (SEQ ID NO:68)
QC L70 R	cagttccagcagggtmnnaaattctgctttttc (SEQ ID NO:69)
QC G94 F	gagtctgatatccgtnnkgcgctggatcgcttc (SEQ ID NO:70)
QC G94 R	gaagcgatccagcgcmnnacggatatcagactc (SEQ ID NO:71)
QC R262 F	tcccgttggtggcgtnnkgtgggtctggcgacc (SEQ ID NO:72)
QC R262 R	ggtcgccagacccacmnnacgccaccaacggga (SEQ ID NO:73)
QC F303 F	tccgtcgcaaaaatgnnktctttcgtaaccatt (SEQ ID NO:74)
QC F303 R	aatggttacgaaagamnncatttttgcgacgga (SEQ ID NO:75)
QC F305 F	gcaaaaatgttttctnnkgtaaccattatcgac (SEQ ID NO:76)
QC F305 R	gtcgataatggttacmnnagaaaacatttttgc (SEQ ID NO:77)
QC V306 F	aaaatgttttctttcnnkaccattatcgacgat (SEQ ID NO:78)
QC V306 R	atcgtcgataatggtmnngaaagaaaacatttt (SEQ ID NO:79)
QC F385 F	gacctgtgcaacgctnnkctgcaagaagccaag (SEQ ID NO:80)
QC F385 R	cttggcttcttgcagmnnagcgttgcacaggtc (SEQ ID NO:81)
QC S412 F	gcatggaaatcctctnnkggcccgctgcaactg (SEQ ID NO:82)
QC S412 R	cagttgcagcgggccmnnagaggatttccatgc (SEQ ID NO:83)
QC Q416 F	tcttctggcccgctgnnkctggtgttcgcttac (SEQ ID NO:84)
QC Q416 R	gtaagcgaacaccagmnncagcgggccagaaga (SEQ ID NO:85)
QC V418 F	ggcccgctgcaactgnnkttcgcttacttcgct (SEQ ID NO:86)
QC V418 R	agcgaagtaagcgaamnncagttgcagcgggcc (SEQ ID NO:87)
QC T442 F	caaaaataccatgacnnkatctctcgtccttcc (SEQ ID NO:88)
QC T442 R	ggaaggacgagagatmnngtcatggtatttttg (SEQ ID NO:89)
QC F450 F	cgtccttcccatatcnnkcgtctgtgcaatgac (SEQ ID NO:90)
QC F450 R	gtcattgcacagacgmnngatatgggaaggacg (SEQ ID NO:91)

II. Generation of a "Winner" Plate for Secondary Assay and Identification of L70R as a Variant with Increased Specific Activity

[0406] Variants that displayed increased specific isoprene production when compared to wild type were chosen for further analysis. Figure 45 shows a typical data set of an SSL plate for an individual residue, in this case L70. From this particular plate, the samples in wells C3 (27), D3 (39), and E3 (51) were chosen for further analysis. Other variants at different residues (listed above) that showed increased isoprene productivity, when subjected to DMAPP analysis, were isolated from their original SSL plates stored at -80 °C (described above), and re-arrayed onto a new "winner" plate for secondary screening. Two wells containing MD09-173 were included as controls. All variants were sequenced (Quintara Biosciences) and subjected to the DMAPP assay as described above. See Table 13-2 for sequencing results. For the DMAPP assay, a single growth of each variant was assayed, and therefore a single lysate generated, but in quadruplicate to generate statistically significant data. Samples were assayed at the OD_{600} indicated in Table 13-2. Protein analysis was performed on all lysates using the Western Breeze Western blot kit (Invitrogen) followed by fluorescence detection on a Storm860 (see below)

III. DMAPP Assay – Growth, Lysis and Isoprene Measurement

[0407] A patch plate was prepared from a glycerol stock plate using a VP-Scientific Replication Tool patch LB Agar CM35/Kan50 large patch plate from overnight glycerol stock Plate. Cultures were incubated at 30°C overnight (20 to 24 hr). Plates were stored at 4°C for up to a week.

[0408] An overnight growth plate was prepared from 500 mL of LB CM35/Kan50 media. 300 µL/well of LB CM35/Kan50 media were dispensed into deep 96 well plate. Using the V&S Replication Tool, the patch inoculum was transferred to a deep 96 well plate. Media was inoculated by dipping the tool then shaking the pin within the well. The overnight growth plate was sealed with a Breathe-Easier Sealing Membrane. The plate was incubated at 30 °C overnight in a Vertiga Shaking Incubator at 800 rpm for 16 to 18 hours.

[0409] A deep 96 well day growth plate was prepared by dispensing 588 µL/well of LB CM35/Kan50 media. The overnight growth plate was removed from the incubator and cultures were diluted 50-fold. 12 µL of overnight oulture was transferred to a day growth plate containing 588 µL/well of supplemented LB media. The overnight growth plate was sealed with a new Breathe-Easier Sealing Membrane and was incubated at 34 °C and 800 rpm for 2.25 hr in the Vertiga Shaking Incubator.

[0410] To induce the expression of IspS, thawed 12 mM IPTG was poured into 50 mL or 100 mL sterile reservoir and dispensed 20 µL/well into each 600 µL/well culture. Overnight

growth plate was resealed with Breathe-Easier Sealing Membrane and incubated at 34°C and 800 rpm for 4 hours in the Vertiga Shaking Incubator.

[0411] To harvest cell, 200 µL of induced culture was transferred to 450 µL Nunc storage plate. The plate was centrifuged at 3300 rpm for 20 min at 4 °C in a low speed benchtop centrifuge. 180 µL supernatant was removed with a pipettor and discarded. The plate was sealed with an aluminum foil membrane, covered with a plastic plate lid and stored frozen at -80 °C.

[0412] The OD_{600} of the plates were read. 150 µL 1x PBS was dispensed into a 96 well Costar Read Plate (#9017). 50 µL of culture sample was then transferred to the read plate. The OD_{600} reading was then taked with a Spectramax Plate Reader.

[0413] Lysis: The harvest plate was defrosted in a room temperature water bath for 4 min and then incubated in Thermomixer at 25°C at 1200 rpm for 1 min. Lysis buffer was dispensed at 80 µL/well to 20 µL/well of harvest cells. 1.25X Lysis Working Stock buffer was prepared from 6.25 ml 1M Tris pH 8, 625 µl 10% Tween 20, 312.5 µl 0.2 M PMSF, 462.5 µl 10 mg/ml DNAse I (Sigma), 1.25 ml 1 M $MgCl_2$, 132.5 µl 25000 U/µl Lysozyme (Epicentre Technologies) and 40.968 ml dIH_20. Plates were incubated on a Thermomixer at 25°C and 1200 rpm for 30 min. 1x Lysis Buffer stock was prepared by diluting 19 ml of 1.25x Lysis Working stock with 4.75 ml dIH_2O.

[0414] DMAPP Working Stock was prepared as follows.

Dimethylallyl Pyrophosphate (triammonium salt) 25 mg (Cayman Chemicals, Cat No. 63180)

final	total vol	diluent	stock vol	stock	dilution	Reagent	Units	Plate(s)
30	840	840	solid	25000	1	DMAPP	mg/mL	1
3	2500	2250	250	30	10	DMAPP	mg/mL	1

[0415] The Diluent was 0.1 M Potassium Phosphate. 200 uL/well was dispensed for transfer to sample wells and was stored on ice.

[0416] DMAPP Reaction: 1x Lysis Buffer was dispensed at 65 µL/well. 15 µL/well of lysate was transferred to the respective sample wells in a 96 Deep well Zinsser Glass Block. DMAPP reagent was dispensed at 20 µL/well. The glass block was sealed with an aluminum foil membrane and incubated at 25 °C at 450 rpm for 45 min. The reaction was stopped by transferring the Glass Block to a 70 °C water bath and incubating for 6 min. GC Analysis was performed as previously described.

IV. Western blot of Isoprene Synthase with Fluorescence labeled Secondary Antibody.

[0417] Samples were prepared and run on NativePAGE™ Novex® Bis-Tris Gels (Invitrogen) according to the manufacturer's protocol. After completion of the run the gels were immediately transferred to Nitrocellulose membranes using the XCell II™ Blot Module (Invitrogen) according to the manufacturer's recommended protocol. After transfer, the membrane was placed in 15 ml of the appropriate Blocking Solution (Ultra filtered Water 31.5 ml, Blocker/Diluent (Part A) 9 ml, Blocker/Diluent (Part B) 4.5 ml) in the covered, plastic dish provided in the kit and incubated for 30 minutes on a rotary shaker set at 1 revolution/sec. The Blocking Solution was decanted and the membrane rinsed 2 times with 20 ml of water for 5 minutes. The membrane was incubated with 15 ml of Primary Antibody (Ab) Solution (24 µl of primary Ab in 15 ml Blocking solution) for 1 hour, followed by washing 3 times 5 minutes with 20 ml of 1x Antibody Wash Solution. The membrane was then incubated in 15 ml of SecondaryAntibody Solution (15ul secondary Ab (Alexa Fluor 488 goat anti-rabbit IgG (H+L, Invitrogen)) in 15 of blocking solution) for 30 minutes. The membrane was washed 3 times at 5 minutes with 20 ml of Antibody Wash, and rinsed two times 2 minutes with 20 ml of water. The membrane was dried between paper towels and stored at room temperature for further detection. The fluorescent bands were detected and quantified using the Storm 860 Molecular Imager (GMI, Inc).

V. Results:

[0418] Table 13-2 shows all of the relevant data for each variant assayed: sequencing results, residue change, average isoprene production, protein concentration, and average specific activity (of all 4 replicates). Figure 46 shows the graphical representation of the data shown in Table 13-2. Specific activity was calculated by multiplying the isoprene produced (µg/l) by 0.0414 and then dividing by protein concentration (mg/ml). This conversion factor (0.0414) accounts for the total headspace volume in a sealed 2 ml GC vial (1.9 ml), the lysate volume (15 ul), the duration of the DMAPP assay (45 min), and the molecular weight of isoprene. Thus, specific activity values are given in nmol isoprene/mg Isps/min.

[0419] The data in Table 13-2 and the graph in Figure 46 show that of all variants analyzed, all three L70R variants displayed higher specific activity than wild type. To analyze the L70R variants further, the specific activity values for all 3 isolates (4 replicates of each) were averaged and compared to the controls (2 isolates, 4 replicates each). Therefore, there were 12 measurements for the L70R variant, and 8 for wild type. These data are shown

below in Table 13-3. When corrected for protein, the L70R variants displayed a 25% increase in activity over MD09-173 (the MEA truncation). Figure 47 shows the average specific activity for all L70R variants compared to MEA. Error bars show one standard deviation. The two data sets for L70R and the MEA control were subjected to a Student's T-Test for statistical analysis, which yielded a P-value of 6.0011×10^{-5}.

Table 13-2. Sequencing Results, Isoprene Production, Protein concentration, and Specific Activity for all residues in the Winner Plate

Residue	WT codon	Mutant codon	Amino acid change	OD600	Avg. Isoprene produced (4 replicates)	Std. Dev. (isoprene)	Protein concentration (mg/ml)	Avg. Specific Activity (4 replicates)	Std. Dev. (Specific Activity)
L70	CTG	TGG	W	2.6488	663.00	18.64	0.139	198.020	5.566
L70	CTG	CGG	R	3.4944	1235.72	48.82	0.127	401.451	15.860
L70	CTG	CGT	R	3.32416	944.77	19.15	0.121	322.523	6.539
L70	CTG	CGT	R	3.37232	947.11	17.74	0.106	371.375	6.957
L70	CTG	TGG	W	2.83584	774.49	32.60	0.129	248.925	10.477
G94	GGT	GAG	E	3.304	1070.41	20.52	0.144	307.731	5.898
G94	GGT	GGG	G	3.40816	982.64	27.37	0.133	306.891	8.549
R262	CGT	CGT	R	3.01616	861.08	29.13	0.116	307.227	10.395
R262	CGT	CGG	R	3.31744	965.44	19.25	0.136	294.311	5.868
F305	TTC	TTT	F	2.90864	788.46	15.15	0.119	274.297	5.270
F305	TTC	CTG	L	2.7776	626.70	22.91	0.141	183.823	6.719
WT1				3.71392	991.65	35.78	0.144	285.216	10.292
F305	TTC	TTC	F	2.604	694.03	35.93	0.118	244.488	12.658
V306	GTA	GTA	V	3.33648	912.56	38.76	nd	nd	nd
V306	GTA	GTA	V	3.17632	892.97	56.10	0.137	269.415	16.927
F385	TTC	TTC	F	2.89184	721.24	29.36	0.134	223.380	9.094
Q416	CAA	CAG	Q	3.00272	953.07	57.38	0.149	264.718	15.938

V418	GTG	ATG	M	2.14144	767.25	27.94	0.164	194.099	7.067
V418	GTG	ACG	T	3.24688	973.57	75.08	0.192	209.801	16.179
V418	GTG	ACG	T	3.13264	936.98	68.50	0.171	226.197	16.536
T442	ACC	GTA	V	3.07552	951.64	38.06	0.154	255.496	10.217
F450	TTC	TTC	F	2.93328	911.44	50.88	0.126	299.018	16.691
V418	GTG	ACG	T	3.08896	1057.71	46.28	0.183	238.887	10.454
WT2				3.37568	960.25	58.16	0.131	304.346	18.434

[0420] Note that sequence of all plasmids is identical to Pdu39 (see above) with the exception of the indicated codon. The L70R variants are highlighted in gray.

Table 13-3. Average Specific Activity of all L70R variants relative to the MEA control.

VariantAverage	Specific Activity	Standard Deviation
L70R	365.116	35.31977
WT (the MEA control)	294.7809	17.19228

See Figure 47 for bar graph.

Example 14

Truncations of *P. alba*, *P. tremuloides*, *P. trichocharpa*, and Kudzu Isoprene Synthases

[0421] This example describes the generation of a series of truncations in the IspS enzymes of *P. alba*, *P. tremuloides*, *P. trichocharpa*, and Kudzu and to determine their effect on activity.

I. Strain Construction

[0422] All isoprene synthase genes were codon optimized for *E. coli*, synthesized, and cloned into pET24a by DNA2.0 (Menlo Park, CA). All truncated constructs were generated using the QuickChange Site-Directed Mutagensis kit (Stratagene) using the previously described templates P. alba pET24a (for plasmids pDu47-3 through -7, Figures 48, 49, 51-60), P. tremuloides pET24a (plasmid pDu48, Figures 49C, 61 and 62), P. trichocharpa pET24a (pDu49, Figures 50A, 63, 64), or pET24d-Kudzu (pDu50 and 50-4, Figures 50B, 50C, 65-68) for PCR amplification. Approximately 50 ng of template DNA was used for

amplification (with an Eppendorf Mastercycler Gradient PCR Machine) of the PCR product with the Forward (For) and Reverse (Rev) primer pairs that correspond to each relevant truncation (QC Trunc -3 F and QC Trunc -3 R, for example, see Table 14-1). PCR reactions mixtures were as follows: 1 µl P. alba pET24a (or other template), 5 µl 10X PfuUltra HF buffer, 1 µl dNTP's (10 mM), 1 µl (50uM) primer-For, 1 µl (50 µM) primer-Rev, 1.5 µl DMSO, 39.5 µl diH_2O and 1 µl PfuUltra HF Polymerase. PCR cycle parameters were as follows: (95 °C 1 min., 95 °C 1 min., 55 °C 1 min., 68 °C 7.30 min.) for 18 cycles then 4°C until cool using an Eppendorf Mastercycler Gradient Machine. The PCR products were treated with 1-2 µl of *Dpn*I (Roche) for 1-3 hour at 37 °C. 5 µl of the *Dpn*I treated products were visualized on a 0.8% E-gel (Invitrogen). 1 µl of each product was transformed into chemically competent *E. coli* Top10 cells (Invitrogen) (according to the manufacturer's protocol). Transformants were selected for on LB medium containing kanamycin at a concentration of 50 µg/ml (Kan50), and incubated overnight at 37 °C. Five colonies of each transformation were selected and grown to stationary phase in 3 ml liquid LB Kan50. Plasmids were purified using a QIAPrep Spin miniprep kit (Qiagen) according to the manufacturer's recommended protocol. Purified plasmids were sequenced (by Quintara Biosciences) with T7 Forward and Reverse primers, compared to the parental sequence, and confirmed for their respective truncation. The resulting plasmids (pDu47-3 through pDu50-4, see Table 14-2) were transformed into chemically competent *E. coli* BL21(DE3) pLysS (Invitrogen) according to the manufacturer's recommended protocol. Table 14-3 describes the strains used for expression of truncated IspS enzymes.

[0423] After overnight incubation at 37 °C, individual colonies were inoculated into individual wells in a 96-well deep-well microtiter plate (VWR) containing 500 µl of liquid LB Kan50 CM35 each. Microtiter plates were then sealed with a semi-permeable membrane (Breathe-Easier, Diversified Biotech), and incubated overnight at 30 °C in a shaking incubator (Vertiga). The next day, 100 µl samples from each well within a 96-well plate were mixed with 50 µl of 50% glycerol in a new 200 µl 96-well plate, and frozen at -80 °C until further analysis. This plate was then used for the DMAPP assay as described in Example 13. Table 14-4 shows the average specific productivity of all samples, and Figure 69 shows the graphical representation of the same data.

[0424] DMAPP activity and protein quantitation was determined as described in Example 13.

[0425] Specific activity was calculated by multiplying the isoprene produced (µg/l) by 0.00776 and then dividing by protein concentration (mg/ml). This conversion factor

(0.00776) accounts for the total headspace volume in a sealed 2 ml GC vial (1.9 ml), the lysate volume (80 µl), the duration of the DMAPP assay (45 min), and the molecular weight of isoprene. Thus, specific activity values are given in nmol isoprene/mg IspS/min.

Table 14-1. Primers

QC Trunc -3 F	gaaggagatatacatatgaccgaagctcgtcgt (SEQ ID NO:92)
QC Trunc -3 R	acgacgagcttcggtcatatgtatatctccttc (SEQ ID NO:93)
QC Trunc -4 F	gaaggagatatacatatggaaaccgaagctcgt (SEQ ID NO:94)
QC Trunc -4 R	acgagcttcggtttccatatgtatatctccttc (SEQ ID NO:95)
QC Trunc -5 F	gaaggagatatacatatgactgaaaccgaagct (SEQ ID NO:96)
QC Trunc -5 R	agcttcggtttcagtcatatgtatatctccttc (SEQ ID NO:97)
QC Trunc -6 F	gaaggagatatacatatggaaactgaaaccgaa (SEQ ID NO:98)
QC Trunc -6 R	ttcggtttcagtttccatatgtatatctccttc (SEQ ID NO:99)
QC Trunc -7 F	gaaggagatatacatatgaccgaaactgaaacc (SEQ ID NO:100)
QC Trunc -7 F	ggtttcagtttcggtcatatgtatatctccttc (SEQ ID NO:101)
QC Kudzu MEA F	agaaggagatataccatggaagctcgtcgttccgcaaac (SEQ ID NO:102)
QC Kudzu MEA R	gtttgcggaacgacgagcttccatggtatatctccttct (SEQ ID NO:103)
QC Kudzu -4 F	agaaggagatataccatggagcataattcccgt (SEQ ID NO:104)
QC Kudzu -4 R	acgggaattatgctccatggtatatctccttct (SEQ ID NO:105)
QC Trem/Trich -2 F	gaaggagatatacatatggaaacgcgtcgttct (SEQ ID NO:106)
QC Trem/Trich -2 R	agaacgacgcgtttccatatgtatatctccttc (SEQ ID NO:107)

Table 14-2. Plasmids

pDu47-3	Mtg pET24a-P.alba TRC (-3)
pDu47-4	Mtg pET24a-P.alba TRC (-4)
pDu47-5	Mtg pET24a-P.alba TRC (-5)
pDu47-6	Mtg pET24a-P.alba TRC (-6)
pDu47-7	Mtg pET24a-P.alba TRC (-7)
pDu48	Mtg pET24a-P.tremu TRC (MET)
pDu49	Mtg pET24a-P.tricho TRC (MET)
pDu50	Mtg pET24d-Kudzu TRC (MEA)
pDu50-4	Mtg pET24d-Kudzu TRC (-4)

Table 14-3. Strains

MD09-197-3	BL21(DE3)pLysS, pDu47-3
MD09-197-4	BL21(DE3)pLysS, pDu47-4
MD09-197-5	BL21(DE3)pLysS, pDu47-5
MD09-197-6	BL21(DE3)pLysS, pDu47-6
MD09-197-7	BL21(DE3)pLysS, pDu47-7
MD09-198	BL21(DE3)pLysS, pDu48
MD09-199	BL21(DE3)pLysS, pDu49
MD09-200	BL21(DE3)pLysS, pDu50
MD09-200-4	BL21(DE3)pLysS, pDu50-4

Table 14-4. Specific Productivity of Variants listed above

Isoprene Produced (µg/l)					OD_{600}		OD
Sample	Sample	Average	Std Dev	%CV	Raw	xDF xCF	Norm
IspS N terminal Truncation Variants	MD09-197-3	3381	154	5	0.3060	3.4	986.6
	MD09-197-4	3000	206	7	0.3160	3.5	847.7
	MD09-197-5	2932	266	9	0.3200	3.6	818.2
	MD09-197-6	2450	217	9	0.3040	3.4	719.4
	MD09-197-7	2285	397	17	0.3020	3.4	675.5
	MD09-198	1916	106	6	0.3330	3.7	513.6
	MD09-199	2031	108	5	0.2140	2.4	847.6
	MD09-200	141	8	6	0.3700	4.1	34.0
	MD09-200-4	1829	197	11	0.2760	3.1	591.5
	MD09-173	2414	201	8	0.3400	3.8	633.9
	MD09-176	2826	354	13	0.3260	3.7	773.9
	BL21 DE3 pLysS + P alba pET24a	2175	117	5	0.2990	3.3	649.6

[0426]

[0427] A second experiment was conducted with the strains outlined in Table 14-5. Control was BL21 DE3 pLysS with P. alba pET24a (full length P. alba IspS).

[0428]

[0429] Table 14-5. Strains

MD09-197-3	BL21(DE3)pLysS, pDu47-3
MD09-197-4	BL21(DE3)pLysS, pDu47-4
MD09-197-5	BL21(DE3)pLysS, pDu47-5
MD09-197-6	BL21(DE3)pLysS, pDu47-6
MD09-197-7	BL21(DE3)pLysS, pDu47-7
MD09-198	BL21(DE3)pLysS, pDu48
MD09-199	BL21(DE3)pLysS, pDu49
MD09-173	BL21(DE3)pLysS, pET24a-P.alba (MEA) Untagged (pDu39)
MD09-174	BL21(DE3)pLysS, pET24a-P.alba (MNV) Untagged (pDu40)
MD09-175	BL21(DE3)pLysS, pET24a-P.alba (MSV) Untagged (pDu41)
MD09-176	BL21(DE3)pLysS, pET24a-P.alba (MTE) Untagged (pDu42)
MD09-177	BL21(DE3)pLysS, pET24a-P.alba (MVS) Untagged (pDu43)
MD09-197-3	BL21(DE3)pLysS, pDu47-3
MD09-197-4	BL21(DE3)pLysS, pDu47-4

[0430]

[0431] Results

[0432] All truncations of *P. alba* IspS and two from *P. tremuloides* and *P. trichocharpa* were assayed in parallel to compare their relevant specific activities via DMAPP assay and quantitative Western blot. At least two samples per variant were assayed for isoprene

production and amount of IspS in mg/ml. Variant MD09-174 produced little isoprene and expressed little protein, yet displayed high specific activity. High specific activities were also displayed by MD09-173, MD09-176, and MD09-197-3 (see Table 14-6 and Figure 70). The highest levels of protein (µg) in 3 µg total protein were displayed by MD09-176 and MD09-197-3, indicating that these variants are more effectively expressed in the *E. coli* BL21 DE3 host strain.

[0433]

[0434] Table 14-6. Specific Activity of truncations.

Strain	Average Specific Activity	Standard Deviation	Average ug IspS/ 3 µg total protein
P. alba FL	240.16239	31.0423851	0.198
MD09-175	331.8755329	8.958408319	0.188
MD09-177	340.1959506	39.72104203	0.150
MD09-176	363.516921	3.376026129	0.202
MD09-174	452.7792122	27.71567075	0.018
MD09-197-7	279.2042431	23.82331163	0.158
MD09-197-6	309.8357305	7.903564316	0.164
MD09-197-5	293.22592	20.97161876	0.165
MD09-197-4	321.3926574	56.13760028	0.186
MD09-197-3	333.0604155	45.92710529	0.207
MD09-173	368.4597405	37.80631246	0.159
MD09-198	297.6476631	56.81405985	0.154
MD09-199	256.7342861	8.239697653	0.216

[0435]

Example 15

Constructs for Three-Dimensional Structure Determination

I. Construction of pMAL-C4X Kudzu

[0436] A synthetic gene, coding for isoprene synthase (IspS) of the Kudzu vine (*Pueraria lobata*) and codon-optimized for E. coli, was purchased from DNA2.0 (Menlo Park, CA) and provided as plasmid p9795 (Figure 71 and 72). The insert was removed by digestion with *Bsp*LU11I/*Pst*I, gel-purified, and religated into *Nco*I/*Pst*I-digested pTrcHis2B (Invitrogen, Carlsbad, California). The resulting plasmid was named pTrcKudzu (Figure 73: map of pTrcKudzu). The stop codon in the insert is before the *Pst*I site, which results in a construct in which the His-Tag is not attached to the IspS protein.

[0437] A PCR reaction was performed to amplify the *E. coli* codon-optimized Kudzu gene using plasmid pTrcKudzu as the DNA template, primers EL-959 and EL-960, 10mM dNTP

(Roche, Indianapolis, IN), and Pfu Ultra II Fusion DNA polymerase (Stratagene, La Jolla, CA) according to manufacturer's protocol. PCR conditions were as follows: 95 °C for 2 min (first cycle only), 95 °C for 25 sec, 60 °C for 25 sec, 72 °C for 30 sec, repeat for 28 cycles, with final extension at 72 °C for 1 min. The PCR product was then purified using the QIAquick PCR Purification Kit (Qiagen Inc, Valencia, CA).

[0438] The Kudzu PCR product (1 µg) was digested using *Eco*RI and *Hind*III restriction endonucleases (Roche) according to manufacturer's protocol. The digest was incubated 37 °C for 30 minutes to minimize digestion of the internal *Eco*RI site that is present in the Kudzu gene. The digested PCR fragment was then purified using the QIAquick PCR Purification Kit. The vector pMAL-C4X (0.5 µg) (New England Biolabs, Ipswich, MA; Figures 75 and 76) was digested using *Eco*RI and *Hind*III restriction endonucleases (Roche) according to manufacturer's protocol. The digested vector was then gel purified using the QIAquick Gel Extraction Kit (Qiagen Inc). A DNA ligation reaction was performed using T4 DNA ligase (New England Biolabs) with a 5:1 ratio of digested Kudzu PCR product to digested pMAL-C4X vector according to manufacturer's protocol. An aliquot of the ligation reaction was then transformed into TOP10 chemically competent cells (Invitrogen Corp). Transformants were selected on LA + 50 µg/µl carbenicillin plates.

[0439] Screening of transformants containing the Kudzu gene was performed by picking colonies and performing PCR with primers EL-957 and EL-966 using PuReTaq Ready-To-Go PCR beads (GE Healthcare, Piscataway, NJ) according to manufacturer's protocol. PCR conditions were as follows: 95 °C for 2 min (first cycle only), 95 °C for 30 sec, 50 °C for 30 sec, 72 °C for 40 sec, repeat for 28 cycles, with final extension at 72 °C for 1 min. PCR products were analyzed on a 2% E-gel (Invitrogen Corp) looking for a 600 bp fragment. Colonies containing the correct sized PCR product insert were submitted for DNA sequencing using primers EL-950, EL-951, EL-953, and EL-957. DNA sequencing confirmed the construction of plasmid pMAL-C4X Kudzu (Figures 77 - 79).

Table 15-1 Primer sequences

Primer name	Primer sequence
EL-950	CGGTGAACTGAAAGGTGACGTCC (SEQ ID NO:108)
EL-951	GGACGTTAACGCTATTAACACCCTG (SEQ ID NO:109)
EL-953	CACATCGTCGATCAGCTCCAGC (SEQ ID NO:110)
EL-957	GGTCGTCAGACTGTCGATGAAGCC (SEQ ID NO:111)
EL-959	GCTTATGAATTCTGTGCGACCTCTTCTCAATTTACTCAG (SEQ ID NO:112)
EL-960	GCTTATAAGCTTAGACATACATCAGCTGGTTAATCGGG (SEQ ID NO:113)

EL-966	CTCCTCCAGCAGGTTCTCACC (SEQ ID NO:114)

[0440] Plasmid pMAL-C4X Kudzu was transformed into OneShot BL21(λDE3) chemically competent cells (Invitrogen Corp). Expression strain transformants were selected on LA + 50 mg/ml carbenicillin plates.

II. IspS Variants for Crystal Structure Trials

[0441] This example describes methods to generate affinity tagged isoprene synthase (IspS) enzymes for expression, purification and crystallization.

Strain Construction

[0442] For constructs in the pET200D-TOPO vector (Invitrogen), PCR products of the IspS enzymes from *P. alba*, *P. tremuloides*, and *P. trichocharpa* were gel extracted and purified (Qiagen), using 0.8% E-gel (Invitrogen), according to the manufacturer's recommended protocol. PCR reactions for pET200 constructs are as follows: Reaction mixture was 1µl (Templates)-pET24a-P.alba, 5 µl 10X PfuUltrall Fusion buffer, 1 µl dNTP's (10 mM), 1 µl primer (50uM) primer F-(MCM219 or 218), 1 µl primer (50uM) primer R-(MCM182), 41 µl diH2O and 1 µl of PfuUltra II Fusion DNA Polymerase from Stratagene; Cycle Parameter were 95°C 1 min., 95°C 1 min, 55°C 20 sec., 72°C 27 sec. for 29 cycles followed by 72°C for 3 min and then 4° C until cool, using an Eppendorf Mastercycler. Similar reactions were performed for *P. tremuloides*, *P. trichocarpa*, and Kudzu. 3 µl of purified product was then ligated to the pET200D/TOPO vector (Invitrogen), according to the manufacturer's protocol. The reaction was incubated for 5 minutes at room temperature, and the 6 µl topoisomerase mixture was then transformed into E. coli Top10 chemically competent cells (Invitrogen) according to the manufacturer's protocol. Transformants were selected for on LB Kan50, and incubated at 37 °C overnight. Five colonies per construct were chosen and screened using PuReTaq Ready-To-Go PCR Beads (Amersham) using the T7 Forward and MCM182 primers (Table 15-2). Clones harboring inserts of the correct size were further verified by plasmid miniprep using the QIAPrep Spin Miniprep kit (Qiagen) followed by sequencing using the T7 Forward and T7 Reverse primers (Quintara Biosciences). One fully sequenced construct for each IspS variant (see below for details and sequence/Figures 79-90), was chosen for further study. 1 µl of each plasmid was transformed into BL21(λDE3) pLysS (Invitrogen) according to the manufacturer's protocol. Transformants were selected for on LB medium with Kan50 + Cm35 and incubated at 37°C overnight. The resulting strains were used for expression and purification of various IspS enzymes for crystallography studies.

[0443] Construction of N-terminally 6His-tagged IspS plasmids, strains and purification is described in Example 11.

Table 15-2. Primers

MCM219	caccatgcgttgtagcgtgtcca (SEQ ID NO: 114)
MCM182	gggcccgtttaaactttaactagactctgcagttagcgttcaaacggcagaa (SEQ ID NO:115)
MCM218	caccatgcgtcgttctgcgaactac (SEQ ID NO:116)

Table 15-3. Plasmids

P. alba pET24a	pET24a with "full length" IspS from P. alba
P. trichocharpa pET24a	pET24a with "full length" IspS from P. trichocharpa
P. tremuloides pET24a	pET24a with "full length" IspS from P. tremuloides
MBP-Kudzu	
pDu27	P. albaFL-pET200/Top 10
pDu30	P. albaTRC-pET200/Top10
pDu31	P. tremTRC-pET200/Top 10
pDu32	P. trichTRC-pET200/Top10
MD09-161	pET24a-P.alba FL C-Term (+) TEV, His tag/MCM331
MD09-163	pET24a-P.alba TRC (MEA) C-Term (+) TEV, His tag/MCM331

Table 15-4. Strains

MBP-Kudzu	
MD08-99	BL21 DE3 pLys + pDu27
MD08-100	BL21 DE3 pLys + pDu30
MD08-102	BL21 DE3 pLys + pDu31
MD08-104	BL21 DE3 pLys + pDu32
MD09-165	BL21(DE3)pLysS, pET24a-P.alba FL C-Term (+) TEV, His tag
MD09-167	BL21(DE3) pLysS, pET24a-P.alba TRC (MEA) C-Term (+) TEV, His tag

III. Digestion of TEV (Tobacco Etch Virus) or EK (Enterokinase)-tagged enzymes

TEV Cleavage (IspS from strains MD09-165 and MD09-167)

[0444] Strains MD09-165 and MD09-167 are described in Example 11. For digestion, enzymes were purified through a Ni charged sepharose (GE Healthcare) and desalted into 50 mM HEPES, 50 mM NaCl pH 7.4 buffer containing 1 mM DTT. Digestion was performed with TurboTEV Protease from Eton Bioscience Inc. One unit of TurboTEV per 10 µg of purified protein was used. The digest was performed at 4°C overnight. Samples were passed through another Ni column equilibrated in the Ni buffer to remove uncleaved enzyme, tag, TurboTEV protease (that is also tagged) and impurities. The Ni column pass though and washes were analyzed using SDS-PAGE gel (NUPAGE, Invitrogen) and DMAPP activity

assays. Samples containing pure enzyme were pooled and desalted into 50 mM NaCl pH 7.4 buffer containing 1 mM DTT and stored at -80°C.

EK Cleavage (IspS from strains MD08-102 and MD08-104)

[0445] For digestion enzymes were purified through a Ni charged sepharose (GE Healthcare) and desalted into 50 mM HEPES, 50 mM NaCl pH 7.4 buffer containing 1 mM DTT.

[0446] Digestion was performed with EKMax (E180-02) (Invitrogen) using 1 unit of EKMax per 20 μg of purified protein at 4 °C overnight. Samples were passed over EK Away resin (Invitrogen) to remove excess enterokinase. Samples were batched onto Ni charged sepharose resin (equilibrated in the Ni wash buffer) and incubated for 30 min at 4 °C, with occasional inverting. This removed uncleaved enzyme, tag, and impurities. The Ni column pass through and washes were analyzed using SDS-PAGE gel (4-12% NUPAGE, Invitrogen) and DMAPP activity assays. Samples containing pure enzyme were pooled and desalted into 50 mM HEPES, 50 mM NaCl pH 7.4 buffer containing 1 mM DTT and stored at -80°C.

IV. Purification of MBP-IspS

[0447] Construction of pMAL-C4X Kudzu for the expression of MBP-Kudzu isoprene synthase is described above. MBP-Kudzu isoprene synthase production from *E. coli* grown in batch culture at the 15-L scale.

Medium Recipe (per liter fermentation medium)

[0448] K_2HPO_4 7.5 g, $MgSO_4$ * $7H_2O$ 2 g, citric acid monohydrate 2 g, ferric ammonium citrate 0.3 g, yeast extract 0.5 g, 1000X Modified Trace Metal Solution 1 ml. All of the components were added together and dissolved in diH_2O. This solution was autoclaved. The pH was adjusted to 7.0 with ammonium hydroxide (30%) and q.s. to volume. Glucose 10 g, thiamine * HCl 0.1 g, and antibiotics were added after sterilization and pH adjustment.

1000X Modified Trace Metal Solution

[0449] Citric Acids * H_2O 40 g, $MnSO_4$ * H_2O 30 g, NaCl 10 g, $FeSO_4$ * $7H_2O$ 1 g, $CoCl_2$ * $6H_2O$ 1 g, ZnSO * $7H_2O$ 1 g, $CuSO_4$ * $5H_2O$ 100 mg, H_3BO_3 100 mg, $NaMoO_4$ * $2H_2O$ 100 mg. Each component is dissolved one at a time in diH_2O, pH to 3.0 with HCl/NaOH, then q.s. to volume and filter sterilized with 0.22 micron filter.

[0450] Fermentation was performed in a 15-L bioreactor with BL21 (DE3) *E. coli* cells containing the pMAL-C4X plasmid expressing a maltose binding protein (MBP)-Kudzu

isoprene synthase fusion molecule. This experiment was carried out to produce isoprene synthase at the desired fermentation pH 7.0 and temperature 30 °C. A frozen vial of the *E. coli* strain was thawed and inoculated into tryptone-yeast extract medium. After the inoculum grew to OD 1.0, measured at 550 nm (OD_{550}), 120 mL was used to inoculate a 15-L bioreactor bringing the initial volume to 9-L.

[0451] Expression of the desired molecule was achieved by adding isopropyl-beta-D-1-thiogalactopyranoside (IPTG). The IPTG concentration was brought to 1 mM when the OD_{550} reached a value of 10. Cells containing the desired product were harvested 3 hrs after IPTG addition.

MBP-IspS Purification

[0452] The broth was centrifuged for 15 min at 10000 x g. The pellet was collected and frozen at -80 °C until further purification. Cells were resuspended in MBP-Bind Buffer (5% glycerol, 20 mM Tris pH 7.4, 200 mM NaCl, 2 mM DTT, 1mg/ml lysozyme) and passed through the french press three times at 20000 psi. The lysate was then ultracentrifuged at 100000 x g for 1 hour to yield a relatively clear solution. The supernatant was pipetted from the top of the tube without disturbing the gelatinous material on the bottom of the centrifuge tube. Gel filtration was performed on the supernatant using a Superdex-200 26/60 column (GE healthcare). The column was developed using MBP-Bind buffer at a flow rate of 3 mL/min at 23 °C. Fractions were tested for DMAPP activity as described below. Active fractions were pooled and loaded onto 25 mL amylose resin (New England Biolabs). The column was washed with 10 column volumes MBP-Bind buffer and the protein was then eluted with 2 column volumes of MBP-Bind buffer containing 10 mM maltose to yield >90% pure MBP-IspS.

V. DMAPP Assay

[0453] The following reaction mixture was used for the DMAPP assay: 25 µL lysate mixture, 5 µL $MgCl_2$ (1 M), 5 µL DMAPP (100mM), and 65 µL 100 mM Tris pH 8, 100 mM NaCl for a total volume of 100 µL. The reaction is performed at 30 °C for 15 minutes in a gas tight 1.8 mL GC tube. Reactions are terminated by the addition of 100 µL 500 mM EDTA (pH 8). The amount of isoprene produced was measured by GC/MS as described above.

Example 16

Three-dimensional structure of IspS

[0454] Seven constructs of plant isoprene synthase (IspS) were prepared to generate crystals suitable for x-ray diffraction. These were: a construct containing N-terminal histidine-tagged maltose binding protein and kudzu IspS (MBP-kudzu), full-length *P. alba* IspS with N-terminal histidine-tag (MD08-99), *P. alba* IspS with the first nineteen N-terminal residues removed (MD08-100), this construct also had the N-terminal his-tag removed after purification. Full-length, untagged *P. alba* IspS (strain RM11608-2). A truncated *P. alba* IspS construct featuring two additional residues before the twin-arginine motif was generated (MD09-167). *P. tricharpa* IspS was generated, which contains both an N-terminal his-tag and N-terminal truncation (MD08-104), and another construct composed of IspS from *P. tremuloides* was generated with an N-terminal his-tag and N-terminal truncation (MD08-102). Construction of strains expressing various isoprene synthases are described above.

[0455] Each construct was purified and a concentrated protein solution was then prepared for surveying possible crystallization conditions. Each construct was purified independently and surveyed as described below. All in-house crystallization screens were set up using the hanging drop vapor diffusion method. At a minimum, each construct was surveyed using the following commercial screens: the Crystal Screen from Hampton Research (Aliso Viejo, CA) and the JCSG+ Suite from Qiagen (Valencia, CA).

[0456] Purified MBP-kudzu using was set up using the following commercial screens: the Crystal Screen from Hampton Research and the JCSG+ Suite from. Additionally, purified MBP-kudzu was sent to the Hauptman-Woodward Institute (Buffalo, NY) for high-throughput screening, where no fewer than 1536 conditions were surveyed. The purified MBP-kudzu fusion precipitated out of solution in the majority of conditions, and no protein crystals were observed.

[0457] The next construct used for crystallization screening was MD08-99 (full-length *P. alba* IspS with N-terminal histidine-tag). MD08-99 was purified and the histidine-tag was removed. The same three initial crystallization screens were performed as for MBP-kudzu. The Hampton Research Crystal Screen and Qiagen JCSG+ Suite were each performed at multiple protein concentrations. Small needle-like crystals were observed in some Hampton Research Crystal Screen conditions. Further attempts to improve the crystals involved co-crystallization with the IspS inhibitor sodium ibandronate (Sigma-Aldrich, St Louis, MO). Taken together, an additional 288 crystallization conditions were attempted with variations of pH, concentration, and crystallization reagents. The nine best crystals were then prepared for data collection and tested in-house on a Rigaku RU200 rotating anode generator and R-AXIS IV++, and they either did not diffract x-rays or were salt crystals.

[0458] The first nineteen N-terminal residues of *P. alba* IspS were removed to produce construct MD08-100. This construct had the N-terminal histidine-tag removed after purification. In house crystallization screens were performed using the Hampton Research Crystal Screen and Qiagen JCSG+ Suite, each with multiple protein concentrations. Initial crystal hits included hexagonal plates that diffracted to 16Å resolution, and small rods that diffracted to 5Å resolution using the in-house x-ray generator. In an attempt to improve the crystals, MD08-100 was co-crystallized with either sodium ibandronate or sodium pyrophosphate (Sigma-Aldrich, St Louis, MO), both of which are inhibitors of the IspS activity. Neither inhibitor resulted in improved crystals or improved diffraction. An additional 168 crystallization conditions were attempted with variations of pH, concentration, and crystallization reagents. The twenty-one most promising MD08-100 crystals were screened for diffraction, with the best resolution obtained being 5Å.

[0459] Full-length, untagged *P. alba* IspS (strain RM11608-2) from a fermentation run was purified. An initial screen was set up using the Hampton Research Crystal Screen, and crystals were observed in four different conditions. All four crystals were tested for diffraction in-house, with three being salt crystals and one not diffracting.

[0460] A truncated *P. alba* IspS construct featuring two additional residues before the twin-arginine motif was generated (MD09-167). This construct contains a C-terminal histidine-tag, and crystallization experiments were set up with the tag either cleaved or not cleaved, at varying protein concentrations, and with or without sodium pyrophosphate. Initial crystallization screens were done as per MBP-kudzu. Crystals from this construct were observed in numerous conditions; optimization included 528 variations of pH, precipitating agents, concentrations, and inhibitors. From the optimization experiments, fifteen different MD09-167 crystals were screened in-house for diffraction. In an effort to improve the resolution, various crystal freezing conditions were tested, with the effect of improving the diffraction limits from 10Å to 6.5Å.

[0461] A new construct containing *P. tricharpa* IspS was generated, which contains both an N-terminal histidine-tag and an N-terminal truncation (MD08-104). Purified MD08-104 with cleaved histidine-tag was surveyed using the Hampton Research Crystal Screen and the Qiagen JCSG+ suite. This construct generated heavier precipitate than the *P. alba* IspS constructs. Very small needles were observed, with none of the crystals being suitable for diffraction.

[0462] Another construct composed of IspS from *P. tremuloides* was generated with an N-terminal histidine-tag and an N-terminal truncation (MD08-102). Purified MD08-102 with

and without cleaved histidine-tag was set up using the Hampton Research Crystal Screen and the Qiagen JCSG+ Suite at varying protein concentrations. Rod and plate-like crystals were observed in some conditions and an additional 120 experiments were performed to improve the crystals by varying pH, concentration, and crystallization reagents. From the optimization experiments, ten crystals were tested in-house, with the initial best diffraction reaching 5Å. Upon further modification of the freezing conditions of the crystals, a crystal was found that diffracted to 3.3Å from the non-cleaved histidine-tagged protein. This crystal was grown by mixing 2 μL of protein (10 mg/ml, with 30mM $MgCl_2$) with 2 μL of precipitant solution [10% (wt/vol) polyethylene glycol 8000, 0.1 M HEPES, pH 7.5, 8% ethylene glycol] and equilibrated against 500 μL of precipitant. A cluster of rod-shaped crystals appeared after three weeks. The crystals belong to the tetragonal space group P43212, and have unit cell dimensions a = 154.2, b = 154.2, c = 142.7.

[0463] In-house x-ray diffraction data were collected under a nitrogen stream at 100 K using a Rigaku RU200 generator and R-AXIS IV++ detector. Before flash-freezing the crystal in liquid nitrogen, it was cryoprotected by swiping it through a solution containing 10% (wt/vol) polyethylene glycol 8000, 0.1 M HEPES, pH 7.5, and 25% ethylene glycol. Data were integrated using Mosflm (Leslie, A. (1998) J. of Appl. Crystallography 30, 1036-1040) and scaled using SCALA (Collaborative Computational Project, N. (1994) Acta Crystallographica Section D 50, 760-763). The data were then phased by molecular replacement using MrBUMP (Keegan, R. M., and Winn, M. D. (2007) Acta Crystallographica Section D 63, 447-457; Vagin, A., and Teplyakov, A. (1997) J. of Appl. Crystallography 30, 1022-1025), with a monomer of limonene synthase (Protein Data Bank ID 2ONH)(Berman, H., *et al.* (2007) Nucl. Acids Res. 35, D301-303) as the starting model. The crystal contains one dimer in the asymmetric unit with a solvent content of 66%.

[0464] A 3.05Å data set from the same crystal was then collected using beamline 11-1 of the Stanford Synchrotron Radiation Laboratory. These data were also processed using Mosflm and SCALA. Data collection and refinement statistics are given in Table 16-1.

[0465] Refinement with Refmac5 (Collaborative Computational Project, N. (1994) Acta Crystallographica Section D 50, 760-763) was used with iterative manual rebuilding steps using the visualization program Coot (Emsley, P., and Cowtan, K. (2004) Acta Crystallographica Section D 60, 2126-2132). During refinement, the geometry of the protein was checked using Molprobity (Davis, I. W., *et al.* (2007) Nucl. Acids Res., gkm216).

[0466] The fold of poplar IspS is similar to bornyl diphosphate synthase (Whittington, D. A., *et al.* (2002) Proc. Natl Acad. Sci. USA 99, 15375-15380), limonene synthase (Hyatt, D.

C., et al. (2007) Proc. Natl Acad. Sci. USA 104, 5360-5365), and tobacco 5-epi-aristolochene synthase (Starks, C. M., *et al.* (1997) Science 277, 1815-1820) . The structure consists of two helical domains, a C-terminal domain containing the active site and N-terminal domain (Figures 90 and 91). Coordinates are provided in Table 16-7.

Table 16-1. Data Collection and Refinement Statistics

Data Collection	
Space Group	$P4_32_12$
Cell dimensions	
a, b, c (Å)	154.2, 154.2, 142.7
a, ß, γ, (°)	90.0, 90.0, 90.0
Resolution (Å)	37.8 – 3.05
R_{merge}	16.4 (72.9)[a]
<I/sI>	10.3 (2.6)
Completeness (%)	99.8 (100)
Redundancy	7.3 (7.4)
Refinement	
Resolution (Å)	37.8 – 3.05
No. measured reflections	248741
No. Unique reflections	34201
R_{work}	21.1
R_{free}	27.1
rmsd bonds, (Å)	0.011
rmsd angles, (°)	1.28
No. of Atoms	
Protein, ions[b]	8331
Water	18

Flexible Loops

[0467] The unique and unexpected discovery coming from the determination of the three dimensional structure of isoprene synthase is that several crucial loops forming the active site are flexible. The discovery can be immediately seen when the known structure of other terpene synthases are compared with the structure of isoprene synthase (Figure 94). Overall, the structures are highly conserved in the conformation of secondary structure and connectivity loops. (In this example of the *Poplar tremuloides* IspS from construct P.tremTRC-pET200, the numbering convention is such that the first number of the complete sequence containing the tag is -35, with the first residue of IspS being 1.) However, three segments, forming a considerable portion of the substrate binding pocket, notably the truncated N-terminus, along with two loops comprised of residues 438-453 (Loop I) and

residues 512-527 (Loop II) are seen to diverge (Figures 95 to 97). This has been attributed to the absence of substrate complexed with the enzyme in our structure determination.

[0468] In comparing the enzyme with BdpS, for example, we find that the loops corresponding to residues 498-513 and 573-587 are composed of the same number of residues and have a homologous, but not identical amino sequence in these regions. We expect that the related terpene synthases will be found to display similar flexibility in the segments as these structure become more thoroughly studied. The residues in terpene synthases corresponding to these variable loop regions are enumerated in Table 16-2.

Table 16-2. Residues corresponding to variable loops in terpene synthases

	Poplar IspS	LS	BdpS	TEAS
N-term I	Met 1	Met 57	Ile 54	Val 14
	Arg 2	Arg 58	Arg 55	Arg 15
	Arg 3	Arg 59	Arg 56	Pro 16
	Ser 4	Ser 60	Ser 57	Val 17
	Ala 5	Gly 61	Gly 58	Ala 18
	Asn 6	Asn 62	Asn 59	Asp 19
	Tyr 7	Tyr 63	Tyr 60	Phe 20
	Glu 8	Asn 64	Gln 61	Ser 21
	Pro 9	Pro 65	Pro 62	Pro 22
	Asn 10	Ser 66	Ala 63	Ser 23
	Ser 11	Arg 67	Leu 64	Leu 24
	Trp 12	Trp 68	Trp 65	Trp 25
	Asp 13	Asp 69	Asp 66	Gly 26
	Tyr 14	Val 70	Ser 67	Asp 27
	Asp 15	Asn 71	Asn 68	Gln 28
	Tyr 16	Phe 72	Tyr 69	Phe 29
N-term II	Leu 17	Ile 73	Ile 70	Leu 30
	Leu 18	Gln 74	Gln 71	Ser 31
	Ser 19	Ser 75	Ser 72	Phe 32
	Ser 20	Leu 76	Leu 73	Ser 34
	Asp 21	Leu 77	Asn 74	Ile 35
	Thr 22	Ser 78	Thr 75	Asp 36
	Asp 23	Asp 79	Pro 76	Asn 37
	Glu 24	Tyr 80	Tyr 77	Gln 38
	Ser 25	Lys 81	Thr 78	Val 39
	Ile 26	Glu 82	Glu 79	Ala 40
	Glu 27	Asp 83	Glu 80	Glu 41
	Val 28	Lys 84	Arg 81	Lys 42

Loop I	Leu 438	Leu 498	Leu 498	Thr 446
	Ala 439	Gly 499	Gly 499	Ala 447
	Ser 440	Thr 500	Thr 500	The 448
	Ala 441	Ser 501	Ser 502	Tyr 449
	Ser 442	Val 502	Tyr 503	Glu 450
	Ala 443	Glu 503	Phe 504	Val 451
	Glu 444	Glu 504	Glu 505	Glu 452
	Ile 445	Val 505	Leu 506	Lys 453
	Ala 446	Ser 506	Ala 507	Ser 454
	Arg 447	Arg 507	Arg 508	Arg 455
	Gly 448	Gly 508	Gly 509	Gly 456
	Glu 449	Asp 509	Asp 510	Gln 457
	Thr 450	Val 510	Val 511	Ile 458
	Ala 451	Pro 511	Pro 512	Ala 459
	Asn 452	Lys 512	Lys 513	Thr 460
	Ser 453	Ser 513	Thr 514	Gly 461
Loop II	Tyr 512	Tyr 576	Tyr 573	Tyr 520
				Ile 521
	His 513	His 577	Leu 574	His 522
	Asn 514	Asn 578	His 575	Asn 523
	Gly 515	Gly 579	Gly 576	Leu 524
	Asp 516	Asp 580	Asp 577	Asp 525
	Ala 517	Gly 581	Gly 578	Gly 526
	His 518	His 582	Phe 579	Tyr 527
	Thr 519	Gly 583	Gly 580	The 528
	Ser 520	Thr 584	Val 581	His 529
	Pro 521	Gln 585	Gln 582	Pro 530
	Asp 522	His 585	His 583	Glu 531
	Glu 523	Pro 586	Ser 584	Lys 532
	Leu 524	Ile 587	Lys 585	Val 533
	Thr 525	Ile 588	Thr 586	Lue 534
	Arg 526	His 589	Tyr 587	Lys 535

[0469] This important finding can be exploited for the engineering of improved isoprene synthase in a straightforward manner. It would be desirable to exploit the flexibility to enhance enzyme performance by making substitutions in the amino aids forming these segments to facilitate the transitions the enzyme must undergo in the steps of binding substrate and allowing rearrangement of substrate in different kinetic steps that are postulated

to occur during enzymatic de-phosphorylation and for electron transfer to convert DMAPP to isoprene.

[0470] The structure provides the new insight that these loops can be present in at least two conformations: the "open" form in the absence of substrate, as we have see in the uncomplexed structure of the isoprene synthase, and a "closed," or active form when the substrate is bound. It would therefore also be beneficial to modify residues coming in contact with the loops in the active form as described in Table 16-3.

Table 16-3. Residues coming within 5 angstroms of flexible elements

	P trem IspS	1N1B	2ONG	5EAS[e]
N-term neigbors	L17, L18, S19, S20, S239, R243, F253, A254, R255, D256, R257, I259, E260, D293, Y295, D296, V297, Y298, G299, T300, E303, Y325, L374, Y375, elements of loop I, elements of loop II, V529, L530, T534	70I, 71Q, 72S, 73L, 298S, 302S, 312F, 313V, 314R, 315D, 316R, 318V, 319E, 352D, 354Y, 355D, 356V, 357Y, 358G, 359T, 362E, 384Y, 433Y, 434H, elements of loop I, elements of loop II , 589I, 590A , 594F	I73, Q74, S75, L76, F299, R303, F313, A314, R315, A316, R317, V319, E320, D353, Y355, D356, V357, Y358, G359, T360, E363, Y385, F434, Y435, elements of loop I, elements of loop II, M590, T591, F595	L30, S31, F32, S33, S248, K252, Y262, A263, R264, D265, R266, V268, E269, D302, F304, D305, A306, Y307, G308, T309, E312, Y334, F383, I384, elements of loop I, elements of loop II, I538, I538, V543
Loop I neighbors	Elements of N-term, D293, Y295, V297, E370, A371, W373, L374, S378, T379, P380, F382, Y385, F386, R433, L434 C435, N436, D437, V454, S455, C456, Y457, M458, T469, V472, I476, Y512, elements of loop II	Elements of N-term, 352D, 354Y, 356V, 429E, 430A, 432W, 433Y, 437Y, 438T, 439P, 441L, 444Y, 445L, 493R, 494L, 495P, 496D, 497D, 514I, 515Q, 516C, 517Y, 518M, 529V, 532V, 536I, 572Y, elements of loop II	Elements of N-term, D353, Y355, V357, E430, A431, W433, F434, H438, K439, P440, L442, Y445, L446, R493, L494, A495, D496, D497, L514, Q515, C516, Y517, M518, R529, V532, I536, Y573, elements of loop II	Elements of N-term, D304, F304, A306, E379, S380, W382, F383, Y387, T388, P389, V391, Y394, L395, R441, V442, I443, D444, D445, I462, E463, C464, C465, M466, M477, F480, A484, Y520, elements of loop II
Loop II neighbors	Elements of N-terminus, E187, L188, R255, R257, F270, E271, Q273, Y274, F285, V288, A439, S440, S442, S508, H509, C510, T511, Y512, R528, V529, L530, S531, V532	Elements of N-terminus, 246D, 247L, 314R, 316R, 329E, 330S, 332F, 333W, 344I, 348I, 499G, 500T, 503Y, 568A, 569Q, 570F, 571I, 572Y, 588H, 589I, 590A, 591G, 592L	Elements of N-terminus, D247, I248, R315, R317, E330, P331, Q333, H334, N345, I347, G499, T500, V502, A569, Q570, L571, M572, Y573, Q589, M590, T591, R592, T593	Elements of N-terminus, E195, Q196, R264, R266, F279, E280, Q282, Y283, I294, I297, A447, T448, E450, V516, E517, V518, I519, Y520, H537, I538, I539, N540, L541

Selection of Sites for Improvement of Plant Isoprene Synthase

[0471] The isoprene synthases of plants were expected to be homologous to the terpene synthases. The three-dimensional structures of three homologous terpene synthases have been determined: *Salvia officinalis* bornyl diphosphate synthase (BdpS; pdb entry 1N1B), *Mentha spicata* limonene synthase (LS; pdb entry 2ONG), and tobacco 5-epi-aristolochene synthase (TEAS; pdb entry 5EAS). These enzymes share only 33% homology but their tertiary structure is conserved. Sequence identity is shown in Table 16-4, and structural homology between the structures is shown in Table 16-5. In addition, the structures of intermediate complexes with all three related enzymes have shown that not only tertiary

folding, but also detailed interactions in the active sites of these enzymes are highly conserved.

Table 16-4. Percent Identity of Terpene Cyclases.

	P trem IspS	1N1B	2ONG	5EAS[e]
P alba IspS[a]	98.6	40.7	41.3	33.2
P trem IspS[b]		41.0	41.4	33.2
1N1B[c]			51.4	33.8
2ONG[d]				33.3

[a] Polar alba isoprene synthase
[b] Polar tremuloides isoprene synthase
[c] bornyl diphosphate synthase
[d] limonene synthase
[e] 5-epi-aristolochene synthase

Table 16-5. Structural Alignment of Terpene Synthases

	1N1B[b]	2ONG[c]	5EAS[d]
P trem IspS[a]	1.40 (465)[e]	1.29 (468)	1.62 (458)
1N1B		1.27 (520)	1.97 (476)
2ONG			1.83 (477)

[a] *Polar tremuloides* isoprene synthase
[b] bornyl diphosphate synthase
[c] limonene synthase
[d] 5-epi-aristolochene synthase
[e] Root mean square deviation in Å for Ca atoms, with the number of aligned residues in parenthesis

[0472] In this example of the *Poplar tremuloides* IspS from construct P.tremTRC-pET200, the numbering convention is such that the first number of the complete sequence containing the tag is -35, with the first residue of IspS being 1.

[0473] A comparison of the active site from the structure of BdpS and the structure of poplar IspS indicates that the active site involved in metal ion binding and phosphate recognition is conserved. In particular, Arg 255, Asp 292, Asp 296, Glu 370, Arg 433 and

Asn 436 of poplar IspS were observed to overlap equivalent residues in BdpS. The positioning of an intermediate of the BdpS was also compared with the poplar IspS structure. Based on this it was possible to identify the analogous binding region and the approach direction that dimethylallyl pyrophosphate would require in order to bind and react with the poplar IspS enzyme.

[0474] Based on the structure of poplar IspS, sites in the poplar IspS were identified as candidates for mutagenesis to produce variant IspS enzymes with improved performance. Briefly, sites were selected in the IspS that might alter the interaction of the metal binding, diphosphate recognition, DMAPP chain binding and/or the approach to the active site.

I. Diphosphate/ Metal Binding Sites

[0475] The side chains of amino acid residues in the poplar IspS that are found in proximity to the metal and diphosphate binding side chains were identified. These residues include Asp 293, Tyr 385, Ser 392, and Asp 437. Engineering of these sites may result in increased enzyme activity.

II. Substrate Access Loops

[0476] The substrate access loops of poplar IspS are in regions that deviate from the BdpS structure. In the BdpS structure the residues create a cover over the active site. It is likely that upon substrate binding the structure of poplar IspS will form a similar structure. As such the residues in these loops, including residues 440-453 and 512-524, may be in a position to alter the activity of the poplar IspS. In the poplar IspS enzyme, residues 440-453 have the sequence SASAEIARGETANS and residues 512-526 have the sequence YHNGDAHTSPDEL.

III. Isoprenyl Binding Site

[0477] The complex of BdpS and the product of the reaction, bornyl diphosphate (PDB entry 1N24), was used to identify residues in the poplar IspS structure that with protein engineering may be used modulate substrate specificity and/or reaction rate (altered on and off rates of substrate and product). These residues include Ser 261, Trp 264, Phe 285, Thr 289, Ser 393, Ser 394, Phe 432, and Try 512.

Table 16-6. Candidate mutagenesis sites.

	Poplar IspS
DPP/Metal Binding Sites	Asp 293
	Tyr 385
	Ser 392
	Asp 437
Substrate Access Loop I	Ser 440
	Ala 441
	Ser 442
	Ala 443
	Glu 444
	Ile 445
	Ala 446
	Arg 447
	Gly 448
	Glu 449
	Thr 450
	Ala 451
	Asn 452
	Ser 453
Substate Access Loop II	Tyr 512
	His 513
	Asn 514
	Gly 515
	Asp 516
	Ala 517
	His 518
	Thr 519
	Ser 520
	Pro 521
	Asp 522
	Glu 523
	Leu 524
Isoprenyl Binding Site	Ser 261
	Trp 264
	Phe 285
	Thr 289
	Ser 393
	Ser 394
	Phe 432

	Tyr 512

Table 16-7. Coordinates of *P. tremuloides* IspS

```
HEADER    ----                          XX-XXX-XX   xxxx
COMPND    ---
REMARK   3
REMARK   3 REFINEMENT.
REMARK   3   PROGRAM     : REFMAC 5.5.0088
REMARK   3   AUTHORS     : MURSHUDOV,VAGIN,DODSON
REMARK   3
REMARK   3    REFINEMENT TARGET : MAXIMUM LIKELIHOOD
REMARK   3
REMARK   3  DATA USED IN REFINEMENT.
REMARK   3   RESOLUTION RANGE HIGH (ANGSTROMS) :   3.05
REMARK   3   RESOLUTION RANGE LOW  (ANGSTROMS) : 110.17
REMARK   3   DATA CUTOFF           (SIGMA(F)) : NONE
REMARK   3   COMPLETENESS FOR RANGE       (%) :  99.67
REMARK   3   NUMBER OF REFLECTIONS          :   32446
REMARK   3
REMARK   3  FIT TO DATA USED IN REFINEMENT.
REMARK   3   CROSS-VALIDATION METHOD        : THROUGHOUT
REMARK   3   FREE R VALUE TEST SET SELECTION  : RANDOM
REMARK   3   R VALUE     (WORKING + TEST SET) :  .21396
REMARK   3   R VALUE          (WORKING SET) :   .21092
REMARK   3   FREE R VALUE                   :   .27112
REMARK   3   FREE R VALUE TEST SET SIZE   (%) :  5.1
REMARK   3   FREE R VALUE TEST SET COUNT     :  1727
REMARK   3
REMARK   3  FIT IN THE HIGHEST RESOLUTION BIN.
REMARK   3   TOTAL NUMBER OF BINS USED          :     20
REMARK   3   BIN RESOLUTION RANGE HIGH          :   3.050
REMARK   3   BIN RESOLUTION RANGE LOW           :   3.129
REMARK   3   REFLECTION IN BIN     (WORKING SET) :    2359
REMARK   3   BIN COMPLETENESS (WORKING+TEST) (%) :   100.00
REMARK   3   BIN R VALUE          (WORKING SET) :    .288
REMARK   3   BIN FREE R VALUE SET COUNT         :     127
REMARK   3   BIN FREE R VALUE                   :    .352
REMARK   3
REMARK   3  NUMBER OF NON-HYDROGEN ATOMS USED IN REFINEMENT.
REMARK   3   ALL ATOMS             :    8349
REMARK   3
REMARK   3  B VALUES.
REMARK   3   FROM WILSON PLOT         (A**2) : NULL
REMARK   3   MEAN B VALUE     (OVERALL, A**2) :  24.592
REMARK   3   OVERALL ANISOTROPIC B VALUE.
REMARK   3    B11 (A**2) :     .41
REMARK   3    B22 (A**2) :     .41
REMARK   3    B33 (A**2) :    -.81
REMARK   3    B12 (A**2) :     .00
REMARK   3    B13 (A**2) :     .00
REMARK   3    B23 (A**2) :     .00
REMARK   3
REMARK   3  ESTIMATED OVERALL COORDINATE ERROR.
REMARK   3   ESU BASED ON R VALUE                            (A): NULL
REMARK   3   ESU BASED ON FREE R VALUE                       (A):   .427
REMARK   3   ESU BASED ON MAXIMUM LIKELIHOOD                 (A):   .327
REMARK   3   ESU FOR B VALUES BASED ON MAXIMUM LIKELIHOOD (A**2):  39.836
```

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REMARK   3
REMARK   3 CORRELATION COEFFICIENTS.
REMARK   3  CORRELATION COEFFICIENT FO-FC      :   .916
REMARK   3  CORRELATION COEFFICIENT FO-FC FREE :   .868
REMARK   3
REMARK   3 RMS DEVIATIONS FROM IDEAL VALUES       COUNT    RMS    WEIGHT
REMARK   3  BOND LENGTHS REFINED ATOMS       (A):  8495 ;  .011 ;  .022
REMARK   3  BOND LENGTHS OTHERS              (A):  5804 ;  .001 ;  .020
REMARK   3  BOND ANGLES REFINED ATOMS   (DEGREES): 11476 ; 1.279 ; 1.953
REMARK   3  BOND ANGLES OTHERS          (DEGREES): 14093 ;  .882 ; 3.000
REMARK   3  TORSION ANGLES, PERIOD 1    (DEGREES):  1020 ; 7.002 ; 5.000
REMARK   3  TORSION ANGLES, PERIOD 2    (DEGREES):  435 ;35.412 ;24.299
REMARK   3  TORSION ANGLES, PERIOD 3    (DEGREES):  1525 ;18.250 ;15.000
REMARK   3  TORSION ANGLES, PERIOD 4    (DEGREES):  58 ;16.811 ;15.000
REMARK   3  CHIRAL-CENTER RESTRAINTS      (A**3):  1266 ;  .070 ;  .200
REMARK   3  GENERAL PLANES REFINED ATOMS     (A):  9416 ;  .005 ;  .020
REMARK   3  GENERAL PLANES OTHERS            (A):  1780 ;  .001 ;  .020
REMARK   3
REMARK   3 ISOTROPIC THERMAL FACTOR RESTRAINTS.    COUNT   RMS    WEIGHT
REMARK   3  MAIN-CHAIN BOND REFINED ATOMS  (A**2):  5104 ;  .514 ; 1.500
REMARK   3  MAIN-CHAIN BOND OTHER ATOMS    (A**2):  2068 ;  .059 ; 1.500
REMARK   3  MAIN-CHAIN ANGLE REFINED ATOMS (A**2):  8204 ; 1.000 ; 2.000
REMARK   3  SIDE-CHAIN BOND REFINED ATOMS  (A**2):  3391 ; 1.218 ; 3.000
REMARK   3  SIDE-CHAIN ANGLE REFINED ATOMS (A**2):  3272 ; 2.157 ; 4.500
REMARK   3
REMARK   3 NCS RESTRAINTS STATISTICS
REMARK   3  NUMBER OF DIFFERENT NCS GROUPS :  1
REMARK   3
REMARK   3 NCS GROUP NUMBER             :  1
REMARK   3   CHAIN NAMES                : A B
REMARK   3   NUMBER OF COMPONENTS NCS GROUP :  1
REMARK   3    COMPONENT C  SSSEQI  TO  C   SSSEQI   CODE
REMARK   3        1    A      17      A      541     6
REMARK   3        1    B      17      B      541     6
REMARK   3              GROUP CHAIN       COUNT   RMS     WEIGHT
REMARK   3  LOOSE POSITIONAL   1   1    (A):   7038 ;   .37 ;  5.00
REMARK   3  LOOSE THERMAL      1   1  (A**2):   7038 ;  1.09 ; 10.00
REMARK   3
REMARK   3 TWIN DETAILS
REMARK   3  NUMBER OF TWIN DOMAINS  : NULL
REMARK   3
REMARK   3
REMARK   3 TLS DETAILS
REMARK   3  NUMBER OF TLS GROUPS  :  8
REMARK   3  ATOM RECORD CONTAINS RESIDUAL B FACTORS ONLY
REMARK   3
REMARK   3  TLS GROUP :  1
REMARK   3   NUMBER OF COMPONENTS GROUP :  1
REMARK   3   COMPONENTS       C SSSEQI   TO  C SSSEQI
REMARK   3   RESIDUE RANGE :   A      17       A      219
REMARK   3   ORIGIN FOR THE GROUP (A): -64.7667  37.6643   -.0896
REMARK   3   T TENSOR
REMARK   3    T11:   .0648 T22:   .0357
REMARK   3    T33:   .0787 T12:   .0200
REMARK   3    T13:   .0129 T23:  -.0089
REMARK   3   L TENSOR
REMARK   3    L11:  3.7204 L22:  1.5111
REMARK   3    L33:  2.6701 L12:   .5715
REMARK   3    L13:   .6692 L23:  -.9699
REMARK   3   S TENSOR
```

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REMARK   3    S11:   .0562 S12:   .0478 S13:  -.1976
REMARK   3    S21:  -.1702 S22:  -.0055 S23:   .1376
REMARK   3    S31:   .0900 S32:  -.2188 S33:  -.0507
REMARK   3
REMARK   3  TLS GROUP :    2
REMARK   3  NUMBER OF COMPONENTS GROUP :    1
REMARK   3  COMPONENTS       C SSSEQI   TO  C SSSEQI
REMARK   3  RESIDUE RANGE :   A      220       A      287
REMARK   3  ORIGIN FOR THE GROUP (A): -59.5787   8.4529   -.7693
REMARK   3  T TENSOR
REMARK   3    T11:   .1615 T22:   .0645
REMARK   3    T33:   .1539 T12:  -.0314
REMARK   3    T13:  -.0461 T23:   .0198
REMARK   3  L TENSOR
REMARK   3    L11:  2.4192 L22:  4.6709
REMARK   3    L33:   .7709 L12: -3.2943
REMARK   3    L13:  -.1814 L23:  -.0705
REMARK   3  S TENSOR
REMARK   3    S11:   .0055 S12:  -.0699 S13:  -.2073
REMARK   3    S21:  -.1805 S22:   .0996 S23:   .3781
REMARK   3    S31:   .2596 S32:   .0887 S33:  -.1051
REMARK   3
REMARK   3  TLS GROUP :    3
REMARK   3  NUMBER OF COMPONENTS GROUP :    1
REMARK   3  COMPONENTS       C SSSEQI   TO  C SSSEQI
REMARK   3  RESIDUE RANGE :   A      288       A      374
REMARK   3  ORIGIN FOR THE GROUP (A): -40.1866   1.6932    .5805
REMARK   3  T TENSOR
REMARK   3    T11:   .1149 T22:   .1003
REMARK   3    T33:   .1629 T12:   .0153
REMARK   3    T13:   .0224 T23:   .0164
REMARK   3  L TENSOR
REMARK   3    L11:   .2271 L22:   .7399
REMARK   3    L33:  4.8529 L12:   .3413
REMARK   3    L13:   .4755 L23:  -.1746
REMARK   3  S TENSOR
REMARK   3    S11:  -.0449 S12:  -.0288 S13:  -.1131
REMARK   3    S21:  -.1346 S22:  -.0665 S23:  -.2749
REMARK   3    S31:  -.0040 S32:   .1558 S33:   .1114
REMARK   3
REMARK   3  TLS GROUP :    4
REMARK   3  NUMBER OF COMPONENTS GROUP :    1
REMARK   3  COMPONENTS       C SSSEQI   TO  C SSSEQI
REMARK   3  RESIDUE RANGE :   A      375       A      541
REMARK   3  ORIGIN FOR THE GROUP (A): -47.2220  21.5399   6.9217
REMARK   3  T TENSOR
REMARK   3    T11:   .1551 T22:   .1194
REMARK   3    T33:   .1485 T12:  -.0666
REMARK   3    T13:   .0275 T23:   .0272
REMARK   3  L TENSOR
REMARK   3    L11:  2.2352 L22:  2.1698
REMARK   3    L33:  2.3370 L12:  -.4501
REMARK   3    L13:  2.2662 L23:  -.1852
REMARK   3  S TENSOR
REMARK   3    S11:   .0233 S12:  -.3041 S13:  -.0323
REMARK   3    S21:   .3375 S22:   .0236 S23:   .0121
REMARK   3    S31:   .0592 S32:  -.2979 S33:  -.0469
REMARK   3
REMARK   3  TLS GROUP :    5
REMARK   3  NUMBER OF COMPONENTS GROUP :    1
```

REMARK 3 COMPONENTS C SSSEQI TO C SSSEQI
REMARK 3 RESIDUE RANGE : B 17 B 219
REMARK 3 ORIGIN FOR THE GROUP (A): -73.9834 -39.9016 -18.5783
REMARK 3 T TENSOR
REMARK 3 T11: .0658 T22: .1153
REMARK 3 T33: .1251 T12: -.0621
REMARK 3 T13: -.0164 T23: -.0098
REMARK 3 L TENSOR
REMARK 3 L11: 4.6230 L22: 1.7260
REMARK 3 L33: 3.8816 L12: -.4202
REMARK 3 L13: -1.8646 L23: -.9046
REMARK 3 S TENSOR
REMARK 3 S11: -.0685 S12: .0375 S13: -.0003
REMARK 3 S21: .1931 S22: .0510 S23: -.0097
REMARK 3 S31: .0317 S32: -.2047 S33: .0175
REMARK 3
REMARK 3 TLS GROUP : 6
REMARK 3 NUMBER OF COMPONENTS GROUP : 1
REMARK 3 COMPONENTS C SSSEQI TO C SSSEQI
REMARK 3 RESIDUE RANGE : B 220 B 287
REMARK 3 ORIGIN FOR THE GROUP (A): -62.1586 -12.7634 -18.1912
REMARK 3 T TENSOR
REMARK 3 T11: .1825 T22: .0804
REMARK 3 T33: .1512 T12: .0549
REMARK 3 T13: .0773 T23: .0208
REMARK 3 L TENSOR
REMARK 3 L11: 5.4421 L22: 4.0606
REMARK 3 L33: 1.5369 L12: 4.6706
REMARK 3 L13: -2.0058 L23: -1.5537
REMARK 3 S TENSOR
REMARK 3 S11: .1622 S12: .0431 S13: .3257
REMARK 3 S21: .1755 S22: .0292 S23: .2977
REMARK 3 S31: -.1910 S32: -.0506 S33: -.1914
REMARK 3
REMARK 3 TLS GROUP : 7
REMARK 3 NUMBER OF COMPONENTS GROUP : 1
REMARK 3 COMPONENTS C SSSEQI TO C SSSEQI
REMARK 3 RESIDUE RANGE : B 288 B 374
REMARK 3 ORIGIN FOR THE GROUP (A): -41.6930 -10.8250 -19.6636
REMARK 3 T TENSOR
REMARK 3 T11: .1424 T22: .0604
REMARK 3 T33: .1153 T12: .0184
REMARK 3 T13: .0146 T23: .0276
REMARK 3 L TENSOR
REMARK 3 L11: .6426 L22: .8163
REMARK 3 L33: 2.3437 L12: -.1831
REMARK 3 L13: -.5246 L23: .4917
REMARK 3 S TENSOR
REMARK 3 S11: .0592 S12: -.0206 S13: .0071
REMARK 3 S21: .0906 S22: -.0229 S23: -.1585
REMARK 3 S31: -.0355 S32: .0262 S33: -.0363
REMARK 3
REMARK 3 TLS GROUP : 8
REMARK 3 NUMBER OF COMPONENTS GROUP : 1
REMARK 3 COMPONENTS C SSSEQI TO C SSSEQI
REMARK 3 RESIDUE RANGE : B 375 B 541
REMARK 3 ORIGIN FOR THE GROUP (A): -53.4886 -28.3212 -26.0670
REMARK 3 T TENSOR
REMARK 3 T11: .1107 T22: .1220
REMARK 3 T33: .1514 T12: .0692

```
REMARK   3    T13:  -.0073 T23:   .0518
REMARK   3   L TENSOR
REMARK   3    L11:  2.6766 L22:  1.8433
REMARK   3    L33:  2.6389 L12:   .1130
REMARK   3    L13: -2.4696 L23:   .6986
REMARK   3   S TENSOR
REMARK   3    S11:   .1115 S12:   .3882 S13:   .0569
REMARK   3    S21:  -.0725 S22:  -.0724 S23:   .1450
REMARK   3    S31:  -.1453 S32:  -.4044 S33:  -.0392
REMARK   3
REMARK   3
REMARK   3  BULK SOLVENT MODELLING.
REMARK   3   METHOD USED :  MASK
REMARK   3   PARAMETERS FOR MASK CALCULATION
REMARK   3   VDW PROBE RADIUS   :  1.40
REMARK   3   ION PROBE RADIUS   :   .80
REMARK   3   SHRINKAGE RADIUS   :   .80
REMARK   3
REMARK   3  OTHER REFINEMENT REMARKS:
REMARK   3  HYDROGENS HAVE BEEN ADDED IN THE RIDING POSITIONS
REMARK   3  U VALUES      : RESIDUAL ONLY
REMARK   3
CISPEP   1 ALA A  446    ARG A  447               .00
CISPEP   2 GLY A  515    ASP A  516               .00
CISPEP   3 THR B   22    ASP B   23              .00
CISPEP   4 ALA B  446    ARG B  447               .00
CISPEP   5 GLY B  515    ASP B  516               .00
CRYST1  155.800  155.800  143.690  90.00  90.00  90.00 P 43 21 2
SCALE1      .006418  .000000  .000000        .00000
SCALE2      .000000  .006418  .000000        .00000
SCALE3      .000000  .000000  .006959        .00000
ATOM      1  N   LEU A  17    -63.930  24.416 -19.202  1.00 30.90           N
ATOM      2  CA  LEU A  17    -64.132  23.019 -19.731  1.00 31.43           C
ATOM      4  CB  LEU A  17    -63.308  22.800 -21.021  1.00 31.35           C
ATOM      7  CG  LEU A  17    -64.002  23.016 -22.386  1.00 31.95           C
ATOM      9  CD1 LEU A  17    -62.989  23.068 -23.550  1.00 31.88           C
ATOM     13  CD2 LEU A  17    -65.052  21.915 -22.676  1.00 31.95           C
ATOM     17  C   LEU A  17    -63.783  21.952 -18.660  1.00 31.39           C
ATOM     18  O   LEU A  17    -63.142  22.291 -17.651  1.00 31.61           O
ATOM     22  N   LEU A  18    -64.216  20.693 -18.877  1.00 31.11           N
ATOM     23  CA  LEU A  18    -63.986  19.529 -17.957  1.00 30.78           C
ATOM     25  CB  LEU A  18    -62.503  19.072 -17.935  1.00 30.97           C
ATOM     28  CG  LEU A  18    -61.303  19.949 -17.496  1.00 31.10           C
ATOM     30  CD1 LEU A  18    -61.406  20.430 -16.064  1.00 30.71           C
ATOM     34  CD2 LEU A  18    -59.977  19.173 -17.703  1.00 31.87           C
ATOM     38  C   LEU A  18    -64.531  19.665 -16.522  1.00 30.38           C
ATOM     39  O   LEU A  18    -64.837  18.667 -15.883  1.00 29.86           O
ATOM     41  N   SER A  19    -64.587  20.900 -16.023  1.00 30.45           N
ATOM     42  CA  SER A  19    -65.335  21.276 -14.815  1.00 30.37           C
ATOM     44  CB  SER A  19    -64.604  22.417 -14.026  1.00 30.02           C
ATOM     47  OG  SER A  19    -64.881  23.741 -14.489  1.00 28.00           O
ATOM     49  C   SER A  19    -66.784  21.654 -15.218  1.00 31.03           C
ATOM     50  O   SER A  19    -67.666  21.711 -14.367  1.00 30.95           O
ATOM     52  N   SER A  20    -67.023  21.880 -16.519  1.00 31.85           N
ATOM     53  CA  SER A  20    -68.355  22.247 -17.051  1.00 32.37           C
ATOM     55  CB  SER A  20    -68.291  22.507 -18.579  1.00 32.39           C
ATOM     58  OG  SER A  20    -67.387  23.542 -18.931  1.00 31.77           O
ATOM     60  C   SER A  20    -69.357  21.124 -16.744  1.00 33.04           C
ATOM     61  O   SER A  20    -69.076  20.254 -15.922  1.00 33.08           O
ATOM     63  N   ASP A  21    -70.522  21.136 -17.393  1.00 33.88           N
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ATOM   64  CA  ASP A  21    -71.512  20.069 -17.206  1.00 34.48      C
ATOM   66  CB  ASP A  21    -72.907  20.655 -17.127  1.00 34.59      C
ATOM   69  CG  ASP A  21    -73.022  21.661 -16.006  1.00 35.54      C
ATOM   70  OD1 ASP A  21    -72.041  21.836 -15.251  1.00 35.31      O
ATOM   71  OD2 ASP A  21    -74.082  22.289 -15.870  1.00 38.72      O
ATOM   72  C   ASP A  21    -71.409  18.975 -18.260  1.00 34.94      C
ATOM   73  O   ASP A  21    -72.134  18.947 -19.269  1.00 34.58      O
ATOM   75  N   THR A  22    -70.457  18.086 -17.989  1.00 35.66      N
ATOM   76  CA  THR A  22    -70.340  16.799 -18.657  1.00 36.27      C
ATOM   78  CB  THR A  22    -68.895  16.576 -19.168  1.00 36.30      C
ATOM   80  OG1 THR A  22    -67.968  17.278 -18.322  1.00 36.04      O
ATOM   82  CG2 THR A  22    -68.755  17.088 -20.604  1.00 36.11      C
ATOM   86  C   THR A  22    -70.792  15.714 -17.648  1.00 36.83      C
ATOM   87  O   THR A  22    -69.968  15.022 -17.035  1.00 37.05      O
ATOM   89  N   ASP A  23    -72.121  15.599 -17.494  1.00 37.27      N
ATOM   90  CA  ASP A  23    -72.790  14.802 -16.441  1.00 37.25      C
ATOM   92  CB  ASP A  23    -72.962  15.659 -15.167  1.00 37.17      C
ATOM   95  CG  ASP A  23    -71.625  16.081 -14.549  1.00 37.74      C
ATOM   96  OD1 ASP A  23    -70.714  15.241 -14.436  1.00 38.88      O
ATOM   97  OD2 ASP A  23    -71.472  17.256 -14.164  1.00 38.91      O
ATOM   98  C   ASP A  23    -74.172  14.351 -16.956  1.00 37.18      C
ATOM   99  O   ASP A  23    -75.137  15.112 -16.846  1.00 37.10      O
ATOM   101 N   GLU A  24    -74.280  13.134 -17.501  1.00 37.23      N
ATOM   102 CA  GLU A  24    -75.406  12.815 -18.410  1.00 37.58      C
ATOM   104 CB  GLU A  24    -74.941  13.007 -19.865  1.00 37.77      C
ATOM   107 CG  GLU A  24    -74.424  14.417 -20.239  1.00 37.98      C
ATOM   110 CD  GLU A  24    -74.121  14.556 -21.746  1.00 38.35      C
ATOM   111 OE1 GLU A  24    -74.284  13.564 -22.503  1.00 38.12      O
ATOM   112 OE2 GLU A  24    -73.721  15.661 -22.174  1.00 38.18      O
ATOM   113 C   GLU A  24    -76.139  11.440 -18.323  1.00 37.79      C
ATOM   114 O   GLU A  24    -77.323  11.397 -17.960  1.00 37.90      O
ATOM   116 N   SER A  25    -75.462  10.345 -18.696  1.00 37.92      N
ATOM   117 CA  SER A  25    -76.140   9.070 -19.048  1.00 38.09      C
ATOM   119 CB  SER A  25    -75.167   8.076 -19.723  1.00 38.11      C
ATOM   122 OG  SER A  25    -74.503   7.239 -18.787  1.00 38.02      O
ATOM   124 C   SER A  25    -76.917   8.374 -17.907  1.00 38.42      C
ATOM   125 O   SER A  25    -76.635   8.581 -16.724  1.00 38.15      O
ATOM   127 N   ILE A  26    -77.861   7.511 -18.312  1.00 39.00      N
ATOM   128 CA  ILE A  26    -78.993   7.042 -17.476  1.00 39.30      C
ATOM   130 CB  ILE A  26    -78.594   5.965 -16.429  1.00 39.34      C
ATOM   132 CG1 ILE A  26    -77.892   4.791 -17.120  1.00 39.37      C
ATOM   135 CD1 ILE A  26    -77.766   3.531 -16.253  1.00 39.46      C
ATOM   139 CG2 ILE A  26    -79.836   5.423 -15.714  1.00 39.29      C
ATOM   143 C   ILE A  26    -79.716   8.260 -16.852  1.00 39.66      C
ATOM   144 O   ILE A  26    -79.274   8.831 -15.838  1.00 39.49      O
ATOM   146 N   GLU A  27    -80.837   8.623 -17.486  1.00 39.99      N
ATOM   147 CA  GLU A  27    -81.450   9.965 -17.383  1.00 40.11      C
ATOM   149 CB  GLU A  27    -82.395  10.183 -18.587  1.00 40.19      C
ATOM   152 CG  GLU A  27    -81.632  10.311 -19.904  1.00 40.60      C
ATOM   155 CD  GLU A  27    -82.528  10.434 -21.116  1.00 41.06      C
ATOM   156 OE1 GLU A  27    -83.328   9.502 -21.367  1.00 41.10      O
ATOM   157 OE2 GLU A  27    -82.409  11.458 -21.830  1.00 41.36      O
ATOM   158 C   GLU A  27    -82.144  10.264 -16.042  1.00 40.02      C
ATOM   159 O   GLU A  27    -81.977   9.518 -15.071  1.00 40.01      O
ATOM   161 N   VAL A  28    -82.899  11.370 -16.005  1.00 39.84      N
ATOM   162 CA  VAL A  28    -83.463  11.960 -14.779  1.00 39.65      C
ATOM   164 CB  VAL A  28    -83.884  10.905 -13.694  1.00 39.78      C
ATOM   166 CG1 VAL A  28    -84.472  11.596 -12.456  1.00 39.87      C
ATOM   170 CG2 VAL A  28    -84.887   9.880 -14.274  1.00 39.49      C
ATOM   174 C   VAL A  28    -82.469  12.980 -14.206  1.00 39.46      C
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ATOM 175 O VAL A 28 -82.798 13.717 -13.270 1.00 39.38 O
ATOM 177 N HIS A 29 -81.264 13.025 -14.786 1.00 39.30 N
ATOM 178 CA HIS A 29 -80.236 14.006 -14.412 1.00 39.23 C
ATOM 180 CB HIS A 29 -78.866 13.344 -14.186 1.00 39.45 C
ATOM 183 CG HIS A 29 -78.910 12.139 -13.296 1.00 41.29 C
ATOM 184 ND1 HIS A 29 -78.407 12.140 -12.007 1.00 42.51 N
ATOM 186 CE1 HIS A 29 -78.585 10.942 -11.472 1.00 43.37 C
ATOM 188 NE2 HIS A 29 -79.181 10.164 -12.365 1.00 43.18 N
ATOM 190 CD2 HIS A 29 -79.393 10.888 -13.515 1.00 42.55 C
ATOM 192 C HIS A 29 -80.090 15.110 -15.464 1.00 38.60 C
ATOM 193 O HIS A 29 -79.049 15.774 -15.499 1.00 38.61 O
ATOM 195 N LYS A 30 -81.110 15.320 -16.311 1.00 37.87 N
ATOM 196 CA LYS A 30 -81.265 16.610 -17.001 1.00 37.22 C
ATOM 198 CB LYS A 30 -82.283 16.542 -18.140 1.00 37.09 C
ATOM 201 CG LYS A 30 -81.764 15.794 -19.360 1.00 37.00 C
ATOM 204 CD LYS A 30 -82.831 15.653 -20.457 1.00 36.89 C
ATOM 207 CE LYS A 30 -82.413 14.637 -21.531 1.00 36.48 C
ATOM 210 NZ LYS A 30 -83.422 14.458 -22.611 1.00 35.46 N
ATOM 214 C LYS A 30 -81.648 17.649 -15.938 1.00 36.88 C
ATOM 215 O LYS A 30 -82.516 18.499 -16.136 1.00 36.71 O
ATOM 217 N ASP A 31 -80.982 17.506 -14.788 1.00 36.58 N
ATOM 218 CA ASP A 31 -80.895 18.476 -13.720 1.00 36.18 C
ATOM 220 CB ASP A 31 -80.518 17.751 -12.396 1.00 36.20 C
ATOM 223 CG ASP A 31 -79.863 18.669 -11.342 1.00 36.65 C
ATOM 224 OD1 ASP A 31 -80.055 19.901 -11.390 1.00 38.17 O
ATOM 225 OD2 ASP A 31 -79.147 18.150 -10.449 1.00 35.46 O
ATOM 226 C ASP A 31 -79.811 19.426 -14.226 1.00 35.74 C
ATOM 227 O ASP A 31 -78.628 19.279 -13.918 1.00 35.44 O
ATOM 229 N LYS A 32 -80.220 20.343 -15.096 1.00 35.30 N
ATOM 230 CA LYS A 32 -79.360 21.449 -15.507 1.00 34.69 C
ATOM 232 CB LYS A 32 -78.698 21.188 -16.849 1.00 34.63 C
ATOM 235 CG LYS A 32 -77.699 20.042 -16.765 1.00 34.51 C
ATOM 238 CD LYS A 32 -76.953 19.853 -18.078 1.00 34.48 C
ATOM 241 CE LYS A 32 -76.859 18.387 -18.503 1.00 33.77 C
ATOM 244 NZ LYS A 32 -77.002 18.244 -19.985 1.00 32.92 N
ATOM 248 C LYS A 32 -80.162 22.745 -15.459 1.00 34.01 C
ATOM 249 O LYS A 32 -80.468 23.380 -16.473 1.00 33.41 O
ATOM 251 N ALA A 33 -80.540 23.051 -14.219 1.00 33.21 N
ATOM 252 CA ALA A 33 -80.785 24.381 -13.766 1.00 32.60 C
ATOM 254 CB ALA A 33 -81.619 24.347 -12.484 1.00 32.28 C
ATOM 258 C ALA A 33 -79.411 25.031 -13.524 1.00 32.31 C
ATOM 259 O ALA A 33 -79.335 26.081 -12.901 1.00 32.80 O
ATOM 261 N LYS A 34 -78.323 24.389 -13.968 1.00 31.70 N
ATOM 262 CA LYS A 34 -77.035 25.071 -14.186 1.00 31.12 C
ATOM 264 CB LYS A 34 -75.863 24.089 -14.128 1.00 31.23 C
ATOM 267 CG LYS A 34 -75.118 24.077 -12.791 1.00 31.76 C
ATOM 270 CD LYS A 34 -73.584 24.412 -12.921 1.00 31.49 C
ATOM 273 CE LYS A 34 -72.685 23.269 -12.506 1.00 30.50 C
ATOM 276 NZ LYS A 34 -72.951 22.090 -13.348 1.00 29.53 N
ATOM 280 C LYS A 34 -77.024 25.884 -15.518 1.00 30.50 C
ATOM 281 O LYS A 34 -76.977 25.353 -16.625 1.00 29.82 O
ATOM 283 N LYS A 35 -76.927 27.191 -15.337 1.00 29.97 N
ATOM 284 CA LYS A 35 -77.632 28.233 -16.098 1.00 29.41 C
ATOM 286 CB LYS A 35 -78.852 27.704 -16.867 1.00 29.53 C
ATOM 289 CG LYS A 35 -80.166 27.594 -16.077 1.00 30.18 C
ATOM 292 CD LYS A 35 -81.030 28.858 -16.203 1.00 31.25 C
ATOM 295 CE LYS A 35 -82.375 28.721 -15.486 1.00 31.85 C
ATOM 298 NZ LYS A 35 -83.298 29.865 -15.783 1.00 31.73 N
ATOM 302 C LYS A 35 -78.053 29.277 -15.026 1.00 28.53 C
ATOM 303 O LYS A 35 -78.246 30.460 -15.307 1.00 28.53 O

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ATOM   305  N   LEU A  36    -78.225  28.791 -13.796  1.00 27.29           N
ATOM   306  CA  LEU A  36    -77.998  29.576 -12.594  1.00 26.21           C
ATOM   308  CB  LEU A  36    -78.088  28.679 -11.364  1.00 25.76           C
ATOM   311  CG  LEU A  36    -79.468  28.350 -10.832  1.00 24.08           C
ATOM   313  CD1 LEU A  36    -79.376  27.233  -9.836  1.00 22.16           C
ATOM   317  CD2 LEU A  36    -80.051  29.586 -10.213  1.00 23.45           C
ATOM   321  C   LEU A  36    -76.587  30.137 -12.665  1.00 25.93           C
ATOM   322  O   LEU A  36    -76.290  31.221 -12.137  1.00 26.11           O
ATOM   324  N   GLU A  37    -75.714  29.332 -13.260  1.00 25.24           N
ATOM   325  CA  GLU A  37    -74.381  29.739 -13.650  1.00 24.85           C
ATOM   327  CB  GLU A  37    -73.678  28.566 -14.313  1.00 24.74           C
ATOM   330  CG  GLU A  37    -72.182  28.667 -14.285  1.00 23.93           C
ATOM   333  CD  GLU A  37    -71.519  27.490 -14.937  1.00 22.32           C
ATOM   334  OE1 GLU A  37    -72.203  26.738 -15.657  1.00 20.57           O
ATOM   335  OE2 GLU A  37    -70.303  27.322 -14.728  1.00 22.27           O
ATOM   336  C   GLU A  37    -74.391  30.927 -14.600  1.00 24.69           C
ATOM   337  O   GLU A  37    -73.666  31.891 -14.389  1.00 24.49           O
ATOM   339  N   ALA A  38    -75.203  30.850 -15.650  1.00 24.68           N
ATOM   340  CA  ALA A  38    -75.352  31.960 -16.599  1.00 24.87           C
ATOM   342  CB  ALA A  38    -76.453  31.656 -17.609  1.00 24.53           C
ATOM   346  C   ALA A  38    -75.643  33.278 -15.880  1.00 25.08           C
ATOM   347  O   ALA A  38    -75.009  34.295 -16.135  1.00 25.21           O
ATOM   349  N   GLU A  39    -76.591  33.228 -14.956  1.00 25.35           N
ATOM   350  CA  GLU A  39    -77.050  34.400 -14.219  1.00 25.51           C
ATOM   352  CB  GLU A  39    -78.283  34.014 -13.396  1.00 25.95           C
ATOM   355  CG  GLU A  39    -79.302  35.119 -13.136  1.00 27.03           C
ATOM   358  CD  GLU A  39    -80.715  34.557 -12.906  1.00 28.70           C
ATOM   359  OE1 GLU A  39    -81.006  33.416 -13.346  1.00 27.40           O
ATOM   360  OE2 GLU A  39    -81.540  35.266 -12.289  1.00 31.12           O
ATOM   361  C   GLU A  39    -75.970  34.966 -13.306  1.00 25.11           C
ATOM   362  O   GLU A  39    -75.870  36.167 -13.164  1.00 25.28           O
ATOM   364  N   VAL A  40    -75.182  34.107 -12.672  1.00 24.86           N
ATOM   365  CA  VAL A  40    -74.079  34.568 -11.824  1.00 24.69           C
ATOM   367  CB  VAL A  40    -73.511  33.420 -10.952  1.00 24.56           C
ATOM   369  CG1 VAL A  40    -72.239  33.857 -10.240  1.00 23.69           C
ATOM   373  CG2 VAL A  40    -74.553  32.955  -9.955  1.00 24.68           C
ATOM   377  C   VAL A  40    -72.971  35.148 -12.698  1.00 24.76           C
ATOM   378  O   VAL A  40    -72.337  36.139 -12.362  1.00 24.16           O
ATOM   380  N   ARG A  41    -72.744  34.506 -13.831  1.00 25.25           N
ATOM   381  CA  ARG A  41    -71.727  34.948 -14.769  1.00 25.66           C
ATOM   383  CB  ARG A  41    -71.576  33.927 -15.896  1.00 25.88           C
ATOM   386  CG  ARG A  41    -70.726  34.385 -17.062  1.00 27.04           C
ATOM   389  CD  ARG A  41    -71.519  35.178 -18.095  1.00 27.90           C
ATOM   392  NE  ARG A  41    -70.653  35.635 -19.180  1.00 29.20           N
ATOM   394  CZ  ARG A  41    -70.946  36.615 -20.034  1.00 29.94           C
ATOM   395  NH1 ARG A  41    -70.077  36.945 -20.980  1.00 29.86           N
ATOM   398  NH2 ARG A  41    -72.096  37.273 -19.957  1.00 30.54           N
ATOM   401  C   ARG A  41    -72.104  36.301 -15.335  1.00 25.60           C
ATOM   402  O   ARG A  41    -71.237  37.113 -15.612  1.00 25.77           O
ATOM   404  N   ARG A  42    -73.400  36.521 -15.537  1.00 25.50           N
ATOM   405  CA  ARG A  42    -73.900  37.810 -15.979  1.00 25.39           C
ATOM   407  CB  ARG A  42    -75.389  37.723 -16.313  1.00 25.09           C
ATOM   410  CG  ARG A  42    -76.077  39.062 -16.445  1.00 23.84           C
ATOM   413  CD  ARG A  42    -77.459  38.906 -16.980  1.00 22.37           C
ATOM   416  NE  ARG A  42    -78.448  38.554 -15.965  1.00 21.69           N
ATOM   418  CZ  ARG A  42    -79.705  38.206 -16.248  1.00 22.99           C
ATOM   419  NH1 ARG A  42    -80.122  38.146 -17.517  1.00 24.16           N
ATOM   422  NH2 ARG A  42    -80.557  37.900 -15.275  1.00 22.94           N
ATOM   425  C   ARG A  42    -73.666  38.889 -14.925  1.00 26.00           C
ATOM   426  O   ARG A  42    -73.173  39.959 -15.244  1.00 26.17           O
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ATOM   428  N   GLU A  43    -74.014  38.621 -13.673  1.00 26.66      N
ATOM   429  CA  GLU A  43    -73.930  39.662 -12.650  1.00 27.47      C
ATOM   431  CB  GLU A  43    -74.749  39.304 -11.401  1.00 27.97      C
ATOM   434  CG  GLU A  43    -76.274  39.266 -11.661  1.00 31.05      C
ATOM   437  CD  GLU A  43    -76.869  40.636 -12.063  1.00 34.68      C
ATOM   438  OE1 GLU A  43    -76.804  41.571 -11.222  1.00 37.63      O
ATOM   439  OE2 GLU A  43    -77.398  40.773 -13.205  1.00 34.52      O
ATOM   440  C   GLU A  43    -72.494  40.035 -12.275  1.00 27.15      C
ATOM   441  O   GLU A  43    -72.292  41.118 -11.716  1.00 27.49      O
ATOM   443  N   ILE A  44    -71.517  39.166 -12.588  1.00 26.57      N
ATOM   444  CA  ILE A  44    -70.090  39.456 -12.334  1.00 25.80      C
ATOM   446  CB  ILE A  44    -69.206  38.187 -12.187  1.00 25.52      C
ATOM   448  CG1 ILE A  44    -69.624  37.320 -11.010  1.00 24.69      C
ATOM   451  CD1 ILE A  44    -68.828  36.061 -10.899  1.00 23.08      C
ATOM   455  CG2 ILE A  44    -67.790  38.581 -11.916  1.00 25.73      C
ATOM   459  C   ILE A  44    -69.522  40.286 -13.472  1.00 25.40      C
ATOM   460  O   ILE A  44    -68.745  41.211 -13.236  1.00 25.26      O
ATOM   462  N   ASN A  45    -69.912  39.945 -14.700  1.00 25.14      N
ATOM   463  CA  ASN A  45    -69.480  40.669 -15.906  1.00 25.02      C
ATOM   465  CB  ASN A  45    -69.696  39.813 -17.151  1.00 24.69      C
ATOM   468  CG  ASN A  45    -68.662  38.735 -17.302  1.00 24.01      C
ATOM   469  OD1 ASN A  45    -67.470  39.013 -17.395  1.00 23.81      O
ATOM   470  ND2 ASN A  45    -69.111  37.490 -17.344  1.00 23.28      N
ATOM   473  C   ASN A  45    -70.177  42.014 -16.114  1.00 25.52      C
ATOM   474  O   ASN A  45    -69.704  42.836 -16.890  1.00 25.40      O
ATOM   476  N   ASN A  46    -71.308  42.210 -15.437  1.00 26.33      N
ATOM   477  CA  ASN A  46    -72.085  43.453 -15.468  1.00 26.72      C
ATOM   479  CB  ASN A  46    -73.102  43.404 -14.322  1.00 26.31      C
ATOM   482  CG  ASN A  46    -73.935  44.641 -14.209  1.00 24.24      C
ATOM   483  OD1 ASN A  46    -73.948  45.472 -15.091  1.00 22.38      O
ATOM   484  ND2 ASN A  46    -74.645  44.766 -13.106  1.00 21.64      N
ATOM   487  C   ASN A  46    -71.185  44.680 -15.349  1.00 28.11      C
ATOM   488  O   ASN A  46    -70.603  44.933 -14.304  1.00 28.16      O
ATOM   490  N   GLU A  47    -71.084  45.441 -16.433  1.00 29.93      N
ATOM   491  CA  GLU A  47    -70.128  46.558 -16.544  1.00 31.30      C
ATOM   493  CB  GLU A  47    -69.933  46.969 -18.013  1.00 31.28      C
ATOM   496  CG  GLU A  47    -69.737  45.795 -19.020  1.00 32.37      C
ATOM   499  CD  GLU A  47    -71.060  45.127 -19.545  1.00 32.69      C
ATOM   500  OE1 GLU A  47    -72.055  45.833 -19.816  1.00 32.16      O
ATOM   501  OE2 GLU A  47    -71.087  43.880 -19.699  1.00 32.41      O
ATOM   502  C   GLU A  47    -70.582  47.774 -15.729  1.00 32.47      C
ATOM   503  O   GLU A  47    -69.760  48.525 -15.230  1.00 32.86      O
ATOM   505  N   LYS A  48    -71.898  47.945 -15.585  1.00 33.93      N
ATOM   506  CA  LYS A  48    -72.491  49.075 -14.861  1.00 34.85      C
ATOM   508  CB  LYS A  48    -73.660  49.672 -15.684  1.00 35.08      C
ATOM   511  CG  LYS A  48    -73.221  50.119 -17.126  1.00 36.58      C
ATOM   514  CD  LYS A  48    -74.035  51.277 -17.751  1.00 37.93      C
ATOM   517  CE  LYS A  48    -75.353  50.799 -18.415  1.00 39.02      C
ATOM   520  NZ  LYS A  48    -75.159  49.990 -19.669  1.00 39.11      N
ATOM   524  C   LYS A  48    -72.926  48.632 -13.465  1.00 35.26      C
ATOM   525  O   LYS A  48    -74.011  48.954 -13.015  1.00 35.04      O
ATOM   527  N   ALA A  49    -72.051  47.890 -12.790  1.00 36.29      N
ATOM   528  CA  ALA A  49    -72.321  47.348 -11.456  1.00 37.18      C
ATOM   530  CB  ALA A  49    -71.828  45.923 -11.353  1.00 37.20      C
ATOM   534  C   ALA A  49    -71.618  48.191 -10.418  1.00 37.88      C
ATOM   535  O   ALA A  49    -70.480  48.610 -10.638  1.00 38.17      O
ATOM   537  N   GLU A  50    -72.278  48.404  -9.280  1.00 38.53      N
ATOM   538  CA  GLU A  50    -71.730  49.242  -8.213  1.00 39.08      C
ATOM   540  CB  GLU A  50    -72.790  49.545  -7.146  1.00 39.43      C
ATOM   543  CG  GLU A  50    -72.708  50.953  -6.600  1.00 40.86      C
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ATOM   546 CD  GLU A  50    -73.089  52.010  -7.639  1.00 42.77      C
ATOM   547 OE1 GLU A  50    -74.225  52.530  -7.570  1.00 45.07      O
ATOM   548 OE2 GLU A  50    -72.265  52.320  -8.530  1.00 43.35      O
ATOM   549 C   GLU A  50    -70.560  48.521  -7.600  1.00 38.89      C
ATOM   550 O   GLU A  50    -70.699  47.378  -7.201  1.00 39.05      O
ATOM   552 N   PHE A  51    -69.411  49.181  -7.536  1.00 38.99      N
ATOM   553 CA  PHE A  51    -68.161  48.502  -7.196  1.00 39.52      C
ATOM   555 CB  PHE A  51    -67.000  49.494  -7.098  1.00 40.05      C
ATOM   558 CG  PHE A  51    -66.460  49.948  -8.431  1.00 42.80      C
ATOM   559 CD1 PHE A  51    -66.135  49.014  -9.435  1.00 45.21      C
ATOM   561 CE1 PHE A  51    -65.612  49.425 -10.675  1.00 46.12      C
ATOM   563 CZ  PHE A  51    -65.403  50.790 -10.917  1.00 47.21      C
ATOM   565 CE2 PHE A  51    -65.726  51.741  -9.913  1.00 46.72      C
ATOM   567 CD2 PHE A  51    -66.247  51.310  -8.679  1.00 45.05      C
ATOM   569 C   PHE A  51    -68.223  47.687  -5.905  1.00 39.05      C
ATOM   570 O   PHE A  51    -67.897  46.506  -5.900  1.00 39.28      O
ATOM   572 N   LEU A  52    -68.648  48.307  -4.813  1.00 38.42      N
ATOM   573 CA  LEU A  52    -68.709  47.610  -3.528  1.00 37.94      C
ATOM   575 CB  LEU A  52    -69.084  48.594  -2.413  1.00 38.53      C
ATOM   578 CG  LEU A  52    -68.057  49.726  -2.181  1.00 40.46      C
ATOM   580 CD1 LEU A  52    -68.691  51.101  -1.787  1.00 41.88      C
ATOM   584 CD2 LEU A  52    -67.020  49.274  -1.141  1.00 41.83      C
ATOM   588 C   LEU A  52    -69.667  46.406  -3.532  1.00 36.72      C
ATOM   589 O   LEU A  52    -69.517  45.494  -2.724  1.00 36.84      O
ATOM   591 N   THR A  53    -70.649  46.398  -4.431  1.00 35.37      N
ATOM   592 CA  THR A  53    -71.545  45.247  -4.569  1.00 34.11      C
ATOM   594 CB  THR A  53    -72.867  45.594  -5.277  1.00 33.87      C
ATOM   596 OG1 THR A  53    -73.339  46.863  -4.828  1.00 33.49      O
ATOM   598 CG2 THR A  53    -73.917  44.535  -4.983  1.00 33.70      C
ATOM   602 C   THR A  53    -70.853  44.148  -5.359  1.00 33.04      C
ATOM   603 O   THR A  53    -70.893  42.977  -4.973  1.00 32.90      O
ATOM   605 N   LEU A  54    -70.228  44.528  -6.467  1.00 31.76      N
ATOM   606 CA  LEU A  54    -69.469  43.578  -7.286  1.00 31.13      C
ATOM   608 CB  LEU A  54    -68.721  44.308  -8.392  1.00 30.92      C
ATOM   611 CG  LEU A  54    -68.028  43.437  -9.424  1.00 30.27      C
ATOM   613 CD1 LEU A  54    -69.034  42.769 -10.310  1.00 29.56      C
ATOM   617 CD2 LEU A  54    -67.108  44.306 -10.242  1.00 31.15      C
ATOM   621 C   LEU A  54    -68.466  42.808  -6.443  1.00 30.60      C
ATOM   622 O   LEU A  54    -68.378  41.587  -6.543  1.00 30.30      O
ATOM   624 N   LEU A  55    -67.725  43.551  -5.618  1.00 30.09      N
ATOM   625 CA  LEU A  55    -66.730  43.000  -4.695  1.00 29.47      C
ATOM   627 CB  LEU A  55    -66.006  44.126  -3.944  1.00 29.44      C
ATOM   630 CG  LEU A  55    -65.069  45.017  -4.781  1.00 29.74      C
ATOM   632 CD1 LEU A  55    -64.609  46.255  -4.003  1.00 29.43      C
ATOM   636 CD2 LEU A  55    -63.859  44.234  -5.286  1.00 29.64      C
ATOM   640 C   LEU A  55    -67.340  42.024  -3.696  1.00 28.87      C
ATOM   641 O   LEU A  55    -66.746  40.991  -3.383  1.00 28.98      O
ATOM   643 N   GLU A  56    -68.525  42.330  -3.198  1.00 28.01      N
ATOM   644 CA  GLU A  56    -69.160  41.419  -2.256  1.00 27.64      C
ATOM   646 CB  GLU A  56    -70.172  42.173  -1.395  1.00 28.19      C
ATOM   649 CG  GLU A  56    -69.497  43.167   -.459  1.00 29.75      C
ATOM   652 CD  GLU A  56    -70.457  43.858    .478  1.00 33.04      C
ATOM   653 OE1 GLU A  56    -71.667  43.538    .481  1.00 34.46      O
ATOM   654 OE2 GLU A  56    -69.988  44.737   1.226  1.00 36.78      O
ATOM   655 C   GLU A  56    -69.776  40.200  -2.945  1.00 26.37      C
ATOM   656 O   GLU A  56    -69.914  39.146  -2.333  1.00 26.02      O
ATOM   658 N   LEU A  57    -70.134  40.347  -4.218  1.00 25.30      N
ATOM   659 CA  LEU A  57    -70.569  39.212  -5.036  1.00 24.17      C
ATOM   661 CB  LEU A  57    -71.125  39.680  -6.382  1.00 23.71      C
ATOM   664 CG  LEU A  57    -71.417  38.568  -7.390  1.00 22.27      C
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ATOM   666 CD1 LEU A  57    -72.515  37.675  -6.858  1.00 19.31      C
ATOM   670 CD2 LEU A  57    -71.752  39.167  -8.768  1.00 20.30      C
ATOM   674 C   LEU A  57    -69.404  38.267  -5.284  1.00 23.69      C
ATOM   675 O   LEU A  57    -69.547  37.051  -5.136  1.00 23.83      O
ATOM   677 N   ILE A  58    -68.261  38.822  -5.682  1.00 22.82      N
ATOM   678 CA  ILE A  58    -67.070  38.019  -5.925  1.00 22.39      C
ATOM   680 CB  ILE A  58    -65.884  38.899  -6.355  1.00 22.21      C
ATOM   682 CG1 ILE A  58    -66.088  39.386  -7.792  1.00 21.83      C
ATOM   685 CD1 ILE A  58    -65.002  40.314  -8.320  1.00 20.43      C
ATOM   689 CG2 ILE A  58    -64.565  38.131  -6.245  1.00 22.64      C
ATOM   693 C   ILE A  58    -66.719  37.227  -4.662  1.00 22.35      C
ATOM   694 O   ILE A  58    -66.520  36.002  -4.706  1.00 21.95      O
ATOM   696 N   ASP A  59    -66.676  37.951  -3.543  1.00 22.32      N
ATOM   697 CA  ASP A  59    -66.396  37.396  -2.215  1.00 22.26      C
ATOM   699 CB  ASP A  59    -66.570  38.500  -1.171  1.00 22.67      C
ATOM   702 CG  ASP A  59    -66.126  38.092   .213  1.00 23.91      C
ATOM   703 OD1 ASP A  59    -65.271  37.182   .338  1.00 23.77      O
ATOM   704 OD2 ASP A  59    -66.641  38.718  1.178  1.00 27.12      O
ATOM   705 C   ASP A  59    -67.304  36.216  -1.901  1.00 21.79      C
ATOM   706 O   ASP A  59    -66.828  35.102  -1.668  1.00 21.71      O
ATOM   708 N   ASN A  60    -68.610  36.466  -1.926  1.00 21.51      N
ATOM   709 CA  ASN A  60    -69.619  35.418  -1.759  1.00 21.28      C
ATOM   711 CB  ASN A  60    -71.012  36.006  -1.958  1.00 21.25      C
ATOM   714 CG  ASN A  60    -71.476  36.827  -.776  1.00 21.82      C
ATOM   715 OD1 ASN A  60    -71.067  36.598   .364  1.00 20.81      O
ATOM   716 ND2 ASN A  60    -72.361  37.783  -1.043  1.00 23.63      N
ATOM   719 C   ASN A  60    -69.445  34.240  -2.725  1.00 21.22      C
ATOM   720 O   ASN A  60    -69.444  33.053  -2.303  1.00 20.95      O
ATOM   722 N   VAL A  61    -69.308  34.566  -4.018  1.00 20.83      N
ATOM   723 CA  VAL A  61    -69.147  33.536  -5.043  1.00 20.57      C
ATOM   725 CB  VAL A  61    -68.915  34.122  -6.466  1.00 20.53      C
ATOM   727 CG1 VAL A  61    -68.382  33.042  -7.430  1.00 19.44      C
ATOM   731 CG2 VAL A  61    -70.190  34.758  -7.006  1.00 19.75      C
ATOM   735 C   VAL A  61    -67.981  32.646  -4.644  1.00 20.62      C
ATOM   736 O   VAL A  61    -68.080  31.431  -4.699  1.00 20.56      O
ATOM   738 N   GLN A  62    -66.888  33.255  -4.209  1.00 20.76      N
ATOM   739 CA  GLN A  62    -65.703  32.481  -3.898  1.00 21.18      C
ATOM   741 CB  GLN A  62    -64.461  33.379  -3.824  1.00 21.39      C
ATOM   744 CG  GLN A  62    -64.007  33.920  -5.165  1.00 21.64      C
ATOM   747 CD  GLN A  62    -62.608  34.512  -5.135  1.00 22.04      C
ATOM   748 OE1 GLN A  62    -61.890  34.483  -6.145  1.00 23.18      O
ATOM   749 NE2 GLN A  62    -62.217  35.062  -3.989  1.00 20.39      N
ATOM   752 C   GLN A  62    -65.891  31.681  -2.607  1.00 21.09      C
ATOM   753 O   GLN A  62    -65.544  30.485  -2.554  1.00 21.30      O
ATOM   755 N   ARG A  63    -66.448  32.325  -1.583  1.00 20.63      N
ATOM   756 CA  ARG A  63    -66.590  31.677  -.273  1.00 20.54      C
ATOM   758 CB  ARG A  63    -67.025  32.686   .786  1.00 20.57      C
ATOM   761 CG  ARG A  63    -66.031  33.823   .930  1.00 22.55      C
ATOM   764 CD  ARG A  63    -66.214  34.632  2.179  1.00 24.93      C
ATOM   767 NE  ARG A  63    -66.123  33.781  3.355  1.00 27.75      N
ATOM   769 CZ  ARG A  63    -66.496  34.151  4.573  1.00 30.24      C
ATOM   770 NH1 ARG A  63    -66.971  35.385  4.782  1.00 31.79      N
ATOM   773 NH2 ARG A  63    -66.399  33.285  5.581  1.00 30.07      N
ATOM   776 C   ARG A  63    -67.557  30.499  -.338  1.00 19.81      C
ATOM   777 O   ARG A  63    -67.283  29.431   .209  1.00 19.67      O
ATOM   779 N   LEU A  64    -68.661  30.684  -1.057  1.00 19.04      N
ATOM   780 CA  LEU A  64    -69.636  29.617  -1.246  1.00 18.44      C
ATOM   782 CB  LEU A  64    -70.865  30.167  -1.954  1.00 18.59      C
ATOM   785 CG  LEU A  64    -71.662  31.170  -1.140  1.00 18.32      C
ATOM   787 CD1 LEU A  64    -72.669  31.852  -2.034  1.00 18.10      C
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ATOM   791 CD2 LEU A 64    -72.334  30.444    .004  1.00 18.29      C
ATOM   795 C   LEU A 64    -69.089  28.436  -2.037  1.00 17.80      C
ATOM   796 O   LEU A 64    -69.802  27.453  -2.252  1.00 17.79      O
ATOM   798 N   GLY A 65    -67.850  28.573  -2.515  1.00 17.07      N
ATOM   799 CA  GLY A 65    -67.084  27.480  -3.081  1.00 16.27      C
ATOM   802 C   GLY A 65    -67.137  27.406  -4.588  1.00 15.77      C
ATOM   803 O   GLY A 65    -66.893  26.347  -5.154  1.00 15.78      O
ATOM   805 N   LEU A 66    -67.439  28.521  -5.246  1.00 15.24      N
ATOM   806 CA  LEU A 66    -67.621  28.537  -6.701  1.00 14.93      C
ATOM   808 CB  LEU A 66    -68.977  29.146  -7.021  1.00 14.84      C
ATOM   811 CG  LEU A 66    -70.204  28.334  -6.619  1.00 13.97      C
ATOM   813 CD1 LEU A 66    -71.391  29.260  -6.650  1.00 13.74      C
ATOM   817 CD2 LEU A 66    -70.415  27.125  -7.534  1.00 11.22      C
ATOM   821 C   LEU A 66    -66.533  29.314  -7.454  1.00 15.09      C
ATOM   822 O   LEU A 66    -66.621  29.497  -8.678  1.00 14.81      O
ATOM   824 N   GLY A 67    -65.510  29.758  -6.720  1.00 15.21      N
ATOM   825 CA  GLY A 67    -64.404  30.526  -7.280  1.00 14.98      C
ATOM   828 C   GLY A 67    -63.873  29.952  -8.569  1.00 14.60      C
ATOM   829 O   GLY A 67    -63.891  30.619  -9.579  1.00 14.63      O
ATOM   831 N   TYR A 68    -63.419  28.706  -8.523  1.00 14.57      N
ATOM   832 CA  TYR A 68    -62.831  28.029  -9.688  1.00 14.72      C
ATOM   834 CB  TYR A 68    -62.608  26.539  -9.372  1.00 14.73      C
ATOM   837 CG  TYR A 68    -63.858  25.689  -9.330  1.00 12.47      C
ATOM   838 CD1 TYR A 68    -64.163  24.826 -10.366  1.00 10.68      C
ATOM   840 CE1 TYR A 68    -65.310  24.043 -10.340  1.00 10.55      C
ATOM   842 CZ  TYR A 68    -66.163  24.119  -9.258  1.00 10.41      C
ATOM   843 OH  TYR A 68    -67.311  23.349  -9.212  1.00  6.97      O
ATOM   845 CE2 TYR A 68    -65.864  24.979  -8.210  1.00 11.44      C
ATOM   847 CD2 TYR A 68    -64.722  25.750  -8.252  1.00 11.29      C
ATOM   849 C   TYR A 68    -63.648  28.141 -10.980  1.00 15.31      C
ATOM   850 O   TYR A 68    -63.106  28.230 -12.083  1.00 15.01      O
ATOM   852 N   ARG A 69    -64.959  28.136 -10.816  1.00 16.03      N
ATOM   853 CA  ARG A 69    -65.884  28.083 -11.922  1.00 16.67      C
ATOM   855 CB  ARG A 69    -67.224  27.649 -11.348  1.00 16.58      C
ATOM   858 CG  ARG A 69    -68.332  27.445 -12.335  1.00 16.07      C
ATOM   861 CD  ARG A 69    -69.378  26.578 -11.701  1.00 14.26      C
ATOM   864 NE  ARG A 69    -68.915  25.205 -11.677  1.00 12.82      N
ATOM   866 CZ  ARG A 69    -69.063  24.346 -12.676  1.00 12.42      C
ATOM   867 NH1 ARG A 69    -69.676  24.694 -13.792  1.00 12.27      N
ATOM   870 NH2 ARG A 69    -68.601  23.119 -12.553  1.00 13.23      N
ATOM   873 C   ARG A 69    -66.010  29.409 -12.692  1.00 17.62      C
ATOM   874 O   ARG A 69    -66.281  29.401 -13.892  1.00 17.10      O
ATOM   876 N   PHE A 70    -65.811  30.529 -11.985  1.00 19.11      N
ATOM   877 CA  PHE A 70    -65.936  31.891 -12.530  1.00 19.96      C
ATOM   879 CB  PHE A 70    -67.024  32.666 -11.763  1.00 19.89      C
ATOM   882 CG  PHE A 70    -68.365  32.010 -11.784  1.00 18.68      C
ATOM   883 CD1 PHE A 70    -69.158  32.082 -12.903  1.00 18.05      C
ATOM   885 CE1 PHE A 70    -70.376  31.452 -12.938  1.00 18.03      C
ATOM   887 CZ  PHE A 70    -70.825  30.754 -11.851  1.00 17.26      C
ATOM   889 CE2 PHE A 70    -70.051  30.672 -10.736  1.00 17.60      C
ATOM   891 CD2 PHE A 70    -68.822  31.300 -10.700  1.00 17.86      C
ATOM   893 C   PHE A 70    -64.627  32.661 -12.400  1.00 21.34      C
ATOM   894 O   PHE A 70    -64.629  33.862 -12.171  1.00 21.25      O
ATOM   896 N   GLU A 71    -63.501  31.977 -12.541  1.00 23.19      N
ATOM   897 CA  GLU A 71    -62.211  32.591 -12.214  1.00 24.60      C
ATOM   899 CB  GLU A 71    -61.127  31.524 -12.073  1.00 25.03      C
ATOM   902 CG  GLU A 71    -59.717  32.059 -11.861  1.00 27.10      C
ATOM   905 CD  GLU A 71    -58.712  30.949 -11.549  1.00 30.10      C
ATOM   906 OE1 GLU A 71    -59.084  30.007 -10.796  1.00 32.05      O
ATOM   907 OE2 GLU A 71    -57.558  31.027 -12.051  1.00 30.50      O
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ATOM 908 C GLU A 71 -61.809 33.644 -13.241 1.00 25.23 C
ATOM 909 O GLU A 71 -61.362 34.717 -12.862 1.00 25.54 O
ATOM 911 N SER A 72 -61.979 33.345 -14.530 1.00 25.91 N
ATOM 912 CA SER A 72 -61.641 34.294 -15.588 1.00 26.37 C
ATOM 914 CB SER A 72 -61.656 33.606 -16.941 1.00 26.32 C
ATOM 917 OG SER A 72 -62.985 33.278 -17.291 1.00 27.28 O
ATOM 919 C SER A 72 -62.609 35.476 -15.608 1.00 26.84 C
ATOM 920 O SER A 72 -62.197 36.601 -15.852 1.00 27.02 O
ATOM 922 N ASP A 73 -63.893 35.214 -15.361 1.00 27.45 N
ATOM 923 CA ASP A 73 -64.895 36.277 -15.246 1.00 27.87 C
ATOM 925 CB ASP A 73 -66.289 35.705 -14.968 1.00 27.99 C
ATOM 928 CG ASP A 73 -66.842 34.913 -16.140 1.00 29.49 C
ATOM 929 OD1 ASP A 73 -67.215 35.530 -17.155 1.00 30.90 O
ATOM 930 OD2 ASP A 73 -66.916 33.667 -16.054 1.00 31.85 O
ATOM 931 C ASP A 73 -64.518 37.221 -14.121 1.00 27.86 C
ATOM 932 O ASP A 73 -64.598 38.435 -14.286 1.00 28.05 O
ATOM 934 N ILE A 74 -64.118 36.652 -12.985 1.00 27.88 N
ATOM 935 CA ILE A 74 -63.698 37.422 -11.821 1.00 27.98 C
ATOM 937 CB ILE A 74 -63.348 36.521 -10.637 1.00 27.71 C
ATOM 939 CG1 ILE A 74 -64.607 36.007 -9.960 1.00 27.60 C
ATOM 942 CD1 ILE A 74 -64.355 34.846 -9.023 1.00 27.67 C
ATOM 946 CG2 ILE A 74 -62.551 37.272 -9.621 1.00 26.82 C
ATOM 950 C ILE A 74 -62.472 38.252 -12.133 1.00 28.80 C
ATOM 951 O ILE A 74 -62.475 39.453 -11.917 1.00 29.00 O
ATOM 953 N ARG A 75 -61.415 37.616 -12.628 1.00 29.80 N
ATOM 954 CA ARG A 75 -60.197 38.341 -12.968 1.00 30.79 C
ATOM 956 CB ARG A 75 -59.286 37.507 -13.841 1.00 31.33 C
ATOM 959 CG ARG A 75 -58.506 36.441 -13.115 1.00 34.25 C
ATOM 962 CD ARG A 75 -57.286 36.009 -13.929 1.00 37.53 C
ATOM 965 NE ARG A 75 -56.238 37.019 -13.799 1.00 40.89 N
ATOM 967 CZ ARG A 75 -54.934 36.807 -13.967 1.00 44.24 C
ATOM 968 NH1 ARG A 75 -54.459 35.602 -14.294 1.00 45.02 N
ATOM 971 NH2 ARG A 75 -54.089 37.821 -13.796 1.00 45.88 N
ATOM 974 C ARG A 75 -60.548 39.596 -13.727 1.00 30.95 C
ATOM 975 O ARG A 75 -60.163 40.685 -13.336 1.00 31.27 O
ATOM 977 N ARG A 76 -61.293 39.435 -14.815 1.00 31.31 N
ATOM 978 CA ARG A 76 -61.712 40.567 -15.638 1.00 31.62 C
ATOM 980 CB ARG A 76 -62.593 40.106 -16.794 1.00 31.97 C
ATOM 983 CG ARG A 76 -61.833 39.392 -17.895 1.00 32.91 C
ATOM 986 CD ARG A 76 -62.615 39.453 -19.205 1.00 34.43 C
ATOM 989 NE ARG A 76 -63.925 38.803 -19.128 1.00 35.66 N
ATOM 991 CZ ARG A 76 -64.115 37.480 -19.106 1.00 37.15 C
ATOM 992 NH1 ARG A 76 -63.085 36.632 -19.129 1.00 37.93 N
ATOM 995 NH2 ARG A 76 -65.347 36.992 -19.048 1.00 37.64 N
ATOM 998 C ARG A 76 -62.453 41.629 -14.849 1.00 31.41 C
ATOM 999 O ARG A 76 -62.144 42.798 -14.966 1.00 31.35 O
ATOM 1001 N ALA A 77 -63.437 41.230 -14.058 1.00 31.53 N
ATOM 1002 CA ALA A 77 -64.136 42.177 -13.211 1.00 31.73 C
ATOM 1004 CB ALA A 77 -65.074 41.468 -12.275 1.00 31.69 C
ATOM 1008 C ALA A 77 -63.107 42.950 -12.423 1.00 32.23 C
ATOM 1009 O ALA A 77 -63.116 44.176 -12.411 1.00 32.42 O
ATOM 1011 N LEU A 78 -62.198 42.223 -11.786 1.00 32.95 N
ATOM 1012 CA LEU A 78 -61.168 42.838 -10.963 1.00 33.51 C
ATOM 1014 CB LEU A 78 -60.319 41.775 -10.265 1.00 33.10 C
ATOM 1017 CG LEU A 78 -60.959 41.077 -9.081 1.00 32.30 C
ATOM 1019 CD1 LEU A 78 -59.960 40.104 -8.472 1.00 30.80 C
ATOM 1023 CD2 LEU A 78 -61.438 42.117 -8.056 1.00 31.89 C
ATOM 1027 C LEU A 78 -60.249 43.752 -11.753 1.00 34.70 C
ATOM 1028 O LEU A 78 -59.790 44.753 -11.214 1.00 35.18 O
ATOM 1030 N ASP A 79 -59.955 43.404 -13.007 1.00 35.91 N

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ATOM   1031  CA  ASP A  79     -59.054  44.205 -13.828  1.00 36.89           C
ATOM   1033  CB  ASP A  79     -58.637  43.452 -15.083  1.00 37.06           C
ATOM   1036  CG  ASP A  79     -57.518  44.150 -15.821  1.00 38.41           C
ATOM   1037  OD1 ASP A  79     -57.800  45.080 -16.615  1.00 39.85           O
ATOM   1038  OD2 ASP A  79     -56.347  43.775 -15.592  1.00 40.78           O
ATOM   1039  C   ASP A  79     -59.721  45.505 -14.220  1.00 37.75           C
ATOM   1040  O   ASP A  79     -59.105  46.568 -14.177  1.00 37.82           O
ATOM   1042  N   ARG A  80     -60.984  45.401 -14.615  1.00 38.99           N
ATOM   1043  CA  ARG A  80     -61.814  46.558 -14.923  1.00 39.88           C
ATOM   1045  CB  ARG A  80     -63.191  46.106 -15.427  1.00 40.41           C
ATOM   1048  CG  ARG A  80     -64.025  47.183 -16.122  1.00 42.77           C
ATOM   1051  CD  ARG A  80     -65.347  46.624 -16.718  1.00 45.79           C
ATOM   1054  NE  ARG A  80     -66.107  45.799 -15.765  1.00 48.55           N
ATOM   1056  CZ  ARG A  80     -66.136  44.457 -15.742  1.00 50.37           C
ATOM   1057  NH1 ARG A  80     -65.450  43.724 -16.636  1.00 49.78           N
ATOM   1060  NH2 ARG A  80     -66.868  43.835 -14.805  1.00 50.77           N
ATOM   1063  C   ARG A  80     -61.946  47.409 -13.668  1.00 39.80           C
ATOM   1064  O   ARG A  80     -61.840  48.630 -13.742  1.00 40.37           O
ATOM   1066  N   PHE A  81     -62.136  46.771 -12.516  1.00 39.62           N
ATOM   1067  CA  PHE A  81     -62.216  47.505 -11.245  1.00 39.61           C
ATOM   1069  CB  PHE A  81     -62.392  46.561 -10.053  1.00 39.74           C
ATOM   1072  CG  PHE A  81     -62.282  47.247  -8.712  1.00 38.81           C
ATOM   1073  CD1 PHE A  81     -63.238  48.153  -8.315  1.00 39.03           C
ATOM   1075  CE1 PHE A  81     -63.153  48.787  -7.100  1.00 39.69           C
ATOM   1077  CZ  PHE A  81     -62.095  48.515  -6.261  1.00 39.54           C
ATOM   1079  CE2 PHE A  81     -61.134  47.608  -6.647  1.00 38.66           C
ATOM   1081  CD2 PHE A  81     -61.228  46.986  -7.865  1.00 38.27           C
ATOM   1083  C   PHE A  81     -61.006  48.378 -10.970  1.00 39.58           C
ATOM   1084  O   PHE A  81     -61.165  49.535 -10.581  1.00 39.76           O
ATOM   1086  N   VAL A  82     -59.810  47.817 -11.142  1.00 39.50           N
ATOM   1087  CA  VAL A  82     -58.575  48.562 -10.892  1.00 39.47           C
ATOM   1089  CB  VAL A  82     -57.314  47.659 -10.977  1.00 39.37           C
ATOM   1091  CG1 VAL A  82     -56.108  48.426 -11.521  1.00 39.06           C
ATOM   1095  CG2 VAL A  82     -57.009  47.079  -9.614  1.00 39.23           C
ATOM   1099  C   VAL A  82     -58.457  49.755 -11.833  1.00 39.54           C
ATOM   1100  O   VAL A  82     -58.222  50.884 -11.378  1.00 39.45           O
ATOM   1102  N   SER A  83     -58.678  49.513 -13.126  1.00 39.65           N
ATOM   1103  CA  SER A  83     -58.469  50.535 -14.157  1.00 39.82           C
ATOM   1105  CB  SER A  83     -58.196  49.880 -15.526  1.00 39.84           C
ATOM   1108  OG  SER A  83     -59.138  48.870 -15.829  1.00 40.00           O
ATOM   1110  C   SER A  83     -59.617  51.561 -14.219  1.00 39.62           C
ATOM   1111  O   SER A  83     -60.149  51.853 -15.286  1.00 39.59           O
ATOM   1113  N   SER A  84     -59.957  52.108 -13.052  1.00 39.44           N
ATOM   1114  CA  SER A  84     -60.926  53.197 -12.910  1.00 39.13           C
ATOM   1116  CB  SER A  84     -62.238  52.834 -13.618  1.00 39.03           C
ATOM   1119  OG  SER A  84     -62.620  51.505 -13.325  1.00 37.97           O
ATOM   1121  C   SER A  84     -61.243  53.580 -11.446  1.00 39.17           C
ATOM   1122  O   SER A  84     -62.189  54.341 -11.230  1.00 39.58           O
ATOM   1124  N   GLY A  85     -60.482  53.077 -10.457  1.00 38.74           N
ATOM   1125  CA  GLY A  85     -60.795  53.282  -9.024  1.00 38.26           C
ATOM   1128  C   GLY A  85     -61.724  52.238  -8.413  1.00 37.79           C
ATOM   1129  O   GLY A  85     -61.529  51.799  -7.273  1.00 36.84           O
ATOM   1131  N   SER A  94     -63.557  54.187   1.994  1.00 28.27           N
ATOM   1132  CA  SER A  94     -64.069  52.892   2.476  1.00 28.03           C
ATOM   1134  CB  SER A  94     -64.856  52.225   1.359  1.00 27.84           C
ATOM   1137  OG  SER A  94     -65.234  50.921   1.743  1.00 28.20           O
ATOM   1139  C   SER A  94     -62.992  51.910   2.934  1.00 27.83           C
ATOM   1140  O   SER A  94     -62.339  51.325   2.090  1.00 28.15           O
ATOM   1142  N   LEU A  95     -62.815  51.705   4.245  1.00 27.70           N
ATOM   1143  CA  LEU A  95     -61.813  50.728   4.751  1.00 27.59           C
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ATOM   1145  CB  LEU A  95     -61.692  50.747   6.282  1.00 27.49      C
ATOM   1148  CG  LEU A  95     -60.871  49.596   6.909  1.00 27.47      C
ATOM   1150  CD1 LEU A  95     -59.400  49.900   6.902  1.00 27.70      C
ATOM   1154  CD2 LEU A  95     -61.292  49.274   8.329  1.00 27.50      C
ATOM   1158  C   LEU A  95     -62.173  49.314   4.318  1.00 27.71      C
ATOM   1159  O   LEU A  95     -61.303  48.537   3.914  1.00 27.73      O
ATOM   1161  N   HIS A  96     -63.461  48.989   4.437  1.00 27.74      N
ATOM   1162  CA  HIS A  96     -64.003  47.715   3.977  1.00 27.54      C
ATOM   1164  CB  HIS A  96     -65.497  47.680   4.230  1.00 27.57      C
ATOM   1167  CG  HIS A  96     -66.161  46.482   3.654  1.00 28.65      C
ATOM   1168  ND1 HIS A  96     -65.790  45.201   3.988  1.00 30.59      N
ATOM   1170  CE1 HIS A  96     -66.540  44.341   3.325  1.00 31.88      C
ATOM   1172  NE2 HIS A  96     -67.384  45.021   2.570  1.00 32.06      N
ATOM   1174  CD2 HIS A  96     -67.166  46.364   2.758  1.00 30.47      C
ATOM   1176  C   HIS A  96     -63.705  47.450   2.492  1.00 27.09      C
ATOM   1177  O   HIS A  96     -63.128  46.425   2.150  1.00 27.18      O
ATOM   1179  N   GLY A  97     -64.079  48.386   1.625  1.00 26.55      N
ATOM   1180  CA  GLY A  97     -63.760  48.300    .205  1.00 26.26      C
ATOM   1183  C   GLY A  97     -62.277  48.112   -.088  1.00 26.23      C
ATOM   1184  O   GLY A  97     -61.918  47.334   -.974  1.00 26.39      O
ATOM   1186  N   THR A  98     -61.415  48.815    .653  1.00 25.83      N
ATOM   1187  CA  THR A  98     -59.967  48.755    .435  1.00 25.36      C
ATOM   1189  CB  THR A  98     -59.204  49.847   1.215  1.00 25.07      C
ATOM   1191  OG1 THR A  98     -59.796  51.123    .980  1.00 23.62      O
ATOM   1193  CG2 THR A  98     -57.755  49.905    .780  1.00 24.88      C
ATOM   1197  C   THR A  98     -59.416  47.389    .845  1.00 25.69      C
ATOM   1198  O   THR A  98     -58.622  46.802    .111  1.00 25.66      O
ATOM   1200  N   ALA A  99     -59.847  46.890   2.008  1.00 25.95      N
ATOM   1201  CA  ALA A  99     -59.468  45.540   2.495  1.00 25.93      C
ATOM   1203  CB  ALA A  99     -59.945  45.330   3.929  1.00 25.82      C
ATOM   1207  C   ALA A  99     -59.984  44.404   1.595  1.00 25.64      C
ATOM   1208  O   ALA A  99     -59.204  43.599   1.102  1.00 25.38      O
ATOM   1210  N   LEU A 100     -61.290  44.348   1.371  1.00 25.46      N
ATOM   1211  CA  LEU A 100     -61.856  43.335    .474  1.00 25.55      C
ATOM   1213  CB  LEU A 100     -63.361  43.540    .326  1.00 25.37      C
ATOM   1216  CG  LEU A 100     -64.118  42.464   -.443  1.00 25.41      C
ATOM   1218  CD1 LEU A 100     -64.038  41.115    .281  1.00 26.01      C
ATOM   1222  CD2 LEU A 100     -65.555  42.893   -.639  1.00 25.19      C
ATOM   1226  C   LEU A 100     -61.196  43.353   -.919  1.00 25.70      C
ATOM   1227  O   LEU A 100     -60.819  42.301  -1.469  1.00 25.36      O
ATOM   1229  N   SER A 101     -61.064  44.550  -1.489  1.00 25.77      N
ATOM   1230  CA  SER A 101     -60.434  44.688  -2.805  1.00 25.67      C
ATOM   1232  CB  SER A 101     -60.629  46.098  -3.375  1.00 25.83      C
ATOM   1235  OG  SER A 101     -59.840  47.064  -2.688  1.00 26.98      O
ATOM   1237  C   SER A 101     -58.947  44.336  -2.756  1.00 25.01      C
ATOM   1238  O   SER A 101     -58.427  43.705  -3.672  1.00 24.94      O
ATOM   1240  N   PHE A 102     -58.270  44.737  -1.687  1.00 24.30      N
ATOM   1241  CA  PHE A 102     -56.852  44.436  -1.560  1.00 23.99      C
ATOM   1243  CB  PHE A 102     -56.295  44.963   -.229  1.00 23.84      C
ATOM   1246  CG  PHE A 102     -54.860  44.606    .027  1.00 23.24      C
ATOM   1247  CD1 PHE A 102     -53.849  45.504   -.259  1.00 23.56      C
ATOM   1249  CE1 PHE A 102     -52.507  45.182   -.007  1.00 24.50      C
ATOM   1251  CZ  PHE A 102     -52.175  43.941    .540  1.00 24.27      C
ATOM   1253  CE2 PHE A 102     -53.180  43.042    .834  1.00 23.95      C
ATOM   1255  CD2 PHE A 102     -54.520  43.376    .576  1.00 23.45      C
ATOM   1257  C   PHE A 102     -56.673  42.928  -1.679  1.00 23.65      C
ATOM   1258  O   PHE A 102     -55.890  42.442  -2.501  1.00 23.55      O
ATOM   1260  N   ARG A 103     -57.443  42.202   -.880  1.00 23.20      N
ATOM   1261  CA  ARG A 103     -57.298  40.765   -.764  1.00 22.84      C
ATOM   1263  CB  ARG A 103     -58.250  40.231    .291  1.00 23.01      C
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ATOM   1266  CG  ARG A 103     -58.054  38.774   .597  1.00 23.93      C
ATOM   1269  CD  ARG A 103     -58.703  38.376  1.937  1.00 23.84      C
ATOM   1272  NE  ARG A 103     -60.150  38.538  1.919  1.00 22.36      N
ATOM   1274  CZ  ARG A 103     -60.982  37.763  1.240  1.00 20.62      C
ATOM   1275  NH1 ARG A 103     -60.512  36.773   .490  1.00 20.19      N
ATOM   1278  NH2 ARG A 103     -62.288  38.003  1.293  1.00 20.32      N
ATOM   1281  C   ARG A 103     -57.602  40.117 -2.082  1.00 22.34      C
ATOM   1282  O   ARG A 103     -56.826  39.303 -2.576  1.00 22.37      O
ATOM   1284  N   LEU A 104     -58.729  40.496 -2.667  1.00 21.98      N
ATOM   1285  CA  LEU A 104     -59.129  39.926 -3.951  1.00 21.60      C
ATOM   1287  CB  LEU A 104     -60.503  40.442 -4.378  1.00 21.23      C
ATOM   1290  CG  LEU A 104     -61.590  39.832 -3.522  1.00 20.30      C
ATOM   1292  CD1 LEU A 104     -62.949  40.401 -3.856  1.00 19.53      C
ATOM   1296  CD2 LEU A 104     -61.554  38.344 -3.725  1.00 19.71      C
ATOM   1300  C   LEU A 104     -58.101  40.198 -5.040  1.00 21.48      C
ATOM   1301  O   LEU A 104     -57.743  39.294 -5.780  1.00 21.62      O
ATOM   1303  N   LEU A 105     -57.623  41.432 -5.139  1.00 21.14      N
ATOM   1304  CA  LEU A 105     -56.655  41.747 -6.173  1.00 21.05      C
ATOM   1306  CB  LEU A 105     -56.352  43.248 -6.205  1.00 20.94      C
ATOM   1309  CG  LEU A 105     -57.465  44.165 -6.732  1.00 20.06      C
ATOM   1311  CD1 LEU A 105     -57.060  45.617 -6.580  1.00 17.92      C
ATOM   1315  CD2 LEU A 105     -57.804  43.857 -8.174  1.00 19.18      C
ATOM   1319  C   LEU A 105     -55.372  40.908 -5.997  1.00 21.32      C
ATOM   1320  O   LEU A 105     -54.840  40.357 -6.976  1.00 21.37      O
ATOM   1322  N   ARG A 106     -54.893  40.777 -4.763  1.00 21.25      N
ATOM   1323  CA  ARG A 106     -53.678  40.003 -4.528  1.00 21.33      C
ATOM   1325  CB  ARG A 106     -53.151  40.211 -3.117  1.00 21.53      C
ATOM   1328  CG  ARG A 106     -51.772  39.588 -2.917  1.00 22.60      C
ATOM   1331  CD  ARG A 106     -51.098  40.091 -1.666  1.00 23.60      C
ATOM   1334  NE  ARG A 106     -50.374  41.330 -1.897  1.00 24.60      N
ATOM   1336  CZ  ARG A 106     -49.606  41.916  -.989  1.00 26.54      C
ATOM   1337  NH1 ARG A 106     -49.469  41.380   .225  1.00 26.98      N
ATOM   1340  NH2 ARG A 106     -48.967  43.041 -1.295  1.00 27.19      N
ATOM   1343  C   ARG A 106     -53.888  38.517 -4.767  1.00 21.19      C
ATOM   1344  O   ARG A 106     -52.998  37.821 -5.278  1.00 21.18      O
ATOM   1346  N   GLN A 107     -55.061  38.028 -4.378  1.00 21.09      N
ATOM   1347  CA  GLN A 107     -55.425  36.635 -4.618  1.00 20.76      C
ATOM   1349  CB  GLN A 107     -56.861  36.378 -4.168  1.00 20.51      C
ATOM   1352  CG  GLN A 107     -57.329  34.941 -4.327  1.00 19.68      C
ATOM   1355  CD  GLN A 107     -58.790  34.772 -4.010  1.00 18.26      C
ATOM   1356  OE1 GLN A 107     -59.395  35.591 -3.334  1.00 17.44      O
ATOM   1357  NE2 GLN A 107     -59.366  33.698 -4.497  1.00 18.48      N
ATOM   1360  C   GLN A 107     -55.304  36.306 -6.094  1.00 20.93      C
ATOM   1361  O   GLN A 107     -54.917  35.212 -6.447  1.00 21.45      O
ATOM   1363  N   HIS A 108     -55.642  37.260 -6.951  1.00 21.09      N
ATOM   1364  CA  HIS A 108     -55.686  37.030 -8.379  1.00 21.28      C
ATOM   1366  CB  HIS A 108     -57.024  37.541 -8.913  1.00 21.02      C
ATOM   1369  CG  HIS A 108     -58.182  36.706 -8.478  1.00 19.70      C
ATOM   1370  ND1 HIS A 108     -58.637  35.632 -9.210  1.00 19.91      N
ATOM   1372  CE1 HIS A 108     -59.641  35.060 -8.571  1.00 19.27      C
ATOM   1374  NE2 HIS A 108     -59.851  35.720 -7.449  1.00 18.10      N
ATOM   1376  CD2 HIS A 108     -58.950  36.753 -7.367  1.00 18.98      C
ATOM   1378  C   HIS A 108     -54.456  37.621 -9.108  1.00 22.21      C
ATOM   1379  O   HIS A 108     -54.505  37.980 -10.304  1.00 21.80      O
ATOM   1381  N   GLY A 109     -53.345  37.686 -8.375  1.00 23.19      N
ATOM   1382  CA  GLY A 109     -52.055  38.007 -8.956  1.00 24.17      C
ATOM   1385  C   GLY A 109     -51.813  39.470 -9.275  1.00 25.25      C
ATOM   1386  O   GLY A 109     -50.767  39.802 -9.845  1.00 25.26      O
ATOM   1388  N   PHE A 110     -52.755  40.349 -8.917  1.00 26.42      N
ATOM   1389  CA  PHE A 110     -52.575  41.783 -9.154  1.00 27.33      C
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ATOM  1391  CB  PHE A 110     -53.895  42.546  -9.067  1.00 27.36           C
ATOM  1394  CG  PHE A 110     -54.838  42.250 -10.193  1.00 27.83           C
ATOM  1395  CD1 PHE A 110     -54.633  42.801 -11.439  1.00 28.69           C
ATOM  1397  CE1 PHE A 110     -55.490  42.529 -12.488  1.00 28.91           C
ATOM  1399  CZ  PHE A 110     -56.568  41.702 -12.295  1.00 28.85           C
ATOM  1401  CE2 PHE A 110     -56.787  41.146 -11.060  1.00 28.67           C
ATOM  1403  CD2 PHE A 110     -55.923  41.418 -10.013  1.00 28.39           C
ATOM  1405  C   PHE A 110     -51.582  42.369  -8.163  1.00 28.25           C
ATOM  1406  O   PHE A 110     -51.449  41.890  -7.024  1.00 28.71           O
ATOM  1408  N   GLU A 111     -50.886  43.411  -8.607  1.00 29.05           N
ATOM  1409  CA  GLU A 111     -49.951  44.142  -7.760  1.00 29.66           C
ATOM  1411  CB  GLU A 111     -48.902  44.803  -8.648  1.00 30.37           C
ATOM  1414  CG  GLU A 111     -47.750  45.509  -7.947  1.00 33.30           C
ATOM  1417  CD  GLU A 111     -46.916  46.342  -8.946  1.00 38.00           C
ATOM  1418  OE1 GLU A 111     -46.312  45.750  -9.885  1.00 39.60           O
ATOM  1419  OE2 GLU A 111     -46.886  47.594  -8.802  1.00 40.87           O
ATOM  1420  C   GLU A 111     -50.724  45.184  -6.935  1.00 28.98           C
ATOM  1421  O   GLU A 111     -51.293  46.123  -7.495  1.00 28.45           O
ATOM  1423  N   VAL A 112     -50.787  44.961  -5.618  1.00 28.47           N
ATOM  1424  CA  VAL A 112     -51.284  45.950  -4.655  1.00 28.09           C
ATOM  1426  CB  VAL A 112     -52.564  45.501  -3.908  1.00 27.76           C
ATOM  1428  CG1 VAL A 112     -53.745  45.466  -4.836  1.00 27.38           C
ATOM  1432  CG2 VAL A 112     -52.360  44.167  -3.252  1.00 27.80           C
ATOM  1436  C   VAL A 112     -50.193  46.199  -3.631  1.00 28.15           C
ATOM  1437  O   VAL A 112     -49.339  45.354  -3.436  1.00 27.90           O
ATOM  1439  N   SER A 113     -50.241  47.354  -2.974  1.00 28.54           N
ATOM  1440  CA  SER A 113     -49.194  47.782  -2.047  1.00 28.93           C
ATOM  1442  CB  SER A 113     -48.563  49.064  -2.564  1.00 29.12           C
ATOM  1445  OG  SER A 113     -47.692  49.644  -1.619  1.00 29.57           O
ATOM  1447  C   SER A 113     -49.780  48.041   -.685  1.00 29.13           C
ATOM  1448  O   SER A 113     -50.937  48.426   -.581  1.00 28.90           O
ATOM  1450  N   GLN A 114     -48.985  47.857    .367  1.00 29.84           N
ATOM  1451  CA  GLN A 114     -49.524  48.019   1.736  1.00 30.40           C
ATOM  1453  CB  GLN A 114     -48.568  47.507   2.830  1.00 30.34           C
ATOM  1456  CG  GLN A 114     -47.199  48.159   2.844  1.00 30.61           C
ATOM  1459  CD  GLN A 114     -46.456  47.928   4.147  1.00 30.77           C
ATOM  1460  OE1 GLN A 114     -46.876  47.129   4.982  1.00 31.92           O
ATOM  1461  NE2 GLN A 114     -45.341  48.624   4.324  1.00 30.02           N
ATOM  1464  C   GLN A 114     -49.939  49.440   2.068  1.00 30.62           C
ATOM  1465  O   GLN A 114     -50.573  49.644   3.094  1.00 30.73           O
ATOM  1467  N   GLU A 115     -49.592  50.407   1.216  1.00 30.94           N
ATOM  1468  CA  GLU A 115     -49.963  51.794   1.458  1.00 31.45           C
ATOM  1470  CB  GLU A 115     -48.881  52.777    .975  1.00 31.86           C
ATOM  1473  CG  GLU A 115     -48.489  52.723   -.509  1.00 33.48           C
ATOM  1476  CD  GLU A 115     -47.006  53.100   -.759  1.00 36.13           C
ATOM  1477  OE1 GLU A 115     -46.106  52.668    .022  1.00 38.72           O
ATOM  1478  OE2 GLU A 115     -46.741  53.811  -1.754  1.00 35.70           O
ATOM  1479  C   GLU A 115     -51.338  52.125    .895  1.00 31.45           C
ATOM  1480  O   GLU A 115     -51.716  53.283    .808  1.00 31.80           O
ATOM  1482  N   ALA A 116     -52.108  51.105    .549  1.00 31.58           N
ATOM  1483  CA  ALA A 116     -53.524  51.286    .284  1.00 31.67           C
ATOM  1485  CB  ALA A 116     -54.071  50.092   -.461  1.00 31.62           C
ATOM  1489  C   ALA A 116     -54.273  51.473   1.596  1.00 31.88           C
ATOM  1490  O   ALA A 116     -55.428  51.874   1.604  1.00 31.82           O
ATOM  1492  N   PHE A 117     -53.608  51.161   2.702  1.00 32.39           N
ATOM  1493  CA  PHE A 117     -54.193  51.271   4.030  1.00 32.87           C
ATOM  1495  CB  PHE A 117     -53.884  50.003   4.856  1.00 32.79           C
ATOM  1498  CG  PHE A 117     -54.539  48.758   4.323  1.00 31.03           C
ATOM  1499  CD1 PHE A 117     -53.782  47.749   3.760  1.00 28.79           C
ATOM  1501  CE1 PHE A 117     -54.379  46.620   3.265  1.00 28.36           C
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ATOM  1503  CZ  PHE A 117    -55.754  46.489   3.316  1.00 29.50      C
ATOM  1505  CE2 PHE A 117    -56.527  47.493   3.872  1.00 29.91      C
ATOM  1507  CD2 PHE A 117    -55.917  48.613   4.375  1.00 30.09      C
ATOM  1509  C   PHE A 117    -53.683  52.493   4.773  1.00 33.71      C
ATOM  1510  O   PHE A 117    -54.012  52.678   5.937  1.00 33.61      O
ATOM  1512  N   SER A 118    -52.886  53.325   4.107  1.00 35.09      N
ATOM  1513  CA  SER A 118    -52.186  54.429   4.779  1.00 36.12      C
ATOM  1515  CB  SER A 118    -51.073  54.990   3.895  1.00 36.09      C
ATOM  1518  OG  SER A 118    -51.607  55.747   2.820  1.00 35.96      O
ATOM  1520  C   SER A 118    -53.134  55.552   5.184  1.00 37.17      C
ATOM  1521  O   SER A 118    -52.873  56.255   6.166  1.00 37.22      O
ATOM  1523  N   GLY A 119    -54.231  55.705   4.436  1.00 38.40      N
ATOM  1524  CA  GLY A 119    -55.227  56.735   4.708  1.00 39.47      C
ATOM  1527  C   GLY A 119    -56.255  56.398   5.778  1.00 40.62      C
ATOM  1528  O   GLY A 119    -57.259  57.086   5.877  1.00 40.74      O
ATOM  1530  N   PHE A 120    -56.024  55.344   6.563  1.00 42.13      N
ATOM  1531  CA  PHE A 120    -56.906  54.971   7.684  1.00 43.27      C
ATOM  1533  CB  PHE A 120    -57.510  53.586   7.455  1.00 43.21      C
ATOM  1536  CG  PHE A 120    -58.176  53.439   6.134  1.00 42.36      C
ATOM  1537  CD1 PHE A 120    -59.418  54.006   5.911  1.00 41.23      C
ATOM  1539  CE1 PHE A 120    -60.035  53.880   4.691  1.00 40.87      C
ATOM  1541  CZ  PHE A 120    -59.414  53.182   3.675  1.00 41.03      C
ATOM  1543  CE2 PHE A 120    -58.167  52.618   3.883  1.00 40.92      C
ATOM  1545  CD2 PHE A 120    -57.556  52.746   5.106  1.00 41.30      C
ATOM  1547  C   PHE A 120    -56.179  54.952   9.019  1.00 44.71      C
ATOM  1548  O   PHE A 120    -56.732  54.489  10.025  1.00 44.80      O
ATOM  1550  N   LYS A 121    -54.939  55.430   9.021  1.00 46.38      N
ATOM  1551  CA  LYS A 121    -54.153  55.519  10.235  1.00 47.81      C
ATOM  1553  CB  LYS A 121    -52.722  55.050   9.957  1.00 47.86      C
ATOM  1556  CG  LYS A 121    -52.648  53.537   9.648  1.00 48.24      C
ATOM  1559  CD  LYS A 121    -51.417  53.119   8.823  1.00 49.41      C
ATOM  1562  CE  LYS A 121    -50.095  53.142   9.621  1.00 49.88      C
ATOM  1565  NZ  LYS A 121    -49.944  52.005  10.584  1.00 49.89      N
ATOM  1569  C   LYS A 121    -54.257  56.964  10.735  1.00 49.00      C
ATOM  1570  O   LYS A 121    -54.712  57.839  10.000  1.00 49.11      O
ATOM  1572  N   ASP A 122    -53.899  57.206  11.995  1.00 50.51      N
ATOM  1573  CA  ASP A 122    -54.078  58.537  12.596  1.00 51.46      C
ATOM  1575  CB  ASP A 122    -54.604  58.443  14.050  1.00 51.29      C
ATOM  1578  CG  ASP A 122    -53.570  57.919  15.036  1.00 50.73      C
ATOM  1579  OD1 ASP A 122    -52.353  58.025  14.777  1.00 49.90      O
ATOM  1580  OD2 ASP A 122    -53.988  57.398  16.088  1.00 49.66      O
ATOM  1581  C   ASP A 122    -52.792  59.358  12.502  1.00 52.60      C
ATOM  1582  O   ASP A 122    -51.830  58.953  11.835  1.00 52.65      O
ATOM  1584  N   GLN A 123    -52.802  60.512  13.172  1.00 53.88      N
ATOM  1585  CA  GLN A 123    -51.680  61.456  13.195  1.00 54.66      C
ATOM  1587  CB  GLN A 123    -51.993  62.594  14.178  1.00 55.01      C
ATOM  1590  CG  GLN A 123    -53.249  63.442  13.831  1.00 56.15      C
ATOM  1593  CD  GLN A 123    -52.943  64.736  13.064  1.00 57.64      C
ATOM  1594  OE1 GLN A 123    -51.779  65.102  12.859  1.00 59.10      O
ATOM  1595  NE2 GLN A 123    -54.001  65.438  12.652  1.00 57.63      N
ATOM  1598  C   GLN A 123    -50.365  60.772  13.591  1.00 54.87      C
ATOM  1599  O   GLN A 123    -49.309  61.078  13.034  1.00 54.67      O
ATOM  1601  N   ASN A 124    -50.458  59.834  14.538  1.00 55.21      N
ATOM  1602  CA  ASN A 124    -49.300  59.137  15.109  1.00 55.39      C
ATOM  1604  CB  ASN A 124    -49.421  59.122  16.637  1.00 55.52      C
ATOM  1607  CG  ASN A 124    -49.833  60.478  17.202  1.00 55.98      C
ATOM  1608  OD1 ASN A 124    -49.093  61.460  17.091  1.00 56.93      O
ATOM  1609  ND2 ASN A 124    -51.026  60.540  17.797  1.00 55.99      N
ATOM  1612  C   ASN A 124    -49.116  57.705  14.589  1.00 55.27      C
ATOM  1613  O   ASN A 124    -48.530  56.864  15.271  1.00 55.18      O
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ATOM   1615  N   GLY A 125     -49.626  57.430  13.391  1.00 55.18           N
ATOM   1616  CA  GLY A 125     -49.311  56.190  12.672  1.00 55.08           C
ATOM   1619  C   GLY A 125     -49.994  54.897  13.119  1.00 54.90           C
ATOM   1620  O   GLY A 125     -49.543  53.806  12.750  1.00 55.24           O
ATOM   1622  N   ASN A 126     -51.072  55.008  13.900  1.00 54.23           N
ATOM   1623  CA  ASN A 126     -51.871  53.853  14.329  1.00 53.39           C
ATOM   1625  CB  ASN A 126     -51.927  53.782  15.852  1.00 53.27           C
ATOM   1628  CG  ASN A 126     -50.596  53.425  16.466  1.00 52.81           C
ATOM   1629  OD1 ASN A 126     -49.636  53.113  15.764  1.00 52.29           O
ATOM   1630  ND2 ASN A 126     -50.532  53.460  17.789  1.00 52.53           N
ATOM   1633  C   ASN A 126     -53.274  53.978  13.771  1.00 52.82           C
ATOM   1634  O   ASN A 126     -53.724  55.081  13.494  1.00 52.69           O
ATOM   1636  N   PHE A 127     -53.968  52.857  13.607  1.00 52.17           N
ATOM   1637  CA  PHE A 127     -55.287  52.875  12.962  1.00 51.56           C
ATOM   1639  CB  PHE A 127     -55.805  51.451  12.721  1.00 51.35           C
ATOM   1642  CG  PHE A 127     -55.119  50.730  11.587  1.00 50.06           C
ATOM   1643  CD1 PHE A 127     -54.068  49.856  11.831  1.00 48.90           C
ATOM   1645  CE1 PHE A 127     -53.437  49.187  10.789  1.00 47.59           C
ATOM   1647  CZ  PHE A 127     -53.857  49.383   9.495  1.00 47.40           C
ATOM   1649  CE2 PHE A 127     -54.906  50.244   9.234  1.00 47.96           C
ATOM   1651  CD2 PHE A 127     -55.533  50.915  10.276  1.00 48.85           C
ATOM   1653  C   PHE A 127     -56.303  53.690  13.776  1.00 51.35           C
ATOM   1654  O   PHE A 127     -56.347  53.594  15.002  1.00 51.09           O
ATOM   1656  N   LEU A 128     -57.100  54.500  13.083  1.00 51.15           N
ATOM   1657  CA  LEU A 128     -58.143  55.280  13.727  1.00 51.09           C
ATOM   1659  CB  LEU A 128     -59.039  55.979  12.694  1.00 51.17           C
ATOM   1662  CG  LEU A 128     -58.463  57.046  11.746  1.00 51.31           C
ATOM   1664  CD1 LEU A 128     -59.571  57.628  10.855  1.00 50.76           C
ATOM   1668  CD2 LEU A 128     -57.762  58.157  12.508  1.00 50.98           C
ATOM   1672  C   LEU A 128     -58.996  54.353  14.581  1.00 51.06           C
ATOM   1673  O   LEU A 128     -59.573  53.393  14.078  1.00 50.94           O
ATOM   1675  N   GLU A 129     -59.053  54.637  15.879  1.00 51.12           N
ATOM   1676  CA  GLU A 129     -59.916  53.913  16.808  1.00 50.99           C
ATOM   1678  CB  GLU A 129     -60.019  54.665  18.132  1.00 51.14           C
ATOM   1681  CG  GLU A 129     -58.850  54.431  19.049  1.00 52.04           C
ATOM   1684  CD  GLU A 129     -58.903  53.069  19.697  1.00 53.22           C
ATOM   1685  OE1 GLU A 129     -58.040  52.219  19.376  1.00 54.19           O
ATOM   1686  OE2 GLU A 129     -59.823  52.848  20.516  1.00 53.51           O
ATOM   1687  C   GLU A 129     -61.314  53.712  16.260  1.00 50.66           C
ATOM   1688  O   GLU A 129     -61.791  52.587  16.200  1.00 50.83           O
ATOM   1690  N   ASN A 130     -61.960  54.799  15.839  1.00 50.28           N
ATOM   1691  CA  ASN A 130     -63.389  54.765  15.486  1.00 50.03           C
ATOM   1693  CB  ASN A 130     -63.910  56.182  15.193  1.00 50.09           C
ATOM   1696  CG  ASN A 130     -63.286  56.805  13.960  1.00 50.37           C
ATOM   1697  OD1 ASN A 130     -62.504  56.177  13.249  1.00 51.44           O
ATOM   1698  ND2 ASN A 130     -63.634  58.056  13.701  1.00 50.27           N
ATOM   1701  C   ASN A 130     -63.804  53.782  14.369  1.00 49.56           C
ATOM   1702  O   ASN A 130     -64.993  53.581  14.131  1.00 49.44           O
ATOM   1704  N   LEU A 131     -62.828  53.175  13.699  1.00 49.21           N
ATOM   1705  CA  LEU A 131     -63.087  52.103  12.729  1.00 48.78           C
ATOM   1707  CB  LEU A 131     -61.846  51.832  11.875  1.00 48.64           C
ATOM   1710  CG  LEU A 131     -61.445  52.939  10.898  1.00 48.26           C
ATOM   1712  CD1 LEU A 131     -60.029  52.709  10.375  1.00 47.76           C
ATOM   1716  CD2 LEU A 131     -62.441  53.039   9.754  1.00 47.32           C
ATOM   1720  C   LEU A 131     -63.516  50.798  13.394  1.00 48.58           C
ATOM   1721  O   LEU A 131     -64.093  49.939  12.731  1.00 48.64           O
ATOM   1723  N   LYS A 132     -63.225  50.645  14.689  1.00 48.23           N
ATOM   1724  CA  LYS A 132     -63.650  49.474  15.465  1.00 47.80           C
ATOM   1726  CB  LYS A 132     -63.156  49.587  16.913  1.00 47.71           C
ATOM   1729  CG  LYS A 132     -63.930  50.615  17.728  1.00 47.80           C
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ATOM 1732 CD LYS A 132 -63.430 50.779 19.153 1.00 47.75 C
ATOM 1735 CE LYS A 132 -64.438 51.577 19.982 1.00 47.22 C
ATOM 1738 NZ LYS A 132 -63.769 52.364 21.033 1.00 46.65 N
ATOM 1742 C LYS A 132 -65.182 49.308 15.446 1.00 47.56 C
ATOM 1743 O LYS A 132 -65.696 48.204 15.616 1.00 47.76 O
ATOM 1745 N GLU A 133 -65.901 50.413 15.249 1.00 47.18 N
ATOM 1746 CA GLU A 133 -67.371 50.412 15.191 1.00 46.79 C
ATOM 1748 CB GLU A 133 -67.898 51.850 15.337 1.00 46.95 C
ATOM 1751 CG GLU A 133 -67.840 52.376 16.776 1.00 47.56 C
ATOM 1754 CD GLU A 133 -67.613 53.886 16.863 1.00 48.41 C
ATOM 1755 OE1 GLU A 133 -68.247 54.648 16.093 1.00 47.67 O
ATOM 1756 OE2 GLU A 133 -66.798 54.304 17.721 1.00 48.92 O
ATOM 1757 C GLU A 133 -67.949 49.770 13.918 1.00 46.10 C
ATOM 1758 O GLU A 133 -69.140 49.446 13.874 1.00 46.11 O
ATOM 1760 N ASP A 134 -67.103 49.601 12.896 1.00 45.11 N
ATOM 1761 CA ASP A 134 -67.477 48.995 11.608 1.00 44.06 C
ATOM 1763 CB ASP A 134 -66.934 49.868 10.474 1.00 43.97 C
ATOM 1766 CG ASP A 134 -67.380 49.411 9.104 1.00 44.08 C
ATOM 1767 OD1 ASP A 134 -68.072 48.373 8.972 1.00 43.42 O
ATOM 1768 OD2 ASP A 134 -67.020 50.116 8.141 1.00 44.84 O
ATOM 1769 C ASP A 134 -66.910 47.570 11.526 1.00 43.12 C
ATOM 1770 O ASP A 134 -65.788 47.357 11.080 1.00 43.19 O
ATOM 1772 N ILE A 135 -67.708 46.594 11.944 1.00 41.85 N
ATOM 1773 CA ILE A 135 -67.216 45.247 12.216 1.00 40.75 C
ATOM 1775 CB ILE A 135 -68.183 44.507 13.170 1.00 40.80 C
ATOM 1777 CG1 ILE A 135 -68.227 45.226 14.524 1.00 41.21 C
ATOM 1780 CD1 ILE A 135 -69.353 46.283 14.633 1.00 42.86 C
ATOM 1784 CG2 ILE A 135 -67.776 43.063 13.373 1.00 40.88 C
ATOM 1788 C ILE A 135 -66.980 44.457 10.933 1.00 39.67 C
ATOM 1789 O ILE A 135 -66.166 43.537 10.901 1.00 39.37 O
ATOM 1791 N LYS A 136 -67.690 44.828 9.877 1.00 38.62 N
ATOM 1792 CA LYS A 136 -67.465 44.256 8.554 1.00 37.88 C
ATOM 1794 CB LYS A 136 -68.525 44.749 7.561 1.00 38.33 C
ATOM 1797 CG LYS A 136 -69.955 44.342 7.879 1.00 40.17 C
ATOM 1800 CD LYS A 136 -70.486 43.262 6.911 1.00 42.97 C
ATOM 1803 CE LYS A 136 -71.624 42.389 7.536 1.00 44.00 C
ATOM 1806 NZ LYS A 136 -72.950 43.086 7.726 1.00 43.82 N
ATOM 1810 C LYS A 136 -66.097 44.687 8.047 1.00 36.38 C
ATOM 1811 O LYS A 136 -65.399 43.914 7.388 1.00 36.24 O
ATOM 1813 N ALA A 137 -65.728 45.931 8.341 1.00 34.51 N
ATOM 1814 CA ALA A 137 -64.463 46.474 7.876 1.00 33.41 C
ATOM 1816 CB ALA A 137 -64.432 47.981 8.058 1.00 33.43 C
ATOM 1820 C ALA A 137 -63.291 45.827 8.600 1.00 32.30 C
ATOM 1821 O ALA A 137 -62.288 45.481 7.995 1.00 31.89 O
ATOM 1823 N ILE A 138 -63.437 45.662 9.905 1.00 31.41 N
ATOM 1824 CA ILE A 138 -62.395 45.074 10.737 1.00 30.60 C
ATOM 1826 CB ILE A 138 -62.770 45.131 12.238 1.00 30.20 C
ATOM 1828 CG1 ILE A 138 -62.914 46.576 12.689 1.00 29.92 C
ATOM 1831 CD1 ILE A 138 -61.681 47.414 12.417 1.00 30.50 C
ATOM 1835 CG2 ILE A 138 -61.706 44.470 13.085 1.00 29.73 C
ATOM 1839 C ILE A 138 -62.140 43.631 10.320 1.00 30.34 C
ATOM 1840 O ILE A 138 -60.972 43.203 10.212 1.00 30.65 O
ATOM 1842 N LEU A 139 -63.227 42.884 10.098 1.00 29.69 N
ATOM 1843 CA LEU A 139 -63.134 41.523 9.562 1.00 29.23 C
ATOM 1845 CB LEU A 139 -64.517 40.917 9.332 1.00 28.92 C
ATOM 1848 CG LEU A 139 -65.066 40.185 10.545 1.00 29.06 C
ATOM 1850 CD1 LEU A 139 -66.541 39.875 10.352 1.00 28.20 C
ATOM 1854 CD2 LEU A 139 -64.250 38.922 10.813 1.00 28.59 C
ATOM 1858 C LEU A 139 -62.382 41.546 8.247 1.00 29.00 C
ATOM 1859 O LEU A 139 -61.444 40.773 8.035 1.00 29.50 O

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ATOM   1861  N   SER A 140     -62.790  42.458   7.372  1.00 28.14           N
ATOM   1862  CA  SER A 140     -62.222  42.526   6.054  1.00 27.40           C
ATOM   1864  CB  SER A 140     -62.912  43.619   5.260  1.00 27.35           C
ATOM   1867  OG  SER A 140     -63.310  43.103   4.015  1.00 28.43           O
ATOM   1869  C   SER A 140     -60.720  42.777   6.123  1.00 26.77           C
ATOM   1870  O   SER A 140     -59.975  42.269   5.298  1.00 27.29           O
ATOM   1872  N   LEU A 141     -60.285  43.563   7.105  1.00 25.89           N
ATOM   1873  CA  LEU A 141     -58.872  43.897   7.283  1.00 25.20           C
ATOM   1875  CB  LEU A 141     -58.717  45.164   8.155  1.00 25.00           C
ATOM   1878  CG  LEU A 141     -57.298  45.670   8.489  1.00 24.35           C
ATOM   1880  CD1 LEU A 141     -56.497  45.974   7.232  1.00 22.75           C
ATOM   1884  CD2 LEU A 141     -57.329  46.893   9.385  1.00 22.81           C
ATOM   1888  C   LEU A 141     -58.140  42.721   7.920  1.00 24.92           C
ATOM   1889  O   LEU A 141     -57.034  42.380   7.521  1.00 24.77           O
ATOM   1891  N   TYR A 142     -58.751  42.101   8.921  1.00 24.51           N
ATOM   1892  CA  TYR A 142     -58.163  40.913   9.514  1.00 24.36           C
ATOM   1894  CB  TYR A 142     -59.120  40.325  10.538  1.00 24.18           C
ATOM   1897  CG  TYR A 142     -58.774  38.941  11.046  1.00 23.72           C
ATOM   1898  CD1 TYR A 142     -57.878  38.763  12.091  1.00 22.97           C
ATOM   1900  CE1 TYR A 142     -57.593  37.500  12.582  1.00 24.25           C
ATOM   1902  CZ  TYR A 142     -58.229  36.386  12.030  1.00 25.75           C
ATOM   1903  OH  TYR A 142     -57.967  35.100  12.500  1.00 26.97           O
ATOM   1905  CE2 TYR A 142     -59.120  36.551  10.988  1.00 25.02           C
ATOM   1907  CD2 TYR A 142     -59.390  37.820  10.511  1.00 24.01           C
ATOM   1909  C   TYR A 142     -57.877  39.896   8.423  1.00 24.39           C
ATOM   1910  O   TYR A 142     -56.822  39.276   8.380  1.00 24.19           O
ATOM   1912  N   GLU A 143     -58.841  39.760   7.527  1.00 24.59           N
ATOM   1913  CA  GLU A 143     -58.820  38.728   6.521  1.00 24.70           C
ATOM   1915  CB  GLU A 143     -60.194  38.636   5.853  1.00 24.69           C
ATOM   1918  CG  GLU A 143     -60.651  37.219   5.547  1.00 27.21           C
ATOM   1921  CD  GLU A 143     -61.127  36.426   6.774  1.00 30.20           C
ATOM   1922  OE1 GLU A 143     -60.261  35.776   7.393  1.00 33.40           O
ATOM   1923  OE2 GLU A 143     -62.351  36.421   7.097  1.00 30.50           O
ATOM   1924  C   GLU A 143     -57.701  39.010   5.518  1.00 24.08           C
ATOM   1925  O   GLU A 143     -56.984  38.090   5.126  1.00 24.53           O
ATOM   1927  N   ALA A 144     -57.537  40.281   5.147  1.00 23.30           N
ATOM   1928  CA  ALA A 144     -56.515  40.715   4.173  1.00 22.79           C
ATOM   1930  CB  ALA A 144     -56.787  42.154   3.740  1.00 22.49           C
ATOM   1934  C   ALA A 144     -55.073  40.598   4.701  1.00 22.42           C
ATOM   1935  O   ALA A 144     -54.128  40.380   3.935  1.00 22.36           O
ATOM   1937  N   SER A 145     -54.909  40.713   6.012  1.00 21.80           N
ATOM   1938  CA  SER A 145     -53.593  40.822   6.600  1.00 21.36           C
ATOM   1940  CB  SER A 145     -53.726  41.170   8.066  1.00 21.21           C
ATOM   1943  OG  SER A 145     -54.337  40.100   8.753  1.00 21.59           O
ATOM   1945  C   SER A 145     -52.797  39.537   6.476  1.00 21.30           C
ATOM   1946  O   SER A 145     -51.571  39.533   6.701  1.00 21.50           O
ATOM   1948  N   PHE A 146     -53.488  38.439   6.154  1.00 21.00           N
ATOM   1949  CA  PHE A 146     -52.827  37.127   6.030  1.00 20.41           C
ATOM   1951  CB  PHE A 146     -53.796  35.979   6.338  1.00 20.20           C
ATOM   1954  CG  PHE A 146     -54.130  35.873   7.798  1.00 19.91           C
ATOM   1955  CD1 PHE A 146     -53.382  35.087   8.637  1.00 20.48           C
ATOM   1957  CE1 PHE A 146     -53.679  35.012   9.992  1.00 20.59           C
ATOM   1959  CZ  PHE A 146     -54.731  35.740  10.508  1.00 19.15           C
ATOM   1961  CE2 PHE A 146     -55.464  36.536   9.691  1.00 19.10           C
ATOM   1963  CD2 PHE A 146     -55.155  36.615   8.343  1.00 20.16           C
ATOM   1965  C   PHE A 146     -52.174  36.964   4.680  1.00 19.76           C
ATOM   1966  O   PHE A 146     -51.305  36.116   4.523  1.00 19.46           O
ATOM   1968  N   LEU A 147     -52.550  37.819   3.729  1.00 19.34           N
ATOM   1969  CA  LEU A 147     -51.933  37.804   2.402  1.00 19.13           C
ATOM   1971  CB  LEU A 147     -52.905  38.367   1.347  1.00 18.67           C
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ATOM  1974 CG  LEU A 147    -53.964  37.334   .919  1.00 18.11      C
ATOM  1976 CD1 LEU A 147    -55.090  37.248  1.961  1.00 15.10      C
ATOM  1980 CD2 LEU A 147    -54.494  37.609  -.499  1.00 16.50      C
ATOM  1984 C   LEU A 147    -50.582  38.525  2.369  1.00 19.10      C
ATOM  1985 O   LEU A 147    -49.992  38.715  1.311  1.00 19.44      O
ATOM  1987 N   ALA A 148    -50.075  38.882  3.542  1.00 19.13      N
ATOM  1988 CA  ALA A 148    -48.967  39.806  3.664  1.00 18.84      C
ATOM  1990 CB  ALA A 148    -48.762  40.167  5.117  1.00 18.78      C
ATOM  1994 C   ALA A 148    -47.723  39.184  3.113  1.00 18.85      C
ATOM  1995 O   ALA A 148    -47.548  37.975  3.206  1.00 18.80      O
ATOM  1997 N   LEU A 149    -46.869  40.013  2.523  1.00 19.08      N
ATOM  1998 CA  LEU A 149    -45.507  39.601  2.215  1.00 19.32      C
ATOM  2000 CB  LEU A 149    -45.056  40.145   .863  1.00 19.14      C
ATOM  2003 CG  LEU A 149    -45.819  39.650  -.364  1.00 19.16      C
ATOM  2005 CD1 LEU A 149    -45.036  39.929 -1.645  1.00 18.43      C
ATOM  2009 CD2 LEU A 149    -46.089  38.175  -.259  1.00 20.09      C
ATOM  2013 C   LEU A 149    -44.527  40.029  3.304  1.00 19.60      C
ATOM  2014 O   LEU A 149    -44.797  40.916  4.113  1.00 19.20      O
ATOM  2016 N   GLU A 150    -43.384  39.361  3.309  1.00 20.42      N
ATOM  2017 CA  GLU A 150    -42.286  39.674  4.215  1.00 21.03      C
ATOM  2019 CB  GLU A 150    -41.098  38.741  3.948  1.00 21.03      C
ATOM  2022 CG  GLU A 150    -40.491  38.176  5.205  1.00 22.23      C
ATOM  2025 CD  GLU A 150    -39.433  37.117  4.941  1.00 24.34      C
ATOM  2026 OE1 GLU A 150    -39.189  36.786  3.753  1.00 24.53      O
ATOM  2027 OE2 GLU A 150    -38.843  36.625  5.940  1.00 25.82      O
ATOM  2028 C   GLU A 150    -41.887  41.130  4.011  1.00 21.29      C
ATOM  2029 O   GLU A 150    -41.619  41.544  2.885  1.00 21.13      O
ATOM  2031 N   GLY A 151    -41.893  41.903  5.094  1.00 21.89      N
ATOM  2032 CA  GLY A 151    -41.636  43.341  5.030  1.00 22.25      C
ATOM  2035 C   GLY A 151    -42.871  44.221  5.152  1.00 22.67      C
ATOM  2036 O   GLY A 151    -42.757  45.397  5.462  1.00 22.84      O
ATOM  2038 N   GLU A 152    -44.055  43.669  4.918  1.00 23.19      N
ATOM  2039 CA  GLU A 152    -45.263  44.474  4.937  1.00 23.76      C
ATOM  2041 CB  GLU A 152    -46.350  43.813  4.100  1.00 23.79      C
ATOM  2044 CG  GLU A 152    -46.037  43.890  2.615  1.00 23.98      C
ATOM  2047 CD  GLU A 152    -47.147  43.368  1.749  1.00 23.72      C
ATOM  2048 OE1 GLU A 152    -47.226  43.771   .574  1.00 22.11      O
ATOM  2049 OE2 GLU A 152    -47.939  42.542  2.241  1.00 25.41      O
ATOM  2050 C   GLU A 152    -45.722  44.719  6.365  1.00 24.47      C
ATOM  2051 O   GLU A 152    -46.586  44.006  6.906  1.00 24.70      O
ATOM  2053 N   ASN A 153    -45.134  45.744  6.969  1.00 25.00      N
ATOM  2054 CA  ASN A 153    -45.287  45.978  8.404  1.00 25.59      C
ATOM  2056 CB  ASN A 153    -44.221  46.957  8.902  1.00 25.55      C
ATOM  2059 CG  ASN A 153    -44.386  48.331  8.308  1.00 25.57      C
ATOM  2060 OD1 ASN A 153    -44.114  48.557  7.128  1.00 24.52      O
ATOM  2061 ND2 ASN A 153    -44.867  49.256  9.117  1.00 27.05      N
ATOM  2064 C   ASN A 153    -46.679  46.486  8.772  1.00 25.92      C
ATOM  2065 O   ASN A 153    -47.172  46.238  9.872  1.00 26.02      O
ATOM  2067 N   ILE A 154    -47.310  47.197  7.847  1.00 26.35      N
ATOM  2068 CA  ILE A 154    -48.638  47.751  8.082  1.00 26.57      C
ATOM  2070 CB  ILE A 154    -49.013  48.779  7.007  1.00 26.45      C
ATOM  2072 CG1 ILE A 154    -48.159  50.023  7.164  1.00 26.36      C
ATOM  2075 CD1 ILE A 154    -48.060  50.790  5.883  1.00 27.92      C
ATOM  2079 CG2 ILE A 154    -50.467  49.152  7.089  1.00 26.25      C
ATOM  2083 C   ILE A 154    -49.674  46.643  8.111  1.00 26.96      C
ATOM  2084 O   ILE A 154    -50.650  46.741  8.851  1.00 27.12      O
ATOM  2086 N   LEU A 155    -49.467  45.588  7.320  1.00 27.35      N
ATOM  2087 CA  LEU A 155    -50.422  44.475  7.304  1.00 27.76      C
ATOM  2089 CB  LEU A 155    -50.238  43.594  6.067  1.00 27.73      C
ATOM  2092 CG  LEU A 155    -51.090  43.990  4.875  1.00 27.31      C
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ATOM  2094 CD1 LEU A 155    -50.980  45.456   4.683  1.00 28.13      C
ATOM  2098 CD2 LEU A 155    -50.633  43.262   3.623  1.00 27.79      C
ATOM  2102 C   LEU A 155    -50.340  43.642   8.582  1.00 28.22      C
ATOM  2103 O   LEU A 155    -51.361  43.237   9.112  1.00 27.95      O
ATOM  2105 N   ASP A 156    -49.128  43.395   9.068  1.00 28.95      N
ATOM  2106 CA  ASP A 156    -48.944  42.723  10.348  1.00 29.71      C
ATOM  2108 CB  ASP A 156    -47.450  42.461  10.639  1.00 30.23      C
ATOM  2111 CG  ASP A 156    -46.938  41.125  10.027  1.00 32.82      C
ATOM  2112 OD1 ASP A 156    -47.765  40.240   9.658  1.00 36.27      O
ATOM  2113 OD2 ASP A 156    -45.700  40.961   9.923  1.00 34.48      O
ATOM  2114 C   ASP A 156    -49.570  43.539  11.469  1.00 29.66      C
ATOM  2115 O   ASP A 156    -50.109  42.969  12.425  1.00 29.81      O
ATOM  2117 N   GLU A 157    -49.514  44.866  11.345  1.00 29.69      N
ATOM  2118 CA  GLU A 157    -50.129  45.768  12.329  1.00 29.57      C
ATOM  2120 CB  GLU A 157    -49.581  47.186  12.178  1.00 29.71      C
ATOM  2123 CG  GLU A 157    -48.164  47.326  12.712  1.00 30.53      C
ATOM  2126 CD  GLU A 157    -47.455  48.544  12.169  1.00 31.96      C
ATOM  2127 OE1 GLU A 157    -48.167  49.491  11.741  1.00 33.56      O
ATOM  2128 OE2 GLU A 157    -46.195  48.546  12.166  1.00 31.54      O
ATOM  2129 C   GLU A 157    -51.649  45.771  12.230  1.00 29.16      C
ATOM  2130 O   GLU A 157    -52.330  45.819  13.241  1.00 29.00      O
ATOM  2132 N   ALA A 158    -52.172  45.716  11.010  1.00 28.86      N
ATOM  2133 CA  ALA A 158    -53.606  45.570  10.792  1.00 28.79      C
ATOM  2135 CB  ALA A 158    -53.893  45.456   9.301  1.00 28.44      C
ATOM  2139 C   ALA A 158    -54.171  44.352  11.536  1.00 28.93      C
ATOM  2140 O   ALA A 158    -55.265  44.402  12.098  1.00 28.77      O
ATOM  2142 N   LYS A 159    -53.416  43.260  11.528  1.00 29.19      N
ATOM  2143 CA  LYS A 159    -53.849  42.022  12.143  1.00 29.57      C
ATOM  2145 CB  LYS A 159    -52.929  40.880  11.710  1.00 29.62      C
ATOM  2148 CG  LYS A 159    -53.297  39.513  12.258  1.00 30.27      C
ATOM  2151 CD  LYS A 159    -52.765  38.365  11.387  1.00 31.78      C
ATOM  2154 CE  LYS A 159    -51.259  38.132  11.525  1.00 33.15      C
ATOM  2157 NZ  LYS A 159    -50.911  36.696  11.248  1.00 33.88      N
ATOM  2161 C   LYS A 159    -53.866  42.160  13.670  1.00 29.99      C
ATOM  2162 O   LYS A 159    -54.767  41.642  14.332  1.00 30.29      O
ATOM  2164 N   VAL A 160    -52.886  42.862  14.236  1.00 30.07      N
ATOM  2165 CA  VAL A 160    -52.840  43.047  15.696  1.00 30.03      C
ATOM  2167 CB  VAL A 160    -51.520  43.691  16.162  1.00 29.88      C
ATOM  2169 CG1 VAL A 160    -51.515  43.863  17.671  1.00 28.94      C
ATOM  2173 CG2 VAL A 160    -50.341  42.848  15.707  1.00 30.23      C
ATOM  2177 C   VAL A 160    -53.996  43.925  16.149  1.00 30.05      C
ATOM  2178 O   VAL A 160    -54.544  43.752  17.234  1.00 30.31      O
ATOM  2180 N   PHE A 161    -54.355  44.862  15.290  1.00 30.08      N
ATOM  2181 CA  PHE A 161    -55.407  45.808  15.558  1.00 30.09      C
ATOM  2183 CB  PHE A 161    -55.255  46.993  14.598  1.00 29.92      C
ATOM  2186 CG  PHE A 161    -56.370  47.974  14.654  1.00 28.52      C
ATOM  2187 CD1 PHE A 161    -56.347  49.005  15.554  1.00 27.92      C
ATOM  2189 CE1 PHE A 161    -57.361  49.903  15.600  1.00 28.06      C
ATOM  2191 CZ  PHE A 161    -58.411  49.783  14.733  1.00 28.76      C
ATOM  2193 CE2 PHE A 161    -58.441  48.757  13.826  1.00 28.31      C
ATOM  2195 CD2 PHE A 161    -57.429  47.869  13.789  1.00 28.16      C
ATOM  2197 C   PHE A 161    -56.746  45.123  15.388  1.00 30.55      C
ATOM  2198 O   PHE A 161    -57.598  45.203  16.258  1.00 30.53      O
ATOM  2200 N   ALA A 162    -56.930  44.438  14.271  1.00 31.34      N
ATOM  2201 CA  ALA A 162    -58.193  43.770  14.023  1.00 32.26      C
ATOM  2203 CB  ALA A 162    -58.217  43.139  12.643  1.00 32.31      C
ATOM  2207 C   ALA A 162    -58.500  42.734  15.118  1.00 33.09      C
ATOM  2208 O   ALA A 162    -59.557  42.814  15.735  1.00 33.83      O
ATOM  2210 N   ILE A 163    -57.587  41.799  15.393  1.00 33.59      N
ATOM  2211 CA  ILE A 163    -57.826  40.799  16.438  1.00 34.02      C
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ATOM  2213  CB  ILE A 163    -56.597  39.907  16.745  1.00 33.98      C
ATOM  2215  CG1 ILE A 163    -56.235  39.008  15.566  1.00 34.37      C
ATOM  2218  CD1 ILE A 163    -54.878  38.317  15.722  1.00 34.38      C
ATOM  2222  CG2 ILE A 163    -56.883  38.995  17.919  1.00 33.38      C
ATOM  2226  C   ILE A 163    -58.225  41.472  17.744  1.00 34.75      C
ATOM  2227  O   ILE A 163    -59.189  41.064  18.373  1.00 35.03      O
ATOM  2229  N   SER A 164    -57.501  42.504  18.156  1.00 35.76      N
ATOM  2230  CA  SER A 164    -57.763  43.117  19.463  1.00 36.59      C
ATOM  2232  CB  SER A 164    -56.828  44.293  19.735  1.00 36.59      C
ATOM  2235  OG  SER A 164    -57.350  45.485  19.164  1.00 36.46      O
ATOM  2237  C   SER A 164    -59.196  43.611  19.556  1.00 37.42      C
ATOM  2238  O   SER A 164    -59.860  43.420  20.571  1.00 37.38      O
ATOM  2240  N   HIS A 165    -59.661  44.251  18.486  1.00 38.51      N
ATOM  2241  CA  HIS A 165    -60.990  44.851  18.467  1.00 39.40      C
ATOM  2243  CB  HIS A 165    -61.008  46.097  17.574  1.00 39.76      C
ATOM  2246  CG  HIS A 165    -60.467  47.323  18.251  1.00 42.06      C
ATOM  2247  ND1 HIS A 165    -59.205  47.821  18.000  1.00 44.21      N
ATOM  2249  CE1 HIS A 165    -58.998  48.893  18.748  1.00 45.04      C
ATOM  2251  NE2 HIS A 165    -60.080  49.106  19.478  1.00 44.99      N
ATOM  2253  CD2 HIS A 165    -61.011  48.135  19.192  1.00 43.76      C
ATOM  2255  C   HIS A 165    -62.078  43.872  18.060  1.00 39.38      C
ATOM  2256  O   HIS A 165    -63.248  44.244  18.067  1.00 39.43      O
ATOM  2258  N   LEU A 166    -61.683  42.632  17.745  1.00 39.54      N
ATOM  2259  CA  LEU A 166    -62.589  41.550  17.326  1.00 39.55      C
ATOM  2261  CB  LEU A 166    -62.001  40.766  16.154  1.00 39.28      C
ATOM  2264  CG  LEU A 166    -62.156  41.339  14.752  1.00 38.23      C
ATOM  2266  CD1 LEU A 166    -61.361  40.501  13.805  1.00 37.53      C
ATOM  2270  CD2 LEU A 166    -63.594  41.367  14.332  1.00 37.21      C
ATOM  2274  C   LEU A 166    -62.842  40.555  18.438  1.00 40.08      C
ATOM  2275  O   LEU A 166    -63.991  40.220  18.733  1.00 40.42      O
ATOM  2277  N   LYS A 167    -61.766  40.074  19.052  1.00 40.58      N
ATOM  2278  CA  LYS A 167    -61.875  39.090  20.133  1.00 41.09      C
ATOM  2280  CB  LYS A 167    -60.491  38.632  20.595  1.00 41.13      C
ATOM  2283  CG  LYS A 167    -59.897  39.399  21.768  1.00 42.16      C
ATOM  2286  CD  LYS A 167    -58.421  39.035  22.013  1.00 44.45      C
ATOM  2289  CE  LYS A 167    -58.070  37.561  21.654  1.00 45.56      C
ATOM  2292  NZ  LYS A 167    -56.610  37.237  21.798  1.00 46.20      N
ATOM  2296  C   LYS A 167    -62.678  39.584  21.337  1.00 41.23      C
ATOM  2297  O   LYS A 167    -62.994  38.793  22.215  1.00 41.47      O
ATOM  2299  N   GLU A 168    -62.995  40.884  21.352  1.00 41.49      N
ATOM  2300  CA  GLU A 168    -63.704  41.583  22.437  1.00 41.42      C
ATOM  2302  CB  GLU A 168    -65.201  41.730  22.100  1.00 41.27      C
ATOM  2305  CG  GLU A 168    -65.995  40.424  22.016  1.00 41.01      C
ATOM  2308  CD  GLU A 168    -66.928  40.328  20.787  1.00 40.84      C
ATOM  2309  OE1 GLU A 168    -66.701  41.040  19.770  1.00 39.82      O
ATOM  2310  OE2 GLU A 168    -67.884  39.509  20.845  1.00 39.04      O
ATOM  2311  C   GLU A 168    -63.484  41.004  23.843  1.00 41.66      C
ATOM  2312  O   GLU A 168    -62.435  41.231  24.469  1.00 41.46      O
ATOM  2314  N   GLU A 172    -71.668  38.961  21.192  1.00 55.65      N
ATOM  2315  CA  GLU A 172    -73.052  39.153  20.721  1.00 56.00      C
ATOM  2317  CB  GLU A 172    -73.876  37.880  20.937  1.00 56.27      C
ATOM  2320  CG  GLU A 172    -73.198  36.620  20.390  1.00 57.12      C
ATOM  2323  CD  GLU A 172    -74.056  35.363  20.516  1.00 58.18      C
ATOM  2324  OE1 GLU A 172    -75.300  35.480  20.622  1.00 58.84      O
ATOM  2325  OE2 GLU A 172    -73.480  34.249  20.498  1.00 58.98      O
ATOM  2326  C   GLU A 172    -73.766  40.386  21.334  1.00 55.70      C
ATOM  2327  O   GLU A 172    -74.956  40.347  21.688  1.00 54.95      O
ATOM  2329  N   LYS A 173    -72.987  41.458  21.486  1.00 55.58      N
ATOM  2330  CA  LYS A 173    -73.496  42.831  21.466  1.00 55.43      C
ATOM  2332  CB  LYS A 173    -72.649  43.741  22.357  1.00 55.51      C
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ATOM 2335 CG LYS A 173 -72.527 43.223 23.793 1.00 56.07 C
ATOM 2338 CD LYS A 173 -72.803 44.291 24.868 1.00 55.87 C
ATOM 2341 CE LYS A 173 -73.111 43.642 26.221 1.00 55.20 C
ATOM 2344 NZ LYS A 173 -72.893 44.576 27.348 1.00 54.63 N
ATOM 2348 C LYS A 173 -73.449 43.297 20.009 1.00 55.01 C
ATOM 2349 O LYS A 173 -74.091 44.274 19.625 1.00 54.97 O
ATOM 2351 N ILE A 174 -72.647 42.581 19.223 1.00 54.57 N
ATOM 2352 CA ILE A 174 -72.713 42.550 17.767 1.00 54.22 C
ATOM 2354 CB ILE A 174 -71.429 41.845 17.227 1.00 54.21 C
ATOM 2356 CG1 ILE A 174 -70.196 42.724 17.474 1.00 54.73 C
ATOM 2359 CD1 ILE A 174 -68.858 41.949 17.553 1.00 55.78 C
ATOM 2363 CG2 ILE A 174 -71.532 41.504 15.759 1.00 54.06 C
ATOM 2367 C ILE A 174 -73.957 41.744 17.384 1.00 53.88 C
ATOM 2368 O ILE A 174 -74.587 41.134 18.250 1.00 53.83 O
ATOM 2370 N GLY A 175 -74.332 41.747 16.107 1.00 53.59 N
ATOM 2371 CA GLY A 175 -75.351 40.817 15.613 1.00 53.51 C
ATOM 2374 C GLY A 175 -75.130 39.395 16.126 1.00 53.43 C
ATOM 2375 O GLY A 175 -74.119 39.105 16.760 1.00 53.80 O
ATOM 2377 N LYS A 176 -76.070 38.495 15.861 1.00 53.10 N
ATOM 2378 CA LYS A 176 -75.926 37.098 16.286 1.00 52.68 C
ATOM 2380 CB LYS A 176 -77.291 36.522 16.677 1.00 52.99 C
ATOM 2383 CG LYS A 176 -78.003 37.387 17.746 1.00 54.12 C
ATOM 2386 CD LYS A 176 -79.201 36.697 18.436 1.00 54.57 C
ATOM 2389 CE LYS A 176 -79.503 37.369 19.792 1.00 54.79 C
ATOM 2392 NZ LYS A 176 -80.458 36.598 20.653 1.00 55.20 N
ATOM 2396 C LYS A 176 -75.246 36.267 15.196 1.00 51.83 C
ATOM 2397 O LYS A 176 -74.393 35.433 15.486 1.00 51.69 O
ATOM 2399 N GLU A 177 -75.609 36.520 13.940 1.00 50.90 N
ATOM 2400 CA GLU A 177 -74.975 35.854 12.800 1.00 50.19 C
ATOM 2402 CB GLU A 177 -75.792 36.062 11.507 1.00 50.41 C
ATOM 2405 CG GLU A 177 -75.506 37.368 10.735 1.00 51.03 C
ATOM 2408 CD GLU A 177 -76.403 37.572 9.507 1.00 52.17 C
ATOM 2409 OE1 GLU A 177 -75.955 38.276 8.569 1.00 52.63 O
ATOM 2410 OE2 GLU A 177 -77.546 37.048 9.479 1.00 52.03 O
ATOM 2411 C GLU A 177 -73.549 36.369 12.607 1.00 49.10 C
ATOM 2412 O GLU A 177 -72.626 35.597 12.321 1.00 49.53 O
ATOM 2414 N LEU A 178 -73.388 37.681 12.770 1.00 47.39 N
ATOM 2415 CA LEU A 178 -72.110 38.371 12.575 1.00 45.63 C
ATOM 2417 CB LEU A 178 -72.352 39.877 12.615 1.00 45.59 C
ATOM 2420 CG LEU A 178 -71.280 40.809 12.085 1.00 45.45 C
ATOM 2422 CD1 LEU A 178 -70.969 40.515 10.620 1.00 45.45 C
ATOM 2426 CD2 LEU A 178 -71.765 42.233 12.279 1.00 44.63 C
ATOM 2430 C LEU A 178 -71.095 37.979 13.634 1.00 44.06 C
ATOM 2431 O LEU A 178 -69.902 38.012 13.387 1.00 43.70 O
ATOM 2433 N ALA A 179 -71.586 37.611 14.810 1.00 42.54 N
ATOM 2434 CA ALA A 179 -70.753 37.041 15.847 1.00 41.66 C
ATOM 2436 CB ALA A 179 -71.545 36.884 17.122 1.00 41.69 C
ATOM 2440 C ALA A 179 -70.193 35.695 15.416 1.00 40.75 C
ATOM 2441 O ALA A 179 -69.078 35.351 15.769 1.00 40.61 O
ATOM 2443 N GLU A 180 -70.974 34.931 14.664 1.00 39.88 N
ATOM 2444 CA GLU A 180 -70.518 33.639 14.143 1.00 39.40 C
ATOM 2446 CB GLU A 180 -71.710 32.781 13.718 1.00 39.74 C
ATOM 2449 CG GLU A 180 -72.650 32.415 14.865 1.00 40.88 C
ATOM 2452 CD GLU A 180 -73.913 31.710 14.398 1.00 42.02 C
ATOM 2453 OE1 GLU A 180 -74.380 32.022 13.271 1.00 43.05 O
ATOM 2454 OE2 GLU A 180 -74.437 30.857 15.166 1.00 41.93 O
ATOM 2455 C GLU A 180 -69.565 33.805 12.960 1.00 38.29 C
ATOM 2456 O GLU A 180 -68.739 32.940 12.699 1.00 38.23 O
ATOM 2458 N GLN A 181 -69.704 34.911 12.240 1.00 36.92 N
ATOM 2459 CA GLN A 181 -68.748 35.299 11.223 1.00 35.74 C

ATOM 2461 CB GLN A 181 -69.272 36.516 10.463 1.00 35.94 C
ATOM 2464 CG GLN A 181 -68.931 36.537 8.975 1.00 36.93 C
ATOM 2467 CD GLN A 181 -69.693 35.492 8.176 1.00 37.72 C
ATOM 2468 OE1 GLN A 181 -70.769 35.067 8.567 1.00 38.78 O
ATOM 2469 NE2 GLN A 181 -69.139 35.083 7.050 1.00 38.11 N
ATOM 2472 C GLN A 181 -67.406 35.632 11.881 1.00 34.64 C
ATOM 2473 O GLN A 181 -66.348 35.411 11.294 1.00 34.73 O
ATOM 2475 N VAL A 182 -67.448 36.158 13.102 1.00 33.29 N
ATOM 2476 CA VAL A 182 -66.224 36.488 13.842 1.00 32.28 C
ATOM 2478 CB VAL A 182 -66.433 37.653 14.855 1.00 32.10 C
ATOM 2480 CG1 VAL A 182 -66.328 38.991 14.166 1.00 31.51 C
ATOM 2484 CG2 VAL A 182 -65.420 37.594 15.957 1.00 31.69 C
ATOM 2488 C VAL A 182 -65.613 35.298 14.575 1.00 31.49 C
ATOM 2489 O VAL A 182 -64.396 35.230 14.668 1.00 31.43 O
ATOM 2491 N SER A 183 -66.422 34.378 15.106 1.00 30.56 N
ATOM 2492 CA SER A 183 -65.860 33.174 15.744 1.00 30.16 C
ATOM 2494 CB SER A 183 -66.926 32.253 16.327 1.00 30.29 C
ATOM 2497 OG SER A 183 -67.796 32.934 17.214 1.00 32.35 O
ATOM 2499 C SER A 183 -65.111 32.403 14.692 1.00 29.30 C
ATOM 2500 O SER A 183 -63.974 31.981 14.903 1.00 29.32 O
ATOM 2502 N HIS A 184 -65.768 32.252 13.546 1.00 28.24 N
ATOM 2503 CA HIS A 184 -65.215 31.578 12.379 1.00 27.36 C
ATOM 2505 CB HIS A 184 -66.245 31.653 11.254 1.00 27.41 C
ATOM 2508 CG HIS A 184 -65.930 30.807 10.064 1.00 26.90 C
ATOM 2509 ND1 HIS A 184 -65.484 29.511 10.166 1.00 27.76 N
ATOM 2511 CE1 HIS A 184 -65.321 29.009 8.955 1.00 27.47 C
ATOM 2513 NE2 HIS A 184 -65.661 29.929 8.075 1.00 26.52 N
ATOM 2515 CD2 HIS A 184 -66.059 31.058 8.742 1.00 26.61 C
ATOM 2517 C HIS A 184 -63.898 32.200 11.940 1.00 26.69 C
ATOM 2518 O HIS A 184 -62.881 31.525 11.862 1.00 26.44 O
ATOM 2520 N ALA A 185 -63.909 33.498 11.675 1.00 26.11 N
ATOM 2521 CA ALA A 185 -62.711 34.176 11.205 1.00 25.63 C
ATOM 2523 CB ALA A 185 -62.970 35.627 11.109 1.00 25.74 C
ATOM 2527 C ALA A 185 -61.552 33.917 12.153 1.00 25.33 C
ATOM 2528 O ALA A 185 -60.451 33.572 11.725 1.00 25.79 O
ATOM 2530 N LEU A 186 -61.814 34.066 13.450 1.00 24.77 N
ATOM 2531 CA LEU A 186 -60.776 33.940 14.470 1.00 24.05 C
ATOM 2533 CB LEU A 186 -61.256 34.498 15.814 1.00 23.63 C
ATOM 2536 CG LEU A 186 -61.516 36.012 15.903 1.00 22.51 C
ATOM 2538 CD1 LEU A 186 -62.057 36.399 17.266 1.00 20.79 C
ATOM 2542 CD2 LEU A 186 -60.273 36.793 15.613 1.00 21.13 C
ATOM 2546 C LEU A 186 -60.316 32.497 14.613 1.00 24.02 C
ATOM 2547 O LEU A 186 -59.169 32.250 14.943 1.00 24.27 O
ATOM 2549 N GLU A 187 -61.201 31.543 14.347 1.00 23.88 N
ATOM 2550 CA GLU A 187 -60.836 30.117 14.348 1.00 23.53 C
ATOM 2552 CB GLU A 187 -62.029 29.270 13.919 1.00 23.66 C
ATOM 2555 CG GLU A 187 -61.945 27.828 14.316 1.00 25.26 C
ATOM 2558 CD GLU A 187 -63.049 26.971 13.693 1.00 28.04 C
ATOM 2559 OE1 GLU A 187 -63.672 27.393 12.681 1.00 28.67 O
ATOM 2560 OE2 GLU A 187 -63.288 25.858 14.225 1.00 29.72 O
ATOM 2561 C GLU A 187 -59.686 29.838 13.395 1.00 22.92 C
ATOM 2562 O GLU A 187 -58.765 29.091 13.729 1.00 22.53 O
ATOM 2564 N LEU A 188 -59.763 30.446 12.209 1.00 22.46 N
ATOM 2565 CA LEU A 188 -58.799 30.246 11.121 1.00 22.07 C
ATOM 2567 CB LEU A 188 -58.802 28.794 10.635 1.00 22.11 C
ATOM 2570 CG LEU A 188 -57.876 28.362 9.493 1.00 22.17 C
ATOM 2572 CD1 LEU A 188 -56.456 28.051 9.961 1.00 21.62 C
ATOM 2576 CD2 LEU A 188 -58.464 27.134 8.822 1.00 22.40 C
ATOM 2580 C LEU A 188 -59.237 31.137 9.985 1.00 21.69 C
ATOM 2581 O LEU A 188 -60.380 31.075 9.563 1.00 21.53 O

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ATOM  2583  N   PRO A 189    -58.333  31.973   9.474  1.00 21.46      N
ATOM  2584  CA  PRO A 189    -58.745  32.935   8.472  1.00 21.18      C
ATOM  2586  CB  PRO A 189    -57.592  33.936   8.486  1.00 21.03      C
ATOM  2589  CG  PRO A 189    -56.423  33.118   8.757  1.00 21.21      C
ATOM  2592  CD  PRO A 189    -56.873  31.992   9.668  1.00 21.61      C
ATOM  2595  C   PRO A 189    -58.946  32.314   7.076  1.00 20.96      C
ATOM  2596  O   PRO A 189    -58.418  31.247   6.793  1.00 21.02      O
ATOM  2597  N   LEU A 190    -59.714  32.994   6.226  1.00 20.89      N
ATOM  2598  CA  LEU A 190    -60.018  32.533   4.867  1.00 20.74      C
ATOM  2600  CB  LEU A 190    -60.597  33.690   4.053  1.00 20.76      C
ATOM  2603  CG  LEU A 190    -62.090  33.924   4.259  1.00 21.35      C
ATOM  2605  CD1 LEU A 190    -62.537  35.196   3.578  1.00 20.54      C
ATOM  2609  CD2 LEU A 190    -62.889  32.712   3.720  1.00 23.39      C
ATOM  2613  C   LEU A 190    -58.814  31.971   4.112  1.00 20.35      C
ATOM  2614  O   LEU A 190    -58.859  30.871   3.546  1.00 20.08      O
ATOM  2616  N   HIS A 191    -57.734  32.746   4.132  1.00 19.81      N
ATOM  2617  CA  HIS A 191    -56.537  32.448   3.364  1.00 18.89      C
ATOM  2619  CB  HIS A 191    -55.548  33.592   3.536  1.00 18.92      C
ATOM  2622  CG  HIS A 191    -54.372  33.520   2.623  1.00 18.51      C
ATOM  2623  ND1 HIS A 191    -54.482  33.647   1.258  1.00 18.08      N
ATOM  2625  CE1 HIS A 191    -53.281  33.544    .718  1.00 18.96      C
ATOM  2627  NE2 HIS A 191    -52.397  33.371   1.684  1.00 17.01      N
ATOM  2629  CD2 HIS A 191    -53.054  33.355   2.884  1.00 17.94      C
ATOM  2631  C   HIS A 191    -55.889  31.142   3.759  1.00 18.32      C
ATOM  2632  O   HIS A 191    -55.217  30.531   2.942  1.00 17.98      O
ATOM  2634  N   ARG A 192    -56.093  30.719   5.006  1.00 18.06      N
ATOM  2635  CA  ARG A 192    -55.502  29.480   5.523  1.00 17.99      C
ATOM  2637  CB  ARG A 192    -54.940  29.722   6.909  1.00 17.77      C
ATOM  2640  CG  ARG A 192    -53.822  30.683   6.881  1.00 18.47      C
ATOM  2643  CD  ARG A 192    -53.082  30.748   8.196  1.00 19.80      C
ATOM  2646  NE  ARG A 192    -52.174  31.900   8.224  1.00 20.33      N
ATOM  2648  CZ  ARG A 192    -51.176  32.048   9.077  1.00 20.10      C
ATOM  2649  NH1 ARG A 192    -50.928  31.113   9.972  1.00 21.72      N
ATOM  2652  NH2 ARG A 192    -50.407  33.119   9.019  1.00 20.79      N
ATOM  2655  C   ARG A 192    -56.477  28.311   5.590  1.00 18.00      C
ATOM  2656  O   ARG A 192    -56.067  27.170   5.871  1.00 18.21      O
ATOM  2658  N   ARG A 193    -57.758  28.588   5.335  1.00 17.59      N
ATOM  2659  CA  ARG A 193    -58.779  27.563   5.382  1.00 17.16      C
ATOM  2661  CB  ARG A 193    -60.141  28.164   5.741  1.00 17.45      C
ATOM  2664  CG  ARG A 193    -61.109  27.132   6.322  1.00 18.70      C
ATOM  2667  CD  ARG A 193    -62.479  27.682   6.686  1.00 20.20      C
ATOM  2670  NE  ARG A 193    -62.423  28.682   7.751  1.00 22.59      N
ATOM  2672  CZ  ARG A 193    -62.386  28.435   9.067  1.00 24.12      C
ATOM  2673  NH1 ARG A 193    -62.395  27.198   9.575  1.00 22.66      N
ATOM  2676  NH2 ARG A 193    -62.348  29.469   9.898  1.00 26.36      N
ATOM  2679  C   ARG A 193    -58.871  26.842   4.058  1.00 16.63      C
ATOM  2680  O   ARG A 193    -58.861  27.461   3.005  1.00 15.93      O
ATOM  2682  N   THR A 194    -58.955  25.518   4.149  1.00 16.72      N
ATOM  2683  CA  THR A 194    -59.332  24.638   3.051  1.00 16.88      C
ATOM  2685  CB  THR A 194    -59.520  23.250   3.592  1.00 16.43      C
ATOM  2687  OG1 THR A 194    -58.252  22.605   3.583  1.00 17.74      O
ATOM  2689  CG2 THR A 194    -60.454  22.441   2.754  1.00 18.43      C
ATOM  2693  C   THR A 194    -60.607  25.112   2.384  1.00 17.28      C
ATOM  2694  O   THR A 194    -61.441  25.734   3.022  1.00 17.44      O
ATOM  2696  N   GLN A 195    -60.765  24.855   1.091  1.00 18.05      N
ATOM  2697  CA  GLN A 195    -61.925  25.402    .397  1.00 18.76      C
ATOM  2699  CB  GLN A 195    -61.768  25.381  -1.114  1.00 18.87      C
ATOM  2702  CG  GLN A 195    -63.145  25.523  -1.761  1.00 20.75      C
ATOM  2705  CD  GLN A 195    -63.095  25.922  -3.179  1.00 23.41      C
ATOM  2706  OE1 GLN A 195    -62.031  26.088  -3.733  1.00 27.07      O
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ATOM  2707 NE2 GLN A 195    -64.248  26.090  -3.791  1.00 25.02      N
ATOM  2710 C   GLN A 195    -63.243  24.704    .765  1.00 18.93      C
ATOM  2711 O   GLN A 195    -64.169  25.333   1.291  1.00 19.42      O
ATOM  2713 N   ARG A 196    -63.345  23.418    .443  1.00 18.90      N
ATOM  2714 CA  ARG A 196    -64.577  22.685    .663  1.00 18.68      C
ATOM  2716 CB  ARG A 196    -64.356  21.186    .454  1.00 18.53      C
ATOM  2719 CG  ARG A 196    -64.851  20.644   -.888  1.00 18.31      C
ATOM  2722 CD  ARG A 196    -64.705  21.622  -2.037  1.00 17.93      C
ATOM  2725 NE  ARG A 196    -65.930  21.720  -2.834  1.00 18.52      N
ATOM  2727 CZ  ARG A 196    -66.480  22.857  -3.256  1.00 18.63      C
ATOM  2728 NH1 ARG A 196    -65.938  24.014  -2.937  1.00 19.84      N
ATOM  2731 NH2 ARG A 196    -67.582  22.844  -3.999  1.00 18.53      N
ATOM  2734 C   ARG A 196    -65.070  22.982   2.061  1.00 19.02      C
ATOM  2735 O   ARG A 196    -66.276  23.085   2.284  1.00 19.30      O
ATOM  2737 N   LEU A 197    -64.127  23.152   2.990  1.00 19.09      N
ATOM  2738 CA  LEU A 197    -64.444  23.432   4.379  1.00 19.19      C
ATOM  2740 CB  LEU A 197    -63.203  23.346   5.262  1.00 19.14      C
ATOM  2743 CG  LEU A 197    -63.135  22.097   6.130  1.00 19.99      C
ATOM  2745 CD1 LEU A 197    -64.476  21.899   6.811  1.00 21.56      C
ATOM  2749 CD2 LEU A 197    -62.016  22.198   7.161  1.00 20.06      C
ATOM  2753 C   LEU A 197    -65.071  24.781   4.553  1.00 19.52      C
ATOM  2754 O   LEU A 197    -66.052  24.902   5.252  1.00 19.85      O
ATOM  2756 N   GLU A 198    -64.488  25.803   3.941  1.00 20.11      N
ATOM  2757 CA  GLU A 198    -65.051  27.147   3.986  1.00 20.47      C
ATOM  2759 CB  GLU A 198    -64.079  28.156   3.385  1.00 20.84      C
ATOM  2762 CG  GLU A 198    -64.659  29.539   3.069  1.00 22.30      C
ATOM  2765 CD  GLU A 198    -65.206  30.260   4.283  1.00 24.40      C
ATOM  2766 OE1 GLU A 198    -64.852  29.894   5.418  1.00 25.34      O
ATOM  2767 OE2 GLU A 198    -65.991  31.217   4.106  1.00 26.83      O
ATOM  2768 C   GLU A 198    -66.360  27.186   3.226  1.00 20.57      C
ATOM  2769 O   GLU A 198    -67.212  28.009   3.529  1.00 20.65      O
ATOM  2771 N   ALA A 199    -66.519  26.298   2.240  1.00 20.76      N
ATOM  2772 CA  ALA A 199    -67.751  26.229   1.452  1.00 20.52      C
ATOM  2774 CB  ALA A 199    -67.521  25.492    .166  1.00 20.44      C
ATOM  2778 C   ALA A 199    -68.907  25.611   2.232  1.00 20.55      C
ATOM  2779 O   ALA A 199    -69.988  26.158   2.202  1.00 20.17      O
ATOM  2781 N   VAL A 200    -68.701  24.493   2.933  1.00 21.10      N
ATOM  2782 CA  VAL A 200    -69.791  23.935   3.774  1.00 21.51      C
ATOM  2784 CB  VAL A 200    -69.509  22.576   4.485  1.00 21.18      C
ATOM  2786 CG1 VAL A 200    -69.618  21.460   3.525  1.00 21.27      C
ATOM  2790 CG2 VAL A 200    -68.161  22.569   5.200  1.00 21.23      C
ATOM  2794 C   VAL A 200    -70.170  24.905   4.860  1.00 21.99      C
ATOM  2795 O   VAL A 200    -71.338  25.022   5.186  1.00 22.99      O
ATOM  2797 N   TRP A 201    -69.204  25.590   5.440  1.00 22.10      N
ATOM  2798 CA  TRP A 201    -69.551  26.565   6.433  1.00 22.58      C
ATOM  2800 CB  TRP A 201    -68.315  27.144   7.121  1.00 22.92      C
ATOM  2803 CG  TRP A 201    -68.667  27.957   8.310  1.00 23.65      C
ATOM  2804 CD1 TRP A 201    -68.758  27.520   9.588  1.00 25.08      C
ATOM  2806 NE1 TRP A 201    -69.127  28.549  10.417  1.00 26.35      N
ATOM  2808 CE2 TRP A 201    -69.290  29.683   9.669  1.00 25.48      C
ATOM  2809 CD2 TRP A 201    -69.010  29.344   8.332  1.00 24.77      C
ATOM  2810 CE3 TRP A 201    -69.095  30.336   7.355  1.00 24.92      C
ATOM  2812 CZ3 TRP A 201    -69.450  31.616   7.739  1.00 24.96      C
ATOM  2814 CH2 TRP A 201    -69.720  31.918   9.078  1.00 25.08      C
ATOM  2816 CZ2 TRP A 201    -69.648  30.968  10.056  1.00 24.68      C
ATOM  2818 C   TRP A 201    -70.351  27.662   5.758  1.00 22.71      C
ATOM  2819 O   TRP A 201    -71.482  27.921   6.140  1.00 22.76      O
ATOM  2821 N   SER A 202    -69.776  28.272   4.727  1.00 23.04      N
ATOM  2822 CA  SER A 202    -70.335  29.500   4.165  1.00 23.29      C
ATOM  2824 CB  SER A 202    -69.304  30.205   3.290  1.00 23.20      C
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ATOM 2827 OG SER A 202 -68.306 30.807 4.111 1.00 23.07 O
ATOM 2829 C SER A 202 -71.666 29.341 3.432 1.00 23.66 C
ATOM 2830 O SER A 202 -72.392 30.310 3.265 1.00 23.38 O
ATOM 2832 N ILE A 203 -71.996 28.124 3.016 1.00 24.49 N
ATOM 2833 CA ILE A 203 -73.321 27.859 2.460 1.00 25.07 C
ATOM 2835 CB ILE A 203 -73.391 26.530 1.653 1.00 24.74 C
ATOM 2837 CG1 ILE A 203 -72.494 26.587 .423 1.00 24.36 C
ATOM 2840 CD1 ILE A 203 -72.344 25.255 -.281 1.00 23.81 C
ATOM 2844 CG2 ILE A 203 -74.795 26.292 1.156 1.00 24.45 C
ATOM 2848 C ILE A 203 -74.338 27.858 3.607 1.00 25.91 C
ATOM 2849 O ILE A 203 -75.350 28.554 3.546 1.00 26.26 O
ATOM 2851 N GLU A 204 -74.051 27.104 4.662 1.00 26.69 N
ATOM 2852 CA GLU A 204 -74.929 27.053 5.824 1.00 27.40 C
ATOM 2854 CB GLU A 204 -74.286 26.217 6.931 1.00 27.65 C
ATOM 2857 CG GLU A 204 -75.132 26.032 8.183 1.00 29.02 C
ATOM 2860 CD GLU A 204 -76.530 25.491 7.903 1.00 30.44 C
ATOM 2861 OE1 GLU A 204 -76.746 24.858 6.844 1.00 31.22 O
ATOM 2862 OE2 GLU A 204 -77.417 25.703 8.753 1.00 31.96 O
ATOM 2863 C GLU A 204 -75.258 28.451 6.342 1.00 27.61 C
ATOM 2864 O GLU A 204 -76.409 28.778 6.526 1.00 27.78 O
ATOM 2866 N ALA A 205 -74.240 29.274 6.547 1.00 28.15 N
ATOM 2867 CA ALA A 205 -74.416 30.637 7.050 1.00 28.41 C
ATOM 2869 CB ALA A 205 -73.062 31.285 7.274 1.00 28.41 C
ATOM 2873 C ALA A 205 -75.234 31.520 6.136 1.00 28.84 C
ATOM 2874 O ALA A 205 -76.050 32.302 6.610 1.00 28.54 O
ATOM 2876 N TYR A 206 -74.978 31.408 4.832 1.00 29.84 N
ATOM 2877 CA TYR A 206 -75.581 32.281 3.805 1.00 30.41 C
ATOM 2879 CB TYR A 206 -74.801 32.170 2.493 1.00 30.20 C
ATOM 2882 CG TYR A 206 -75.180 33.173 1.425 1.00 29.62 C
ATOM 2883 CD1 TYR A 206 -74.721 34.482 1.484 1.00 30.32 C
ATOM 2885 CE1 TYR A 206 -75.047 35.412 .489 1.00 29.70 C
ATOM 2887 CZ TYR A 206 -75.830 35.028 -.578 1.00 28.41 C
ATOM 2888 OH TYR A 206 -76.155 35.956 -1.548 1.00 26.74 O
ATOM 2890 CE2 TYR A 206 -76.291 33.724 -.659 1.00 28.16 C
ATOM 2892 CD2 TYR A 206 -75.958 32.806 .335 1.00 28.39 C
ATOM 2894 C TYR A 206 -77.038 31.918 3.561 1.00 31.15 C
ATOM 2895 O TYR A 206 -77.858 32.781 3.268 1.00 31.30 O
ATOM 2897 N ARG A 207 -77.341 30.631 3.676 1.00 32.05 N
ATOM 2898 CA ARG A 207 -78.691 30.128 3.555 1.00 32.81 C
ATOM 2900 CB ARG A 207 -78.684 28.623 3.813 1.00 32.86 C
ATOM 2903 CG ARG A 207 -80.028 27.941 3.673 1.00 34.01 C
ATOM 2906 CD ARG A 207 -80.066 26.632 4.450 1.00 35.11 C
ATOM 2909 NE ARG A 207 -79.096 25.669 3.939 1.00 35.35 N
ATOM 2911 CZ ARG A 207 -79.353 24.737 3.022 1.00 36.00 C
ATOM 2912 NH1 ARG A 207 -80.562 24.611 2.478 1.00 35.55 N
ATOM 2915 NH2 ARG A 207 -78.381 23.918 2.640 1.00 37.05 N
ATOM 2918 C ARG A 207 -79.609 30.826 4.550 1.00 33.57 C
ATOM 2919 O ARG A 207 -80.783 31.003 4.263 1.00 33.82 O
ATOM 2921 N LYS A 208 -79.064 31.223 5.707 1.00 34.58 N
ATOM 2922 CA LYS A 208 -79.835 31.830 6.812 1.00 35.21 C
ATOM 2924 CB LYS A 208 -79.137 31.599 8.159 1.00 35.05 C
ATOM 2927 CG LYS A 208 -78.847 30.147 8.496 1.00 34.78 C
ATOM 2930 CD LYS A 208 -78.583 29.974 9.980 1.00 34.44 C
ATOM 2933 CE LYS A 208 -77.992 28.619 10.309 1.00 34.16 C
ATOM 2936 NZ LYS A 208 -76.540 28.693 10.572 1.00 33.81 N
ATOM 2940 C LYS A 208 -80.075 33.333 6.663 1.00 36.06 C
ATOM 2941 O LYS A 208 -81.032 33.857 7.226 1.00 36.19 O
ATOM 2943 N LYS A 209 -79.197 34.032 5.946 1.00 36.93 N
ATOM 2944 CA LYS A 209 -79.412 35.445 5.652 1.00 37.77 C
ATOM 2946 CB LYS A 209 -78.284 35.998 4.779 1.00 38.18 C

ATOM 2949 CG LYS A 209 -76.928 36.134 5.458 1.00 39.90 C
ATOM 2952 CD LYS A 209 -75.982 37.023 4.621 1.00 42.39 C
ATOM 2955 CE LYS A 209 -74.531 37.016 5.169 1.00 44.21 C
ATOM 2958 NZ LYS A 209 -74.350 37.688 6.509 1.00 44.75 N
ATOM 2962 C LYS A 209 -80.738 35.600 4.911 1.00 37.89 C
ATOM 2963 O LYS A 209 -81.049 34.785 4.036 1.00 38.20 O
ATOM 2965 N GLU A 210 -81.518 36.632 5.243 1.00 37.87 N
ATOM 2966 CA GLU A 210 -82.847 36.797 4.630 1.00 37.72 C
ATOM 2968 CB GLU A 210 -83.821 37.578 5.549 1.00 38.19 C
ATOM 2971 CG GLU A 210 -83.850 39.130 5.404 1.00 39.68 C
ATOM 2974 CD GLU A 210 -85.270 39.736 5.534 1.00 41.27 C
ATOM 2975 OE1 GLU A 210 -86.172 39.100 6.136 1.00 41.67 O
ATOM 2976 OE2 GLU A 210 -85.482 40.859 5.019 1.00 42.17 O
ATOM 2977 C GLU A 210 -82.760 37.394 3.219 1.00 36.68 C
ATOM 2978 O GLU A 210 -83.605 37.103 2.371 1.00 36.39 O
ATOM 2980 N ASP A 211 -81.725 38.198 2.969 1.00 35.65 N
ATOM 2981 CA ASP A 211 -81.481 38.777 1.632 1.00 34.94 C
ATOM 2983 CB ASP A 211 -81.064 40.257 1.740 1.00 35.22 C
ATOM 2986 CG ASP A 211 -79.811 40.477 2.599 1.00 35.84 C
ATOM 2987 OD1 ASP A 211 -79.379 39.557 3.341 1.00 35.60 O
ATOM 2988 OD2 ASP A 211 -79.276 41.606 2.536 1.00 36.73 O
ATOM 2989 C ASP A 211 -80.451 37.989 .811 1.00 33.73 C
ATOM 2990 O ASP A 211 -79.753 38.556 -.021 1.00 33.40 O
ATOM 2992 N ALA A 212 -80.366 36.682 1.057 1.00 32.53 N
ATOM 2993 CA ALA A 212 -79.506 35.783 .293 1.00 31.40 C
ATOM 2995 CB ALA A 212 -79.569 34.382 .889 1.00 30.79 C
ATOM 2999 C ALA A 212 -79.940 35.762 -1.176 1.00 30.60 C
ATOM 3000 O ALA A 212 -81.124 35.594 -1.467 1.00 30.37 O
ATOM 3002 N ASN A 213 -79.000 35.967 -2.097 1.00 29.71 N
ATOM 3003 CA ASN A 213 -79.304 35.809 -3.520 1.00 29.27 C
ATOM 3005 CB ASN A 213 -78.144 36.315 -4.402 1.00 29.30 C
ATOM 3008 CG ASN A 213 -78.442 36.217 -5.911 1.00 29.07 C
ATOM 3009 OD1 ASN A 213 -78.437 37.215 -6.624 1.00 29.38 O
ATOM 3010 ND2 ASN A 213 -78.691 35.015 -6.389 1.00 28.37 N
ATOM 3013 C ASN A 213 -79.634 34.328 -3.785 1.00 28.81 C
ATOM 3014 O ASN A 213 -78.784 33.455 -3.658 1.00 29.04 O
ATOM 3016 N GLN A 214 -80.880 34.053 -4.145 1.00 28.04 N
ATOM 3017 CA GLN A 214 -81.376 32.692 -4.191 1.00 27.32 C
ATOM 3019 CB GLN A 214 -82.906 32.700 -4.178 1.00 27.47 C
ATOM 3022 CG GLN A 214 -83.505 33.269 -2.889 1.00 27.68 C
ATOM 3025 CD GLN A 214 -83.294 32.359 -1.688 1.00 27.54 C
ATOM 3026 OE1 GLN A 214 -83.940 31.320 -1.571 1.00 28.19 O
ATOM 3027 NE2 GLN A 214 -82.392 32.748 -.790 1.00 26.90 N
ATOM 3030 C GLN A 214 -80.858 31.902 -5.385 1.00 26.71 C
ATOM 3031 O GLN A 214 -80.863 30.668 -5.355 1.00 26.91 O
ATOM 3033 N VAL A 215 -80.439 32.600 -6.442 1.00 25.81 N
ATOM 3034 CA VAL A 215 -79.789 31.947 -7.588 1.00 24.88 C
ATOM 3036 CB VAL A 215 -79.651 32.894 -8.808 1.00 24.81 C
ATOM 3038 CG1 VAL A 215 -78.459 32.483 -9.680 1.00 24.94 C
ATOM 3042 CG2 VAL A 215 -80.935 32.907 -9.620 1.00 23.74 C
ATOM 3046 C VAL A 215 -78.415 31.427 -7.176 1.00 24.18 C
ATOM 3047 O VAL A 215 -78.073 30.282 -7.430 1.00 23.74 O
ATOM 3049 N LEU A 216 -77.650 32.283 -6.510 1.00 23.78 N
ATOM 3050 CA LEU A 216 -76.299 31.961 -6.036 1.00 23.33 C
ATOM 3052 CB LEU A 216 -75.680 33.195 -5.373 1.00 23.10 C
ATOM 3055 CG LEU A 216 -74.194 33.192 -5.059 1.00 22.91 C
ATOM 3057 CD1 LEU A 216 -73.383 32.962 -6.312 1.00 22.88 C
ATOM 3061 CD2 LEU A 216 -73.826 34.518 -4.424 1.00 22.03 C
ATOM 3065 C LEU A 216 -76.333 30.797 -5.050 1.00 22.92 C
ATOM 3066 O LEU A 216 -75.598 29.826 -5.201 1.00 23.38 O

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ATOM   3068  N   LEU A 217    -77.214  30.890  -4.060  1.00 22.09           N
ATOM   3069  CA  LEU A 217    -77.367  29.851  -3.054  1.00 21.14           C
ATOM   3071  CB  LEU A 217    -78.488  30.225  -2.090  1.00 21.11           C
ATOM   3074  CG  LEU A 217    -78.782  29.236   -.961  1.00 21.08           C
ATOM   3076  CD1 LEU A 217    -77.703  29.267    .101  1.00 19.87           C
ATOM   3080  CD2 LEU A 217    -80.146  29.535   -.360  1.00 21.46           C
ATOM   3084  C   LEU A 217    -77.682  28.517  -3.685  1.00 20.38           C
ATOM   3085  O   LEU A 217    -77.133  27.508  -3.286  1.00 20.04           O
ATOM   3087  N   GLU A 218    -78.579  28.512  -4.661  1.00 19.97           N
ATOM   3088  CA  GLU A 218    -79.027  27.260  -5.273  1.00 19.72           C
ATOM   3090  CB  GLU A 218    -80.220  27.499  -6.212  1.00 19.87           C
ATOM   3093  CG  GLU A 218    -81.005  26.228  -6.627  1.00 21.03           C
ATOM   3096  CD  GLU A 218    -82.303  26.535  -7.424  1.00 22.59           C
ATOM   3097  OE1 GLU A 218    -82.643  27.730  -7.619  1.00 23.61           O
ATOM   3098  OE2 GLU A 218    -82.983  25.578  -7.863  1.00 22.31           O
ATOM   3099  C   GLU A 218    -77.854  26.613  -6.009  1.00 19.03           C
ATOM   3100  O   GLU A 218    -77.522  25.452  -5.764  1.00 18.97           O
ATOM   3102  N   LEU A 219    -77.203  27.381  -6.878  1.00 18.06           N
ATOM   3103  CA  LEU A 219    -76.012  26.907  -7.573  1.00 17.15           C
ATOM   3105  CB  LEU A 219    -75.439  28.029  -8.418  1.00 16.75           C
ATOM   3108  CG  LEU A 219    -74.196  27.717  -9.231  1.00 16.01           C
ATOM   3110  CD1 LEU A 219    -74.511  26.832 -10.404  1.00 12.99           C
ATOM   3114  CD2 LEU A 219    -73.577  29.028  -9.675  1.00 16.20           C
ATOM   3118  C   LEU A 219    -74.973  26.409  -6.570  1.00 16.75           C
ATOM   3119  O   LEU A 219    -74.377  25.355  -6.757  1.00 16.47           O
ATOM   3121  N   ALA A 220    -74.786  27.169  -5.496  1.00 16.40           N
ATOM   3122  CA  ALA A 220    -73.858  26.808  -4.422  1.00 16.15           C
ATOM   3124  CB  ALA A 220    -73.906  27.830  -3.302  1.00 16.13           C
ATOM   3128  C   ALA A 220    -74.137  25.436  -3.862  1.00 16.03           C
ATOM   3129  O   ALA A 220    -73.253  24.603  -3.799  1.00 16.30           O
ATOM   3131  N   ILE A 221    -75.371  25.201  -3.447  1.00 16.24           N
ATOM   3132  CA  ILE A 221    -75.731  23.916  -2.857  1.00 16.33           C
ATOM   3134  CB  ILE A 221    -77.203  23.895  -2.352  1.00 15.94           C
ATOM   3136  CG1 ILE A 221    -77.410  24.879  -1.203  1.00 15.36           C
ATOM   3139  CD1 ILE A 221    -78.842  25.234   -.962  1.00 14.49           C
ATOM   3143  CG2 ILE A 221    -77.571  22.537  -1.836  1.00 15.18           C
ATOM   3147  C   ILE A 221    -75.509  22.841  -3.911  1.00 17.06           C
ATOM   3148  O   ILE A 221    -74.899  21.819  -3.653  1.00 16.51           O
ATOM   3150  N   LEU A 222    -75.981  23.138  -5.117  1.00 18.53           N
ATOM   3151  CA  LEU A 222    -76.006  22.207  -6.243  1.00 19.25           C
ATOM   3153  CB  LEU A 222    -76.657  22.891  -7.445  1.00 19.18           C
ATOM   3156  CG  LEU A 222    -77.037  21.972  -8.597  1.00 19.65           C
ATOM   3158  CD1 LEU A 222    -78.318  22.489  -9.268  1.00 19.24           C
ATOM   3162  CD2 LEU A 222    -75.869  21.788  -9.597  1.00 18.75           C
ATOM   3166  C   LEU A 222    -74.618  21.751  -6.630  1.00 20.07           C
ATOM   3167  O   LEU A 222    -74.381  20.558  -6.778  1.00 20.55           O
ATOM   3169  N   ASP A 223    -73.710  22.711  -6.797  1.00 20.92           N
ATOM   3170  CA  ASP A 223    -72.330  22.427  -7.189  1.00 21.43           C
ATOM   3172  CB  ASP A 223    -71.621  23.723  -7.585  1.00 21.63           C
ATOM   3175  CG  ASP A 223    -70.202  23.495  -8.070  1.00 22.51           C
ATOM   3176  OD1 ASP A 223    -69.296  23.282  -7.225  1.00 24.67           O
ATOM   3177  OD2 ASP A 223    -69.990  23.544  -9.296  1.00 22.73           O
ATOM   3178  C   ASP A 223    -71.573  21.722  -6.060  1.00 21.79           C
ATOM   3179  O   ASP A 223    -70.843  20.764  -6.313  1.00 21.73           O
ATOM   3181  N   TYR A 224    -71.755  22.182  -4.820  1.00 22.14           N
ATOM   3182  CA  TYR A 224    -71.120  21.529  -3.686  1.00 22.22           C
ATOM   3184  CB  TYR A 224    -71.462  22.190  -2.355  1.00 22.38           C
ATOM   3187  CG  TYR A 224    -70.673  21.542  -1.249  1.00 22.65           C
ATOM   3188  CD1 TYR A 224    -69.356  21.864  -1.053  1.00 22.59           C
ATOM   3190  CE1 TYR A 224    -68.622  21.258   -.098  1.00 23.38           C
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ATOM 3192 CZ TYR A 224 -69.177 20.288 .670 1.00 23.22 C
ATOM 3193 OH TYR A 224 -68.402 19.684 1.620 1.00 23.93 O
ATOM 3195 CE2 TYR A 224 -70.483 19.931 .500 1.00 23.36 C
ATOM 3197 CD2 TYR A 224 -71.221 20.547 -.464 1.00 23.41 C
ATOM 3199 C TYR A 224 -71.485 20.065 -3.605 1.00 22.52 C
ATOM 3200 O TYR A 224 -70.641 19.233 -3.311 1.00 22.93 O
ATOM 3202 N ASN A 225 -72.742 19.749 -3.856 1.00 22.94 N
ATOM 3203 CA ASN A 225 -73.187 18.374 -3.801 1.00 23.44 C
ATOM 3205 CB ASN A 225 -74.706 18.310 -3.729 1.00 23.34 C
ATOM 3208 CG ASN A 225 -75.210 18.579 -2.352 1.00 22.62 C
ATOM 3209 OD1 ASN A 225 -74.749 17.977 -1.407 1.00 23.33 O
ATOM 3210 ND2 ASN A 225 -76.146 19.494 -2.223 1.00 22.52 N
ATOM 3213 C ASN A 225 -72.694 17.523 -4.959 1.00 24.26 C
ATOM 3214 O ASN A 225 -72.408 16.328 -4.767 1.00 24.88 O
ATOM 3216 N MET A 226 -72.607 18.119 -6.150 1.00 24.67 N
ATOM 3217 CA MET A 226 -72.167 17.395 -7.349 1.00 24.95 C
ATOM 3219 CB MET A 226 -72.421 18.237 -8.594 1.00 25.37 C
ATOM 3222 CG MET A 226 -71.785 17.713 -9.873 1.00 27.23 C
ATOM 3225 SD MET A 226 -70.837 19.010 -10.708 1.00 31.73 S
ATOM 3226 CE MET A 226 -72.185 20.000 -11.367 1.00 31.30 C
ATOM 3230 C MET A 226 -70.688 17.045 -7.247 1.00 24.70 C
ATOM 3231 O MET A 226 -70.291 15.929 -7.568 1.00 24.91 O
ATOM 3233 N ILE A 227 -69.873 17.995 -6.799 1.00 24.43 N
ATOM 3234 CA ILE A 227 -68.456 17.726 -6.598 1.00 24.18 C
ATOM 3236 CB ILE A 227 -67.656 18.971 -6.154 1.00 24.15 C
ATOM 3238 CG1 ILE A 227 -67.628 20.021 -7.253 1.00 23.64 C
ATOM 3241 CD1 ILE A 227 -66.853 21.246 -6.880 1.00 23.11 C
ATOM 3245 CG2 ILE A 227 -66.229 18.603 -5.827 1.00 24.36 C
ATOM 3249 C ILE A 227 -68.329 16.645 -5.546 1.00 23.98 C
ATOM 3250 O ILE A 227 -67.609 15.689 -5.747 1.00 24.35 O
ATOM 3252 N GLN A 228 -69.048 16.779 -4.439 1.00 23.79 N
ATOM 3253 CA GLN A 228 -69.020 15.754 -3.382 1.00 23.66 C
ATOM 3255 CB GLN A 228 -70.077 16.010 -2.305 1.00 23.64 C
ATOM 3258 CG GLN A 228 -69.972 15.049 -1.145 1.00 22.91 C
ATOM 3261 CD GLN A 228 -70.891 15.417 -.033 1.00 23.26 C
ATOM 3262 OE1 GLN A 228 -72.082 15.098 -.069 1.00 25.64 O
ATOM 3263 NE2 GLN A 228 -70.357 16.083 .978 1.00 21.77 N
ATOM 3266 C GLN A 228 -69.243 14.349 -3.893 1.00 23.54 C
ATOM 3267 O GLN A 228 -68.664 13.412 -3.357 1.00 23.59 O
ATOM 3269 N SER A 229 -70.105 14.194 -4.893 1.00 23.27 N
ATOM 3270 CA SER A 229 -70.394 12.868 -5.406 1.00 23.35 C
ATOM 3272 CB SER A 229 -71.753 12.812 -6.095 1.00 23.31 C
ATOM 3275 OG SER A 229 -71.836 13.823 -7.060 1.00 24.31 O
ATOM 3277 C SER A 229 -69.287 12.394 -6.331 1.00 23.19 C
ATOM 3278 O SER A 229 -69.130 11.194 -6.512 1.00 23.44 O
ATOM 3280 N VAL A 230 -68.512 13.306 -6.914 1.00 23.14 N
ATOM 3281 CA VAL A 230 -67.269 12.874 -7.552 1.00 23.00 C
ATOM 3283 CB VAL A 230 -66.469 13.998 -8.253 1.00 22.75 C
ATOM 3285 CG1 VAL A 230 -65.091 13.470 -8.667 1.00 21.87 C
ATOM 3289 CG2 VAL A 230 -67.222 14.539 -9.459 1.00 21.74 C
ATOM 3293 C VAL A 230 -66.417 12.268 -6.452 1.00 23.35 C
ATOM 3294 O VAL A 230 -65.917 11.173 -6.589 1.00 23.68 O
ATOM 3296 N TYR A 231 -66.284 12.968 -5.340 1.00 23.96 N
ATOM 3297 CA TYR A 231 -65.414 12.509 -4.274 1.00 24.60 C
ATOM 3299 CB TYR A 231 -65.486 13.426 -3.051 1.00 24.69 C
ATOM 3302 CG TYR A 231 -64.963 14.837 -3.211 1.00 24.11 C
ATOM 3303 CD1 TYR A 231 -64.071 15.190 -4.214 1.00 24.31 C
ATOM 3305 CE1 TYR A 231 -63.592 16.491 -4.322 1.00 24.63 C
ATOM 3307 CZ TYR A 231 -63.994 17.441 -3.406 1.00 25.13 C
ATOM 3308 OH TYR A 231 -63.554 18.754 -3.456 1.00 24.64 O

ATOM 3310 CE2 TYR A 231 -64.863 17.086 -2.402 1.00 25.76 C
ATOM 3312 CD2 TYR A 231 -65.329 15.800 -2.308 1.00 24.28 C
ATOM 3314 C TYR A 231 -65.785 11.111 -3.833 1.00 25.26 C
ATOM 3315 O TYR A 231 -64.917 10.315 -3.488 1.00 25.44 O
ATOM 3317 N GLN A 232 -67.079 10.819 -3.833 1.00 26.04 N
ATOM 3318 CA GLN A 232 -67.566 9.532 -3.362 1.00 26.57 C
ATOM 3320 CB GLN A 232 -69.060 9.621 -3.057 1.00 26.44 C
ATOM 3323 CG GLN A 232 -69.339 10.397 -1.778 1.00 26.25 C
ATOM 3326 CD GLN A 232 -70.786 10.819 -1.630 1.00 26.53 C
ATOM 3327 OE1 GLN A 232 -71.667 10.305 -2.318 1.00 27.77 O
ATOM 3328 NE2 GLN A 232 -71.040 11.759 -.723 1.00 25.51 N
ATOM 3331 C GLN A 232 -67.238 8.414 -4.351 1.00 27.44 C
ATOM 3332 O GLN A 232 -66.852 7.319 -3.935 1.00 27.33 O
ATOM 3334 N ARG A 233 -67.373 8.691 -5.649 1.00 28.66 N
ATOM 3335 CA ARG A 233 -66.905 7.768 -6.685 1.00 29.86 C
ATOM 3337 CB ARG A 233 -67.212 8.292 -8.090 1.00 30.08 C
ATOM 3340 CG ARG A 233 -66.378 7.634 -9.179 1.00 32.80 C
ATOM 3343 CD ARG A 233 -66.913 7.923 -10.572 1.00 36.74 C
ATOM 3346 NE ARG A 233 -66.962 9.363 -10.860 1.00 40.33 N
ATOM 3348 CZ ARG A 233 -68.069 10.119 -10.891 1.00 43.12 C
ATOM 3349 NH1 ARG A 233 -69.276 9.600 -10.655 1.00 44.55 N
ATOM 3352 NH2 ARG A 233 -67.971 11.418 -11.169 1.00 43.38 N
ATOM 3355 C ARG A 233 -65.401 7.518 -6.514 1.00 30.34 C
ATOM 3356 O ARG A 233 -64.962 6.374 -6.412 1.00 30.55 O
ATOM 3358 N ASP A 234 -64.621 8.591 -6.461 1.00 31.00 N
ATOM 3359 CA ASP A 234 -63.187 8.487 -6.205 1.00 31.48 C
ATOM 3361 CB ASP A 234 -62.594 9.870 -5.942 1.00 31.56 C
ATOM 3364 CG ASP A 234 -62.573 10.741 -7.167 1.00 32.78 C
ATOM 3365 OD1 ASP A 234 -62.911 10.249 -8.276 1.00 34.25 O
ATOM 3366 OD2 ASP A 234 -62.215 11.930 -7.011 1.00 34.81 O
ATOM 3367 C ASP A 234 -62.885 7.596 -5.010 1.00 31.70 C
ATOM 3368 O ASP A 234 -61.985 6.780 -5.053 1.00 31.56 O
ATOM 3370 N LEU A 235 -63.647 7.766 -3.943 1.00 32.43 N
ATOM 3371 CA LEU A 235 -63.366 7.102 -2.685 1.00 33.04 C
ATOM 3373 CB LEU A 235 -64.072 7.833 -1.553 1.00 32.57 C
ATOM 3376 CG LEU A 235 -63.884 7.252 -.167 1.00 30.85 C
ATOM 3378 CD1 LEU A 235 -62.428 7.261 .174 1.00 28.78 C
ATOM 3382 CD2 LEU A 235 -64.703 8.050 .823 1.00 29.93 C
ATOM 3386 C LEU A 235 -63.789 5.637 -2.686 1.00 34.69 C
ATOM 3387 O LEU A 235 -63.123 4.812 -2.065 1.00 35.29 O
ATOM 3389 N ARG A 236 -64.893 5.299 -3.354 1.00 36.09 N
ATOM 3390 CA ARG A 236 -65.290 3.893 -3.458 1.00 37.26 C
ATOM 3392 CB ARG A 236 -66.672 3.736 -4.103 1.00 37.64 C
ATOM 3395 CG ARG A 236 -67.839 4.000 -3.157 1.00 39.15 C
ATOM 3398 CD ARG A 236 -69.162 3.528 -3.741 1.00 40.25 C
ATOM 3401 NE ARG A 236 -69.385 4.046 -5.095 1.00 41.64 N
ATOM 3403 CZ ARG A 236 -69.837 5.269 -5.392 1.00 42.54 C
ATOM 3404 NH1 ARG A 236 -70.115 6.147 -4.430 1.00 42.18 N
ATOM 3407 NH2 ARG A 236 -70.012 5.621 -6.668 1.00 43.04 N
ATOM 3410 C ARG A 236 -64.266 3.108 -4.262 1.00 37.81 C
ATOM 3411 O ARG A 236 -64.104 1.912 -4.060 1.00 38.07 O
ATOM 3413 N GLU A 237 -63.584 3.801 -5.168 1.00 38.69 N
ATOM 3414 CA GLU A 237 -62.639 3.189 -6.102 1.00 39.45 C
ATOM 3416 CB GLU A 237 -62.452 4.108 -7.338 1.00 40.25 C
ATOM 3419 CG GLU A 237 -62.268 3.387 -8.710 1.00 43.02 C
ATOM 3422 CD GLU A 237 -60.835 3.458 -9.287 1.00 46.64 C
ATOM 3423 OE1 GLU A 237 -60.093 4.440 -8.997 1.00 48.03 O
ATOM 3424 OE2 GLU A 237 -60.466 2.519 -10.047 1.00 48.35 O
ATOM 3425 C GLU A 237 -61.310 2.905 -5.408 1.00 38.70 C
ATOM 3426 O GLU A 237 -60.832 1.782 -5.440 1.00 38.33 O

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ATOM   3428  N   THR A 238     -60.726   3.908  -4.764  1.00 38.40           N
ATOM   3429  CA  THR A 238     -59.504   3.669  -4.009  1.00 38.74           C
ATOM   3431  CB  THR A 238     -58.710   4.965  -3.593  1.00 38.78           C
ATOM   3433  OG1 THR A 238     -59.294   5.583  -2.444  1.00 38.38           O
ATOM   3435  CG2 THR A 238     -58.612   5.963  -4.743  1.00 38.94           C
ATOM   3439  C   THR A 238     -59.802   2.834  -2.773  1.00 39.05           C
ATOM   3440  O   THR A 238     -58.886   2.294  -2.153  1.00 39.17           O
ATOM   3442  N   SER A 239     -61.076   2.717  -2.408  1.00 39.34           N
ATOM   3443  CA  SER A 239     -61.443   1.841  -1.304  1.00 39.47           C
ATOM   3445  CB  SER A 239     -62.844   2.149   -.792  1.00 39.34           C
ATOM   3448  OG  SER A 239     -63.087   1.428    .396  1.00 39.94           O
ATOM   3450  C   SER A 239     -61.313    .367  -1.699  1.00 39.53           C
ATOM   3451  O   SER A 239     -60.834   -.439   -.900  1.00 39.53           O
ATOM   3453  N   ARG A 240     -61.728    .021  -2.921  1.00 39.69           N
ATOM   3454  CA  ARG A 240     -61.559  -1.341  -3.439  1.00 39.79           C
ATOM   3456  CB  ARG A 240     -62.105  -1.492  -4.867  1.00 40.34           C
ATOM   3459  CG  ARG A 240     -63.624  -1.715  -4.947  1.00 43.03           C
ATOM   3462  CD  ARG A 240     -64.104  -2.125  -6.364  1.00 46.66           C
ATOM   3465  NE  ARG A 240     -63.780  -1.136  -7.416  1.00 50.46           N
ATOM   3467  CZ  ARG A 240     -64.535   -.082  -7.775  1.00 53.13           C
ATOM   3468  NH1 ARG A 240     -64.112    .732  -8.749  1.00 53.13           N
ATOM   3471  NH2 ARG A 240     -65.707    .178  -7.178  1.00 54.02           N
ATOM   3474  C   ARG A 240     -60.089  -1.704  -3.414  1.00 38.94           C
ATOM   3475  O   ARG A 240     -59.732  -2.795  -2.978  1.00 39.09           O
ATOM   3477  N   TRP A 241     -59.246   -.775  -3.862  1.00 37.92           N
ATOM   3478  CA  TRP A 241     -57.787   -.947  -3.842  1.00 36.93           C
ATOM   3480  CB  TRP A 241     -57.099    .318  -4.388  1.00 36.57           C
ATOM   3483  CG  TRP A 241     -55.624    .333  -4.209  1.00 34.71           C
ATOM   3484  CD1 TRP A 241     -54.702   -.312  -4.969  1.00 33.50           C
ATOM   3486  NE1 TRP A 241     -53.441   -.068  -4.482  1.00 32.62           N
ATOM   3488  CE2 TRP A 241     -53.538    .747  -3.392  1.00 31.16           C
ATOM   3489  CD2 TRP A 241     -54.896   1.022  -3.191  1.00 32.61           C
ATOM   3490  CE3 TRP A 241     -55.268   1.837  -2.117  1.00 32.63           C
ATOM   3492  CZ3 TRP A 241     -54.293   2.345  -1.307  1.00 31.31           C
ATOM   3494  CH2 TRP A 241     -52.956   2.053  -1.537  1.00 31.81           C
ATOM   3496  CZ2 TRP A 241     -52.560   1.252  -2.577  1.00 31.18           C
ATOM   3498  C   TRP A 241     -57.263  -1.274  -2.444  1.00 36.67           C
ATOM   3499  O   TRP A 241     -56.540  -2.247  -2.252  1.00 36.32           O
ATOM   3501  N   TRP A 242     -57.647   -.460  -1.471  1.00 36.59           N
ATOM   3502  CA  TRP A 242     -57.150   -.593   -.100  1.00 36.80           C
ATOM   3504  CB  TRP A 242     -57.694    .582    .734  1.00 36.47           C
ATOM   3507  CG  TRP A 242     -57.113    .754   2.107  1.00 35.59           C
ATOM   3508  CD1 TRP A 242     -57.806    .831   3.270  1.00 35.14           C
ATOM   3510  NE1 TRP A 242     -56.950    .999   4.328  1.00 34.47           N
ATOM   3512  CE2 TRP A 242     -55.667   1.032   3.859  1.00 34.64           C
ATOM   3513  CD2 TRP A 242     -55.728    .884   2.461  1.00 35.26           C
ATOM   3514  CE3 TRP A 242     -54.531    .882   1.732  1.00 35.22           C
ATOM   3516  CZ3 TRP A 242     -53.342   1.024   2.409  1.00 34.30           C
ATOM   3518  CH2 TRP A 242     -53.318   1.169   3.799  1.00 34.70           C
ATOM   3520  CZ2 TRP A 242     -54.467   1.173   4.542  1.00 34.63           C
ATOM   3522  C   TRP A 242     -57.482  -1.975    .524  1.00 37.34           C
ATOM   3523  O   TRP A 242     -56.628  -2.623   1.126  1.00 36.53           O
ATOM   3525  N   ARG A 243     -58.720  -2.421    .348  1.00 38.54           N
ATOM   3526  CA  ARG A 243     -59.149  -3.734    .822  1.00 39.71           C
ATOM   3528  CB  ARG A 243     -60.669  -3.896    .687  1.00 40.10           C
ATOM   3531  CG  ARG A 243     -61.495  -3.134   1.747  1.00 42.18           C
ATOM   3534  CD  ARG A 243     -62.826  -2.623   1.169  1.00 45.18           C
ATOM   3537  NE  ARG A 243     -63.506  -3.656    .369  1.00 48.22           N
ATOM   3539  CZ  ARG A 243     -64.374  -3.431   -.629  1.00 49.95           C
ATOM   3540  NH1 ARG A 243     -64.717  -2.182   -.991  1.00 50.13           N
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ATOM 3543 NH2 ARG A 243 -64.911 -4.477 -1.273 1.00 49.77 N
ATOM 3546 C ARG A 243 -58.438 -4.852 .068 1.00 40.08 C
ATOM 3547 O ARG A 243 -58.084 -5.870 .665 1.00 40.45 O
ATOM 3549 N ARG A 244 -58.236 -4.663 -1.236 1.00 40.42 N
ATOM 3550 CA ARG A 244 -57.499 -5.621 -2.063 1.00 40.65 C
ATOM 3552 CB ARG A 244 -57.370 -5.100 -3.503 1.00 41.29 C
ATOM 3555 CG ARG A 244 -56.939 -6.126 -4.560 1.00 43.27 C
ATOM 3558 CD ARG A 244 -58.090 -7.062 -4.952 1.00 46.01 C
ATOM 3561 NE ARG A 244 -57.595 -8.337 -5.485 1.00 48.77 N
ATOM 3563 CZ ARG A 244 -57.075 -9.332 -4.752 1.00 51.17 C
ATOM 3564 NH1 ARG A 244 -56.968 -9.234 -3.422 1.00 51.63 N
ATOM 3567 NH2 ARG A 244 -56.656 -10.448 -5.353 1.00 52.11 N
ATOM 3570 C ARG A 244 -56.120 -5.861 -1.465 1.00 40.12 C
ATOM 3571 O ARG A 244 -55.728 -7.000 -1.235 1.00 39.96 O
ATOM 3573 N VAL A 245 -55.399 -4.778 -1.201 1.00 39.78 N
ATOM 3574 CA VAL A 245 -54.099 -4.858 -.543 1.00 39.68 C
ATOM 3576 CB VAL A 245 -53.430 -3.458 -.437 1.00 39.70 C
ATOM 3578 CG1 VAL A 245 -53.133 -2.914 -1.824 1.00 39.54 C
ATOM 3582 CG2 VAL A 245 -52.145 -3.507 .395 1.00 39.41 C
ATOM 3586 C VAL A 245 -54.262 -5.472 .841 1.00 39.73 C
ATOM 3587 O VAL A 245 -53.455 -6.291 1.253 1.00 39.53 O
ATOM 3589 N GLY A 246 -55.312 -5.051 1.544 1.00 40.11 N
ATOM 3590 CA GLY A 246 -55.705 -5.617 2.839 1.00 40.35 C
ATOM 3593 C GLY A 246 -54.621 -5.648 3.894 1.00 40.58 C
ATOM 3594 O GLY A 246 -54.396 -6.676 4.510 1.00 40.68 O
ATOM 3596 N LEU A 247 -53.963 -4.522 4.129 1.00 41.15 N
ATOM 3597 CA LEU A 247 -52.778 -4.519 4.982 1.00 41.71 C
ATOM 3599 CB LEU A 247 -51.808 -3.422 4.537 1.00 41.60 C
ATOM 3602 CG LEU A 247 -50.334 -3.815 4.441 1.00 40.83 C
ATOM 3604 CD1 LEU A 247 -50.158 -5.014 3.539 1.00 40.54 C
ATOM 3608 CD2 LEU A 247 -49.534 -2.644 3.918 1.00 39.92 C
ATOM 3612 C LEU A 247 -53.136 -4.385 6.471 1.00 42.60 C
ATOM 3613 O LEU A 247 -52.588 -5.111 7.313 1.00 42.06 O
ATOM 3615 N ALA A 248 -54.064 -3.475 6.788 1.00 43.75 N
ATOM 3616 CA ALA A 248 -54.603 -3.352 8.162 1.00 44.52 C
ATOM 3618 CB ALA A 248 -55.712 -2.296 8.210 1.00 44.31 C
ATOM 3622 C ALA A 248 -55.129 -4.706 8.695 1.00 45.10 C
ATOM 3623 O ALA A 248 -54.969 -5.041 9.875 1.00 44.96 O
ATOM 3625 N THR A 249 -55.742 -5.477 7.802 1.00 45.91 N
ATOM 3626 CA THR A 249 -56.328 -6.768 8.154 1.00 46.50 C
ATOM 3628 CB THR A 249 -57.303 -7.277 7.041 1.00 46.48 C
ATOM 3630 OG1 THR A 249 -56.583 -8.039 6.063 1.00 46.20 O
ATOM 3632 CG2 THR A 249 -58.033 -6.102 6.350 1.00 46.70 C
ATOM 3636 C THR A 249 -55.257 -7.840 8.447 1.00 47.06 C
ATOM 3637 O THR A 249 -55.531 -8.813 9.159 1.00 47.22 O
ATOM 3639 N LYS A 250 -54.049 -7.661 7.905 1.00 47.52 N
ATOM 3640 CA LYS A 250 -52.952 -8.620 8.096 1.00 47.91 C
ATOM 3642 CB LYS A 250 -52.319 -8.976 6.744 1.00 48.09 C
ATOM 3645 CG LYS A 250 -52.911 -10.229 6.088 1.00 48.91 C
ATOM 3648 CD LYS A 250 -52.210 -11.510 6.585 1.00 49.88 C
ATOM 3651 CE LYS A 250 -53.066 -12.760 6.349 1.00 50.12 C
ATOM 3654 NZ LYS A 250 -52.385 -14.011 6.791 1.00 49.99 N
ATOM 3658 C LYS A 250 -51.880 -8.129 9.078 1.00 48.13 C
ATOM 3659 O LYS A 250 -51.252 -8.939 9.759 1.00 47.89 O
ATOM 3661 N LEU A 251 -51.667 -6.812 9.134 1.00 48.63 N
ATOM 3662 CA LEU A 251 -50.758 -6.187 10.114 1.00 48.83 C
ATOM 3664 CB LEU A 251 -49.981 -5.020 9.485 1.00 48.74 C
ATOM 3667 CG LEU A 251 -48.569 -5.296 8.960 1.00 48.51 C
ATOM 3669 CD1 LEU A 251 -48.472 -6.594 8.174 1.00 47.96 C
ATOM 3673 CD2 LEU A 251 -48.102 -4.115 8.116 1.00 48.76 C

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ATOM  3677  C   LEU A 251     -51.559  -5.703  11.324  1.00 49.17           C
ATOM  3678  O   LEU A 251     -52.176  -4.632  11.304  1.00 49.28           O
ATOM  3680  N   HIS A 252     -51.521  -6.486  12.393  1.00 49.53           N
ATOM  3681  CA  HIS A 252     -52.470  -6.322  13.494  1.00 50.02           C
ATOM  3683  CB  HIS A 252     -52.598  -7.647  14.266  1.00 50.42           C
ATOM  3686  CG  HIS A 252     -52.860  -8.834  13.380  1.00 52.23           C
ATOM  3687  ND1 HIS A 252     -54.032  -8.989  12.667  1.00 53.75           N
ATOM  3689  CE1 HIS A 252     -53.978 -10.113  11.973  1.00 54.43           C
ATOM  3691  NE2 HIS A 252     -52.810 -10.689  12.201  1.00 54.52           N
ATOM  3693  CD2 HIS A 252     -52.090  -9.910  13.077  1.00 53.70           C
ATOM  3695  C   HIS A 252     -52.161  -5.147  14.441  1.00 49.64           C
ATOM  3696  O   HIS A 252     -52.951  -4.849  15.336  1.00 49.61           O
ATOM  3698  N   PHE A 253     -51.027  -4.483  14.229  1.00 49.37           N
ATOM  3699  CA  PHE A 253     -50.652  -3.273  14.973  1.00 49.15           C
ATOM  3701  CB  PHE A 253     -49.144  -3.273  15.260  1.00 49.07           C
ATOM  3704  CG  PHE A 253     -48.307  -3.112  14.025  1.00 48.30           C
ATOM  3705  CD1 PHE A 253     -48.028  -1.851  13.518  1.00 48.10           C
ATOM  3707  CE1 PHE A 253     -47.290  -1.702  12.349  1.00 48.21           C
ATOM  3709  CZ  PHE A 253     -46.825  -2.825  11.675  1.00 47.88           C
ATOM  3711  CE2 PHE A 253     -47.101  -4.090  12.175  1.00 47.66           C
ATOM  3713  CD2 PHE A 253     -47.842  -4.226  13.338  1.00 47.74           C
ATOM  3715  C   PHE A 253     -50.974  -2.006  14.176  1.00 49.31           C
ATOM  3716  O   PHE A 253     -50.846   -.893  14.702  1.00 49.01           O
ATOM  3718  N   ALA A 254     -51.365  -2.185  12.910  1.00 49.48           N
ATOM  3719  CA  ALA A 254     -51.412  -1.095  11.931  1.00 49.63           C
ATOM  3721  CB  ALA A 254     -51.344  -1.663  10.524  1.00 49.64           C
ATOM  3725  C   ALA A 254     -52.650   -.224  12.061  1.00 49.77           C
ATOM  3726  O   ALA A 254     -53.761   -.735  12.219  1.00 49.86           O
ATOM  3728  N   ARG A 255     -52.452  1.090  11.975  1.00 49.93           N
ATOM  3729  CA  ARG A 255     -53.562  2.042  11.908  1.00 50.27           C
ATOM  3731  CB  ARG A 255     -53.094  3.468  12.237  1.00 50.43           C
ATOM  3734  CG  ARG A 255     -52.678  3.736  13.696  1.00 50.82           C
ATOM  3737  CD  ARG A 255     -52.242  5.211  13.887  1.00 51.32           C
ATOM  3740  NE  ARG A 255     -51.003  5.522  13.155  1.00 51.81           N
ATOM  3742  CZ  ARG A 255     -50.571  6.746  12.829  1.00 51.67           C
ATOM  3743  NH1 ARG A 255     -51.264  7.839  13.146  1.00 51.63           N
ATOM  3746  NH2 ARG A 255     -49.427  6.877  12.162  1.00 51.52           N
ATOM  3749  C   ARG A 255     -54.160  2.040  10.497  1.00 50.32           C
ATOM  3750  O   ARG A 255     -53.416  2.081   9.504  1.00 50.35           O
ATOM  3752  N   ASP A 256     -55.492  2.005  10.412  1.00 50.17           N
ATOM  3753  CA  ASP A 256     -56.190  2.090   9.128  1.00 50.18           C
ATOM  3755  CB  ASP A 256     -57.259  1.009   9.037  1.00 50.37           C
ATOM  3758  CG  ASP A 256     -58.095  1.130   7.780  1.00 50.96           C
ATOM  3759  OD1 ASP A 256     -59.252  1.601   7.881  1.00 52.00           O
ATOM  3760  OD2 ASP A 256     -57.581   .787   6.693  1.00 50.94           O
ATOM  3761  C   ASP A 256     -56.838  3.470   8.945  1.00 49.85           C
ATOM  3762  O   ASP A 256     -57.812  3.804   9.624  1.00 50.13           O
ATOM  3764  N   ARG A 257     -56.315  4.263   8.013  1.00 49.11           N
ATOM  3765  CA  ARG A 257     -56.712  5.665   7.913  1.00 48.59           C
ATOM  3767  CB  ARG A 257     -55.622  6.553   8.529  1.00 48.79           C
ATOM  3770  CG  ARG A 257     -55.318  6.275  10.006  1.00 49.85           C
ATOM  3773  CD  ARG A 257     -56.538  6.480  10.908  1.00 51.01           C
ATOM  3776  NE  ARG A 257     -56.198  7.274  12.089  1.00 51.80           N
ATOM  3778  CZ  ARG A 257     -55.779  6.791  13.260  1.00 52.00           C
ATOM  3779  NH1 ARG A 257     -55.643  5.486  13.468  1.00 51.64           N
ATOM  3782  NH2 ARG A 257     -55.501  7.638  14.245  1.00 52.62           N
ATOM  3785  C   ARG A 257     -56.988  6.112   6.477  1.00 47.58           C
ATOM  3786  O   ARG A 257     -56.476  7.144   6.031  1.00 47.40           O
ATOM  3788  N   LEU A 258     -57.814  5.352   5.761  1.00 46.18           N
ATOM  3789  CA  LEU A 258     -58.094  5.672   4.358  1.00 44.78           C
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ATOM  3791 CB  LEU A 258    -58.777   4.508   3.629  1.00 44.57      C
ATOM  3794 CG  LEU A 258    -58.917   4.731   2.121  1.00 43.79      C
ATOM  3796 CD1 LEU A 258    -57.557   4.661   1.478  1.00 43.89      C
ATOM  3800 CD2 LEU A 258    -59.850   3.733   1.492  1.00 42.88      C
ATOM  3804 C   LEU A 258    -58.970   6.907   4.259  1.00 43.52      C
ATOM  3805 O   LEU A 258    -58.643   7.849   3.545  1.00 43.42      O
ATOM  3807 N   ILE A 259    -60.080   6.895   4.983  1.00 41.98      N
ATOM  3808 CA  ILE A 259    -61.072   7.948   4.843  1.00 40.89      C
ATOM  3810 CB  ILE A 259    -62.349   7.703   5.693  1.00 41.02      C
ATOM  3812 CG1 ILE A 259    -62.846   6.248   5.570  1.00 41.82      C
ATOM  3815 CD1 ILE A 259    -64.029   5.872   6.508  1.00 42.29      C
ATOM  3819 CG2 ILE A 259    -63.446   8.662   5.262  1.00 40.47      C
ATOM  3823 C   ILE A 259    -60.424   9.253   5.273  1.00 39.74      C
ATOM  3824 O   ILE A 259    -60.607  10.291   4.635  1.00 39.25      O
ATOM  3826 N   GLU A 260    -59.650   9.191   6.355  1.00 38.46      N
ATOM  3827 CA  GLU A 260    -58.951  10.366   6.846  1.00 37.44      C
ATOM  3829 CB  GLU A 260    -58.183  10.072   8.140  1.00 37.74      C
ATOM  3832 CG  GLU A 260    -59.041   9.934   9.393  1.00 38.71      C
ATOM  3835 CD  GLU A 260    -59.469   8.501   9.693  1.00 41.00      C
ATOM  3836 OE1 GLU A 260    -59.273   7.594   8.842  1.00 42.70      O
ATOM  3837 OE2 GLU A 260    -60.012   8.281  10.800  1.00 42.43      O
ATOM  3838 C   GLU A 260    -57.995  10.841   5.764  1.00 35.94      C
ATOM  3839 O   GLU A 260    -57.981  12.020   5.418  1.00 36.10      O
ATOM  3841 N   SER A 261    -57.222   9.908   5.212  1.00 34.02      N
ATOM  3842 CA  SER A 261    -56.263  10.229   4.152  1.00 32.47      C
ATOM  3844 CB  SER A 261    -55.407   9.015   3.774  1.00 32.51      C
ATOM  3847 OG  SER A 261    -54.253   8.940   4.584  1.00 33.14      O
ATOM  3849 C   SER A 261    -56.894  10.764   2.889  1.00 30.82      C
ATOM  3850 O   SER A 261    -56.199  11.306   2.062  1.00 30.79      O
ATOM  3852 N   PHE A 262    -58.194  10.589   2.713  1.00 29.25      N
ATOM  3853 CA  PHE A 262    -58.861  11.091   1.514  1.00 27.98      C
ATOM  3855 CB  PHE A 262    -60.011  10.185   1.119  1.00 27.57      C
ATOM  3858 CG  PHE A 262    -60.473  10.423   -.251  1.00 26.11      C
ATOM  3859 CD1 PHE A 262    -59.763   9.914  -1.318  1.00 25.14      C
ATOM  3861 CE1 PHE A 262    -60.169  10.147  -2.605  1.00 24.32      C
ATOM  3863 CZ  PHE A 262    -61.284  10.917  -2.840  1.00 24.36      C
ATOM  3865 CE2 PHE A 262    -61.987  11.445  -1.785  1.00 25.23      C
ATOM  3867 CD2 PHE A 262    -61.575  11.201   -.492  1.00 25.61      C
ATOM  3869 C   PHE A 262    -59.394  12.507   1.707  1.00 27.29      C
ATOM  3870 O   PHE A 262    -59.275  13.359   .821  1.00 27.39      O
ATOM  3872 N   TYR A 263    -60.025  12.723   2.856  1.00 26.19      N
ATOM  3873 CA  TYR A 263    -60.415  14.052   3.310  1.00 25.22      C
ATOM  3875 CB  TYR A 263    -60.975  13.942   4.735  1.00 25.21      C
ATOM  3878 CG  TYR A 263    -61.037  15.199   5.578  1.00 25.37      C
ATOM  3879 CD1 TYR A 263    -62.020  16.152   5.385  1.00 24.95      C
ATOM  3881 CE1 TYR A 263    -62.084  17.282   6.197  1.00 26.54      C
ATOM  3883 CZ  TYR A 263    -61.158  17.455   7.229  1.00 27.44      C
ATOM  3884 OH  TYR A 263    -61.186  18.567   8.059  1.00 28.97      O
ATOM  3886 CE2 TYR A 263    -60.185  16.512   7.438  1.00 27.10      C
ATOM  3888 CD2 TYR A 263    -60.136  15.390   6.626  1.00 26.91      C
ATOM  3890 C   TYR A 263    -59.190  14.946   3.238  1.00 24.29      C
ATOM  3891 O   TYR A 263    -59.267  16.077   2.757  1.00 24.13      O
ATOM  3893 N   TRP A 264    -58.055  14.415   3.682  1.00 23.01      N
ATOM  3894 CA  TRP A 264    -56.789  15.121   3.567  1.00 22.32      C
ATOM  3896 CB  TRP A 264    -55.642  14.261   4.119  1.00 22.26      C
ATOM  3899 CG  TRP A 264    -54.326  14.874   3.860  1.00 22.16      C
ATOM  3900 CD1 TRP A 264    -53.614  14.821   2.699  1.00 22.68      C
ATOM  3902 NE1 TRP A 264    -52.456  15.538   2.818  1.00 23.08      N
ATOM  3904 CE2 TRP A 264    -52.407  16.083   4.072  1.00 23.07      C
ATOM  3905 CD2 TRP A 264    -53.579  15.686   4.753  1.00 22.18      C
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ATOM  3906 CE3 TRP A 264    -53.782  16.119   6.066  1.00 22.57      C
ATOM  3908 CZ3 TRP A 264    -52.824  16.925   6.657  1.00 23.43      C
ATOM  3910 CH2 TRP A 264    -51.656  17.297   5.955  1.00 24.14      C
ATOM  3912 CZ2 TRP A 264    -51.433  16.886   4.663  1.00 23.64      C
ATOM  3914 C   TRP A 264    -56.485  15.523   2.112  1.00 21.50      C
ATOM  3915 O   TRP A 264    -56.179  16.682   1.820  1.00 21.29      O
ATOM  3917 N   ALA A 265    -56.561  14.547   1.213  1.00 20.41      N
ATOM  3918 CA  ALA A 265    -56.242  14.760   -.187  1.00 19.63      C
ATOM  3920 CB  ALA A 265    -56.298  13.437   -.953  1.00 19.39      C
ATOM  3924 C   ALA A 265    -57.176  15.792   -.798  1.00 19.07      C
ATOM  3925 O   ALA A 265    -56.760  16.573  -1.633  1.00 18.99      O
ATOM  3927 N   VAL A 266    -58.431  15.814   -.359  1.00 18.78      N
ATOM  3928 CA  VAL A 266    -59.396  16.828   -.818  1.00 18.56      C
ATOM  3930 CB  VAL A 266    -60.839  16.541   -.278  1.00 18.41      C
ATOM  3932 CG1 VAL A 266    -61.405  15.298   -.935  1.00 18.88      C
ATOM  3936 CG2 VAL A 266    -61.780  17.709   -.505  1.00 17.21      C
ATOM  3940 C   VAL A 266    -58.947  18.257   -.450  1.00 18.43      C
ATOM  3941 O   VAL A 266    -59.250  19.200  -1.171  1.00 18.83      O
ATOM  3943 N   GLY A 267    -58.230  18.411    .663  1.00 17.96      N
ATOM  3944 CA  GLY A 267    -57.714  19.712   1.067  1.00 17.45      C
ATOM  3947 C   GLY A 267    -56.687  20.180    .070  1.00 17.20      C
ATOM  3948 O   GLY A 267    -56.574  21.365   -.215  1.00 17.41      O
ATOM  3950 N   VAL A 268    -55.959  19.219   -.480  1.00 16.88      N
ATOM  3951 CA  VAL A 268    -54.822  19.487  -1.319  1.00 16.62      C
ATOM  3953 CB  VAL A 268    -53.833  18.300  -1.290  1.00 16.19      C
ATOM  3955 CG1 VAL A 268    -52.691  18.536  -2.240  1.00 15.50      C
ATOM  3959 CG2 VAL A 268    -53.310  18.121    .103  1.00 15.30      C
ATOM  3963 C   VAL A 268    -55.262  19.788  -2.736  1.00 17.15      C
ATOM  3964 O   VAL A 268    -54.748  20.710  -3.350  1.00 17.12      O
ATOM  3966 N   ALA A 269    -56.217  19.014  -3.243  1.00 17.99      N
ATOM  3967 CA  ALA A 269    -56.688  19.158  -4.622  1.00 18.79      C
ATOM  3969 CB  ALA A 269    -55.958  18.183  -5.551  1.00 18.26      C
ATOM  3973 C   ALA A 269    -58.196  18.938  -4.672  1.00 19.70      C
ATOM  3974 O   ALA A 269    -58.665  17.834  -4.958  1.00 19.50      O
ATOM  3976 N   PHE A 270    -58.945  20.011  -4.417  1.00 21.09      N
ATOM  3977 CA  PHE A 270    -60.393  19.910  -4.211  1.00 22.32      C
ATOM  3979 CB  PHE A 270    -60.925  21.108  -3.404  1.00 22.49      C
ATOM  3982 CG  PHE A 270    -61.193  22.321  -4.246  1.00 23.31      C
ATOM  3983 CD1 PHE A 270    -62.423  22.483  -4.883  1.00 24.16      C
ATOM  3985 CE1 PHE A 270    -62.662  23.569  -5.683  1.00 23.84      C
ATOM  3987 CZ  PHE A 270    -61.675  24.497  -5.871  1.00 23.93      C
ATOM  3989 CE2 PHE A 270    -60.448  24.349  -5.242  1.00 23.33      C
ATOM  3991 CD2 PHE A 270    -60.213  23.268  -4.443  1.00 23.11      C
ATOM  3993 C   PHE A 270    -61.173  19.820  -5.515  1.00 23.21      C
ATOM  3994 O   PHE A 270    -62.142  19.069  -5.599  1.00 23.48      O
ATOM  3996 N   GLU A 271    -60.771  20.599  -6.522  1.00 24.16      N
ATOM  3997 CA  GLU A 271    -61.595  20.744  -7.741  1.00 25.01      C
ATOM  3999 CB  GLU A 271    -61.065  21.863  -8.655  1.00 25.19      C
ATOM  4002 CG  GLU A 271    -59.563  21.909  -8.794  1.00 27.45      C
ATOM  4005 CD  GLU A 271    -58.857  22.910  -7.857  1.00 30.03      C
ATOM  4006 OE1 GLU A 271    -58.905  24.145  -8.147  1.00 29.41      O
ATOM  4007 OE2 GLU A 271    -58.227  22.431  -6.865  1.00 30.71      O
ATOM  4008 C   GLU A 271    -61.799  19.391  -8.484  1.00 24.95      C
ATOM  4009 O   GLU A 271    -60.972  18.480  -8.352  1.00 25.70      O
ATOM  4011 N   PRO A 272    -62.918  19.242  -9.224  1.00 24.59      N
ATOM  4012 CA  PRO A 272    -63.399  17.915  -9.656  1.00 24.38      C
ATOM  4014 CB  PRO A 272    -64.675  18.243 -10.430  1.00 24.25      C
ATOM  4017 CG  PRO A 272    -65.105  19.536  -9.869  1.00 24.53      C
ATOM  4020 CD  PRO A 272    -63.855  20.295  -9.639  1.00 24.42      C
ATOM  4023 C   PRO A 272    -62.475  17.111 -10.549  1.00 24.29      C
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ATOM  4024  O   PRO A 272     -62.406  15.886 -10.410  1.00 24.45           O
ATOM  4025  N   GLN A 273     -61.777  17.781 -11.462  1.00 24.13           N
ATOM  4026  CA  GLN A 273     -60.998  17.064 -12.461  1.00 24.13           C
ATOM  4028  CB  GLN A 273     -60.523  17.983 -13.567  1.00 23.84           C
ATOM  4031  CG  GLN A 273     -59.556  19.041 -13.117  1.00 24.37           C
ATOM  4034  CD  GLN A 273     -60.222  20.360 -12.775  1.00 25.22           C
ATOM  4035  OE1 GLN A 273     -61.392  20.412 -12.367  1.00 25.71           O
ATOM  4036  NE2 GLN A 273     -59.468  21.441 -12.932  1.00 24.95           N
ATOM  4039  C   GLN A 273     -59.808  16.327 -11.877  1.00 24.33           C
ATOM  4040  O   GLN A 273     -59.224  15.486 -12.555  1.00 24.91           O
ATOM  4042  N   TYR A 274     -59.462  16.607 -10.626  1.00 24.27           N
ATOM  4043  CA  TYR A 274     -58.211  16.119 -10.067  1.00 24.38           C
ATOM  4045  CB  TYR A 274     -57.639  17.180  -9.138  1.00 24.36           C
ATOM  4048  CG  TYR A 274     -57.066  18.398  -9.819  1.00 24.35           C
ATOM  4049  CD1 TYR A 274     -56.249  18.291 -10.935  1.00 24.13           C
ATOM  4051  CE1 TYR A 274     -55.716  19.409 -11.542  1.00 23.75           C
ATOM  4053  CZ  TYR A 274     -55.968  20.646 -11.019  1.00 24.14           C
ATOM  4054  OH  TYR A 274     -55.431  21.762 -11.597  1.00 24.45           O
ATOM  4056  CE2 TYR A 274     -56.755  20.780  -9.903  1.00 24.92           C
ATOM  4058  CD2 TYR A 274     -57.297  19.658  -9.308  1.00 24.74           C
ATOM  4060  C   TYR A 274     -58.319  14.796  -9.310  1.00 24.63           C
ATOM  4061  O   TYR A 274     -57.681  14.613  -8.276  1.00 24.47           O
ATOM  4063  N   SER A 275     -59.097  13.852  -9.821  1.00 25.00           N
ATOM  4064  CA  SER A 275     -59.254  12.575  -9.116  1.00 25.11           C
ATOM  4066  CB  SER A 275     -60.244  11.664  -9.842  1.00 25.14           C
ATOM  4069  OG  SER A 275     -61.537  12.252  -9.852  1.00 25.96           O
ATOM  4071  C   SER A 275     -57.907  11.885  -8.963  1.00 24.94           C
ATOM  4072  O   SER A 275     -57.544  11.439  -7.877  1.00 24.57           O
ATOM  4074  N   ASP A 276     -57.149  11.822 -10.052  1.00 25.01           N
ATOM  4075  CA  ASP A 276     -55.840  11.187  -9.990  1.00 24.92           C
ATOM  4077  CB  ASP A 276     -55.102  11.257 -11.324  1.00 25.02           C
ATOM  4080  CG  ASP A 276     -55.827  10.495 -12.407  1.00 26.27           C
ATOM  4081  OD1 ASP A 276     -56.372   9.411 -12.080  1.00 26.65           O
ATOM  4082  OD2 ASP A 276     -55.880  10.991 -13.563  1.00 28.21           O
ATOM  4083  C   ASP A 276     -55.026  11.798  -8.881  1.00 24.30           C
ATOM  4084  O   ASP A 276     -54.454  11.064  -8.099  1.00 24.64           O
ATOM  4086  N   CYS A 277     -55.005  13.124  -8.772  1.00 23.61           N
ATOM  4087  CA  CYS A 277     -54.210  13.746  -7.715  1.00 22.91           C
ATOM  4089  CB  CYS A 277     -54.262  15.268  -7.748  1.00 22.83           C
ATOM  4092  SG  CYS A 277     -53.048  15.994  -6.615  1.00 22.43           S
ATOM  4094  C   CYS A 277     -54.653  13.251  -6.357  1.00 22.39           C
ATOM  4095  O   CYS A 277     -53.822  12.833  -5.559  1.00 22.23           O
ATOM  4097  N   ARG A 278     -55.962  13.262  -6.115  1.00 22.01           N
ATOM  4098  CA  ARG A 278     -56.519  12.813  -4.829  1.00 21.40           C
ATOM  4100  CB  ARG A 278     -58.021  13.053  -4.753  1.00 21.07           C
ATOM  4103  CG  ARG A 278     -58.382  14.509  -4.754  1.00 20.39           C
ATOM  4106  CD  ARG A 278     -59.852  14.698  -4.527  1.00 20.05           C
ATOM  4109  NE  ARG A 278     -60.683  14.331  -5.675  1.00 18.86           N
ATOM  4111  CZ  ARG A 278     -60.993  15.144  -6.679  1.00 18.58           C
ATOM  4112  NH1 ARG A 278     -60.530  16.391  -6.730  1.00 18.45           N
ATOM  4115  NH2 ARG A 278     -61.775  14.702  -7.647  1.00 19.04           N
ATOM  4118  C   ARG A 278     -56.224  11.358  -4.530  1.00 21.12           C
ATOM  4119  O   ARG A 278     -55.804  11.050  -3.434  1.00 21.59           O
ATOM  4121  N   ASN A 279     -56.412  10.467  -5.493  1.00 20.94           N
ATOM  4122  CA  ASN A 279     -56.168   9.044  -5.243  1.00 21.08           C
ATOM  4124  CB  ASN A 279     -56.672   8.182  -6.401  1.00 21.54           C
ATOM  4127  CG  ASN A 279     -58.199   8.346  -6.642  1.00 23.94           C
ATOM  4128  OD1 ASN A 279     -58.920   8.941  -5.823  1.00 26.47           O
ATOM  4129  ND2 ASN A 279     -58.685   7.825  -7.769  1.00 25.52           N
ATOM  4132  C   ASN A 279     -54.699   8.798  -4.972  1.00 20.30           C
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ATOM  4133  O   ASN A 279     -54.337   8.200  -3.977  1.00 19.95           O
ATOM  4135  N   SER A 280     -53.851   9.297  -5.856  1.00 20.02           N
ATOM  4136  CA  SER A 280     -52.409   9.335  -5.612  1.00 19.32           C
ATOM  4138  CB  SER A 280     -51.725  10.304  -6.580  1.00 19.35           C
ATOM  4141  OG  SER A 280     -50.624   9.705  -7.212  1.00 19.77           O
ATOM  4143  C   SER A 280     -52.122   9.745  -4.166  1.00 18.55           C
ATOM  4144  O   SER A 280     -51.514   8.976  -3.436  1.00 18.98           O
ATOM  4146  N   VAL A 281     -52.580  10.923  -3.743  1.00 17.45           N
ATOM  4147  CA  VAL A 281     -52.235  11.444  -2.416  1.00 17.01           C
ATOM  4149  CB  VAL A 281     -52.650  12.934  -2.235  1.00 17.20           C
ATOM  4151  CG1 VAL A 281     -52.492  13.376   -.787  1.00 16.76           C
ATOM  4155  CG2 VAL A 281     -51.826  13.847  -3.128  1.00 17.13           C
ATOM  4159  C   VAL A 281     -52.861  10.607  -1.301  1.00 16.82           C
ATOM  4160  O   VAL A 281     -52.217  10.314   -.289  1.00 16.81           O
ATOM  4162  N   ALA A 282     -54.118  10.225  -1.481  1.00 16.55           N
ATOM  4163  CA  ALA A 282     -54.774   9.304   -.559  1.00 16.31           C
ATOM  4165  CB  ALA A 282     -56.174   8.951  -1.060  1.00 16.08           C
ATOM  4169  C   ALA A 282     -53.946   8.036   -.355  1.00 16.31           C
ATOM  4170  O   ALA A 282     -53.671   7.653    .762  1.00 16.16           O
ATOM  4172  N   LYS A 283     -53.539   7.395  -1.443  1.00 16.92           N
ATOM  4173  CA  LYS A 283     -52.773   6.139  -1.368  1.00 17.39           C
ATOM  4175  CB  LYS A 283     -52.454   5.596  -2.773  1.00 17.31           C
ATOM  4178  CG  LYS A 283     -53.680   5.066  -3.519  1.00 17.85           C
ATOM  4181  CD  LYS A 283     -53.389   4.527  -4.941  1.00 18.98           C
ATOM  4184  CE  LYS A 283     -54.709   4.275  -5.718  1.00 19.79           C
ATOM  4187  NZ  LYS A 283     -54.695   3.091  -6.625  1.00 20.11           N
ATOM  4191  C   LYS A 283     -51.483   6.338   -.591  1.00 17.82           C
ATOM  4192  O   LYS A 283     -51.170   5.577    .331  1.00 17.37           O
ATOM  4194  N   MET A 284     -50.744   7.381   -.964  1.00 18.49           N
ATOM  4195  CA  MET A 284     -49.434   7.622   -.373  1.00 18.82           C
ATOM  4197  CB  MET A 284     -48.688   8.795  -1.047  1.00 18.84           C
ATOM  4200  CG  MET A 284     -48.118   8.506  -2.444  1.00 18.47           C
ATOM  4203  SD  MET A 284     -47.540   6.819  -2.718  1.00 19.50           S
ATOM  4204  CE  MET A 284     -49.088   5.982  -3.094  1.00 19.36           C
ATOM  4208  C   MET A 284     -49.575   7.848   1.115  1.00 18.95           C
ATOM  4209  O   MET A 284     -48.901   7.166   1.892  1.00 19.29           O
ATOM  4211  N   PHE A 285     -50.465   8.762   1.507  1.00 18.94           N
ATOM  4212  CA  PHE A 285     -50.671   9.082   2.930  1.00 19.26           C
ATOM  4214  CB  PHE A 285     -51.714  10.185   3.073  1.00 19.72           C
ATOM  4217  CG  PHE A 285     -51.575  11.016   4.328  1.00 21.97           C
ATOM  4218  CD1 PHE A 285     -50.335  11.202   4.954  1.00 24.49           C
ATOM  4220  CE1 PHE A 285     -50.209  11.996   6.086  1.00 25.11           C
ATOM  4222  CZ  PHE A 285     -51.321  12.634   6.597  1.00 26.40           C
ATOM  4224  CE2 PHE A 285     -52.566  12.470   5.977  1.00 26.44           C
ATOM  4226  CD2 PHE A 285     -52.678  11.670   4.846  1.00 24.55           C
ATOM  4228  C   PHE A 285     -51.097   7.879   3.770  1.00 18.74           C
ATOM  4229  O   PHE A 285     -50.700   7.729   4.924  1.00 18.31           O
ATOM  4231  N   SER A 286     -51.903   7.019   3.169  1.00 18.49           N
ATOM  4232  CA  SER A 286     -52.281   5.772   3.791  1.00 18.38           C
ATOM  4234  CB  SER A 286     -53.302   5.065   2.926  1.00 18.45           C
ATOM  4237  OG  SER A 286     -54.389   5.949   2.687  1.00 19.82           O
ATOM  4239  C   SER A 286     -51.070   4.888   4.048  1.00 18.08           C
ATOM  4240  O   SER A 286     -50.931   4.376   5.146  1.00 18.18           O
ATOM  4242  N   PHE A 287     -50.195   4.714   3.054  1.00 17.72           N
ATOM  4243  CA  PHE A 287     -48.911   4.024   3.279  1.00 17.23           C
ATOM  4245  CB  PHE A 287     -48.133   3.801   1.977  1.00 17.09           C
ATOM  4248  CG  PHE A 287     -48.513   2.555   1.258  1.00 17.26           C
ATOM  4249  CD1 PHE A 287     -48.220   1.315   1.802  1.00 18.31           C
ATOM  4251  CE1 PHE A 287     -48.583    .129   1.131  1.00 18.47           C
ATOM  4253  CZ  PHE A 287     -49.237    .198   -.091  1.00 17.88           C
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ATOM 4255 CE2 PHE A 287 -49.530 1.441 -.642 1.00 17.57 C
ATOM 4257 CD2 PHE A 287 -49.168 2.608 .031 1.00 17.79 C
ATOM 4259 C PHE A 287 -48.022 4.787 4.277 1.00 16.92 C
ATOM 4260 O PHE A 287 -47.369 4.173 5.143 1.00 17.18 O
ATOM 4262 N VAL A 288 -47.989 6.113 4.174 1.00 16.00 N
ATOM 4263 CA VAL A 288 -47.148 6.883 5.080 1.00 15.45 C
ATOM 4265 CB VAL A 288 -47.289 8.399 4.863 1.00 15.21 C
ATOM 4267 CG1 VAL A 288 -46.433 9.162 5.852 1.00 14.24 C
ATOM 4271 CG2 VAL A 288 -46.898 8.757 3.450 1.00 14.46 C
ATOM 4275 C VAL A 288 -47.479 6.499 6.527 1.00 15.46 C
ATOM 4276 O VAL A 288 -46.590 6.160 7.299 1.00 14.79 O
ATOM 4278 N THR A 289 -48.759 6.494 6.880 1.00 15.62 N
ATOM 4279 CA THR A 289 -49.110 6.272 8.274 1.00 16.09 C
ATOM 4281 CB THR A 289 -50.602 6.557 8.588 1.00 15.72 C
ATOM 4283 OG1 THR A 289 -51.422 5.827 7.708 1.00 16.52 O
ATOM 4285 CG2 THR A 289 -50.927 8.007 8.371 1.00 16.56 C
ATOM 4289 C THR A 289 -48.677 4.879 8.727 1.00 16.34 C
ATOM 4290 O THR A 289 -48.234 4.707 9.881 1.00 16.68 O
ATOM 4292 N ILE A 290 -48.737 3.904 7.820 1.00 16.29 N
ATOM 4293 CA ILE A 290 -48.347 2.538 8.166 1.00 16.56 C
ATOM 4295 CB ILE A 290 -48.734 1.516 7.096 1.00 16.48 C
ATOM 4297 CG1 ILE A 290 -50.247 1.440 6.944 1.00 16.91 C
ATOM 4300 CD1 ILE A 290 -50.677 .564 5.811 1.00 16.52 C
ATOM 4304 CG2 ILE A 290 -48.262 .145 7.488 1.00 16.52 C
ATOM 4308 C ILE A 290 -46.842 2.456 8.402 1.00 16.94 C
ATOM 4309 O ILE A 290 -46.404 1.968 9.443 1.00 17.06 O
ATOM 4311 N ILE A 291 -46.048 2.942 7.451 1.00 17.22 N
ATOM 4312 CA ILE A 291 -44.595 2.969 7.640 1.00 17.20 C
ATOM 4314 CB ILE A 291 -43.842 3.534 6.405 1.00 17.32 C
ATOM 4316 CG1 ILE A 291 -44.172 2.744 5.125 1.00 17.61 C
ATOM 4319 CD1 ILE A 291 -44.004 1.265 5.250 1.00 18.21 C
ATOM 4323 CG2 ILE A 291 -42.336 3.550 6.637 1.00 16.64 C
ATOM 4327 C ILE A 291 -44.262 3.794 8.886 1.00 17.36 C
ATOM 4328 O ILE A 291 -43.420 3.413 9.670 1.00 17.06 O
ATOM 4330 N ASP A 292 -44.950 4.906 9.093 1.00 18.12 N
ATOM 4331 CA ASP A 292 -44.627 5.755 10.227 1.00 18.83 C
ATOM 4333 CB ASP A 292 -45.511 7.017 10.285 1.00 19.22 C
ATOM 4336 CG ASP A 292 -45.185 7.920 11.485 1.00 19.93 C
ATOM 4337 OD1 ASP A 292 -44.062 8.460 11.544 1.00 21.80 O
ATOM 4338 OD2 ASP A 292 -46.048 8.080 12.375 1.00 20.46 O
ATOM 4339 C ASP A 292 -44.745 4.947 11.509 1.00 18.96 C
ATOM 4340 O ASP A 292 -43.902 5.094 12.394 1.00 19.05 O
ATOM 4342 N ASP A 293 -45.774 4.097 11.610 1.00 19.05 N
ATOM 4343 CA ASP A 293 -45.951 3.273 12.817 1.00 18.99 C
ATOM 4345 CB ASP A 293 -47.237 2.443 12.790 1.00 18.95 C
ATOM 4348 CG ASP A 293 -48.496 3.272 12.921 1.00 19.27 C
ATOM 4349 OD1 ASP A 293 -48.483 4.361 13.523 1.00 21.51 O
ATOM 4350 OD2 ASP A 293 -49.536 2.812 12.421 1.00 19.61 O
ATOM 4351 C ASP A 293 -44.783 2.322 12.935 1.00 19.07 C
ATOM 4352 O ASP A 293 -44.244 2.135 14.024 1.00 19.35 O
ATOM 4354 N ILE A 294 -44.390 1.730 11.805 1.00 19.10 N
ATOM 4355 CA ILE A 294 -43.320 .727 11.786 1.00 19.04 C
ATOM 4357 CB ILE A 294 -43.137 .109 10.386 1.00 18.49 C
ATOM 4359 CG1 ILE A 294 -44.343 -.754 10.038 1.00 17.60 C
ATOM 4362 CD1 ILE A 294 -44.204 -1.504 8.752 1.00 16.77 C
ATOM 4366 CG2 ILE A 294 -41.895 -.745 10.348 1.00 18.77 C
ATOM 4370 C ILE A 294 -41.974 1.273 12.298 1.00 19.55 C
ATOM 4371 O ILE A 294 -41.234 .550 12.974 1.00 19.75 O
ATOM 4373 N TYR A 295 -41.649 2.525 11.983 1.00 19.75 N
ATOM 4374 CA TYR A 295 -40.411 3.103 12.476 1.00 19.91 C

ATOM 4376 CB TYR A 295 -39.856 4.178 11.542 1.00 19.66 C
ATOM 4379 CG TYR A 295 -39.206 3.695 10.245 1.00 18.19 C
ATOM 4380 CD1 TYR A 295 -37.821 3.727 10.075 1.00 16.19 C
ATOM 4382 CE1 TYR A 295 -37.222 3.331 8.882 1.00 14.68 C
ATOM 4384 CZ TYR A 295 -38.004 2.906 7.828 1.00 15.04 C
ATOM 4385 OH TYR A 295 -37.428 2.485 6.631 1.00 12.25 O
ATOM 4387 CE2 TYR A 295 -39.383 2.871 7.975 1.00 16.48 C
ATOM 4389 CD2 TYR A 295 -39.975 3.271 9.172 1.00 17.01 C
ATOM 4391 C TYR A 295 -40.647 3.677 13.858 1.00 20.73 C
ATOM 4392 O TYR A 295 -39.749 3.635 14.717 1.00 21.64 O
ATOM 4394 N ASP A 296 -41.843 4.200 14.103 1.00 21.38 N
ATOM 4395 CA ASP A 296 -42.100 4.865 15.391 1.00 22.20 C
ATOM 4397 CB ASP A 296 -43.421 5.644 15.391 1.00 22.69 C
ATOM 4400 CG ASP A 296 -43.567 6.548 16.607 1.00 23.85 C
ATOM 4401 OD1 ASP A 296 -42.568 7.179 17.014 1.00 25.49 O
ATOM 4402 OD2 ASP A 296 -44.689 6.648 17.145 1.00 26.12 O
ATOM 4403 C ASP A 296 -42.106 3.890 16.549 1.00 22.10 C
ATOM 4404 O ASP A 296 -41.376 4.082 17.506 1.00 22.14 O
ATOM 4406 N VAL A 297 -42.900 2.828 16.435 1.00 22.25 N
ATOM 4407 CA VAL A 297 -43.163 1.937 17.570 1.00 22.22 C
ATOM 4409 CB VAL A 297 -44.635 2.116 18.057 1.00 22.07 C
ATOM 4411 CG1 VAL A 297 -44.958 3.587 18.215 1.00 21.63 C
ATOM 4415 CG2 VAL A 297 -45.618 1.459 17.099 1.00 20.76 C
ATOM 4419 C VAL A 297 -42.861 .422 17.373 1.00 22.49 C
ATOM 4420 O VAL A 297 -42.517 -.255 18.343 1.00 22.40 O
ATOM 4422 N TYR A 298 -42.990 -.117 16.157 1.00 22.69 N
ATOM 4423 CA TYR A 298 -43.065 -1.579 15.993 1.00 22.90 C
ATOM 4425 CB TYR A 298 -44.089 -1.974 14.934 1.00 22.77 C
ATOM 4428 CG TYR A 298 -44.341 -3.469 14.932 1.00 23.74 C
ATOM 4429 CD1 TYR A 298 -45.249 -4.043 15.819 1.00 25.72 C
ATOM 4431 CE1 TYR A 298 -45.484 -5.435 15.833 1.00 26.12 C
ATOM 4433 CZ TYR A 298 -44.798 -6.247 14.954 1.00 25.59 C
ATOM 4434 OH TYR A 298 -45.027 -7.593 14.970 1.00 25.33 O
ATOM 4436 CE2 TYR A 298 -43.890 -5.702 14.062 1.00 24.79 C
ATOM 4438 CD2 TYR A 298 -43.661 -4.317 14.061 1.00 24.20 C
ATOM 4440 C TYR A 298 -41.750 -2.258 15.649 1.00 23.02 C
ATOM 4441 O TYR A 298 -41.387 -3.257 16.256 1.00 22.80 O
ATOM 4443 N GLY A 299 -41.069 -1.747 14.634 1.00 23.47 N
ATOM 4444 CA GLY A 299 -39.839 -2.361 14.149 1.00 23.36 C
ATOM 4447 C GLY A 299 -38.631 -1.978 14.984 1.00 23.27 C
ATOM 4448 O GLY A 299 -38.532 -.858 15.501 1.00 23.35 O
ATOM 4450 N THR A 300 -37.702 -2.918 15.098 1.00 23.11 N
ATOM 4451 CA THR A 300 -36.459 -2.682 15.797 1.00 22.90 C
ATOM 4453 CB THR A 300 -35.869 -3.957 16.386 1.00 22.83 C
ATOM 4455 OG1 THR A 300 -35.328 -4.756 15.328 1.00 22.61 O
ATOM 4457 CG2 THR A 300 -36.928 -4.732 17.162 1.00 22.18 C
ATOM 4461 C THR A 300 -35.482 -2.120 14.796 1.00 23.00 C
ATOM 4462 O THR A 300 -35.606 -2.364 13.602 1.00 23.13 O
ATOM 4464 N LEU A 301 -34.496 -1.394 15.309 1.00 23.07 N
ATOM 4465 CA LEU A 301 -33.596 -.572 14.498 1.00 22.84 C
ATOM 4467 CB LEU A 301 -32.515 .007 15.403 1.00 22.80 C
ATOM 4470 CG LEU A 301 -31.965 1.412 15.182 1.00 22.39 C
ATOM 4472 CD1 LEU A 301 -32.983 2.365 14.587 1.00 22.44 C
ATOM 4476 CD2 LEU A 301 -31.482 1.919 16.536 1.00 22.19 C
ATOM 4480 C LEU A 301 -32.964 -1.358 13.361 1.00 22.95 C
ATOM 4481 O LEU A 301 -32.910 -.888 12.232 1.00 22.50 O
ATOM 4483 N ASP A 302 -32.511 -2.569 13.673 1.00 23.35 N
ATOM 4484 CA ASP A 302 -31.929 -3.469 12.670 1.00 23.65 C
ATOM 4486 CB ASP A 302 -31.332 -4.747 13.328 1.00 24.12 C
ATOM 4489 CG ASP A 302 -29.984 -4.498 14.057 1.00 25.23 C

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ATOM   4490  OD1 ASP A 302     -29.003  -4.051  13.409  1.00 26.43           O
ATOM   4491  OD2 ASP A 302     -29.896  -4.780  15.277  1.00 26.92           O
ATOM   4492  C   ASP A 302     -32.945  -3.859  11.581  1.00 23.11           C
ATOM   4493  O   ASP A 302     -32.544  -4.086  10.445  1.00 23.05           O
ATOM   4495  N   GLU A 303     -34.235  -3.965  11.927  1.00 22.63           N
ATOM   4496  CA  GLU A 303     -35.295  -4.248  10.931  1.00 22.40           C
ATOM   4498  CB  GLU A 303     -36.625  -4.675  11.589  1.00 22.20           C
ATOM   4501  CG  GLU A 303     -36.537  -5.956  12.426  1.00 22.66           C
ATOM   4504  CD  GLU A 303     -37.832  -6.341  13.159  1.00 22.69           C
ATOM   4505  OE1 GLU A 303     -38.614  -5.449  13.568  1.00 22.23           O
ATOM   4506  OE2 GLU A 303     -38.051  -7.558  13.338  1.00 21.64           O
ATOM   4507  C   GLU A 303     -35.533  -3.017  10.067  1.00 22.35           C
ATOM   4508  O   GLU A 303     -35.658  -3.105   8.841  1.00 22.27           O
ATOM   4510  N   LEU A 304     -35.597  -1.866  10.724  1.00 22.34           N
ATOM   4511  CA  LEU A 304     -35.776   -.607  10.040  1.00 22.26           C
ATOM   4513  CB  LEU A 304     -35.861    .537  11.052  1.00 22.49           C
ATOM   4516  CG  LEU A 304     -37.089    .517  11.973  1.00 23.05           C
ATOM   4518  CD1 LEU A 304     -37.109   1.708  12.932  1.00 23.46           C
ATOM   4522  CD2 LEU A 304     -38.353    .511  11.142  1.00 23.96           C
ATOM   4526  C   LEU A 304     -34.634   -.383   9.063  1.00 22.09           C
ATOM   4527  O   LEU A 304     -34.873    .094   7.969  1.00 22.32           O
ATOM   4529  N   GLU A 305     -33.408   -.740   9.450  1.00 21.91           N
ATOM   4530  CA  GLU A 305     -32.259   -.685   8.541  1.00 21.93           C
ATOM   4532  CB  GLU A 305     -30.988  -1.194   9.219  1.00 22.35           C
ATOM   4535  CG  GLU A 305     -30.363   -.258  10.249  1.00 24.12           C
ATOM   4538  CD  GLU A 305     -29.751   1.002   9.649  1.00 26.11           C
ATOM   4539  OE1 GLU A 305     -29.275   1.846  10.454  1.00 25.68           O
ATOM   4540  OE2 GLU A 305     -29.756   1.146   8.391  1.00 27.67           O
ATOM   4541  C   GLU A 305     -32.475  -1.524   7.295  1.00 21.54           C
ATOM   4542  O   GLU A 305     -32.010  -1.162   6.220  1.00 21.75           O
ATOM   4544  N   LEU A 306     -33.155  -2.660   7.448  1.00 21.21           N
ATOM   4545  CA  LEU A 306     -33.459  -3.557   6.316  1.00 20.66           C
ATOM   4547  CB  LEU A 306     -33.880  -4.956   6.795  1.00 20.26           C
ATOM   4550  CG  LEU A 306     -32.725  -5.854   7.220  1.00 19.57           C
ATOM   4552  CD1 LEU A 306     -33.261  -7.150   7.777  1.00 20.18           C
ATOM   4556  CD2 LEU A 306     -31.791  -6.120   6.061  1.00 18.29           C
ATOM   4560  C   LEU A 306     -34.535  -2.967   5.416  1.00 20.23           C
ATOM   4561  O   LEU A 306     -34.412  -2.966   4.197  1.00 19.97           O
ATOM   4563  N   PHE A 307     -35.588  -2.457   6.023  1.00 19.99           N
ATOM   4564  CA  PHE A 307     -36.635  -1.861   5.237  1.00 20.00           C
ATOM   4566  CB  PHE A 307     -37.771  -1.388   6.118  1.00 20.08           C
ATOM   4569  CG  PHE A 307     -39.011  -1.115   5.370  1.00 19.05           C
ATOM   4570  CD1 PHE A 307     -39.895  -2.118   5.119  1.00 18.77           C
ATOM   4572  CE1 PHE A 307     -41.037  -1.873   4.421  1.00 20.07           C
ATOM   4574  CZ  PHE A 307     -41.296   -.621   3.959  1.00 19.63           C
ATOM   4576  CE2 PHE A 307     -40.411    .391   4.199  1.00 19.27           C
ATOM   4578  CD2 PHE A 307     -39.278    .142   4.900  1.00 19.17           C
ATOM   4580  C   PHE A 307     -36.087   -.695   4.447  1.00 20.25           C
ATOM   4581  O   PHE A 307     -36.356   -.589   3.242  1.00 20.08           O
ATOM   4583  N   THR A 308     -35.325    .167   5.137  1.00 20.51           N
ATOM   4584  CA  THR A 308     -34.737   1.379   4.538  1.00 20.60           C
ATOM   4586  CB  THR A 308     -33.860   2.177   5.541  1.00 20.41           C
ATOM   4588  OG1 THR A 308     -34.672   2.661   6.611  1.00 20.05           O
ATOM   4590  CG2 THR A 308     -33.198   3.376   4.864  1.00 20.38           C
ATOM   4594  C   THR A 308     -33.895   1.009   3.331  1.00 20.82           C
ATOM   4595  O   THR A 308     -34.057   1.571   2.243  1.00 20.45           O
ATOM   4597  N   ASP A 309     -33.020    .031   3.522  1.00 21.32           N
ATOM   4598  CA  ASP A 309     -32.138   -.399   2.449  1.00 21.88           C
ATOM   4600  CB  ASP A 309     -31.042  -1.324   2.971  1.00 22.44           C
ATOM   4603  CG  ASP A 309     -30.164  -1.847   1.857  1.00 25.69           C
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ATOM  4604 OD1 ASP A 309    -29.599 -1.010  1.089 1.00 28.02       O
ATOM  4605 OD2 ASP A 309    -30.076 -3.100  1.730 1.00 30.59       O
ATOM  4606 C   ASP A 309    -32.928 -1.085  1.357 1.00 21.17       C
ATOM  4607 O   ASP A 309    -32.601  -.948   .188 1.00 20.95       O
ATOM  4609 N   ALA A 310    -33.965 -1.818  1.757 1.00 20.99       N
ATOM  4610 CA  ALA A 310    -34.885 -2.474   .828 1.00 20.91       C
ATOM  4612 CB  ALA A 310    -35.931 -3.244  1.591 1.00 20.77       C
ATOM  4616 C   ALA A 310    -35.567 -1.501  -.123 1.00 21.08       C
ATOM  4617 O   ALA A 310    -35.745 -1.816 -1.305 1.00 20.76       O
ATOM  4619 N   VAL A 311    -35.958  -.334   .402 1.00 21.51       N
ATOM  4620 CA  VAL A 311    -36.594   .719  -.396 1.00 21.50       C
ATOM  4622 CB  VAL A 311    -37.424  1.715   .477 1.00 21.73       C
ATOM  4624 CG1 VAL A 311    -38.724  1.076   .941 1.00 21.01       C
ATOM  4628 CG2 VAL A 311    -37.765  2.993  -.292 1.00 21.88       C
ATOM  4632 C   VAL A 311    -35.553  1.445 -1.230 1.00 21.67       C
ATOM  4633 O   VAL A 311    -35.811  1.728 -2.389 1.00 21.71       O
ATOM  4635 N   GLU A 312    -34.381  1.724  -.663 1.00 22.25       N
ATOM  4636 CA  GLU A 312    -33.248  2.284 -1.443 1.00 23.00       C
ATOM  4638 CB  GLU A 312    -31.951  2.331  -.608 1.00 23.36       C
ATOM  4641 CG  GLU A 312    -31.897  3.383   .511 1.00 24.72       C
ATOM  4644 CD  GLU A 312    -30.526  3.469  1.189 1.00 27.09       C
ATOM  4645 OE1 GLU A 312    -30.083  4.608  1.458 1.00 30.07       O
ATOM  4646 OE2 GLU A 312    -29.885  2.418  1.454 1.00 27.86       O
ATOM  4647 C   GLU A 312    -32.954  1.498 -2.731 1.00 23.13       C
ATOM  4648 O   GLU A 312    -32.851  2.064 -3.803 1.00 22.88       O
ATOM  4650 N   ARG A 313    -32.819   .188 -2.615 1.00 23.74       N
ATOM  4651 CA  ARG A 313    -32.400  -.628 -3.743 1.00 24.46       C
ATOM  4653 CB  ARG A 313    -31.758 -1.916 -3.232 1.00 25.01       C
ATOM  4656 CG  ARG A 313    -30.421 -1.667 -2.481 1.00 27.74       C
ATOM  4659 CD  ARG A 313    -29.715 -2.963 -2.072 1.00 31.41       C
ATOM  4662 NE  ARG A 313    -30.675 -3.921 -1.499 1.00 34.94       N
ATOM  4664 CZ  ARG A 313    -31.203 -4.974 -2.138 1.00 37.87       C
ATOM  4665 NH1 ARG A 313    -30.861 -5.282 -3.402 1.00 38.35       N
ATOM  4668 NH2 ARG A 313    -32.079 -5.746 -1.495 1.00 38.82       N
ATOM  4671 C   ARG A 313    -33.523  -.914 -4.739 1.00 24.27       C
ATOM  4672 O   ARG A 313    -33.257 -1.178 -5.898 1.00 24.17       O
ATOM  4674 N   TRP A 314    -34.770  -.873 -4.282 1.00 24.59       N
ATOM  4675 CA  TRP A 314    -35.939 -1.042 -5.142 1.00 24.66       C
ATOM  4677 CB  TRP A 314    -36.175   .234 -5.961 1.00 24.39       C
ATOM  4680 CG  TRP A 314    -37.575   .382 -6.386 1.00 22.61       C
ATOM  4681 CD1 TRP A 314    -38.073   .204 -7.635 1.00 21.66       C
ATOM  4683 NE1 TRP A 314    -39.429   .403 -7.634 1.00 21.42       N
ATOM  4685 CE2 TRP A 314    -39.829   .707 -6.360 1.00 20.99       C
ATOM  4686 CD2 TRP A 314    -38.683   .701 -5.550 1.00 21.41       C
ATOM  4687 CE3 TRP A 314    -38.817   .991 -4.191 1.00 21.48       C
ATOM  4689 CZ3 TRP A 314    -40.080  1.277 -3.693 1.00 21.38       C
ATOM  4691 CH2 TRP A 314    -41.204  1.269 -4.523 1.00 20.84       C
ATOM  4693 CZ2 TRP A 314    -41.099   .985 -5.857 1.00 20.87       C
ATOM  4695 C   TRP A 314    -35.831 -2.286 -6.038 1.00 25.65       C
ATOM  4696 O   TRP A 314    -36.069 -2.238 -7.259 1.00 25.69       O
ATOM  4698 N   ASP A 315    -35.480 -3.400 -5.404 1.00 26.79       N
ATOM  4699 CA  ASP A 315    -35.253 -4.667 -6.087 1.00 28.01       C
ATOM  4701 CB  ASP A 315    -33.801 -5.097 -5.890 1.00 28.07       C
ATOM  4704 CG  ASP A 315    -33.553 -6.536 -6.296 1.00 29.92       C
ATOM  4705 OD1 ASP A 315    -34.262 -7.026 -7.197 1.00 32.58       O
ATOM  4706 OD2 ASP A 315    -32.648 -7.194 -5.722 1.00 32.73       O
ATOM  4707 C   ASP A 315    -36.202 -5.710 -5.518 1.00 28.91       C
ATOM  4708 O   ASP A 315    -36.019 -6.163 -4.399 1.00 29.17       O
ATOM  4710 N   VAL A 316    -37.218 -6.091 -6.283 1.00 30.25       N
ATOM  4711 CA  VAL A 316    -38.233 -7.012 -5.778 1.00 31.47       C
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ATOM 4713 CB VAL A 316 -39.396 -7.156 -6.755 1.00 31.56 C
ATOM 4715 CG1 VAL A 316 -40.668 -7.590 -6.027 1.00 30.99 C
ATOM 4719 CG2 VAL A 316 -39.033 -8.141 -7.862 1.00 31.84 C
ATOM 4723 C VAL A 316 -37.663 -8.405 -5.540 1.00 32.86 C
ATOM 4724 O VAL A 316 -38.170 -9.153 -4.708 1.00 32.99 O
ATOM 4726 N ASN A 317 -36.607 -8.750 -6.278 1.00 34.55 N
ATOM 4727 CA ASN A 317 -35.940 -10.060 -6.160 1.00 35.53 C
ATOM 4729 CB ASN A 317 -35.013 -10.298 -7.367 1.00 35.68 C
ATOM 4732 CG ASN A 317 -35.752 -10.264 -8.713 1.00 35.92 C
ATOM 4733 OD1 ASN A 317 -36.634 -11.092 -8.971 1.00 36.95 O
ATOM 4734 ND2 ASN A 317 -35.368 -9.323 -9.585 1.00 34.17 N
ATOM 4737 C ASN A 317 -35.126 -10.225 -4.871 1.00 36.40 C
ATOM 4738 O ASN A 317 -34.385 -11.195 -4.747 1.00 36.47 O
ATOM 4740 N ALA A 318 -35.239 -9.265 -3.944 1.00 37.52 N
ATOM 4741 CA ALA A 318 -34.614 -9.335 -2.613 1.00 38.45 C
ATOM 4743 CB ALA A 318 -33.371 -8.465 -2.557 1.00 38.43 C
ATOM 4747 C ALA A 318 -35.631 -8.902 -1.554 1.00 39.28 C
ATOM 4748 O ALA A 318 -35.361 -8.094 -.662 1.00 39.55 O
ATOM 4750 N ILE A 319 -36.823 -9.456 -1.698 1.00 40.17 N
ATOM 4751 CA ILE A 319 -37.905 -9.310 -.740 1.00 40.49 C
ATOM 4753 CB ILE A 319 -39.275 -9.588 -1.469 1.00 40.64 C
ATOM 4755 CG1 ILE A 319 -40.473 -9.078 -.683 1.00 40.88 C
ATOM 4758 CD1 ILE A 319 -41.799 -9.535 -1.280 1.00 40.86 C
ATOM 4762 CG2 ILE A 319 -39.460 -11.082 -1.801 1.00 40.50 C
ATOM 4766 C ILE A 319 -37.656 -10.319 .393 1.00 40.69 C
ATOM 4767 O ILE A 319 -38.136 -10.138 1.504 1.00 40.88 O
ATOM 4769 N ASN A 320 -36.886 -11.374 .104 1.00 40.79 N
ATOM 4770 CA ASN A 320 -36.689 -12.483 1.049 1.00 40.64 C
ATOM 4772 CB ASN A 320 -36.240 -13.761 .314 1.00 40.73 C
ATOM 4775 CG ASN A 320 -37.370 -14.422 -.468 1.00 40.98 C
ATOM 4776 OD1 ASN A 320 -38.556 -14.309 -.119 1.00 40.77 O
ATOM 4777 ND2 ASN A 320 -37.001 -15.131 -1.529 1.00 41.31 N
ATOM 4780 C ASN A 320 -35.711 -12.175 2.169 1.00 40.16 C
ATOM 4781 O ASN A 320 -35.546 -12.978 3.077 1.00 40.15 O
ATOM 4783 N ASP A 321 -35.067 -11.017 2.101 1.00 39.66 N
ATOM 4784 CA ASP A 321 -34.111 -10.615 3.126 1.00 39.51 C
ATOM 4786 CB ASP A 321 -33.114 -9.571 2.575 1.00 40.17 C
ATOM 4789 CG ASP A 321 -32.595 -9.904 1.152 1.00 42.12 C
ATOM 4790 OD1 ASP A 321 -32.425 -11.115 .820 1.00 44.15 O
ATOM 4791 OD2 ASP A 321 -32.354 -8.934 .375 1.00 43.28 O
ATOM 4792 C ASP A 321 -34.851 -10.030 4.337 1.00 38.27 C
ATOM 4793 O ASP A 321 -34.304 -9.987 5.443 1.00 38.15 O
ATOM 4795 N LEU A 322 -36.089 -9.583 4.108 1.00 36.72 N
ATOM 4796 CA LEU A 322 -36.887 -8.875 5.104 1.00 35.38 C
ATOM 4798 CB LEU A 322 -37.894 -7.942 4.422 1.00 35.15 C
ATOM 4801 CG LEU A 322 -37.370 -6.840 3.503 1.00 34.83 C
ATOM 4803 CD1 LEU A 322 -38.479 -6.286 2.626 1.00 34.45 C
ATOM 4807 CD2 LEU A 322 -36.742 -5.740 4.316 1.00 34.89 C
ATOM 4811 C LEU A 322 -37.683 -9.834 5.963 1.00 34.57 C
ATOM 4812 O LEU A 322 -37.975 -10.933 5.527 1.00 34.27 O
ATOM 4814 N PRO A 323 -38.039 -9.402 7.189 1.00 33.93 N
ATOM 4815 CA PRO A 323 -39.070 -9.917 8.067 1.00 33.49 C
ATOM 4817 CB PRO A 323 -39.151 -8.840 9.141 1.00 33.31 C
ATOM 4820 CG PRO A 323 -37.791 -8.419 9.311 1.00 33.67 C
ATOM 4823 CD PRO A 323 -37.154 -8.496 7.941 1.00 34.20 C
ATOM 4826 C PRO A 323 -40.429 -10.036 7.425 1.00 33.33 C
ATOM 4827 O PRO A 323 -40.776 -9.232 6.579 1.00 33.35 O
ATOM 4828 N ASP A 324 -41.209 -11.005 7.891 1.00 33.37 N
ATOM 4829 CA ASP A 324 -42.511 -11.329 7.313 1.00 33.36 C
ATOM 4831 CB ASP A 324 -43.137 -12.542 8.037 1.00 33.59 C

ATOM 4834 CG ASP A 324 -42.496 -13.881 7.619 1.00 34.18 C
ATOM 4835 OD1 ASP A 324 -41.885 -13.915 6.518 1.00 36.44 O
ATOM 4836 OD2 ASP A 324 -42.607 -14.887 8.371 1.00 32.19 O
ATOM 4837 C ASP A 324 -43.484 -10.149 7.289 1.00 32.90 C
ATOM 4838 O ASP A 324 -44.108 -9.885 6.255 1.00 33.36 O
ATOM 4840 N TYR A 325 -43.606 -9.423 8.392 1.00 32.10 N
ATOM 4841 CA TYR A 325 -44.515 -8.279 8.400 1.00 31.65 C
ATOM 4843 CB TYR A 325 -44.718 -7.726 9.815 1.00 31.68 C
ATOM 4846 CG TYR A 325 -43.618 -6.846 10.352 1.00 31.35 C
ATOM 4847 CD1 TYR A 325 -42.507 -7.389 10.992 1.00 31.31 C
ATOM 4849 CE1 TYR A 325 -41.497 -6.574 11.504 1.00 31.46 C
ATOM 4851 CZ TYR A 325 -41.613 -5.192 11.392 1.00 32.41 C
ATOM 4852 OH TYR A 325 -40.637 -4.336 11.893 1.00 32.78 O
ATOM 4854 CE2 TYR A 325 -42.723 -4.644 10.769 1.00 32.17 C
ATOM 4856 CD2 TYR A 325 -43.713 -5.470 10.261 1.00 31.47 C
ATOM 4858 C TYR A 325 -44.094 -7.179 7.424 1.00 31.17 C
ATOM 4859 O TYR A 325 -44.947 -6.458 6.920 1.00 31.09 O
ATOM 4861 N MET A 326 -42.796 -7.068 7.145 1.00 30.73 N
ATOM 4862 CA MET A 326 -42.277 -6.036 6.225 1.00 30.49 C
ATOM 4864 CB MET A 326 -40.832 -5.702 6.565 1.00 30.16 C
ATOM 4867 CG MET A 326 -40.725 -4.918 7.830 1.00 29.57 C
ATOM 4870 SD MET A 326 -39.057 -4.376 8.166 1.00 28.39 S
ATOM 4871 CE MET A 326 -39.407 -2.787 8.933 1.00 26.18 C
ATOM 4875 C MET A 326 -42.371 -6.418 4.748 1.00 30.59 C
ATOM 4876 O MET A 326 -42.786 -5.603 3.920 1.00 30.48 O
ATOM 4878 N LYS A 327 -41.936 -7.643 4.438 1.00 30.68 N
ATOM 4879 CA LYS A 327 -42.170 -8.299 3.143 1.00 30.56 C
ATOM 4881 CB LYS A 327 -42.267 -9.830 3.326 1.00 30.84 C
ATOM 4884 CG LYS A 327 -41.052 -10.607 2.844 1.00 32.35 C
ATOM 4887 CD LYS A 327 -40.990 -12.019 3.412 1.00 34.43 C
ATOM 4890 CE LYS A 327 -40.221 -12.941 2.462 1.00 35.77 C
ATOM 4893 NZ LYS A 327 -39.691 -14.162 3.150 1.00 37.20 N
ATOM 4897 C LYS A 327 -43.453 -7.811 2.515 1.00 29.89 C
ATOM 4898 O LYS A 327 -43.447 -7.220 1.436 1.00 29.85 O
ATOM 4900 N LEU A 328 -44.544 -8.046 3.230 1.00 29.10 N
ATOM 4901 CA LEU A 328 -45.871 -7.781 2.730 1.00 28.77 C
ATOM 4903 CB LEU A 328 -46.899 -8.336 3.709 1.00 28.81 C
ATOM 4906 CG LEU A 328 -48.349 -8.364 3.257 1.00 28.82 C
ATOM 4908 CD1 LEU A 328 -48.519 -9.260 2.046 1.00 29.09 C
ATOM 4912 CD2 LEU A 328 -49.202 -8.845 4.411 1.00 29.16 C
ATOM 4916 C LEU A 328 -46.057 -6.291 2.564 1.00 28.61 C
ATOM 4917 O LEU A 328 -46.582 -5.828 1.554 1.00 29.00 O
ATOM 4919 N CYS A 329 -45.612 -5.532 3.557 1.00 28.24 N
ATOM 4920 CA CYS A 329 -45.737 -4.086 3.504 1.00 27.95 C
ATOM 4922 CB CYS A 329 -45.311 -3.459 4.834 1.00 28.21 C
ATOM 4925 SG CYS A 329 -45.280 -1.630 4.817 1.00 32.39 S
ATOM 4927 C CYS A 329 -44.921 -3.541 2.327 1.00 26.34 C
ATOM 4928 O CYS A 329 -45.459 -2.853 1.475 1.00 26.23 O
ATOM 4930 N PHE A 330 -43.642 -3.882 2.269 1.00 24.82 N
ATOM 4931 CA PHE A 330 -42.790 -3.514 1.130 1.00 23.82 C
ATOM 4933 CB PHE A 330 -41.397 -4.137 1.283 1.00 23.64 C
ATOM 4936 CG PHE A 330 -40.492 -3.873 .117 1.00 22.63 C
ATOM 4937 CD1 PHE A 330 -39.845 -2.658 -.008 1.00 21.68 C
ATOM 4939 CE1 PHE A 330 -39.020 -2.393 -1.082 1.00 21.07 C
ATOM 4941 CZ PHE A 330 -38.829 -3.343 -2.046 1.00 22.00 C
ATOM 4943 CE2 PHE A 330 -39.474 -4.568 -1.944 1.00 22.60 C
ATOM 4945 CD2 PHE A 330 -40.309 -4.824 -.865 1.00 22.36 C
ATOM 4947 C PHE A 330 -43.348 -3.863 -.281 1.00 22.99 C
ATOM 4948 O PHE A 330 -43.350 -3.012 -1.182 1.00 22.98 O
ATOM 4950 N LEU A 331 -43.789 -5.101 -.492 1.00 21.65 N

ATOM 4951 CA LEU A 331 -44.306 -5.484 -1.816 1.00 20.74 C
ATOM 4953 CB LEU A 331 -44.573 -6.990 -1.912 1.00 20.57 C
ATOM 4956 CG LEU A 331 -44.959 -7.575 -3.277 1.00 19.82 C
ATOM 4958 CD1 LEU A 331 -43.936 -7.246 -4.329 1.00 19.00 C
ATOM 4962 CD2 LEU A 331 -45.128 -9.092 -3.165 1.00 19.11 C
ATOM 4966 C LEU A 331 -45.568 -4.710 -2.159 1.00 19.98 C
ATOM 4967 O LEU A 331 -45.753 -4.324 -3.300 1.00 20.15 O
ATOM 4969 N ALA A 332 -46.431 -4.495 -1.172 1.00 19.09 N
ATOM 4970 CA ALA A 332 -47.619 -3.675 -1.353 1.00 18.46 C
ATOM 4972 CB ALA A 332 -48.406 -3.587 -.045 1.00 18.20 C
ATOM 4976 C ALA A 332 -47.248 -2.279 -1.856 1.00 17.91 C
ATOM 4977 O ALA A 332 -47.890 -1.745 -2.744 1.00 17.98 O
ATOM 4979 N LEU A 333 -46.197 -1.706 -1.295 1.00 17.62 N
ATOM 4980 CA LEU A 333 -45.753 -.353 -1.637 1.00 17.60 C
ATOM 4982 CB LEU A 333 -44.725 .132 -.598 1.00 17.59 C
ATOM 4985 CG LEU A 333 -44.122 1.533 -.761 1.00 17.16 C
ATOM 4987 CD1 LEU A 333 -45.166 2.629 -.554 1.00 16.99 C
ATOM 4991 CD2 LEU A 333 -42.979 1.704 .200 1.00 15.89 C
ATOM 4995 C LEU A 333 -45.100 -.320 -3.005 1.00 17.70 C
ATOM 4996 O LEU A 333 -45.321 .603 -3.795 1.00 17.86 O
ATOM 4998 N TYR A 334 -44.248 -1.319 -3.234 1.00 17.63 N
ATOM 4999 CA TYR A 334 -43.542 -1.531 -4.489 1.00 17.44 C
ATOM 5001 CB TYR A 334 -42.893 -2.908 -4.444 1.00 17.50 C
ATOM 5004 CG TYR A 334 -41.897 -3.169 -5.523 1.00 18.03 C
ATOM 5005 CD1 TYR A 334 -40.698 -2.473 -5.569 1.00 18.83 C
ATOM 5007 CE1 TYR A 334 -39.764 -2.725 -6.542 1.00 18.13 C
ATOM 5009 CZ TYR A 334 -40.016 -3.678 -7.478 1.00 18.78 C
ATOM 5010 OH TYR A 334 -39.096 -3.929 -8.439 1.00 21.71 O
ATOM 5012 CE2 TYR A 334 -41.180 -4.391 -7.462 1.00 19.74 C
ATOM 5014 CD2 TYR A 334 -42.118 -4.139 -6.472 1.00 19.59 C
ATOM 5016 C TYR A 334 -44.500 -1.497 -5.649 1.00 17.43 C
ATOM 5017 O TYR A 334 -44.264 -.803 -6.636 1.00 17.64 O
ATOM 5019 N ASN A 335 -45.589 -2.253 -5.504 1.00 17.30 N
ATOM 5020 CA ASN A 335 -46.574 -2.448 -6.553 1.00 17.23 C
ATOM 5022 CB ASN A 335 -47.544 -3.551 -6.166 1.00 17.32 C
ATOM 5025 CG ASN A 335 -46.952 -4.920 -6.332 1.00 18.16 C
ATOM 5026 OD1 ASN A 335 -45.913 -5.090 -6.989 1.00 18.99 O
ATOM 5027 ND2 ASN A 335 -47.616 -5.921 -5.749 1.00 18.49 N
ATOM 5030 C ASN A 335 -47.365 -1.218 -6.812 1.00 17.12 C
ATOM 5031 O ASN A 335 -47.613 -.852 -7.965 1.00 17.36 O
ATOM 5033 N THR A 336 -47.789 -.602 -5.722 1.00 17.20 N
ATOM 5034 CA THR A 336 -48.601 .593 -5.779 1.00 17.36 C
ATOM 5036 CB THR A 336 -48.888 1.104 -4.381 1.00 17.20 C
ATOM 5038 OG1 THR A 336 -49.611 .103 -3.657 1.00 16.26 O
ATOM 5040 CG2 THR A 336 -49.688 2.384 -4.452 1.00 17.18 C
ATOM 5044 C THR A 336 -47.893 1.691 -6.550 1.00 17.84 C
ATOM 5045 O THR A 336 -48.511 2.388 -7.360 1.00 18.07 O
ATOM 5047 N ILE A 337 -46.595 1.831 -6.298 1.00 18.14 N
ATOM 5048 CA ILE A 337 -45.817 2.904 -6.895 1.00 18.50 C
ATOM 5050 CB ILE A 337 -44.584 3.209 -6.066 1.00 18.31 C
ATOM 5052 CG1 ILE A 337 -45.014 3.997 -4.837 1.00 18.58 C
ATOM 5055 CD1 ILE A 337 -44.043 3.866 -3.735 1.00 20.66 C
ATOM 5059 CG2 ILE A 337 -43.570 3.988 -6.867 1.00 16.98 C
ATOM 5063 C ILE A 337 -45.447 2.548 -8.314 1.00 19.29 C
ATOM 5064 O ILE A 337 -45.556 3.387 -9.214 1.00 19.17 O
ATOM 5066 N ASN A 338 -45.033 1.299 -8.513 1.00 20.16 N
ATOM 5067 CA ASN A 338 -44.861 .767 -9.864 1.00 20.93 C
ATOM 5069 CB ASN A 338 -44.409 -.695 -9.830 1.00 21.07 C
ATOM 5072 CG ASN A 338 -42.953 -.845 -9.439 1.00 21.61 C
ATOM 5073 OD1 ASN A 338 -42.232 .143 -9.308 1.00 22.40 O

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ATOM  5074 ND2 ASN A 338    -42.509  -2.086  -9.260  1.00 21.92      N
ATOM  5077 C   ASN A 338    -46.123    .914 -10.719  1.00 21.44      C
ATOM  5078 O   ASN A 338    -46.022   1.202 -11.904  1.00 21.25      O
ATOM  5080 N   GLU A 339    -47.303    .747 -10.128  1.00 22.21      N
ATOM  5081 CA  GLU A 339    -48.532   1.000 -10.880  1.00 23.31      C
ATOM  5083 CB  GLU A 339    -49.768    .464 -10.164  1.00 24.13      C
ATOM  5086 CG  GLU A 339    -50.146   -.936 -10.660  1.00 28.69      C
ATOM  5089 CD  GLU A 339    -50.939  -1.740  -9.638  1.00 35.06      C
ATOM  5090 OE1 GLU A 339    -51.899  -1.136  -9.067  1.00 39.51      O
ATOM  5091 OE2 GLU A 339    -50.596  -2.952  -9.414  1.00 36.64      O
ATOM  5092 C   GLU A 339    -48.725   2.463 -11.269  1.00 22.71      C
ATOM  5093 O   GLU A 339    -49.215   2.743 -12.372  1.00 22.48      O
ATOM  5095 N   ILE A 340    -48.339   3.390 -10.390  1.00 22.19      N
ATOM  5096 CA  ILE A 340    -48.406   4.813 -10.734  1.00 21.64      C
ATOM  5098 CB  ILE A 340    -48.135   5.739  -9.538  1.00 21.33      C
ATOM  5100 CG1 ILE A 340    -49.229   5.596  -8.482  1.00 21.29      C
ATOM  5103 CD1 ILE A 340    -48.925   6.306  -7.150  1.00 20.00      C
ATOM  5107 CG2 ILE A 340    -48.091   7.177  -9.982  1.00 20.28      C
ATOM  5111 C   ILE A 340    -47.414   5.128 -11.861  1.00 21.78      C
ATOM  5112 O   ILE A 340    -47.786   5.826 -12.818  1.00 22.13      O
ATOM  5114 N   ALA A 341    -46.179   4.609 -11.771  1.00 21.34      N
ATOM  5115 CA  ALA A 341    -45.147   4.892 -12.787  1.00 21.03      C
ATOM  5117 CB  ALA A 341    -43.837   4.268 -12.406  1.00 20.55      C
ATOM  5121 C   ALA A 341    -45.592   4.426 -14.183  1.00 21.32      C
ATOM  5122 O   ALA A 341    -45.228   5.036 -15.217  1.00 21.11      O
ATOM  5124 N   TYR A 342    -46.393   3.355 -14.196  1.00 21.45      N
ATOM  5125 CA  TYR A 342    -47.008   2.861 -15.414  1.00 21.41      C
ATOM  5127 CB  TYR A 342    -47.627   1.468 -15.208  1.00 21.31      C
ATOM  5130 CG  TYR A 342    -48.336    .957 -16.450  1.00 19.60      C
ATOM  5131 CD1 TYR A 342    -47.613    .463 -17.521  1.00 16.69      C
ATOM  5133 CE1 TYR A 342    -48.231    .032 -18.643  1.00 15.50      C
ATOM  5135 CZ  TYR A 342    -49.595    .085 -18.728  1.00 15.88      C
ATOM  5136 OH  TYR A 342    -50.196   -.352 -19.877  1.00 16.46      O
ATOM  5138 CE2 TYR A 342    -50.352    .558 -17.681  1.00 16.50      C
ATOM  5140 CD2 TYR A 342    -49.725    .997 -16.556  1.00 18.17      C
ATOM  5142 C   TYR A 342    -48.064   3.830 -15.899  1.00 22.08      C
ATOM  5143 O   TYR A 342    -48.094   4.169 -17.048  1.00 22.07      O
ATOM  5145 N   ASP A 343    -48.942   4.283 -15.032  1.00 23.41      N
ATOM  5146 CA  ASP A 343    -49.970   5.211 -15.481  1.00 24.66      C
ATOM  5148 CB  ASP A 343    -50.851   5.674 -14.318  1.00 25.10      C
ATOM  5151 CG  ASP A 343    -51.720   4.552 -13.732  1.00 26.06      C
ATOM  5152 OD1 ASP A 343    -52.107   3.613 -14.477  1.00 26.39      O
ATOM  5153 OD2 ASP A 343    -52.032   4.642 -12.516  1.00 27.29      O
ATOM  5154 C   ASP A 343    -49.316   6.420 -16.142  1.00 25.22      C
ATOM  5155 O   ASP A 343    -49.755   6.874 -17.192  1.00 25.47      O
ATOM  5157 N   ASN A 344    -48.260   6.936 -15.528  1.00 25.87      N
ATOM  5158 CA  ASN A 344    -47.508   8.042 -16.127  1.00 26.41      C
ATOM  5160 CB  ASN A 344    -46.498   8.605 -15.134  1.00 26.56      C
ATOM  5163 CG  ASN A 344    -47.152   9.407 -14.073  1.00 26.95      C
ATOM  5164 OD1 ASN A 344    -47.495  10.568 -14.296  1.00 29.13      O
ATOM  5165 ND2 ASN A 344    -47.367   8.799 -12.916  1.00 26.36      N
ATOM  5168 C   ASN A 344    -46.785   7.674 -17.416  1.00 26.53      C
ATOM  5169 O   ASN A 344    -46.658   8.508 -18.304  1.00 26.74      O
ATOM  5171 N   LEU A 345    -46.280   6.448 -17.510  1.00 26.56      N
ATOM  5172 CA  LEU A 345    -45.634   6.019 -18.739  1.00 26.37      C
ATOM  5174 CB  LEU A 345    -44.890   4.693 -18.550  1.00 26.32      C
ATOM  5177 CG  LEU A 345    -43.995   4.339 -19.750  1.00 25.96      C
ATOM  5179 CD1 LEU A 345    -42.706   5.133 -19.665  1.00 25.07      C
ATOM  5183 CD2 LEU A 345    -43.724   2.835 -19.874  1.00 24.75      C
ATOM  5187 C   LEU A 345    -46.679   5.908 -19.856  1.00 26.38      C
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ATOM  5188  O   LEU A 345     -46.435   6.335 -20.966  1.00 26.52           O
ATOM  5190  N   LYS A 346     -47.839   5.340 -19.563  1.00 26.59           N
ATOM  5191  CA  LYS A 346     -48.880   5.176 -20.572  1.00 26.89           C
ATOM  5193  CB  LYS A 346     -50.065   4.367 -20.011  1.00 26.80           C
ATOM  5196  CG  LYS A 346     -51.073   3.931 -21.062  1.00 26.26           C
ATOM  5199  CD  LYS A 346     -52.210   3.080 -20.517  1.00 26.15           C
ATOM  5202  CE  LYS A 346     -53.227   3.849 -19.689  1.00 26.40           C
ATOM  5205  NZ  LYS A 346     -53.136   3.506 -18.223  1.00 27.67           N
ATOM  5209  C   LYS A 346     -49.372   6.537 -21.071  1.00 27.52           C
ATOM  5210  O   LYS A 346     -49.562   6.742 -22.272  1.00 27.57           O
ATOM  5212  N   ASP A 347     -49.567   7.472 -20.148  1.00 28.10           N
ATOM  5213  CA  ASP A 347     -50.309   8.689 -20.465  1.00 28.58           C
ATOM  5215  CB  ASP A 347     -51.305   9.017 -19.329  1.00 28.85           C
ATOM  5218  CG  ASP A 347     -52.426   7.950 -19.197  1.00 30.01           C
ATOM  5219  OD1 ASP A 347     -52.827   7.349 -20.223  1.00 30.51           O
ATOM  5220  OD2 ASP A 347     -52.910   7.704 -18.069  1.00 32.61           O
ATOM  5221  C   ASP A 347     -49.407   9.871 -20.804  1.00 28.22           C
ATOM  5222  O   ASP A 347     -49.778  10.710 -21.611  1.00 28.39           O
ATOM  5224  N   LYS A 348     -48.228   9.930 -20.206  1.00 28.03           N
ATOM  5225  CA  LYS A 348     -47.301  11.021 -20.467  1.00 28.01           C
ATOM  5227  CB  LYS A 348     -46.785  11.648 -19.164  1.00 28.39           C
ATOM  5230  CG  LYS A 348     -47.834  12.305 -18.257  1.00 30.18           C
ATOM  5233  CD  LYS A 348     -47.143  12.898 -17.003  1.00 32.40           C
ATOM  5236  CE  LYS A 348     -48.124  13.121 -15.874  1.00 33.59           C
ATOM  5239  NZ  LYS A 348     -49.319  13.878 -16.341  1.00 35.48           N
ATOM  5243  C   LYS A 348     -46.107  10.551 -21.260  1.00 27.25           C
ATOM  5244  O   LYS A 348     -45.241  11.345 -21.566  1.00 27.60           O
ATOM  5246  N   GLY A 349     -46.036   9.271 -21.583  1.00 26.47           N
ATOM  5247  CA  GLY A 349     -44.863   8.742 -22.261  1.00 26.01           C
ATOM  5250  C   GLY A 349     -43.559   9.109 -21.587  1.00 25.67           C
ATOM  5251  O   GLY A 349     -42.613   9.472 -22.250  1.00 25.85           O
ATOM  5253  N   GLU A 350     -43.498   9.032 -20.269  1.00 25.55           N
ATOM  5254  CA  GLU A 350     -42.272   9.374 -19.555  1.00 25.76           C
ATOM  5256  CB  GLU A 350     -42.332  10.814 -19.021  1.00 26.34           C
ATOM  5259  CG  GLU A 350     -42.179  11.928 -20.106  1.00 29.04           C
ATOM  5262  CD  GLU A 350     -40.745  12.101 -20.598  1.00 32.08           C
ATOM  5263  OE1 GLU A 350     -39.853  12.170 -19.716  1.00 35.46           O
ATOM  5264  OE2 GLU A 350     -40.516  12.174 -21.839  1.00 31.64           O
ATOM  5265  C   GLU A 350     -42.084   8.414 -18.400  1.00 24.87           C
ATOM  5266  O   GLU A 350     -43.067   8.046 -17.760  1.00 25.16           O
ATOM  5268  N   ASN A 351     -40.833   8.009 -18.145  1.00 23.71           N
ATOM  5269  CA  ASN A 351     -40.494   7.189 -16.980  1.00 22.88           C
ATOM  5271  CB  ASN A 351     -39.351   6.229 -17.287  1.00 22.88           C
ATOM  5274  CG  ASN A 351     -39.141   5.215 -16.184  1.00 22.98           C
ATOM  5275  OD1 ASN A 351     -39.006   5.584 -15.035  1.00 22.68           O
ATOM  5276  ND2 ASN A 351     -39.139   3.924 -16.529  1.00 24.38           N
ATOM  5279  C   ASN A 351     -40.126   8.058 -15.786  1.00 22.40           C
ATOM  5280  O   ASN A 351     -39.097   8.741 -15.785  1.00 22.66           O
ATOM  5282  N   ILE A 352     -40.965   8.021 -14.760  1.00 21.55           N
ATOM  5283  CA  ILE A 352     -40.770   8.860 -13.591  1.00 20.75           C
ATOM  5285  CB  ILE A 352     -42.002   9.788 -13.360  1.00 20.95           C
ATOM  5287  CG1 ILE A 352     -43.263   8.970 -13.022  1.00 20.82           C
ATOM  5290  CD1 ILE A 352     -44.237   9.698 -12.122  1.00 20.21           C
ATOM  5294  CG2 ILE A 352     -42.266  10.669 -14.582  1.00 19.85           C
ATOM  5298  C   ILE A 352     -40.516   8.016 -12.339  1.00 20.37           C
ATOM  5299  O   ILE A 352     -40.574   8.513 -11.224  1.00 20.55           O
ATOM  5301  N   LEU A 353     -40.236   6.733 -12.519  1.00 19.98           N
ATOM  5302  CA  LEU A 353     -40.061   5.828 -11.387  1.00 19.42           C
ATOM  5304  CB  LEU A 353     -39.894   4.392 -11.870  1.00 19.27           C
ATOM  5307  CG  LEU A 353     -39.989   3.318 -10.799  1.00 19.01           C
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ATOM 5309 CD1 LEU A 353 -41.164 3.574 -9.867 1.00 18.35 C
ATOM 5313 CD2 LEU A 353 -40.085 1.938 -11.468 1.00 18.74 C
ATOM 5317 C LEU A 353 -38.890 6.240 -10.523 1.00 19.11 C
ATOM 5318 O LEU A 353 -39.022 6.319 -9.314 1.00 18.96 O
ATOM 5320 N PRO A 354 -37.746 6.549 -11.142 1.00 19.06 N
ATOM 5321 CA PRO A 354 -36.631 7.069 -10.367 1.00 19.29 C
ATOM 5323 CB PRO A 354 -35.749 7.717 -11.438 1.00 19.25 C
ATOM 5326 CG PRO A 354 -35.997 6.942 -12.638 1.00 19.08 C
ATOM 5329 CD PRO A 354 -37.409 6.472 -12.572 1.00 19.00 C
ATOM 5332 C PRO A 354 -37.024 8.122 -9.328 1.00 19.33 C
ATOM 5333 O PRO A 354 -36.534 8.057 -8.193 1.00 19.73 O
ATOM 5334 N TYR A 355 -37.891 9.063 -9.721 1.00 18.83 N
ATOM 5335 CA TYR A 355 -38.206 10.221 -8.898 1.00 18.79 C
ATOM 5337 CB TYR A 355 -38.836 11.359 -9.707 1.00 19.10 C
ATOM 5340 CG TYR A 355 -38.142 11.708 -11.009 1.00 20.15 C
ATOM 5341 CD1 TYR A 355 -36.940 12.403 -11.027 1.00 20.78 C
ATOM 5343 CE1 TYR A 355 -36.321 12.719 -12.232 1.00 22.19 C
ATOM 5345 CZ TYR A 355 -36.918 12.347 -13.438 1.00 22.19 C
ATOM 5346 OH TYR A 355 -36.341 12.660 -14.657 1.00 23.29 O
ATOM 5348 CE2 TYR A 355 -38.113 11.677 -13.430 1.00 21.62 C
ATOM 5350 CD2 TYR A 355 -38.720 11.371 -12.227 1.00 21.05 C
ATOM 5352 C TYR A 355 -39.155 9.864 -7.777 1.00 18.43 C
ATOM 5353 O TYR A 355 -39.081 10.460 -6.709 1.00 18.61 O
ATOM 5355 N LEU A 356 -40.058 8.917 -8.023 1.00 17.92 N
ATOM 5356 CA LEU A 356 -40.993 8.467 -6.994 1.00 17.38 C
ATOM 5358 CB LEU A 356 -42.136 7.658 -7.597 1.00 17.17 C
ATOM 5361 CG LEU A 356 -42.956 8.366 -8.682 1.00 17.56 C
ATOM 5363 CD1 LEU A 356 -43.933 7.419 -9.371 1.00 17.47 C
ATOM 5367 CD2 LEU A 356 -43.698 9.548 -8.112 1.00 18.08 C
ATOM 5371 C LEU A 356 -40.241 7.623 -5.978 1.00 17.10 C
ATOM 5372 O LEU A 356 -40.332 7.859 -4.783 1.00 17.62 O
ATOM 5374 N THR A 357 -39.464 6.656 -6.442 1.00 16.64 N
ATOM 5375 CA THR A 357 -38.775 5.769 -5.513 1.00 16.18 C
ATOM 5377 CB THR A 357 -38.104 4.554 -6.213 1.00 16.04 C
ATOM 5379 OG1 THR A 357 -37.092 4.996 -7.123 1.00 15.93 O
ATOM 5381 CG2 THR A 357 -39.142 3.732 -6.962 1.00 14.99 C
ATOM 5385 C THR A 357 -37.764 6.544 -4.686 1.00 16.16 C
ATOM 5386 O THR A 357 -37.599 6.278 -3.506 1.00 16.07 O
ATOM 5388 N LYS A 358 -37.107 7.524 -5.291 1.00 16.20 N
ATOM 5389 CA LYS A 358 -36.186 8.365 -4.543 1.00 16.46 C
ATOM 5391 CB LYS A 358 -35.518 9.386 -5.453 1.00 16.80 C
ATOM 5394 CG LYS A 358 -34.612 10.388 -4.741 1.00 18.30 C
ATOM 5397 CD LYS A 358 -33.352 9.738 -4.168 1.00 20.21 C
ATOM 5400 CE LYS A 358 -32.335 10.811 -3.768 1.00 21.96 C
ATOM 5403 NZ LYS A 358 -31.163 10.275 -3.019 1.00 22.95 N
ATOM 5407 C LYS A 358 -36.936 9.083 -3.440 1.00 16.26 C
ATOM 5408 O LYS A 358 -36.448 9.161 -2.320 1.00 16.15 O
ATOM 5410 N ALA A 359 -38.126 9.593 -3.763 1.00 16.11 N
ATOM 5411 CA ALA A 359 -38.937 10.332 -2.798 1.00 16.10 C
ATOM 5413 CB ALA A 359 -40.221 10.768 -3.406 1.00 15.71 C
ATOM 5417 C ALA A 359 -39.215 9.476 -1.588 1.00 16.52 C
ATOM 5418 O ALA A 359 -39.247 9.970 -.442 1.00 16.82 O
ATOM 5420 N TRP A 360 -39.398 8.187 -1.843 1.00 16.79 N
ATOM 5421 CA TRP A 360 -39.704 7.247 -.780 1.00 17.25 C
ATOM 5423 CB TRP A 360 -40.390 6.006 -1.352 1.00 17.41 C
ATOM 5426 CG TRP A 360 -41.852 6.129 -1.318 1.00 17.06 C
ATOM 5427 CD1 TRP A 360 -42.664 6.451 -2.346 1.00 17.94 C
ATOM 5429 NE1 TRP A 360 -43.967 6.489 -1.926 1.00 18.03 N
ATOM 5431 CE2 TRP A 360 -44.002 6.193 -.592 1.00 17.72 C
ATOM 5432 CD2 TRP A 360 -42.684 5.965 -.179 1.00 16.60 C

ATOM 5433 CE3 TRP A 360 -42.441 5.654 1.155 1.00 16.65 C
ATOM 5435 CZ3 TRP A 360 -43.508 5.573 2.022 1.00 16.91 C
ATOM 5437 CH2 TRP A 360 -44.811 5.807 1.586 1.00 17.82 C
ATOM 5439 CZ2 TRP A 360 -45.080 6.114 .282 1.00 18.49 C
ATOM 5441 C TRP A 360 -38.490 6.865 .073 1.00 17.52 C
ATOM 5442 O TRP A 360 -38.603 6.767 1.297 1.00 17.38 O
ATOM 5444 N ALA A 361 -37.344 6.651 -.568 1.00 17.82 N
ATOM 5445 CA ALA A 361 -36.122 6.336 .157 1.00 18.11 C
ATOM 5447 CB ALA A 361 -34.982 6.050 -.805 1.00 17.92 C
ATOM 5451 C ALA A 361 -35.781 7.507 1.063 1.00 18.52 C
ATOM 5452 O ALA A 361 -35.434 7.327 2.229 1.00 18.48 O
ATOM 5454 N ASP A 362 -35.911 8.711 .521 1.00 19.16 N
ATOM 5455 CA ASP A 362 -35.627 9.925 1.276 1.00 19.90 C
ATOM 5457 CB ASP A 362 -35.797 11.167 .387 1.00 20.39 C
ATOM 5460 CG ASP A 362 -34.596 11.424 -.530 1.00 21.84 C
ATOM 5461 OD1 ASP A 362 -33.630 10.625 -.561 1.00 22.88 O
ATOM 5462 OD2 ASP A 362 -34.630 12.453 -1.231 1.00 24.83 O
ATOM 5463 C ASP A 362 -36.532 10.039 2.510 1.00 19.91 C
ATOM 5464 O ASP A 362 -36.074 10.427 3.591 1.00 19.76 O
ATOM 5466 N LEU A 363 -37.813 9.707 2.346 1.00 19.95 N
ATOM 5467 CA LEU A 363 -38.747 9.688 3.478 1.00 19.85 C
ATOM 5469 CB LEU A 363 -40.175 9.415 3.006 1.00 19.70 C
ATOM 5472 CG LEU A 363 -41.219 9.293 4.123 1.00 18.58 C
ATOM 5474 CD1 LEU A 363 -41.189 10.551 4.965 1.00 18.37 C
ATOM 5478 CD2 LEU A 363 -42.597 9.073 3.551 1.00 16.43 C
ATOM 5482 C LEU A 363 -38.368 8.613 4.488 1.00 20.24 C
ATOM 5483 O LEU A 363 -38.314 8.875 5.691 1.00 20.52 O
ATOM 5485 N CYS A 364 -38.129 7.397 3.997 1.00 20.29 N
ATOM 5486 CA CYS A 364 -37.741 6.308 4.874 1.00 20.39 C
ATOM 5488 CB CYS A 364 -37.595 4.985 4.111 1.00 20.37 C
ATOM 5491 SG CYS A 364 -39.208 4.201 3.666 1.00 20.69 S
ATOM 5493 C CYS A 364 -36.467 6.683 5.646 1.00 20.59 C
ATOM 5494 O CYS A 364 -36.386 6.445 6.863 1.00 20.82 O
ATOM 5496 N ASN A 365 -35.495 7.314 4.980 1.00 20.35 N
ATOM 5497 CA ASN A 365 -34.282 7.716 5.697 1.00 20.14 C
ATOM 5499 CB ASN A 365 -33.188 8.203 4.754 1.00 20.18 C
ATOM 5502 CG ASN A 365 -32.359 7.064 4.184 1.00 20.55 C
ATOM 5503 OD1 ASN A 365 -31.706 6.316 4.925 1.00 20.40 O
ATOM 5504 ND2 ASN A 365 -32.365 6.938 2.854 1.00 21.25 N
ATOM 5507 C ASN A 365 -34.590 8.746 6.779 1.00 19.92 C
ATOM 5508 O ASN A 365 -33.997 8.685 7.857 1.00 19.94 O
ATOM 5510 N ALA A 366 -35.531 9.658 6.507 1.00 19.58 N
ATOM 5511 CA ALA A 366 -36.036 10.578 7.537 1.00 19.39 C
ATOM 5513 CB ALA A 366 -37.083 11.507 6.971 1.00 18.79 C
ATOM 5517 C ALA A 366 -36.597 9.784 8.730 1.00 19.75 C
ATOM 5518 O ALA A 366 -36.215 10.049 9.891 1.00 19.53 O
ATOM 5520 N PHE A 367 -37.460 8.797 8.447 1.00 19.69 N
ATOM 5521 CA PHE A 367 -37.985 7.925 9.502 1.00 20.11 C
ATOM 5523 CB PHE A 367 -38.952 6.857 8.967 1.00 20.47 C
ATOM 5526 CG PHE A 367 -40.293 7.370 8.494 1.00 21.35 C
ATOM 5527 CD1 PHE A 367 -40.985 8.347 9.180 1.00 21.54 C
ATOM 5529 CE1 PHE A 367 -42.224 8.775 8.732 1.00 21.47 C
ATOM 5531 CZ PHE A 367 -42.798 8.213 7.612 1.00 21.87 C
ATOM 5533 CE2 PHE A 367 -42.135 7.230 6.924 1.00 22.60 C
ATOM 5535 CD2 PHE A 367 -40.894 6.798 7.373 1.00 22.90 C
ATOM 5537 C PHE A 367 -36.871 7.179 10.252 1.00 20.12 C
ATOM 5538 O PHE A 367 -36.940 7.009 11.476 1.00 19.88 O
ATOM 5540 N LEU A 368 -35.868 6.696 9.516 1.00 20.30 N
ATOM 5541 CA LEU A 368 -34.775 5.931 10.133 1.00 20.19 C
ATOM 5543 CB LEU A 368 -33.783 5.413 9.085 1.00 20.08 C

ATOM 5546 CG LEU A 368 -32.743 4.363 9.514 1.00 19.30 C
ATOM 5548 CD1 LEU A 368 -33.384 3.227 10.260 1.00 18.66 C
ATOM 5552 CD2 LEU A 368 -31.968 3.807 8.319 1.00 18.16 C
ATOM 5556 C LEU A 368 -34.063 6.812 11.128 1.00 20.41 C
ATOM 5557 O LEU A 368 -33.842 6.407 12.257 1.00 20.01 O
ATOM 5559 N GLN A 369 -33.751 8.036 10.711 1.00 20.89 N
ATOM 5560 CA GLN A 369 -33.037 8.970 11.564 1.00 21.49 C
ATOM 5562 CB GLN A 369 -32.782 10.280 10.832 1.00 21.58 C
ATOM 5565 CG GLN A 369 -32.071 11.359 11.677 1.00 21.20 C
ATOM 5568 CD GLN A 369 -30.639 11.006 11.976 1.00 20.04 C
ATOM 5569 OE1 GLN A 369 -30.282 10.650 13.108 1.00 19.10 O
ATOM 5570 NE2 GLN A 369 -29.803 11.095 10.956 1.00 18.75 N
ATOM 5573 C GLN A 369 -33.763 9.265 12.870 1.00 22.21 C
ATOM 5574 O GLN A 369 -33.122 9.343 13.909 1.00 22.41 O
ATOM 5576 N GLU A 370 -35.080 9.455 12.822 1.00 23.05 N
ATOM 5577 CA GLU A 370 -35.856 9.718 14.046 1.00 23.71 C
ATOM 5579 CB GLU A 370 -37.329 10.041 13.726 1.00 24.04 C
ATOM 5582 CG GLU A 370 -37.484 11.293 12.862 1.00 26.84 C
ATOM 5585 CD GLU A 370 -38.897 11.910 12.834 1.00 30.36 C
ATOM 5586 OE1 GLU A 370 -39.886 11.161 12.586 1.00 31.90 O
ATOM 5587 OE2 GLU A 370 -38.992 13.164 13.014 1.00 31.62 O
ATOM 5588 C GLU A 370 -35.755 8.523 14.994 1.00 23.60 C
ATOM 5589 O GLU A 370 -35.534 8.689 16.199 1.00 23.33 O
ATOM 5591 N ALA A 371 -35.904 7.322 14.435 1.00 23.72 N
ATOM 5592 CA ALA A 371 -35.771 6.091 15.201 1.00 23.91 C
ATOM 5594 CB ALA A 371 -35.991 4.868 14.312 1.00 23.76 C
ATOM 5598 C ALA A 371 -34.392 6.051 15.840 1.00 24.20 C
ATOM 5599 O ALA A 371 -34.277 5.804 17.035 1.00 24.54 O
ATOM 5601 N LYS A 372 -33.355 6.333 15.049 1.00 24.38 N
ATOM 5602 CA LYS A 372 -31.979 6.273 15.530 1.00 24.39 C
ATOM 5604 CB LYS A 372 -30.970 6.466 14.393 1.00 24.43 C
ATOM 5607 CG LYS A 372 -30.623 5.164 13.645 1.00 25.20 C
ATOM 5610 CD LYS A 372 -29.188 5.149 13.069 1.00 26.09 C
ATOM 5613 CE LYS A 372 -29.114 5.437 11.557 1.00 27.01 C
ATOM 5616 NZ LYS A 372 -29.002 4.200 10.709 1.00 26.82 N
ATOM 5620 C LYS A 372 -31.717 7.268 16.645 1.00 24.59 C
ATOM 5621 O LYS A 372 -31.096 6.908 17.627 1.00 25.13 O
ATOM 5623 N TRP A 373 -32.181 8.507 16.520 1.00 24.78 N
ATOM 5624 CA TRP A 373 -32.006 9.473 17.610 1.00 24.90 C
ATOM 5626 CB TRP A 373 -32.565 10.863 17.266 1.00 24.75 C
ATOM 5629 CG TRP A 373 -31.701 11.677 16.338 1.00 23.59 C
ATOM 5630 CD1 TRP A 373 -30.344 11.663 16.259 1.00 22.38 C
ATOM 5632 NE1 TRP A 373 -29.915 12.539 15.298 1.00 21.59 N
ATOM 5634 CE2 TRP A 373 -30.999 13.162 14.744 1.00 21.69 C
ATOM 5635 CD2 TRP A 373 -32.147 12.644 15.376 1.00 22.41 C
ATOM 5636 CE3 TRP A 373 -33.409 13.110 14.976 1.00 21.98 C
ATOM 5638 CZ3 TRP A 373 -33.480 14.072 13.979 1.00 22.08 C
ATOM 5640 CH2 TRP A 373 -32.313 14.567 13.366 1.00 22.31 C
ATOM 5642 CZ2 TRP A 373 -31.067 14.124 13.736 1.00 21.87 C
ATOM 5644 C TRP A 373 -32.678 8.970 18.881 1.00 25.53 C
ATOM 5645 O TRP A 373 -32.101 9.072 19.972 1.00 25.99 O
ATOM 5647 N LEU A 374 -33.881 8.420 18.739 1.00 25.84 N
ATOM 5648 CA LEU A 374 -34.667 7.980 19.893 1.00 26.29 C
ATOM 5650 CB LEU A 374 -36.070 7.562 19.443 1.00 26.32 C
ATOM 5653 CG LEU A 374 -37.227 7.646 20.444 1.00 26.39 C
ATOM 5655 CD1 LEU A 374 -38.456 8.286 19.761 1.00 26.95 C
ATOM 5659 CD2 LEU A 374 -37.583 6.281 21.050 1.00 26.24 C
ATOM 5663 C LEU A 374 -33.982 6.824 20.623 1.00 26.77 C
ATOM 5664 O LEU A 374 -33.995 6.758 21.860 1.00 26.95 O
ATOM 5666 N TYR A 375 -33.383 5.919 19.854 1.00 27.23 N

ATOM 5667 CA TYR A 375 -32.706 4.761 20.425 1.00 27.74 C
ATOM 5669 CB TYR A 375 -32.195 3.814 19.328 1.00 27.78 C
ATOM 5672 CG TYR A 375 -31.526 2.556 19.848 1.00 28.74 C
ATOM 5673 CD1 TYR A 375 -32.264 1.394 20.090 1.00 29.61 C
ATOM 5675 CE1 TYR A 375 -31.652 .232 20.573 1.00 29.89 C
ATOM 5677 CZ TYR A 375 -30.287 .226 20.817 1.00 30.15 C
ATOM 5678 OH TYR A 375 -29.676 -.917 21.286 1.00 30.57 O
ATOM 5680 CE2 TYR A 375 -29.530 1.367 20.579 1.00 30.05 C
ATOM 5682 CD2 TYR A 375 -30.152 2.522 20.096 1.00 29.74 C
ATOM 5684 C TYR A 375 -31.553 5.248 21.275 1.00 27.97 C
ATOM 5685 O TYR A 375 -31.404 4.837 22.422 1.00 28.00 O
ATOM 5687 N ASN A 376 -30.763 6.158 20.719 1.00 28.32 N
ATOM 5688 CA ASN A 376 -29.531 6.590 21.368 1.00 28.71 C
ATOM 5690 CB ASN A 376 -28.569 7.161 20.329 1.00 28.60 C
ATOM 5693 CG ASN A 376 -28.215 6.159 19.255 1.00 28.32 C
ATOM 5694 OD1 ASN A 376 -27.961 4.977 19.527 1.00 25.72 O
ATOM 5695 ND2 ASN A 376 -28.195 6.631 18.015 1.00 29.29 N
ATOM 5698 C ASN A 376 -29.728 7.617 22.484 1.00 29.05 C
ATOM 5699 O ASN A 376 -28.752 8.021 23.136 1.00 29.03 O
ATOM 5701 N LYS A 377 -30.977 8.021 22.716 1.00 29.16 N
ATOM 5702 CA LYS A 377 -31.254 9.178 23.549 1.00 29.27 C
ATOM 5704 CB LYS A 377 -31.051 8.879 25.050 1.00 29.52 C
ATOM 5707 CG LYS A 377 -32.202 8.112 25.723 1.00 30.36 C
ATOM 5710 CD LYS A 377 -32.202 6.638 25.340 1.00 31.54 C
ATOM 5713 CE LYS A 377 -33.322 5.862 26.031 1.00 32.30 C
ATOM 5716 NZ LYS A 377 -33.559 4.509 25.411 1.00 32.13 N
ATOM 5720 C LYS A 377 -30.337 10.299 23.080 1.00 28.92 C
ATOM 5721 O LYS A 377 -29.590 10.867 23.875 1.00 28.94 O
ATOM 5723 N SER A 378 -30.377 10.575 21.776 1.00 28.52 N
ATOM 5724 CA SER A 378 -29.652 11.700 21.201 1.00 28.30 C
ATOM 5726 CB SER A 378 -29.623 11.620 19.678 1.00 28.33 C
ATOM 5729 OG SER A 378 -28.919 10.482 19.237 1.00 29.36 O
ATOM 5731 C SER A 378 -30.355 12.977 21.594 1.00 27.97 C
ATOM 5732 O SER A 378 -31.483 12.947 22.108 1.00 27.91 O
ATOM 5734 N THR A 379 -29.684 14.098 21.344 1.00 27.60 N
ATOM 5735 CA THR A 379 -30.257 15.422 21.581 1.00 27.24 C
ATOM 5737 CB THR A 379 -29.929 15.950 23.002 1.00 27.23 C
ATOM 5739 OG1 THR A 379 -28.512 16.102 23.158 1.00 26.85 O
ATOM 5741 CG2 THR A 379 -30.467 15.007 24.067 1.00 27.48 C
ATOM 5745 C THR A 379 -29.738 16.414 20.548 1.00 26.83 C
ATOM 5746 O THR A 379 -28.834 17.190 20.844 1.00 26.69 O
ATOM 5748 N PRO A 380 -30.305 16.390 19.331 1.00 26.56 N
ATOM 5749 CA PRO A 380 -29.884 17.315 18.278 1.00 26.52 C
ATOM 5751 CB PRO A 380 -30.380 16.648 16.992 1.00 26.46 C
ATOM 5754 CG PRO A 380 -31.281 15.533 17.408 1.00 26.41 C
ATOM 5757 CD PRO A 380 -31.395 15.508 18.887 1.00 26.53 C
ATOM 5760 C PRO A 380 -30.469 18.728 18.386 1.00 26.55 C
ATOM 5761 O PRO A 380 -31.472 18.966 19.063 1.00 26.69 O
ATOM 5762 N THR A 381 -29.840 19.661 17.692 1.00 26.51 N
ATOM 5763 CA THR A 381 -30.299 21.034 17.699 1.00 26.51 C
ATOM 5765 CB THR A 381 -29.261 21.955 17.033 1.00 26.99 C
ATOM 5767 OG1 THR A 381 -28.919 21.431 15.732 1.00 27.65 O
ATOM 5769 CG2 THR A 381 -28.003 22.082 17.930 1.00 26.41 C
ATOM 5773 C THR A 381 -31.635 21.167 16.970 1.00 26.06 C
ATOM 5774 O THR A 381 -31.972 20.347 16.112 1.00 26.03 O
ATOM 5776 N PHE A 382 -32.386 22.218 17.294 1.00 25.52 N
ATOM 5777 CA PHE A 382 -33.681 22.436 16.654 1.00 24.83 C
ATOM 5779 CB PHE A 382 -34.284 23.793 17.011 1.00 24.53 C
ATOM 5782 CG PHE A 382 -35.495 24.113 16.211 1.00 23.77 C
ATOM 5783 CD1 PHE A 382 -36.745 23.715 16.637 1.00 24.50 C

ATOM 5785 CE1 PHE A 382 -37.873 23.977 15.878 1.00 24.49 C
ATOM 5787 CZ PHE A 382 -37.744 24.630 14.673 1.00 24.41 C
ATOM 5789 CE2 PHE A 382 -36.490 25.014 14.235 1.00 23.88 C
ATOM 5791 CD2 PHE A 382 -35.381 24.752 14.999 1.00 23.29 C
ATOM 5793 C PHE A 382 -33.542 22.342 15.150 1.00 24.49 C
ATOM 5794 O PHE A 382 -34.361 21.731 14.485 1.00 24.32 O
ATOM 5796 N ASP A 383 -32.498 22.969 14.627 1.00 24.42 N
ATOM 5797 CA ASP A 383 -32.257 23.005 13.190 1.00 24.19 C
ATOM 5799 CB ASP A 383 -31.101 23.966 12.867 1.00 24.21 C
ATOM 5802 CG ASP A 383 -31.473 25.423 13.050 1.00 23.72 C
ATOM 5803 OD1 ASP A 383 -32.634 25.794 12.837 1.00 25.60 O
ATOM 5804 OD2 ASP A 383 -30.594 26.220 13.383 1.00 24.03 O
ATOM 5805 C ASP A 383 -31.982 21.612 12.599 1.00 24.06 C
ATOM 5806 O ASP A 383 -32.393 21.342 11.473 1.00 24.00 O
ATOM 5808 N ASP A 384 -31.298 20.739 13.336 1.00 23.78 N
ATOM 5809 CA ASP A 384 -31.078 19.379 12.848 1.00 24.11 C
ATOM 5811 CB ASP A 384 -29.981 18.651 13.632 1.00 24.54 C
ATOM 5814 CG ASP A 384 -28.573 19.009 13.159 1.00 26.32 C
ATOM 5815 OD1 ASP A 384 -28.441 19.852 12.232 1.00 28.55 O
ATOM 5816 OD2 ASP A 384 -27.599 18.451 13.728 1.00 27.18 O
ATOM 5817 C ASP A 384 -32.351 18.550 12.905 1.00 23.83 C
ATOM 5818 O ASP A 384 -32.670 17.825 11.955 1.00 24.24 O
ATOM 5820 N TYR A 385 -33.070 18.637 14.017 1.00 23.31 N
ATOM 5821 CA TYR A 385 -34.294 17.861 14.179 1.00 22.89 C
ATOM 5823 CB TYR A 385 -34.833 17.979 15.608 1.00 22.86 C
ATOM 5826 CG TYR A 385 -36.144 17.245 15.807 1.00 22.65 C
ATOM 5827 CD1 TYR A 385 -36.163 15.868 16.030 1.00 22.36 C
ATOM 5829 CE1 TYR A 385 -37.351 15.189 16.206 1.00 22.77 C
ATOM 5831 CZ TYR A 385 -38.545 15.887 16.146 1.00 23.54 C
ATOM 5832 OH TYR A 385 -39.733 15.212 16.309 1.00 24.38 O
ATOM 5834 CE2 TYR A 385 -38.554 17.258 15.913 1.00 22.76 C
ATOM 5836 CD2 TYR A 385 -37.360 17.923 15.744 1.00 22.12 C
ATOM 5838 C TYR A 385 -35.375 18.299 13.190 1.00 22.55 C
ATOM 5839 O TYR A 385 -36.050 17.467 12.584 1.00 22.85 O
ATOM 5841 N PHE A 386 -35.537 19.609 13.042 1.00 22.08 N
ATOM 5842 CA PHE A 386 -36.626 20.155 12.248 1.00 21.62 C
ATOM 5844 CB PHE A 386 -36.857 21.628 12.568 1.00 21.73 C
ATOM 5847 CG PHE A 386 -38.033 22.209 11.851 1.00 21.54 C
ATOM 5848 CD1 PHE A 386 -39.311 21.933 12.273 1.00 21.29 C
ATOM 5850 CE1 PHE A 386 -40.380 22.444 11.623 1.00 22.11 C
ATOM 5852 CZ PHE A 386 -40.193 23.240 10.517 1.00 23.28 C
ATOM 5854 CE2 PHE A 386 -38.920 23.502 10.069 1.00 23.10 C
ATOM 5856 CD2 PHE A 386 -37.853 22.989 10.737 1.00 22.15 C
ATOM 5858 C PHE A 386 -36.369 19.987 10.769 1.00 21.09 C
ATOM 5859 O PHE A 386 -37.278 19.700 10.006 1.00 20.91 O
ATOM 5861 N GLY A 387 -35.127 20.177 10.362 1.00 20.68 N
ATOM 5862 CA GLY A 387 -34.747 19.917 8.985 1.00 20.43 C
ATOM 5865 C GLY A 387 -35.151 18.521 8.544 1.00 19.95 C
ATOM 5866 O GLY A 387 -35.553 18.327 7.398 1.00 20.24 O
ATOM 5868 N ASN A 388 -35.032 17.554 9.451 1.00 19.12 N
ATOM 5869 CA ASN A 388 -35.451 16.182 9.202 1.00 18.73 C
ATOM 5871 CB ASN A 388 -34.744 15.272 10.205 1.00 18.90 C
ATOM 5874 CG ASN A 388 -34.863 13.795 9.871 1.00 18.35 C
ATOM 5875 OD1 ASN A 388 -34.163 13.284 8.993 1.00 17.24 O
ATOM 5876 ND2 ASN A 388 -35.714 13.092 10.614 1.00 17.01 N
ATOM 5879 C ASN A 388 -36.968 16.033 9.350 1.00 18.65 C
ATOM 5880 O ASN A 388 -37.624 15.370 8.551 1.00 18.82 O
ATOM 5882 N ALA A 389 -37.527 16.670 10.371 1.00 18.38 N
ATOM 5883 CA ALA A 389 -38.926 16.477 10.728 1.00 18.02 C
ATOM 5885 CB ALA A 389 -39.203 17.107 12.084 1.00 17.83 C

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ATOM  5889 C   ALA A 389    -39.949  16.966   9.700  1.00 17.90      C
ATOM  5890 O   ALA A 389    -41.095  16.544   9.760  1.00 17.74      O
ATOM  5892 N   TRP A 390    -39.585  17.860   8.783  1.00 18.11      N
ATOM  5893 CA  TRP A 390    -40.543  18.254   7.731  1.00 18.46      C
ATOM  5895 CB  TRP A 390    -40.459  19.737   7.329  1.00 18.59      C
ATOM  5898 CG  TRP A 390    -39.143  20.224   6.821  1.00 19.26      C
ATOM  5899 CD1 TRP A 390    -38.224  20.947   7.519  1.00 20.64      C
ATOM  5901 NE1 TRP A 390    -37.138  21.224   6.729  1.00 20.62      N
ATOM  5903 CE2 TRP A 390    -37.352  20.694   5.485  1.00 19.57      C
ATOM  5904 CD2 TRP A 390    -38.607  20.066   5.504  1.00 19.15      C
ATOM  5905 CE3 TRP A 390    -39.060  19.448   4.344  1.00 20.13      C
ATOM  5907 CZ3 TRP A 390    -38.254  19.477   3.224  1.00 20.27      C
ATOM  5909 CH2 TRP A 390    -37.017  20.110   3.239  1.00 19.38      C
ATOM  5911 CZ2 TRP A 390    -36.549  20.724   4.356  1.00 19.49      C
ATOM  5913 C   TRP A 390    -40.407  17.343   6.527  1.00 18.73      C
ATOM  5914 O   TRP A 390    -41.369  17.143   5.788  1.00 18.32      O
ATOM  5916 N   LYS A 391    -39.200  16.806   6.336  1.00 19.30      N
ATOM  5917 CA  LYS A 391    -38.969  15.692   5.404  1.00 19.70      C
ATOM  5919 CB  LYS A 391    -37.459  15.392   5.244  1.00 19.92      C
ATOM  5922 CG  LYS A 391    -36.812  15.953   3.935  1.00 22.08      C
ATOM  5925 CD  LYS A 391    -35.257  16.217   4.040  1.00 23.92      C
ATOM  5928 CE  LYS A 391    -34.918  17.698   4.426  1.00 24.43      C
ATOM  5931 NZ  LYS A 391    -33.699  17.901   5.307  1.00 23.23      N
ATOM  5935 C   LYS A 391    -39.731  14.441   5.861  1.00 19.46      C
ATOM  5936 O   LYS A 391    -40.284  13.709   5.032  1.00 20.07      O
ATOM  5938 N   SER A 392    -39.793  14.202   7.170  1.00 18.95      N
ATOM  5939 CA  SER A 392    -40.455  12.998   7.666  1.00 18.63      C
ATOM  5941 CB  SER A 392    -39.850  12.508   9.000  1.00 18.75      C
ATOM  5944 OG  SER A 392    -40.314  13.230  10.126  1.00 18.94      O
ATOM  5946 C   SER A 392    -41.964  13.152   7.771  1.00 18.20      C
ATOM  5947 O   SER A 392    -42.654  12.182   8.031  1.00 18.12      O
ATOM  5949 N   SER A 393    -42.477  14.360   7.567  1.00 18.07      N
ATOM  5950 CA  SER A 393    -43.929  14.591   7.556  1.00 18.02      C
ATOM  5952 CB  SER A 393    -44.229  16.078   7.504  1.00 18.08      C
ATOM  5955 OG  SER A 393    -43.995  16.558   6.192  1.00 18.01      O
ATOM  5957 C   SER A 393    -44.594  13.971   6.340  1.00 17.87      C
ATOM  5958 O   SER A 393    -45.778  13.661   6.372  1.00 18.03      O
ATOM  5960 N   SER A 394    -43.823  13.841   5.264  1.00 17.69      N
ATOM  5961 CA  SER A 394    -44.284  13.306   3.989  1.00 17.59      C
ATOM  5963 CB  SER A 394    -45.329  12.180   4.149  1.00 17.61      C
ATOM  5966 OG  SER A 394    -46.648  12.681   4.294  1.00 17.18      O
ATOM  5968 C   SER A 394    -44.828  14.415   3.115  1.00 17.42      C
ATOM  5969 O   SER A 394    -45.345  14.146   2.024  1.00 17.31      O
ATOM  5971 N   GLY A 395    -44.711  15.654   3.592  1.00 17.23      N
ATOM  5972 CA  GLY A 395    -45.088  16.827   2.807  1.00 17.26      C
ATOM  5975 C   GLY A 395    -44.478  16.749   1.415  1.00 17.29      C
ATOM  5976 O   GLY A 395    -45.203  16.653    .413  1.00 18.06      O
ATOM  5978 N   PRO A 396    -43.145  16.754   1.331  1.00 16.72      N
ATOM  5979 CA  PRO A 396    -42.582  16.610    .006  1.00 16.40      C
ATOM  5981 CB  PRO A 396    -41.080  16.549    .259  1.00 16.62      C
ATOM  5984 CG  PRO A 396    -40.903  16.749   1.775  1.00 17.11      C
ATOM  5987 CD  PRO A 396    -42.157  17.252   2.296  1.00 16.87      C
ATOM  5990 C   PRO A 396    -43.053  15.374   -.748  1.00 15.89      C
ATOM  5991 O   PRO A 396    -43.501  15.498  -1.894  1.00 15.90      O
ATOM  5992 N   LEU A 397    -42.973  14.197   -.135  1.00 15.27      N
ATOM  5993 CA  LEU A 397    -43.287  12.976   -.886  1.00 14.57      C
ATOM  5995 CB  LEU A 397    -43.332  11.733   -.008  1.00 14.36      C
ATOM  5998 CG  LEU A 397    -43.541  10.431   -.781  1.00 14.02      C
ATOM  6000 CD1 LEU A 397    -42.690   9.348   -.206  1.00 15.04      C
ATOM  6004 CD2 LEU A 397    -44.985   9.976   -.805  1.00 13.75      C
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ATOM   6008  C   LEU A 397     -44.618  13.182  -1.542  1.00 14.39           C
ATOM   6009  O   LEU A 397     -44.736  12.999  -2.745  1.00 14.57           O
ATOM   6011  N   GLN A 398     -45.604  13.607   -.751  1.00 14.08           N
ATOM   6012  CA  GLN A 398     -46.962  13.828  -1.245  1.00 13.91           C
ATOM   6014  CB  GLN A 398     -47.860  14.363   -.136  1.00 13.99           C
ATOM   6017  CG  GLN A 398     -48.274  13.321    .909  1.00 14.01           C
ATOM   6020  CD  GLN A 398     -49.189  13.902   1.983  1.00 13.41           C
ATOM   6021  OE1 GLN A 398     -49.941  14.847   1.740  1.00 14.65           O
ATOM   6022  NE2 GLN A 398     -49.122  13.344   3.168  1.00 12.17           N
ATOM   6025  C   GLN A 398     -47.015  14.800  -2.403  1.00 13.84           C
ATOM   6026  O   GLN A 398     -47.677  14.547  -3.396  1.00 13.46           O
ATOM   6028  N   LEU A 399     -46.319  15.922  -2.272  1.00 14.11           N
ATOM   6029  CA  LEU A 399     -46.359  16.942  -3.315  1.00 14.37           C
ATOM   6031  CB  LEU A 399     -45.900  18.282  -2.756  1.00 14.26           C
ATOM   6034  CG  LEU A 399     -46.882  18.830  -1.704  1.00 14.44           C
ATOM   6036  CD1 LEU A 399     -46.250  19.960   -.919  1.00 16.43           C
ATOM   6040  CD2 LEU A 399     -48.191  19.304  -2.317  1.00 12.20           C
ATOM   6044  C   LEU A 399     -45.582  16.525  -4.578  1.00 14.68           C
ATOM   6045  O   LEU A 399     -46.043  16.784  -5.687  1.00 14.70           O
ATOM   6047  N   ILE A 400     -44.443  15.844  -4.419  1.00 14.92           N
ATOM   6048  CA  ILE A 400     -43.748  15.221  -5.564  1.00 15.08           C
ATOM   6050  CB  ILE A 400     -42.549  14.355  -5.129  1.00 15.35           C
ATOM   6052  CG1 ILE A 400     -41.406  15.254  -4.611  1.00 16.83           C
ATOM   6055  CD1 ILE A 400     -40.234  14.490  -3.958  1.00 17.18           C
ATOM   6059  CG2 ILE A 400     -42.060  13.486  -6.292  1.00 14.03           C
ATOM   6063  C   ILE A 400     -44.682  14.329  -6.358  1.00 15.08           C
ATOM   6064  O   ILE A 400     -44.672  14.362  -7.574  1.00 15.18           O
ATOM   6066  N   PHE A 401     -45.474  13.524  -5.650  1.00 15.16           N
ATOM   6067  CA  PHE A 401     -46.501  12.674  -6.258  1.00 14.90           C
ATOM   6069  CB  PHE A 401     -47.052  11.663  -5.240  1.00 14.51           C
ATOM   6072  CG  PHE A 401     -46.294  10.378  -5.201  1.00 12.92           C
ATOM   6073  CD1 PHE A 401     -46.727   9.282  -5.931  1.00 11.98           C
ATOM   6075  CE1 PHE A 401     -46.032   8.093  -5.917  1.00 11.20           C
ATOM   6077  CZ  PHE A 401     -44.881   7.985  -5.165  1.00 12.03           C
ATOM   6079  CE2 PHE A 401     -44.431   9.078  -4.428  1.00 11.98           C
ATOM   6081  CD2 PHE A 401     -45.143  10.263  -4.453  1.00 12.09           C
ATOM   6083  C   PHE A 401     -47.641  13.509  -6.806  1.00 15.39           C
ATOM   6084  O   PHE A 401     -48.183  13.215  -7.858  1.00 15.51           O
ATOM   6086  N   ALA A 402     -48.022  14.545  -6.080  1.00 16.15           N
ATOM   6087  CA  ALA A 402     -49.110  15.393  -6.525  1.00 16.90           C
ATOM   6089  CB  ALA A 402     -49.391  16.473  -5.505  1.00 16.99           C
ATOM   6093  C   ALA A 402     -48.722  16.003  -7.856  1.00 17.50           C
ATOM   6094  O   ALA A 402     -49.549  16.100  -8.770  1.00 17.48           O
ATOM   6096  N   TYR A 403     -47.444  16.367  -7.963  1.00 18.28           N
ATOM   6097  CA  TYR A 403     -46.916  17.046  -9.142  1.00 18.94           C
ATOM   6099  CB  TYR A 403     -45.412  17.252  -9.043  1.00 19.03           C
ATOM   6102  CG  TYR A 403     -44.823  17.801 -10.314  1.00 19.79           C
ATOM   6103  CD1 TYR A 403     -44.973  19.138 -10.652  1.00 20.80           C
ATOM   6105  CE1 TYR A 403     -44.436  19.643 -11.827  1.00 20.73           C
ATOM   6107  CZ  TYR A 403     -43.759  18.804 -12.674  1.00 21.16           C
ATOM   6108  OH  TYR A 403     -43.231  19.283 -13.836  1.00 22.98           O
ATOM   6110  CE2 TYR A 403     -43.608  17.476 -12.370  1.00 21.23           C
ATOM   6112  CD2 TYR A 403     -44.137  16.980 -11.195  1.00 20.93           C
ATOM   6114  C   TYR A 403     -47.198  16.293 -10.413  1.00 19.39           C
ATOM   6115  O   TYR A 403     -47.567  16.904 -11.422  1.00 19.57           O
ATOM   6117  N   PHE A 404     -47.023  14.976 -10.376  1.00 19.74           N
ATOM   6118  CA  PHE A 404     -47.239  14.177 -11.573  1.00 20.35           C
ATOM   6120  CB  PHE A 404     -46.533  12.841 -11.466  1.00 19.96           C
ATOM   6123  CG  PHE A 404     -45.048  12.971 -11.387  1.00 18.81           C
ATOM   6124  CD1 PHE A 404     -44.292  13.115 -12.528  1.00 17.42           C
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ATOM 6126 CE1 PHE A 404 -42.935 13.239 -12.457 1.00 17.24 C
ATOM 6128 CZ PHE A 404 -42.312 13.237 -11.237 1.00 17.40 C
ATOM 6130 CE2 PHE A 404 -43.056 13.106 -10.093 1.00 17.72 C
ATOM 6132 CD2 PHE A 404 -44.413 12.975 -10.170 1.00 17.93 C
ATOM 6134 C PHE A 404 -48.713 13.994 -11.894 1.00 21.59 C
ATOM 6135 O PHE A 404 -49.072 13.717 -13.046 1.00 21.71 O
ATOM 6137 N ALA A 405 -49.572 14.169 -10.896 1.00 22.87 N
ATOM 6138 CA ALA A 405 -50.990 13.939 -11.099 1.00 24.06 C
ATOM 6140 CB ALA A 405 -51.604 13.408 -9.833 1.00 24.15 C
ATOM 6144 C ALA A 405 -51.724 15.192 -11.556 1.00 25.21 C
ATOM 6145 O ALA A 405 -52.876 15.114 -11.939 1.00 25.51 O
ATOM 6147 N VAL A 406 -51.056 16.336 -11.530 1.00 26.52 N
ATOM 6148 CA VAL A 406 -51.713 17.617 -11.759 1.00 27.68 C
ATOM 6150 CB VAL A 406 -51.694 18.406 -10.434 1.00 27.60 C
ATOM 6152 CG1 VAL A 406 -51.654 19.913 -10.663 1.00 28.07 C
ATOM 6156 CG2 VAL A 406 -52.883 18.009 -9.596 1.00 27.41 C
ATOM 6160 C VAL A 406 -51.097 18.429 -12.925 1.00 29.10 C
ATOM 6161 O VAL A 406 -51.810 19.104 -13.678 1.00 28.53 O
ATOM 6163 N VAL A 407 -49.772 18.356 -13.059 1.00 30.90 N
ATOM 6164 CA VAL A 407 -49.052 19.003 -14.151 1.00 32.15 C
ATOM 6166 CB VAL A 407 -47.574 19.228 -13.777 1.00 32.25 C
ATOM 6168 CG1 VAL A 407 -46.770 19.780 -14.964 1.00 32.22 C
ATOM 6172 CG2 VAL A 407 -47.490 20.154 -12.583 1.00 32.25 C
ATOM 6176 C VAL A 407 -49.134 18.160 -15.421 1.00 33.36 C
ATOM 6177 O VAL A 407 -48.688 17.009 -15.454 1.00 33.40 O
ATOM 6179 N GLN A 408 -49.693 18.767 -16.463 1.00 34.93 N
ATOM 6180 CA GLN A 408 -49.930 18.102 -17.749 1.00 36.16 C
ATOM 6182 CB GLN A 408 -50.779 19.016 -18.638 1.00 36.63 C
ATOM 6185 CG GLN A 408 -51.625 18.270 -19.672 1.00 38.95 C
ATOM 6188 CD GLN A 408 -52.991 18.930 -19.887 1.00 41.80 C
ATOM 6189 OE1 GLN A 408 -53.739 19.150 -18.921 1.00 43.40 O
ATOM 6190 NE2 GLN A 408 -53.323 19.244 -21.151 1.00 41.68 N
ATOM 6193 C GLN A 408 -48.630 17.725 -18.470 1.00 36.22 C
ATOM 6194 O GLN A 408 -48.456 16.588 -18.920 1.00 35.86 O
ATOM 6196 N ASN A 409 -47.726 18.694 -18.578 1.00 36.64 N
ATOM 6197 CA ASN A 409 -46.400 18.441 -19.136 1.00 36.85 C
ATOM 6199 CB ASN A 409 -46.134 19.306 -20.373 1.00 36.73 C
ATOM 6202 CG ASN A 409 -46.808 18.752 -21.604 1.00 36.19 C
ATOM 6203 OD1 ASN A 409 -46.178 18.072 -22.420 1.00 35.00 O
ATOM 6204 ND2 ASN A 409 -48.110 18.994 -21.720 1.00 34.99 N
ATOM 6207 C ASN A 409 -45.312 18.613 -18.095 1.00 36.96 C
ATOM 6208 O ASN A 409 -45.032 19.720 -17.618 1.00 36.81 O
ATOM 6210 N ILE A 410 -44.713 17.488 -17.734 1.00 37.10 N
ATOM 6211 CA ILE A 410 -43.625 17.508 -16.792 1.00 37.27 C
ATOM 6213 CB ILE A 410 -43.265 16.092 -16.295 1.00 37.38 C
ATOM 6215 CG1 ILE A 410 -42.745 15.209 -17.426 1.00 37.84 C
ATOM 6218 CD1 ILE A 410 -42.416 13.824 -16.985 1.00 38.96 C
ATOM 6222 CG2 ILE A 410 -44.491 15.437 -15.676 1.00 37.67 C
ATOM 6226 C ILE A 410 -42.467 18.179 -17.492 1.00 37.12 C
ATOM 6227 O ILE A 410 -42.150 17.839 -18.617 1.00 36.87 O
ATOM 6229 N LYS A 411 -41.896 19.187 -16.851 1.00 37.38 N
ATOM 6230 CA LYS A 411 -40.680 19.813 -17.332 1.00 37.73 C
ATOM 6232 CB LYS A 411 -40.756 21.332 -17.171 1.00 38.15 C
ATOM 6235 CG LYS A 411 -41.979 21.962 -17.837 1.00 39.89 C
ATOM 6238 CD LYS A 411 -41.797 23.463 -18.080 1.00 42.48 C
ATOM 6241 CE LYS A 411 -43.029 24.069 -18.795 1.00 44.22 C
ATOM 6244 NZ LYS A 411 -42.977 25.576 -18.904 1.00 45.31 N
ATOM 6248 C LYS A 411 -39.562 19.244 -16.489 1.00 37.38 C
ATOM 6249 O LYS A 411 -39.721 19.112 -15.281 1.00 37.28 O
ATOM 6251 N LYS A 412 -38.445 18.886 -17.122 1.00 37.24 N

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ATOM   6252  CA  LYS A 412     -37.333  18.243 -16.413  1.00 36.95           C
ATOM   6254  CB  LYS A 412     -36.286  17.701 -17.384  1.00 37.14           C
ATOM   6257  CG  LYS A 412     -35.233  16.818 -16.720  1.00 37.89           C
ATOM   6260  CD  LYS A 412     -34.334  16.125 -17.757  1.00 39.54           C
ATOM   6263  CE  LYS A 412     -33.263  17.068 -18.348  1.00 40.08           C
ATOM   6266  NZ  LYS A 412     -32.161  17.399 -17.376  1.00 40.16           N
ATOM   6270  C   LYS A 412     -36.664  19.177 -15.419  1.00 36.42           C
ATOM   6271  O   LYS A 412     -36.246  18.728 -14.357  1.00 36.56           O
ATOM   6273  N   GLU A 413     -36.570  20.466 -15.744  1.00 35.77           N
ATOM   6274  CA  GLU A 413     -35.948  21.423 -14.820  1.00 35.38           C
ATOM   6276  CB  GLU A 413     -35.688  22.792 -15.489  1.00 35.73           C
ATOM   6279  CG  GLU A 413     -36.510  24.013 -14.973  1.00 37.10           C
ATOM   6282  CD  GLU A 413     -35.621  25.235 -14.633  1.00 38.51           C
ATOM   6283  OE1 GLU A 413     -34.778  25.125 -13.714  1.00 39.24           O
ATOM   6284  OE2 GLU A 413     -35.768  26.306 -15.266  1.00 39.04           O
ATOM   6285  C   GLU A 413     -36.760  21.551 -13.522  1.00 34.43           C
ATOM   6286  O   GLU A 413     -36.196  21.801 -12.460  1.00 34.34           O
ATOM   6288  N   GLU A 414     -38.074  21.360 -13.616  1.00 33.45           N
ATOM   6289  CA  GLU A 414     -38.956  21.407 -12.452  1.00 32.80           C
ATOM   6291  CB  GLU A 414     -40.435  21.425 -12.864  1.00 32.83           C
ATOM   6294  CG  GLU A 414     -40.923  22.736 -13.478  1.00 33.15           C
ATOM   6297  CD  GLU A 414     -42.360  22.668 -14.003  1.00 33.82           C
ATOM   6298  OE1 GLU A 414     -42.876  21.560 -14.231  1.00 35.31           O
ATOM   6299  OE2 GLU A 414     -42.985  23.727 -14.204  1.00 33.98           O
ATOM   6300  C   GLU A 414     -38.715  20.222 -11.536  1.00 32.18           C
ATOM   6301  O   GLU A 414     -38.407  20.409 -10.372  1.00 32.25           O
ATOM   6303  N   ILE A 415     -38.863  19.002 -12.044  1.00 31.63           N
ATOM   6304  CA  ILE A 415     -38.725  17.819 -11.181  1.00 31.28           C
ATOM   6306  CB  ILE A 415     -39.131  16.472 -11.852  1.00 31.14           C
ATOM   6308  CG1 ILE A 415     -38.349  16.204 -13.133  1.00 31.13           C
ATOM   6311  CD1 ILE A 415     -38.786  14.926 -13.836  1.00 30.72           C
ATOM   6315  CG2 ILE A 415     -40.611  16.454 -12.160  1.00 31.12           C
ATOM   6319  C   ILE A 415     -37.316  17.705 -10.636  1.00 31.08           C
ATOM   6320  O   ILE A 415     -37.105  17.188  -9.539  1.00 31.22           O
ATOM   6322  N   GLU A 416     -36.345  18.208 -11.381  1.00 30.67           N
ATOM   6323  CA  GLU A 416     -34.998  18.270 -10.850  1.00 30.55           C
ATOM   6325  CB  GLU A 416     -34.011  18.654 -11.955  1.00 30.91           C
ATOM   6328  CG  GLU A 416     -32.654  17.967 -11.845  1.00 32.55           C
ATOM   6331  CD  GLU A 416     -31.802  18.130 -13.109  1.00 34.91           C
ATOM   6332  OE1 GLU A 416     -32.337  18.563 -14.161  1.00 35.53           O
ATOM   6333  OE2 GLU A 416     -30.590  17.816 -13.052  1.00 36.45           O
ATOM   6334  C   GLU A 416     -34.962  19.249  -9.650  1.00 29.74           C
ATOM   6335  O   GLU A 416     -34.143  19.097  -8.738  1.00 29.73           O
ATOM   6337  N   ASN A 417     -35.864  20.234  -9.652  1.00 28.69           N
ATOM   6338  CA  ASN A 417     -36.060  21.134  -8.503  1.00 27.92           C
ATOM   6340  CB  ASN A 417     -36.632  22.477  -8.963  1.00 27.75           C
ATOM   6343  CG  ASN A 417     -35.572  23.532  -9.095  1.00 26.84           C
ATOM   6344  OD1 ASN A 417     -35.160  24.132  -8.105  1.00 24.88           O
ATOM   6345  ND2 ASN A 417     -35.117  23.765 -10.318  1.00 26.28           N
ATOM   6348  C   ASN A 417     -36.917  20.580  -7.356  1.00 27.41           C
ATOM   6349  O   ASN A 417     -36.650  20.838  -6.187  1.00 27.15           O
ATOM   6351  N   LEU A 418     -37.955  19.834  -7.675  1.00 27.09           N
ATOM   6352  CA  LEU A 418     -38.694  19.156  -6.628  1.00 27.02           C
ATOM   6354  CB  LEU A 418     -39.921  18.423  -7.200  1.00 26.95           C
ATOM   6357  CG  LEU A 418     -41.030  19.284  -7.826  1.00 25.97           C
ATOM   6359  CD1 LEU A 418     -42.127  18.429  -8.447  1.00 24.88           C
ATOM   6363  CD2 LEU A 418     -41.623  20.226  -6.803  1.00 24.50           C
ATOM   6367  C   LEU A 418     -37.763  18.196  -5.860  1.00 27.26           C
ATOM   6368  O   LEU A 418     -37.834  18.123  -4.644  1.00 27.07           O
ATOM   6370  N   GLN A 419     -36.873  17.494  -6.561  1.00 27.67           N
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ATOM  6371 CA  GLN A 419    -35.924  16.575  -5.909  1.00 28.28      C
ATOM  6373 CB  GLN A 419    -35.155  15.758  -6.945  1.00 28.36      C
ATOM  6376 CG  GLN A 419    -35.747  14.375  -7.146  1.00 29.43      C
ATOM  6379 CD  GLN A 419    -35.052  13.573  -8.215  1.00 29.76      C
ATOM  6380 OE1 GLN A 419    -34.355  14.112  -9.066  1.00 29.93      O
ATOM  6381 NE2 GLN A 419    -35.252  12.270  -8.184  1.00 31.33      N
ATOM  6384 C   GLN A 419    -34.922  17.219  -4.947  1.00 28.73      C
ATOM  6385 O   GLN A 419    -34.540  16.608  -3.952  1.00 28.90      O
ATOM  6387 N   LYS A 420    -34.490  18.440  -5.240  1.00 29.27      N
ATOM  6388 CA  LYS A 420    -33.608  19.166  -4.335  1.00 29.81      C
ATOM  6390 CB  LYS A 420    -32.758  20.163  -5.129  1.00 30.24      C
ATOM  6393 CG  LYS A 420    -31.592  19.513  -5.867  1.00 31.75      C
ATOM  6396 CD  LYS A 420    -31.259  20.217  -7.183  1.00 34.14      C
ATOM  6399 CE  LYS A 420    -30.140  19.463  -7.953  1.00 36.21      C
ATOM  6402 NZ  LYS A 420    -30.073  19.759  -9.439  1.00 36.76      N
ATOM  6406 C   LYS A 420    -34.375  19.872  -3.204  1.00 29.98      C
ATOM  6407 O   LYS A 420    -33.759  20.547  -2.384  1.00 30.44      O
ATOM  6409 N   TYR A 421    -35.706  19.694  -3.162  1.00 30.07      N
ATOM  6410 CA  TYR A 421    -36.646  20.309  -2.171  1.00 29.73      C
ATOM  6412 CB  TYR A 421    -36.298  19.949   -.712  1.00 29.59      C
ATOM  6415 CG  TYR A 421    -36.386  18.468   -.470  1.00 30.57      C
ATOM  6416 CD1 TYR A 421    -37.582  17.785   -.643  1.00 30.87      C
ATOM  6418 CE1 TYR A 421    -37.665  16.414   -.448  1.00 31.28      C
ATOM  6420 CZ  TYR A 421    -36.549  15.705   -.068  1.00 31.90      C
ATOM  6421 OH  TYR A 421    -36.620  14.347    .124  1.00 32.43      O
ATOM  6423 CE2 TYR A 421    -35.355  16.354    .119  1.00 32.68      C
ATOM  6425 CD2 TYR A 421    -35.274  17.736   -.095  1.00 32.42      C
ATOM  6427 C   TYR A 421    -36.850  21.816  -2.347  1.00 29.24      C
ATOM  6428 O   TYR A 421    -36.709  22.590  -1.401  1.00 29.26      O
ATOM  6430 N   HIS A 422    -37.219  22.214  -3.563  1.00 28.65      N
ATOM  6431 CA  HIS A 422    -37.540  23.604  -3.859  1.00 28.26      C
ATOM  6433 CB  HIS A 422    -38.150  23.715  -5.256  1.00 28.33      C
ATOM  6436 CG  HIS A 422    -38.299  25.124  -5.748  1.00 28.44      C
ATOM  6437 ND1 HIS A 422    -37.225  25.904  -6.106  1.00 28.97      N
ATOM  6439 CE1 HIS A 422    -37.660  27.082  -6.520  1.00 29.40      C
ATOM  6441 NE2 HIS A 422    -38.977  27.090  -6.443  1.00 28.14      N
ATOM  6443 CD2 HIS A 422    -39.399  25.879  -5.965  1.00 27.76      C
ATOM  6445 C   HIS A 422    -38.511  24.147  -2.816  1.00 27.74      C
ATOM  6446 O   HIS A 422    -39.357  23.408  -2.310  1.00 27.53      O
ATOM  6448 N   ASP A 423    -38.384  25.437  -2.505  1.00 27.12      N
ATOM  6449 CA  ASP A 423    -39.186  26.072  -1.454  1.00 26.63      C
ATOM  6451 CB  ASP A 423    -38.877  27.575  -1.349  1.00 27.05      C
ATOM  6454 CG  ASP A 423    -37.456  27.875   -.851  1.00 28.35      C
ATOM  6455 OD1 ASP A 423    -36.951  27.121    .018  1.00 30.99      O
ATOM  6456 OD2 ASP A 423    -36.860  28.884  -1.322  1.00 27.89      O
ATOM  6457 C   ASP A 423    -40.689  25.883  -1.698  1.00 25.71      C
ATOM  6458 O   ASP A 423    -41.487  25.831   -.749  1.00 26.26      O
ATOM  6460 N   ILE A 424    -41.075  25.781  -2.966  1.00 24.01      N
ATOM  6461 CA  ILE A 424    -42.479  25.596  -3.327  1.00 22.72      C
ATOM  6463 CB  ILE A 424    -42.639  25.391  -4.843  1.00 22.40      C
ATOM  6465 CG1 ILE A 424    -44.029  25.668  -5.318  1.00 21.78      C
ATOM  6468 CD1 ILE A 424    -44.086  25.499  -6.793  1.00 22.22      C
ATOM  6472 CG2 ILE A 424    -42.340  23.985  -5.255  1.00 22.87      C
ATOM  6476 C   ILE A 424    -43.103  24.442  -2.562  1.00 21.91      C
ATOM  6477 O   ILE A 424    -44.238  24.574  -2.115  1.00 21.73      O
ATOM  6479 N   ILE A 425    -42.365  23.334  -2.399  1.00 21.23      N
ATOM  6480 CA  ILE A 425    -42.853  22.173  -1.634  1.00 20.73      C
ATOM  6482 CB  ILE A 425    -42.622  20.820  -2.330  1.00 20.10      C
ATOM  6484 CG1 ILE A 425    -41.158  20.409  -2.290  1.00 18.72      C
ATOM  6487 CD1 ILE A 425    -40.923  19.075  -2.948  1.00 18.27      C
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ATOM 6491 CG2 ILE A 425 -43.146 20.840 -3.741 1.00 19.57 C
ATOM 6495 C ILE A 425 -42.252 22.060 -.242 1.00 21.21 C
ATOM 6496 O ILE A 425 -42.810 21.370 .613 1.00 21.30 O
ATOM 6498 N SER A 426 -41.129 22.721 -.002 1.00 21.56 N
ATOM 6499 CA SER A 426 -40.492 22.620 1.299 1.00 22.23 C
ATOM 6501 CB SER A 426 -39.043 23.082 1.234 1.00 22.36 C
ATOM 6504 OG SER A 426 -38.977 24.501 1.342 1.00 24.09 O
ATOM 6506 C SER A 426 -41.242 23.460 2.334 1.00 22.39 C
ATOM 6507 O SER A 426 -41.390 23.051 3.491 1.00 22.95 O
ATOM 6509 N ARG A 427 -41.701 24.643 1.937 1.00 22.08 N
ATOM 6510 CA ARG A 427 -42.332 25.541 2.905 1.00 21.87 C
ATOM 6512 CB ARG A 427 -42.466 26.955 2.345 1.00 21.99 C
ATOM 6515 CG ARG A 427 -41.170 27.696 2.493 1.00 23.36 C
ATOM 6518 CD ARG A 427 -40.954 28.727 1.433 1.00 26.07 C
ATOM 6521 NE ARG A 427 -39.680 29.407 1.667 1.00 28.18 N
ATOM 6523 CZ ARG A 427 -39.127 30.298 .844 1.00 29.21 C
ATOM 6524 NH1 ARG A 427 -39.723 30.633 -.298 1.00 28.60 N
ATOM 6527 NH2 ARG A 427 -37.962 30.854 1.173 1.00 30.48 N
ATOM 6530 C ARG A 427 -43.651 25.003 3.434 1.00 21.21 C
ATOM 6531 O ARG A 427 -43.817 24.891 4.645 1.00 21.11 O
ATOM 6533 N PRO A 428 -44.573 24.622 2.541 1.00 20.52 N
ATOM 6534 CA PRO A 428 -45.789 23.999 3.040 1.00 20.27 C
ATOM 6536 CB PRO A 428 -46.410 23.369 1.791 1.00 20.44 C
ATOM 6539 CG PRO A 428 -45.864 24.119 .666 1.00 20.63 C
ATOM 6542 CD PRO A 428 -44.521 24.644 1.074 1.00 20.54 C
ATOM 6545 C PRO A 428 -45.450 22.917 4.050 1.00 19.75 C
ATOM 6546 O PRO A 428 -46.089 22.834 5.095 1.00 19.77 O
ATOM 6547 N SER A 429 -44.424 22.123 3.747 1.00 18.97 N
ATOM 6548 CA SER A 429 -44.008 21.045 4.636 1.00 18.45 C
ATOM 6550 CB SER A 429 -42.954 20.180 3.972 1.00 18.35 C
ATOM 6553 OG SER A 429 -43.452 19.716 2.733 1.00 19.12 O
ATOM 6555 C SER A 429 -43.519 21.525 5.985 1.00 17.97 C
ATOM 6556 O SER A 429 -43.733 20.846 6.968 1.00 17.88 O
ATOM 6558 N HIS A 430 -42.879 22.689 6.053 1.00 17.73 N
ATOM 6559 CA HIS A 430 -42.593 23.289 7.359 1.00 17.71 C
ATOM 6561 CB HIS A 430 -41.937 24.668 7.241 1.00 17.97 C
ATOM 6564 CG HIS A 430 -40.558 24.663 6.651 1.00 18.87 C
ATOM 6565 ND1 HIS A 430 -39.940 23.524 6.186 1.00 19.85 N
ATOM 6567 CE1 HIS A 430 -38.746 23.836 5.709 1.00 19.43 C
ATOM 6569 NE2 HIS A 430 -38.573 25.137 5.838 1.00 19.06 N
ATOM 6571 CD2 HIS A 430 -39.693 25.681 6.418 1.00 19.32 C
ATOM 6573 C HIS A 430 -43.914 23.444 8.131 1.00 17.31 C
ATOM 6574 O HIS A 430 -44.023 23.013 9.287 1.00 17.06 O
ATOM 6576 N ILE A 431 -44.913 24.050 7.475 1.00 16.74 N
ATOM 6577 CA ILE A 431 -46.218 24.304 8.091 1.00 16.15 C
ATOM 6579 CB ILE A 431 -47.174 25.057 7.174 1.00 16.18 C
ATOM 6581 CG1 ILE A 431 -46.613 26.428 6.801 1.00 17.05 C
ATOM 6584 CD1 ILE A 431 -46.441 27.352 7.994 1.00 18.34 C
ATOM 6588 CG2 ILE A 431 -48.496 25.263 7.860 1.00 15.28 C
ATOM 6592 C ILE A 431 -46.899 23.021 8.476 1.00 15.75 C
ATOM 6593 O ILE A 431 -47.624 22.980 9.445 1.00 15.95 O
ATOM 6595 N PHE A 432 -46.663 21.969 7.714 1.00 15.59 N
ATOM 6596 CA PHE A 432 -47.192 20.652 8.041 1.00 15.52 C
ATOM 6598 CB PHE A 432 -46.837 19.683 6.913 1.00 15.23 C
ATOM 6601 CG PHE A 432 -47.451 18.318 7.031 1.00 15.98 C
ATOM 6602 CD1 PHE A 432 -48.324 17.972 8.052 1.00 16.55 C
ATOM 6604 CE1 PHE A 432 -48.867 16.700 8.102 1.00 16.04 C
ATOM 6606 CZ PHE A 432 -48.559 15.774 7.130 1.00 15.29 C
ATOM 6608 CE2 PHE A 432 -47.718 16.107 6.114 1.00 15.37 C
ATOM 6610 CD2 PHE A 432 -47.172 17.364 6.061 1.00 16.74 C

ATOM 6612 C PHE A 432 -46.640 20.191 9.392 1.00 15.54 C
ATOM 6613 O PHE A 432 -47.383 20.006 10.343 1.00 15.37 O
ATOM 6615 N ARG A 433 -45.328 20.041 9.483 1.00 15.98 N
ATOM 6616 CA ARG A 433 -44.695 19.542 10.709 1.00 16.20 C
ATOM 6618 CB ARG A 433 -43.176 19.476 10.526 1.00 15.85 C
ATOM 6621 CG ARG A 433 -42.411 19.183 11.804 1.00 16.11 C
ATOM 6624 CD ARG A 433 -42.848 17.890 12.489 1.00 15.70 C
ATOM 6627 NE ARG A 433 -42.811 16.747 11.588 1.00 15.64 N
ATOM 6629 CZ ARG A 433 -43.377 15.571 11.838 1.00 16.27 C
ATOM 6630 NH1 ARG A 433 -44.029 15.359 12.965 1.00 16.82 N
ATOM 6633 NH2 ARG A 433 -43.302 14.598 10.948 1.00 16.96 N
ATOM 6636 C ARG A 433 -45.029 20.411 11.935 1.00 16.46 C
ATOM 6637 O ARG A 433 -45.296 19.890 13.031 1.00 16.31 O
ATOM 6639 N LEU A 434 -45.006 21.731 11.724 1.00 16.47 N
ATOM 6640 CA LEU A 434 -45.123 22.701 12.800 1.00 15.98 C
ATOM 6642 CB LEU A 434 -44.771 24.114 12.303 1.00 15.83 C
ATOM 6645 CG LEU A 434 -43.287 24.486 12.218 1.00 14.95 C
ATOM 6647 CD1 LEU A 434 -43.130 25.918 11.826 1.00 15.09 C
ATOM 6651 CD2 LEU A 434 -42.600 24.281 13.536 1.00 14.37 C
ATOM 6655 C LEU A 434 -46.517 22.660 13.387 1.00 16.19 C
ATOM 6656 O LEU A 434 -46.669 22.564 14.604 1.00 15.92 O
ATOM 6658 N CYS A 435 -47.529 22.715 12.520 1.00 16.78 N
ATOM 6659 CA CYS A 435 -48.936 22.591 12.940 1.00 17.48 C
ATOM 6661 CB CYS A 435 -49.870 22.617 11.726 1.00 17.54 C
ATOM 6664 SG CYS A 435 -50.110 24.233 10.985 1.00 18.80 S
ATOM 6666 C CYS A 435 -49.192 21.296 13.708 1.00 17.84 C
ATOM 6667 O CYS A 435 -50.043 21.250 14.597 1.00 17.92 O
ATOM 6669 N ASN A 436 -48.446 20.257 13.333 1.00 18.24 N
ATOM 6670 CA ASN A 436 -48.603 18.913 13.846 1.00 18.50 C
ATOM 6672 CB ASN A 436 -47.936 17.949 12.867 1.00 18.63 C
ATOM 6675 CG ASN A 436 -48.156 16.487 13.213 1.00 18.58 C
ATOM 6676 OD1 ASN A 436 -48.810 16.129 14.185 1.00 18.80 O
ATOM 6677 ND2 ASN A 436 -47.588 15.633 12.398 1.00 19.29 N
ATOM 6680 C ASN A 436 -47.975 18.755 15.210 1.00 18.83 C
ATOM 6681 O ASN A 436 -48.551 18.153 16.115 1.00 19.00 O
ATOM 6683 N ASP A 437 -46.763 19.255 15.351 1.00 19.29 N
ATOM 6684 CA ASP A 437 -46.097 19.179 16.634 1.00 19.62 C
ATOM 6686 CB ASP A 437 -44.615 19.522 16.510 1.00 19.45 C
ATOM 6689 CG ASP A 437 -43.849 18.480 15.734 1.00 19.36 C
ATOM 6690 OD1 ASP A 437 -44.491 17.586 15.158 1.00 19.89 O
ATOM 6691 OD2 ASP A 437 -42.608 18.543 15.699 1.00 19.86 O
ATOM 6692 C ASP A 437 -46.799 20.106 17.597 1.00 20.01 C
ATOM 6693 O ASP A 437 -46.916 19.790 18.779 1.00 20.30 O
ATOM 6695 N LEU A 438 -47.288 21.233 17.092 1.00 20.40 N
ATOM 6696 CA LEU A 438 -47.996 22.174 17.940 1.00 21.03 C
ATOM 6698 CB LEU A 438 -48.510 23.363 17.126 1.00 21.01 C
ATOM 6701 CG LEU A 438 -47.575 24.565 17.078 1.00 20.32 C
ATOM 6703 CD1 LEU A 438 -47.938 25.524 15.952 1.00 19.14 C
ATOM 6707 CD2 LEU A 438 -47.611 25.263 18.415 1.00 19.73 C
ATOM 6711 C LEU A 438 -49.153 21.496 18.679 1.00 21.81 C
ATOM 6712 O LEU A 438 -49.277 21.633 19.902 1.00 21.55 O
ATOM 6714 N ALA A 439 -49.973 20.754 17.932 1.00 22.76 N
ATOM 6715 CA ALA A 439 -51.138 20.055 18.486 1.00 23.58 C
ATOM 6717 CB ALA A 439 -51.905 19.360 17.386 1.00 23.57 C
ATOM 6721 C ALA A 439 -50.746 19.042 19.542 1.00 24.47 C
ATOM 6722 O ALA A 439 -51.386 18.951 20.575 1.00 24.63 O
ATOM 6724 N SER A 440 -49.685 18.291 19.276 1.00 25.78 N
ATOM 6725 CA SER A 440 -49.242 17.227 20.168 1.00 26.84 C
ATOM 6727 CB SER A 440 -48.566 16.130 19.353 1.00 26.92 C
ATOM 6730 OG SER A 440 -47.321 16.582 18.859 1.00 27.46 O

ATOM 6732 C SER A 440 -48.270 17.691 21.244 1.00 27.68 C
ATOM 6733 O SER A 440 -47.934 16.923 22.132 1.00 28.00 O
ATOM 6735 N ALA A 441 -47.822 18.935 21.174 1.00 28.83 N
ATOM 6736 CA ALA A 441 -46.760 19.419 22.056 1.00 29.73 C
ATOM 6738 CB ALA A 441 -46.529 20.910 21.841 1.00 29.84 C
ATOM 6742 C ALA A 441 -46.982 19.132 23.539 1.00 30.57 C
ATOM 6743 O ALA A 441 -46.306 18.274 24.093 1.00 30.50 O
ATOM 6745 N SER A 442 -47.929 19.827 24.172 1.00 31.90 N
ATOM 6746 CA SER A 442 -47.999 19.862 25.654 1.00 32.95 C
ATOM 6748 CB SER A 442 -49.043 20.870 26.169 1.00 32.91 C
ATOM 6751 OG SER A 442 -50.331 20.614 25.650 1.00 33.50 O
ATOM 6753 C SER A 442 -48.219 18.497 26.289 1.00 33.69 C
ATOM 6754 O SER A 442 -47.754 18.246 27.397 1.00 33.59 O
ATOM 6756 N ALA A 443 -48.922 17.623 25.578 1.00 34.93 N
ATOM 6757 CA ALA A 443 -49.050 16.231 25.980 1.00 35.81 C
ATOM 6759 CB ALA A 443 -49.981 15.488 25.030 1.00 35.72 C
ATOM 6763 C ALA A 443 -47.663 15.580 25.996 1.00 36.71 C
ATOM 6764 O ALA A 443 -47.198 15.115 27.047 1.00 36.94 O
ATOM 6766 N GLU A 444 -46.999 15.567 24.838 1.00 37.47 N
ATOM 6767 CA GLU A 444 -45.688 14.930 24.718 1.00 37.93 C
ATOM 6769 CB GLU A 444 -45.164 14.996 23.277 1.00 37.99 C
ATOM 6772 CG GLU A 444 -45.952 14.100 22.326 1.00 39.24 C
ATOM 6775 CD GLU A 444 -45.419 14.080 20.886 1.00 41.03 C
ATOM 6776 OE1 GLU A 444 -44.612 14.958 20.510 1.00 42.16 O
ATOM 6777 OE2 GLU A 444 -45.827 13.178 20.119 1.00 42.36 O
ATOM 6778 C GLU A 444 -44.694 15.534 25.708 1.00 38.09 C
ATOM 6779 O GLU A 444 -43.924 14.803 26.324 1.00 38.17 O
ATOM 6781 N ILE A 445 -44.739 16.851 25.889 1.00 38.41 N
ATOM 6782 CA ILE A 445 -43.829 17.530 26.814 1.00 38.75 C
ATOM 6784 CB ILE A 445 -43.802 19.065 26.587 1.00 38.69 C
ATOM 6786 CG1 ILE A 445 -43.314 19.396 25.170 1.00 38.18 C
ATOM 6789 CD1 ILE A 445 -43.702 20.775 24.712 1.00 37.58 C
ATOM 6793 CG2 ILE A 445 -42.909 19.753 27.617 1.00 38.26 C
ATOM 6797 C ILE A 445 -44.243 17.194 28.246 1.00 39.35 C
ATOM 6798 O ILE A 445 -45.039 17.901 28.870 1.00 39.44 O
ATOM 6800 N ALA A 446 -43.696 16.092 28.750 1.00 40.02 N
ATOM 6801 CA ALA A 446 -44.082 15.540 30.045 1.00 40.51 C
ATOM 6803 CB ALA A 446 -43.815 16.552 31.170 1.00 40.55 C
ATOM 6807 C ALA A 446 -45.559 15.130 30.029 1.00 40.86 C
ATOM 6808 O ALA A 446 -46.407 16.021 30.121 1.00 40.77 O
ATOM 6810 N ARG A 447 -45.925 13.842 29.899 1.00 41.31 N
ATOM 6811 CA ARG A 447 -45.072 12.633 29.691 1.00 41.58 C
ATOM 6813 CB ARG A 447 -45.272 12.092 28.258 1.00 41.84 C
ATOM 6816 CG ARG A 447 -46.667 11.495 27.991 1.00 42.69 C
ATOM 6819 CD ARG A 447 -46.778 10.901 26.582 1.00 43.92 C
ATOM 6822 NE ARG A 447 -47.764 11.589 25.744 1.00 45.34 N
ATOM 6824 CZ ARG A 447 -47.887 11.435 24.420 1.00 46.56 C
ATOM 6825 NH1 ARG A 447 -47.077 10.623 23.742 1.00 46.71 N
ATOM 6828 NH2 ARG A 447 -48.828 12.107 23.757 1.00 46.97 N
ATOM 6831 C ARG A 447 -43.581 12.728 30.054 1.00 41.38 C
ATOM 6832 O ARG A 447 -43.231 12.747 31.238 1.00 41.92 O
ATOM 6834 N GLY A 448 -42.710 12.736 29.051 1.00 40.88 N
ATOM 6835 CA GLY A 448 -41.312 13.128 29.234 1.00 40.44 C
ATOM 6838 C GLY A 448 -40.579 13.316 27.915 1.00 40.08 C
ATOM 6839 O GLY A 448 -39.364 13.488 27.901 1.00 40.05 O
ATOM 6841 N GLU A 449 -41.323 13.332 26.809 1.00 39.56 N
ATOM 6842 CA GLU A 449 -40.750 13.132 25.486 1.00 39.19 C
ATOM 6844 CB GLU A 449 -41.827 12.668 24.502 1.00 39.52 C
ATOM 6847 CG GLU A 449 -42.403 11.290 24.810 1.00 40.61 C
ATOM 6850 CD GLU A 449 -43.348 10.782 23.715 1.00 42.21 C

ATOM 6851 OE1 GLU A 449 -43.068 11.019 22.503 1.00 41.83 O
ATOM 6852 OE2 GLU A 449 -44.368 10.141 24.082 1.00 42.41 O
ATOM 6853 C GLU A 449 -40.037 14.365 24.921 1.00 38.34 C
ATOM 6854 O GLU A 449 -40.511 15.497 25.031 1.00 38.01 O
ATOM 6856 N THR A 450 -38.904 14.106 24.279 1.00 37.37 N
ATOM 6857 CA THR A 450 -38.047 15.138 23.726 1.00 36.37 C
ATOM 6859 CB THR A 450 -36.607 14.985 24.285 1.00 36.39 C
ATOM 6861 OG1 THR A 450 -35.846 16.153 23.982 1.00 36.63 O
ATOM 6863 CG2 THR A 450 -35.888 13.749 23.706 1.00 36.52 C
ATOM 6867 C THR A 450 -38.013 15.100 22.190 1.00 35.36 C
ATOM 6868 O THR A 450 -37.175 15.764 21.583 1.00 35.43 O
ATOM 6870 N ALA A 451 -38.917 14.338 21.563 1.00 33.98 N
ATOM 6871 CA ALA A 451 -38.920 14.182 20.096 1.00 32.81 C
ATOM 6873 CB ALA A 451 -39.030 12.708 19.708 1.00 32.99 C
ATOM 6877 C ALA A 451 -40.043 14.987 19.459 1.00 31.46 C
ATOM 6878 O ALA A 451 -41.050 14.432 18.996 1.00 31.06 O
ATOM 6880 N ASN A 452 -39.848 16.302 19.432 1.00 29.88 N
ATOM 6881 CA ASN A 452 -40.881 17.225 18.973 1.00 28.81 C
ATOM 6883 CB ASN A 452 -41.957 17.329 20.051 1.00 28.57 C
ATOM 6886 CG ASN A 452 -42.969 18.380 19.757 1.00 28.30 C
ATOM 6887 OD1 ASN A 452 -42.622 19.517 19.468 1.00 29.35 O
ATOM 6888 ND2 ASN A 452 -44.236 18.018 19.836 1.00 28.36 N
ATOM 6891 C ASN A 452 -40.285 18.590 18.641 1.00 27.76 C
ATOM 6892 O ASN A 452 -39.365 19.018 19.296 1.00 28.04 O
ATOM 6894 N SER A 453 -40.807 19.269 17.630 1.00 26.77 N
ATOM 6895 CA SER A 453 -40.226 20.533 17.182 1.00 26.38 C
ATOM 6897 CB SER A 453 -40.912 21.015 15.903 1.00 26.40 C
ATOM 6900 OG SER A 453 -40.796 20.044 14.876 1.00 25.79 O
ATOM 6902 C SER A 453 -40.253 21.643 18.233 1.00 26.12 C
ATOM 6903 O SER A 453 -39.280 22.361 18.385 1.00 25.97 O
ATOM 6905 N VAL A 454 -41.368 21.784 18.942 1.00 26.15 N
ATOM 6906 CA VAL A 454 -41.518 22.780 20.022 1.00 26.21 C
ATOM 6908 CB VAL A 454 -42.975 22.818 20.532 1.00 26.04 C
ATOM 6910 CG1 VAL A 454 -43.122 23.787 21.694 1.00 25.24 C
ATOM 6914 CG2 VAL A 454 -43.913 23.190 19.401 1.00 26.32 C
ATOM 6918 C VAL A 454 -40.617 22.451 21.211 1.00 26.63 C
ATOM 6919 O VAL A 454 -40.173 23.328 21.959 1.00 26.53 O
ATOM 6921 N SER A 455 -40.374 21.160 21.380 1.00 27.21 N
ATOM 6922 CA SER A 455 -39.541 20.651 22.437 1.00 27.60 C
ATOM 6924 CB SER A 455 -39.677 19.141 22.490 1.00 27.31 C
ATOM 6927 OG SER A 455 -38.922 18.625 23.545 1.00 28.13 O
ATOM 6929 C SER A 455 -38.096 21.045 22.181 1.00 28.29 C
ATOM 6930 O SER A 455 -37.445 21.628 23.043 1.00 28.63 O
ATOM 6932 N CYS A 456 -37.599 20.748 20.988 1.00 29.04 N
ATOM 6933 CA CYS A 456 -36.219 21.082 20.640 1.00 29.65 C
ATOM 6935 CB CYS A 456 -35.868 20.535 19.256 1.00 29.52 C
ATOM 6938 SG CYS A 456 -35.959 18.734 19.163 1.00 29.71 S
ATOM 6940 C CYS A 456 -35.955 22.589 20.710 1.00 30.26 C
ATOM 6941 O CYS A 456 -34.887 23.007 21.162 1.00 30.49 O
ATOM 6943 N TYR A 457 -36.924 23.399 20.283 1.00 30.88 N
ATOM 6944 CA TYR A 457 -36.767 24.850 20.308 1.00 31.45 C
ATOM 6946 CB TYR A 457 -37.967 25.557 19.648 1.00 31.55 C
ATOM 6949 CG TYR A 457 -37.691 26.991 19.178 1.00 32.09 C
ATOM 6950 CD1 TYR A 457 -37.378 27.269 17.843 1.00 31.69 C
ATOM 6952 CE1 TYR A 457 -37.128 28.569 17.418 1.00 31.73 C
ATOM 6954 CZ TYR A 457 -37.186 29.613 18.328 1.00 32.84 C
ATOM 6955 OH TYR A 457 -36.945 30.917 17.927 1.00 33.81 O
ATOM 6957 CE2 TYR A 457 -37.492 29.364 19.658 1.00 32.72 C
ATOM 6959 CD2 TYR A 457 -37.746 28.064 20.074 1.00 32.44 C
ATOM 6961 C TYR A 457 -36.571 25.295 21.758 1.00 31.99 C

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ATOM  6962  O   TYR A 457    -35.648  26.053  22.052  1.00 31.98      O
ATOM  6964  N   MET A 458    -37.419  24.799  22.661  1.00 32.76      N
ATOM  6965  CA  MET A 458    -37.211  24.987  24.105  1.00 33.37      C
ATOM  6967  CB  MET A 458    -38.151  24.097  24.921  1.00 33.43      C
ATOM  6970  CG  MET A 458    -39.570  24.593  25.059  1.00 33.70      C
ATOM  6973  SD  MET A 458    -40.641  23.312  25.737  1.00 34.59      S
ATOM  6974  CE  MET A 458    -39.709  22.763  27.179  1.00 34.71      C
ATOM  6978  C   MET A 458    -35.784  24.641  24.517  1.00 33.78      C
ATOM  6979  O   MET A 458    -35.101  25.437  25.151  1.00 33.73      O
ATOM  6981  N   ARG A 459    -35.347  23.445  24.145  1.00 34.46      N
ATOM  6982  CA  ARG A 459    -34.051  22.926  24.581  1.00 35.15      C
ATOM  6984  CB  ARG A 459    -33.876  21.447  24.171  1.00 35.68      C
ATOM  6987  CG  ARG A 459    -32.494  20.864  24.500  1.00 37.23      C
ATOM  6990  CD  ARG A 459    -32.491  19.345  24.752  1.00 39.80      C
ATOM  6993  NE  ARG A 459    -33.140  18.538  23.711  1.00 42.88      N
ATOM  6995  CZ  ARG A 459    -32.704  18.407  22.453  1.00 45.43      C
ATOM  6996  NH1 ARG A 459    -31.615  19.062  22.035  1.00 47.50      N
ATOM  6999  NH2 ARG A 459    -33.366  17.629  21.595  1.00 44.77      N
ATOM  7002  C   ARG A 459    -32.878  23.749  24.072  1.00 34.92      C
ATOM  7003  O   ARG A 459    -32.007  24.109  24.849  1.00 35.06      O
ATOM  7005  N   THR A 460    -32.854  24.047  22.778  1.00 34.96      N
ATOM  7006  CA  THR A 460    -31.674  24.678  22.163  1.00 34.91      C
ATOM  7008  CB  THR A 460    -31.494  24.263  20.680  1.00 34.88      C
ATOM  7010  OG1 THR A 460    -32.330  25.067  19.841  1.00 34.39      O
ATOM  7012  CG2 THR A 460    -31.825  22.776  20.488  1.00 35.44      C
ATOM  7016  C   THR A 460    -31.672  26.210  22.258  1.00 34.78      C
ATOM  7017  O   THR A 460    -30.673  26.837  21.911  1.00 34.92      O
ATOM  7019  N   LYS A 461    -32.781  26.806  22.701  1.00 34.41      N
ATOM  7020  CA  LYS A 461    -32.811  28.231  23.039  1.00 34.25      C
ATOM  7022  CB  LYS A 461    -33.921  28.947  22.265  1.00 34.56      C
ATOM  7025  CG  LYS A 461    -33.717  28.986  20.750  1.00 35.84      C
ATOM  7028  CD  LYS A 461    -32.519  29.859  20.347  1.00 37.64      C
ATOM  7031  CE  LYS A 461    -32.232  29.804  18.838  1.00 38.44      C
ATOM  7034  NZ  LYS A 461    -33.141  30.671  18.027  1.00 38.31      N
ATOM  7038  C   LYS A 461    -32.974  28.476  24.544  1.00 33.73      C
ATOM  7039  O   LYS A 461    -32.994  29.626  24.983  1.00 33.23      O
ATOM  7041  N   GLY A 462    -33.078  27.395  25.321  1.00 33.48      N
ATOM  7042  CA  GLY A 462    -33.173  27.464  26.784  1.00 33.23      C
ATOM  7045  C   GLY A 462    -34.332  28.320  27.239  1.00 32.95      C
ATOM  7046  O   GLY A 462    -34.144  29.258  28.004  1.00 33.17      O
ATOM  7048  N   ILE A 463    -35.528  28.000  26.757  1.00 32.52      N
ATOM  7049  CA  ILE A 463    -36.694  28.843  26.971  1.00 32.32      C
ATOM  7051  CB  ILE A 463    -37.006  29.724  25.734  1.00 32.47      C
ATOM  7053  CG1 ILE A 463    -37.152  28.866  24.463  1.00 32.41      C
ATOM  7056  CD1 ILE A 463    -37.359  29.675  23.191  1.00 32.02      C
ATOM  7060  CG2 ILE A 463    -35.937  30.810  25.571  1.00 32.44      C
ATOM  7064  C   ILE A 463    -37.902  28.006  27.309  1.00 32.15      C
ATOM  7065  O   ILE A 463    -37.886  26.799  27.145  1.00 32.01      O
ATOM  7067  N   SER A 464    -38.950  28.670  27.780  1.00 32.27      N
ATOM  7068  CA  SER A 464    -40.163  28.006  28.239  1.00 32.52      C
ATOM  7070  CB  SER A 464    -40.964  28.974  29.110  1.00 32.65      C
ATOM  7073  OG  SER A 464    -41.112  30.224  28.457  1.00 32.69      O
ATOM  7075  C   SER A 464    -41.036  27.522  27.079  1.00 32.53      C
ATOM  7076  O   SER A 464    -40.968  28.069  25.986  1.00 32.62      O
ATOM  7078  N   GLU A 465    -41.857  26.500  27.332  1.00 32.47      N
ATOM  7079  CA  GLU A 465    -42.836  26.010  26.353  1.00 32.33      C
ATOM  7081  CB  GLU A 465    -43.689  24.868  26.935  1.00 32.34      C
ATOM  7084  CG  GLU A 465    -44.756  24.312  25.974  1.00 32.37      C
ATOM  7087  CD  GLU A 465    -45.675  23.279  26.611  1.00 32.47      C
ATOM  7088  OE1 GLU A 465    -45.297  22.659  27.630  1.00 31.63      O
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ATOM  7089  OE2 GLU A 465    -46.785  23.086  26.074  1.00 32.77       O
ATOM  7090  C   GLU A 465    -43.758  27.124  25.864  1.00 32.33       C
ATOM  7091  O   GLU A 465    -44.078  27.183  24.676  1.00 32.60       O
ATOM  7093  N   GLU A 466    -44.196  28.001  26.767  1.00 32.08       N
ATOM  7094  CA  GLU A 466    -45.085  29.097  26.380  1.00 31.79       C
ATOM  7096  CB  GLU A 466    -45.606  29.832  27.624  1.00 31.91       C
ATOM  7099  CG  GLU A 466    -46.503  31.041  27.304  1.00 32.82       C
ATOM  7102  CD  GLU A 466    -47.426  31.472  28.452  1.00 33.67       C
ATOM  7103  OE1 GLU A 466    -47.519  30.756  29.478  1.00 35.09       O
ATOM  7104  OE2 GLU A 466    -48.077  32.533  28.312  1.00 33.12       O
ATOM  7105  C   GLU A 466    -44.392  30.052  25.386  1.00 31.13       C
ATOM  7106  O   GLU A 466    -45.032  30.603  24.492  1.00 30.87       O
ATOM  7108  N   LEU A 467    -43.077  30.194  25.531  1.00 30.57       N
ATOM  7109  CA  LEU A 467    -42.265  31.102  24.708  1.00 30.18       C
ATOM  7111  CB  LEU A 467    -41.055  31.604  25.524  1.00 30.38       C
ATOM  7114  CG  LEU A 467    -40.674  33.087  25.463  1.00 30.39       C
ATOM  7116  CD1 LEU A 467    -41.608  33.900  26.362  1.00 30.23       C
ATOM  7120  CD2 LEU A 467    -39.214  33.308  25.872  1.00 30.31       C
ATOM  7124  C   LEU A 467    -41.773  30.401  23.439  1.00 29.47       C
ATOM  7125  O   LEU A 467    -41.660  31.010  22.382  1.00 29.17       O
ATOM  7127  N   ALA A 468    -41.445  29.121  23.562  1.00 28.93       N
ATOM  7128  CA  ALA A 468    -41.095  28.310  22.404  1.00 28.45       C
ATOM  7130  CB  ALA A 468    -40.613  26.935  22.830  1.00 28.10       C
ATOM  7134  C   ALA A 468    -42.306  28.193  21.494  1.00 28.08       C
ATOM  7135  O   ALA A 468    -42.179  28.321  20.285  1.00 28.24       O
ATOM  7137  N   THR A 469    -43.479  27.964  22.080  1.00 27.58       N
ATOM  7138  CA  THR A 469    -44.719  27.870  21.322  1.00 27.26       C
ATOM  7140  CB  THR A 469    -45.928  27.710  22.261  1.00 27.28       C
ATOM  7142  OG1 THR A 469    -46.063  26.330  22.627  1.00 27.55       O
ATOM  7144  CG2 THR A 469    -47.222  28.185  21.597  1.00 27.34       C
ATOM  7148  C   THR A 469    -44.916  29.099  20.449  1.00 27.10       C
ATOM  7149  O   THR A 469    -45.176  28.989  19.250  1.00 27.11       O
ATOM  7151  N   GLU A 470    -44.774  30.267  21.061  1.00 26.88       N
ATOM  7152  CA  GLU A 470    -44.944  31.542  20.376  1.00 26.84       C
ATOM  7154  CB  GLU A 470    -44.832  32.663  21.400  1.00 27.07       C
ATOM  7157  CG  GLU A 470    -45.357  34.003  20.958  1.00 28.47       C
ATOM  7160  CD  GLU A 470    -45.140  35.087  22.008  1.00 30.51       C
ATOM  7161  OE1 GLU A 470    -45.029  34.775  23.221  1.00 31.53       O
ATOM  7162  OE2 GLU A 470    -45.083  36.269  21.608  1.00 32.59       O
ATOM  7163  C   GLU A 470    -43.926  31.750  19.239  1.00 26.48       C
ATOM  7164  O   GLU A 470    -44.261  32.296  18.184  1.00 26.29       O
ATOM  7166  N   SER A 471    -42.686  31.316  19.452  1.00 26.12       N
ATOM  7167  CA  SER A 471    -41.660  31.386  18.408  1.00 25.85       C
ATOM  7169  CB  SER A 471    -40.296  30.933  18.941  1.00 25.96       C
ATOM  7172  OG  SER A 471    -39.656  31.939  19.711  1.00 26.53       O
ATOM  7174  C   SER A 471    -42.036  30.529  17.208  1.00 25.35       C
ATOM  7175  O   SER A 471    -41.761  30.899  16.067  1.00 25.43       O
ATOM  7177  N   VAL A 472    -42.653  29.381  17.482  1.00 24.95       N
ATOM  7178  CA  VAL A 472    -43.097  28.451  16.438  1.00 24.65       C
ATOM  7180  CB  VAL A 472    -43.485  27.055  17.024  1.00 24.57       C
ATOM  7182  CG1 VAL A 472    -44.257  26.222  16.016  1.00 23.23       C
ATOM  7186  CG2 VAL A 472    -42.232  26.309  17.494  1.00 23.83       C
ATOM  7190  C   VAL A 472    -44.252  29.039  15.631  1.00 24.71       C
ATOM  7191  O   VAL A 472    -44.369  28.776  14.440  1.00 24.63       O
ATOM  7193  N   MET A 473    -45.073  29.866  16.269  1.00 24.79       N
ATOM  7194  CA  MET A 473    -46.143  30.591  15.565  1.00 24.94       C
ATOM  7196  CB  MET A 473    -47.059  31.266  16.576  1.00 25.11       C
ATOM  7199  CG  MET A 473    -47.683  30.335  17.560  1.00 25.11       C
ATOM  7202  SD  MET A 473    -48.967  29.391  16.780  1.00 25.35       S
ATOM  7203  CE  MET A 473    -50.064  29.163  18.189  1.00 26.11       C
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ATOM  7207  C   MET A 473    -45.613  31.672  14.605  1.00 24.86      C
ATOM  7208  O   MET A 473    -46.132  31.849  13.513  1.00 24.57      O
ATOM  7210  N   ASN A 474    -44.589  32.405  15.032  1.00 24.89      N
ATOM  7211  CA  ASN A 474    -43.951  33.383  14.166  1.00 25.00      C
ATOM  7213  CB  ASN A 474    -43.009  34.278  14.966  1.00 25.12      C
ATOM  7216  CG  ASN A 474    -43.700  34.966  16.127  1.00 25.77      C
ATOM  7217  OD1 ASN A 474    -43.058  35.312  17.114  1.00 26.96      O
ATOM  7218  ND2 ASN A 474    -45.015  35.163  16.021  1.00 26.31      N
ATOM  7221  C   ASN A 474    -43.195  32.707  13.024  1.00 24.84      C
ATOM  7222  O   ASN A 474    -42.979  33.313  11.973  1.00 25.07      O
ATOM  7224  N   LEU A 475    -42.792  31.455  13.227  1.00 24.46      N
ATOM  7225  CA  LEU A 475    -42.218  30.671  12.142  1.00 24.06      C
ATOM  7227  CB  LEU A 475    -41.596  29.367  12.653  1.00 24.27      C
ATOM  7230  CG  LEU A 475    -40.307  29.072  11.886  1.00 25.08      C
ATOM  7232  CD1 LEU A 475    -39.207  30.000  12.419  1.00 25.89      C
ATOM  7236  CD2 LEU A 475    -39.887  27.622  11.985  1.00 25.33      C
ATOM  7240  C   LEU A 475    -43.278  30.365  11.085  1.00 23.26      C
ATOM  7241  O   LEU A 475    -43.018  30.479   9.884  1.00 22.90      O
ATOM  7243  N   ILE A 476    -44.471  29.978  11.534  1.00 22.53      N
ATOM  7244  CA  ILE A 476    -45.544  29.632  10.606  1.00 21.93      C
ATOM  7246  CB  ILE A 476    -46.773  29.017  11.308  1.00 21.58      C
ATOM  7248  CG1 ILE A 476    -46.499  27.550  11.664  1.00 21.32      C
ATOM  7251  CD1 ILE A 476    -47.552  26.902  12.598  1.00 20.33      C
ATOM  7255  CG2 ILE A 476    -47.994  29.104  10.428  1.00 20.46      C
ATOM  7259  C   ILE A 476    -45.926  30.887   9.853  1.00 22.07      C
ATOM  7260  O   ILE A 476    -46.007  30.869   8.626  1.00 22.47      O
ATOM  7262  N   ASP A 477    -46.122  31.982  10.584  1.00 21.81      N
ATOM  7263  CA  ASP A 477    -46.483  33.245   9.970  1.00 21.56      C
ATOM  7265  CB  ASP A 477    -46.643  34.337  11.032  1.00 21.89      C
ATOM  7268  CG  ASP A 477    -47.962  34.217  11.817  1.00 23.39      C
ATOM  7269  OD1 ASP A 477    -48.854  33.441  11.375  1.00 24.41      O
ATOM  7270  OD2 ASP A 477    -48.103  34.902  12.875  1.00 23.80      O
ATOM  7271  C   ASP A 477    -45.425  33.626   8.947  1.00 21.06      C
ATOM  7272  O   ASP A 477    -45.759  33.913   7.795  1.00 20.78      O
ATOM  7274  N   GLU A 478    -44.156  33.591   9.361  1.00 20.63      N
ATOM  7275  CA  GLU A 478    -43.027  33.919   8.467  1.00 20.45      C
ATOM  7277  CB  GLU A 478    -41.680  33.793   9.200  1.00 20.66      C
ATOM  7280  CG  GLU A 478    -40.422  34.044   8.339  1.00 22.27      C
ATOM  7283  CD  GLU A 478    -39.107  33.579   9.018  1.00 24.72      C
ATOM  7284  OE1 GLU A 478    -38.553  34.367   9.817  1.00 26.19      O
ATOM  7285  OE2 GLU A 478    -38.619  32.442   8.745  1.00 25.66      O
ATOM  7286  C   GLU A 478    -43.041  33.042   7.217  1.00 19.54      C
ATOM  7287  O   GLU A 478    -42.879  33.544   6.102  1.00 19.02      O
ATOM  7289  N   THR A 479    -43.250  31.743   7.413  1.00 18.76      N
ATOM  7290  CA  THR A 479    -43.358  30.808   6.294  1.00 18.45      C
ATOM  7292  CB  THR A 479    -43.503  29.339   6.774  1.00 18.26      C
ATOM  7294  OG1 THR A 479    -42.334  28.955   7.494  1.00 17.30      O
ATOM  7296  CG2 THR A 479    -43.669  28.394   5.592  1.00 17.93      C
ATOM  7300  C   THR A 479    -44.504  31.173   5.314  1.00 18.39      C
ATOM  7301  O   THR A 479    -44.280  31.200   4.103  1.00 18.58      O
ATOM  7303  N   TRP A 480    -45.709  31.457   5.818  1.00 17.85      N
ATOM  7304  CA  TRP A 480    -46.801  31.909   4.942  1.00 17.44      C
ATOM  7306  CB  TRP A 480    -48.086  32.225   5.728  1.00 17.67      C
ATOM  7309  CG  TRP A 480    -48.969  31.042   5.888  1.00 17.09      C
ATOM  7310  CD1 TRP A 480    -48.996  30.195   6.936  1.00 16.76      C
ATOM  7312  NE1 TRP A 480    -49.914  29.216   6.724  1.00 17.08      N
ATOM  7314  CE2 TRP A 480    -50.501  29.410   5.507  1.00 17.86      C
ATOM  7315  CD2 TRP A 480    -49.930  30.559   4.954  1.00 17.15      C
ATOM  7316  CE3 TRP A 480    -50.356  30.980   3.696  1.00 18.31      C
ATOM  7318  CZ3 TRP A 480    -51.337  30.244   3.039  1.00 19.10      C
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ATOM  7320 CH2 TRP A 480    -51.897  29.107   3.622  1.00 18.83      C
ATOM  7322 CZ2 TRP A 480    -51.493  28.673   4.855  1.00 18.86      C
ATOM  7324 C   TRP A 480    -46.426  33.124   4.097  1.00 17.10      C
ATOM  7325 O   TRP A 480    -46.824  33.215   2.943  1.00 17.22      O
ATOM  7327 N   LYS A 481    -45.675  34.062   4.659  1.00 16.60      N
ATOM  7328 CA  LYS A 481    -45.275  35.215   3.886  1.00 16.23      C
ATOM  7330 CB  LYS A 481    -44.566  36.243   4.747  1.00 16.42      C
ATOM  7333 CG  LYS A 481    -45.417  36.954   5.769  1.00 16.42      C
ATOM  7336 CD  LYS A 481    -44.555  37.979   6.505  1.00 16.40      C
ATOM  7339 CE  LYS A 481    -45.199  38.504   7.782  1.00 16.66      C
ATOM  7342 NZ  LYS A 481    -44.184  38.717   8.846  1.00 16.72      N
ATOM  7346 C   LYS A 481    -44.357  34.782   2.767  1.00 15.94      C
ATOM  7347 O   LYS A 481    -44.451  35.291   1.674  1.00 16.09      O
ATOM  7349 N   LYS A 482    -43.461  33.849   3.034  1.00 15.98      N
ATOM  7350 CA  LYS A 482    -42.559  33.369   1.996  1.00 16.30      C
ATOM  7352 CB  LYS A 482    -41.409  32.563   2.594  1.00 16.51      C
ATOM  7355 CG  LYS A 482    -40.354  33.445   3.286  1.00 17.46      C
ATOM  7358 CD  LYS A 482    -39.486  32.647   4.241  1.00 18.48      C
ATOM  7361 CE  LYS A 482    -38.625  33.548   5.096  1.00 18.94      C
ATOM  7364 NZ  LYS A 482    -37.865  32.773   6.129  1.00 20.40      N
ATOM  7368 C   LYS A 482    -43.296  32.561    .938  1.00 16.40      C
ATOM  7369 O   LYS A 482    -42.941  32.614   -.229  1.00 16.85      O
ATOM  7371 N   MET A 483    -44.328  31.824   1.332  1.00 16.57      N
ATOM  7372 CA  MET A 483    -45.149  31.100    .366  1.00 16.67      C
ATOM  7374 CB  MET A 483    -46.128  30.156   1.057  1.00 16.55      C
ATOM  7377 CG  MET A 483    -45.496  28.923   1.675  1.00 16.50      C
ATOM  7380 SD  MET A 483    -46.715  27.684   2.194  1.00 17.39      S
ATOM  7381 CE  MET A 483    -47.937  28.704   3.025  1.00 17.27      C
ATOM  7385 C   MET A 483    -45.928  32.069   -.495  1.00 17.06      C
ATOM  7386 O   MET A 483    -46.027  31.867  -1.688  1.00 17.17      O
ATOM  7388 N   ASN A 484    -46.483  33.110    .118  1.00 17.72      N
ATOM  7389 CA  ASN A 484    -47.305  34.093   -.587  1.00 18.35      C
ATOM  7391 CB  ASN A 484    -47.861  35.129    .397  1.00 18.26      C
ATOM  7394 CG  ASN A 484    -48.994  34.601   1.248  1.00 17.35      C
ATOM  7395 OD1 ASN A 484    -49.597  33.577    .934  1.00 17.54      O
ATOM  7396 ND2 ASN A 484    -49.304  35.317   2.331  1.00 14.10      N
ATOM  7399 C   ASN A 484    -46.541  34.839  -1.677  1.00 19.51      C
ATOM  7400 O   ASN A 484    -47.123  35.250  -2.685  1.00 19.49      O
ATOM  7402 N   LYS A 485    -45.243  35.035  -1.463  1.00 20.86      N
ATOM  7403 CA  LYS A 485    -44.394  35.681  -2.456  1.00 22.12      C
ATOM  7405 CB  LYS A 485    -43.070  36.092  -1.823  1.00 22.08      C
ATOM  7408 CG  LYS A 485    -42.229  37.060  -2.641  1.00 23.09      C
ATOM  7411 CD  LYS A 485    -40.783  37.072  -2.109  1.00 25.38      C
ATOM  7414 CE  LYS A 485    -40.098  38.460  -2.135  1.00 26.12      C
ATOM  7417 NZ  LYS A 485    -38.943  38.555  -3.086  1.00 26.61      N
ATOM  7421 C   LYS A 485    -44.164  34.743  -3.656  1.00 23.36      C
ATOM  7422 O   LYS A 485    -44.120  35.191  -4.802  1.00 23.00      O
ATOM  7424 N   GLU A 486    -44.027  33.442  -3.400  1.00 24.99      N
ATOM  7425 CA  GLU A 486    -43.902  32.479  -4.491  1.00 26.35      C
ATOM  7427 CB  GLU A 486    -43.627  31.061  -3.978  1.00 26.55      C
ATOM  7430 CG  GLU A 486    -42.985  30.130  -5.033  1.00 28.29      C
ATOM  7433 CD  GLU A 486    -41.466  30.324  -5.191  1.00 31.11      C
ATOM  7434 OE1 GLU A 486    -40.981  30.466  -6.341  1.00 32.07      O
ATOM  7435 OE2 GLU A 486    -40.744  30.335  -4.159  1.00 33.04      O
ATOM  7436 C   GLU A 486    -45.157  32.501  -5.362  1.00 27.13      C
ATOM  7437 O   GLU A 486    -45.064  32.618  -6.583  1.00 27.57      O
ATOM  7439 N   LYS A 487    -46.325  32.422  -4.739  1.00 28.12      N
ATOM  7440 CA  LYS A 487    -47.582  32.378  -5.485  1.00 29.12      C
ATOM  7442 CB  LYS A 487    -48.788  32.260  -4.542  1.00 29.21      C
ATOM  7445 CG  LYS A 487    -50.167  32.296  -5.235  1.00 28.57      C
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ATOM 7448 CD LYS A 487 -50.403 31.040 -6.036 1.00 27.91 C
ATOM 7451 CE LYS A 487 -51.615 31.141 -6.936 1.00 28.38 C
ATOM 7454 NZ LYS A 487 -52.874 31.460 -6.211 1.00 28.03 N
ATOM 7458 C LYS A 487 -47.756 33.603 -6.352 1.00 30.18 C
ATOM 7459 O LYS A 487 -48.308 33.514 -7.446 1.00 30.21 O
ATOM 7461 N LEU A 488 -47.295 34.743 -5.844 1.00 31.64 N
ATOM 7462 CA LEU A 488 -47.422 36.026 -6.532 1.00 32.65 C
ATOM 7464 CB LEU A 488 -47.426 37.144 -5.494 1.00 32.43 C
ATOM 7467 CG LEU A 488 -48.091 38.446 -5.907 1.00 32.50 C
ATOM 7469 CD1 LEU A 488 -49.593 38.288 -5.943 1.00 32.66 C
ATOM 7473 CD2 LEU A 488 -47.707 39.554 -4.943 1.00 33.38 C
ATOM 7477 C LEU A 488 -46.286 36.242 -7.542 1.00 33.99 C
ATOM 7478 O LEU A 488 -46.536 36.539 -8.705 1.00 33.72 O
ATOM 7480 N GLY A 489 -45.046 36.045 -7.091 1.00 35.85 N
ATOM 7481 CA GLY A 489 -43.845 36.361 -7.874 1.00 37.37 C
ATOM 7484 C GLY A 489 -43.278 35.221 -8.709 1.00 38.76 C
ATOM 7485 O GLY A 489 -42.414 34.467 -8.250 1.00 39.06 O
ATOM 7487 N GLY A 490 -43.760 35.119 -9.947 1.00 40.26 N
ATOM 7488 CA GLY A 490 -43.285 34.130 -10.927 1.00 41.03 C
ATOM 7491 C GLY A 490 -42.193 33.194 -10.436 1.00 41.61 C
ATOM 7492 O GLY A 490 -41.010 33.547 -10.423 1.00 41.62 O
ATOM 7494 N SER A 491 -42.590 31.996 -10.023 1.00 42.17 N
ATOM 7495 CA SER A 491 -41.619 30.962 -9.662 1.00 42.54 C
ATOM 7497 CB SER A 491 -42.279 29.909 -8.741 1.00 42.63 C
ATOM 7500 OG SER A 491 -43.451 29.345 -9.294 1.00 42.44 O
ATOM 7502 C SER A 491 -41.032 30.349 -10.952 1.00 42.50 C
ATOM 7503 O SER A 491 -41.117 30.961 -12.030 1.00 42.57 O
ATOM 7505 N LEU A 492 -40.405 29.177 -10.843 1.00 42.18 N
ATOM 7506 CA LEU A 492 -40.185 28.333 -12.021 1.00 41.96 C
ATOM 7508 CB LEU A 492 -39.110 27.270 -11.782 1.00 42.39 C
ATOM 7511 CG LEU A 492 -37.695 27.671 -11.353 1.00 44.21 C
ATOM 7513 CD1 LEU A 492 -36.783 26.438 -11.498 1.00 45.26 C
ATOM 7517 CD2 LEU A 492 -37.120 28.896 -12.129 1.00 45.51 C
ATOM 7521 C LEU A 492 -41.479 27.610 -12.356 1.00 40.88 C
ATOM 7522 O LEU A 492 -41.713 27.244 -13.504 1.00 40.78 O
ATOM 7524 N PHE A 493 -42.308 27.409 -11.339 1.00 39.61 N
ATOM 7525 CA PHE A 493 -43.500 26.595 -11.460 1.00 38.85 C
ATOM 7527 CB PHE A 493 -43.783 25.911 -10.124 1.00 38.62 C
ATOM 7530 CG PHE A 493 -42.725 24.937 -9.713 1.00 37.16 C
ATOM 7531 CD1 PHE A 493 -42.901 23.587 -9.916 1.00 35.26 C
ATOM 7533 CE1 PHE A 493 -41.934 22.698 -9.546 1.00 34.86 C
ATOM 7535 CZ PHE A 493 -40.769 23.143 -8.966 1.00 35.09 C
ATOM 7537 CE2 PHE A 493 -40.574 24.482 -8.759 1.00 35.45 C
ATOM 7539 CD2 PHE A 493 -41.549 25.374 -9.130 1.00 36.36 C
ATOM 7541 C PHE A 493 -44.714 27.412 -11.890 1.00 38.62 C
ATOM 7542 O PHE A 493 -44.756 28.621 -11.702 1.00 38.86 O
ATOM 7544 N ALA A 494 -45.698 26.731 -12.469 1.00 38.32 N
ATOM 7545 CA ALA A 494 -46.977 27.337 -12.843 1.00 38.09 C
ATOM 7547 CB ALA A 494 -47.658 26.486 -13.906 1.00 38.17 C
ATOM 7551 C ALA A 494 -47.891 27.479 -11.623 1.00 37.76 C
ATOM 7552 O ALA A 494 -48.039 26.541 -10.845 1.00 38.15 O
ATOM 7554 N LYS A 495 -48.541 28.629 -11.484 1.00 37.15 N
ATOM 7555 CA LYS A 495 -49.321 28.947 -10.270 1.00 36.53 C
ATOM 7557 CB LYS A 495 -50.116 30.258 -10.477 1.00 36.90 C
ATOM 7560 CG LYS A 495 -49.235 31.524 -10.582 1.00 37.72 C
ATOM 7563 CD LYS A 495 -50.061 32.826 -10.585 1.00 38.87 C
ATOM 7566 CE LYS A 495 -49.140 34.065 -10.665 1.00 39.78 C
ATOM 7569 NZ LYS A 495 -49.786 35.369 -10.282 1.00 39.78 N
ATOM 7573 C LYS A 495 -50.238 27.809 -9.724 1.00 35.25 C
ATOM 7574 O LYS A 495 -50.261 27.563 -8.523 1.00 34.91 O

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ATOM   7576  N   PRO A 496     -50.978  27.107 -10.599  1.00 33.76           N
ATOM   7577  CA  PRO A 496     -51.846  26.015 -10.162  1.00 32.74           C
ATOM   7579  CB  PRO A 496     -52.222  25.340 -11.474  1.00 32.99           C
ATOM   7582  CG  PRO A 496     -52.337  26.470 -12.385  1.00 33.75           C
ATOM   7585  CD  PRO A 496     -51.196  27.400 -12.022  1.00 33.83           C
ATOM   7588  C   PRO A 496     -51.194  24.998  -9.267  1.00 31.24           C
ATOM   7589  O   PRO A 496     -51.822  24.522  -8.331  1.00 31.54           O
ATOM   7590  N   PHE A 497     -49.954  24.642  -9.566  1.00 29.40           N
ATOM   7591  CA  PHE A 497     -49.229  23.726  -8.708  1.00 27.76           C
ATOM   7593  CB  PHE A 497     -48.162  22.948  -9.474  1.00 27.62           C
ATOM   7596  CG  PHE A 497     -47.351  22.040  -8.597  1.00 26.33           C
ATOM   7597  CD1 PHE A 497     -47.944  20.969  -7.974  1.00 24.96           C
ATOM   7599  CE1 PHE A 497     -47.218  20.151  -7.156  1.00 25.04           C
ATOM   7601  CZ  PHE A 497     -45.875  20.396  -6.940  1.00 24.79           C
ATOM   7603  CE2 PHE A 497     -45.274  21.457  -7.549  1.00 24.73           C
ATOM   7605  CD2 PHE A 497     -46.010  22.282  -8.366  1.00 25.48           C
ATOM   7607  C   PHE A 497     -48.592  24.407  -7.494  1.00 26.59           C
ATOM   7608  O   PHE A 497     -48.361  23.738  -6.500  1.00 26.77           O
ATOM   7610  N   VAL A 498     -48.291  25.704  -7.535  1.00 24.83           N
ATOM   7611  CA  VAL A 498     -47.869  26.338  -6.289  1.00 23.86           C
ATOM   7613  CB  VAL A 498     -47.181  27.722  -6.455  1.00 23.47           C
ATOM   7615  CG1 VAL A 498     -48.163  28.755  -6.759  1.00 24.57           C
ATOM   7619  CG2 VAL A 498     -46.151  27.690  -7.551  1.00 23.54           C
ATOM   7623  C   VAL A 498     -49.094  26.396  -5.355  1.00 22.97           C
ATOM   7624  O   VAL A 498     -48.978  26.130  -4.161  1.00 23.39           O
ATOM   7626  N   GLU A 499     -50.268  26.687  -5.903  1.00 21.68           N
ATOM   7627  CA  GLU A 499     -51.473  26.719  -5.106  1.00 20.84           C
ATOM   7629  CB  GLU A 499     -52.677  27.136  -5.930  1.00 20.99           C
ATOM   7632  CG  GLU A 499     -53.957  27.352  -5.099  1.00 21.25           C
ATOM   7635  CD  GLU A 499     -53.930  28.630  -4.265  1.00 21.77           C
ATOM   7636  OE1 GLU A 499     -52.982  29.448  -4.383  1.00 20.74           O
ATOM   7637  OE2 GLU A 499     -54.876  28.812  -3.476  1.00 22.76           O
ATOM   7638  C   GLU A 499     -51.766  25.371  -4.497  1.00 20.35           C
ATOM   7639  O   GLU A 499     -52.137  25.308  -3.318  1.00 20.78           O
ATOM   7641  N   THR A 500     -51.629  24.286  -5.264  1.00 19.40           N
ATOM   7642  CA  THR A 500     -51.894  22.970  -4.667  1.00 18.94           C
ATOM   7644  CB  THR A 500     -51.993  21.782  -5.683  1.00 18.96           C
ATOM   7646  OG1 THR A 500     -50.708  21.475  -6.202  1.00 19.44           O
ATOM   7648  CG2 THR A 500     -52.991  22.071  -6.835  1.00 18.75           C
ATOM   7652  C   THR A 500     -50.895  22.674  -3.526  1.00 18.20           C
ATOM   7653  O   THR A 500     -51.280  22.100  -2.519  1.00 17.68           O
ATOM   7655  N   ALA A 501     -49.646  23.119  -3.666  1.00 17.49           N
ATOM   7656  CA  ALA A 501     -48.663  23.021  -2.593  1.00 17.18           C
ATOM   7658  CB  ALA A 501     -47.348  23.563  -3.051  1.00 16.98           C
ATOM   7662  C   ALA A 501     -49.120  23.770  -1.338  1.00 17.38           C
ATOM   7663  O   ALA A 501     -49.098  23.219   -.230  1.00 17.45           O
ATOM   7665  N   ILE A 502     -49.517  25.031  -1.508  1.00 17.29           N
ATOM   7666  CA  ILE A 502     -49.971  25.857   -.386  1.00 17.07           C
ATOM   7668  CB  ILE A 502     -50.353  27.304   -.846  1.00 17.09           C
ATOM   7670  CG1 ILE A 502     -49.092  28.069  -1.286  1.00 17.17           C
ATOM   7673  CD1 ILE A 502     -49.345  29.345  -2.116  1.00 16.25           C
ATOM   7677  CG2 ILE A 502     -51.110  28.076   .265  1.00 16.14           C
ATOM   7681  C   ILE A 502     -51.155  25.168   .285  1.00 17.24           C
ATOM   7682  O   ILE A 502     -51.265  25.163  1.516  1.00 17.03           O
ATOM   7684  N   ASN A 503     -52.022  24.559   -.522  1.00 17.32           N
ATOM   7685  CA  ASN A 503     -53.167  23.823   .022  1.00 17.75           C
ATOM   7687  CB  ASN A 503     -53.986  23.221  -1.121  1.00 17.70           C
ATOM   7690  CG  ASN A 503     -54.760  24.261  -1.888  1.00 18.41           C
ATOM   7691  OD1 ASN A 503     -55.058  25.334  -1.382  1.00 18.94           O
ATOM   7692  ND2 ASN A 503     -55.107  23.939  -3.119  1.00 20.42           N
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ATOM  7695  C   ASN A 503    -52.803  22.727   1.075  1.00 17.74      C
ATOM  7696  O   ASN A 503    -53.619  22.387   1.949  1.00 17.96      O
ATOM  7698  N   LEU A 504    -51.589  22.185   .993  1.00 17.23      N
ATOM  7699  CA  LEU A 504    -51.105  21.249   1.994  1.00 17.10      C
ATOM  7701  CB  LEU A 504    -49.745  20.686   1.583  1.00 17.28      C
ATOM  7704  CG  LEU A 504    -49.213  19.528   2.426  1.00 17.29      C
ATOM  7706  CD1 LEU A 504    -49.570  18.196   1.762  1.00 17.22      C
ATOM  7710  CD2 LEU A 504    -47.708  19.686   2.616  1.00 16.83      C
ATOM  7714  C   LEU A 504    -50.971  21.939   3.347  1.00 16.97      C
ATOM  7715  O   LEU A 504    -51.237  21.330   4.379  1.00 16.84      O
ATOM  7717  N   ALA A 505    -50.535  23.201   3.330  1.00 16.90      N
ATOM  7718  CA  ALA A 505    -50.433  24.015   4.540  1.00 16.68      C
ATOM  7720  CB  ALA A 505    -49.739  25.309   4.243  1.00 16.54      C
ATOM  7724  C   ALA A 505    -51.826  24.281   5.074  1.00 16.77      C
ATOM  7725  O   ALA A 505    -52.087  24.123   6.266  1.00 16.80      O
ATOM  7727  N   ARG A 506    -52.726  24.664   4.172  1.00 16.82      N
ATOM  7728  CA  ARG A 506    -54.128  24.875   4.521  1.00 16.84      C
ATOM  7730  CB  ARG A 506    -54.944  25.274   3.286  1.00 16.86      C
ATOM  7733  CG  ARG A 506    -54.649  26.661   2.795  1.00 16.27      C
ATOM  7736  CD  ARG A 506    -55.586  27.090   1.726  1.00 15.26      C
ATOM  7739  NE  ARG A 506    -55.240  28.436   1.273  1.00 15.31      N
ATOM  7741  CZ  ARG A 506    -54.744  28.758   .082  1.00 14.28      C
ATOM  7742  NH1 ARG A 506    -54.519  27.856   -.856  1.00 14.12      N
ATOM  7745  NH2 ARG A 506    -54.471  30.018   -.176  1.00 15.94      N
ATOM  7748  C   ARG A 506    -54.732  23.631   5.122  1.00 16.96      C
ATOM  7749  O   ARG A 506    -55.480  23.707   6.089  1.00 16.71      O
ATOM  7751  N   GLN A 507    -54.415  22.481   4.542  1.00 17.37      N
ATOM  7752  CA  GLN A 507    -54.962  21.233   5.048  1.00 17.87      C
ATOM  7754  CB  GLN A 507    -54.712  20.075   4.087  1.00 17.80      C
ATOM  7757  CG  GLN A 507    -55.293  18.740   4.571  1.00 17.24      C
ATOM  7760  CD  GLN A 507    -56.777  18.805   4.860  1.00 16.23      C
ATOM  7761  OE1 GLN A 507    -57.506  19.585   4.250  1.00 16.66      O
ATOM  7762  NE2 GLN A 507    -57.233  17.980   5.790  1.00 14.96      N
ATOM  7765  C   GLN A 507    -54.401  20.890   6.423  1.00 18.28      C
ATOM  7766  O   GLN A 507    -55.148  20.419   7.287  1.00 18.53      O
ATOM  7768  N   SER A 508    -53.096  21.113   6.609  1.00 18.50      N
ATOM  7769  CA  SER A 508    -52.435  20.924   7.908  1.00 18.54      C
ATOM  7771  CB  SER A 508    -50.979  21.385   7.856  1.00 18.40      C
ATOM  7774  OG  SER A 508    -50.259  20.694   6.857  1.00 18.51      O
ATOM  7776  C   SER A 508    -53.147  21.752   8.942  1.00 18.78      C
ATOM  7777  O   SER A 508    -53.535  21.278  10.006  1.00 18.33      O
ATOM  7779  N   HIS A 509    -53.324  23.014   8.599  1.00 19.37      N
ATOM  7780  CA  HIS A 509    -54.014  23.922   9.466  1.00 19.92      C
ATOM  7782  CB  HIS A 509    -54.126  25.295   8.818  1.00 20.07      C
ATOM  7785  CG  HIS A 509    -53.000  26.188   9.174  1.00 19.82      C
ATOM  7786  ND1 HIS A 509    -52.079  26.631   8.255  1.00 19.73      N
ATOM  7788  CE1 HIS A 509    -51.187  27.383   8.866  1.00 20.25      C
ATOM  7790  NE2 HIS A 509    -51.485  27.426  10.149  1.00 21.66      N
ATOM  7792  CD2 HIS A 509    -52.615  26.682  10.368  1.00 20.98      C
ATOM  7794  C   HIS A 509    -55.389  23.448   9.839  1.00 20.41      C
ATOM  7795  O   HIS A 509    -55.821  23.694  10.934  1.00 20.22      O
ATOM  7797  N   CYS A 510    -56.093  22.808   8.918  1.00 21.33      N
ATOM  7798  CA  CYS A 510    -57.470  22.396   9.189  1.00 22.03      C
ATOM  7800  CB  CYS A 510    -58.278  22.383   7.894  1.00 21.90      C
ATOM  7803  SG  CYS A 510    -58.522  24.055   7.270  1.00 21.93      S
ATOM  7805  C   CYS A 510    -57.527  21.054   9.908  1.00 22.60      C
ATOM  7806  O   CYS A 510    -58.423  20.822  10.706  1.00 22.23      O
ATOM  7808  N   THR A 511    -56.553  20.194   9.627  1.00 23.67      N
ATOM  7809  CA  THR A 511    -56.421  18.920  10.305  1.00 24.81      C
ATOM  7811  CB  THR A 511    -55.437  18.000   9.565  1.00 24.70      C
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ATOM  7813 OG1 THR A 511    -56.071  17.485   8.394  1.00 24.45       O
ATOM  7815 CG2 THR A 511    -55.003  16.844  10.448  1.00 24.23       C
ATOM  7819 C   THR A 511    -55.965  19.086  11.756  1.00 26.22       C
ATOM  7820 O   THR A 511    -56.685  18.717  12.679  1.00 26.12       O
ATOM  7822 N   TYR A 512    -54.775  19.643  11.959  1.00 28.08       N
ATOM  7823 CA  TYR A 512    -54.177  19.657  13.298  1.00 29.63       C
ATOM  7825 CB  TYR A 512    -52.663  19.783  13.238  1.00 29.67       C
ATOM  7828 CG  TYR A 512    -52.117  18.579  12.560  1.00 29.56       C
ATOM  7829 CD1 TYR A 512    -51.965  17.395  13.246  1.00 29.66       C
ATOM  7831 CE1 TYR A 512    -51.507  16.273  12.614  1.00 30.94       C
ATOM  7833 CZ  TYR A 512    -51.217  16.326  11.263  1.00 32.04       C
ATOM  7834 OH  TYR A 512    -50.757  15.209  10.608  1.00 33.78       O
ATOM  7836 CE2 TYR A 512    -51.390  17.492  10.557  1.00 31.29       C
ATOM  7838 CD2 TYR A 512    -51.847  18.600  11.205  1.00 30.53       C
ATOM  7840 C   TYR A 512    -54.812  20.676  14.206  1.00 31.11       C
ATOM  7841 O   TYR A 512    -55.494  20.277  15.139  1.00 31.34       O
ATOM  7843 N   HIS A 513    -54.583  21.969  13.966  1.00 32.89       N
ATOM  7844 CA  HIS A 513    -55.505  23.023  14.442  1.00 34.48       C
ATOM  7846 CB  HIS A 513    -56.372  23.461  13.225  1.00 35.13       C
ATOM  7849 CG  HIS A 513    -57.704  24.108  13.529  1.00 37.10       C
ATOM  7850 ND1 HIS A 513    -58.265  25.040  12.678  1.00 38.69       N
ATOM  7852 CE1 HIS A 513    -59.442  25.416  13.151  1.00 39.23       C
ATOM  7854 NE2 HIS A 513    -59.678  24.751  14.268  1.00 38.18       N
ATOM  7856 CD2 HIS A 513    -58.615  23.915  14.519  1.00 38.17       C
ATOM  7858 C   HIS A 513    -56.337  22.503  15.610  1.00 35.00       C
ATOM  7859 O   HIS A 513    -56.302  23.074  16.712  1.00 35.48       O
ATOM  7861 N   ASN A 514    -57.079  21.419  15.351  1.00 35.23       N
ATOM  7862 CA  ASN A 514    -57.934  20.768  16.347  1.00 35.46       C
ATOM  7864 CB  ASN A 514    -58.342  19.343  15.903  1.00 35.39       C
ATOM  7867 CG  ASN A 514    -59.383  19.345  14.786  1.00 34.01       C
ATOM  7868 OD1 ASN A 514    -59.336  20.185  13.896  1.00 33.36       O
ATOM  7869 ND2 ASN A 514    -60.315  18.406  14.833  1.00 31.13       N
ATOM  7872 C   ASN A 514    -57.464  20.751  17.818  1.00 36.15       C
ATOM  7873 O   ASN A 514    -56.397  20.211  18.153  1.00 36.13       O
ATOM  7875 N   GLY A 515    -58.277  21.430  18.640  1.00 36.95       N
ATOM  7876 CA  GLY A 515    -58.427  21.235  20.079  1.00 37.43       C
ATOM  7879 C   GLY A 515    -59.724  20.470  20.381  1.00 38.18       C
ATOM  7880 O   GLY A 515    -59.636  19.418  21.021  1.00 38.57       O
ATOM  7882 N   ASP A 516    -60.930  20.921  19.969  1.00 38.73       N
ATOM  7883 CA  ASP A 516    -61.249  22.194  19.293  1.00 39.26       C
ATOM  7885 CB  ASP A 516    -61.607  21.904  17.845  1.00 39.51       C
ATOM  7888 CG  ASP A 516    -60.523  22.291  16.894  1.00 42.32       C
ATOM  7889 OD1 ASP A 516    -59.613  23.084  17.286  1.00 45.56       O
ATOM  7890 OD2 ASP A 516    -60.578  21.797  15.740  1.00 45.52       O
ATOM  7891 C   ASP A 516    -62.466  22.913  19.884  1.00 39.38       C
ATOM  7892 O   ASP A 516    -63.032  22.454  20.880  1.00 39.74       O
ATOM  7894 N   ALA A 517    -62.850  24.038  19.259  1.00 39.40       N
ATOM  7895 CA  ALA A 517    -64.140  24.752  19.481  1.00 39.50       C
ATOM  7897 CB  ALA A 517    -65.117  24.403  18.333  1.00 39.27       C
ATOM  7901 C   ALA A 517    -64.837  24.566  20.863  1.00 39.90       C
ATOM  7902 O   ALA A 517    -64.173  24.428  21.899  1.00 39.89       O
ATOM  7904 N   HIS A 518    -66.175  24.617  20.876  1.00 40.33       N
ATOM  7905 CA  HIS A 518    -66.973  24.112  22.016  1.00 40.73       C
ATOM  7907 CB  HIS A 518    -68.091  25.092  22.396  1.00 41.22       C
ATOM  7910 CG  HIS A 518    -67.578  26.419  22.866  1.00 43.58       C
ATOM  7911 ND1 HIS A 518    -67.426  26.725  24.207  1.00 45.88       N
ATOM  7913 CE1 HIS A 518    -66.938  27.950  24.320  1.00 46.42       C
ATOM  7915 NE2 HIS A 518    -66.760  28.446  23.102  1.00 46.25       N
ATOM  7917 CD2 HIS A 518    -67.145  27.506  22.174  1.00 45.24       C
ATOM  7919 C   HIS A 518    -67.526  22.725  21.655  1.00 40.17       C
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ATOM 7920 O HIS A 518 -68.738 22.501 21.571 1.00 40.02 O
ATOM 7922 N THR A 519 -66.581 21.812 21.448 1.00 39.64 N
ATOM 7923 CA THR A 519 -66.808 20.466 20.918 1.00 39.16 C
ATOM 7925 CB THR A 519 -67.414 20.469 19.453 1.00 39.16 C
ATOM 7927 OG1 THR A 519 -66.847 21.529 18.665 1.00 39.04 O
ATOM 7929 CG2 THR A 519 -68.942 20.633 19.480 1.00 38.82 C
ATOM 7933 C THR A 519 -65.428 19.771 20.978 1.00 38.85 C
ATOM 7934 O THR A 519 -64.391 20.433 20.878 1.00 38.66 O
ATOM 7936 N SER A 520 -65.407 18.455 21.170 1.00 38.37 N
ATOM 7937 CA SER A 520 -64.160 17.745 21.500 1.00 38.08 C
ATOM 7939 CB SER A 520 -64.514 16.320 21.931 1.00 38.06 C
ATOM 7942 OG SER A 520 -64.560 15.475 20.805 1.00 38.66 O
ATOM 7944 C SER A 520 -63.136 17.771 20.327 1.00 37.86 C
ATOM 7945 O SER A 520 -63.420 18.369 19.289 1.00 37.50 O
ATOM 7947 N PRO A 521 -61.948 17.122 20.482 1.00 37.98 N
ATOM 7948 CA PRO A 521 -60.944 17.170 19.379 1.00 37.92 C
ATOM 7950 CB PRO A 521 -59.674 16.527 19.987 1.00 37.87 C
ATOM 7953 CG PRO A 521 -60.091 15.919 21.330 1.00 38.28 C
ATOM 7956 CD PRO A 521 -61.577 16.137 21.526 1.00 38.13 C
ATOM 7959 C PRO A 521 -61.432 16.446 18.110 1.00 37.96 C
ATOM 7960 O PRO A 521 -61.769 17.118 17.140 1.00 38.09 O
ATOM 7961 N ASP A 522 -61.483 15.108 18.107 1.00 38.07 N
ATOM 7962 CA ASP A 522 -62.351 14.393 17.161 1.00 38.14 C
ATOM 7964 CB ASP A 522 -62.132 12.877 17.204 1.00 38.31 C
ATOM 7967 CG ASP A 522 -60.769 12.456 16.640 1.00 39.45 C
ATOM 7968 OD1 ASP A 522 -60.160 13.200 15.827 1.00 39.72 O
ATOM 7969 OD2 ASP A 522 -60.302 11.361 17.025 1.00 41.59 O
ATOM 7970 C ASP A 522 -63.760 14.780 17.591 1.00 37.92 C
ATOM 7971 O ASP A 522 -63.908 15.608 18.474 1.00 38.01 O
ATOM 7973 N GLU A 523 -64.799 14.239 16.974 1.00 37.79 N
ATOM 7974 CA GLU A 523 -66.150 14.818 17.121 1.00 37.83 C
ATOM 7976 CB GLU A 523 -66.618 14.919 18.591 1.00 37.85 C
ATOM 7979 CG GLU A 523 -66.346 13.678 19.483 1.00 39.40 C
ATOM 7982 CD GLU A 523 -66.916 13.802 20.931 1.00 41.49 C
ATOM 7983 OE1 GLU A 523 -67.714 14.737 21.207 1.00 42.81 O
ATOM 7984 OE2 GLU A 523 -66.566 12.957 21.800 1.00 42.04 O
ATOM 7985 C GLU A 523 -66.242 16.203 16.430 1.00 37.51 C
ATOM 7986 O GLU A 523 -67.338 16.751 16.283 1.00 37.70 O
ATOM 7988 N LEU A 524 -65.097 16.775 16.043 1.00 37.03 N
ATOM 7989 CA LEU A 524 -65.044 17.863 15.067 1.00 36.58 C
ATOM 7991 CB LEU A 524 -64.174 19.022 15.559 1.00 36.56 C
ATOM 7994 CG LEU A 524 -63.963 20.225 14.624 1.00 36.35 C
ATOM 7996 CD1 LEU A 524 -63.400 21.376 15.418 1.00 35.74 C
ATOM 8000 CD2 LEU A 524 -65.242 20.681 13.910 1.00 36.53 C
ATOM 8004 C LEU A 524 -64.478 17.287 13.782 1.00 36.20 C
ATOM 8005 O LEU A 524 -65.106 17.363 12.733 1.00 36.14 O
ATOM 8007 N THR A 525 -63.298 16.686 13.869 1.00 35.83 N
ATOM 8008 CA THR A 525 -62.756 15.935 12.748 1.00 35.66 C
ATOM 8010 CB THR A 525 -61.585 15.015 13.173 1.00 35.48 C
ATOM 8012 OG1 THR A 525 -60.776 15.678 14.152 1.00 35.55 O
ATOM 8014 CG2 THR A 525 -60.720 14.641 11.978 1.00 34.73 C
ATOM 8018 C THR A 525 -63.875 15.098 12.123 1.00 35.89 C
ATOM 8019 O THR A 525 -64.040 15.095 10.909 1.00 35.98 O
ATOM 8021 N ARG A 526 -64.667 14.420 12.954 1.00 36.06 N
ATOM 8022 CA ARG A 526 -65.739 13.574 12.448 1.00 36.18 C
ATOM 8024 CB ARG A 526 -66.340 12.718 13.555 1.00 36.56 C
ATOM 8027 CG ARG A 526 -67.416 11.754 13.054 1.00 38.35 C
ATOM 8030 CD ARG A 526 -67.781 10.702 14.092 1.00 41.00 C
ATOM 8033 NE ARG A 526 -67.740 11.207 15.470 1.00 43.08 N
ATOM 8035 CZ ARG A 526 -68.637 12.033 16.024 1.00 44.51 C

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ATOM  8036 NH1 ARG A 526    -69.681  12.500  15.336  1.00 44.46           N
ATOM  8039 NH2 ARG A 526    -68.476  12.406  17.288  1.00 45.02           N
ATOM  8042 C   ARG A 526    -66.834  14.384  11.774  1.00 35.68           C
ATOM  8043 O   ARG A 526    -67.253  14.035  10.675  1.00 35.84           O
ATOM  8045 N   LYS A 527    -67.309  15.447  12.424  1.00 35.06           N
ATOM  8046 CA  LYS A 527    -68.285  16.343  11.780  1.00 34.61           C
ATOM  8048 CB  LYS A 527    -68.680  17.528  12.683  1.00 34.74           C
ATOM  8051 CG  LYS A 527    -69.818  17.225  13.651  1.00 35.40           C
ATOM  8054 CD  LYS A 527    -70.301  18.452  14.441  1.00 35.99           C
ATOM  8057 CE  LYS A 527    -71.280  18.021  15.556  1.00 36.42           C
ATOM  8060 NZ  LYS A 527    -71.652  19.095  16.530  1.00 36.31           N
ATOM  8064 C   LYS A 527    -67.723  16.860  10.457  1.00 33.77           C
ATOM  8065 O   LYS A 527    -68.377  16.763   9.423  1.00 33.75           O
ATOM  8067 N   ARG A 528    -66.501  17.388  10.499  1.00 32.71           N
ATOM  8068 CA  ARG A 528    -65.840  17.929   9.310  1.00 31.79           C
ATOM  8070 CB  ARG A 528    -64.425  18.464   9.644  1.00 31.74           C
ATOM  8073 CG  ARG A 528    -64.419  19.844  10.330  1.00 30.90           C
ATOM  8076 CD  ARG A 528    -63.021  20.439  10.527  1.00 29.75           C
ATOM  8079 NE  ARG A 528    -63.098  21.745  11.190  1.00 29.55           N
ATOM  8081 CZ  ARG A 528    -62.056  22.513  11.528  1.00 29.96           C
ATOM  8082 NH1 ARG A 528    -60.801  22.145  11.284  1.00 29.74           N
ATOM  8085 NH2 ARG A 528    -62.269  23.677  12.130  1.00 30.71           N
ATOM  8088 C   ARG A 528    -65.796  16.904   8.172  1.00 30.99           C
ATOM  8089 O   ARG A 528    -66.226  17.206   7.068  1.00 30.97           O
ATOM  8091 N   VAL A 529    -65.313  15.694   8.450  1.00 30.12           N
ATOM  8092 CA  VAL A 529    -65.239  14.631   7.438  1.00 29.43           C
ATOM  8094 CB  VAL A 529    -64.557  13.354   7.972  1.00 29.39           C
ATOM  8096 CG1 VAL A 529    -64.785  12.187   7.023  1.00 28.89           C
ATOM  8100 CG2 VAL A 529    -63.062  13.589   8.186  1.00 29.44           C
ATOM  8104 C   VAL A 529    -66.609  14.243   6.887  1.00 28.95           C
ATOM  8105 O   VAL A 529    -66.755  14.016   5.690  1.00 29.09           O
ATOM  8107 N   LEU A 530    -67.615  14.153   7.744  1.00 28.18           N
ATOM  8108 CA  LEU A 530    -68.956  13.874   7.246  1.00 27.72           C
ATOM  8110 CB  LEU A 530    -69.971  13.715   8.395  1.00 27.75           C
ATOM  8113 CG  LEU A 530    -70.334  12.274   8.775  1.00 27.36           C
ATOM  8115 CD1 LEU A 530    -69.096  11.415   9.050  1.00 26.86           C
ATOM  8119 CD2 LEU A 530    -71.273  12.279   9.968  1.00 27.14           C
ATOM  8123 C   LEU A 530    -69.401  14.963   6.256  1.00 27.16           C
ATOM  8124 O   LEU A 530    -69.861  14.652   5.161  1.00 27.42           O
ATOM  8126 N   SER A 531    -69.230  16.229   6.635  1.00 26.21           N
ATOM  8127 CA  SER A 531    -69.730  17.359   5.853  1.00 25.12           C
ATOM  8129 CB  SER A 531    -69.519  18.657   6.618  1.00 25.01           C
ATOM  8132 OG  SER A 531    -68.167  18.791   6.985  1.00 23.94           O
ATOM  8134 C   SER A 531    -69.055  17.476   4.507  1.00 24.48           C
ATOM  8135 O   SER A 531    -69.687  17.886   3.538  1.00 24.14           O
ATOM  8137 N   VAL A 532    -67.774  17.115   4.461  1.00 23.89           N
ATOM  8138 CA  VAL A 532    -66.962  17.226   3.246  1.00 23.53           C
ATOM  8140 CB  VAL A 532    -65.470  17.437   3.575  1.00 23.09           C
ATOM  8142 CG1 VAL A 532    -64.633  17.355   2.348  1.00 22.32           C
ATOM  8146 CG2 VAL A 532    -65.268  18.773   4.198  1.00 23.07           C
ATOM  8150 C   VAL A 532    -67.100  16.028   2.316  1.00 23.67           C
ATOM  8151 O   VAL A 532    -67.137  16.209   1.099  1.00 23.58           O
ATOM  8153 N   ILE A 533    -67.187  14.824   2.886  1.00 23.85           N
ATOM  8154 CA  ILE A 533    -67.172  13.578   2.107  1.00 24.08           C
ATOM  8156 CB  ILE A 533    -66.172  12.555   2.691  1.00 24.10           C
ATOM  8158 CG1 ILE A 533    -64.745  13.079   2.631  1.00 23.47           C
ATOM  8161 CD1 ILE A 533    -64.178  13.083   1.255  1.00 23.42           C
ATOM  8165 CG2 ILE A 533    -66.254  11.231   1.932  1.00 24.56           C
ATOM  8169 C   ILE A 533    -68.522  12.859   1.990  1.00 24.27           C
ATOM  8170 O   ILE A 533    -68.991  12.620    .887  1.00 24.34           O
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ATOM  8172  N   THR A 534    -69.133  12.487   3.111  1.00 24.57       N
ATOM  8173  CA  THR A 534    -70.279  11.564   3.072  1.00 24.92       C
ATOM  8175  CB  THR A 534    -70.200  10.522   4.207  1.00 24.93       C
ATOM  8177  OG1 THR A 534    -70.491  11.149   5.458  1.00 25.28       O
ATOM  8179  CG2 THR A 534    -68.804   9.885   4.257  1.00 24.75       C
ATOM  8183  C   THR A 534    -71.673  12.209   3.083  1.00 25.00       C
ATOM  8184  O   THR A 534    -72.601  11.646   2.522  1.00 24.94       O
ATOM  8186  N   GLU A 535    -71.821  13.374   3.708  1.00 25.26       N
ATOM  8187  CA  GLU A 535    -73.132  14.024   3.833  1.00 25.34       C
ATOM  8189  CB  GLU A 535    -73.333  14.523   5.255  1.00 25.44       C
ATOM  8192  CG  GLU A 535    -73.753  13.424   6.196  1.00 25.80       C
ATOM  8195  CD  GLU A 535    -74.307  13.963   7.468  1.00 25.72       C
ATOM  8196  OE1 GLU A 535    -75.375  13.487   7.881  1.00 24.50       O
ATOM  8197  OE2 GLU A 535    -73.678  14.877   8.039  1.00 27.03       O
ATOM  8198  C   GLU A 535    -73.363  15.179   2.859  1.00 25.26       C
ATOM  8199  O   GLU A 535    -72.686  16.206   2.939  1.00 25.02       O
ATOM  8201  N   PRO A 536    -74.351  15.030   1.959  1.00 25.25       N
ATOM  8202  CA  PRO A 536    -74.655  16.111   1.050  1.00 25.18       C
ATOM  8204  CB  PRO A 536    -75.661  15.484    .076  1.00 25.15       C
ATOM  8207  CG  PRO A 536    -75.825  14.077    .476  1.00 24.98       C
ATOM  8210  CD  PRO A 536    -75.363  13.965   1.868  1.00 25.26       C
ATOM  8213  C   PRO A 536    -75.289  17.265   1.801  1.00 25.30       C
ATOM  8214  O   PRO A 536    -75.826  17.070   2.883  1.00 25.57       O
ATOM  8215  N   ILE A 537    -75.213  18.458   1.230  1.00 25.36       N
ATOM  8216  CA  ILE A 537    -75.807  19.638   1.827  1.00 25.34       C
ATOM  8218  CB  ILE A 537    -75.201  20.918   1.221  1.00 25.14       C
ATOM  8220  CG1 ILE A 537    -73.787  21.131   1.744  1.00 24.32       C
ATOM  8223  CD1 ILE A 537    -73.228  22.472   1.406  1.00 23.22       C
ATOM  8227  CG2 ILE A 537    -76.030  22.131   1.569  1.00 25.54       C
ATOM  8231  C   ILE A 537    -77.313  19.603   1.611  1.00 25.67       C
ATOM  8232  O   ILE A 537    -77.786  19.132    .579  1.00 25.47       O
ATOM  8234  N   LEU A 538    -78.071  20.088   2.586  1.00 26.22       N
ATOM  8235  CA  LEU A 538    -79.514  20.051   2.467  1.00 26.65       C
ATOM  8237  CB  LEU A 538    -80.213  20.525   3.749  1.00 26.78       C
ATOM  8240  CG  LEU A 538    -80.162  19.609   4.989  1.00 26.64       C
ATOM  8242  CD1 LEU A 538    -81.218  20.033   6.007  1.00 26.16       C
ATOM  8246  CD2 LEU A 538    -80.346  18.138   4.633  1.00 26.12       C
ATOM  8250  C   LEU A 538    -79.925  20.881   1.262  1.00 27.08       C
ATOM  8253  N   PRO A 539    -80.786  20.306    .414  1.00 28.03       N
ATOM  8254  CA  PRO A 539    -81.117  20.855   -.888  1.00 28.44       C
ATOM  8256  CB  PRO A 539    -82.093  19.828  -1.449  1.00 28.40       C
ATOM  8259  CG  PRO A 539    -82.793  19.328   -.253  1.00 28.30       C
ATOM  8262  CD  PRO A 539    -81.720  19.228    .787  1.00 28.11       C
ATOM  8265  C   PRO A 539    -81.813  22.194   -.804  1.00 28.89       C
ATOM  8266  O   PRO A 539    -82.396  22.535    .226  1.00 28.97       O
ATOM  8267  N   PHE A 540    -81.774  22.932  -1.906  1.00 29.32       N
ATOM  8268  CA  PHE A 540    -82.380  24.245  -1.962  1.00 29.50       C
ATOM  8270  CB  PHE A 540    -82.146  24.874  -3.326  1.00 29.56       C
ATOM  8273  CG  PHE A 540    -82.757  26.227  -3.463  1.00 29.75       C
ATOM  8274  CD1 PHE A 540    -83.874  26.429  -4.255  1.00 29.47       C
ATOM  8276  CE1 PHE A 540    -84.441  27.681  -4.364  1.00 29.46       C
ATOM  8278  CZ  PHE A 540    -83.901  28.743  -3.674  1.00 29.81       C
ATOM  8280  CE2 PHE A 540    -82.791  28.553  -2.877  1.00 30.21       C
ATOM  8282  CD2 PHE A 540    -82.229  27.300  -2.770  1.00 30.17       C
ATOM  8284  C   PHE A 540    -83.865  24.129  -1.722  1.00 29.66       C
ATOM  8285  O   PHE A 540    -84.568  23.551  -2.545  1.00 29.66       O
ATOM  8287  N   GLU A 541    -84.337  24.673   -.601  1.00 29.90       N
ATOM  8288  CA  GLU A 541    -85.761  24.605   -.233  1.00 30.06       C
ATOM  8290  CB  GLU A 541    -85.951  23.724   1.017  1.00 30.15       C
ATOM  8293  CG  GLU A 541    -87.411  23.361   1.367  1.00 30.64       C
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ATOM   8296  CD  GLU A 541     -88.091  24.351   2.322  1.00 31.35           C
ATOM   8297  OE1 GLU A 541     -87.468  25.370   2.680  1.00 32.67           O
ATOM   8298  OE2 GLU A 541     -89.254  24.114   2.719  1.00 30.48           O
ATOM   8299  C   GLU A 541     -86.315  26.011   -.010  1.00 29.89           C
ATOM   8300  O   GLU A 541     -86.835  26.636   -.936  1.00 29.71           O
ATOM   8302  N   LEU B  17     -69.666 -25.325   2.227  1.00 33.20           N
ATOM   8303  CA  LEU B  17     -69.356 -25.417    .755  1.00 33.49           C
ATOM   8305  CB  LEU B  17     -70.240 -26.475    .048  1.00 33.44           C
ATOM   8308  CG  LEU B  17     -70.077 -27.986    .328  1.00 33.60           C
ATOM   8310  CD1 LEU B  17     -71.285 -28.778   -.217  1.00 32.76           C
ATOM   8314  CD2 LEU B  17     -68.763 -28.553   -.230  1.00 33.21           C
ATOM   8318  C   LEU B  17     -69.513 -24.044    .055  1.00 33.54           C
ATOM   8319  O   LEU B  17     -70.550 -23.380    .195  1.00 33.77           O
ATOM   8323  N   LEU B  18     -68.481 -23.637   -.696  1.00 33.44           N
ATOM   8324  CA  LEU B  18     -68.476 -22.362  -1.454  1.00 33.07           C
ATOM   8326  CB  LEU B  18     -67.029 -21.960  -1.840  1.00 33.21           C
ATOM   8329  CG  LEU B  18     -66.065 -21.488   -.721  1.00 34.06           C
ATOM   8331  CD1 LEU B  18     -64.607 -21.351  -1.235  1.00 34.51           C
ATOM   8335  CD2 LEU B  18     -66.516 -20.164   -.061  1.00 33.43           C
ATOM   8339  C   LEU B  18     -69.379 -22.400  -2.714  1.00 32.37           C
ATOM   8340  O   LEU B  18     -69.710 -21.355  -3.274  1.00 32.29           O
ATOM   8342  N   SER B  19     -69.765 -23.597  -3.153  1.00 31.62           N
ATOM   8343  CA  SER B  19     -70.711 -23.749  -4.253  1.00 31.16           C
ATOM   8345  CB  SER B  19     -70.443 -25.067  -5.033  1.00 31.09           C
ATOM   8348  OG  SER B  19     -70.977 -26.243  -4.421  1.00 29.36           O
ATOM   8350  C   SER B  19     -72.168 -23.663  -3.759  1.00 31.45           C
ATOM   8351  O   SER B  19     -73.076 -23.432  -4.551  1.00 31.13           O
ATOM   8353  N   SER B  20     -72.386 -23.824  -2.451  1.00 31.91           N
ATOM   8354  CA  SER B  20     -73.749 -23.900  -1.879  1.00 32.34           C
ATOM   8356  CB  SER B  20     -73.706 -24.122   -.357  1.00 32.35           C
ATOM   8359  OG  SER B  20     -73.393 -25.473   -.055  1.00 32.34           O
ATOM   8361  C   SER B  20     -74.601 -22.670  -2.204  1.00 32.69           C
ATOM   8362  O   SER B  20     -74.072 -21.600  -2.487  1.00 32.89           O
ATOM   8364  N   ASP B  21     -75.921 -22.831  -2.119  1.00 33.13           N
ATOM   8365  CA  ASP B  21     -76.874 -21.901  -2.745  1.00 33.40           C
ATOM   8367  CB  ASP B  21     -78.179 -22.628  -3.045  1.00 33.64           C
ATOM   8370  CG  ASP B  21     -77.943 -23.883  -3.828  1.00 35.35           C
ATOM   8371  OD1 ASP B  21     -77.031 -23.866  -4.684  1.00 38.26           O
ATOM   8372  OD2 ASP B  21     -78.631 -24.890  -3.590  1.00 37.55           O
ATOM   8373  C   ASP B  21     -77.141 -20.649  -1.940  1.00 33.23           C
ATOM   8374  O   ASP B  21     -78.039 -20.616  -1.106  1.00 32.91           O
ATOM   8376  N   THR B  22     -76.348 -19.621  -2.229  1.00 33.46           N
ATOM   8377  CA  THR B  22     -76.443 -18.307  -1.593  1.00 33.79           C
ATOM   8379  CB  THR B  22     -76.460 -18.378   -.016  1.00 33.74           C
ATOM   8381  OG1 THR B  22     -75.426 -19.250    .460  1.00 32.97           O
ATOM   8383  CG2 THR B  22     -77.805 -18.838    .535  1.00 33.55           C
ATOM   8387  C   THR B  22     -75.217 -17.479  -2.018  1.00 34.24           C
ATOM   8388  O   THR B  22     -74.102 -17.988  -1.892  1.00 33.95           O
ATOM   8390  N   ASP B  23     -75.361 -16.248  -2.543  1.00 34.99           N
ATOM   8391  CA  ASP B  23     -76.603 -15.620  -3.103  1.00 35.61           C
ATOM   8393  CB  ASP B  23     -77.242 -16.538  -4.170  1.00 35.51           C
ATOM   8396  CG  ASP B  23     -76.196 -17.236  -5.034  1.00 36.08           C
ATOM   8397  OD1 ASP B  23     -75.084 -16.685  -5.194  1.00 35.58           O
ATOM   8398  OD2 ASP B  23     -76.473 -18.344  -5.541  1.00 37.65           O
ATOM   8399  C   ASP B  23     -77.662 -15.083  -2.097  1.00 36.10           C
ATOM   8400  O   ASP B  23     -78.644 -15.770  -1.799  1.00 36.13           O
ATOM   8402  N   GLU B  24     -77.487 -13.845  -1.616  1.00 36.74           N
ATOM   8403  CA  GLU B  24     -78.358 -13.316   -.543  1.00 37.59           C
ATOM   8405  CB  GLU B  24     -77.765 -13.666    .838  1.00 37.88           C
ATOM   8408  CG  GLU B  24     -77.624 -15.173   1.120  1.00 38.51           C
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ATOM 8411 CD GLU B 24 -77.314 -15.510 2.588 1.00 39.48 C
ATOM 8412 OE1 GLU B 24 -77.171 -14.581 3.434 1.00 39.60 O
ATOM 8413 OE2 GLU B 24 -77.221 -16.725 2.884 1.00 39.51 O
ATOM 8414 C GLU B 24 -78.730 -11.809 -.559 1.00 38.11 C
ATOM 8415 O GLU B 24 -79.840 -11.453 -.972 1.00 38.20 O
ATOM 8417 N SER B 25 -77.825 -10.941 -.089 1.00 38.70 N
ATOM 8418 CA SER B 25 -78.192 -9.560 .312 1.00 39.21 C
ATOM 8420 CB SER B 25 -76.995 -8.783 .916 1.00 39.29 C
ATOM 8423 OG SER B 25 -76.267 -8.037 -.056 1.00 39.40 O
ATOM 8425 C SER B 25 -78.853 -8.738 -.802 1.00 39.69 C
ATOM 8426 O SER B 25 -78.707 -9.050 -1.995 1.00 39.75 O
ATOM 8428 N ILE B 26 -79.544 -7.670 -.378 1.00 40.21 N
ATOM 8429 CA ILE B 26 -80.554 -6.962 -1.189 1.00 40.55 C
ATOM 8431 CB ILE B 26 -79.925 -6.082 -2.319 1.00 40.66 C
ATOM 8433 CG1 ILE B 26 -79.083 -4.951 -1.700 1.00 40.73 C
ATOM 8436 CD1 ILE B 26 -78.596 -3.877 -2.698 1.00 40.68 C
ATOM 8440 CG2 ILE B 26 -81.018 -5.475 -3.203 1.00 40.88 C
ATOM 8444 C ILE B 26 -81.575 -7.999 -1.714 1.00 40.72 C
ATOM 8445 O ILE B 26 -81.311 -8.710 -2.690 1.00 40.80 O
ATOM 8447 N GLU B 27 -82.729 -8.070 -1.037 1.00 40.86 N
ATOM 8448 CA GLU B 27 -83.694 -9.190 -1.160 1.00 40.88 C
ATOM 8450 CB GLU B 27 -84.782 -9.060 -.061 1.00 40.95 C
ATOM 8453 CG GLU B 27 -84.235 -9.257 1.379 1.00 41.28 C
ATOM 8456 CD GLU B 27 -85.123 -8.657 2.484 1.00 41.74 C
ATOM 8457 OE1 GLU B 27 -85.593 -7.504 2.344 1.00 41.14 O
ATOM 8458 OE2 GLU B 27 -85.332 -9.337 3.514 1.00 42.36 O
ATOM 8459 C GLU B 27 -84.290 -9.355 -2.587 1.00 40.75 C
ATOM 8460 O GLU B 27 -83.664 -8.936 -3.569 1.00 40.88 O
ATOM 8462 N VAL B 28 -85.461 -9.994 -2.712 1.00 40.40 N
ATOM 8463 CA VAL B 28 -86.033 -10.361 -4.027 1.00 39.97 C
ATOM 8465 CB VAL B 28 -86.034 -9.157 -5.053 1.00 40.03 C
ATOM 8467 CG1 VAL B 28 -86.494 -9.600 -6.444 1.00 39.63 C
ATOM 8471 CG2 VAL B 28 -86.900 -7.994 -4.525 1.00 39.86 C
ATOM 8475 C VAL B 28 -85.335 -11.600 -4.625 1.00 39.63 C
ATOM 8476 O VAL B 28 -85.858 -12.204 -5.567 1.00 39.63 O
ATOM 8478 N HIS B 29 -84.175 -11.980 -4.069 1.00 39.21 N
ATOM 8479 CA HIS B 29 -83.431 -13.177 -4.504 1.00 38.81 C
ATOM 8481 CB HIS B 29 -81.914 -12.913 -4.665 1.00 38.97 C
ATOM 8484 CG HIS B 29 -81.571 -11.721 -5.512 1.00 39.99 C
ATOM 8485 ND1 HIS B 29 -81.181 -11.825 -6.834 1.00 40.79 N
ATOM 8487 CE1 HIS B 29 -80.931 -10.615 -7.312 1.00 40.76 C
ATOM 8489 NE2 HIS B 29 -81.134 -9.734 -6.346 1.00 40.27 N
ATOM 8491 CD2 HIS B 29 -81.525 -10.400 -5.209 1.00 40.17 C
ATOM 8493 C HIS B 29 -83.611 -14.340 -3.523 1.00 38.05 C
ATOM 8494 O HIS B 29 -82.782 -15.259 -3.526 1.00 38.02 O
ATOM 8496 N LYS B 30 -84.667 -14.321 -2.694 1.00 37.06 N
ATOM 8497 CA LYS B 30 -85.107 -15.559 -2.022 1.00 36.33 C
ATOM 8499 CB LYS B 30 -86.056 -15.286 -.836 1.00 36.27 C
ATOM 8502 CG LYS B 30 -85.352 -14.818 .461 1.00 36.09 C
ATOM 8505 CD LYS B 30 -86.355 -14.599 1.612 1.00 36.03 C
ATOM 8508 CE LYS B 30 -85.811 -13.659 2.701 1.00 36.24 C
ATOM 8511 NZ LYS B 30 -86.802 -13.356 3.789 1.00 35.65 N
ATOM 8515 C LYS B 30 -85.710 -16.510 -3.094 1.00 35.69 C
ATOM 8516 O LYS B 30 -86.706 -17.205 -2.879 1.00 35.35 O
ATOM 8518 N ASP B 31 -85.075 -16.484 -4.268 1.00 35.13 N
ATOM 8519 CA ASP B 31 -85.145 -17.519 -5.282 1.00 34.64 C
ATOM 8521 CB ASP B 31 -84.592 -16.962 -6.623 1.00 34.60 C
ATOM 8524 CG ASP B 31 -84.419 -18.032 -7.725 1.00 34.24 C
ATOM 8525 OD1 ASP B 31 -84.914 -19.165 -7.570 1.00 34.58 O
ATOM 8526 OD2 ASP B 31 -83.776 -17.732 -8.761 1.00 31.56 O

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ATOM  8527  C   ASP B  31    -84.304 -18.675  -4.721  1.00 34.31      C
ATOM  8528  O   ASP B  31    -83.122 -18.838  -5.038  1.00 34.03      O
ATOM  8530  N   LYS B  32    -84.917 -19.429  -3.813  1.00 33.94      N
ATOM  8531  CA  LYS B  32    -84.380 -20.710  -3.369  1.00 33.36      C
ATOM  8533  CB  LYS B  32    -83.772 -20.607  -1.973  1.00 33.45      C
ATOM  8536  CG  LYS B  32    -82.540 -19.693  -1.951  1.00 33.56      C
ATOM  8539  CD  LYS B  32    -82.025 -19.455   -.532  1.00 34.17      C
ATOM  8542  CE  LYS B  32    -81.671 -17.987   -.283  1.00 34.16      C
ATOM  8545  NZ  LYS B  32    -80.746 -17.437  -1.311  1.00 34.07      N
ATOM  8549  C   LYS B  32    -85.490 -21.764  -3.499  1.00 32.57      C
ATOM  8550  O   LYS B  32    -85.908 -22.412  -2.538  1.00 32.10      O
ATOM  8552  N   ALA B  33    -85.976 -21.859  -4.738  1.00 31.66      N
ATOM  8553  CA  ALA B  33    -86.576 -23.055  -5.259  1.00 30.94      C
ATOM  8555  CB  ALA B  33    -87.247 -22.773  -6.597  1.00 30.47      C
ATOM  8559  C   ALA B  33    -85.442 -24.081  -5.403  1.00 30.55      C
ATOM  8560  O   ALA B  33    -85.684 -25.230  -5.751  1.00 31.12      O
ATOM  8562  N   LYS B  34    -84.200 -23.660  -5.161  1.00 29.73      N
ATOM  8563  CA  LYS B  34    -83.107 -24.585  -4.839  1.00 29.09      C
ATOM  8565  CB  LYS B  34    -81.776 -23.817  -4.865  1.00 29.30      C
ATOM  8568  CG  LYS B  34    -80.678 -24.474  -5.726  1.00 29.76      C
ATOM  8571  CD  LYS B  34    -79.633 -23.458  -6.283  1.00 28.74      C
ATOM  8574  CE  LYS B  34    -78.417 -24.186  -6.890  1.00 27.56      C
ATOM  8577  NZ  LYS B  34    -78.745 -25.174  -7.935  1.00 26.16      N
ATOM  8581  C   LYS B  34    -83.376 -25.320  -3.472  1.00 28.37      C
ATOM  8582  O   LYS B  34    -83.254 -24.755  -2.374  1.00 27.82      O
ATOM  8584  N   LYS B  35    -83.635 -26.620  -3.604  1.00 27.53      N
ATOM  8585  CA  LYS B  35    -84.629 -27.429  -2.851  1.00 26.77      C
ATOM  8587  CB  LYS B  35    -85.729 -26.602  -2.170  1.00 26.81      C
ATOM  8590  CG  LYS B  35    -87.089 -26.520  -2.907  1.00 27.05      C
ATOM  8593  CD  LYS B  35    -88.096 -27.604  -2.452  1.00 27.41      C
ATOM  8596  CE  LYS B  35    -89.394 -27.636  -3.300  1.00 27.21      C
ATOM  8599  NZ  LYS B  35    -90.501 -26.792  -2.762  1.00 26.28      N
ATOM  8603  C   LYS B  35    -85.257 -28.357  -3.920  1.00 26.03      C
ATOM  8604  O   LYS B  35    -85.853 -29.386  -3.626  1.00 26.00      O
ATOM  8606  N   LEU B  36    -85.171 -27.909  -5.168  1.00 24.98      N
ATOM  8607  CA  LEU B  36    -85.095 -28.783  -6.319  1.00 24.02      C
ATOM  8609  CB  LEU B  36    -85.004 -27.930  -7.594  1.00 23.83      C
ATOM  8612  CG  LEU B  36    -86.208 -27.103  -8.062  1.00 22.23      C
ATOM  8614  CD1 LEU B  36    -85.762 -25.873  -8.802  1.00 19.93      C
ATOM  8618  CD2 LEU B  36    -87.092 -27.930  -8.951  1.00 22.11      C
ATOM  8622  C   LEU B  36    -83.834 -29.659  -6.185  1.00 23.58      C
ATOM  8623  O   LEU B  36    -83.840 -30.842  -6.508  1.00 23.38      O
ATOM  8625  N   GLU B  37    -82.742 -29.046  -5.739  1.00 23.18      N
ATOM  8626  CA  GLU B  37    -81.510 -29.753  -5.396  1.00 22.88      C
ATOM  8628  CB  GLU B  37    -80.466 -28.766  -4.855  1.00 22.76      C
ATOM  8631  CG  GLU B  37    -79.038 -29.297  -4.874  1.00 22.24      C
ATOM  8634  CD  GLU B  37    -78.085 -28.505  -4.009  1.00 21.06      C
ATOM  8635  OE1 GLU B  37    -78.368 -27.331  -3.737  1.00 19.65      O
ATOM  8636  OE2 GLU B  37    -77.037 -29.059  -3.615  1.00 20.62      O
ATOM  8637  C   GLU B  37    -81.748 -30.856  -4.364  1.00 22.95      C
ATOM  8638  O   GLU B  37    -81.164 -31.933  -4.458  1.00 22.99      O
ATOM  8640  N   ALA B  38    -82.591 -30.575  -3.372  1.00 23.02      N
ATOM  8641  CA  ALA B  38    -82.973 -31.565  -2.364  1.00 22.93      C
ATOM  8643  CB  ALA B  38    -83.966 -30.959  -1.374  1.00 22.73      C
ATOM  8647  C   ALA B  38    -83.580 -32.778  -3.044  1.00 23.05      C
ATOM  8648  O   ALA B  38    -83.170 -33.909  -2.813  1.00 22.52      O
ATOM  8650  N   GLU B  39    -84.546 -32.506  -3.912  1.00 23.66      N
ATOM  8651  CA  GLU B  39    -85.273 -33.534  -4.642  1.00 24.08      C
ATOM  8653  CB  GLU B  39    -86.403 -32.891  -5.453  1.00 24.28      C
ATOM  8656  CG  GLU B  39    -87.405 -33.869  -6.075  1.00 25.14      C
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ATOM 8659 CD GLU B 39 -88.773 -33.227 -6.341 1.00 26.43 C
ATOM 8660 OE1 GLU B 39 -89.232 -32.381 -5.519 1.00 25.90 O
ATOM 8661 OE2 GLU B 39 -89.387 -33.584 -7.375 1.00 26.99 O
ATOM 8662 C GLU B 39 -84.362 -34.359 -5.545 1.00 24.18 C
ATOM 8663 O GLU B 39 -84.483 -35.579 -5.575 1.00 24.32 O
ATOM 8665 N VAL B 40 -83.450 -33.710 -6.269 1.00 24.43 N
ATOM 8666 CA VAL B 40 -82.533 -34.437 -7.153 1.00 24.59 C
ATOM 8668 CB VAL B 40 -81.734 -33.496 -8.087 1.00 24.65 C
ATOM 8670 CG1 VAL B 40 -80.611 -34.258 -8.792 1.00 24.14 C
ATOM 8674 CG2 VAL B 40 -82.662 -32.852 -9.106 1.00 23.89 C
ATOM 8678 C VAL B 40 -81.592 -35.304 -6.328 1.00 24.99 C
ATOM 8679 O VAL B 40 -81.265 -36.407 -6.717 1.00 24.77 O
ATOM 8681 N ARG B 41 -81.184 -34.811 -5.171 1.00 25.79 N
ATOM 8682 CA ARG B 41 -80.387 -35.613 -4.248 1.00 26.75 C
ATOM 8684 CB ARG B 41 -80.032 -34.823 -2.998 1.00 27.38 C
ATOM 8687 CG ARG B 41 -78.568 -34.777 -2.757 1.00 30.18 C
ATOM 8690 CD ARG B 41 -78.281 -34.610 -1.273 1.00 34.43 C
ATOM 8693 NE ARG B 41 -76.896 -34.198 -1.016 1.00 37.07 N
ATOM 8695 CZ ARG B 41 -76.350 -33.045 -1.416 1.00 38.54 C
ATOM 8696 NH1 ARG B 41 -75.083 -32.797 -1.112 1.00 40.04 N
ATOM 8699 NH2 ARG B 41 -77.037 -32.145 -2.128 1.00 38.45 N
ATOM 8702 C ARG B 41 -81.081 -36.860 -3.762 1.00 26.60 C
ATOM 8703 O ARG B 41 -80.446 -37.894 -3.627 1.00 26.89 O
ATOM 8705 N ARG B 42 -82.363 -36.733 -3.423 1.00 26.41 N
ATOM 8706 CA ARG B 42 -83.159 -37.870 -3.002 1.00 26.09 C
ATOM 8708 CB ARG B 42 -84.588 -37.452 -2.674 1.00 25.99 C
ATOM 8711 CG ARG B 42 -85.426 -38.562 -2.049 1.00 25.45 C
ATOM 8714 CD ARG B 42 -86.783 -38.078 -1.645 1.00 24.26 C
ATOM 8717 NE ARG B 42 -87.549 -37.602 -2.794 1.00 23.73 N
ATOM 8719 CZ ARG B 42 -88.547 -36.722 -2.717 1.00 24.51 C
ATOM 8720 NH1 ARG B 42 -88.912 -36.195 -1.545 1.00 24.99 N
ATOM 8723 NH2 ARG B 42 -89.185 -36.354 -3.816 1.00 24.46 N
ATOM 8726 C ARG B 42 -83.167 -38.894 -4.118 1.00 26.28 C
ATOM 8727 O ARG B 42 -82.864 -40.054 -3.888 1.00 26.39 O
ATOM 8729 N GLU B 43 -83.476 -38.460 -5.334 1.00 26.52 N
ATOM 8730 CA GLU B 43 -83.476 -39.370 -6.479 1.00 27.00 C
ATOM 8732 CB GLU B 43 -83.982 -38.676 -7.753 1.00 27.50 C
ATOM 8735 CG GLU B 43 -85.469 -38.275 -7.699 1.00 29.78 C
ATOM 8738 CD GLU B 43 -86.342 -39.301 -6.974 1.00 32.52 C
ATOM 8739 OE1 GLU B 43 -86.388 -40.455 -7.445 1.00 35.06 O
ATOM 8740 OE2 GLU B 43 -86.966 -38.963 -5.936 1.00 33.80 O
ATOM 8741 C GLU B 43 -82.147 -40.059 -6.769 1.00 26.37 C
ATOM 8742 O GLU B 43 -82.162 -41.126 -7.355 1.00 26.63 O
ATOM 8744 N ILE B 44 -81.018 -39.472 -6.373 1.00 25.85 N
ATOM 8745 CA ILE B 44 -79.717 -40.126 -6.555 1.00 25.55 C
ATOM 8747 CB ILE B 44 -78.547 -39.121 -6.692 1.00 25.26 C
ATOM 8749 CG1 ILE B 44 -78.706 -38.273 -7.953 1.00 24.47 C
ATOM 8752 CD1 ILE B 44 -77.690 -37.163 -8.114 1.00 23.21 C
ATOM 8756 CG2 ILE B 44 -77.207 -39.863 -6.778 1.00 25.35 C
ATOM 8760 C ILE B 44 -79.404 -41.109 -5.428 1.00 25.84 C
ATOM 8761 O ILE B 44 -78.925 -42.208 -5.698 1.00 25.97 O
ATOM 8763 N ASN B 45 -79.663 -40.708 -4.177 1.00 26.25 N
ATOM 8764 CA ASN B 45 -79.403 -41.542 -2.983 1.00 26.34 C
ATOM 8766 CB ASN B 45 -79.284 -40.681 -1.719 1.00 26.01 C
ATOM 8769 CG ASN B 45 -78.072 -39.789 -1.723 1.00 24.65 C
ATOM 8770 OD1 ASN B 45 -76.957 -40.226 -1.434 1.00 22.47 O
ATOM 8771 ND2 ASN B 45 -78.288 -38.516 -2.009 1.00 23.36 N
ATOM 8774 C ASN B 45 -80.488 -42.586 -2.731 1.00 27.18 C
ATOM 8775 O ASN B 45 -80.374 -43.390 -1.806 1.00 27.30 O
ATOM 8777 N ASN B 46 -81.553 -42.541 -3.527 1.00 28.17 N

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ATOM   8778  CA  ASN B  46     -82.619 -43.536  -3.489  1.00 29.02           C
ATOM   8780  CB  ASN B  46     -83.558 -43.289  -4.665  1.00 29.05           C
ATOM   8783  CG  ASN B  46     -84.615 -44.345  -4.806  1.00 28.82           C
ATOM   8784  OD1 ASN B  46     -84.861 -45.132  -3.895  1.00 28.14           O
ATOM   8785  ND2 ASN B  46     -85.255 -44.369  -5.968  1.00 29.67           N
ATOM   8788  C   ASN B  46     -82.076 -44.958  -3.549  1.00 30.14           C
ATOM   8789  O   ASN B  46     -81.566 -45.408  -4.581  1.00 30.30           O
ATOM   8791  N   GLU B  47     -82.218 -45.674  -2.446  1.00 31.36           N
ATOM   8792  CA  GLU B  47     -81.575 -46.968  -2.295  1.00 32.61           C
ATOM   8794  CB  GLU B  47     -81.617 -47.430  -.823  1.00 33.09           C
ATOM   8797  CG  GLU B  47     -80.974 -46.466   .218  1.00 34.19           C
ATOM   8800  CD  GLU B  47     -81.919 -45.337   .721  1.00 34.57           C
ATOM   8801  OE1 GLU B  47     -82.911 -45.012   .029  1.00 34.53           O
ATOM   8802  OE2 GLU B  47     -81.652 -44.762  1.805  1.00 34.30           O
ATOM   8803  C   GLU B  47     -82.205 -48.046  -3.172  1.00 33.18           C
ATOM   8804  O   GLU B  47     -81.604 -49.088  -3.370  1.00 33.44           O
ATOM   8806  N   LYS B  48     -83.408 -47.808  -3.692  1.00 34.11           N
ATOM   8807  CA  LYS B  48     -84.164 -48.853  -4.396  1.00 34.85           C
ATOM   8809  CB  LYS B  48     -85.379 -49.254  -3.542  1.00 35.09           C
ATOM   8812  CG  LYS B  48     -85.003 -49.723  -2.127  1.00 36.00           C
ATOM   8815  CD  LYS B  48     -86.174 -50.338  -1.350  1.00 37.13           C
ATOM   8818  CE  LYS B  48     -87.312 -49.340  -1.094  1.00 37.90           C
ATOM   8821  NZ  LYS B  48     -86.908 -48.161  -.272  1.00 38.31           N
ATOM   8825  C   LYS B  48     -84.586 -48.487  -5.835  1.00 35.13           C
ATOM   8826  O   LYS B  48     -85.544 -49.030  -6.361  1.00 34.60           O
ATOM   8828  N   ALA B  49     -83.858 -47.576  -6.474  1.00 36.09           N
ATOM   8829  CA  ALA B  49     -84.093 -47.261  -7.886  1.00 36.87           C
ATOM   8831  CB  ALA B  49     -83.550 -45.880  -8.238  1.00 36.73           C
ATOM   8835  C   ALA B  49     -83.406 -48.325  -8.714  1.00 37.56           C
ATOM   8836  O   ALA B  49     -82.315 -48.761  -8.363  1.00 37.62           O
ATOM   8838  N   GLU B  50     -84.028 -48.754  -9.807  1.00 38.54           N
ATOM   8839  CA  GLU B  50     -83.399 -49.772 -10.652  1.00 39.40           C
ATOM   8841  CB  GLU B  50     -84.380 -50.384 -11.673  1.00 39.71           C
ATOM   8844  CG  GLU B  50     -83.959 -51.808 -12.179  1.00 41.33           C
ATOM   8847  CD  GLU B  50     -83.733 -52.860 -11.039  1.00 42.88           C
ATOM   8848  OE1 GLU B  50     -84.683 -53.628 -10.718  1.00 42.94           O
ATOM   8849  OE2 GLU B  50     -82.603 -52.921 -10.472  1.00 42.96           O
ATOM   8850  C   GLU B  50     -82.171 -49.163 -11.330  1.00 39.43           C
ATOM   8851  O   GLU B  50     -82.211 -48.017 -11.791  1.00 39.66           O
ATOM   8853  N   PHE B  51     -81.084 -49.929 -11.376  1.00 39.32           N
ATOM   8854  CA  PHE B  51     -79.763 -49.360 -11.636  1.00 39.32           C
ATOM   8856  CB  PHE B  51     -78.675 -50.429 -11.476  1.00 39.62           C
ATOM   8859  CG  PHE B  51     -78.470 -50.889 -10.032  1.00 41.82           C
ATOM   8860  CD1 PHE B  51     -78.093 -49.978  -9.032  1.00 42.93           C
ATOM   8862  CE1 PHE B  51     -77.892 -50.391  -7.705  1.00 43.30           C
ATOM   8864  CZ  PHE B  51     -78.059 -51.729  -7.359  1.00 44.33           C
ATOM   8866  CE2 PHE B  51     -78.430 -52.659  -8.341  1.00 44.75           C
ATOM   8868  CD2 PHE B  51     -78.633 -52.234  -9.677  1.00 44.06           C
ATOM   8870  C   PHE B  51     -79.646 -48.625 -12.976  1.00 38.57           C
ATOM   8871  O   PHE B  51     -79.045 -47.564 -13.046  1.00 38.50           O
ATOM   8873  N   LEU B  52     -80.262 -49.155 -14.024  1.00 37.99           N
ATOM   8874  CA  LEU B  52     -80.176 -48.539 -15.351  1.00 37.42           C
ATOM   8876  CB  LEU B  52     -80.774 -49.476 -16.399  1.00 37.66           C
ATOM   8879  CG  LEU B  52     -80.502 -49.168 -17.876  1.00 38.39           C
ATOM   8881  CD1 LEU B  52     -80.171 -50.452 -18.652  1.00 38.46           C
ATOM   8885  CD2 LEU B  52     -81.703 -48.432 -18.500  1.00 39.23           C
ATOM   8889  C   LEU B  52     -80.824 -47.143 -15.431  1.00 36.69           C
ATOM   8890  O   LEU B  52     -80.383 -46.312 -16.224  1.00 36.59           O
ATOM   8892  N   THR B  53     -81.859 -46.879 -14.625  1.00 35.87           N
ATOM   8893  CA  THR B  53     -82.409 -45.510 -14.513  1.00 34.91           C
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ATOM  8895  CB  THR B  53    -83.784 -45.421 -13.805  1.00 34.72       C
ATOM  8897  OG1 THR B  53    -84.724 -46.269 -14.455  1.00 34.04       O
ATOM  8899  CG2 THR B  53    -84.316 -43.981 -13.855  1.00 34.81       C
ATOM  8903  C   THR B  53    -81.454 -44.642 -13.722  1.00 34.05       C
ATOM  8904  O   THR B  53    -81.170 -43.513 -14.121  1.00 34.16       O
ATOM  8906  N   LEU B  54    -80.987 -45.167 -12.593  1.00 32.84       N
ATOM  8907  CA  LEU B  54    -80.027 -44.461 -11.772  1.00 32.16       C
ATOM  8909  CB  LEU B  54    -79.506 -45.354 -10.662  1.00 32.27       C
ATOM  8912  CG  LEU B  54    -78.521 -44.702  -9.698  1.00 32.56       C
ATOM  8914  CD1 LEU B  54    -79.275 -43.760  -8.769  1.00 32.38       C
ATOM  8918  CD2 LEU B  54    -77.755 -45.789  -8.917  1.00 33.29       C
ATOM  8922  C   LEU B  54    -78.870 -44.006 -12.634  1.00 31.50       C
ATOM  8923  O   LEU B  54    -78.509 -42.840 -12.607  1.00 31.98       O
ATOM  8925  N   LEU B  55    -78.297 -44.914 -13.418  1.00 30.43       N
ATOM  8926  CA  LEU B  55    -77.220 -44.540 -14.333  1.00 29.36       C
ATOM  8928  CB  LEU B  55    -76.765 -45.733 -15.173  1.00 29.23       C
ATOM  8931  CG  LEU B  55    -76.157 -46.902 -14.391  1.00 28.60       C
ATOM  8933  CD1 LEU B  55    -75.697 -48.004 -15.348  1.00 27.60       C
ATOM  8937  CD2 LEU B  55    -75.020 -46.440 -13.469  1.00 27.20       C
ATOM  8941  C   LEU B  55    -77.678 -43.406 -15.230  1.00 28.60       C
ATOM  8942  O   LEU B  55    -77.063 -42.365 -15.267  1.00 28.17       O
ATOM  8944  N   GLU B  56    -78.786 -43.594 -15.919  1.00 28.23       N
ATOM  8945  CA  GLU B  56    -79.326 -42.530 -16.759  1.00 28.64       C
ATOM  8947  CB  GLU B  56    -80.567 -43.031 -17.524  1.00 29.27       C
ATOM  8950  CG  GLU B  56    -80.229 -43.783 -18.829  1.00 31.73       C
ATOM  8953  CD  GLU B  56    -81.265 -44.860 -19.206  1.00 35.52       C
ATOM  8954  OE1 GLU B  56    -82.474 -44.693 -18.889  1.00 36.97       O
ATOM  8955  OE2 GLU B  56    -80.856 -45.877 -19.825  1.00 37.55       O
ATOM  8956  C   GLU B  56    -79.632 -41.203 -15.995  1.00 27.77       C
ATOM  8957  O   GLU B  56    -79.561 -40.103 -16.582  1.00 27.84       O
ATOM  8959  N   LEU B  57    -79.976 -41.303 -14.710  1.00 26.29       N
ATOM  8960  CA  LEU B  57    -80.158 -40.120 -13.895  1.00 25.06       C
ATOM  8962  CB  LEU B  57    -80.724 -40.462 -12.514  1.00 24.83       C
ATOM  8965  CG  LEU B  57    -80.952 -39.298 -11.544  1.00 23.72       C
ATOM  8967  CD1 LEU B  57    -81.909 -38.278 -12.117  1.00 21.43       C
ATOM  8971  CD2 LEU B  57    -81.477 -39.830 -10.227  1.00 22.41       C
ATOM  8975  C   LEU B  57    -78.801 -39.459 -13.780  1.00 24.40       C
ATOM  8976  O   LEU B  57    -78.591 -38.373 -14.306  1.00 24.70       O
ATOM  8978  N   ILE B  58    -77.855 -40.133 -13.144  1.00 23.56       N
ATOM  8979  CA  ILE B  58    -76.509 -39.574 -12.991  1.00 22.91       C
ATOM  8981  CB  ILE B  58    -75.454 -40.635 -12.599  1.00 22.49       C
ATOM  8983  CG1 ILE B  58    -75.753 -41.251 -11.235  1.00 22.09       C
ATOM  8986  CD1 ILE B  58    -74.936 -42.464 -10.926  1.00 20.88       C
ATOM  8990  CG2 ILE B  58    -74.103 -39.992 -12.534  1.00 22.63       C
ATOM  8994  C   ILE B  58    -76.062 -38.927 -14.302  1.00 22.64       C
ATOM  8995  O   ILE B  58    -75.603 -37.796 -14.315  1.00 22.38       O
ATOM  8997  N   ASP B  59    -76.228 -39.646 -15.404  1.00 22.56       N
ATOM  8998  CA  ASP B  59    -75.715 -39.196 -16.684  1.00 22.76       C
ATOM  9000  CB  ASP B  59    -75.926 -40.269 -17.757  1.00 22.93       C
ATOM  9003  CG  ASP B  59    -75.274 -39.904 -19.088  1.00 24.58       C
ATOM  9004  OD1 ASP B  59    -74.157 -39.322 -19.081  1.00 25.70       O
ATOM  9005  OD2 ASP B  59    -75.897 -40.186 -20.142  1.00 27.51       O
ATOM  9006  C   ASP B  59    -76.343 -37.863 -17.104  1.00 22.40       C
ATOM  9007  O   ASP B  59    -75.634 -36.939 -17.520  1.00 22.40       O
ATOM  9009  N   ASN B  60    -77.662 -37.767 -16.991  1.00 21.91       N
ATOM  9010  CA  ASN B  60    -78.349 -36.500 -17.217  1.00 21.70       C
ATOM  9012  CB  ASN B  60    -79.867 -36.674 -17.088  1.00 22.12       C
ATOM  9015  CG  ASN B  60    -80.477 -37.390 -18.268  1.00 22.76       C
ATOM  9016  OD1 ASN B  60    -80.027 -37.233 -19.393  1.00 24.28       O
ATOM  9017  ND2 ASN B  60    -81.515 -38.172 -18.017  1.00 24.36       N
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ATOM 9020 C ASN B 60 -77.898 -35.427 -16.234 1.00 21.17 C
ATOM 9021 O ASN B 60 -77.700 -34.273 -16.614 1.00 20.85 O
ATOM 9023 N VAL B 61 -77.745 -35.805 -14.968 1.00 20.60 N
ATOM 9024 CA VAL B 61 -77.382 -34.841 -13.942 1.00 20.48 C
ATOM 9026 CB VAL B 61 -77.277 -35.490 -12.551 1.00 20.26 C
ATOM 9028 CG1 VAL B 61 -76.585 -34.562 -11.565 1.00 19.92 C
ATOM 9032 CG2 VAL B 61 -78.668 -35.857 -12.049 1.00 20.66 C
ATOM 9036 C VAL B 61 -76.068 -34.208 -14.335 1.00 20.66 C
ATOM 9037 O VAL B 61 -75.871 -32.998 -14.182 1.00 20.74 O
ATOM 9039 N GLN B 62 -75.187 -35.048 -14.875 1.00 20.92 N
ATOM 9040 CA GLN B 62 -73.854 -34.636 -15.285 1.00 20.69 C
ATOM 9042 CB GLN B 62 -72.917 -35.847 -15.404 1.00 20.77 C
ATOM 9045 CG GLN B 62 -72.456 -36.369 -14.035 1.00 20.91 C
ATOM 9048 CD GLN B 62 -71.328 -37.383 -14.112 1.00 20.75 C
ATOM 9049 OE1 GLN B 62 -70.512 -37.498 -13.192 1.00 20.93 O
ATOM 9050 NE2 GLN B 62 -71.291 -38.135 -15.195 1.00 20.39 N
ATOM 9053 C GLN B 62 -73.900 -33.834 -16.567 1.00 20.32 C
ATOM 9054 O GLN B 62 -73.410 -32.712 -16.569 1.00 20.79 O
ATOM 9056 N ARG B 63 -74.512 -34.373 -17.625 1.00 19.87 N
ATOM 9057 CA ARG B 63 -74.520 -33.696 -18.940 1.00 19.81 C
ATOM 9059 CB ARG B 63 -75.240 -34.536 -20.013 1.00 19.75 C
ATOM 9062 CG ARG B 63 -74.492 -35.846 -20.345 1.00 21.69 C
ATOM 9065 CD ARG B 63 -75.158 -36.786 -21.368 1.00 24.89 C
ATOM 9068 NE ARG B 63 -74.674 -36.558 -22.741 1.00 29.32 N
ATOM 9070 CZ ARG B 63 -75.323 -35.878 -23.702 1.00 33.71 C
ATOM 9071 NH1 ARG B 63 -76.537 -35.345 -23.510 1.00 36.67 N
ATOM 9074 NH2 ARG B 63 -74.761 -35.736 -24.894 1.00 34.58 N
ATOM 9077 C ARG B 63 -75.099 -32.276 -18.822 1.00 19.39 C
ATOM 9078 O ARG B 63 -74.553 -31.310 -19.395 1.00 19.63 O
ATOM 9080 N LEU B 64 -76.155 -32.148 -18.017 1.00 18.62 N
ATOM 9081 CA LEU B 64 -76.811 -30.856 -17.753 1.00 17.96 C
ATOM 9083 CB LEU B 64 -78.136 -31.077 -17.008 1.00 17.97 C
ATOM 9086 CG LEU B 64 -79.264 -31.737 -17.809 1.00 17.08 C
ATOM 9088 CD1 LEU B 64 -80.276 -32.354 -16.879 1.00 15.15 C
ATOM 9092 CD2 LEU B 64 -79.904 -30.734 -18.737 1.00 15.30 C
ATOM 9096 C LEU B 64 -75.975 -29.847 -16.966 1.00 17.39 C
ATOM 9097 O LEU B 64 -76.370 -28.685 -16.825 1.00 17.38 O
ATOM 9099 N GLY B 65 -74.848 -30.286 -16.432 1.00 16.73 N
ATOM 9100 CA GLY B 65 -73.917 -29.374 -15.818 1.00 16.65 C
ATOM 9103 C GLY B 65 -74.077 -29.249 -14.319 1.00 16.68 C
ATOM 9104 O GLY B 65 -73.565 -28.302 -13.718 1.00 16.79 O
ATOM 9106 N LEU B 66 -74.758 -30.209 -13.702 1.00 16.60 N
ATOM 9107 CA LEU B 66 -74.978 -30.177 -12.264 1.00 16.58 C
ATOM 9109 CB LEU B 66 -76.465 -30.389 -11.957 1.00 16.35 C
ATOM 9112 CG LEU B 66 -77.363 -29.187 -12.234 1.00 15.57 C
ATOM 9114 CD1 LEU B 66 -78.828 -29.602 -12.163 1.00 15.26 C
ATOM 9118 CD2 LEU B 66 -77.063 -28.051 -11.270 1.00 13.66 C
ATOM 9122 C LEU B 66 -74.129 -31.203 -11.513 1.00 16.94 C
ATOM 9123 O LEU B 66 -74.152 -31.251 -10.279 1.00 17.50 O
ATOM 9125 N GLY B 67 -73.373 -32.017 -12.236 1.00 17.03 N
ATOM 9126 CA GLY B 67 -72.541 -33.036 -11.602 1.00 17.13 C
ATOM 9129 C GLY B 67 -71.642 -32.557 -10.461 1.00 17.08 C
ATOM 9130 O GLY B 67 -71.378 -33.317 -9.522 1.00 17.33 O
ATOM 9132 N TYR B 68 -71.159 -31.316 -10.541 1.00 16.83 N
ATOM 9133 CA TYR B 68 -70.217 -30.804 -9.552 1.00 16.64 C
ATOM 9135 CB TYR B 68 -69.654 -29.437 -9.951 1.00 16.25 C
ATOM 9138 CG TYR B 68 -70.609 -28.273 -9.802 1.00 13.51 C
ATOM 9139 CD1 TYR B 68 -70.521 -27.411 -8.738 1.00 10.49 C
ATOM 9141 CE1 TYR B 68 -71.407 -26.342 -8.608 1.00 10.25 C
ATOM 9143 CZ TYR B 68 -72.382 -26.135 -9.555 1.00 9.74 C

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ATOM  9144 OH  TYR B  68    -73.253 -25.086  -9.450  1.00  7.62           O
ATOM  9146 CE2 TYR B  68    -72.484 -26.978 -10.625  1.00 11.14           C
ATOM  9148 CD2 TYR B  68    -71.603 -28.037 -10.748  1.00 12.56           C
ATOM  9150 C   TYR B  68    -70.828 -30.700  -8.172  1.00 17.79           C
ATOM  9151 O   TYR B  68    -70.107 -30.811  -7.182  1.00 18.00           O
ATOM  9153 N   ARG B  69    -72.146 -30.485  -8.090  1.00 18.85           N
ATOM  9154 CA  ARG B  69    -72.784 -30.269  -6.789  1.00 19.46           C
ATOM  9156 CB  ARG B  69    -73.708 -29.047  -6.819  1.00 19.23           C
ATOM  9159 CG  ARG B  69    -75.030 -29.219  -7.509  1.00 18.83           C
ATOM  9162 CD  ARG B  69    -76.053 -28.192  -6.985  1.00 17.73           C
ATOM  9165 NE  ARG B  69    -75.642 -26.830  -7.297  1.00 16.01           N
ATOM  9167 CZ  ARG B  69    -75.330 -25.889  -6.417  1.00 14.68           C
ATOM  9168 NH1 ARG B  69    -75.400 -26.093  -5.112  1.00 14.99           N
ATOM  9171 NH2 ARG B  69    -74.959 -24.707  -6.861  1.00 15.04           N
ATOM  9174 C   ARG B  69    -73.490 -31.489  -6.234  1.00 20.50           C
ATOM  9175 O   ARG B  69    -74.084 -31.418  -5.163  1.00 20.67           O
ATOM  9177 N   PHE B  70    -73.416 -32.607  -6.959  1.00 22.04           N
ATOM  9178 CA  PHE B  70    -73.853 -33.917  -6.450  1.00 23.03           C
ATOM  9180 CB  PHE B  70    -75.081 -34.428  -7.211  1.00 22.94           C
ATOM  9183 CG  PHE B  70    -76.236 -33.503  -7.157  1.00 21.78           C
ATOM  9184 CD1 PHE B  70    -77.024 -33.441  -6.028  1.00 20.54           C
ATOM  9186 CE1 PHE B  70    -78.076 -32.571  -5.959  1.00 20.32           C
ATOM  9188 CZ  PHE B  70    -78.353 -31.752  -7.025  1.00 20.73           C
ATOM  9190 CE2 PHE B  70    -77.564 -31.796  -8.160  1.00 21.24           C
ATOM  9192 CD2 PHE B  70    -76.511 -32.665  -8.220  1.00 21.22           C
ATOM  9194 C   PHE B  70    -72.765 -34.962  -6.570  1.00 24.33           C
ATOM  9195 O   PHE B  70    -73.069 -36.142  -6.614  1.00 24.56           O
ATOM  9197 N   GLU B  71    -71.500 -34.547  -6.624  1.00 26.01           N
ATOM  9198 CA  GLU B  71    -70.413 -35.506  -6.804  1.00 27.04           C
ATOM  9200 CB  GLU B  71    -69.042 -34.824  -6.885  1.00 27.48           C
ATOM  9203 CG  GLU B  71    -67.851 -35.816  -6.794  1.00 28.94           C
ATOM  9206 CD  GLU B  71    -66.491 -35.192  -7.081  1.00 30.38           C
ATOM  9207 OE1 GLU B  71    -66.398 -34.192  -7.835  1.00 30.52           O
ATOM  9208 OE2 GLU B  71    -65.501 -35.730  -6.544  1.00 32.16           O
ATOM  9209 C   GLU B  71    -70.436 -36.531  -5.680  1.00 27.46           C
ATOM  9210 O   GLU B  71    -70.449 -37.723  -5.937  1.00 27.67           O
ATOM  9212 N   SER B  72    -70.464 -36.087  -4.435  1.00 28.04           N
ATOM  9213 CA  SER B  72    -70.381 -37.044  -3.348  1.00 28.86           C
ATOM  9215 CB  SER B  72    -70.388 -36.340  -1.983  1.00 29.09           C
ATOM  9218 OG  SER B  72    -71.649 -35.751  -1.687  1.00 30.21           O
ATOM  9220 C   SER B  72    -71.519 -38.058  -3.481  1.00 29.30           C
ATOM  9221 O   SER B  72    -71.304 -39.265  -3.384  1.00 29.24           O
ATOM  9223 N   ASP B  73    -72.719 -37.560  -3.756  1.00 30.03           N
ATOM  9224 CA  ASP B  73    -73.897 -38.417  -3.874  1.00 30.63           C
ATOM  9226 CB  ASP B  73    -75.184 -37.598  -4.116  1.00 30.74           C
ATOM  9229 CG  ASP B  73    -75.419 -36.509  -3.052  1.00 31.84           C
ATOM  9230 OD1 ASP B  73    -75.562 -36.830  -1.841  1.00 31.70           O
ATOM  9231 OD2 ASP B  73    -75.473 -35.317  -3.443  1.00 33.81           O
ATOM  9232 C   ASP B  73    -73.722 -39.443  -4.994  1.00 30.81           C
ATOM  9233 O   ASP B  73    -74.130 -40.590  -4.835  1.00 31.39           O
ATOM  9235 N   ILE B  74    -73.122 -39.031  -6.112  1.00 30.96           N
ATOM  9236 CA  ILE B  74    -72.917 -39.912  -7.282  1.00 31.04           C
ATOM  9238 CB  ILE B  74    -72.461 -39.114  -8.524  1.00 30.88           C
ATOM  9240 CG1 ILE B  74    -73.585 -38.213  -9.018  1.00 30.99           C
ATOM  9243 CD1 ILE B  74    -73.105 -37.120  -9.923  1.00 31.54           C
ATOM  9247 CG2 ILE B  74    -72.052 -40.035  -9.642  1.00 29.85           C
ATOM  9251 C   ILE B  74    -71.885 -41.005  -6.999  1.00 31.45           C
ATOM  9252 O   ILE B  74    -72.098 -42.165  -7.347  1.00 31.31           O
ATOM  9254 N   ARG B  75    -70.768 -40.628  -6.380  1.00 31.93           N
ATOM  9255 CA  ARG B  75    -69.778 -41.601  -5.947  1.00 32.38           C
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ATOM 9257 CB ARG B 75 -68.629 -40.959 -5.137 1.00 32.87 C
ATOM 9260 CG ARG B 75 -67.310 -40.751 -5.915 1.00 35.01 C
ATOM 9263 CD ARG B 75 -66.089 -40.489 -5.003 1.00 37.62 C
ATOM 9266 NE ARG B 75 -65.260 -41.687 -4.783 1.00 41.03 N
ATOM 9268 CZ ARG B 75 -64.461 -42.253 -5.700 1.00 44.29 C
ATOM 9269 NH1 ARG B 75 -64.385 -41.751 -6.931 1.00 46.22 N
ATOM 9272 NH2 ARG B 75 -63.741 -43.341 -5.404 1.00 44.30 N
ATOM 9275 C ARG B 75 -70.478 -42.673 -5.126 1.00 32.18 C
ATOM 9276 O ARG B 75 -70.307 -43.849 -5.398 1.00 32.19 O
ATOM 9278 N ARG B 76 -71.280 -42.275 -4.143 1.00 32.21 N
ATOM 9279 CA ARG B 76 -71.975 -43.256 -3.307 1.00 32.61 C
ATOM 9281 CB ARG B 76 -72.737 -42.582 -2.162 1.00 32.75 C
ATOM 9284 CG ARG B 76 -71.880 -42.320 -.929 1.00 33.44 C
ATOM 9287 CD ARG B 76 -72.720 -42.046 .334 1.00 34.16 C
ATOM 9290 NE ARG B 76 -73.797 -41.074 .124 1.00 34.53 N
ATOM 9292 CZ ARG B 76 -73.627 -39.765 -.063 1.00 34.38 C
ATOM 9293 NH1 ARG B 76 -72.414 -39.219 -.092 1.00 34.34 N
ATOM 9296 NH2 ARG B 76 -74.689 -38.993 -.241 1.00 34.71 N
ATOM 9299 C ARG B 76 -72.918 -44.159 -4.112 1.00 32.81 C
ATOM 9300 O ARG B 76 -72.863 -45.379 -3.995 1.00 32.86 O
ATOM 9302 N ALA B 77 -73.780 -43.559 -4.923 1.00 33.10 N
ATOM 9303 CA ALA B 77 -74.655 -44.307 -5.813 1.00 33.27 C
ATOM 9305 CB ALA B 77 -75.321 -43.366 -6.770 1.00 33.26 C
ATOM 9309 C ALA B 77 -73.884 -45.370 -6.578 1.00 33.80 C
ATOM 9310 O ALA B 77 -74.235 -46.542 -6.559 1.00 33.75 O
ATOM 9312 N LEU B 78 -72.816 -44.952 -7.242 1.00 34.77 N
ATOM 9313 CA LEU B 78 -71.987 -45.868 -8.019 1.00 35.41 C
ATOM 9315 CB LEU B 78 -70.845 -45.109 -8.702 1.00 35.01 C
ATOM 9318 CG LEU B 78 -71.220 -44.092 -9.782 1.00 34.37 C
ATOM 9320 CD1 LEU B 78 -69.945 -43.502 -10.381 1.00 33.93 C
ATOM 9324 CD2 LEU B 78 -72.109 -44.692 -10.873 1.00 32.94 C
ATOM 9328 C LEU B 78 -71.409 -46.974 -7.142 1.00 36.50 C
ATOM 9329 O LEU B 78 -71.336 -48.124 -7.552 1.00 36.87 O
ATOM 9331 N ASP B 79 -71.005 -46.619 -5.931 1.00 37.74 N
ATOM 9332 CA ASP B 79 -70.308 -47.545 -5.056 1.00 38.74 C
ATOM 9334 CB ASP B 79 -69.787 -46.810 -3.819 1.00 38.99 C
ATOM 9337 CG ASP B 79 -68.499 -47.386 -3.313 1.00 40.08 C
ATOM 9338 OD1 ASP B 79 -68.494 -48.591 -2.976 1.00 42.32 O
ATOM 9339 OD2 ASP B 79 -67.494 -46.638 -3.261 1.00 41.24 O
ATOM 9340 C ASP B 79 -71.207 -48.705 -4.645 1.00 39.42 C
ATOM 9341 O ASP B 79 -70.736 -49.835 -4.505 1.00 39.58 O
ATOM 9343 N ARG B 80 -72.495 -48.424 -4.450 1.00 40.26 N
ATOM 9344 CA ARG B 80 -73.471 -49.470 -4.143 1.00 40.92 C
ATOM 9346 CB ARG B 80 -74.823 -48.881 -3.716 1.00 41.46 C
ATOM 9349 CG ARG B 80 -74.871 -48.247 -2.308 1.00 42.87 C
ATOM 9352 CD ARG B 80 -76.316 -47.826 -1.936 1.00 44.62 C
ATOM 9355 NE ARG B 80 -76.946 -46.968 -2.949 1.00 45.87 N
ATOM 9357 CZ ARG B 80 -76.741 -45.651 -3.089 1.00 46.82 C
ATOM 9358 NH1 ARG B 80 -75.905 -44.989 -2.282 1.00 46.27 N
ATOM 9361 NH2 ARG B 80 -77.378 -44.988 -4.059 1.00 47.22 N
ATOM 9364 C ARG B 80 -73.667 -50.341 -5.371 1.00 40.77 C
ATOM 9365 O ARG B 80 -73.642 -51.563 -5.275 1.00 41.06 O
ATOM 9367 N PHE B 81 -73.863 -49.705 -6.520 1.00 40.56 N
ATOM 9368 CA PHE B 81 -73.986 -50.418 -7.787 1.00 40.59 C
ATOM 9370 CB PHE B 81 -73.984 -49.426 -8.956 1.00 40.73 C
ATOM 9373 CG PHE B 81 -73.898 -50.063 -10.323 1.00 40.84 C
ATOM 9374 CD1 PHE B 81 -75.000 -50.668 -10.893 1.00 41.39 C
ATOM 9376 CE1 PHE B 81 -74.925 -51.236 -12.167 1.00 41.67 C
ATOM 9378 CZ PHE B 81 -73.741 -51.191 -12.877 1.00 41.33 C
ATOM 9380 CE2 PHE B 81 -72.638 -50.580 -12.326 1.00 41.19 C

ATOM 9382 CD2 PHE B 81 -72.720 -50.012 -11.057 1.00 41.39 C
ATOM 9384 C PHE B 81 -72.871 -51.441 -7.953 1.00 40.47 C
ATOM 9385 O PHE B 81 -73.134 -52.583 -8.311 1.00 40.85 O
ATOM 9387 N VAL B 82 -71.633 -51.051 -7.683 1.00 40.26 N
ATOM 9388 CA VAL B 82 -70.522 -51.986 -7.821 1.00 40.24 C
ATOM 9390 CB VAL B 82 -69.173 -51.386 -7.379 1.00 40.28 C
ATOM 9392 CG1 VAL B 82 -68.164 -52.493 -7.063 1.00 39.98 C
ATOM 9396 CG2 VAL B 82 -68.644 -50.462 -8.451 1.00 40.09 C
ATOM 9400 C VAL B 82 -70.788 -53.230 -7.005 1.00 40.16 C
ATOM 9401 O VAL B 82 -70.880 -54.313 -7.559 1.00 40.13 O
ATOM 9403 N SER B 83 -70.953 -53.056 -5.698 1.00 40.26 N
ATOM 9404 CA SER B 83 -71.070 -54.174 -4.749 1.00 40.43 C
ATOM 9406 CB SER B 83 -70.797 -53.666 -3.331 1.00 40.54 C
ATOM 9409 OG SER B 83 -71.256 -52.330 -3.191 1.00 40.89 O
ATOM 9411 C SER B 83 -72.415 -54.912 -4.831 1.00 40.34 C
ATOM 9412 O SER B 83 -73.137 -55.046 -3.845 1.00 39.99 O
ATOM 9414 N SER B 84 -72.698 -55.400 -6.038 1.00 40.57 N
ATOM 9415 CA SER B 84 -73.902 -56.154 -6.411 1.00 40.63 C
ATOM 9417 CB SER B 84 -75.154 -55.679 -5.651 1.00 40.56 C
ATOM 9420 OG SER B 84 -75.292 -54.268 -5.663 1.00 39.82 O
ATOM 9422 C SER B 84 -74.104 -56.026 -7.940 1.00 40.85 C
ATOM 9423 O SER B 84 -75.104 -55.462 -8.395 1.00 41.24 O
ATOM 9425 N GLY B 85 -73.136 -56.524 -8.720 1.00 40.75 N
ATOM 9426 CA GLY B 85 -73.201 -56.506 -10.191 1.00 40.64 C
ATOM 9429 C GLY B 85 -73.225 -55.120 -10.815 1.00 40.64 C
ATOM 9430 O GLY B 85 -74.133 -54.794 -11.590 1.00 40.32 O
ATOM 9432 N THR B 93 -74.847 -57.360 -18.759 1.00 36.30 N
ATOM 9433 CA THR B 93 -75.593 -58.129 -19.774 1.00 35.99 C
ATOM 9435 CB THR B 93 -76.251 -59.379 -19.152 1.00 35.87 C
ATOM 9437 OG1 THR B 93 -76.347 -60.389 -20.158 1.00 35.64 O
ATOM 9439 CG2 THR B 93 -77.646 -59.062 -18.548 1.00 34.95 C
ATOM 9443 C THR B 93 -76.625 -57.274 -20.583 1.00 35.90 C
ATOM 9444 O THR B 93 -77.764 -57.688 -20.843 1.00 35.74 O
ATOM 9446 N SER B 94 -76.175 -56.076 -20.963 1.00 35.58 N
ATOM 9447 CA SER B 94 -76.874 -55.150 -21.866 1.00 34.97 C
ATOM 9449 CB SER B 94 -78.074 -54.472 -21.190 1.00 35.06 C
ATOM 9452 OG SER B 94 -77.702 -53.260 -20.541 1.00 34.37 O
ATOM 9454 C SER B 94 -75.831 -54.097 -22.232 1.00 34.39 C
ATOM 9455 O SER B 94 -75.212 -53.518 -21.341 1.00 34.11 O
ATOM 9457 N LEU B 95 -75.619 -53.864 -23.522 1.00 33.77 N
ATOM 9458 CA LEU B 95 -74.490 -53.045 -23.952 1.00 33.33 C
ATOM 9460 CB LEU B 95 -74.373 -53.010 -25.475 1.00 33.30 C
ATOM 9463 CG LEU B 95 -73.154 -52.246 -26.006 1.00 33.27 C
ATOM 9465 CD1 LEU B 95 -71.909 -52.455 -25.137 1.00 32.89 C
ATOM 9469 CD2 LEU B 95 -72.864 -52.649 -27.438 1.00 33.19 C
ATOM 9473 C LEU B 95 -74.551 -51.623 -23.413 1.00 33.00 C
ATOM 9474 O LEU B 95 -73.588 -51.151 -22.809 1.00 32.83 O
ATOM 9476 N HIS B 96 -75.678 -50.949 -23.633 1.00 32.64 N
ATOM 9477 CA HIS B 96 -75.853 -49.576 -23.171 1.00 32.39 C
ATOM 9479 CB HIS B 96 -77.246 -49.069 -23.527 1.00 32.64 C
ATOM 9482 CG HIS B 96 -77.528 -47.689 -23.025 1.00 34.16 C
ATOM 9483 ND1 HIS B 96 -76.565 -46.703 -22.981 1.00 36.21 N
ATOM 9485 CE1 HIS B 96 -77.096 -45.594 -22.496 1.00 36.92 C
ATOM 9487 NE2 HIS B 96 -78.371 -45.827 -22.227 1.00 37.06 N
ATOM 9489 CD2 HIS B 96 -78.664 -47.130 -22.548 1.00 35.43 C
ATOM 9491 C HIS B 96 -75.612 -49.445 -21.665 1.00 31.78 C
ATOM 9492 O HIS B 96 -74.936 -48.523 -21.215 1.00 31.95 O
ATOM 9494 N GLY B 97 -76.156 -50.372 -20.887 1.00 31.10 N
ATOM 9495 CA GLY B 97 -75.907 -50.396 -19.446 1.00 30.52 C
ATOM 9498 C GLY B 97 -74.434 -50.532 -19.085 1.00 29.95 C

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ATOM  9499  O   GLY B  97    -73.936 -49.797 -18.241  1.00 30.21      O
ATOM  9501  N   THR B  98    -73.740 -51.470 -19.726  1.00 29.15      N
ATOM  9502  CA  THR B  98    -72.314 -51.690 -19.490  1.00 28.55      C
ATOM  9504  CB  THR B  98    -71.803 -52.955 -20.248  1.00 28.48      C
ATOM  9506  OG1 THR B  98    -72.678 -54.066 -19.997  1.00 28.41      O
ATOM  9508  CG2 THR B  98    -70.405 -53.331 -19.816  1.00 27.74      C
ATOM  9512  C   THR B  98    -71.492 -50.452 -19.894  1.00 28.31      C
ATOM  9513  O   THR B  98    -70.658 -49.979 -19.127  1.00 28.13      O
ATOM  9515  N   ALA B  99    -71.750 -49.910 -21.080  1.00 28.04      N
ATOM  9516  CA  ALA B  99    -70.984 -48.758 -21.578  1.00 27.88      C
ATOM  9518  CB  ALA B  99    -71.387 -48.406 -23.014  1.00 27.78      C
ATOM  9522  C   ALA B  99    -71.127 -47.538 -20.684  1.00 27.62      C
ATOM  9523  O   ALA B  99    -70.135 -46.885 -20.361  1.00 27.84      O
ATOM  9525  N   LEU B 100    -72.357 -47.233 -20.290  1.00 27.20      N
ATOM  9526  CA  LEU B 100    -72.613 -46.088 -19.422  1.00 27.08      C
ATOM  9528  CB  LEU B 100    -74.122 -45.900 -19.230  1.00 26.95      C
ATOM  9531  CG  LEU B 100    -74.560 -44.715 -18.367  1.00 26.27      C
ATOM  9533  CD1 LEU B 100    -73.753 -43.478 -18.734  1.00 26.19      C
ATOM  9537  CD2 LEU B 100    -76.052 -44.445 -18.504  1.00 25.20      C
ATOM  9541  C   LEU B 100    -71.928 -46.221 -18.046  1.00 27.23      C
ATOM  9542  O   LEU B 100    -71.368 -45.243 -17.523  1.00 27.16      O
ATOM  9544  N   SER B 101    -71.980 -47.429 -17.472  1.00 27.00      N
ATOM  9545  CA  SER B 101    -71.475 -47.682 -16.117  1.00 26.63      C
ATOM  9547  CB  SER B 101    -72.039 -48.992 -15.568  1.00 26.49      C
ATOM  9550  OG  SER B 101    -71.758 -50.063 -16.442  1.00 26.38      O
ATOM  9552  C   SER B 101    -69.956 -47.740 -16.090  1.00 26.47      C
ATOM  9553  O   SER B 101    -69.326 -47.324 -15.121  1.00 26.35      O
ATOM  9555  N   PHE B 102    -69.381 -48.288 -17.154  1.00 26.29      N
ATOM  9556  CA  PHE B 102    -67.934 -48.332 -17.322  1.00 25.91      C
ATOM  9558  CB  PHE B 102    -67.588 -49.005 -18.652  1.00 25.96      C
ATOM  9561  CG  PHE B 102    -66.133 -49.020 -18.958  1.00 25.81      C
ATOM  9562  CD1 PHE B 102    -65.360 -50.115 -18.633  1.00 25.96      C
ATOM  9564  CE1 PHE B 102    -63.999 -50.122 -18.909  1.00 26.94      C
ATOM  9566  CZ  PHE B 102    -63.403 -49.026 -19.519  1.00 26.27      C
ATOM  9568  CE2 PHE B 102    -64.174 -47.930 -19.848  1.00 26.19      C
ATOM  9570  CD2 PHE B 102    -65.531 -47.933 -19.573  1.00 26.04      C
ATOM  9572  C   PHE B 102    -67.416 -46.911 -17.315  1.00 25.56      C
ATOM  9573  O   PHE B 102    -66.486 -46.564 -16.568  1.00 25.37      O
ATOM  9575  N   ARG B 103    -68.050 -46.095 -18.152  1.00 25.20      N
ATOM  9576  CA  ARG B 103    -67.663 -44.696 -18.322  1.00 25.09      C
ATOM  9578  CB  ARG B 103    -68.510 -44.026 -19.400  1.00 25.12      C
ATOM  9581  CG  ARG B 103    -68.194 -42.561 -19.572  1.00 25.41      C
ATOM  9584  CD  ARG B 103    -68.744 -42.035 -20.889  1.00 26.68      C
ATOM  9587  NE  ARG B 103    -70.197 -41.843 -20.877  1.00 27.49      N
ATOM  9589  CZ  ARG B 103    -70.826 -40.851 -20.246  1.00 26.56      C
ATOM  9590  NH1 ARG B 103    -70.139 -39.963 -19.531  1.00 27.11      N
ATOM  9593  NH2 ARG B 103    -72.148 -40.759 -20.310  1.00 25.20      N
ATOM  9596  C   ARG B 103    -67.785 -43.898 -17.033  1.00 24.61      C
ATOM  9597  O   ARG B 103    -66.865 -43.168 -16.659  1.00 24.67      O
ATOM  9599  N   LEU B 104    -68.927 -44.013 -16.371  1.00 23.79      N
ATOM  9600  CA  LEU B 104    -69.125 -43.263 -15.148  1.00 23.23      C
ATOM  9602  CB  LEU B 104    -70.591 -43.342 -14.693  1.00 23.01      C
ATOM  9605  CG  LEU B 104    -71.607 -42.620 -15.584  1.00 21.36      C
ATOM  9607  CD1 LEU B 104    -73.002 -42.860 -15.067  1.00 19.31      C
ATOM  9611  CD2 LEU B 104    -71.310 -41.157 -15.633  1.00 19.57      C
ATOM  9615  C   LEU B 104    -68.156 -43.781 -14.071  1.00 23.15      C
ATOM  9616  O   LEU B 104    -67.445 -43.007 -13.423  1.00 23.40      O
ATOM  9618  N   LEU B 105    -68.106 -45.091 -13.894  1.00 22.79      N
ATOM  9619  CA  LEU B 105    -67.203 -45.659 -12.916  1.00 22.40      C
ATOM  9621  CB  LEU B 105    -67.303 -47.178 -12.912  1.00 22.42      C
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ATOM 9624 CG LEU B 105 -68.505 -47.709 -12.163 1.00 21.82 C
ATOM 9626 CD1 LEU B 105 -68.810 -49.120 -12.591 1.00 21.95 C
ATOM 9630 CD2 LEU B 105 -68.201 -47.648 -10.692 1.00 22.14 C
ATOM 9634 C LEU B 105 -65.767 -45.239 -13.196 1.00 22.33 C
ATOM 9635 O LEU B 105 -65.049 -44.823 -12.275 1.00 22.13 O
ATOM 9637 N ARG B 106 -65.331 -45.342 -14.451 1.00 22.08 N
ATOM 9638 CA ARG B 106 -63.953 -44.973 -14.730 1.00 22.20 C
ATOM 9640 CB ARG B 106 -63.521 -45.266 -16.151 1.00 22.33 C
ATOM 9643 CG ARG B 106 -62.075 -44.827 -16.329 1.00 23.60 C
ATOM 9646 CD ARG B 106 -61.383 -45.445 -17.513 1.00 24.71 C
ATOM 9649 NE ARG B 106 -61.078 -46.852 -17.319 1.00 24.66 N
ATOM 9651 CZ ARG B 106 -60.418 -47.582 -18.206 1.00 25.75 C
ATOM 9652 NH1 ARG B 106 -59.995 -47.028 -19.337 1.00 26.41 N
ATOM 9655 NH2 ARG B 106 -60.182 -48.866 -17.971 1.00 26.54 N
ATOM 9658 C ARG B 106 -63.732 -43.504 -14.438 1.00 21.75 C
ATOM 9659 O ARG B 106 -62.801 -43.145 -13.725 1.00 21.50 O
ATOM 9661 N GLN B 107 -64.609 -42.680 -15.003 1.00 21.69 N
ATOM 9662 CA GLN B 107 -64.630 -41.239 -14.794 1.00 21.64 C
ATOM 9664 CB GLN B 107 -65.964 -40.664 -15.261 1.00 21.71 C
ATOM 9667 CG GLN B 107 -66.169 -39.178 -14.929 1.00 21.97 C
ATOM 9670 CD GLN B 107 -67.588 -38.723 -15.172 1.00 21.54 C
ATOM 9671 OE1 GLN B 107 -68.355 -39.365 -15.906 1.00 20.08 O
ATOM 9672 NE2 GLN B 107 -67.948 -37.600 -14.556 1.00 21.45 N
ATOM 9675 C GLN B 107 -64.454 -40.850 -13.352 1.00 21.70 C
ATOM 9676 O GLN B 107 -63.776 -39.865 -13.078 1.00 22.14 O
ATOM 9678 N HIS B 108 -65.091 -41.599 -12.450 1.00 21.53 N
ATOM 9679 CA HIS B 108 -65.049 -41.326 -11.019 1.00 21.63 C
ATOM 9681 CB HIS B 108 -66.447 -41.535 -10.429 1.00 21.47 C
ATOM 9684 CG HIS B 108 -67.416 -40.445 -10.752 1.00 20.91 C
ATOM 9685 ND1 HIS B 108 -67.541 -39.315 -9.976 1.00 20.66 N
ATOM 9687 CE1 HIS B 108 -68.476 -38.535 -10.490 1.00 20.90 C
ATOM 9689 NE2 HIS B 108 -68.966 -39.118 -11.567 1.00 19.67 N
ATOM 9691 CD2 HIS B 108 -68.326 -40.320 -11.747 1.00 20.76 C
ATOM 9693 C HIS B 108 -64.024 -42.209 -10.269 1.00 22.22 C
ATOM 9694 O HIS B 108 -64.220 -42.553 -9.104 1.00 22.17 O
ATOM 9696 N GLY B 109 -62.950 -42.613 -10.933 1.00 22.91 N
ATOM 9697 CA GLY B 109 -61.846 -43.288 -10.245 1.00 23.85 C
ATOM 9700 C GLY B 109 -61.986 -44.748 -9.800 1.00 24.50 C
ATOM 9701 O GLY B 109 -61.053 -45.306 -9.189 1.00 24.12 O
ATOM 9703 N PHE B 110 -63.128 -45.371 -10.094 1.00 25.16 N
ATOM 9704 CA PHE B 110 -63.309 -46.791 -9.800 1.00 25.67 C
ATOM 9706 CB PHE B 110 -64.782 -47.187 -9.891 1.00 25.80 C
ATOM 9709 CG PHE B 110 -65.625 -46.656 -8.772 1.00 26.12 C
ATOM 9710 CD1 PHE B 110 -65.564 -47.230 -7.510 1.00 27.13 C
ATOM 9712 CE1 PHE B 110 -66.353 -46.751 -6.468 1.00 27.42 C
ATOM 9714 CZ PHE B 110 -67.215 -45.691 -6.692 1.00 26.93 C
ATOM 9716 CE2 PHE B 110 -67.284 -45.119 -7.954 1.00 26.49 C
ATOM 9718 CD2 PHE B 110 -66.494 -45.601 -8.981 1.00 25.96 C
ATOM 9720 C PHE B 110 -62.505 -47.615 -10.793 1.00 25.92 C
ATOM 9721 O PHE B 110 -62.232 -47.157 -11.898 1.00 26.41 O
ATOM 9723 N GLU B 111 -62.134 -48.832 -10.406 1.00 26.06 N
ATOM 9724 CA GLU B 111 -61.403 -49.724 -11.304 1.00 26.17 C
ATOM 9726 CB GLU B 111 -60.444 -50.609 -10.511 1.00 26.50 C
ATOM 9729 CG GLU B 111 -59.372 -51.272 -11.374 1.00 28.11 C
ATOM 9732 CD GLU B 111 -58.607 -52.377 -10.646 1.00 30.70 C
ATOM 9733 OE1 GLU B 111 -58.660 -52.436 -9.390 1.00 31.99 O
ATOM 9734 OE2 GLU B 111 -57.948 -53.190 -11.338 1.00 32.09 O
ATOM 9735 C GLU B 111 -62.355 -50.598 -12.130 1.00 25.60 C
ATOM 9736 O GLU B 111 -63.116 -51.388 -11.585 1.00 25.48 O
ATOM 9738 N VAL B 112 -62.314 -50.439 -13.447 1.00 25.24 N

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ATOM  9739 CA  VAL B 112    -63.026 -51.331 -14.357  1.00 24.90      C
ATOM  9741 CB  VAL B 112    -64.308 -50.712 -14.908  1.00 24.92      C
ATOM  9743 CG1 VAL B 112    -65.268 -50.437 -13.771  1.00 25.26      C
ATOM  9747 CG2 VAL B 112    -63.999 -49.450 -15.706  1.00 24.77      C
ATOM  9751 C   VAL B 112    -62.144 -51.701 -15.522  1.00 24.66      C
ATOM  9752 O   VAL B 112    -61.217 -50.964 -15.862  1.00 23.80      O
ATOM  9754 N   SER B 113    -62.467 -52.842 -16.132  1.00 24.88      N
ATOM  9755 CA  SER B 113    -61.604 -53.494 -17.109  1.00 25.21      C
ATOM  9757 CB  SER B 113    -61.286 -54.913 -16.654  1.00 24.94      C
ATOM  9760 OG  SER B 113    -60.357 -55.523 -17.528  1.00 24.31      O
ATOM  9762 C   SER B 113    -62.233 -53.532 -18.492  1.00 25.88      C
ATOM  9763 O   SER B 113    -63.446 -53.651 -18.630  1.00 25.86      O
ATOM  9765 N   GLN B 114    -61.406 -53.438 -19.526  1.00 26.92      N
ATOM  9766 CA  GLN B 114    -61.928 -53.491 -20.880  1.00 27.83      C
ATOM  9768 CB  GLN B 114    -60.846 -53.194 -21.917  1.00 27.75      C
ATOM  9771 CG  GLN B 114    -59.559 -53.952 -21.726  1.00 28.05      C
ATOM  9774 CD  GLN B 114    -58.739 -54.077 -23.007  1.00 28.39      C
ATOM  9775 OE1 GLN B 114    -59.086 -53.515 -24.051  1.00 29.05      O
ATOM  9776 NE2 GLN B 114    -57.637 -54.808 -22.925  1.00 27.62      N
ATOM  9779 C   GLN B 114    -62.615 -54.827 -21.158  1.00 28.78      C
ATOM  9780 O   GLN B 114    -63.484 -54.905 -22.022  1.00 29.10      O
ATOM  9782 N   GLU B 115    -62.248 -55.861 -20.401  1.00 29.99      N
ATOM  9783 CA  GLU B 115    -62.888 -57.181 -20.505  1.00 30.89      C
ATOM  9785 CB  GLU B 115    -62.252 -58.202 -19.549  1.00 31.10      C
ATOM  9788 CG  GLU B 115    -60.740 -58.394 -19.697  1.00 32.35      C
ATOM  9791 CD  GLU B 115    -60.320 -58.796 -21.106  1.00 34.20      C
ATOM  9792 OE1 GLU B 115    -60.965 -59.699 -21.688  1.00 34.94      O
ATOM  9793 OE2 GLU B 115    -59.348 -58.201 -21.634  1.00 35.60      O
ATOM  9794 C   GLU B 115    -64.380 -57.120 -20.224  1.00 31.26      C
ATOM  9795 O   GLU B 115    -65.125 -57.971 -20.691  1.00 31.54      O
ATOM  9797 N   ALA B 116    -64.825 -56.127 -19.465  1.00 31.91      N
ATOM  9798 CA  ALA B 116    -66.255 -55.937 -19.259  1.00 32.69      C
ATOM  9800 CB  ALA B 116    -66.521 -54.648 -18.513  1.00 32.62      C
ATOM  9804 C   ALA B 116    -66.999 -55.950 -20.597  1.00 33.33      C
ATOM  9805 O   ALA B 116    -68.156 -56.364 -20.668  1.00 33.26      O
ATOM  9807 N   PHE B 117    -66.316 -55.521 -21.655  1.00 34.16      N
ATOM  9808 CA  PHE B 117    -66.889 -55.498 -22.996  1.00 34.98      C
ATOM  9810 CB  PHE B 117    -66.310 -54.314 -23.766  1.00 35.02      C
ATOM  9813 CG  PHE B 117    -66.868 -52.997 -23.345  1.00 35.06      C
ATOM  9814 CD1 PHE B 117    -66.061 -52.046 -22.729  1.00 35.33      C
ATOM  9816 CE1 PHE B 117    -66.576 -50.825 -22.342  1.00 35.16      C
ATOM  9818 CZ  PHE B 117    -67.907 -50.544 -22.570  1.00 35.37      C
ATOM  9820 CE2 PHE B 117    -68.723 -51.488 -23.187  1.00 35.28      C
ATOM  9822 CD2 PHE B 117    -68.201 -52.701 -23.571  1.00 34.68      C
ATOM  9824 C   PHE B 117    -66.676 -56.766 -23.830  1.00 35.86      C
ATOM  9825 O   PHE B 117    -66.934 -56.755 -25.037  1.00 35.91      O
ATOM  9827 N   SER B 118    -66.215 -57.853 -23.212  1.00 36.98      N
ATOM  9828 CA  SER B 118    -65.924 -59.086 -23.960  1.00 37.76      C
ATOM  9830 CB  SER B 118    -64.836 -59.907 -23.262  1.00 37.73      C
ATOM  9833 OG  SER B 118    -65.272 -60.346 -21.987  1.00 37.77      O
ATOM  9835 C   SER B 118    -67.178 -59.939 -24.215  1.00 38.48      C
ATOM  9836 O   SER B 118    -67.207 -60.724 -25.157  1.00 38.42      O
ATOM  9838 N   GLY B 119    -68.221 -59.765 -23.407  1.00 39.51      N
ATOM  9839 CA  GLY B 119    -69.481 -60.473 -23.629  1.00 40.51      C
ATOM  9842 C   GLY B 119    -70.287 -60.034 -24.848  1.00 41.51      C
ATOM  9843 O   GLY B 119    -71.444 -60.433 -25.002  1.00 41.53      O
ATOM  9845 N   PHE B 120    -69.688 -59.210 -25.709  1.00 42.79      N
ATOM  9846 CA  PHE B 120    -70.382 -58.621 -26.864  1.00 43.81      C
ATOM  9848 CB  PHE B 120    -70.643 -57.121 -26.601  1.00 43.76      C
ATOM  9851 CG  PHE B 120    -71.367 -56.853 -25.293  1.00 43.65      C
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ATOM 9852 CD1 PHE B 120 -72.762 -56.874 -25.230 1.00 43.48 C
ATOM 9854 CE1 PHE B 120 -73.437 -56.650 -24.023 1.00 43.03 C
ATOM 9856 CZ PHE B 120 -72.717 -56.413 -22.865 1.00 43.09 C
ATOM 9858 CE2 PHE B 120 -71.323 -56.397 -22.909 1.00 43.38 C
ATOM 9860 CD2 PHE B 120 -70.655 -56.619 -24.120 1.00 43.41 C
ATOM 9862 C PHE B 120 -69.607 -58.832 -28.175 1.00 44.81 C
ATOM 9863 O PHE B 120 -69.930 -58.238 -29.205 1.00 44.65 O
ATOM 9865 N LYS B 121 -68.602 -59.705 -28.126 1.00 46.19 N
ATOM 9866 CA LYS B 121 -67.757 -60.004 -29.272 1.00 47.31 C
ATOM 9868 CB LYS B 121 -66.275 -59.928 -28.870 1.00 47.47 C
ATOM 9871 CG LYS B 121 -65.743 -58.495 -28.637 1.00 48.13 C
ATOM 9874 CD LYS B 121 -64.532 -58.439 -27.675 1.00 48.89 C
ATOM 9877 CE LYS B 121 -63.261 -59.094 -28.241 1.00 49.20 C
ATOM 9880 NZ LYS B 121 -62.541 -58.232 -29.218 1.00 49.04 N
ATOM 9884 C LYS B 121 -68.096 -61.400 -29.810 1.00 48.15 C
ATOM 9885 O LYS B 121 -68.199 -62.361 -29.043 1.00 48.36 O
ATOM 9887 N ASP B 122 -68.270 -61.510 -31.126 1.00 49.04 N
ATOM 9888 CA ASP B 122 -68.611 -62.788 -31.754 1.00 49.60 C
ATOM 9890 CB ASP B 122 -69.070 -62.596 -33.217 1.00 49.52 C
ATOM 9893 CG ASP B 122 -67.989 -62.015 -34.126 1.00 49.18 C
ATOM 9894 OD1 ASP B 122 -66.792 -62.306 -33.938 1.00 48.96 O
ATOM 9895 OD2 ASP B 122 -68.351 -61.268 -35.057 1.00 48.82 O
ATOM 9896 C ASP B 122 -67.455 -63.785 -31.651 1.00 50.31 C
ATOM 9897 O ASP B 122 -66.369 -63.441 -31.171 1.00 50.33 O
ATOM 9899 N GLN B 123 -67.705 -65.014 -32.098 1.00 51.05 N
ATOM 9900 CA GLN B 123 -66.716 -66.095 -32.057 1.00 51.61 C
ATOM 9902 CB GLN B 123 -67.263 -67.330 -32.785 1.00 51.82 C
ATOM 9905 CG GLN B 123 -68.483 -67.986 -32.117 1.00 52.32 C
ATOM 9908 CD GLN B 123 -68.117 -69.137 -31.184 1.00 52.64 C
ATOM 9909 OE1 GLN B 123 -67.146 -69.062 -30.432 1.00 53.02 O
ATOM 9910 NE2 GLN B 123 -68.904 -70.207 -31.230 1.00 52.04 N
ATOM 9913 C GLN B 123 -65.358 -65.694 -32.659 1.00 51.78 C
ATOM 9914 O GLN B 123 -64.309 -66.000 -32.090 1.00 51.67 O
ATOM 9916 N ASN B 124 -65.388 -65.004 -33.799 1.00 52.05 N
ATOM 9917 CA ASN B 124 -64.166 -64.547 -34.473 1.00 52.25 C
ATOM 9919 CB ASN B 124 -64.486 -64.042 -35.884 1.00 52.25 C
ATOM 9922 CG ASN B 124 -64.911 -65.158 -36.819 1.00 51.88 C
ATOM 9923 OD1 ASN B 124 -65.918 -65.825 -36.592 1.00 51.43 O
ATOM 9924 ND2 ASN B 124 -64.144 -65.364 -37.880 1.00 51.23 N
ATOM 9927 C ASN B 124 -63.382 -63.466 -33.716 1.00 52.43 C
ATOM 9928 O ASN B 124 -62.189 -63.287 -33.959 1.00 52.33 O
ATOM 9930 N GLY B 125 -64.051 -62.747 -32.815 1.00 52.66 N
ATOM 9931 CA GLY B 125 -63.396 -61.745 -31.968 1.00 52.68 C
ATOM 9934 C GLY B 125 -63.916 -60.329 -32.135 1.00 52.63 C
ATOM 9935 O GLY B 125 -63.539 -59.447 -31.367 1.00 52.57 O
ATOM 9937 N ASN B 126 -64.782 -60.117 -33.129 1.00 52.54 N
ATOM 9938 CA ASN B 126 -65.343 -58.793 -33.443 1.00 52.41 C
ATOM 9940 CB ASN B 126 -65.575 -58.671 -34.949 1.00 52.40 C
ATOM 9943 CG ASN B 126 -64.322 -58.951 -35.751 1.00 52.64 C
ATOM 9944 OD1 ASN B 126 -63.426 -59.665 -35.297 1.00 52.77 O
ATOM 9945 ND2 ASN B 126 -64.249 -58.390 -36.952 1.00 53.00 N
ATOM 9948 C ASN B 126 -66.656 -58.524 -32.712 1.00 52.10 C
ATOM 9949 O ASN B 126 -67.253 -59.432 -32.153 1.00 52.27 O
ATOM 9951 N PHE B 127 -67.111 -57.279 -32.724 1.00 51.61 N
ATOM 9952 CA PHE B 127 -68.362 -56.936 -32.055 1.00 51.23 C
ATOM 9954 CB PHE B 127 -68.506 -55.416 -31.905 1.00 51.21 C
ATOM 9957 CG PHE B 127 -67.702 -54.848 -30.770 1.00 50.58 C
ATOM 9958 CD1 PHE B 127 -66.513 -54.192 -31.003 1.00 50.15 C
ATOM 9960 CE1 PHE B 127 -65.777 -53.686 -29.948 1.00 50.15 C
ATOM 9962 CZ PHE B 127 -66.225 -53.839 -28.647 1.00 49.71 C

ATOM 9964 CE2 PHE B 127 -67.399 -54.496 -28.405 1.00 49.50 C
ATOM 9966 CD2 PHE B 127 -68.132 -54.999 -29.459 1.00 49.99 C
ATOM 9968 C PHE B 127 -69.537 -57.505 -32.821 1.00 50.99 C
ATOM 9969 O PHE B 127 -69.468 -57.641 -34.040 1.00 50.92 O
ATOM 9971 N LEU B 128 -70.609 -57.840 -32.106 1.00 50.83 N
ATOM 9972 CA LEU B 128 -71.799 -58.422 -32.731 1.00 50.76 C
ATOM 9974 CB LEU B 128 -72.780 -58.953 -31.669 1.00 50.80 C
ATOM 9977 CG LEU B 128 -72.341 -60.098 -30.734 1.00 50.91 C
ATOM 9979 CD1 LEU B 128 -73.483 -60.532 -29.813 1.00 50.61 C
ATOM 9983 CD2 LEU B 128 -71.818 -61.303 -31.497 1.00 50.79 C
ATOM 9987 C LEU B 128 -72.500 -57.407 -33.646 1.00 50.55 C
ATOM 9988 O LEU B 128 -73.105 -56.455 -33.171 1.00 50.34 O
ATOM 9990 N GLU B 129 -72.402 -57.628 -34.957 1.00 50.50 N
ATOM 9991 CA GLU B 129 -73.038 -56.783 -35.982 1.00 50.48 C
ATOM 9993 CB GLU B 129 -73.150 -57.551 -37.310 1.00 50.68 C
ATOM 9996 CG GLU B 129 -72.262 -57.024 -38.434 1.00 51.36 C
ATOM 9999 CD GLU B 129 -72.799 -55.745 -39.060 1.00 51.88 C
ATOM 10000 OE1 GLU B 129 -72.110 -54.707 -38.961 1.00 52.72 O
ATOM 10001 OE2 GLU B 129 -73.906 -55.773 -39.643 1.00 51.58 O
ATOM 10002 C GLU B 129 -74.428 -56.264 -35.629 1.00 50.25 C
ATOM 10003 O GLU B 129 -74.737 -55.110 -35.899 1.00 50.18 O
ATOM 10005 N ASN B 130 -75.263 -57.125 -35.047 1.00 50.06 N
ATOM 10006 CA ASN B 130 -76.678 -56.806 -34.785 1.00 49.71 C
ATOM 10008 CB ASN B 130 -77.477 -58.100 -34.550 1.00 49.69 C
ATOM 10011 CG ASN B 130 -77.053 -58.837 -33.291 1.00 49.39 C
ATOM 10012 OD1 ASN B 130 -76.357 -59.848 -33.361 1.00 48.74 O
ATOM 10013 ND2 ASN B 130 -77.468 -58.329 -32.134 1.00 48.99 N
ATOM 10016 C ASN B 130 -76.934 -55.800 -33.646 1.00 49.37 C
ATOM 10017 O ASN B 130 -78.083 -55.456 -33.366 1.00 49.29 O
ATOM 10019 N LEU B 131 -75.868 -55.336 -32.996 1.00 48.98 N
ATOM 10020 CA LEU B 131 -75.957 -54.279 -31.988 1.00 48.56 C
ATOM 10022 CB LEU B 131 -74.797 -54.392 -30.991 1.00 48.44 C
ATOM 10025 CG LEU B 131 -74.759 -55.671 -30.148 1.00 48.19 C
ATOM 10027 CD1 LEU B 131 -73.382 -55.852 -29.523 1.00 47.23 C
ATOM 10031 CD2 LEU B 131 -75.861 -55.670 -29.083 1.00 47.77 C
ATOM 10035 C LEU B 131 -75.968 -52.875 -32.604 1.00 48.29 C
ATOM 10036 O LEU B 131 -76.022 -51.895 -31.874 1.00 48.44 O
ATOM 10038 N LYS B 132 -75.927 -52.771 -33.934 1.00 47.95 N
ATOM 10039 CA LYS B 132 -76.020 -51.471 -34.621 1.00 47.64 C
ATOM 10041 CB LYS B 132 -75.548 -51.590 -36.080 1.00 47.63 C
ATOM 10044 CG LYS B 132 -76.595 -52.235 -36.998 1.00 48.19 C
ATOM 10047 CD LYS B 132 -76.111 -52.483 -38.429 1.00 48.16 C
ATOM 10050 CE LYS B 132 -77.239 -53.040 -39.290 1.00 47.23 C
ATOM 10053 NZ LYS B 132 -76.725 -53.936 -40.331 1.00 47.01 N
ATOM 10057 C LYS B 132 -77.449 -50.907 -34.597 1.00 47.13 C
ATOM 10058 O LYS B 132 -77.683 -49.772 -35.005 1.00 46.87 O
ATOM 10060 N GLU B 133 -78.403 -51.716 -34.149 1.00 46.77 N
ATOM 10061 CA GLU B 133 -79.806 -51.315 -34.107 1.00 46.49 C
ATOM 10063 CB GLU B 133 -80.691 -52.458 -34.622 1.00 46.56 C
ATOM 10066 CG GLU B 133 -80.732 -52.515 -36.155 1.00 47.01 C
ATOM 10069 CD GLU B 133 -80.737 -53.926 -36.715 1.00 47.40 C
ATOM 10070 OE1 GLU B 133 -81.500 -54.775 -36.206 1.00 47.97 O
ATOM 10071 OE2 GLU B 133 -79.983 -54.177 -37.679 1.00 47.22 O
ATOM 10072 C GLU B 133 -80.260 -50.830 -32.723 1.00 45.92 C
ATOM 10073 O GLU B 133 -81.369 -50.308 -32.600 1.00 46.14 O
ATOM 10075 N ASP B 134 -79.424 -51.002 -31.691 1.00 44.98 N
ATOM 10076 CA ASP B 134 -79.611 -50.277 -30.428 1.00 44.14 C
ATOM 10078 CB ASP B 134 -79.375 -51.162 -29.197 1.00 43.95 C
ATOM 10081 CG ASP B 134 -79.646 -50.419 -27.883 1.00 43.57 C
ATOM 10082 OD1 ASP B 134 -80.014 -49.230 -27.919 1.00 42.21 O

ATOM 10083 OD2 ASP B 134 -79.488 -51.011 -26.802 1.00 43.69 O
ATOM 10084 C ASP B 134 -78.662 -49.073 -30.426 1.00 43.47 C
ATOM 10085 O ASP B 134 -77.478 -49.196 -30.104 1.00 43.55 O
ATOM 10087 N ILE B 135 -79.198 -47.908 -30.776 1.00 42.47 N
ATOM 10088 CA ILE B 135 -78.375 -46.739 -31.033 1.00 41.65 C
ATOM 10090 CB ILE B 135 -79.080 -45.783 -32.012 1.00 41.45 C
ATOM 10092 CG1 ILE B 135 -78.877 -46.313 -33.434 1.00 41.74 C
ATOM 10095 CD1 ILE B 135 -79.174 -45.331 -34.540 1.00 42.77 C
ATOM 10099 CG2 ILE B 135 -78.533 -44.391 -31.905 1.00 41.68 C
ATOM 10103 C ILE B 135 -77.901 -46.059 -29.746 1.00 41.14 C
ATOM 10104 O ILE B 135 -76.752 -45.624 -29.676 1.00 41.11 O
ATOM 10106 N LYS B 136 -78.742 -45.998 -28.714 1.00 40.53 N
ATOM 10107 CA LYS B 136 -78.281 -45.480 -27.409 1.00 40.10 C
ATOM 10109 CB LYS B 136 -79.431 -45.361 -26.375 1.00 40.40 C
ATOM 10112 CG LYS B 136 -79.910 -46.697 -25.786 1.00 42.49 C
ATOM 10115 CD LYS B 136 -81.002 -46.574 -24.698 1.00 44.79 C
ATOM 10118 CE LYS B 136 -81.599 -47.994 -24.363 1.00 46.03 C
ATOM 10121 NZ LYS B 136 -82.231 -48.149 -22.994 1.00 46.23 N
ATOM 10125 C LYS B 136 -77.104 -46.327 -26.863 1.00 38.85 C
ATOM 10126 O LYS B 136 -76.246 -45.806 -26.143 1.00 38.91 O
ATOM 10128 N ALA B 137 -77.062 -47.617 -27.219 1.00 37.27 N
ATOM 10129 CA ALA B 137 -75.935 -48.486 -26.864 1.00 35.88 C
ATOM 10131 CB ALA B 137 -76.255 -49.952 -27.116 1.00 35.69 C
ATOM 10135 C ALA B 137 -74.708 -48.085 -27.645 1.00 34.63 C
ATOM 10136 O ALA B 137 -73.647 -47.894 -27.055 1.00 34.70 O
ATOM 10138 N ILE B 138 -74.845 -47.946 -28.965 1.00 33.12 N
ATOM 10139 CA ILE B 138 -73.693 -47.597 -29.805 1.00 31.97 C
ATOM 10141 CB ILE B 138 -74.020 -47.572 -31.296 1.00 31.50 C
ATOM 10143 CG1 ILE B 138 -74.433 -48.955 -31.774 1.00 31.28 C
ATOM 10146 CD1 ILE B 138 -73.460 -50.052 -31.417 1.00 30.86 C
ATOM 10150 CG2 ILE B 138 -72.819 -47.138 -32.073 1.00 30.61 C
ATOM 10154 C ILE B 138 -73.124 -46.245 -29.413 1.00 31.57 C
ATOM 10155 O ILE B 138 -71.909 -46.090 -29.305 1.00 31.77 O
ATOM 10157 N LEU B 139 -73.997 -45.268 -29.192 1.00 30.92 N
ATOM 10158 CA LEU B 139 -73.555 -43.962 -28.713 1.00 30.29 C
ATOM 10160 CB LEU B 139 -74.732 -43.000 -28.530 1.00 30.13 C
ATOM 10163 CG LEU B 139 -74.778 -41.890 -29.574 1.00 29.96 C
ATOM 10165 CD1 LEU B 139 -73.496 -41.060 -29.508 1.00 28.26 C
ATOM 10169 CD2 LEU B 139 -76.022 -41.019 -29.397 1.00 29.48 C
ATOM 10173 C LEU B 139 -72.835 -44.136 -27.397 1.00 29.95 C
ATOM 10174 O LEU B 139 -71.709 -43.687 -27.232 1.00 30.45 O
ATOM 10176 N SER B 140 -73.492 -44.807 -26.463 1.00 29.33 N
ATOM 10177 CA SER B 140 -72.916 -45.061 -25.150 1.00 28.84 C
ATOM 10179 CB SER B 140 -73.900 -45.878 -24.298 1.00 28.93 C
ATOM 10182 OG SER B 140 -73.527 -45.870 -22.930 1.00 30.33 O
ATOM 10184 C SER B 140 -71.555 -45.770 -25.243 1.00 27.78 C
ATOM 10185 O SER B 140 -70.637 -45.454 -24.489 1.00 27.46 O
ATOM 10187 N LEU B 141 -71.432 -46.719 -26.167 1.00 26.82 N
ATOM 10188 CA LEU B 141 -70.178 -47.433 -26.348 1.00 26.34 C
ATOM 10190 CB LEU B 141 -70.366 -48.658 -27.256 1.00 26.16 C
ATOM 10193 CG LEU B 141 -69.098 -49.472 -27.584 1.00 26.09 C
ATOM 10195 CD1 LEU B 141 -68.355 -49.960 -26.330 1.00 24.64 C
ATOM 10199 CD2 LEU B 141 -69.455 -50.643 -28.481 1.00 25.94 C
ATOM 10203 C LEU B 141 -69.124 -46.476 -26.914 1.00 25.89 C
ATOM 10204 O LEU B 141 -68.025 -46.346 -26.366 1.00 25.77 O
ATOM 10206 N TYR B 142 -69.471 -45.809 -28.008 1.00 25.41 N
ATOM 10207 CA TYR B 142 -68.609 -44.804 -28.610 1.00 25.03 C
ATOM 10209 CB TYR B 142 -69.399 -43.982 -29.617 1.00 24.80 C
ATOM 10212 CG TYR B 142 -68.736 -42.695 -30.043 1.00 24.47 C
ATOM 10213 CD1 TYR B 142 -67.761 -42.686 -31.029 1.00 24.18 C

ATOM 10215 CE1 TYR B 142 -67.166 -41.516 -31.438 1.00 24.70 C
ATOM 10217 CZ TYR B 142 -67.548 -40.315 -30.871 1.00 25.80 C
ATOM 10218 OH TYR B 142 -66.940 -39.129 -31.279 1.00 27.63 O
ATOM 10220 CE2 TYR B 142 -68.522 -40.299 -29.890 1.00 25.57 C
ATOM 10222 CD2 TYR B 142 -69.110 -41.485 -29.485 1.00 24.73 C
ATOM 10224 C TYR B 142 -68.095 -43.883 -27.537 1.00 25.17 C
ATOM 10225 O TYR B 142 -66.886 -43.732 -27.360 1.00 25.40 O
ATOM 10227 N GLU B 143 -69.038 -43.293 -26.807 1.00 25.12 N
ATOM 10228 CA GLU B 143 -68.744 -42.256 -25.828 1.00 25.10 C
ATOM 10230 CB GLU B 143 -70.046 -41.726 -25.226 1.00 25.33 C
ATOM 10233 CG GLU B 143 -70.006 -40.244 -24.849 1.00 27.57 C
ATOM 10236 CD GLU B 143 -70.321 -39.313 -26.023 1.00 30.43 C
ATOM 10237 OE1 GLU B 143 -69.343 -38.764 -26.583 1.00 32.89 O
ATOM 10238 OE2 GLU B 143 -71.526 -39.130 -26.377 1.00 30.86 O
ATOM 10239 C GLU B 143 -67.794 -42.746 -24.729 1.00 24.43 C
ATOM 10240 O GLU B 143 -67.026 -41.959 -24.179 1.00 24.06 O
ATOM 10242 N ALA B 144 -67.840 -44.050 -24.449 1.00 24.01 N
ATOM 10243 CA ALA B 144 -67.033 -44.681 -23.399 1.00 23.74 C
ATOM 10245 CB ALA B 144 -67.726 -45.943 -22.883 1.00 23.48 C
ATOM 10249 C ALA B 144 -65.631 -45.025 -23.864 1.00 23.57 C
ATOM 10250 O ALA B 144 -64.720 -45.171 -23.060 1.00 23.69 O
ATOM 10252 N SER B 145 -65.455 -45.168 -25.165 1.00 23.45 N
ATOM 10253 CA SER B 145 -64.168 -45.568 -25.701 1.00 23.44 C
ATOM 10255 CB SER B 145 -64.300 -45.856 -27.214 1.00 23.63 C
ATOM 10258 OG SER B 145 -64.822 -44.748 -27.952 1.00 24.24 O
ATOM 10260 C SER B 145 -63.065 -44.520 -25.416 1.00 23.24 C
ATOM 10261 O SER B 145 -61.877 -44.848 -25.288 1.00 23.25 O
ATOM 10263 N PHE B 146 -63.454 -43.257 -25.285 1.00 22.92 N
ATOM 10264 CA PHE B 146 -62.464 -42.189 -25.170 1.00 22.35 C
ATOM 10266 CB PHE B 146 -63.090 -40.837 -25.478 1.00 22.09 C
ATOM 10269 CG PHE B 146 -63.505 -40.717 -26.911 1.00 22.40 C
ATOM 10270 CD1 PHE B 146 -62.619 -40.229 -27.868 1.00 21.98 C
ATOM 10272 CE1 PHE B 146 -62.985 -40.156 -29.201 1.00 21.80 C
ATOM 10274 CZ PHE B 146 -64.241 -40.579 -29.594 1.00 21.91 C
ATOM 10276 CE2 PHE B 146 -65.123 -41.098 -28.649 1.00 22.29 C
ATOM 10278 CD2 PHE B 146 -64.751 -41.170 -27.323 1.00 22.34 C
ATOM 10280 C PHE B 146 -61.762 -42.208 -23.837 1.00 21.91 C
ATOM 10281 O PHE B 146 -60.669 -41.683 -23.733 1.00 22.30 O
ATOM 10283 N LEU B 147 -62.361 -42.864 -22.841 1.00 21.27 N
ATOM 10284 CA LEU B 147 -61.727 -43.050 -21.535 1.00 20.49 C
ATOM 10286 CB LEU B 147 -62.791 -43.333 -20.478 1.00 20.14 C
ATOM 10289 CG LEU B 147 -63.609 -42.109 -20.102 1.00 18.87 C
ATOM 10291 CD1 LEU B 147 -64.813 -42.020 -20.959 1.00 15.94 C
ATOM 10295 CD2 LEU B 147 -63.988 -42.189 -18.642 1.00 18.62 C
ATOM 10299 C LEU B 147 -60.678 -44.163 -21.498 1.00 20.41 C
ATOM 10300 O LEU B 147 -60.243 -44.552 -20.415 1.00 20.44 O
ATOM 10302 N ALA B 148 -60.268 -44.664 -22.662 1.00 20.28 N
ATOM 10303 CA ALA B 148 -59.330 -45.784 -22.745 1.00 20.33 C
ATOM 10305 CB ALA B 148 -59.188 -46.231 -24.194 1.00 20.15 C
ATOM 10309 C ALA B 148 -57.952 -45.462 -22.170 1.00 20.54 C
ATOM 10310 O ALA B 148 -57.435 -44.366 -22.341 1.00 20.23 O
ATOM 10312 N LEU B 149 -57.366 -46.435 -21.486 1.00 21.19 N
ATOM 10313 CA LEU B 149 -55.969 -46.354 -21.067 1.00 22.02 C
ATOM 10315 CB LEU B 149 -55.768 -47.073 -19.725 1.00 21.90 C
ATOM 10318 CG LEU B 149 -56.541 -46.496 -18.523 1.00 21.50 C
ATOM 10320 CD1 LEU B 149 -55.979 -47.006 -17.223 1.00 20.96 C
ATOM 10324 CD2 LEU B 149 -56.520 -44.974 -18.505 1.00 20.95 C
ATOM 10328 C LEU B 149 -55.054 -46.930 -22.159 1.00 22.84 C
ATOM 10329 O LEU B 149 -55.507 -47.678 -23.017 1.00 22.91 O
ATOM 10331 N GLU B 150 -53.781 -46.550 -22.163 1.00 23.93 N

ATOM 10332 CA GLU B 150 -52.858 -47.071 -23.174 1.00 25.03 C
ATOM 10334 CB GLU B 150 -51.472 -46.431 -23.012 1.00 25.41 C
ATOM 10337 CG GLU B 150 -50.530 -46.608 -24.213 1.00 27.44 C
ATOM 10340 CD GLU B 150 -49.132 -45.987 -23.992 1.00 30.04 C
ATOM 10341 OE1 GLU B 150 -48.925 -45.330 -22.943 1.00 31.41 O
ATOM 10342 OE2 GLU B 150 -48.242 -46.161 -24.867 1.00 30.34 O
ATOM 10343 C GLU B 150 -52.787 -48.600 -23.024 1.00 25.36 C
ATOM 10344 O GLU B 150 -52.613 -49.098 -21.911 1.00 25.58 O
ATOM 10346 N GLY B 151 -52.968 -49.337 -24.122 1.00 25.79 N
ATOM 10347 CA GLY B 151 -52.959 -50.816 -24.086 1.00 26.11 C
ATOM 10350 C GLY B 151 -54.323 -51.522 -24.047 1.00 26.44 C
ATOM 10351 O GLY B 151 -54.393 -52.747 -24.135 1.00 26.91 O
ATOM 10353 N GLU B 152 -55.407 -50.768 -23.899 1.00 26.58 N
ATOM 10354 CA GLU B 152 -56.757 -51.319 -23.971 1.00 26.57 C
ATOM 10356 CB GLU B 152 -57.697 -50.531 -23.065 1.00 26.74 C
ATOM 10359 CG GLU B 152 -57.291 -50.595 -21.596 1.00 27.63 C
ATOM 10362 CD GLU B 152 -58.271 -49.893 -20.668 1.00 28.86 C
ATOM 10363 OE1 GLU B 152 -58.239 -50.192 -19.449 1.00 28.80 O
ATOM 10364 OE2 GLU B 152 -59.066 -49.044 -21.154 1.00 29.26 O
ATOM 10365 C GLU B 152 -57.254 -51.303 -25.415 1.00 26.53 C
ATOM 10366 O GLU B 152 -57.937 -50.381 -25.869 1.00 26.00 O
ATOM 10368 N ASN B 153 -56.888 -52.354 -26.127 1.00 26.77 N
ATOM 10369 CA ASN B 153 -57.189 -52.498 -27.545 1.00 27.05 C
ATOM 10371 CB ASN B 153 -56.345 -53.640 -28.104 1.00 27.12 C
ATOM 10374 CG ASN B 153 -56.770 -54.992 -27.549 1.00 27.81 C
ATOM 10375 OD1 ASN B 153 -56.540 -55.307 -26.379 1.00 27.65 O
ATOM 10376 ND2 ASN B 153 -57.426 -55.782 -28.382 1.00 29.43 N
ATOM 10379 C ASN B 153 -58.659 -52.788 -27.873 1.00 27.09 C
ATOM 10380 O ASN B 153 -59.053 -52.658 -29.029 1.00 27.11 O
ATOM 10382 N ILE B 154 -59.448 -53.223 -26.884 1.00 27.17 N
ATOM 10383 CA ILE B 154 -60.865 -53.544 -27.100 1.00 27.11 C
ATOM 10385 CB ILE B 154 -61.454 -54.369 -25.956 1.00 26.99 C
ATOM 10387 CG1 ILE B 154 -60.811 -55.750 -25.907 1.00 27.16 C
ATOM 10390 CD1 ILE B 154 -61.309 -56.622 -24.746 1.00 27.41 C
ATOM 10394 CG2 ILE B 154 -62.953 -54.519 -26.124 1.00 26.65 C
ATOM 10398 C ILE B 154 -61.704 -52.284 -27.229 1.00 27.43 C
ATOM 10399 O ILE B 154 -62.718 -52.279 -27.939 1.00 27.39 O
ATOM 10401 N LEU B 155 -61.296 -51.226 -26.522 1.00 27.76 N
ATOM 10402 CA LEU B 155 -61.964 -49.918 -26.609 1.00 27.75 C
ATOM 10404 CB LEU B 155 -61.578 -49.024 -25.430 1.00 27.31 C
ATOM 10407 CG LEU B 155 -61.968 -49.544 -24.052 1.00 26.64 C
ATOM 10409 CD1 LEU B 155 -61.444 -48.631 -22.981 1.00 25.82 C
ATOM 10413 CD2 LEU B 155 -63.465 -49.674 -23.944 1.00 26.45 C
ATOM 10417 C LEU B 155 -61.620 -49.226 -27.924 1.00 28.32 C
ATOM 10418 O LEU B 155 -62.499 -48.672 -28.583 1.00 28.72 O
ATOM 10420 N ASP B 156 -60.348 -49.264 -28.309 1.00 28.84 N
ATOM 10421 CA ASP B 156 -59.934 -48.737 -29.601 1.00 29.43 C
ATOM 10423 CB ASP B 156 -58.423 -48.928 -29.823 1.00 29.92 C
ATOM 10426 CG ASP B 156 -57.566 -47.912 -29.045 1.00 31.35 C
ATOM 10427 OD1 ASP B 156 -57.803 -46.680 -29.162 1.00 33.23 O
ATOM 10428 OD2 ASP B 156 -56.640 -48.351 -28.324 1.00 33.08 O
ATOM 10429 C ASP B 156 -60.719 -49.411 -30.717 1.00 29.36 C
ATOM 10430 O ASP B 156 -61.075 -48.768 -31.697 1.00 29.33 O
ATOM 10432 N GLU B 157 -60.981 -50.705 -30.558 1.00 29.63 N
ATOM 10433 CA GLU B 157 -61.845 -51.457 -31.479 1.00 29.98 C
ATOM 10435 CB GLU B 157 -61.729 -52.971 -31.234 1.00 30.30 C
ATOM 10438 CG GLU B 157 -60.664 -53.647 -32.087 1.00 31.79 C
ATOM 10441 CD GLU B 157 -60.075 -54.901 -31.439 1.00 33.87 C
ATOM 10442 OE1 GLU B 157 -60.793 -55.560 -30.640 1.00 35.07 O
ATOM 10443 OE2 GLU B 157 -58.894 -55.223 -31.743 1.00 33.70 O

ATOM 10444 C GLU B 157 -63.304 -51.030 -31.349 1.00 29.53 C
ATOM 10445 O GLU B 157 -63.999 -50.878 -32.351 1.00 29.53 O
ATOM 10447 N ALA B 158 -63.758 -50.853 -30.112 1.00 29.11 N
ATOM 10448 CA ALA B 158 -65.104 -50.370 -29.840 1.00 28.87 C
ATOM 10450 CB ALA B 158 -65.307 -50.195 -28.351 1.00 28.82 C
ATOM 10454 C ALA B 158 -65.383 -49.065 -30.567 1.00 28.73 C
ATOM 10455 O ALA B 158 -66.485 -48.857 -31.065 1.00 28.80 O
ATOM 10457 N LYS B 159 -64.385 -48.197 -30.642 1.00 28.65 N
ATOM 10458 CA LYS B 159 -64.553 -46.910 -31.296 1.00 28.98 C
ATOM 10460 CB LYS B 159 -63.439 -45.950 -30.857 1.00 29.16 C
ATOM 10463 CG LYS B 159 -63.558 -44.536 -31.426 1.00 29.82 C
ATOM 10466 CD LYS B 159 -62.812 -43.493 -30.592 1.00 30.96 C
ATOM 10469 CE LYS B 159 -61.295 -43.610 -30.691 1.00 31.57 C
ATOM 10472 NZ LYS B 159 -60.630 -42.426 -30.079 1.00 31.49 N
ATOM 10476 C LYS B 159 -64.594 -47.041 -32.826 1.00 29.08 C
ATOM 10477 O LYS B 159 -65.385 -46.372 -33.486 1.00 28.73 O
ATOM 10479 N VAL B 160 -63.736 -47.891 -33.386 1.00 29.53 N
ATOM 10480 CA VAL B 160 -63.686 -48.087 -34.836 1.00 29.89 C
ATOM 10482 CB VAL B 160 -62.466 -48.971 -35.282 1.00 29.93 C
ATOM 10484 CG1 VAL B 160 -62.576 -49.375 -36.756 1.00 29.58 C
ATOM 10488 CG2 VAL B 160 -61.152 -48.244 -35.040 1.00 29.41 C
ATOM 10492 C VAL B 160 -65.001 -48.723 -35.263 1.00 30.32 C
ATOM 10493 O VAL B 160 -65.507 -48.459 -36.362 1.00 30.41 O
ATOM 10495 N PHE B 161 -65.558 -49.540 -34.371 1.00 30.83 N
ATOM 10496 CA PHE B 161 -66.854 -50.178 -34.599 1.00 31.34 C
ATOM 10498 CB PHE B 161 -67.090 -51.321 -33.599 1.00 31.34 C
ATOM 10501 CG PHE B 161 -68.492 -51.834 -33.603 1.00 31.09 C
ATOM 10502 CD1 PHE B 161 -68.940 -52.636 -34.633 1.00 31.61 C
ATOM 10504 CE1 PHE B 161 -70.249 -53.098 -34.649 1.00 31.48 C
ATOM 10506 CZ PHE B 161 -71.114 -52.748 -33.628 1.00 30.76 C
ATOM 10508 CE2 PHE B 161 -70.677 -51.944 -32.606 1.00 30.19 C
ATOM 10510 CD2 PHE B 161 -69.378 -51.486 -32.597 1.00 30.70 C
ATOM 10512 C PHE B 161 -67.992 -49.173 -34.504 1.00 31.65 C
ATOM 10513 O PHE B 161 -68.785 -49.038 -35.432 1.00 31.62 O
ATOM 10515 N ALA B 162 -68.068 -48.483 -33.373 1.00 32.26 N
ATOM 10516 CA ALA B 162 -69.135 -47.519 -33.129 1.00 32.84 C
ATOM 10518 CB ALA B 162 -68.948 -46.854 -31.778 1.00 32.66 C
ATOM 10522 C ALA B 162 -69.224 -46.474 -34.245 1.00 33.40 C
ATOM 10523 O ALA B 162 -70.229 -46.408 -34.937 1.00 33.45 O
ATOM 10525 N ILE B 163 -68.164 -45.697 -34.444 1.00 34.38 N
ATOM 10526 CA ILE B 163 -68.166 -44.610 -35.439 1.00 35.23 C
ATOM 10528 CB ILE B 163 -66.734 -44.062 -35.733 1.00 35.18 C
ATOM 10530 CG1 ILE B 163 -66.092 -43.457 -34.488 1.00 35.21 C
ATOM 10533 CD1 ILE B 163 -64.620 -43.171 -34.663 1.00 35.96 C
ATOM 10537 CG2 ILE B 163 -66.778 -42.977 -36.799 1.00 34.72 C
ATOM 10541 C ILE B 163 -68.778 -45.052 -36.766 1.00 36.18 C
ATOM 10542 O ILE B 163 -69.588 -44.335 -37.360 1.00 35.87 O
ATOM 10544 N SER B 164 -68.379 -46.240 -37.217 1.00 37.67 N
ATOM 10545 CA SER B 164 -68.761 -46.752 -38.539 1.00 38.74 C
ATOM 10547 CB SER B 164 -68.104 -48.117 -38.815 1.00 38.80 C
ATOM 10550 OG SER B 164 -68.733 -49.158 -38.077 1.00 39.07 O
ATOM 10552 C SER B 164 -70.277 -46.861 -38.699 1.00 39.51 C
ATOM 10553 O SER B 164 -70.820 -46.494 -39.737 1.00 39.96 O
ATOM 10555 N HIS B 165 -70.962 -47.363 -37.680 1.00 40.28 N
ATOM 10556 CA HIS B 165 -72.410 -47.485 -37.767 1.00 41.07 C
ATOM 10558 CB HIS B 165 -72.911 -48.686 -36.957 1.00 41.38 C
ATOM 10561 CG HIS B 165 -72.571 -50.005 -37.587 1.00 42.65 C
ATOM 10562 ND1 HIS B 165 -71.647 -50.875 -37.046 1.00 43.54 N
ATOM 10564 CE1 HIS B 165 -71.535 -51.938 -37.825 1.00 43.54 C
ATOM 10566 NE2 HIS B 165 -72.346 -51.785 -38.858 1.00 43.25 N

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ATOM  10568 CD2 HIS B 165    -73.001 -50.582 -38.737  1.00 43.31      C
ATOM  10570 C   HIS B 165    -73.125 -46.193 -37.380  1.00 41.21      C
ATOM  10571 O   HIS B 165    -74.257 -45.980 -37.805  1.00 41.53      O
ATOM  10573 N   LEU B 166    -72.459 -45.326 -36.614  1.00 41.32      N
ATOM  10574 CA  LEU B 166    -73.042 -44.039 -36.201  1.00 41.31      C
ATOM  10576 CB  LEU B 166    -72.317 -43.460 -34.973  1.00 41.14      C
ATOM  10579 CG  LEU B 166    -72.732 -43.975 -33.589  1.00 40.03      C
ATOM  10581 CD1 LEU B 166    -71.673 -43.634 -32.579  1.00 38.86      C
ATOM  10585 CD2 LEU B 166    -74.077 -43.421 -33.151  1.00 38.52      C
ATOM  10589 C   LEU B 166    -73.045 -42.992 -37.313  1.00 41.80      C
ATOM  10590 O   LEU B 166    -74.006 -42.230 -37.442  1.00 41.73      O
ATOM  10592 N   LYS B 167    -71.982 -42.947 -38.116  1.00 42.47      N
ATOM  10593 CA  LYS B 167    -71.847 -41.891 -39.137  1.00 43.00      C
ATOM  10595 CB  LYS B 167    -70.416 -41.822 -39.702  1.00 43.12      C
ATOM  10598 CG  LYS B 167    -69.937 -43.068 -40.450  1.00 44.12      C
ATOM  10601 CD  LYS B 167    -69.138 -42.725 -41.736  1.00 45.36      C
ATOM  10604 CE  LYS B 167    -67.898 -41.842 -41.483  1.00 45.65      C
ATOM  10607 NZ  LYS B 167    -67.267 -41.400 -42.762  1.00 44.94      N
ATOM  10611 C   LYS B 167    -72.873 -41.950 -40.283  1.00 42.99      C
ATOM  10612 O   LYS B 167    -72.826 -41.124 -41.182  1.00 42.95      O
ATOM  10614 N   GLU B 168    -73.791 -42.912 -40.244  1.00 43.23      N
ATOM  10615 CA  GLU B 168    -74.928 -42.940 -41.167  1.00 43.44      C
ATOM  10617 CB  GLU B 168    -74.652 -43.969 -42.272  1.00 43.58      C
ATOM  10620 CG  GLU B 168    -73.918 -43.363 -43.501  1.00 44.36      C
ATOM  10623 CD  GLU B 168    -72.618 -44.082 -43.895  1.00 44.53      C
ATOM  10624 OE1 GLU B 168    -71.853 -44.494 -42.992  1.00 44.71      O
ATOM  10625 OE2 GLU B 168    -72.351 -44.197 -45.115  1.00 43.31      O
ATOM  10626 C   GLU B 168    -76.263 -43.214 -40.442  1.00 43.24      C
ATOM  10627 O   GLU B 168    -76.932 -42.291 -39.942  1.00 42.54      O
ATOM  10629 N   GLY B 175    -83.548 -42.037 -36.239  1.00 49.43      N
ATOM  10630 CA  GLY B 175    -84.473 -41.266 -35.416  1.00 49.54      C
ATOM  10633 C   GLY B 175    -84.709 -39.884 -36.001  1.00 49.76      C
ATOM  10634 O   GLY B 175    -84.828 -39.741 -37.220  1.00 49.70      O
ATOM  10636 N   LYS B 176    -84.766 -38.870 -35.131  1.00 49.95      N
ATOM  10637 CA  LYS B 176    -85.014 -37.468 -35.534  1.00 50.05      C
ATOM  10639 CB  LYS B 176    -86.522 -37.225 -35.730  1.00 50.27      C
ATOM  10642 CG  LYS B 176    -87.301 -36.813 -34.460  1.00 51.33      C
ATOM  10645 CD  LYS B 176    -88.553 -37.658 -34.202  1.00 52.21      C
ATOM  10648 CE  LYS B 176    -88.841 -37.754 -32.695  1.00 52.36      C
ATOM  10651 NZ  LYS B 176    -90.029 -38.607 -32.422  1.00 52.15      N
ATOM  10655 C   LYS B 176    -84.427 -36.432 -34.554  1.00 49.75      C
ATOM  10656 O   LYS B 176    -83.990 -35.370 -34.972  1.00 49.88      O
ATOM  10658 N   GLU B 177    -84.473 -36.729 -33.254  1.00 49.46      N
ATOM  10659 CA  GLU B 177    -83.769 -35.959 -32.221  1.00 48.92      C
ATOM  10661 CB  GLU B 177    -84.628 -35.813 -30.946  1.00 49.03      C
ATOM  10664 CG  GLU B 177    -84.196 -36.691 -29.732  1.00 49.60      C
ATOM  10667 CD  GLU B 177    -85.278 -36.871 -28.662  1.00 50.10      C
ATOM  10668 OE1 GLU B 177    -84.998 -37.576 -27.670  1.00 49.78      O
ATOM  10669 OE2 GLU B 177    -86.401 -36.336 -28.808  1.00 50.78      O
ATOM  10670 C   GLU B 177    -82.469 -36.703 -31.924  1.00 48.19      C
ATOM  10671 O   GLU B 177    -81.421 -36.085 -31.721  1.00 48.68      O
ATOM  10673 N   LEU B 178    -82.557 -38.037 -31.900  1.00 46.98      N
ATOM  10674 CA  LEU B 178    -81.398 -38.924 -31.817  1.00 45.91      C
ATOM  10676 CB  LEU B 178    -81.838 -40.387 -31.945  1.00 45.70      C
ATOM  10679 CG  LEU B 178    -81.111 -41.408 -31.074  1.00 45.24      C
ATOM  10681 CD1 LEU B 178    -81.498 -41.225 -29.609  1.00 44.88      C
ATOM  10685 CD2 LEU B 178    -81.413 -42.826 -31.539  1.00 44.19      C
ATOM  10689 C   LEU B 178    -80.423 -38.571 -32.934  1.00 45.27      C
ATOM  10690 O   LEU B 178    -79.211 -38.624 -32.759  1.00 44.99      O
ATOM  10692 N   ALA B 179    -80.970 -38.203 -34.088  1.00 44.75      N
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ATOM 10693 CA ALA B 179 -80.174 -37.661 -35.181 1.00 44.24 C
ATOM 10695 CB ALA B 179 -81.088 -37.069 -36.231 1.00 44.30 C
ATOM 10699 C ALA B 179 -79.192 -36.602 -34.683 1.00 43.65 C
ATOM 10700 O ALA B 179 -78.028 -36.604 -35.061 1.00 43.56 O
ATOM 10702 N GLU B 180 -79.675 -35.707 -33.827 1.00 43.01 N
ATOM 10703 CA GLU B 180 -78.863 -34.610 -33.311 1.00 42.49 C
ATOM 10705 CB GLU B 180 -79.749 -33.477 -32.789 1.00 42.85 C
ATOM 10708 CG GLU B 180 -80.574 -32.800 -33.881 1.00 44.23 C
ATOM 10711 CD GLU B 180 -80.991 -31.382 -33.519 1.00 45.80 C
ATOM 10712 OE1 GLU B 180 -80.098 -30.580 -33.156 1.00 46.69 O
ATOM 10713 OE2 GLU B 180 -82.203 -31.065 -33.610 1.00 46.71 O
ATOM 10714 C GLU B 180 -77.944 -35.075 -32.210 1.00 41.39 C
ATOM 10715 O GLU B 180 -76.843 -34.562 -32.071 1.00 41.27 O
ATOM 10717 N GLN B 181 -78.404 -36.035 -31.419 1.00 40.20 N
ATOM 10718 CA GLN B 181 -77.570 -36.632 -30.394 1.00 39.45 C
ATOM 10720 CB GLN B 181 -78.280 -37.809 -29.736 1.00 39.88 C
ATOM 10723 CG GLN B 181 -78.005 -37.959 -28.249 1.00 41.64 C
ATOM 10726 CD GLN B 181 -78.873 -37.036 -27.404 1.00 44.00 C
ATOM 10727 OE1 GLN B 181 -80.109 -36.992 -27.581 1.00 45.65 O
ATOM 10728 NE2 GLN B 181 -78.235 -36.291 -26.474 1.00 43.41 N
ATOM 10731 C GLN B 181 -76.270 -37.120 -31.003 1.00 38.28 C
ATOM 10732 O GLN B 181 -75.203 -36.767 -30.523 1.00 38.27 O
ATOM 10734 N VAL B 182 -76.358 -37.911 -32.072 1.00 37.05 N
ATOM 10735 CA VAL B 182 -75.160 -38.515 -32.675 1.00 36.20 C
ATOM 10737 CB VAL B 182 -75.486 -39.661 -33.681 1.00 36.11 C
ATOM 10739 CG1 VAL B 182 -76.493 -40.641 -33.080 1.00 36.13 C
ATOM 10743 CG2 VAL B 182 -75.977 -39.106 -35.004 1.00 36.06 C
ATOM 10747 C VAL B 182 -74.238 -37.495 -33.364 1.00 35.44 C
ATOM 10748 O VAL B 182 -73.012 -37.682 -33.375 1.00 35.19 O
ATOM 10750 N SER B 183 -74.811 -36.432 -33.936 1.00 34.41 N
ATOM 10751 CA SER B 183 -73.998 -35.416 -34.630 1.00 33.74 C
ATOM 10753 CB SER B 183 -74.858 -34.438 -35.422 1.00 33.58 C
ATOM 10756 OG SER B 183 -76.003 -35.085 -35.925 1.00 34.52 O
ATOM 10758 C SER B 183 -73.184 -34.644 -33.625 1.00 32.88 C
ATOM 10759 O SER B 183 -72.055 -34.251 -33.906 1.00 33.25 O
ATOM 10761 N HIS B 184 -73.788 -34.427 -32.461 1.00 31.83 N
ATOM 10762 CA HIS B 184 -73.150 -33.787 -31.326 1.00 30.98 C
ATOM 10764 CB HIS B 184 -74.188 -33.627 -30.212 1.00 31.14 C
ATOM 10767 CG HIS B 184 -73.710 -32.849 -29.030 1.00 31.91 C
ATOM 10768 ND1 HIS B 184 -73.326 -31.527 -29.114 1.00 33.18 N
ATOM 10770 CE1 HIS B 184 -72.960 -31.107 -27.914 1.00 33.10 C
ATOM 10772 NE2 HIS B 184 -73.106 -32.102 -27.056 1.00 31.85 N
ATOM 10774 CD2 HIS B 184 -73.583 -33.200 -27.727 1.00 31.86 C
ATOM 10776 C HIS B 184 -71.968 -34.632 -30.865 1.00 30.13 C
ATOM 10777 O HIS B 184 -70.863 -34.122 -30.709 1.00 29.95 O
ATOM 10779 N ALA B 185 -72.194 -35.931 -30.683 1.00 29.27 N
ATOM 10780 CA ALA B 185 -71.123 -36.856 -30.281 1.00 28.64 C
ATOM 10782 CB ALA B 185 -71.689 -38.233 -29.986 1.00 28.44 C
ATOM 10786 C ALA B 185 -70.017 -36.965 -31.330 1.00 28.08 C
ATOM 10787 O ALA B 185 -68.839 -37.043 -30.992 1.00 28.26 O
ATOM 10789 N LEU B 186 -70.394 -36.984 -32.602 1.00 27.40 N
ATOM 10790 CA LEU B 186 -69.412 -37.101 -33.674 1.00 26.84 C
ATOM 10792 CB LEU B 186 -70.088 -37.481 -35.000 1.00 26.75 C
ATOM 10795 CG LEU B 186 -70.085 -38.983 -35.320 1.00 26.70 C
ATOM 10797 CD1 LEU B 186 -70.214 -39.868 -34.075 1.00 27.07 C
ATOM 10801 CD2 LEU B 186 -71.179 -39.306 -36.303 1.00 26.29 C
ATOM 10805 C LEU B 186 -68.594 -35.822 -33.815 1.00 26.45 C
ATOM 10806 O LEU B 186 -67.449 -35.875 -34.237 1.00 26.48 O
ATOM 10808 N GLU B 187 -69.186 -34.685 -33.454 1.00 25.93 N
ATOM 10809 CA GLU B 187 -68.479 -33.406 -33.403 1.00 25.57 C

ATOM 10811 CB GLU B 187 -69.447 -32.310 -32.962 1.00 25.61 C
ATOM 10814 CG GLU B 187 -69.035 -30.899 -33.325 1.00 26.29 C
ATOM 10817 CD GLU B 187 -69.930 -29.857 -32.671 1.00 27.10 C
ATOM 10818 OE1 GLU B 187 -70.312 -30.057 -31.487 1.00 26.51 O
ATOM 10819 OE2 GLU B 187 -70.251 -28.846 -33.344 1.00 27.54 O
ATOM 10820 C GLU B 187 -67.307 -33.490 -32.418 1.00 25.13 C
ATOM 10821 O GLU B 187 -66.155 -33.165 -32.749 1.00 24.85 O
ATOM 10823 N LEU B 188 -67.625 -33.938 -31.204 1.00 24.58 N
ATOM 10824 CA LEU B 188 -66.644 -34.137 -30.148 1.00 24.06 C
ATOM 10826 CB LEU B 188 -66.343 -32.817 -29.451 1.00 24.12 C
ATOM 10829 CG LEU B 188 -65.042 -32.714 -28.670 1.00 23.61 C
ATOM 10831 CD1 LEU B 188 -63.895 -32.872 -29.629 1.00 23.12 C
ATOM 10835 CD2 LEU B 188 -64.976 -31.368 -27.964 1.00 23.18 C
ATOM 10839 C LEU B 188 -67.248 -35.087 -29.140 1.00 23.70 C
ATOM 10840 O LEU B 188 -68.392 -34.901 -28.743 1.00 23.68 O
ATOM 10842 N PRO B 189 -66.493 -36.106 -28.713 1.00 23.34 N
ATOM 10843 CA PRO B 189 -67.031 -36.983 -27.692 1.00 23.08 C
ATOM 10845 CB PRO B 189 -66.018 -38.115 -27.638 1.00 22.96 C
ATOM 10848 CG PRO B 189 -64.743 -37.452 -27.940 1.00 23.22 C
ATOM 10851 CD PRO B 189 -65.059 -36.350 -28.929 1.00 23.54 C
ATOM 10854 C PRO B 189 -67.053 -36.229 -26.387 1.00 22.86 C
ATOM 10855 O PRO B 189 -66.284 -35.285 -26.215 1.00 23.03 O
ATOM 10856 N LEU B 190 -67.912 -36.628 -25.465 1.00 22.56 N
ATOM 10857 CA LEU B 190 -68.152 -35.773 -24.323 1.00 22.41 C
ATOM 10859 CB LEU B 190 -69.567 -35.970 -23.766 1.00 23.04 C
ATOM 10862 CG LEU B 190 -69.853 -37.136 -22.848 1.00 23.41 C
ATOM 10864 CD1 LEU B 190 -69.303 -36.733 -21.481 1.00 25.02 C
ATOM 10868 CD2 LEU B 190 -71.342 -37.411 -22.820 1.00 21.69 C
ATOM 10872 C LEU B 190 -67.065 -35.899 -23.266 1.00 21.56 C
ATOM 10873 O LEU B 190 -66.860 -34.976 -22.477 1.00 21.67 O
ATOM 10875 N HIS B 191 -66.320 -36.998 -23.283 1.00 20.39 N
ATOM 10876 CA HIS B 191 -65.089 -37.037 -22.490 1.00 19.40 C
ATOM 10878 CB HIS B 191 -64.399 -38.393 -22.597 1.00 19.19 C
ATOM 10881 CG HIS B 191 -63.222 -38.530 -21.689 1.00 19.32 C
ATOM 10882 ND1 HIS B 191 -63.347 -38.562 -20.317 1.00 20.95 N
ATOM 10884 CE1 HIS B 191 -62.145 -38.659 -19.771 1.00 21.15 C
ATOM 10886 NE2 HIS B 191 -61.245 -38.689 -20.741 1.00 19.36 N
ATOM 10888 CD2 HIS B 191 -61.893 -38.604 -21.948 1.00 19.49 C
ATOM 10890 C HIS B 191 -64.094 -35.913 -22.841 1.00 18.62 C
ATOM 10891 O HIS B 191 -63.150 -35.677 -22.085 1.00 18.59 O
ATOM 10893 N ARG B 192 -64.307 -35.216 -23.957 1.00 17.72 N
ATOM 10894 CA ARG B 192 -63.394 -34.150 -24.394 1.00 17.57 C
ATOM 10896 CB ARG B 192 -62.838 -34.504 -25.773 1.00 17.81 C
ATOM 10899 CG ARG B 192 -61.971 -35.736 -25.781 1.00 18.59 C
ATOM 10902 CD ARG B 192 -61.484 -36.067 -27.181 1.00 20.10 C
ATOM 10905 NE ARG B 192 -60.462 -37.116 -27.165 1.00 21.62 N
ATOM 10907 CZ ARG B 192 -59.919 -37.648 -28.254 1.00 22.77 C
ATOM 10908 NH1 ARG B 192 -60.304 -37.248 -29.454 1.00 24.20 N
ATOM 10911 NH2 ARG B 192 -58.987 -38.581 -28.149 1.00 23.37 N
ATOM 10914 C ARG B 192 -63.983 -32.726 -24.440 1.00 17.01 C
ATOM 10915 O ARG B 192 -63.242 -31.739 -24.526 1.00 15.78 O
ATOM 10917 N ARG B 193 -65.309 -32.634 -24.392 1.00 17.01 N
ATOM 10918 CA ARG B 193 -66.015 -31.350 -24.453 1.00 16.99 C
ATOM 10920 CB ARG B 193 -67.476 -31.582 -24.892 1.00 17.29 C
ATOM 10923 CG ARG B 193 -68.192 -30.318 -25.377 1.00 18.42 C
ATOM 10926 CD ARG B 193 -69.664 -30.559 -25.646 1.00 19.63 C
ATOM 10929 NE ARG B 193 -69.912 -31.592 -26.648 1.00 21.16 N
ATOM 10931 CZ ARG B 193 -69.868 -31.398 -27.971 1.00 23.56 C
ATOM 10932 NH1 ARG B 193 -69.575 -30.210 -28.496 1.00 23.37 N
ATOM 10935 NH2 ARG B 193 -70.112 -32.413 -28.789 1.00 25.37 N

ATOM 10938 C ARG B 193 -65.974 -30.658 -23.087 1.00 16.46 C
ATOM 10939 O ARG B 193 -66.040 -31.323 -22.034 1.00 16.47 O
ATOM 10941 N THR B 194 -65.864 -29.335 -23.078 1.00 15.84 N
ATOM 10942 CA THR B 194 -65.886 -28.629 -21.799 1.00 15.67 C
ATOM 10944 CB THR B 194 -65.354 -27.199 -21.884 1.00 15.48 C
ATOM 10946 OG1 THR B 194 -66.077 -26.478 -22.882 1.00 15.55 O
ATOM 10948 CG2 THR B 194 -63.877 -27.189 -22.211 1.00 14.65 C
ATOM 10952 C THR B 194 -67.310 -28.613 -21.270 1.00 15.79 C
ATOM 10953 O THR B 194 -68.264 -28.652 -22.030 1.00 15.73 O
ATOM 10955 N GLN B 195 -67.444 -28.557 -19.957 1.00 16.20 N
ATOM 10956 CA GLN B 195 -68.737 -28.711 -19.328 1.00 16.84 C
ATOM 10958 CB GLN B 195 -68.601 -28.781 -17.816 1.00 17.07 C
ATOM 10961 CG GLN B 195 -69.921 -28.440 -17.153 1.00 18.86 C
ATOM 10964 CD GLN B 195 -69.999 -28.875 -15.746 1.00 20.95 C
ATOM 10965 OE1 GLN B 195 -69.099 -29.511 -15.245 1.00 24.63 O
ATOM 10966 NE2 GLN B 195 -71.071 -28.529 -15.082 1.00 22.36 N
ATOM 10969 C GLN B 195 -69.757 -27.623 -19.669 1.00 16.93 C
ATOM 10970 O GLN B 195 -70.858 -27.931 -20.136 1.00 16.98 O
ATOM 10972 N ARG B 196 -69.430 -26.366 -19.386 1.00 16.92 N
ATOM 10973 CA ARG B 196 -70.358 -25.301 -19.685 1.00 17.06 C
ATOM 10975 CB ARG B 196 -69.719 -23.932 -19.459 1.00 17.00 C
ATOM 10978 CG ARG B 196 -70.095 -23.289 -18.120 1.00 17.09 C
ATOM 10981 CD ARG B 196 -70.283 -24.320 -16.995 1.00 17.56 C
ATOM 10984 NE ARG B 196 -71.452 -24.043 -16.146 1.00 17.64 N
ATOM 10986 CZ ARG B 196 -72.289 -24.965 -15.664 1.00 17.93 C
ATOM 10987 NH1 ARG B 196 -72.136 -26.244 -15.966 1.00 17.72 N
ATOM 10990 NH2 ARG B 196 -73.305 -24.611 -14.878 1.00 18.27 N
ATOM 10993 C ARG B 196 -70.881 -25.481 -21.098 1.00 17.42 C
ATOM 10994 O ARG B 196 -72.079 -25.519 -21.317 1.00 17.66 O
ATOM 10996 N LEU B 197 -69.984 -25.676 -22.044 1.00 18.04 N
ATOM 10997 CA LEU B 197 -70.379 -25.925 -23.425 1.00 18.51 C
ATOM 10999 CB LEU B 197 -69.133 -26.085 -24.289 1.00 18.52 C
ATOM 11002 CG LEU B 197 -68.998 -25.185 -25.508 1.00 18.06 C
ATOM 11004 CD1 LEU B 197 -68.209 -23.932 -25.205 1.00 15.52 C
ATOM 11008 CD2 LEU B 197 -68.293 -26.002 -26.574 1.00 20.21 C
ATOM 11012 C LEU B 197 -71.290 -27.163 -23.580 1.00 19.14 C
ATOM 11013 O LEU B 197 -72.226 -27.150 -24.372 1.00 19.52 O
ATOM 11015 N GLU B 198 -71.030 -28.235 -22.842 1.00 19.72 N
ATOM 11016 CA GLU B 198 -71.918 -29.396 -22.909 1.00 20.43 C
ATOM 11018 CB GLU B 198 -71.272 -30.631 -22.270 1.00 20.65 C
ATOM 11021 CG GLU B 198 -72.176 -31.880 -22.172 1.00 22.51 C
ATOM 11024 CD GLU B 198 -72.635 -32.460 -23.522 1.00 25.57 C
ATOM 11025 OE1 GLU B 198 -72.315 -31.896 -24.581 1.00 28.90 O
ATOM 11026 OE2 GLU B 198 -73.326 -33.506 -23.540 1.00 28.09 O
ATOM 11027 C GLU B 198 -73.271 -29.101 -22.259 1.00 20.72 C
ATOM 11028 O GLU B 198 -74.281 -29.693 -22.644 1.00 20.82 O
ATOM 11030 N ALA B 199 -73.282 -28.199 -21.270 1.00 20.86 N
ATOM 11031 CA ALA B 199 -74.508 -27.814 -20.565 1.00 20.66 C
ATOM 11033 CB ALA B 199 -74.176 -27.013 -19.326 1.00 20.36 C
ATOM 11037 C ALA B 199 -75.472 -27.033 -21.461 1.00 20.84 C
ATOM 11038 O ALA B 199 -76.644 -27.404 -21.590 1.00 20.84 O
ATOM 11040 N VAL B 200 -75.002 -25.961 -22.092 1.00 21.12 N
ATOM 11041 CA VAL B 200 -75.903 -25.177 -22.942 1.00 21.60 C
ATOM 11043 CB VAL B 200 -75.215 -24.042 -23.701 1.00 21.30 C
ATOM 11045 CG1 VAL B 200 -74.660 -23.055 -22.738 1.00 21.26 C
ATOM 11049 CG2 VAL B 200 -74.135 -24.575 -24.626 1.00 21.28 C
ATOM 11053 C VAL B 200 -76.603 -26.077 -23.944 1.00 22.32 C
ATOM 11054 O VAL B 200 -77.791 -25.908 -24.218 1.00 22.32 O
ATOM 11056 N TRP B 201 -75.872 -27.047 -24.472 1.00 23.16 N
ATOM 11057 CA TRP B 201 -76.441 -27.946 -25.454 1.00 24.02 C

ATOM 11059 CB TRP B 201 -75.348 -28.718 -26.195 1.00 24.36 C
ATOM 11062 CG TRP B 201 -75.898 -29.510 -27.331 1.00 24.84 C
ATOM 11063 CD1 TRP B 201 -76.060 -29.092 -28.613 1.00 25.41 C
ATOM 11065 NE1 TRP B 201 -76.599 -30.094 -29.374 1.00 25.61 N
ATOM 11067 CE2 TRP B 201 -76.807 -31.184 -28.579 1.00 25.34 C
ATOM 11068 CD2 TRP B 201 -76.374 -30.847 -27.279 1.00 25.56 C
ATOM 11069 CE3 TRP B 201 -76.466 -31.800 -26.264 1.00 27.13 C
ATOM 11071 CZ3 TRP B 201 -76.989 -33.046 -26.574 1.00 28.66 C
ATOM 11073 CH2 TRP B 201 -77.419 -33.347 -27.885 1.00 28.01 C
ATOM 11075 CZ2 TRP B 201 -77.332 -32.425 -28.894 1.00 26.09 C
ATOM 11077 C TRP B 201 -77.411 -28.938 -24.833 1.00 24.22 C
ATOM 11078 O TRP B 201 -78.473 -29.172 -25.383 1.00 24.83 O
ATOM 11080 N SER B 202 -77.034 -29.541 -23.715 1.00 24.39 N
ATOM 11081 CA SER B 202 -77.818 -30.626 -23.144 1.00 24.50 C
ATOM 11083 CB SER B 202 -76.968 -31.455 -22.184 1.00 24.42 C
ATOM 11086 OG SER B 202 -75.848 -32.021 -22.848 1.00 23.80 O
ATOM 11088 C SER B 202 -79.067 -30.099 -22.441 1.00 24.98 C
ATOM 11089 O SER B 202 -80.057 -30.816 -22.324 1.00 24.73 O
ATOM 11091 N ILE B 203 -79.032 -28.849 -21.982 1.00 25.60 N
ATOM 11092 CA ILE B 203 -80.219 -28.255 -21.372 1.00 25.98 C
ATOM 11094 CB ILE B 203 -79.908 -26.967 -20.591 1.00 25.85 C
ATOM 11096 CG1 ILE B 203 -79.086 -27.326 -19.348 1.00 25.76 C
ATOM 11099 CD1 ILE B 203 -78.779 -26.159 -18.431 1.00 26.28 C
ATOM 11103 CG2 ILE B 203 -81.212 -26.253 -20.206 1.00 24.51 C
ATOM 11107 C ILE B 203 -81.280 -28.016 -22.443 1.00 26.67 C
ATOM 11108 O ILE B 203 -82.428 -28.398 -22.260 1.00 26.96 O
ATOM 11110 N GLU B 204 -80.879 -27.412 -23.563 1.00 27.30 N
ATOM 11111 CA GLU B 204 -81.758 -27.205 -24.720 1.00 27.49 C
ATOM 11113 CB GLU B 204 -81.036 -26.384 -25.804 1.00 27.67 C
ATOM 11116 CG GLU B 204 -81.849 -26.077 -27.073 1.00 28.50 C
ATOM 11119 CD GLU B 204 -82.987 -25.072 -26.855 1.00 29.81 C
ATOM 11120 OE1 GLU B 204 -83.158 -24.600 -25.711 1.00 31.40 O
ATOM 11121 OE2 GLU B 204 -83.710 -24.750 -27.832 1.00 29.57 O
ATOM 11122 C GLU B 204 -82.201 -28.542 -25.287 1.00 27.52 C
ATOM 11123 O GLU B 204 -83.321 -28.667 -25.738 1.00 27.67 O
ATOM 11125 N ALA B 205 -81.326 -29.539 -25.266 1.00 27.74 N
ATOM 11126 CA ALA B 205 -81.684 -30.872 -25.728 1.00 28.09 C
ATOM 11128 CB ALA B 205 -80.472 -31.789 -25.726 1.00 27.75 C
ATOM 11132 C ALA B 205 -82.771 -31.448 -24.839 1.00 28.81 C
ATOM 11133 O ALA B 205 -83.811 -31.877 -25.325 1.00 28.90 O
ATOM 11135 N TYR B 206 -82.517 -31.433 -23.531 1.00 29.72 N
ATOM 11136 CA TYR B 206 -83.408 -32.020 -22.527 1.00 30.30 C
ATOM 11138 CB TYR B 206 -82.760 -31.915 -21.149 1.00 30.24 C
ATOM 11141 CG TYR B 206 -83.276 -32.889 -20.127 1.00 29.79 C
ATOM 11142 CD1 TYR B 206 -83.055 -34.245 -20.286 1.00 30.71 C
ATOM 11144 CE1 TYR B 206 -83.498 -35.161 -19.360 1.00 30.78 C
ATOM 11146 CZ TYR B 206 -84.159 -34.731 -18.238 1.00 30.03 C
ATOM 11147 OH TYR B 206 -84.582 -35.684 -17.343 1.00 30.51 O
ATOM 11149 CE2 TYR B 206 -84.394 -33.379 -18.042 1.00 29.42 C
ATOM 11151 CD2 TYR B 206 -83.945 -32.463 -18.989 1.00 29.05 C
ATOM 11153 C TYR B 206 -84.744 -31.308 -22.467 1.00 31.19 C
ATOM 11154 O TYR B 206 -85.790 -31.930 -22.311 1.00 31.44 O
ATOM 11156 N ARG B 207 -84.683 -29.988 -22.558 1.00 32.21 N
ATOM 11157 CA ARG B 207 -85.853 -29.128 -22.521 1.00 33.04 C
ATOM 11159 CB ARG B 207 -85.394 -27.700 -22.843 1.00 32.86 C
ATOM 11162 CG ARG B 207 -86.441 -26.637 -22.846 1.00 32.82 C
ATOM 11165 CD ARG B 207 -85.905 -25.360 -23.462 1.00 32.76 C
ATOM 11168 NE ARG B 207 -85.148 -24.561 -22.504 1.00 32.80 N
ATOM 11170 CZ ARG B 207 -85.676 -23.709 -21.628 1.00 33.40 C
ATOM 11171 NH1 ARG B 207 -86.989 -23.526 -21.555 1.00 34.29 N

ATOM 11174 NH2 ARG B 207 -84.884 -23.030 -20.808 1.00 33.89 N
ATOM 11177 C ARG B 207 -86.971 -29.606 -23.478 1.00 34.14 C
ATOM 11178 O ARG B 207 -88.144 -29.521 -23.128 1.00 34.34 O
ATOM 11180 N LYS B 208 -86.607 -30.137 -24.652 1.00 35.32 N
ATOM 11181 CA LYS B 208 -87.581 -30.535 -25.688 1.00 36.16 C
ATOM 11183 CB LYS B 208 -86.960 -30.468 -27.090 1.00 36.01 C
ATOM 11186 CG LYS B 208 -86.126 -29.234 -27.368 1.00 35.85 C
ATOM 11189 CD LYS B 208 -85.934 -29.023 -28.861 1.00 35.98 C
ATOM 11192 CE LYS B 208 -84.774 -28.086 -29.186 1.00 35.63 C
ATOM 11195 NZ LYS B 208 -83.566 -28.843 -29.596 1.00 35.17 N
ATOM 11199 C LYS B 208 -88.166 -31.937 -25.490 1.00 37.25 C
ATOM 11200 O LYS B 208 -89.212 -32.250 -26.054 1.00 37.50 O
ATOM 11202 N LYS B 209 -87.484 -32.788 -24.730 1.00 38.58 N
ATOM 11203 CA LYS B 209 -88.026 -34.106 -24.383 1.00 39.89 C
ATOM 11205 CB LYS B 209 -87.013 -34.923 -23.578 1.00 40.23 C
ATOM 11208 CG LYS B 209 -85.914 -35.604 -24.373 1.00 41.47 C
ATOM 11211 CD LYS B 209 -84.858 -36.178 -23.417 1.00 43.71 C
ATOM 11214 CE LYS B 209 -84.448 -37.612 -23.764 1.00 45.15 C
ATOM 11217 NZ LYS B 209 -85.390 -38.621 -23.163 1.00 45.73 N
ATOM 11221 C LYS B 209 -89.288 -33.950 -23.530 1.00 40.51 C
ATOM 11222 O LYS B 209 -89.230 -33.367 -22.441 1.00 40.84 O
ATOM 11224 N GLU B 210 -90.418 -34.477 -24.000 1.00 40.92 N
ATOM 11225 CA GLU B 210 -91.652 -34.386 -23.223 1.00 41.27 C
ATOM 11227 CB GLU B 210 -92.855 -34.935 -23.998 1.00 41.77 C
ATOM 11230 CG GLU B 210 -92.822 -36.446 -24.265 1.00 43.47 C
ATOM 11233 CD GLU B 210 -94.049 -36.922 -25.032 1.00 45.23 C
ATOM 11234 OE1 GLU B 210 -95.188 -36.590 -24.612 1.00 45.02 O
ATOM 11235 OE2 GLU B 210 -93.863 -37.629 -26.053 1.00 46.74 O
ATOM 11236 C GLU B 210 -91.494 -35.121 -21.895 1.00 40.71 C
ATOM 11237 O GLU B 210 -91.996 -34.667 -20.864 1.00 40.99 O
ATOM 11239 N ASP B 211 -90.773 -36.240 -21.924 1.00 39.76 N
ATOM 11240 CA ASP B 211 -90.533 -37.050 -20.721 1.00 38.96 C
ATOM 11242 CB ASP B 211 -90.151 -38.476 -21.123 1.00 39.10 C
ATOM 11245 CG ASP B 211 -89.101 -38.499 -22.212 1.00 40.26 C
ATOM 11246 OD1 ASP B 211 -89.327 -37.827 -23.254 1.00 41.25 O
ATOM 11247 OD2 ASP B 211 -88.055 -39.160 -22.020 1.00 41.66 O
ATOM 11248 C ASP B 211 -89.440 -36.468 -19.826 1.00 37.75 C
ATOM 11249 O ASP B 211 -89.009 -37.131 -18.892 1.00 37.62 O
ATOM 11251 N ALA B 212 -88.989 -35.245 -20.115 1.00 36.47 N
ATOM 11252 CA ALA B 212 -87.941 -34.587 -19.335 1.00 35.36 C
ATOM 11254 CB ALA B 212 -87.516 -33.294 -20.011 1.00 35.23 C
ATOM 11258 C ALA B 212 -88.423 -34.307 -17.920 1.00 34.40 C
ATOM 11259 O ALA B 212 -89.559 -33.870 -17.728 1.00 34.42 O
ATOM 11261 N ASN B 213 -87.565 -34.574 -16.937 1.00 33.24 N
ATOM 11262 CA ASN B 213 -87.890 -34.333 -15.533 1.00 32.67 C
ATOM 11264 CB ASN B 213 -86.840 -34.986 -14.623 1.00 32.58 C
ATOM 11267 CG ASN B 213 -87.204 -34.912 -13.152 1.00 32.67 C
ATOM 11268 OD1 ASN B 213 -87.891 -33.994 -12.722 1.00 32.62 O
ATOM 11269 ND2 ASN B 213 -86.734 -35.882 -12.371 1.00 33.18 N
ATOM 11272 C ASN B 213 -87.990 -32.825 -15.266 1.00 32.19 C
ATOM 11273 O ASN B 213 -87.010 -32.092 -15.376 1.00 32.38 O
ATOM 11275 N GLN B 214 -89.182 -32.356 -14.923 1.00 31.48 N
ATOM 11276 CA GLN B 214 -89.389 -30.924 -14.756 1.00 30.85 C
ATOM 11278 CB GLN B 214 -90.889 -30.581 -14.693 1.00 30.82 C
ATOM 11281 CG GLN B 214 -91.684 -30.869 -16.002 1.00 30.80 C
ATOM 11284 CD GLN B 214 -90.990 -30.378 -17.291 1.00 29.69 C
ATOM 11285 OE1 GLN B 214 -90.893 -29.174 -17.543 1.00 29.07 O
ATOM 11286 NE2 GLN B 214 -90.526 -31.321 -18.113 1.00 27.71 N
ATOM 11289 C GLN B 214 -88.638 -30.369 -13.543 1.00 30.37 C
ATOM 11290 O GLN B 214 -88.263 -29.200 -13.533 1.00 30.80 O

ATOM 11292 N VAL B 215 -88.393 -31.200 -12.532 1.00 29.54 N
ATOM 11293 CA VAL B 215 -87.566 -30.779 -11.395 1.00 28.56 C
ATOM 11295 CB VAL B 215 -87.564 -31.818 -10.260 1.00 28.64 C
ATOM 11297 CG1 VAL B 215 -86.758 -31.299 -9.075 1.00 27.94 C
ATOM 11301 CG2 VAL B 215 -88.999 -32.167 -9.856 1.00 28.26 C
ATOM 11305 C VAL B 215 -86.124 -30.545 -11.845 1.00 27.63 C
ATOM 11306 O VAL B 215 -85.566 -29.472 -11.615 1.00 27.58 O
ATOM 11308 N LEU B 216 -85.546 -31.548 -12.504 1.00 26.37 N
ATOM 11309 CA LEU B 216 -84.143 -31.509 -12.930 1.00 25.47 C
ATOM 11311 CB LEU B 216 -83.714 -32.866 -13.490 1.00 25.46 C
ATOM 11314 CG LEU B 216 -82.274 -32.995 -13.979 1.00 24.97 C
ATOM 11316 CD1 LEU B 216 -81.289 -32.640 -12.883 1.00 24.62 C
ATOM 11320 CD2 LEU B 216 -82.042 -34.407 -14.472 1.00 24.55 C
ATOM 11324 C LEU B 216 -83.861 -30.447 -13.972 1.00 24.68 C
ATOM 11325 O LEU B 216 -82.819 -29.820 -13.929 1.00 24.91 O
ATOM 11327 N LEU B 217 -84.776 -30.269 -14.916 1.00 23.79 N
ATOM 11328 CA LEU B 217 -84.625 -29.260 -15.960 1.00 23.13 C
ATOM 11330 CB LEU B 217 -85.765 -29.384 -16.972 1.00 23.36 C
ATOM 11333 CG LEU B 217 -85.808 -28.374 -18.123 1.00 23.18 C
ATOM 11335 CD1 LEU B 217 -84.462 -28.268 -18.796 1.00 22.69 C
ATOM 11339 CD2 LEU B 217 -86.861 -28.786 -19.126 1.00 23.38 C
ATOM 11343 C LEU B 217 -84.631 -27.853 -15.383 1.00 22.51 C
ATOM 11344 O LEU B 217 -83.903 -26.973 -15.855 1.00 22.08 O
ATOM 11346 N GLU B 218 -85.481 -27.647 -14.375 1.00 21.84 N
ATOM 11347 CA GLU B 218 -85.619 -26.339 -13.725 1.00 21.26 C
ATOM 11349 CB GLU B 218 -86.813 -26.341 -12.768 1.00 21.27 C
ATOM 11352 CG GLU B 218 -87.206 -24.956 -12.246 1.00 21.35 C
ATOM 11355 CD GLU B 218 -88.501 -24.964 -11.441 1.00 20.89 C
ATOM 11356 OE1 GLU B 218 -89.097 -26.052 -11.263 1.00 20.47 O
ATOM 11357 OE2 GLU B 218 -88.915 -23.874 -10.986 1.00 20.15 O
ATOM 11358 C GLU B 218 -84.348 -26.001 -12.969 1.00 20.58 C
ATOM 11359 O GLU B 218 -83.877 -24.865 -12.982 1.00 20.31 O
ATOM 11361 N LEU B 219 -83.802 -27.015 -12.312 1.00 19.87 N
ATOM 11362 CA LEU B 219 -82.559 -26.885 -11.592 1.00 19.12 C
ATOM 11364 CB LEU B 219 -82.310 -28.132 -10.746 1.00 18.58 C
ATOM 11367 CG LEU B 219 -81.159 -28.054 -9.762 1.00 17.07 C
ATOM 11369 CD1 LEU B 219 -81.321 -26.847 -8.872 1.00 16.10 C
ATOM 11373 CD2 LEU B 219 -81.107 -29.311 -8.954 1.00 15.22 C
ATOM 11377 C LEU B 219 -81.443 -26.675 -12.599 1.00 19.16 C
ATOM 11378 O LEU B 219 -80.684 -25.721 -12.478 1.00 19.42 O
ATOM 11380 N ALA B 220 -81.368 -27.546 -13.606 1.00 19.04 N
ATOM 11381 CA ALA B 220 -80.356 -27.431 -14.669 1.00 19.04 C
ATOM 11383 CB ALA B 220 -80.648 -28.398 -15.817 1.00 18.64 C
ATOM 11387 C ALA B 220 -80.257 -26.004 -15.196 1.00 19.06 C
ATOM 11388 O ALA B 220 -79.159 -25.472 -15.321 1.00 19.08 O
ATOM 11390 N ILE B 221 -81.410 -25.393 -15.475 1.00 19.19 N
ATOM 11391 CA ILE B 221 -81.473 -24.016 -15.963 1.00 19.22 C
ATOM 11393 CB ILE B 221 -82.898 -23.638 -16.423 1.00 19.03 C
ATOM 11395 CG1 ILE B 221 -83.229 -24.323 -17.755 1.00 18.52 C
ATOM 11398 CD1 ILE B 221 -84.687 -24.645 -17.928 1.00 17.52 C
ATOM 11402 CG2 ILE B 221 -83.024 -22.121 -16.564 1.00 18.03 C
ATOM 11406 C ILE B 221 -81.030 -23.013 -14.906 1.00 19.62 C
ATOM 11407 O ILE B 221 -80.137 -22.190 -15.136 1.00 19.53 O
ATOM 11409 N LEU B 222 -81.666 -23.096 -13.745 1.00 20.27 N
ATOM 11410 CA LEU B 222 -81.412 -22.161 -12.654 1.00 20.63 C
ATOM 11412 CB LEU B 222 -82.203 -22.561 -11.412 1.00 20.50 C
ATOM 11415 CG LEU B 222 -82.195 -21.523 -10.296 1.00 20.76 C
ATOM 11417 CD1 LEU B 222 -83.439 -21.675 -9.431 1.00 21.02 C
ATOM 11421 CD2 LEU B 222 -80.924 -21.625 -9.453 1.00 20.21 C
ATOM 11425 C LEU B 222 -79.925 -22.089 -12.341 1.00 20.98 C

ATOM 11426 O LEU B 222 -79.337 -21.011 -12.381 1.00 21.40 O
ATOM 11428 N ASP B 223 -79.319 -23.240 -12.064 1.00 21.24 N
ATOM 11429 CA ASP B 223 -77.907 -23.298 -11.709 1.00 21.48 C
ATOM 11431 CB ASP B 223 -77.509 -24.724 -11.314 1.00 21.66 C
ATOM 11434 CG ASP B 223 -76.168 -24.792 -10.589 1.00 22.70 C
ATOM 11435 OD1 ASP B 223 -75.095 -24.775 -11.244 1.00 24.25 O
ATOM 11436 OD2 ASP B 223 -76.190 -24.893 -9.349 1.00 24.85 O
ATOM 11437 C ASP B 223 -77.017 -22.768 -12.835 1.00 21.64 C
ATOM 11438 O ASP B 223 -76.035 -22.104 -12.548 1.00 21.66 O
ATOM 11440 N TYR B 224 -77.361 -23.023 -14.100 1.00 22.07 N
ATOM 11441 CA TYR B 224 -76.517 -22.561 -15.218 1.00 22.47 C
ATOM 11443 CB TYR B 224 -76.980 -23.111 -16.589 1.00 22.35 C
ATOM 11446 CG TYR B 224 -76.032 -22.733 -17.724 1.00 22.25 C
ATOM 11447 CD1 TYR B 224 -75.002 -23.576 -18.116 1.00 21.46 C
ATOM 11449 CE1 TYR B 224 -74.126 -23.216 -19.135 1.00 21.43 C
ATOM 11451 CZ TYR B 224 -74.260 -21.991 -19.761 1.00 21.62 C
ATOM 11452 OH TYR B 224 -73.387 -21.618 -20.760 1.00 20.46 O
ATOM 11454 CE2 TYR B 224 -75.270 -21.132 -19.387 1.00 22.04 C
ATOM 11456 CD2 TYR B 224 -76.144 -21.500 -18.373 1.00 22.73 C
ATOM 11458 C TYR B 224 -76.414 -21.023 -15.262 1.00 23.06 C
ATOM 11459 O TYR B 224 -75.323 -20.467 -15.507 1.00 22.89 O
ATOM 11461 N ASN B 225 -77.543 -20.350 -15.027 1.00 23.66 N
ATOM 11462 CA ASN B 225 -77.593 -18.884 -15.072 1.00 24.16 C
ATOM 11464 CB ASN B 225 -79.040 -18.367 -15.107 1.00 24.12 C
ATOM 11467 CG ASN B 225 -79.778 -18.761 -16.365 1.00 23.89 C
ATOM 11468 OD1 ASN B 225 -79.182 -18.877 -17.437 1.00 24.33 O
ATOM 11469 ND2 ASN B 225 -81.088 -18.965 -16.244 1.00 22.05 N
ATOM 11472 C ASN B 225 -76.880 -18.265 -13.881 1.00 24.73 C
ATOM 11473 O ASN B 225 -76.195 -17.247 -14.027 1.00 25.09 O
ATOM 11475 N MET B 226 -77.067 -18.864 -12.703 1.00 25.15 N
ATOM 11476 CA MET B 226 -76.423 -18.390 -11.479 1.00 25.53 C
ATOM 11478 CB MET B 226 -76.806 -19.278 -10.282 1.00 26.11 C
ATOM 11481 CG MET B 226 -75.905 -19.169 -9.023 1.00 27.59 C
ATOM 11484 SD MET B 226 -75.676 -20.788 -8.214 1.00 30.67 S
ATOM 11485 CE MET B 226 -77.308 -21.005 -7.476 1.00 29.78 C
ATOM 11489 C MET B 226 -74.920 -18.380 -11.692 1.00 25.16 C
ATOM 11490 O MET B 226 -74.258 -17.387 -11.391 1.00 25.10 O
ATOM 11492 N ILE B 227 -74.388 -19.473 -12.239 1.00 24.88 N
ATOM 11493 CA ILE B 227 -72.944 -19.564 -12.501 1.00 24.70 C
ATOM 11495 CB ILE B 227 -72.476 -20.994 -12.882 1.00 24.45 C
ATOM 11497 CG1 ILE B 227 -72.656 -21.947 -11.695 1.00 23.80 C
ATOM 11500 CD1 ILE B 227 -72.094 -23.332 -11.885 1.00 21.97 C
ATOM 11504 CG2 ILE B 227 -71.030 -20.969 -13.266 1.00 24.90 C
ATOM 11508 C ILE B 227 -72.529 -18.550 -13.566 1.00 24.45 C
ATOM 11509 O ILE B 227 -71.578 -17.810 -13.373 1.00 24.42 O
ATOM 11511 N GLN B 228 -73.264 -18.484 -14.668 1.00 24.31 N
ATOM 11512 CA GLN B 228 -73.038 -17.414 -15.639 1.00 24.19 C
ATOM 11514 CB GLN B 228 -74.143 -17.363 -16.688 1.00 24.02 C
ATOM 11517 CG GLN B 228 -73.788 -16.488 -17.864 1.00 23.42 C
ATOM 11520 CD GLN B 228 -74.807 -16.567 -18.983 1.00 23.70 C
ATOM 11521 OE1 GLN B 228 -75.790 -15.813 -19.015 1.00 24.07 O
ATOM 11522 NE2 GLN B 228 -74.564 -17.465 -19.927 1.00 23.49 N
ATOM 11525 C GLN B 228 -72.913 -16.037 -14.987 1.00 24.37 C
ATOM 11526 O GLN B 228 -72.145 -15.210 -15.470 1.00 24.45 O
ATOM 11528 N SER B 229 -73.653 -15.776 -13.909 1.00 24.45 N
ATOM 11529 CA SER B 229 -73.578 -14.459 -13.264 1.00 24.76 C
ATOM 11531 CB SER B 229 -74.815 -14.163 -12.397 1.00 24.84 C
ATOM 11534 OG SER B 229 -74.711 -14.718 -11.096 1.00 25.81 O
ATOM 11536 C SER B 229 -72.270 -14.279 -12.469 1.00 24.64 C
ATOM 11537 O SER B 229 -71.726 -13.172 -12.408 1.00 24.95 O

ATOM 11539 N VAL B 230 -71.751 -15.350 -11.878 1.00 24.20 N
ATOM 11540 CA VAL B 230 -70.415 -15.277 -11.299 1.00 23.99 C
ATOM 11542 CB VAL B 230 -70.006 -16.581 -10.574 1.00 23.92 C
ATOM 11544 CG1 VAL B 230 -68.546 -16.510 -10.105 1.00 23.71 C
ATOM 11548 CG2 VAL B 230 -70.923 -16.853 -9.409 1.00 23.52 C
ATOM 11552 C VAL B 230 -69.386 -14.966 -12.400 1.00 24.12 C
ATOM 11553 O VAL B 230 -68.397 -14.291 -12.136 1.00 24.01 O
ATOM 11555 N TYR B 231 -69.612 -15.461 -13.621 1.00 24.30 N
ATOM 11556 CA TYR B 231 -68.672 -15.235 -14.728 1.00 24.53 C
ATOM 11558 CB TYR B 231 -68.997 -16.104 -15.946 1.00 24.08 C
ATOM 11561 CG TYR B 231 -68.892 -17.605 -15.754 1.00 23.29 C
ATOM 11562 CD1 TYR B 231 -68.173 -18.168 -14.706 1.00 23.08 C
ATOM 11564 CE1 TYR B 231 -68.073 -19.547 -14.565 1.00 22.01 C
ATOM 11566 CZ TYR B 231 -68.685 -20.369 -15.479 1.00 21.16 C
ATOM 11567 OH TYR B 231 -68.607 -21.746 -15.353 1.00 20.18 O
ATOM 11569 CE2 TYR B 231 -69.387 -19.825 -16.523 1.00 21.64 C
ATOM 11571 CD2 TYR B 231 -69.476 -18.464 -16.662 1.00 22.15 C
ATOM 11573 C TYR B 231 -68.658 -13.772 -15.166 1.00 25.37 C
ATOM 11574 O TYR B 231 -67.602 -13.221 -15.528 1.00 25.25 O
ATOM 11576 N GLN B 232 -69.832 -13.148 -15.129 1.00 26.11 N
ATOM 11577 CA GLN B 232 -69.978 -11.797 -15.622 1.00 26.68 C
ATOM 11579 CB GLN B 232 -71.430 -11.541 -15.995 1.00 26.45 C
ATOM 11582 CG GLN B 232 -71.883 -12.385 -17.176 1.00 25.67 C
ATOM 11585 CD GLN B 232 -73.388 -12.394 -17.381 1.00 24.91 C
ATOM 11586 OE1 GLN B 232 -74.140 -11.761 -16.637 1.00 24.81 O
ATOM 11587 NE2 GLN B 232 -73.834 -13.113 -18.407 1.00 23.39 N
ATOM 11590 C GLN B 232 -69.445 -10.802 -14.593 1.00 27.90 C
ATOM 11591 O GLN B 232 -68.909 -9.752 -14.958 1.00 27.96 O
ATOM 11593 N ARG B 233 -69.572 -11.145 -13.312 1.00 29.35 N
ATOM 11594 CA ARG B 233 -68.908 -10.396 -12.241 1.00 30.59 C
ATOM 11596 CB ARG B 233 -69.490 -10.775 -10.867 1.00 30.99 C
ATOM 11599 CG ARG B 233 -68.824 -10.114 -9.661 1.00 32.72 C
ATOM 11602 CD ARG B 233 -69.695 -10.210 -8.391 1.00 35.70 C
ATOM 11605 NE ARG B 233 -70.162 -11.578 -8.086 1.00 38.29 N
ATOM 11607 CZ ARG B 233 -71.403 -12.053 -8.276 1.00 39.65 C
ATOM 11608 NH1 ARG B 233 -72.367 -11.287 -8.787 1.00 40.23 N
ATOM 11611 NH2 ARG B 233 -71.687 -13.320 -7.949 1.00 39.61 N
ATOM 11614 C ARG B 233 -67.390 -10.632 -12.303 1.00 31.10 C
ATOM 11615 O ARG B 233 -66.615 -9.693 -12.181 1.00 31.19 O
ATOM 11617 N ASP B 234 -66.954 -11.868 -12.517 1.00 31.91 N
ATOM 11618 CA ASP B 234 -65.530 -12.102 -12.750 1.00 32.63 C
ATOM 11620 CB ASP B 234 -65.220 -13.566 -13.090 1.00 32.53 C
ATOM 11623 CG ASP B 234 -65.336 -14.493 -11.894 1.00 32.90 C
ATOM 11624 OD1 ASP B 234 -65.477 -14.028 -10.746 1.00 33.06 O
ATOM 11625 OD2 ASP B 234 -65.293 -15.713 -12.107 1.00 34.22 O
ATOM 11626 C ASP B 234 -65.058 -11.206 -13.886 1.00 33.10 C
ATOM 11627 O ASP B 234 -64.097 -10.458 -13.723 1.00 33.55 O
ATOM 11629 N LEU B 235 -65.753 -11.256 -15.017 1.00 33.49 N
ATOM 11630 CA LEU B 235 -65.311 -10.550 -16.216 1.00 34.06 C
ATOM 11632 CB LEU B 235 -66.139 -10.996 -17.422 1.00 33.80 C
ATOM 11635 CG LEU B 235 -65.769 -10.403 -18.775 1.00 32.13 C
ATOM 11637 CD1 LEU B 235 -64.303 -10.679 -19.050 1.00 30.94 C
ATOM 11641 CD2 LEU B 235 -66.670 -10.959 -19.870 1.00 29.93 C
ATOM 11645 C LEU B 235 -65.345 -9.023 -16.103 1.00 35.40 C
ATOM 11646 O LEU B 235 -64.500 -8.352 -16.682 1.00 35.61 O
ATOM 11648 N ARG B 236 -66.327 -8.473 -15.386 1.00 36.92 N
ATOM 11649 CA ARG B 236 -66.380 -7.019 -15.137 1.00 38.06 C
ATOM 11651 CB ARG B 236 -67.650 -6.607 -14.367 1.00 38.43 C
ATOM 11654 CG ARG B 236 -68.882 -6.321 -15.230 1.00 39.58 C
ATOM 11657 CD ARG B 236 -69.958 -5.520 -14.459 1.00 40.93 C

ATOM 11660 NE ARG B 236 -70.383 -6.149 -13.199 1.00 41.74 N
ATOM 11662 CZ ARG B 236 -71.208 -7.195 -13.095 1.00 42.20 C
ATOM 11663 NH1 ARG B 236 -71.719 -7.784 -14.175 1.00 41.61 N
ATOM 11666 NH2 ARG B 236 -71.517 -7.672 -11.892 1.00 42.99 N
ATOM 11669 C ARG B 236 -65.170 -6.550 -14.343 1.00 38.57 C
ATOM 11670 O ARG B 236 -64.593 -5.524 -14.665 1.00 38.61 O
ATOM 11672 N GLU B 237 -64.822 -7.292 -13.291 1.00 39.42 N
ATOM 11673 CA GLU B 237 -63.625 -7.017 -12.480 1.00 40.18 C
ATOM 11675 CB GLU B 237 -63.471 -8.033 -11.317 1.00 40.67 C
ATOM 11678 CG GLU B 237 -64.336 -7.750 -10.057 1.00 42.61 C
ATOM 11681 CD GLU B 237 -64.258 -8.858 -8.961 1.00 45.07 C
ATOM 11682 OE1 GLU B 237 -64.051 -10.066 -9.282 1.00 46.74 O
ATOM 11683 OE2 GLU B 237 -64.436 -8.511 -7.764 1.00 45.87 O
ATOM 11684 C GLU B 237 -62.352 -7.024 -13.344 1.00 39.93 C
ATOM 11685 O GLU B 237 -61.593 -6.050 -13.332 1.00 39.96 O
ATOM 11687 N THR B 238 -62.123 -8.104 -14.095 1.00 39.56 N
ATOM 11688 CA THR B 238 -60.900 -8.200 -14.895 1.00 39.42 C
ATOM 11690 CB THR B 238 -60.492 -9.666 -15.268 1.00 39.39 C
ATOM 11692 OG1 THR B 238 -61.222 -10.123 -16.413 1.00 39.37 O
ATOM 11694 CG2 THR B 238 -60.683 -10.612 -14.095 1.00 38.73 C
ATOM 11698 C THR B 238 -60.961 -7.326 -16.156 1.00 39.48 C
ATOM 11699 O THR B 238 -59.930 -7.062 -16.761 1.00 39.48 O
ATOM 11701 N SER B 239 -62.149 -6.871 -16.549 1.00 39.62 N
ATOM 11702 CA SER B 239 -62.264 -5.882 -17.631 1.00 39.63 C
ATOM 11704 CB SER B 239 -63.689 -5.810 -18.172 1.00 39.56 C
ATOM 11707 OG SER B 239 -63.945 -6.917 -19.010 1.00 38.96 O
ATOM 11709 C SER B 239 -61.796 -4.496 -17.181 1.00 39.99 C
ATOM 11710 O SER B 239 -61.108 -3.807 -17.933 1.00 40.10 O
ATOM 11712 N ARG B 240 -62.168 -4.088 -15.965 1.00 40.35 N
ATOM 11713 CA ARG B 240 -61.624 -2.864 -15.363 1.00 40.68 C
ATOM 11715 CB ARG B 240 -62.025 -2.712 -13.881 1.00 41.26 C
ATOM 11718 CG ARG B 240 -63.231 -1.782 -13.621 1.00 43.86 C
ATOM 11721 CD ARG B 240 -63.334 -1.375 -12.130 1.00 47.07 C
ATOM 11724 NE ARG B 240 -63.365 -2.537 -11.222 1.00 50.14 N
ATOM 11726 CZ ARG B 240 -64.462 -3.077 -10.671 1.00 52.32 C
ATOM 11727 NH1 ARG B 240 -64.342 -4.141 -9.875 1.00 53.16 N
ATOM 11730 NH2 ARG B 240 -65.677 -2.577 -10.899 1.00 53.18 N
ATOM 11733 C ARG B 240 -60.113 -2.914 -15.464 1.00 39.91 C
ATOM 11734 O ARG B 240 -59.490 -2.000 -15.988 1.00 39.86 O
ATOM 11736 N TRP B 241 -59.541 -4.002 -14.962 1.00 39.14 N
ATOM 11737 CA TRP B 241 -58.105 -4.217 -15.004 1.00 38.37 C
ATOM 11739 CB TRP B 241 -57.773 -5.635 -14.521 1.00 38.17 C
ATOM 11742 CG TRP B 241 -56.373 -6.005 -14.773 1.00 36.58 C
ATOM 11743 CD1 TRP B 241 -55.290 -5.668 -14.022 1.00 36.32 C
ATOM 11745 NE1 TRP B 241 -54.152 -6.176 -14.587 1.00 35.63 N
ATOM 11747 CE2 TRP B 241 -54.494 -6.846 -15.731 1.00 34.31 C
ATOM 11748 CD2 TRP B 241 -55.883 -6.757 -15.874 1.00 33.99 C
ATOM 11749 CE3 TRP B 241 -56.484 -7.357 -16.977 1.00 33.28 C
ATOM 11751 CZ3 TRP B 241 -55.691 -8.034 -17.883 1.00 32.79 C
ATOM 11753 CH2 TRP B 241 -54.313 -8.101 -17.720 1.00 33.06 C
ATOM 11755 CZ2 TRP B 241 -53.697 -7.515 -16.648 1.00 34.16 C
ATOM 11757 C TRP B 241 -57.561 -3.999 -16.409 1.00 38.25 C
ATOM 11758 O TRP B 241 -56.607 -3.252 -16.603 1.00 38.13 O
ATOM 11760 N TRP B 242 -58.186 -4.644 -17.386 1.00 38.21 N
ATOM 11761 CA TRP B 242 -57.695 -4.628 -18.765 1.00 38.27 C
ATOM 11763 CB TRP B 242 -58.479 -5.640 -19.609 1.00 38.31 C
ATOM 11766 CG TRP B 242 -57.948 -5.872 -20.990 1.00 38.61 C
ATOM 11767 CD1 TRP B 242 -58.642 -5.754 -22.156 1.00 39.11 C
ATOM 11769 NE1 TRP B 242 -57.828 -6.046 -23.224 1.00 39.31 N
ATOM 11771 CE2 TRP B 242 -56.582 -6.363 -22.759 1.00 38.95 C

ATOM 11772 CD2 TRP B 242 -56.617 -6.263 -21.356 1.00 38.66 C
ATOM 11773 CE3 TRP B 242 -55.454 -6.528 -20.637 1.00 38.98 C
ATOM 11775 CZ3 TRP B 242 -54.314 -6.886 -21.326 1.00 39.20 C
ATOM 11777 CH2 TRP B 242 -54.313 -6.985 -22.716 1.00 39.12 C
ATOM 11779 CZ2 TRP B 242 -55.434 -6.724 -23.451 1.00 39.22 C
ATOM 11781 C TRP B 242 -57.739 -3.241 -19.400 1.00 38.27 C
ATOM 11782 O TRP B 242 -56.814 -2.873 -20.108 1.00 37.81 O
ATOM 11784 N ARG B 243 -58.809 -2.489 -19.140 1.00 38.79 N
ATOM 11785 CA ARG B 243 -58.936 -1.097 -19.607 1.00 39.37 C
ATOM 11787 CB ARG B 243 -60.351 -.552 -19.346 1.00 39.66 C
ATOM 11790 CG ARG B 243 -61.324 -.792 -20.520 1.00 41.96 C
ATOM 11793 CD ARG B 243 -62.687 -1.338 -20.085 1.00 44.82 C
ATOM 11796 NE ARG B 243 -63.461 -.380 -19.296 1.00 47.15 N
ATOM 11798 CZ ARG B 243 -64.389 -.704 -18.386 1.00 49.26 C
ATOM 11799 NH1 ARG B 243 -64.685 -1.976 -18.109 1.00 49.18 N
ATOM 11802 NH2 ARG B 243 -65.028 .262 -17.729 1.00 50.40 N
ATOM 11805 C ARG B 243 -57.890 -.183 -18.980 1.00 39.28 C
ATOM 11806 O ARG B 243 -57.246 .577 -19.681 1.00 39.40 O
ATOM 11808 N ARG B 244 -57.724 -.282 -17.665 1.00 39.52 N
ATOM 11809 CA ARG B 244 -56.734 .489 -16.888 1.00 39.61 C
ATOM 11811 CB ARG B 244 -56.774 .041 -15.409 1.00 40.25 C
ATOM 11814 CG ARG B 244 -56.115 .971 -14.383 1.00 42.01 C
ATOM 11817 CD ARG B 244 -57.029 2.154 -14.017 1.00 44.39 C
ATOM 11820 NE ARG B 244 -56.391 3.115 -13.103 1.00 46.36 N
ATOM 11822 CZ ARG B 244 -55.434 3.984 -13.441 1.00 48.06 C
ATOM 11823 NH1 ARG B 244 -54.951 4.043 -14.686 1.00 48.90 N
ATOM 11826 NH2 ARG B 244 -54.947 4.805 -12.519 1.00 48.82 N
ATOM 11829 C ARG B 244 -55.323 .322 -17.437 1.00 38.83 C
ATOM 11830 O ARG B 244 -54.594 1.300 -17.567 1.00 38.39 O
ATOM 11832 N VAL B 245 -54.953 -.922 -17.738 1.00 38.52 N
ATOM 11833 CA VAL B 245 -53.694 -1.241 -18.437 1.00 38.43 C
ATOM 11835 CB VAL B 245 -53.491 -2.760 -18.614 1.00 38.31 C
ATOM 11837 CG1 VAL B 245 -53.247 -3.426 -17.283 1.00 37.77 C
ATOM 11841 CG2 VAL B 245 -52.344 -3.036 -19.561 1.00 37.66 C
ATOM 11845 C VAL B 245 -53.650 -.638 -19.832 1.00 38.68 C
ATOM 11846 O VAL B 245 -52.615 -.153 -20.247 1.00 38.57 O
ATOM 11848 N GLY B 246 -54.765 -.724 -20.559 1.00 39.26 N
ATOM 11849 CA GLY B 246 -54.974 -.012 -21.834 1.00 39.62 C
ATOM 11852 C GLY B 246 -53.962 -.262 -22.942 1.00 40.08 C
ATOM 11853 O GLY B 246 -53.617 .650 -23.700 1.00 39.89 O
ATOM 11855 N LEU B 247 -53.502 -1.500 -23.062 1.00 40.75 N
ATOM 11856 CA LEU B 247 -52.347 -1.778 -23.905 1.00 41.34 C
ATOM 11858 CB LEU B 247 -51.655 -3.065 -23.459 1.00 41.15 C
ATOM 11861 CG LEU B 247 -50.132 -3.026 -23.298 1.00 40.49 C
ATOM 11863 CD1 LEU B 247 -49.622 -1.769 -22.605 1.00 39.50 C
ATOM 11867 CD2 LEU B 247 -49.695 -4.242 -22.526 1.00 39.98 C
ATOM 11871 C LEU B 247 -52.744 -1.836 -25.370 1.00 42.50 C
ATOM 11872 O LEU B 247 -52.005 -1.358 -26.225 1.00 42.33 O
ATOM 11874 N ALA B 248 -53.925 -2.390 -25.654 1.00 44.14 N
ATOM 11875 CA ALA B 248 -54.439 -2.494 -27.041 1.00 45.16 C
ATOM 11877 CB ALA B 248 -55.705 -3.347 -27.087 1.00 45.15 C
ATOM 11881 C ALA B 248 -54.692 -1.140 -27.739 1.00 45.98 C
ATOM 11882 O ALA B 248 -54.604 -1.053 -28.971 1.00 46.37 O
ATOM 11884 N THR B 249 -55.004 -.095 -26.975 1.00 46.64 N
ATOM 11885 CA THR B 249 -55.142 1.234 -27.570 1.00 47.25 C
ATOM 11887 CB THR B 249 -55.905 2.253 -26.655 1.00 47.44 C
ATOM 11889 OG1 THR B 249 -55.001 2.845 -25.706 1.00 47.52 O
ATOM 11891 CG2 THR B 249 -57.104 1.592 -25.928 1.00 47.44 C
ATOM 11895 C THR B 249 -53.756 1.793 -27.931 1.00 47.59 C
ATOM 11896 O THR B 249 -53.553 2.279 -29.049 1.00 48.07 O

ATOM 11898 N LYS B 250 -52.808 1.710 -26.995 1.00 47.67 N
ATOM 11899 CA LYS B 250 -51.469 2.299 -27.185 1.00 47.68 C
ATOM 11901 CB LYS B 250 -50.793 2.553 -25.833 1.00 47.68 C
ATOM 11904 CG LYS B 250 -51.428 3.673 -24.999 1.00 47.77 C
ATOM 11907 CD LYS B 250 -51.142 5.086 -25.552 1.00 47.59 C
ATOM 11910 CE LYS B 250 -49.676 5.496 -25.441 1.00 46.75 C
ATOM 11913 NZ LYS B 250 -49.479 6.878 -25.948 1.00 46.49 N
ATOM 11917 C LYS B 250 -50.541 1.465 -28.082 1.00 47.72 C
ATOM 11918 O LYS B 250 -49.591 1.988 -28.663 1.00 47.54 O
ATOM 11920 N LEU B 251 -50.804 .169 -28.184 1.00 47.82 N
ATOM 11921 CA LEU B 251 -50.072 -.675 -29.118 1.00 47.96 C
ATOM 11923 CB LEU B 251 -49.584 -1.970 -28.447 1.00 48.04 C
ATOM 11926 CG LEU B 251 -48.109 -2.064 -28.033 1.00 47.39 C
ATOM 11928 CD1 LEU B 251 -47.659 -.881 -27.186 1.00 46.47 C
ATOM 11932 CD2 LEU B 251 -47.894 -3.376 -27.304 1.00 46.78 C
ATOM 11936 C LEU B 251 -50.985 -.964 -30.306 1.00 48.19 C
ATOM 11937 O LEU B 251 -51.975 -1.693 -30.194 1.00 48.38 O
ATOM 11939 N HIS B 252 -50.627 -.396 -31.449 1.00 48.42 N
ATOM 11940 CA HIS B 252 -51.521 -.329 -32.601 1.00 48.62 C
ATOM 11942 CB HIS B 252 -51.110 .850 -33.492 1.00 48.99 C
ATOM 11945 CG HIS B 252 -51.000 2.145 -32.742 1.00 50.56 C
ATOM 11946 ND1 HIS B 252 -52.095 2.935 -32.453 1.00 52.11 N
ATOM 11948 CE1 HIS B 252 -51.704 3.993 -31.766 1.00 52.68 C
ATOM 11950 NE2 HIS B 252 -50.397 3.912 -31.585 1.00 52.86 N
ATOM 11952 CD2 HIS B 252 -49.932 2.764 -32.181 1.00 51.68 C
ATOM 11954 C HIS B 252 -51.582 -1.636 -33.383 1.00 48.14 C
ATOM 11955 O HIS B 252 -52.615 -1.975 -33.935 1.00 48.02 O
ATOM 11957 N PHE B 253 -50.481 -2.372 -33.405 1.00 48.10 N
ATOM 11958 CA PHE B 253 -50.422 -3.702 -34.044 1.00 48.18 C
ATOM 11960 CB PHE B 253 -48.965 -4.070 -34.375 1.00 48.16 C
ATOM 11963 CG PHE B 253 -48.119 -4.311 -33.163 1.00 47.85 C
ATOM 11964 CD1 PHE B 253 -47.900 -5.596 -32.702 1.00 48.56 C
ATOM 11966 CE1 PHE B 253 -47.140 -5.812 -31.576 1.00 48.98 C
ATOM 11968 CZ PHE B 253 -46.602 -4.729 -30.895 1.00 48.50 C
ATOM 11970 CE2 PHE B 253 -46.817 -3.454 -31.349 1.00 47.40 C
ATOM 11972 CD2 PHE B 253 -47.569 -3.249 -32.465 1.00 47.22 C
ATOM 11974 C PHE B 253 -51.038 -4.819 -33.185 1.00 48.30 C
ATOM 11975 O PHE B 253 -51.344 -5.903 -33.691 1.00 47.63 O
ATOM 11977 N ALA B 254 -51.204 -4.541 -31.888 1.00 48.86 N
ATOM 11978 CA ALA B 254 -51.653 -5.531 -30.903 1.00 49.13 C
ATOM 11980 CB ALA B 254 -51.290 -5.071 -29.494 1.00 49.02 C
ATOM 11984 C ALA B 254 -53.153 -5.806 -30.982 1.00 49.46 C
ATOM 11985 O ALA B 254 -53.967 -4.870 -31.011 1.00 49.50 O
ATOM 11987 N ARG B 255 -53.501 -7.097 -31.006 1.00 49.75 N
ATOM 11988 CA ARG B 255 -54.896 -7.549 -30.918 1.00 49.89 C
ATOM 11990 CB ARG B 255 -55.028 -9.051 -31.245 1.00 49.94 C
ATOM 11993 CG ARG B 255 -54.839 -9.439 -32.724 1.00 49.93 C
ATOM 11996 CD ARG B 255 -54.709 -10.967 -32.904 1.00 49.79 C
ATOM 11999 NE ARG B 255 -53.527 -11.505 -32.219 1.00 50.11 N
ATOM 12001 CZ ARG B 255 -53.276 -12.801 -32.010 1.00 50.54 C
ATOM 12002 NH1 ARG B 255 -54.117 -13.736 -32.439 1.00 51.36 N
ATOM 12005 NH2 ARG B 255 -52.175 -13.172 -31.360 1.00 50.21 N
ATOM 12008 C ARG B 255 -55.425 -7.308 -29.511 1.00 49.83 C
ATOM 12009 O ARG B 255 -54.666 -6.975 -28.599 1.00 49.95 O
ATOM 12011 N ASP B 256 -56.736 -7.463 -29.350 1.00 49.72 N
ATOM 12012 CA ASP B 256 -57.360 -7.483 -28.034 1.00 49.55 C
ATOM 12014 CB ASP B 256 -58.183 -6.222 -27.812 1.00 49.52 C
ATOM 12017 CG ASP B 256 -59.134 -6.362 -26.654 1.00 50.30 C
ATOM 12018 OD1 ASP B 256 -60.310 -5.944 -26.780 1.00 50.45 O
ATOM 12019 OD2 ASP B 256 -58.702 -6.926 -25.622 1.00 51.68 O

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ATOM  12020  C   ASP B 256    -58.254  -8.721 -27.931  1.00 49.15           C
ATOM  12021  O   ASP B 256    -59.159  -8.901 -28.737  1.00 49.28           O
ATOM  12023  N   ARG B 257    -57.998  -9.565 -26.937  1.00 48.61           N
ATOM  12024  CA  ARG B 257    -58.743 -10.809 -26.765  1.00 48.20           C
ATOM  12026  CB  ARG B 257    -57.949 -11.984 -27.373  1.00 48.41           C
ATOM  12029  CG  ARG B 257    -57.505 -11.799 -28.821  1.00 49.37           C
ATOM  12032  CD  ARG B 257    -58.693 -11.636 -29.784  1.00 50.80           C
ATOM  12035  NE  ARG B 257    -58.908 -12.814 -30.627  1.00 52.11           N
ATOM  12037  CZ  ARG B 257    -58.678 -12.876 -31.944  1.00 52.99           C
ATOM  12038  NH1 ARG B 257    -58.214 -11.820 -32.623  1.00 52.37           N
ATOM  12041  NH2 ARG B 257    -58.918 -14.016 -32.596  1.00 52.97           N
ATOM  12044  C   ARG B 257    -59.032 -11.089 -25.280  1.00 47.32           C
ATOM  12045  O   ARG B 257    -58.579 -12.101 -24.735  1.00 47.46           O
ATOM  12047  N   LEU B 258    -59.770 -10.201 -24.616  1.00 45.94           N
ATOM  12048  CA  LEU B 258    -60.108 -10.430 -23.205  1.00 44.67           C
ATOM  12050  CB  LEU B 258    -60.332  -9.130 -22.438  1.00 44.61           C
ATOM  12053  CG  LEU B 258    -60.422  -9.323 -20.920  1.00 43.83           C
ATOM  12055  CD1 LEU B 258    -59.045  -9.552 -20.339  1.00 43.48           C
ATOM  12059  CD2 LEU B 258    -61.073  -8.139 -20.262  1.00 43.85           C
ATOM  12063  C   LEU B 258    -61.347 -11.286 -23.090  1.00 43.49           C
ATOM  12064  O   LEU B 258    -61.375 -12.220 -22.295  1.00 43.84           O
ATOM  12066  N   ILE B 259    -62.364 -10.968 -23.883  1.00 41.92           N
ATOM  12067  CA  ILE B 259    -63.617 -11.711 -23.841  1.00 40.80           C
ATOM  12069  CB  ILE B 259    -64.718 -11.132 -24.783  1.00 41.05           C
ATOM  12071  CG1 ILE B 259    -64.852  -9.598 -24.653  1.00 41.61           C
ATOM  12074  CD1 ILE B 259    -65.200  -8.874 -25.985  1.00 42.16           C
ATOM  12078  CG2 ILE B 259    -66.065 -11.816 -24.496  1.00 40.46           C
ATOM  12082  C   ILE B 259    -63.319 -13.151 -24.250  1.00 39.50           C
ATOM  12083  O   ILE B 259    -63.782 -14.082 -23.598  1.00 39.30           O
ATOM  12085  N   GLU B 260    -62.524 -13.318 -25.316  1.00 37.99           N
ATOM  12086  CA  GLU B 260    -62.120 -14.652 -25.812  1.00 36.60           C
ATOM  12088  CB  GLU B 260    -61.329 -14.574 -27.142  1.00 36.75           C
ATOM  12091  CG  GLU B 260    -62.167 -14.319 -28.425  1.00 37.79           C
ATOM  12094  CD  GLU B 260    -62.134 -12.851 -28.905  1.00 39.47           C
ATOM  12095  OE1 GLU B 260    -62.207 -11.923 -28.055  1.00 39.97           O
ATOM  12096  OE2 GLU B 260    -62.033 -12.628 -30.139  1.00 40.31           O
ATOM  12097  C   GLU B 260    -61.282 -15.381 -24.770  1.00 34.83           C
ATOM  12098  O   GLU B 260    -61.465 -16.568 -24.544  1.00 34.69           O
ATOM  12100  N   SER B 261    -60.365 -14.669 -24.131  1.00 32.89           N
ATOM  12101  CA  SER B 261    -59.508 -15.292 -23.139  1.00 31.48           C
ATOM  12103  CB  SER B 261    -58.341 -14.376 -22.768  1.00 31.55           C
ATOM  12106  OG  SER B 261    -57.298 -14.493 -23.728  1.00 31.75           O
ATOM  12108  C   SER B 261    -60.294 -15.716 -21.900  1.00 30.04           C
ATOM  12109  O   SER B 261    -59.921 -16.674 -21.208  1.00 29.70           O
ATOM  12111  N   PHE B 262    -61.389 -15.021 -21.618  1.00 28.25           N
ATOM  12112  CA  PHE B 262    -62.203 -15.404 -20.480  1.00 26.75           C
ATOM  12114  CB  PHE B 262    -63.111 -14.278 -20.009  1.00 26.36           C
ATOM  12117  CG  PHE B 262    -63.532 -14.453 -18.603  1.00 24.33           C
ATOM  12118  CD1 PHE B 262    -62.697 -14.092 -17.584  1.00 22.66           C
ATOM  12120  CE1 PHE B 262    -63.047 -14.283 -16.301  1.00 22.65           C
ATOM  12122  CZ  PHE B 262    -64.245 -14.873 -16.007  1.00 23.93           C
ATOM  12124  CE2 PHE B 262    -65.076 -15.267 -17.010  1.00 24.08           C
ATOM  12126  CD2 PHE B 262    -64.711 -15.067 -18.304  1.00 23.96           C
ATOM  12128  C   PHE B 262    -63.017 -16.660 -20.751  1.00 26.02           C
ATOM  12129  O   PHE B 262    -63.074 -17.546 -19.909  1.00 26.32           O
ATOM  12131  N   TYR B 263    -63.652 -16.732 -21.915  1.00 24.98           N
ATOM  12132  CA  TYR B 263    -64.299 -17.969 -22.396  1.00 24.14           C
ATOM  12134  CB  TYR B 263    -64.701 -17.756 -23.853  1.00 24.00           C
ATOM  12137  CG  TYR B 263    -65.080 -18.961 -24.667  1.00 24.32           C
ATOM  12138  CD1 TYR B 263    -66.302 -19.604 -24.489  1.00 25.03           C
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ATOM 12140 CE1 TYR B 263 -66.666 -20.694 -25.285 1.00 25.81 C
ATOM 12142 CZ TYR B 263 -65.798 -21.132 -26.287 1.00 27.06 C
ATOM 12143 OH TYR B 263 -66.106 -22.191 -27.123 1.00 27.14 O
ATOM 12145 CE2 TYR B 263 -64.590 -20.489 -26.479 1.00 26.80 C
ATOM 12147 CD2 TYR B 263 -64.250 -19.404 -25.680 1.00 25.65 C
ATOM 12149 C TYR B 263 -63.351 -19.162 -22.256 1.00 23.35 C
ATOM 12150 O TYR B 263 -63.712 -20.219 -21.740 1.00 22.80 O
ATOM 12152 N TRP B 264 -62.119 -18.955 -22.702 1.00 22.64 N
ATOM 12153 CA TRP B 264 -61.047 -19.918 -22.523 1.00 21.95 C
ATOM 12155 CB TRP B 264 -59.737 -19.334 -23.061 1.00 21.84 C
ATOM 12158 CG TRP B 264 -58.603 -20.278 -22.964 1.00 22.90 C
ATOM 12159 CD1 TRP B 264 -57.700 -20.387 -21.943 1.00 23.98 C
ATOM 12161 NE1 TRP B 264 -56.800 -21.386 -22.214 1.00 23.95 N
ATOM 12163 CE2 TRP B 264 -57.124 -21.949 -23.417 1.00 23.51 C
ATOM 12164 CD2 TRP B 264 -58.252 -21.273 -23.915 1.00 23.40 C
ATOM 12165 CE3 TRP B 264 -58.776 -21.652 -25.147 1.00 23.68 C
ATOM 12167 CZ3 TRP B 264 -58.178 -22.669 -25.826 1.00 24.44 C
ATOM 12169 CH2 TRP B 264 -57.060 -23.324 -25.310 1.00 24.97 C
ATOM 12171 CZ2 TRP B 264 -56.521 -22.978 -24.103 1.00 24.44 C
ATOM 12173 C TRP B 264 -60.897 -20.326 -21.050 1.00 21.11 C
ATOM 12174 O TRP B 264 -60.768 -21.511 -20.748 1.00 20.98 O
ATOM 12176 N ALA B 265 -60.916 -19.344 -20.147 1.00 20.17 N
ATOM 12177 CA ALA B 265 -60.774 -19.602 -18.712 1.00 19.36 C
ATOM 12179 CB ALA B 265 -60.621 -18.305 -17.944 1.00 19.30 C
ATOM 12183 C ALA B 265 -61.947 -20.397 -18.171 1.00 18.63 C
ATOM 12184 O ALA B 265 -61.763 -21.349 -17.434 1.00 18.64 O
ATOM 12186 N VAL B 266 -63.159 -20.034 -18.557 1.00 18.11 N
ATOM 12187 CA VAL B 266 -64.335 -20.758 -18.075 1.00 17.60 C
ATOM 12189 CB VAL B 266 -65.652 -20.221 -18.675 1.00 17.38 C
ATOM 12191 CG1 VAL B 266 -65.902 -18.803 -18.199 1.00 17.09 C
ATOM 12195 CG2 VAL B 266 -66.817 -21.120 -18.312 1.00 15.40 C
ATOM 12199 C VAL B 266 -64.221 -22.246 -18.376 1.00 17.67 C
ATOM 12200 O VAL B 266 -64.766 -23.058 -17.647 1.00 18.27 O
ATOM 12202 N GLY B 267 -63.516 -22.607 -19.444 1.00 17.43 N
ATOM 12203 CA GLY B 267 -63.316 -24.013 -19.789 1.00 16.98 C
ATOM 12206 C GLY B 267 -62.253 -24.683 -18.947 1.00 16.55 C
ATOM 12207 O GLY B 267 -62.360 -25.859 -18.609 1.00 16.37 O
ATOM 12209 N VAL B 268 -61.215 -23.939 -18.608 1.00 16.30 N
ATOM 12210 CA VAL B 268 -60.160 -24.500 -17.794 1.00 16.23 C
ATOM 12212 CB VAL B 268 -58.893 -23.651 -17.840 1.00 15.68 C
ATOM 12214 CG1 VAL B 268 -57.857 -24.194 -16.894 1.00 15.01 C
ATOM 12218 CG2 VAL B 268 -58.361 -23.674 -19.235 1.00 15.01 C
ATOM 12222 C VAL B 268 -60.654 -24.718 -16.374 1.00 16.86 C
ATOM 12223 O VAL B 268 -60.421 -25.784 -15.813 1.00 16.93 O
ATOM 12225 N ALA B 269 -61.362 -23.733 -15.817 1.00 17.64 N
ATOM 12226 CA ALA B 269 -61.911 -23.838 -14.461 1.00 18.46 C
ATOM 12228 CB ALA B 269 -60.958 -23.215 -13.472 1.00 18.15 C
ATOM 12232 C ALA B 269 -63.312 -23.213 -14.340 1.00 19.34 C
ATOM 12233 O ALA B 269 -63.448 -22.030 -14.047 1.00 19.78 O
ATOM 12235 N PHE B 270 -64.347 -24.028 -14.529 1.00 20.34 N
ATOM 12236 CA PHE B 270 -65.724 -23.535 -14.631 1.00 21.21 C
ATOM 12238 CB PHE B 270 -66.564 -24.483 -15.482 1.00 21.34 C
ATOM 12241 CG PHE B 270 -67.083 -25.667 -14.718 1.00 22.46 C
ATOM 12242 CD1 PHE B 270 -68.294 -25.596 -14.039 1.00 23.19 C
ATOM 12244 CE1 PHE B 270 -68.756 -26.672 -13.315 1.00 23.27 C
ATOM 12246 CZ PHE B 270 -68.003 -27.836 -13.258 1.00 23.35 C
ATOM 12248 CE2 PHE B 270 -66.794 -27.918 -13.932 1.00 22.73 C
ATOM 12250 CD2 PHE B 270 -66.340 -26.843 -14.646 1.00 22.88 C
ATOM 12252 C PHE B 270 -66.464 -23.366 -13.316 1.00 21.98 C
ATOM 12253 O PHE B 270 -67.408 -22.583 -13.268 1.00 21.93 O

ATOM 12255 N GLU B 271 -66.102 -24.126 -12.275 1.00 23.01 N
ATOM 12256 CA GLU B 271 -66.929 -24.142 -11.037 1.00 23.99 C
ATOM 12258 CB GLU B 271 -66.679 -25.353 -10.113 1.00 24.25 C
ATOM 12261 CG GLU B 271 -65.286 -25.877 -10.092 1.00 26.22 C
ATOM 12264 CD GLU B 271 -65.013 -26.914 -11.183 1.00 29.01 C
ATOM 12265 OE1 GLU B 271 -65.563 -28.032 -11.090 1.00 31.36 O
ATOM 12266 OE2 GLU B 271 -64.232 -26.622 -12.121 1.00 30.98 O
ATOM 12267 C GLU B 271 -66.795 -22.831 -10.281 1.00 23.90 C
ATOM 12268 O GLU B 271 -65.702 -22.296 -10.181 1.00 24.29 O
ATOM 12270 N PRO B 272 -67.913 -22.316 -9.745 1.00 24.09 N
ATOM 12271 CA PRO B 272 -68.005 -20.885 -9.428 1.00 24.11 C
ATOM 12273 CB PRO B 272 -69.380 -20.751 -8.751 1.00 24.03 C
ATOM 12276 CG PRO B 272 -70.083 -22.069 -8.997 1.00 24.12 C
ATOM 12279 CD PRO B 272 -69.013 -23.083 -9.132 1.00 23.99 C
ATOM 12282 C PRO B 272 -66.900 -20.386 -8.501 1.00 24.28 C
ATOM 12283 O PRO B 272 -66.421 -19.261 -8.676 1.00 24.40 O
ATOM 12284 N GLN B 273 -66.480 -21.222 -7.547 1.00 24.20 N
ATOM 12285 CA GLN B 273 -65.500 -20.809 -6.551 1.00 24.20 C
ATOM 12287 CB GLN B 273 -65.437 -21.840 -5.426 1.00 24.42 C
ATOM 12290 CG GLN B 273 -64.750 -23.176 -5.775 1.00 25.17 C
ATOM 12293 CD GLN B 273 -65.717 -24.334 -6.007 1.00 26.13 C
ATOM 12294 OE1 GLN B 273 -66.857 -24.141 -6.453 1.00 27.46 O
ATOM 12295 NE2 GLN B 273 -65.251 -25.554 -5.721 1.00 25.05 N
ATOM 12298 C GLN B 273 -64.086 -20.546 -7.088 1.00 24.27 C
ATOM 12299 O GLN B 273 -63.221 -20.151 -6.329 1.00 24.32 O
ATOM 12301 N TYR B 274 -63.842 -20.759 -8.380 1.00 24.59 N
ATOM 12302 CA TYR B 274 -62.509 -20.551 -8.962 1.00 24.85 C
ATOM 12304 CB TYR B 274 -62.129 -21.724 -9.880 1.00 24.62 C
ATOM 12307 CG TYR B 274 -62.009 -23.054 -9.184 1.00 24.35 C
ATOM 12308 CD1 TYR B 274 -61.395 -23.169 -7.946 1.00 24.62 C
ATOM 12310 CE1 TYR B 274 -61.280 -24.391 -7.314 1.00 25.10 C
ATOM 12312 CZ TYR B 274 -61.771 -25.525 -7.920 1.00 24.92 C
ATOM 12313 OH TYR B 274 -61.661 -26.748 -7.299 1.00 24.73 O
ATOM 12315 CE2 TYR B 274 -62.366 -25.437 -9.150 1.00 24.76 C
ATOM 12317 CD2 TYR B 274 -62.477 -24.203 -9.779 1.00 24.70 C
ATOM 12319 C TYR B 274 -62.409 -19.235 -9.745 1.00 25.27 C
ATOM 12320 O TYR B 274 -61.956 -19.210 -10.895 1.00 25.42 O
ATOM 12322 N SER B 275 -62.808 -18.134 -9.121 1.00 25.40 N
ATOM 12323 CA SER B 275 -62.755 -16.849 -9.802 1.00 25.43 C
ATOM 12325 CB SER B 275 -63.615 -15.814 -9.071 1.00 25.53 C
ATOM 12328 OG SER B 275 -65.006 -16.068 -9.291 1.00 25.52 O
ATOM 12330 C SER B 275 -61.300 -16.403 -9.948 1.00 25.36 C
ATOM 12331 O SER B 275 -60.885 -15.903 -10.996 1.00 25.17 O
ATOM 12333 N ASP B 276 -60.517 -16.617 -8.901 1.00 25.41 N
ATOM 12334 CA ASP B 276 -59.095 -16.353 -8.979 1.00 25.42 C
ATOM 12336 CB ASP B 276 -58.390 -16.794 -7.712 1.00 25.44 C
ATOM 12339 CG ASP B 276 -58.728 -15.925 -6.558 1.00 26.32 C
ATOM 12340 OD1 ASP B 276 -59.302 -14.857 -6.818 1.00 27.50 O
ATOM 12341 OD2 ASP B 276 -58.442 -16.299 -5.398 1.00 30.16 O
ATOM 12342 C ASP B 276 -58.495 -17.069 -10.157 1.00 25.20 C
ATOM 12343 O ASP B 276 -57.745 -16.461 -10.929 1.00 25.66 O
ATOM 12345 N CYS B 277 -58.814 -18.353 -10.305 1.00 24.60 N
ATOM 12346 CA CYS B 277 -58.228 -19.110 -11.391 1.00 24.30 C
ATOM 12348 CB CYS B 277 -58.684 -20.561 -11.392 1.00 24.28 C
ATOM 12351 SG CYS B 277 -57.737 -21.574 -12.569 1.00 23.82 S
ATOM 12353 C CYS B 277 -58.593 -18.448 -12.698 1.00 24.09 C
ATOM 12354 O CYS B 277 -57.727 -18.013 -13.450 1.00 23.87 O
ATOM 12356 N ARG B 278 -59.893 -18.329 -12.933 1.00 24.22 N
ATOM 12357 CA ARG B 278 -60.400 -17.746 -14.171 1.00 23.98 C
ATOM 12359 CB ARG B 278 -61.917 -17.556 -14.123 1.00 23.93 C

ATOM 12362 CG ARG B 278 -62.662 -18.871 -14.283 1.00 24.07 C
ATOM 12365 CD ARG B 278 -64.132 -18.670 -14.607 1.00 24.48 C
ATOM 12368 NE ARG B 278 -64.874 -18.141 -13.472 1.00 23.75 N
ATOM 12370 CZ ARG B 278 -65.254 -18.856 -12.419 1.00 23.72 C
ATOM 12371 NH1 ARG B 278 -64.973 -20.149 -12.326 1.00 22.86 N
ATOM 12374 NH2 ARG B 278 -65.927 -18.262 -11.443 1.00 25.08 N
ATOM 12377 C ARG B 278 -59.701 -16.453 -14.491 1.00 23.56 C
ATOM 12378 O ARG B 278 -59.296 -16.265 -15.628 1.00 23.87 O
ATOM 12380 N ASN B 279 -59.512 -15.593 -13.495 1.00 23.24 N
ATOM 12381 CA ASN B 279 -58.854 -14.301 -13.734 1.00 23.48 C
ATOM 12383 CB ASN B 279 -59.055 -13.340 -12.574 1.00 24.05 C
ATOM 12386 CG ASN B 279 -60.510 -13.017 -12.346 1.00 26.58 C
ATOM 12387 OD1 ASN B 279 -61.378 -13.310 -13.189 1.00 28.96 O
ATOM 12388 ND2 ASN B 279 -60.799 -12.416 -11.194 1.00 30.30 N
ATOM 12391 C ASN B 279 -57.376 -14.404 -14.027 1.00 22.58 C
ATOM 12392 O ASN B 279 -56.903 -13.749 -14.941 1.00 22.73 O
ATOM 12394 N SER B 280 -56.648 -15.205 -13.251 1.00 21.62 N
ATOM 12395 CA SER B 280 -55.243 -15.483 -13.550 1.00 20.73 C
ATOM 12397 CB SER B 280 -54.696 -16.597 -12.659 1.00 20.85 C
ATOM 12400 OG SER B 280 -53.805 -16.099 -11.683 1.00 21.55 O
ATOM 12402 C SER B 280 -55.091 -15.896 -15.004 1.00 20.04 C
ATOM 12403 O SER B 280 -54.293 -15.312 -15.738 1.00 19.87 O
ATOM 12405 N VAL B 281 -55.875 -16.893 -15.413 1.00 19.24 N
ATOM 12406 CA VAL B 281 -55.720 -17.491 -16.720 1.00 18.77 C
ATOM 12408 CB VAL B 281 -56.482 -18.834 -16.815 1.00 18.74 C
ATOM 12410 CG1 VAL B 281 -56.467 -19.404 -18.251 1.00 18.34 C
ATOM 12414 CG2 VAL B 281 -55.863 -19.844 -15.848 1.00 18.13 C
ATOM 12418 C VAL B 281 -56.142 -16.486 -17.787 1.00 18.89 C
ATOM 12419 O VAL B 281 -55.483 -16.364 -18.832 1.00 18.75 O
ATOM 12421 N ALA B 282 -57.210 -15.739 -17.505 1.00 18.85 N
ATOM 12422 CA ALA B 282 -57.709 -14.723 -18.439 1.00 18.80 C
ATOM 12424 CB ALA B 282 -59.051 -14.191 -17.991 1.00 18.32 C
ATOM 12428 C ALA B 282 -56.718 -13.576 -18.615 1.00 18.94 C
ATOM 12429 O ALA B 282 -56.582 -13.021 -19.700 1.00 19.16 O
ATOM 12431 N LYS B 283 -56.022 -13.211 -17.553 1.00 19.24 N
ATOM 12432 CA LYS B 283 -55.037 -12.145 -17.658 1.00 19.62 C
ATOM 12434 CB LYS B 283 -54.649 -11.615 -16.276 1.00 19.68 C
ATOM 12437 CG LYS B 283 -55.779 -10.923 -15.518 1.00 19.95 C
ATOM 12440 CD LYS B 283 -55.265 -10.398 -14.196 1.00 21.72 C
ATOM 12443 CE LYS B 283 -56.364 -10.236 -13.164 1.00 23.83 C
ATOM 12446 NZ LYS B 283 -56.129 -9.003 -12.351 1.00 24.72 N
ATOM 12450 C LYS B 283 -53.802 -12.643 -18.396 1.00 19.77 C
ATOM 12451 O LYS B 283 -53.237 -11.929 -19.208 1.00 20.05 O
ATOM 12453 N MET B 284 -53.387 -13.871 -18.117 1.00 19.88 N
ATOM 12454 CA MET B 284 -52.136 -14.367 -18.652 1.00 19.90 C
ATOM 12456 CB MET B 284 -51.719 -15.676 -17.960 1.00 20.08 C
ATOM 12459 CG MET B 284 -51.125 -15.505 -16.560 1.00 20.62 C
ATOM 12462 SD MET B 284 -49.782 -14.295 -16.485 1.00 23.69 S
ATOM 12463 CE MET B 284 -50.600 -12.872 -15.754 1.00 23.82 C
ATOM 12467 C MET B 284 -52.257 -14.572 -20.145 1.00 19.82 C
ATOM 12468 O MET B 284 -51.326 -14.269 -20.889 1.00 20.21 O
ATOM 12470 N PHE B 285 -53.401 -15.088 -20.579 1.00 19.72 N
ATOM 12471 CA PHE B 285 -53.620 -15.428 -21.986 1.00 19.66 C
ATOM 12473 CB PHE B 285 -54.863 -16.324 -22.114 1.00 20.09 C
ATOM 12476 CG PHE B 285 -54.986 -17.077 -23.427 1.00 21.18 C
ATOM 12477 CD1 PHE B 285 -53.877 -17.362 -24.232 1.00 22.86 C
ATOM 12479 CE1 PHE B 285 -54.013 -18.070 -25.424 1.00 22.58 C
ATOM 12481 CZ PHE B 285 -55.254 -18.518 -25.806 1.00 23.49 C
ATOM 12483 CE2 PHE B 285 -56.365 -18.254 -25.002 1.00 23.36 C
ATOM 12485 CD2 PHE B 285 -56.222 -17.551 -23.823 1.00 21.76 C

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ATOM  12487  C   PHE B 285     -53.781 -14.148 -22.781  1.00 19.18           C
ATOM  12488  O   PHE B 285     -53.333 -14.046 -23.914  1.00 18.98           O
ATOM  12490  N   SER B 286     -54.410 -13.161 -22.164  1.00 18.92           N
ATOM  12491  CA  SER B 286     -54.488 -11.843 -22.753  1.00 19.15           C
ATOM  12493  CB  SER B 286     -55.292 -10.894 -21.863  1.00 19.38           C
ATOM  12496  OG  SER B 286     -56.684 -11.180 -21.957  1.00 20.24           O
ATOM  12498  C   SER B 286     -53.106 -11.267 -23.032  1.00 18.91           C
ATOM  12499  O   SER B 286     -52.894 -10.668 -24.087  1.00 19.48           O
ATOM  12501  N   PHE B 287     -52.172 -11.446 -22.102  1.00 18.48           N
ATOM  12502  CA  PHE B 287     -50.768 -11.065 -22.339  1.00 18.30           C
ATOM  12504  CB  PHE B 287     -49.958 -11.035 -21.044  1.00 18.27           C
ATOM  12507  CG  PHE B 287     -50.040  -9.740 -20.324  1.00 18.59           C
ATOM  12508  CD1 PHE B 287     -49.375  -8.624 -20.813  1.00 20.02           C
ATOM  12510  CE1 PHE B 287     -49.456  -7.410 -20.152  1.00 20.57           C
ATOM  12512  CZ  PHE B 287     -50.208  -7.308 -18.985  1.00 20.02           C
ATOM  12514  CE2 PHE B 287     -50.869  -8.417 -18.503  1.00 19.78           C
ATOM  12516  CD2 PHE B 287     -50.781  -9.623 -19.164  1.00 19.05           C
ATOM  12518  C   PHE B 287     -50.067 -11.978 -23.339  1.00 18.01           C
ATOM  12519  O   PHE B 287     -49.374 -11.498 -24.229  1.00 18.00           O
ATOM  12521  N   VAL B 288     -50.236 -13.286 -23.194  1.00 17.69           N
ATOM  12522  CA  VAL B 288     -49.720 -14.206 -24.197  1.00 17.66           C
ATOM  12524  CB  VAL B 288     -50.168 -15.649 -23.930  1.00 17.37           C
ATOM  12526  CG1 VAL B 288     -49.937 -16.529 -25.134  1.00 16.24           C
ATOM  12530  CG2 VAL B 288     -49.414 -16.185 -22.758  1.00 17.21           C
ATOM  12534  C   VAL B 288     -50.081 -13.761 -25.633  1.00 18.08           C
ATOM  12535  O   VAL B 288     -49.207 -13.710 -26.492  1.00 18.08           O
ATOM  12537  N   THR B 289     -51.327 -13.396 -25.895  1.00 18.42           N
ATOM  12538  CA  THR B 289     -51.683 -13.001 -27.256  1.00 19.33           C
ATOM  12540  CB  THR B 289     -53.171 -12.736 -27.401  1.00 19.35           C
ATOM  12542  OG1 THR B 289     -53.573 -11.895 -26.321  1.00 21.59           O
ATOM  12544  CG2 THR B 289     -53.973 -14.046 -27.350  1.00 19.09           C
ATOM  12548  C   THR B 289     -50.901 -11.766 -27.723  1.00 19.71           C
ATOM  12549  O   THR B 289     -50.469 -11.707 -28.891  1.00 19.88           O
ATOM  12551  N   ILE B 290     -50.689 -10.796 -26.829  1.00 19.94           N
ATOM  12552  CA  ILE B 290     -49.943  -9.585 -27.225  1.00 20.39           C
ATOM  12554  CB  ILE B 290     -50.069  -8.410 -26.221  1.00 20.50           C
ATOM  12556  CG1 ILE B 290     -51.510  -8.137 -25.823  1.00 21.25           C
ATOM  12559  CD1 ILE B 290     -51.650  -6.854 -25.002  1.00 21.58           C
ATOM  12563  CG2 ILE B 290     -49.546  -7.134 -26.853  1.00 20.39           C
ATOM  12567  C   ILE B 290     -48.434  -9.840 -27.438  1.00 20.45           C
ATOM  12568  O   ILE B 290     -47.853  -9.317 -28.393  1.00 20.76           O
ATOM  12570  N   ILE B 291     -47.808 -10.616 -26.546  1.00 20.21           N
ATOM  12571  CA  ILE B 291     -46.375 -10.869 -26.618  1.00 19.87           C
ATOM  12573  CB  ILE B 291     -45.840 -11.603 -25.407  1.00 19.79           C
ATOM  12575  CG1 ILE B 291     -46.205 -10.879 -24.102  1.00 19.71           C
ATOM  12578  CD1 ILE B 291     -45.326  -9.734 -23.748  1.00 19.77           C
ATOM  12582  CG2 ILE B 291     -44.336 -11.747 -25.516  1.00 18.91           C
ATOM  12586  C   ILE B 291     -46.134 -11.735 -27.825  1.00 20.44           C
ATOM  12587  O   ILE B 291     -45.233 -11.481 -28.600  1.00 20.35           O
ATOM  12589  N   ASP B 292     -46.965 -12.751 -28.005  1.00 21.33           N
ATOM  12590  CA  ASP B 292     -46.915 -13.563 -29.228  1.00 22.13           C
ATOM  12592  CB  ASP B 292     -48.120 -14.508 -29.316  1.00 22.40           C
ATOM  12595  CG  ASP B 292     -47.847 -15.741 -30.160  1.00 23.47           C
ATOM  12596  OD1 ASP B 292     -46.852 -15.765 -30.923  1.00 24.83           O
ATOM  12597  OD2 ASP B 292     -48.637 -16.707 -30.038  1.00 25.22           O
ATOM  12598  C   ASP B 292     -46.856 -12.716 -30.507  1.00 22.28           C
ATOM  12599  O   ASP B 292     -46.088 -13.033 -31.399  1.00 22.73           O
ATOM  12601  N   ASP B 293     -47.656 -11.658 -30.611  1.00 22.22           N
ATOM  12602  CA  ASP B 293     -47.630 -10.828 -31.822  1.00 22.43           C
ATOM  12604  CB  ASP B 293     -48.840  -9.894 -31.885  1.00 23.03           C
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ATOM  12607  CG  ASP B 293     -50.157 -10.644 -31.959  1.00 24.69           C
ATOM  12608  OD1 ASP B 293     -50.113 -11.900 -32.025  1.00 28.66           O
ATOM  12609  OD2 ASP B 293     -51.231  -9.986 -31.930  1.00 23.57           O
ATOM  12610  C   ASP B 293     -46.354  -9.997 -31.921  1.00 21.94           C
ATOM  12611  O   ASP B 293     -45.898  -9.674 -33.019  1.00 22.31           O
ATOM  12613  N   ILE B 294     -45.783  -9.643 -30.780  1.00 21.05           N
ATOM  12614  CA  ILE B 294     -44.513  -8.941 -30.770  1.00 20.53           C
ATOM  12616  CB  ILE B 294     -44.166  -8.448 -29.344  1.00 20.42           C
ATOM  12618  CG1 ILE B 294     -45.150  -7.349 -28.945  1.00 19.66           C
ATOM  12621  CD1 ILE B 294     -45.057  -6.956 -27.536  1.00 18.81           C
ATOM  12625  CG2 ILE B 294     -42.726  -7.924 -29.253  1.00 19.99           C
ATOM  12629  C   ILE B 294     -43.416  -9.845 -31.343  1.00 20.44           C
ATOM  12630  O   ILE B 294     -42.650  -9.431 -32.205  1.00 20.17           O
ATOM  12632  N   TYR B 295     -43.355 -11.088 -30.886  1.00 20.65           N
ATOM  12633  CA  TYR B 295     -42.313 -12.008 -31.353  1.00 20.76           C
ATOM  12635  CB  TYR B 295     -42.145 -13.198 -30.412  1.00 20.29           C
ATOM  12638  CG  TYR B 295     -41.393 -12.926 -29.129  1.00 17.92           C
ATOM  12639  CD1 TYR B 295     -40.117 -13.409 -28.936  1.00 17.62           C
ATOM  12641  CE1 TYR B 295     -39.427 -13.195 -27.747  1.00 17.12           C
ATOM  12643  CZ  TYR B 295     -40.022 -12.493 -26.730  1.00 16.61           C
ATOM  12644  OH  TYR B 295     -39.357 -12.281 -25.528  1.00 14.46           O
ATOM  12646  CE2 TYR B 295     -41.296 -12.008 -26.911  1.00 16.82           C
ATOM  12648  CD2 TYR B 295     -41.972 -12.235 -28.102  1.00 16.39           C
ATOM  12650  C   TYR B 295     -42.619 -12.519 -32.749  1.00 21.65           C
ATOM  12651  O   TYR B 295     -41.698 -12.751 -33.540  1.00 22.13           O
ATOM  12653  N   ASP B 296     -43.905 -12.677 -33.049  1.00 22.47           N
ATOM  12654  CA  ASP B 296     -44.327 -13.316 -34.285  1.00 23.52           C
ATOM  12656  CB  ASP B 296     -45.761 -13.851 -34.185  1.00 23.99           C
ATOM  12659  CG  ASP B 296     -46.134 -14.744 -35.369  1.00 26.22           C
ATOM  12660  OD1 ASP B 296     -45.508 -15.832 -35.538  1.00 27.70           O
ATOM  12661  OD2 ASP B 296     -47.052 -14.348 -36.128  1.00 28.78           O
ATOM  12662  C   ASP B 296     -44.228 -12.392 -35.478  1.00 23.68           C
ATOM  12663  O   ASP B 296     -43.673 -12.784 -36.502  1.00 24.01           O
ATOM  12665  N   VAL B 297     -44.765 -11.178 -35.364  1.00 23.90           N
ATOM  12666  CA  VAL B 297     -44.801 -10.273 -36.524  1.00 23.99           C
ATOM  12668  CB  VAL B 297     -46.251 -10.003 -36.973  1.00 23.87           C
ATOM  12670  CG1 VAL B 297     -46.949 -11.310 -37.197  1.00 23.75           C
ATOM  12674  CG2 VAL B 297     -47.002  -9.136 -35.966  1.00 23.05           C
ATOM  12678  C   VAL B 297     -44.060  -8.940 -36.383  1.00 24.27           C
ATOM  12679  O   VAL B 297     -43.485  -8.465 -37.342  1.00 23.84           O
ATOM  12681  N   TYR B 298     -44.058  -8.347 -35.199  1.00 24.87           N
ATOM  12682  CA  TYR B 298     -43.760  -6.926 -35.078  1.00 25.67           C
ATOM  12684  CB  TYR B 298     -44.656  -6.294 -34.010  1.00 26.06           C
ATOM  12687  CG  TYR B 298     -44.520  -4.789 -33.932  1.00 27.95           C
ATOM  12688  CD1 TYR B 298     -45.097  -3.968 -34.901  1.00 29.74           C
ATOM  12690  CE1 TYR B 298     -44.982  -2.574 -34.843  1.00 29.93           C
ATOM  12692  CZ  TYR B 298     -44.282  -1.991 -33.806  1.00 29.96           C
ATOM  12693  OH  TYR B 298     -44.165   -.631 -33.746  1.00 30.01           O
ATOM  12695  CE2 TYR B 298     -43.697  -2.777 -32.829  1.00 30.39           C
ATOM  12697  CD2 TYR B 298     -43.811  -4.181 -32.899  1.00 29.96           C
ATOM  12699  C   TYR B 298     -42.318  -6.592 -34.755  1.00 25.76           C
ATOM  12700  O   TYR B 298     -41.696  -5.830 -35.470  1.00 26.54           O
ATOM  12702  N   GLY B 299     -41.798  -7.111 -33.653  1.00 25.89           N
ATOM  12703  CA  GLY B 299     -40.473  -6.706 -33.167  1.00 25.78           C
ATOM  12706  C   GLY B 299     -39.346  -7.341 -33.951  1.00 25.52           C
ATOM  12707  O   GLY B 299     -39.513  -8.410 -34.525  1.00 26.04           O
ATOM  12709  N   THR B 300     -38.196  -6.685 -33.990  1.00 25.32           N
ATOM  12710  CA  THR B 300     -37.063  -7.237 -34.716  1.00 25.16           C
ATOM  12712  CB  THR B 300     -36.088  -6.164 -35.295  1.00 25.08           C
ATOM  12714  OG1 THR B 300     -35.191  -5.710 -34.281  1.00 25.07           O
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ATOM 12716 CG2 THR B 300 -36.833 -4.978 -35.875 1.00 25.08 C
ATOM 12720 C THR B 300 -36.324 -8.139 -33.771 1.00 25.13 C
ATOM 12721 O THR B 300 -36.335 -7.950 -32.570 1.00 25.28 O
ATOM 12723 N LEU B 301 -35.662 -9.129 -34.332 1.00 25.50 N
ATOM 12724 CA LEU B 301 -34.918 -10.093 -33.538 1.00 25.42 C
ATOM 12726 CB LEU B 301 -34.148 -11.020 -34.479 1.00 25.17 C
ATOM 12729 CG LEU B 301 -33.624 -12.338 -33.941 1.00 24.95 C
ATOM 12731 CD1 LEU B 301 -34.715 -13.233 -33.437 1.00 24.42 C
ATOM 12735 CD2 LEU B 301 -32.900 -12.998 -35.080 1.00 26.50 C
ATOM 12739 C LEU B 301 -33.995 -9.425 -32.485 1.00 25.54 C
ATOM 12740 O LEU B 301 -33.843 -9.959 -31.394 1.00 25.35 O
ATOM 12742 N ASP B 302 -33.417 -8.257 -32.782 1.00 25.68 N
ATOM 12743 CA ASP B 302 -32.598 -7.550 -31.774 1.00 26.02 C
ATOM 12745 CB ASP B 302 -31.800 -6.377 -32.378 1.00 26.37 C
ATOM 12748 CG ASP B 302 -30.563 -6.833 -33.167 1.00 28.27 C
ATOM 12749 OD1 ASP B 302 -29.508 -6.156 -33.048 1.00 29.05 O
ATOM 12750 OD2 ASP B 302 -30.652 -7.852 -33.910 1.00 31.04 O
ATOM 12751 C ASP B 302 -33.472 -7.037 -30.630 1.00 25.69 C
ATOM 12752 O ASP B 302 -33.110 -7.142 -29.447 1.00 25.90 O
ATOM 12754 N GLU B 303 -34.622 -6.473 -30.993 1.00 25.04 N
ATOM 12755 CA GLU B 303 -35.600 -6.029 -30.011 1.00 24.33 C
ATOM 12757 CB GLU B 303 -36.783 -5.346 -30.697 1.00 24.20 C
ATOM 12760 CG GLU B 303 -36.399 -4.109 -31.466 1.00 24.23 C
ATOM 12763 CD GLU B 303 -37.589 -3.382 -32.063 1.00 24.23 C
ATOM 12764 OE1 GLU B 303 -38.496 -4.065 -32.604 1.00 22.66 O
ATOM 12765 OE2 GLU B 303 -37.592 -2.121 -31.995 1.00 23.93 O
ATOM 12766 C GLU B 303 -36.103 -7.212 -29.193 1.00 23.87 C
ATOM 12767 O GLU B 303 -36.396 -7.058 -28.011 1.00 23.59 O
ATOM 12769 N LEU B 304 -36.204 -8.383 -29.825 1.00 23.39 N
ATOM 12770 CA LEU B 304 -36.766 -9.570 -29.166 1.00 23.23 C
ATOM 12772 CB LEU B 304 -37.180 -10.624 -30.208 1.00 22.83 C
ATOM 12775 CG LEU B 304 -38.381 -10.217 -31.074 1.00 22.06 C
ATOM 12777 CD1 LEU B 304 -38.822 -11.321 -32.037 1.00 20.11 C
ATOM 12781 CD2 LEU B 304 -39.551 -9.800 -30.163 1.00 21.94 C
ATOM 12785 C LEU B 304 -35.810 -10.147 -28.106 1.00 23.37 C
ATOM 12786 O LEU B 304 -36.248 -10.785 -27.141 1.00 23.22 O
ATOM 12788 N GLU B 305 -34.514 -9.892 -28.283 1.00 23.30 N
ATOM 12789 CA GLU B 305 -33.512 -10.308 -27.324 1.00 23.18 C
ATOM 12791 CB GLU B 305 -32.114 -10.176 -27.899 1.00 23.58 C
ATOM 12794 CG GLU B 305 -31.832 -11.142 -29.047 1.00 25.27 C
ATOM 12797 CD GLU B 305 -31.306 -12.488 -28.585 1.00 27.91 C
ATOM 12798 OE1 GLU B 305 -30.946 -13.303 -29.470 1.00 29.87 O
ATOM 12799 OE2 GLU B 305 -31.244 -12.728 -27.351 1.00 29.28 O
ATOM 12800 C GLU B 305 -33.633 -9.440 -26.104 1.00 22.52 C
ATOM 12801 O GLU B 305 -33.793 -9.956 -25.005 1.00 23.39 O
ATOM 12803 N LEU B 306 -33.576 -8.124 -26.274 1.00 21.51 N
ATOM 12804 CA LEU B 306 -33.715 -7.224 -25.114 1.00 20.70 C
ATOM 12806 CB LEU B 306 -33.899 -5.764 -25.544 1.00 20.59 C
ATOM 12809 CG LEU B 306 -32.769 -5.065 -26.293 1.00 20.12 C
ATOM 12811 CD1 LEU B 306 -32.992 -3.576 -26.203 1.00 19.89 C
ATOM 12815 CD2 LEU B 306 -31.402 -5.437 -25.739 1.00 19.81 C
ATOM 12819 C LEU B 306 -34.896 -7.645 -24.237 1.00 19.91 C
ATOM 12820 O LEU B 306 -34.771 -7.778 -23.031 1.00 19.53 O
ATOM 12822 N PHE B 307 -36.030 -7.883 -24.872 1.00 19.48 N
ATOM 12823 CA PHE B 307 -37.231 -8.267 -24.170 1.00 19.36 C
ATOM 12825 CB PHE B 307 -38.400 -8.406 -25.138 1.00 19.54 C
ATOM 12828 CG PHE B 307 -39.729 -8.296 -24.482 1.00 19.66 C
ATOM 12829 CD1 PHE B 307 -40.365 -7.079 -24.400 1.00 21.03 C
ATOM 12831 CE1 PHE B 307 -41.590 -6.968 -23.787 1.00 21.62 C
ATOM 12833 CZ PHE B 307 -42.182 -8.072 -23.248 1.00 20.25 C

ATOM 12835 CE2 PHE B 307 -41.553 -9.292 -23.329 1.00 20.07 C
ATOM 12837 CD2 PHE B 307 -40.338 -9.400 -23.939 1.00 19.62 C
ATOM 12839 C PHE B 307 -37.039 -9.577 -23.443 1.00 19.22 C
ATOM 12840 O PHE B 307 -37.354 -9.684 -22.260 1.00 19.50 O
ATOM 12842 N THR B 308 -36.532 -10.583 -24.143 1.00 18.96 N
ATOM 12843 CA THR B 308 -36.321 -11.874 -23.511 1.00 18.84 C
ATOM 12845 CB THR B 308 -35.774 -12.879 -24.490 1.00 18.62 C
ATOM 12847 OG1 THR B 308 -36.687 -12.988 -25.579 1.00 18.88 O
ATOM 12849 CG2 THR B 308 -35.626 -14.228 -23.833 1.00 18.74 C
ATOM 12853 C THR B 308 -35.384 -11.737 -22.317 1.00 19.04 C
ATOM 12854 O THR B 308 -35.686 -12.244 -21.233 1.00 18.69 O
ATOM 12856 N ASP B 309 -34.264 -11.031 -22.511 1.00 19.36 N
ATOM 12857 CA ASP B 309 -33.335 -10.751 -21.421 1.00 19.65 C
ATOM 12859 CB ASP B 309 -32.121 -9.983 -21.942 1.00 19.92 C
ATOM 12862 CG ASP B 309 -31.171 -9.536 -20.814 1.00 23.51 C
ATOM 12863 OD1 ASP B 309 -30.520 -10.412 -20.175 1.00 27.27 O
ATOM 12864 OD2 ASP B 309 -31.076 -8.299 -20.561 1.00 27.40 O
ATOM 12865 C ASP B 309 -34.048 -9.977 -20.295 1.00 19.08 C
ATOM 12866 O ASP B 309 -33.912 -10.308 -19.124 1.00 18.55 O
ATOM 12868 N ALA B 310 -34.836 -8.975 -20.665 1.00 18.93 N
ATOM 12869 CA ALA B 310 -35.546 -8.151 -19.688 1.00 19.12 C
ATOM 12871 CB ALA B 310 -36.346 -7.062 -20.380 1.00 18.79 C
ATOM 12875 C ALA B 310 -36.462 -8.965 -18.784 1.00 19.36 C
ATOM 12876 O ALA B 310 -36.560 -8.696 -17.577 1.00 19.58 O
ATOM 12878 N VAL B 311 -37.143 -9.942 -19.370 1.00 19.61 N
ATOM 12879 CA VAL B 311 -37.996 -10.845 -18.611 1.00 19.68 C
ATOM 12881 CB VAL B 311 -38.867 -11.682 -19.555 1.00 19.46 C
ATOM 12883 CG1 VAL B 311 -39.948 -10.825 -20.123 1.00 18.49 C
ATOM 12887 CG2 VAL B 311 -39.469 -12.863 -18.843 1.00 19.31 C
ATOM 12891 C VAL B 311 -37.161 -11.726 -17.673 1.00 20.46 C
ATOM 12892 O VAL B 311 -37.479 -11.843 -16.494 1.00 20.25 O
ATOM 12894 N GLU B 312 -36.085 -12.317 -18.189 1.00 21.67 N
ATOM 12895 CA GLU B 312 -35.198 -13.168 -17.384 1.00 22.65 C
ATOM 12897 CB GLU B 312 -34.056 -13.708 -18.239 1.00 23.03 C
ATOM 12900 CG GLU B 312 -34.454 -14.764 -19.261 1.00 24.88 C
ATOM 12903 CD GLU B 312 -33.335 -15.077 -20.267 1.00 27.34 C
ATOM 12904 OE1 GLU B 312 -33.485 -16.057 -21.028 1.00 29.07 O
ATOM 12905 OE2 GLU B 312 -32.316 -14.342 -20.313 1.00 28.63 O
ATOM 12906 C GLU B 312 -34.598 -12.443 -16.167 1.00 23.09 C
ATOM 12907 O GLU B 312 -34.506 -13.007 -15.082 1.00 23.04 O
ATOM 12909 N ARG B 313 -34.186 -11.199 -16.335 1.00 23.67 N
ATOM 12910 CA ARG B 313 -33.590 -10.486 -15.222 1.00 24.60 C
ATOM 12912 CB ARG B 313 -32.609 -9.436 -15.735 1.00 25.26 C
ATOM 12915 CG ARG B 313 -31.333 -10.030 -16.398 1.00 27.83 C
ATOM 12918 CD ARG B 313 -30.289 -8.943 -16.754 1.00 31.87 C
ATOM 12921 NE ARG B 313 -30.922 -7.793 -17.430 1.00 35.71 N
ATOM 12923 CZ ARG B 313 -31.341 -6.661 -16.837 1.00 38.42 C
ATOM 12924 NH1 ARG B 313 -31.189 -6.452 -15.522 1.00 39.15 N
ATOM 12927 NH2 ARG B 313 -31.919 -5.711 -17.576 1.00 39.25 N
ATOM 12930 C ARG B 313 -34.638 -9.879 -14.280 1.00 24.67 C
ATOM 12931 O ARG B 313 -34.359 -9.645 -13.117 1.00 24.09 O
ATOM 12933 N TRP B 314 -35.843 -9.635 -14.781 1.00 25.60 N
ATOM 12934 CA TRP B 314 -36.971 -9.180 -13.951 1.00 26.20 C
ATOM 12936 CB TRP B 314 -37.488 -10.339 -13.097 1.00 25.90 C
ATOM 12939 CG TRP B 314 -38.912 -10.184 -12.662 1.00 23.93 C
ATOM 12940 CD1 TRP B 314 -39.355 -9.854 -11.424 1.00 22.76 C
ATOM 12942 NE1 TRP B 314 -40.727 -9.804 -11.412 1.00 21.93 N
ATOM 12944 CE2 TRP B 314 -41.189 -10.107 -12.659 1.00 20.38 C
ATOM 12945 CD2 TRP B 314 -40.074 -10.352 -13.473 1.00 21.17 C
ATOM 12946 CE3 TRP B 314 -40.277 -10.684 -14.811 1.00 20.19 C

ATOM 12948 CZ3 TRP B 314 -41.549 -10.766 -15.280 1.00 19.79 C
ATOM 12950 CH2 TRP B 314 -42.640 -10.512 -14.445 1.00 21.00 C
ATOM 12952 CZ2 TRP B 314 -42.474 -10.179 -13.130 1.00 20.60 C
ATOM 12954 C TRP B 314 -36.620 -7.966 -13.076 1.00 27.57 C
ATOM 12955 O TRP B 314 -36.890 -7.935 -11.870 1.00 27.56 O
ATOM 12957 N ASP B 315 -36.039 -6.959 -13.718 1.00 29.12 N
ATOM 12958 CA ASP B 315 -35.452 -5.822 -13.027 1.00 30.46 C
ATOM 12960 CB ASP B 315 -33.935 -5.796 -13.315 1.00 30.84 C
ATOM 12963 CG ASP B 315 -33.227 -4.551 -12.772 1.00 32.75 C
ATOM 12964 OD1 ASP B 315 -33.747 -3.904 -11.830 1.00 35.67 O
ATOM 12965 OD2 ASP B 315 -32.128 -4.222 -13.295 1.00 34.91 O
ATOM 12966 C ASP B 315 -36.157 -4.592 -13.557 1.00 31.10 C
ATOM 12967 O ASP B 315 -35.888 -4.157 -14.674 1.00 31.35 O
ATOM 12969 N VAL B 316 -37.088 -4.044 -12.781 1.00 32.06 N
ATOM 12970 CA VAL B 316 -37.864 -2.896 -13.262 1.00 32.65 C
ATOM 12972 CB VAL B 316 -39.016 -2.510 -12.334 1.00 32.45 C
ATOM 12974 CG1 VAL B 316 -39.911 -1.499 -13.012 1.00 32.15 C
ATOM 12978 CG2 VAL B 316 -38.490 -1.960 -11.040 1.00 32.91 C
ATOM 12982 C VAL B 316 -36.964 -1.692 -13.442 1.00 33.43 C
ATOM 12983 O VAL B 316 -37.228 -.854 -14.294 1.00 33.74 O
ATOM 12985 N ASN B 317 -35.881 -1.628 -12.663 1.00 34.29 N
ATOM 12986 CA ASN B 317 -34.937 -.510 -12.730 1.00 34.63 C
ATOM 12988 CB ASN B 317 -33.995 -.526 -11.505 1.00 34.50 C
ATOM 12991 CG ASN B 317 -34.692 -.084 -10.201 1.00 34.08 C
ATOM 12992 OD1 ASN B 317 -35.198 1.042 -10.104 1.00 33.72 O
ATOM 12993 ND2 ASN B 317 -34.690 -.961 -9.193 1.00 31.22 N
ATOM 12996 C ASN B 317 -34.124 -.481 -14.029 1.00 35.21 C
ATOM 12997 O ASN B 317 -33.196 .296 -14.127 1.00 35.52 O
ATOM 12999 N ALA B 318 -34.470 -1.318 -15.013 1.00 35.89 N
ATOM 13000 CA ALA B 318 -33.757 -1.382 -16.299 1.00 36.48 C
ATOM 13002 CB ALA B 318 -32.727 -2.508 -16.253 1.00 36.49 C
ATOM 13006 C ALA B 318 -34.695 -1.525 -17.534 1.00 37.02 C
ATOM 13007 O ALA B 318 -34.297 -1.984 -18.616 1.00 36.52 O
ATOM 13009 N ILE B 319 -35.952 -1.137 -17.339 1.00 37.76 N
ATOM 13010 CA ILE B 319 -36.848 -.733 -18.424 1.00 38.08 C
ATOM 13012 CB ILE B 319 -37.926 .247 -17.893 1.00 38.11 C
ATOM 13014 CG1 ILE B 319 -39.110 -.495 -17.293 1.00 38.08 C
ATOM 13017 CD1 ILE B 319 -40.068 .451 -16.596 1.00 38.27 C
ATOM 13021 CG2 ILE B 319 -38.408 1.189 -18.996 1.00 37.84 C
ATOM 13025 C ILE B 319 -36.134 .053 -19.516 1.00 38.29 C
ATOM 13026 O ILE B 319 -36.192 -.324 -20.677 1.00 38.68 O
ATOM 13028 N ASN B 320 -35.460 1.141 -19.125 1.00 38.36 N
ATOM 13029 CA ASN B 320 -34.977 2.168 -20.074 1.00 38.17 C
ATOM 13031 CB ASN B 320 -34.278 3.331 -19.331 1.00 38.16 C
ATOM 13034 CG ASN B 320 -35.258 4.207 -18.514 1.00 37.87 C
ATOM 13035 OD1 ASN B 320 -36.366 4.542 -18.955 1.00 36.50 O
ATOM 13036 ND2 ASN B 320 -34.827 4.589 -17.322 1.00 38.12 N
ATOM 13039 C ASN B 320 -34.082 1.643 -21.206 1.00 37.78 C
ATOM 13040 O ASN B 320 -33.856 2.332 -22.181 1.00 37.76 O
ATOM 13042 N ASP B 321 -33.600 .416 -21.083 1.00 37.46 N
ATOM 13043 CA ASP B 321 -32.852 -.224 -22.162 1.00 37.25 C
ATOM 13045 CB ASP B 321 -32.091 -1.467 -21.629 1.00 37.83 C
ATOM 13048 CG ASP B 321 -31.351 -1.207 -20.285 1.00 39.33 C
ATOM 13049 OD1 ASP B 321 -31.247 -.021 -19.871 1.00 40.72 O
ATOM 13050 OD2 ASP B 321 -30.887 -2.199 -19.648 1.00 39.62 O
ATOM 13051 C ASP B 321 -33.764 -.636 -23.339 1.00 35.99 C
ATOM 13052 O ASP B 321 -33.273 -.904 -24.436 1.00 35.87 O
ATOM 13054 N LEU B 322 -35.076 -.674 -23.111 1.00 34.66 N
ATOM 13055 CA LEU B 322 -36.024 -1.263 -24.061 1.00 33.77 C
ATOM 13057 CB LEU B 322 -37.180 -1.961 -23.327 1.00 33.65 C

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ATOM  13060  CG  LEU B 322     -36.994  -3.260 -22.544  1.00 32.41           C
ATOM  13062  CD1 LEU B 322     -38.223  -3.482 -21.693  1.00 31.54           C
ATOM  13066  CD2 LEU B 322     -36.769  -4.432 -23.460  1.00 30.73           C
ATOM  13070  C   LEU B 322     -36.670   -.243 -24.982  1.00 33.32           C
ATOM  13071  O   LEU B 322     -36.910    .893 -24.570  1.00 33.37           O
ATOM  13073  N   PRO B 323     -37.005   -.667 -26.218  1.00 32.72           N
ATOM  13074  CA  PRO B 323     -37.856    .068 -27.126  1.00 32.42           C
ATOM  13076  CB  PRO B 323     -38.239   -.985 -28.158  1.00 32.28           C
ATOM  13079  CG  PRO B 323     -37.098  -1.849 -28.231  1.00 32.46           C
ATOM  13082  CD  PRO B 323     -36.498  -1.891 -26.857  1.00 32.79           C
ATOM  13085  C   PRO B 323     -39.115    .576 -26.453  1.00 32.50           C
ATOM  13086  O   PRO B 323     -39.655   -.083 -25.550  1.00 32.46           O
ATOM  13087  N   ASP B 324     -39.590   1.725 -26.923  1.00 32.44           N
ATOM  13088  CA  ASP B 324     -40.729   2.387 -26.318  1.00 32.44           C
ATOM  13090  CB  ASP B 324     -41.059   3.678 -27.071  1.00 32.91           C
ATOM  13093  CG  ASP B 324     -40.241   4.873 -26.576  1.00 34.17           C
ATOM  13094  OD1 ASP B 324     -39.507   4.728 -25.562  1.00 35.83           O
ATOM  13095  OD2 ASP B 324     -40.351   5.960 -27.196  1.00 35.42           O
ATOM  13096  C   ASP B 324     -41.967   1.504 -26.186  1.00 31.78           C
ATOM  13097  O   ASP B 324     -42.546   1.440 -25.102  1.00 31.77           O
ATOM  13099  N   TYR B 325     -42.368    .821 -27.258  1.00 30.99           N
ATOM  13100  CA  TYR B 325     -43.519   -.086 -27.167  1.00 30.49           C
ATOM  13102  CB  TYR B 325     -43.941   -.640 -28.536  1.00 30.28           C
ATOM  13105  CG  TYR B 325     -43.027  -1.688 -29.134  1.00 30.25           C
ATOM  13106  CD1 TYR B 325     -41.917  -1.332 -29.893  1.00 29.81           C
ATOM  13108  CE1 TYR B 325     -41.089  -2.300 -30.449  1.00 29.74           C
ATOM  13110  CZ  TYR B 325     -41.371  -3.643 -30.258  1.00 30.22           C
ATOM  13111  OH  TYR B 325     -40.565  -4.625 -30.805  1.00 31.28           O
ATOM  13113  CE2 TYR B 325     -42.466  -4.015 -29.519  1.00 30.23           C
ATOM  13115  CD2 TYR B 325     -43.288  -3.038 -28.963  1.00 30.49           C
ATOM  13117  C   TYR B 325     -43.284  -1.221 -26.168  1.00 30.14           C
ATOM  13118  O   TYR B 325     -44.219  -1.638 -25.483  1.00 30.19           O
ATOM  13120  N   MET B 326     -42.048  -1.700 -26.060  1.00 29.74           N
ATOM  13121  CA  MET B 326     -41.755  -2.820 -25.155  1.00 29.82           C
ATOM  13123  CB  MET B 326     -40.461  -3.541 -25.549  1.00 29.69           C
ATOM  13126  CG  MET B 326     -40.650  -4.510 -26.686  1.00 28.83           C
ATOM  13129  SD  MET B 326     -39.123  -5.272 -27.204  1.00 26.99           S
ATOM  13130  CE  MET B 326     -39.761  -6.499 -28.328  1.00 29.13           C
ATOM  13134  C   MET B 326     -41.696  -2.402 -23.683  1.00 29.92           C
ATOM  13135  O   MET B 326     -42.032  -3.204 -22.801  1.00 29.75           O
ATOM  13137  N   LYS B 327     -41.251  -1.166 -23.429  1.00 29.68           N
ATOM  13138  CA  LYS B 327     -41.318   -.578 -22.088  1.00 29.46           C
ATOM  13140  CB  LYS B 327     -41.016    .921 -22.114  1.00 29.93           C
ATOM  13143  CG  LYS B 327     -39.572   1.305 -21.951  1.00 31.63           C
ATOM  13146  CD  LYS B 327     -39.410   2.803 -22.249  1.00 34.93           C
ATOM  13149  CE  LYS B 327     -37.986   3.291 -22.021  1.00 36.86           C
ATOM  13152  NZ  LYS B 327     -37.642   4.436 -22.917  1.00 37.83           N
ATOM  13156  C   LYS B 327     -42.708   -.752 -21.531  1.00 28.46           C
ATOM  13157  O   LYS B 327     -42.879  -1.314 -20.461  1.00 28.54           O
ATOM  13159  N   LEU B 328     -43.696   -.258 -22.268  1.00 27.39           N
ATOM  13160  CA  LEU B 328     -45.056   -.216 -21.785  1.00 26.79           C
ATOM  13162  CB  LEU B 328     -45.946    .519 -22.773  1.00 26.68           C
ATOM  13165  CG  LEU B 328     -47.265   1.034 -22.212  1.00 26.00           C
ATOM  13167  CD1 LEU B 328     -47.010   1.964 -21.036  1.00 24.88           C
ATOM  13171  CD2 LEU B 328     -48.051   1.740 -23.308  1.00 24.55           C
ATOM  13175  C   LEU B 328     -45.560  -1.628 -21.587  1.00 26.70           C
ATOM  13176  O   LEU B 328     -46.110  -1.983 -20.543  1.00 27.03           O
ATOM  13178  N   CYS B 329     -45.341  -2.453 -22.591  1.00 26.39           N
ATOM  13179  CA  CYS B 329     -45.750  -3.843 -22.524  1.00 26.12           C
ATOM  13181  CB  CYS B 329     -45.382  -4.526 -23.838  1.00 26.47           C
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ATOM  13184  SG  CYS B 329    -45.857  -6.236 -23.880  1.00 30.60       S
ATOM  13186  C   CYS B 329    -45.124  -4.568 -21.319  1.00 24.45       C
ATOM  13187  O   CYS B 329    -45.829  -5.105 -20.486  1.00 23.93       O
ATOM  13189  N   PHE B 330    -43.801  -4.553 -21.228  1.00 23.30       N
ATOM  13190  CA  PHE B 330    -43.087  -5.220 -20.141  1.00 22.47       C
ATOM  13192  CB  PHE B 330    -41.575  -5.019 -20.267  1.00 22.42       C
ATOM  13195  CG  PHE B 330    -40.800  -5.518 -19.076  1.00 22.37       C
ATOM  13196  CD1 PHE B 330    -40.502  -6.864 -18.940  1.00 22.47       C
ATOM  13198  CE1 PHE B 330    -39.799  -7.339 -17.836  1.00 21.64       C
ATOM  13200  CZ  PHE B 330    -39.379  -6.472 -16.866  1.00 21.50       C
ATOM  13202  CE2 PHE B 330    -39.659  -5.122 -16.983  1.00 21.92       C
ATOM  13204  CD2 PHE B 330    -40.374  -4.648 -18.084  1.00 22.29       C
ATOM  13206  C   PHE B 330    -43.524  -4.739 -18.765  1.00 21.87       C
ATOM  13207  O   PHE B 330    -43.779  -5.552 -17.875  1.00 21.98       O
ATOM  13209  N   LEU B 331    -43.594  -3.427 -18.573  1.00 20.88       N
ATOM  13210  CA  LEU B 331    -43.997  -2.894 -17.276  1.00 20.25       C
ATOM  13212  CB  LEU B 331    -43.927  -1.354 -17.257  1.00 20.06       C
ATOM  13215  CG  LEU B 331    -44.124   -.628 -15.912  1.00 19.21       C
ATOM  13217  CD1 LEU B 331    -43.542  -1.408 -14.737  1.00 18.78       C
ATOM  13221  CD2 LEU B 331    -43.555   .770 -15.957  1.00 15.75       C
ATOM  13225  C   LEU B 331    -45.398  -3.408 -16.902  1.00 19.99       C
ATOM  13226  O   LEU B 331    -45.606  -3.860 -15.771  1.00 19.67       O
ATOM  13228  N   ALA B 332    -46.336  -3.373 -17.860  1.00 19.56       N
ATOM  13229  CA  ALA B 332    -47.695  -3.882 -17.629  1.00 19.24       C
ATOM  13231  CB  ALA B 332    -48.528  -3.802 -18.891  1.00 18.58       C
ATOM  13235  C   ALA B 332    -47.637  -5.321 -17.108  1.00 19.23       C
ATOM  13236  O   ALA B 332    -48.235  -5.650 -16.079  1.00 19.18       O
ATOM  13238  N   LEU B 333    -46.891  -6.162 -17.816  1.00 19.16       N
ATOM  13239  CA  LEU B 333    -46.727  -7.554 -17.438  1.00 19.08       C
ATOM  13241  CB  LEU B 333    -45.830  -8.260 -18.462  1.00 18.97       C
ATOM  13244  CG  LEU B 333    -45.511  -9.758 -18.307  1.00 19.18       C
ATOM  13246  CD1 LEU B 333    -46.779 -10.611 -18.121  1.00 18.09       C
ATOM  13250  CD2 LEU B 333    -44.676 -10.262 -19.499  1.00 17.17       C
ATOM  13254  C   LEU B 333    -46.111  -7.616 -16.042  1.00 19.16       C
ATOM  13255  O   LEU B 333    -46.629  -8.279 -15.137  1.00 18.97       O
ATOM  13257  N   TYR B 334    -45.013  -6.887 -15.884  1.00 19.23       N
ATOM  13258  CA  TYR B 334    -44.212  -6.906 -14.664  1.00 19.33       C
ATOM  13260  CB  TYR B 334    -43.092  -5.873 -14.785  1.00 19.43       C
ATOM  13263  CG  TYR B 334    -42.190  -5.748 -13.596  1.00 19.44       C
ATOM  13264  CD1 TYR B 334    -41.006  -6.464 -13.524  1.00 20.60       C
ATOM  13266  CE1 TYR B 334    -40.148  -6.347 -12.442  1.00 20.77       C
ATOM  13268  CZ  TYR B 334    -40.474  -5.503 -11.417  1.00 21.51       C
ATOM  13269  OH  TYR B 334    -39.628  -5.387 -10.353  1.00 21.42       O
ATOM  13271  CE2 TYR B 334    -41.646  -4.768 -11.466  1.00 22.15       C
ATOM  13273  CD2 TYR B 334    -42.495  -4.892 -12.565  1.00 20.55       C
ATOM  13275  C   TYR B 334    -45.065  -6.614 -13.443  1.00 19.37       C
ATOM  13276  O   TYR B 334    -44.980  -7.337 -12.441  1.00 19.94       O
ATOM  13278  N   ASN B 335    -45.888  -5.565 -13.527  1.00 18.83       N
ATOM  13279  CA  ASN B 335    -46.784  -5.236 -12.443  1.00 18.37       C
ATOM  13281  CB  ASN B 335    -47.452  -3.896 -12.675  1.00 18.52       C
ATOM  13284  CG  ASN B 335    -46.493  -2.742 -12.518  1.00 19.27       C
ATOM  13285  OD1 ASN B 335    -45.421  -2.906 -11.953  1.00 21.25       O
ATOM  13286  ND2 ASN B 335    -46.872  -1.566 -13.022  1.00 19.24       N
ATOM  13289  C   ASN B 335    -47.812  -6.333 -12.291  1.00 18.22       C
ATOM  13290  O   ASN B 335    -47.966  -6.891 -11.207  1.00 18.53       O
ATOM  13292  N   THR B 336    -48.481  -6.697 -13.379  1.00 17.95       N
ATOM  13293  CA  THR B 336    -49.525  -7.728 -13.301  1.00 17.61       C
ATOM  13295  CB  THR B 336    -49.980  -8.204 -14.676  1.00 17.36       C
ATOM  13297  OG1 THR B 336    -50.249  -7.065 -15.500  1.00 17.02       O
ATOM  13299  CG2 THR B 336    -51.228  -9.044 -14.551  1.00 16.07       C
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ATOM 13303 C THR B 336 -49.065 -8.941 -12.501 1.00 17.75 C
ATOM 13304 O THR B 336 -49.788 -9.429 -11.621 1.00 18.09 O
ATOM 13306 N ILE B 337 -47.859 -9.411 -12.785 1.00 17.69 N
ATOM 13307 CA ILE B 337 -47.384 -10.630 -12.165 1.00 17.74 C
ATOM 13309 CB ILE B 337 -46.228 -11.245 -12.949 1.00 17.40 C
ATOM 13311 CG1 ILE B 337 -46.795 -11.865 -14.227 1.00 18.44 C
ATOM 13314 CD1 ILE B 337 -45.767 -12.192 -15.300 1.00 19.26 C
ATOM 13318 CG2 ILE B 337 -45.568 -12.320 -12.152 1.00 16.25 C
ATOM 13322 C ILE B 337 -47.053 -10.395 -10.699 1.00 18.32 C
ATOM 13323 O ILE B 337 -47.497 -11.175 -9.838 1.00 18.06 O
ATOM 13325 N ASN B 338 -46.321 -9.311 -10.404 1.00 18.89 N
ATOM 13326 CA ASN B 338 -45.985 -8.978 -9.007 1.00 19.49 C
ATOM 13328 CB ASN B 338 -45.189 -7.690 -8.917 1.00 19.43 C
ATOM 13331 CG ASN B 338 -43.789 -7.836 -9.444 1.00 20.83 C
ATOM 13332 OD1 ASN B 338 -43.292 -8.954 -9.634 1.00 21.52 O
ATOM 13333 ND2 ASN B 338 -43.124 -6.697 -9.676 1.00 22.32 N
ATOM 13336 C ASN B 338 -47.229 -8.835 -8.146 1.00 20.05 C
ATOM 13337 O ASN B 338 -47.182 -9.055 -6.953 1.00 19.81 O
ATOM 13339 N GLU B 339 -48.337 -8.459 -8.770 1.00 20.81 N
ATOM 13340 CA GLU B 339 -49.589 -8.347 -8.086 1.00 21.81 C
ATOM 13342 CB GLU B 339 -50.563 -7.544 -8.933 1.00 22.69 C
ATOM 13345 CG GLU B 339 -51.240 -6.422 -8.148 1.00 27.28 C
ATOM 13348 CD GLU B 339 -52.571 -5.959 -8.768 1.00 32.79 C
ATOM 13349 OE1 GLU B 339 -52.761 -4.713 -8.897 1.00 36.20 O
ATOM 13350 OE2 GLU B 339 -53.416 -6.837 -9.114 1.00 34.35 O
ATOM 13351 C GLU B 339 -50.170 -9.732 -7.762 1.00 21.59 C
ATOM 13352 O GLU B 339 -50.690 -9.946 -6.666 1.00 21.38 O
ATOM 13354 N ILE B 340 -50.094 -10.676 -8.700 1.00 21.48 N
ATOM 13355 CA ILE B 340 -50.486 -12.049 -8.384 1.00 21.27 C
ATOM 13357 CB ILE B 340 -50.437 -12.990 -9.603 1.00 21.17 C
ATOM 13359 CG1 ILE B 340 -51.478 -12.589 -10.643 1.00 20.99 C
ATOM 13362 CD1 ILE B 340 -51.245 -13.202 -12.017 1.00 19.72 C
ATOM 13366 CG2 ILE B 340 -50.702 -14.444 -9.177 1.00 21.09 C
ATOM 13370 C ILE B 340 -49.557 -12.585 -7.278 1.00 21.40 C
ATOM 13371 O ILE B 340 -50.023 -13.238 -6.334 1.00 21.74 O
ATOM 13373 N ALA B 341 -48.256 -12.301 -7.380 1.00 20.90 N
ATOM 13374 CA ALA B 341 -47.312 -12.721 -6.349 1.00 20.62 C
ATOM 13376 CB ALA B 341 -45.922 -12.260 -6.694 1.00 20.53 C
ATOM 13380 C ALA B 341 -47.720 -12.195 -4.969 1.00 20.59 C
ATOM 13381 O ALA B 341 -47.606 -12.901 -3.950 1.00 20.57 O
ATOM 13383 N TYR B 342 -48.208 -10.958 -4.949 1.00 20.62 N
ATOM 13384 CA TYR B 342 -48.600 -10.303 -3.707 1.00 20.59 C
ATOM 13386 CB TYR B 342 -48.790 -8.792 -3.907 1.00 20.05 C
ATOM 13389 CG TYR B 342 -49.309 -8.143 -2.674 1.00 18.29 C
ATOM 13390 CD1 TYR B 342 -48.443 -7.683 -1.698 1.00 17.62 C
ATOM 13392 CE1 TYR B 342 -48.914 -7.111 -.518 1.00 17.91 C
ATOM 13394 CZ TYR B 342 -50.285 -7.005 -.298 1.00 18.18 C
ATOM 13395 OH TYR B 342 -50.763 -6.433 .877 1.00 16.00 O
ATOM 13397 CE2 TYR B 342 -51.169 -7.467 -1.275 1.00 18.10 C
ATOM 13399 CD2 TYR B 342 -50.670 -8.037 -2.450 1.00 17.67 C
ATOM 13401 C TYR B 342 -49.863 -10.928 -3.118 1.00 21.48 C
ATOM 13402 O TYR B 342 -49.960 -11.089 -1.913 1.00 20.91 O
ATOM 13404 N ASP B 343 -50.832 -11.273 -3.959 1.00 22.93 N
ATOM 13405 CA ASP B 343 -52.048 -11.925 -3.470 1.00 24.30 C
ATOM 13407 CB ASP B 343 -53.010 -12.282 -4.608 1.00 24.59 C
ATOM 13410 CG ASP B 343 -53.577 -11.060 -5.334 1.00 26.66 C
ATOM 13411 OD1 ASP B 343 -53.619 -9.936 -4.756 1.00 28.24 O
ATOM 13412 OD2 ASP B 343 -54.004 -11.247 -6.506 1.00 29.56 O
ATOM 13413 C ASP B 343 -51.660 -13.208 -2.761 1.00 24.97 C
ATOM 13414 O ASP B 343 -52.128 -13.495 -1.658 1.00 24.95 O

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ATOM  13416  N   ASN B 344     -50.792 -13.973  -3.413  1.00 25.90           N
ATOM  13417  CA  ASN B 344     -50.322 -15.252  -2.884  1.00 26.59           C
ATOM  13419  CB  ASN B 344     -49.623 -16.043  -3.978  1.00 26.74           C
ATOM  13422  CG  ASN B 344     -50.594 -16.639  -4.933  1.00 28.21           C
ATOM  13423  OD1 ASN B 344     -51.080 -17.737  -4.688  1.00 32.10           O
ATOM  13424  ND2 ASN B 344     -50.923 -15.916  -6.016  1.00 28.40           N
ATOM  13427  C   ASN B 344     -49.421 -15.146  -1.655  1.00 26.78           C
ATOM  13428  O   ASN B 344     -49.424 -16.053   -.821  1.00 27.06           O
ATOM  13430  N   LEU B 345     -48.647 -14.067  -1.533  1.00 26.74           N
ATOM  13431  CA  LEU B 345     -47.970 -13.793   -.261  1.00 26.59           C
ATOM  13433  CB  LEU B 345     -47.005 -12.618   -.396  1.00 26.25           C
ATOM  13436  CG  LEU B 345     -46.046 -12.376    .764  1.00 24.65           C
ATOM  13438  CD1 LEU B 345     -45.258 -13.621   1.115  1.00 22.50           C
ATOM  13442  CD2 LEU B 345     -45.119 -11.251    .387  1.00 23.54           C
ATOM  13446  C   LEU B 345     -49.004 -13.503    .840  1.00 27.00           C
ATOM  13447  O   LEU B 345     -48.903 -14.014   1.947  1.00 26.93           O
ATOM  13449  N   LYS B 346     -50.008 -12.697    .518  1.00 27.54           N
ATOM  13450  CA  LYS B 346     -51.012 -12.300   1.491  1.00 27.96           C
ATOM  13452  CB  LYS B 346     -51.998 -11.288    .889  1.00 28.13           C
ATOM  13455  CG  LYS B 346     -52.822 -10.527   1.926  1.00 28.70           C
ATOM  13458  CD  LYS B 346     -53.781  -9.526   1.281  1.00 29.73           C
ATOM  13461  CE  LYS B 346     -55.205 -10.063   1.133  1.00 31.17           C
ATOM  13464  NZ  LYS B 346     -55.839  -9.661   -.171  1.00 32.83           N
ATOM  13468  C   LYS B 346     -51.788 -13.498   1.984  1.00 28.31           C
ATOM  13469  O   LYS B 346     -52.074 -13.600   3.177  1.00 28.52           O
ATOM  13471  N   ASP B 347     -52.149 -14.396   1.075  1.00 28.56           N
ATOM  13472  CA  ASP B 347     -53.102 -15.441   1.427  1.00 29.11           C
ATOM  13474  CB  ASP B 347     -54.068 -15.736    .268  1.00 29.50           C
ATOM  13477  CG  ASP B 347     -54.902 -14.500   -.150  1.00 31.04           C
ATOM  13478  OD1 ASP B 347     -54.961 -13.500    .616  1.00 31.35           O
ATOM  13479  OD2 ASP B 347     -55.496 -14.534  -1.261  1.00 33.39           O
ATOM  13480  C   ASP B 347     -52.403 -16.699   1.891  1.00 28.79           C
ATOM  13481  O   ASP B 347     -52.824 -17.321   2.854  1.00 29.02           O
ATOM  13483  N   LYS B 348     -51.326 -17.068   1.222  1.00 28.74           N
ATOM  13484  CA  LYS B 348     -50.612 -18.293   1.564  1.00 28.84           C
ATOM  13486  CB  LYS B 348     -50.290 -19.101    .299  1.00 29.24           C
ATOM  13489  CG  LYS B 348     -51.513 -19.470   -.576  1.00 30.97           C
ATOM  13492  CD  LYS B 348     -51.051 -20.300  -1.803  1.00 33.66           C
ATOM  13495  CE  LYS B 348     -52.033 -20.244  -2.989  1.00 34.52           C
ATOM  13498  NZ  LYS B 348     -53.445 -20.542  -2.607  1.00 35.61           N
ATOM  13502  C   LYS B 348     -49.330 -18.029   2.358  1.00 27.97           C
ATOM  13503  O   LYS B 348     -48.763 -18.948   2.925  1.00 27.88           O
ATOM  13505  N   GLY B 349     -48.874 -16.785   2.403  1.00 27.21           N
ATOM  13506  CA  GLY B 349     -47.625 -16.473   3.075  1.00 26.87           C
ATOM  13509  C   GLY B 349     -46.437 -17.227   2.514  1.00 26.71           C
ATOM  13510  O   GLY B 349     -45.576 -17.669   3.271  1.00 26.65           O
ATOM  13512  N   GLU B 350     -46.409 -17.390   1.191  1.00 26.61           N
ATOM  13513  CA  GLU B 350     -45.263 -17.953    .470  1.00 26.43           C
ATOM  13515  CB  GLU B 350     -45.624 -19.310   -.128  1.00 26.85           C
ATOM  13518  CG  GLU B 350     -45.685 -20.453    .888  1.00 29.63           C
ATOM  13521  CD  GLU B 350     -44.304 -21.036   1.227  1.00 34.21           C
ATOM  13522  OE1 GLU B 350     -43.417 -21.045    .328  1.00 36.93           O
ATOM  13523  OE2 GLU B 350     -44.106 -21.498   2.384  1.00 35.89           O
ATOM  13524  C   GLU B 350     -44.900 -16.981   -.637  1.00 25.49           C
ATOM  13525  O   GLU B 350     -45.774 -16.312  -1.181  1.00 25.35           O
ATOM  13527  N   ASN B 351     -43.616 -16.866   -.955  1.00 24.74           N
ATOM  13528  CA  ASN B 351     -43.206 -16.046  -2.090  1.00 24.47           C
ATOM  13530  CB  ASN B 351     -41.851 -15.369  -1.867  1.00 24.94           C
ATOM  13533  CG  ASN B 351     -41.428 -14.489  -3.062  1.00 26.98           C
ATOM  13534  OD1 ASN B 351     -41.976 -14.605  -4.170  1.00 28.96           O
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ATOM 13535 ND2 ASN B 351 -40.457 -13.601 -2.834 1.00 29.55 N
ATOM 13538 C ASN B 351 -43.095 -16.918 -3.303 1.00 23.33 C
ATOM 13539 O ASN B 351 -42.120 -17.641 -3.429 1.00 23.47 O
ATOM 13541 N ILE B 352 -44.060 -16.823 -4.208 1.00 22.09 N
ATOM 13542 CA ILE B 352 -44.048 -17.644 -5.410 1.00 21.22 C
ATOM 13544 CB ILE B 352 -45.452 -18.213 -5.675 1.00 21.23 C
ATOM 13546 CG1 ILE B 352 -46.464 -17.080 -5.913 1.00 21.11 C
ATOM 13549 CD1 ILE B 352 -47.346 -17.305 -7.126 1.00 20.33 C
ATOM 13553 CG2 ILE B 352 -45.875 -19.116 -4.519 1.00 19.79 C
ATOM 13557 C ILE B 352 -43.508 -16.947 -6.689 1.00 20.88 C
ATOM 13558 O ILE B 352 -43.486 -17.553 -7.758 1.00 20.76 O
ATOM 13560 N LEU B 353 -43.030 -15.705 -6.574 1.00 20.44 N
ATOM 13561 CA LEU B 353 -42.603 -14.907 -7.750 1.00 19.84 C
ATOM 13563 CB LEU B 353 -42.055 -13.527 -7.325 1.00 19.67 C
ATOM 13566 CG LEU B 353 -42.003 -12.339 -8.311 1.00 18.47 C
ATOM 13568 CD1 LEU B 353 -43.306 -12.083 -9.008 1.00 17.03 C
ATOM 13572 CD2 LEU B 353 -41.604 -11.064 -7.597 1.00 17.08 C
ATOM 13576 C LEU B 353 -41.587 -15.628 -8.633 1.00 19.81 C
ATOM 13577 O LEU B 353 -41.720 -15.596 -9.851 1.00 19.55 O
ATOM 13579 N PRO B 354 -40.578 -16.299 -8.024 1.00 20.01 N
ATOM 13580 CA PRO B 354 -39.571 -17.010 -8.822 1.00 19.73 C
ATOM 13582 CB PRO B 354 -38.781 -17.796 -7.779 1.00 19.55 C
ATOM 13585 CG PRO B 354 -38.928 -17.037 -6.542 1.00 19.61 C
ATOM 13588 CD PRO B 354 -40.289 -16.413 -6.578 1.00 19.90 C
ATOM 13591 C PRO B 354 -40.187 -17.971 -9.804 1.00 19.87 C
ATOM 13592 O PRO B 354 -39.693 -18.103 -10.918 1.00 20.08 O
ATOM 13593 N TYR B 355 -41.264 -18.636 -9.387 1.00 20.14 N
ATOM 13594 CA TYR B 355 -41.909 -19.665 -10.216 1.00 20.24 C
ATOM 13596 CB TYR B 355 -42.878 -20.520 -9.394 1.00 20.40 C
ATOM 13599 CG TYR B 355 -42.189 -21.153 -8.214 1.00 21.82 C
ATOM 13600 CD1 TYR B 355 -41.119 -21.999 -8.412 1.00 22.86 C
ATOM 13602 CE1 TYR B 355 -40.457 -22.564 -7.353 1.00 25.07 C
ATOM 13604 CZ TYR B 355 -40.850 -22.285 -6.053 1.00 25.58 C
ATOM 13605 OH TYR B 355 -40.153 -22.887 -5.020 1.00 27.33 O
ATOM 13607 CE2 TYR B 355 -41.918 -21.433 -5.815 1.00 23.93 C
ATOM 13609 CD2 TYR B 355 -42.577 -20.867 -6.900 1.00 23.10 C
ATOM 13611 C TYR B 355 -42.625 -19.001 -11.361 1.00 19.67 C
ATOM 13612 O TYR B 355 -42.455 -19.405 -12.510 1.00 19.75 O
ATOM 13614 N LEU B 356 -43.385 -17.954 -11.030 1.00 18.97 N
ATOM 13615 CA LEU B 356 -44.180 -17.205 -12.004 1.00 18.26 C
ATOM 13617 CB LEU B 356 -45.039 -16.157 -11.293 1.00 18.03 C
ATOM 13620 CG LEU B 356 -46.056 -16.727 -10.312 1.00 18.13 C
ATOM 13622 CD1 LEU B 356 -46.691 -15.613 -9.500 1.00 19.37 C
ATOM 13626 CD2 LEU B 356 -47.106 -17.521 -11.046 1.00 17.93 C
ATOM 13630 C LEU B 356 -43.298 -16.536 -13.056 1.00 17.76 C
ATOM 13631 O LEU B 356 -43.598 -16.567 -14.259 1.00 16.93 O
ATOM 13633 N THR B 357 -42.201 -15.949 -12.600 1.00 17.56 N
ATOM 13634 CA THR B 357 -41.335 -15.215 -13.501 1.00 17.63 C
ATOM 13636 CB THR B 357 -40.438 -14.236 -12.759 1.00 17.69 C
ATOM 13638 OG1 THR B 357 -39.530 -14.974 -11.934 1.00 18.39 O
ATOM 13640 CG2 THR B 357 -41.288 -13.242 -11.927 1.00 16.47 C
ATOM 13644 C THR B 357 -40.477 -16.145 -14.356 1.00 17.55 C
ATOM 13645 O THR B 357 -40.154 -15.793 -15.498 1.00 17.17 O
ATOM 13647 N LYS B 358 -40.127 -17.321 -13.824 1.00 17.37 N
ATOM 13648 CA LYS B 358 -39.462 -18.337 -14.649 1.00 17.55 C
ATOM 13650 CB LYS B 358 -39.030 -19.542 -13.827 1.00 17.87 C
ATOM 13653 CG LYS B 358 -38.450 -20.718 -14.640 1.00 18.75 C
ATOM 13656 CD LYS B 358 -37.013 -20.497 -15.112 1.00 20.18 C
ATOM 13659 CE LYS B 358 -36.361 -21.843 -15.457 1.00 21.49 C
ATOM 13662 NZ LYS B 358 -35.189 -21.702 -16.361 1.00 22.89 N

ATOM 13666 C LYS B 358 -40.403 -18.777 -15.754 1.00 17.43 C
ATOM 13667 O LYS B 358 -40.031 -18.775 -16.926 1.00 17.52 O
ATOM 13669 N ALA B 359 -41.633 -19.120 -15.384 1.00 17.42 N
ATOM 13670 CA ALA B 359 -42.654 -19.471 -16.359 1.00 17.52 C
ATOM 13672 CB ALA B 359 -44.011 -19.434 -15.738 1.00 17.16 C
ATOM 13676 C ALA B 359 -42.585 -18.521 -17.531 1.00 18.18 C
ATOM 13677 O ALA B 359 -42.513 -18.956 -18.675 1.00 18.50 O
ATOM 13679 N TRP B 360 -42.556 -17.223 -17.245 1.00 19.14 N
ATOM 13680 CA TRP B 360 -42.526 -16.206 -18.301 1.00 19.77 C
ATOM 13682 CB TRP B 360 -42.922 -14.837 -17.746 1.00 20.15 C
ATOM 13685 CG TRP B 360 -44.377 -14.653 -17.813 1.00 20.50 C
ATOM 13686 CD1 TRP B 360 -45.259 -14.729 -16.788 1.00 22.15 C
ATOM 13688 NE1 TRP B 360 -46.536 -14.533 -17.248 1.00 22.84 N
ATOM 13690 CE2 TRP B 360 -46.487 -14.348 -18.603 1.00 21.68 C
ATOM 13691 CD2 TRP B 360 -45.134 -14.418 -18.987 1.00 20.85 C
ATOM 13692 CE3 TRP B 360 -44.802 -14.253 -20.334 1.00 21.21 C
ATOM 13694 CZ3 TRP B 360 -45.821 -14.025 -21.245 1.00 20.75 C
ATOM 13696 CH2 TRP B 360 -47.166 -13.961 -20.827 1.00 21.21 C
ATOM 13698 CZ2 TRP B 360 -47.515 -14.123 -19.516 1.00 20.97 C
ATOM 13700 C TRP B 360 -41.215 -16.110 -19.081 1.00 19.96 C
ATOM 13701 O TRP B 360 -41.242 -15.791 -20.271 1.00 19.94 O
ATOM 13703 N ALA B 361 -40.089 -16.368 -18.420 1.00 20.14 N
ATOM 13704 CA ALA B 361 -38.790 -16.437 -19.102 1.00 20.41 C
ATOM 13706 CB ALA B 361 -37.676 -16.581 -18.102 1.00 20.67 C
ATOM 13710 C ALA B 361 -38.763 -17.618 -20.041 1.00 20.55 C
ATOM 13711 O ALA B 361 -38.330 -17.510 -21.187 1.00 20.76 O
ATOM 13713 N ASP B 362 -39.230 -18.749 -19.534 1.00 20.57 N
ATOM 13714 CA ASP B 362 -39.360 -19.965 -20.326 1.00 20.97 C
ATOM 13716 CB ASP B 362 -39.984 -21.082 -19.470 1.00 21.39 C
ATOM 13719 CG ASP B 362 -38.938 -21.902 -18.693 1.00 22.80 C
ATOM 13720 OD1 ASP B 362 -38.836 -23.109 -18.970 1.00 28.57 O
ATOM 13721 OD2 ASP B 362 -38.210 -21.384 -17.825 1.00 22.78 O
ATOM 13722 C ASP B 362 -40.179 -19.748 -21.618 1.00 20.66 C
ATOM 13723 O ASP B 362 -39.740 -20.141 -22.701 1.00 20.69 O
ATOM 13725 N LEU B 363 -41.346 -19.110 -21.501 1.00 20.22 N
ATOM 13726 CA LEU B 363 -42.245 -18.885 -22.648 1.00 19.82 C
ATOM 13728 CB LEU B 363 -43.592 -18.327 -22.164 1.00 19.11 C
ATOM 13731 CG LEU B 363 -44.644 -17.945 -23.209 1.00 17.02 C
ATOM 13733 CD1 LEU B 363 -44.829 -19.033 -24.214 1.00 16.20 C
ATOM 13737 CD2 LEU B 363 -45.979 -17.618 -22.586 1.00 14.21 C
ATOM 13741 C LEU B 363 -41.633 -17.950 -23.706 1.00 20.76 C
ATOM 13742 O LEU B 363 -41.656 -18.235 -24.910 1.00 21.00 O
ATOM 13744 N CYS B 364 -41.088 -16.826 -23.253 1.00 21.42 N
ATOM 13745 CA CYS B 364 -40.427 -15.884 -24.147 1.00 21.67 C
ATOM 13747 CB CYS B 364 -39.969 -14.639 -23.376 1.00 21.86 C
ATOM 13750 SG CYS B 364 -41.327 -13.638 -22.722 1.00 23.36 S
ATOM 13752 C CYS B 364 -39.229 -16.547 -24.835 1.00 21.52 C
ATOM 13753 O CYS B 364 -39.010 -16.323 -26.037 1.00 21.67 O
ATOM 13755 N ASN B 365 -38.454 -17.352 -24.095 1.00 20.83 N
ATOM 13756 CA ASN B 365 -37.306 -18.025 -24.713 1.00 20.65 C
ATOM 13758 CB ASN B 365 -36.425 -18.756 -23.691 1.00 20.74 C
ATOM 13761 CG ASN B 365 -35.330 -17.865 -23.100 1.00 20.53 C
ATOM 13762 OD1 ASN B 365 -34.553 -17.229 -23.830 1.00 18.26 O
ATOM 13763 ND2 ASN B 365 -35.252 -17.841 -21.763 1.00 20.69 N
ATOM 13766 C ASN B 365 -37.756 -18.987 -25.811 1.00 20.43 C
ATOM 13767 O ASN B 365 -36.998 -19.253 -26.759 1.00 20.11 O
ATOM 13769 N ALA B 366 -38.987 -19.492 -25.667 1.00 20.01 N
ATOM 13770 CA ALA B 366 -39.618 -20.340 -26.665 1.00 19.70 C
ATOM 13772 CB ALA B 366 -40.766 -21.113 -26.045 1.00 19.53 C
ATOM 13776 C ALA B 366 -40.099 -19.494 -27.838 1.00 19.74 C

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ATOM  13777  O   ALA B 366    -39.846 -19.824 -28.989  1.00 19.61           O
ATOM  13779  N   PHE B 367    -40.791 -18.399 -27.553  1.00 19.99           N
ATOM  13780  CA  PHE B 367    -41.138 -17.446 -28.606  1.00 20.36           C
ATOM  13782  CB  PHE B 367    -41.805 -16.194 -28.026  1.00 20.62           C
ATOM  13785  CG  PHE B 367    -43.200 -16.403 -27.537  1.00 21.75           C
ATOM  13786  CD1 PHE B 367    -44.136 -17.071 -28.315  1.00 23.00           C
ATOM  13788  CE1 PHE B 367    -45.435 -17.242 -27.874  1.00 23.60           C
ATOM  13790  CZ  PHE B 367    -45.819 -16.731 -26.648  1.00 23.64           C
ATOM  13792  CE2 PHE B 367    -44.901 -16.049 -25.871  1.00 23.56           C
ATOM  13794  CD2 PHE B 367    -43.599 -15.883 -26.316  1.00 22.91           C
ATOM  13796  C   PHE B 367    -39.906 -16.986 -29.393  1.00 20.19           C
ATOM  13797  O   PHE B 367    -39.934 -16.903 -30.615  1.00 19.98           O
ATOM  13799  N   LEU B 368    -38.839 -16.659 -28.675  1.00 20.24           N
ATOM  13800  CA  LEU B 368    -37.629 -16.161 -29.298  1.00 20.31           C
ATOM  13802  CB  LEU B 368    -36.569 -15.900 -28.232  1.00 20.27           C
ATOM  13805  CG  LEU B 368    -35.235 -15.313 -28.694  1.00 20.12           C
ATOM  13807  CD1 LEU B 368    -35.417 -14.069 -29.592  1.00 20.05           C
ATOM  13811  CD2 LEU B 368    -34.409 -14.987 -27.465  1.00 18.60           C
ATOM  13815  C   LEU B 368    -37.122 -17.179 -30.295  1.00 20.53           C
ATOM  13816  O   LEU B 368    -36.844 -16.844 -31.446  1.00 20.49           O
ATOM  13818  N   GLN B 369    -37.032 -18.426 -29.832  1.00 20.80           N
ATOM  13819  CA  GLN B 369    -36.565 -19.557 -30.638  1.00 20.90           C
ATOM  13821  CB  GLN B 369    -36.614 -20.857 -29.815  1.00 20.98           C
ATOM  13824  CG  GLN B 369    -36.343 -22.159 -30.576  1.00 20.75           C
ATOM  13827  CD  GLN B 369    -34.946 -22.238 -31.126  1.00 20.29           C
ATOM  13828  OE1 GLN B 369    -34.718 -21.984 -32.305  1.00 20.17           O
ATOM  13829  NE2 GLN B 369    -33.996 -22.581 -30.272  1.00 20.33           N
ATOM  13832  C   GLN B 369    -37.365 -19.718 -31.910  1.00 21.04           C
ATOM  13833  O   GLN B 369    -36.803 -20.097 -32.929  1.00 20.82           O
ATOM  13835  N   GLU B 370    -38.668 -19.453 -31.863  1.00 21.80           N
ATOM  13836  CA  GLU B 370    -39.480 -19.512 -33.087  1.00 22.73           C
ATOM  13838  CB  GLU B 370    -40.996 -19.518 -32.801  1.00 23.18           C
ATOM  13841  CG  GLU B 370    -41.449 -20.608 -31.809  1.00 25.92           C
ATOM  13844  CD  GLU B 370    -42.927 -21.064 -31.957  1.00 29.74           C
ATOM  13845  OE1 GLU B 370    -43.840 -20.191 -32.101  1.00 30.13           O
ATOM  13846  OE2 GLU B 370    -43.156 -22.316 -31.892  1.00 31.94           O
ATOM  13847  C   GLU B 370    -39.079 -18.358 -34.016  1.00 22.62           C
ATOM  13848  O   GLU B 370    -38.933 -18.565 -35.221  1.00 22.53           O
ATOM  13850  N   ALA B 371    -38.864 -17.166 -33.456  1.00 22.65           N
ATOM  13851  CA  ALA B 371    -38.427 -16.023 -34.254  1.00 22.95           C
ATOM  13853  CB  ALA B 371    -38.375 -14.753 -33.424  1.00 22.97           C
ATOM  13857  C   ALA B 371    -37.070 -16.296 -34.891  1.00 23.13           C
ATOM  13858  O   ALA B 371    -36.900 -16.063 -36.091  1.00 23.38           O
ATOM  13860  N   LYS B 372    -36.113 -16.804 -34.107  1.00 23.15           N
ATOM  13861  CA  LYS B 372    -34.776 -17.102 -34.640  1.00 23.10           C
ATOM  13863  CB  LYS B 372    -33.808 -17.633 -33.575  1.00 22.85           C
ATOM  13866  CG  LYS B 372    -33.414 -16.616 -32.514  1.00 24.28           C
ATOM  13869  CD  LYS B 372    -31.973 -16.806 -31.969  1.00 26.34           C
ATOM  13872  CE  LYS B 372    -31.919 -17.407 -30.544  1.00 27.84           C
ATOM  13875  NZ  LYS B 372    -31.673 -16.405 -29.458  1.00 27.93           N
ATOM  13879  C   LYS B 372    -34.887 -18.093 -35.790  1.00 23.16           C
ATOM  13880  O   LYS B 372    -34.231 -17.920 -36.804  1.00 23.73           O
ATOM  13882  N   TRP B 373    -35.720 -19.122 -35.658  1.00 23.11           N
ATOM  13883  CA  TRP B 373    -35.844 -20.094 -36.742  1.00 22.99           C
ATOM  13885  CB  TRP B 373    -36.746 -21.274 -36.370  1.00 22.71           C
ATOM  13888  CG  TRP B 373    -36.081 -22.343 -35.562  1.00 20.71           C
ATOM  13889  CD1 TRP B 373    -34.770 -22.740 -35.623  1.00 19.89           C
ATOM  13891  NE1 TRP B 373    -34.540 -23.757 -34.734  1.00 19.05           N
ATOM  13893  CE2 TRP B 373    -35.715 -24.050 -34.090  1.00 18.91           C
ATOM  13894  CD2 TRP B 373    -36.707 -23.184 -34.599  1.00 18.41           C
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ATOM 13895 CE3 TRP B 373 -38.007 -23.288 -34.105 1.00 15.66 C
ATOM 13897 CZ3 TRP B 373 -38.271 -24.216 -33.130 1.00 15.41 C
ATOM 13899 CH2 TRP B 373 -37.276 -25.069 -32.647 1.00 16.33 C
ATOM 13901 CZ2 TRP B 373 -35.994 -25.005 -33.112 1.00 17.53 C
ATOM 13903 C TRP B 373 -36.374 -19.416 -37.991 1.00 23.59 C
ATOM 13904 O TRP B 373 -35.878 -19.653 -39.096 1.00 23.60 O
ATOM 13906 N LEU B 374 -37.374 -18.559 -37.801 1.00 24.32 N
ATOM 13907 CA LEU B 374 -38.008 -17.859 -38.915 1.00 24.66 C
ATOM 13909 CB LEU B 374 -39.181 -17.019 -38.428 1.00 24.85 C
ATOM 13912 CG LEU B 374 -40.112 -16.449 -39.496 1.00 25.45 C
ATOM 13914 CD1 LEU B 374 -41.002 -17.535 -40.070 1.00 24.83 C
ATOM 13918 CD2 LEU B 374 -40.959 -15.293 -38.885 1.00 26.92 C
ATOM 13922 C LEU B 374 -37.009 -16.975 -39.618 1.00 24.64 C
ATOM 13923 O LEU B 374 -36.934 -16.992 -40.830 1.00 24.33 O
ATOM 13925 N TYR B 375 -36.232 -16.220 -38.850 1.00 25.09 N
ATOM 13926 CA TYR B 375 -35.283 -15.274 -39.433 1.00 25.71 C
ATOM 13928 CB TYR B 375 -34.534 -14.479 -38.349 1.00 25.91 C
ATOM 13931 CG TYR B 375 -33.536 -13.468 -38.892 1.00 27.11 C
ATOM 13932 CD1 TYR B 375 -33.950 -12.200 -39.305 1.00 27.98 C
ATOM 13934 CE1 TYR B 375 -33.039 -11.271 -39.811 1.00 28.61 C
ATOM 13936 CZ TYR B 375 -31.693 -11.605 -39.904 1.00 29.13 C
ATOM 13937 OH TYR B 375 -30.790 -10.685 -40.397 1.00 29.83 O
ATOM 13939 CE2 TYR B 375 -31.256 -12.863 -39.501 1.00 28.79 C
ATOM 13941 CD2 TYR B 375 -32.177 -13.783 -38.995 1.00 28.03 C
ATOM 13943 C TYR B 375 -34.305 -16.036 -40.301 1.00 25.64 C
ATOM 13944 O TYR B 375 -34.201 -15.788 -41.503 1.00 25.74 O
ATOM 13946 N ASN B 376 -33.635 -17.000 -39.685 1.00 25.73 N
ATOM 13947 CA ASN B 376 -32.599 -17.777 -40.346 1.00 25.78 C
ATOM 13949 CB ASN B 376 -31.739 -18.497 -39.303 1.00 25.73 C
ATOM 13952 CG ASN B 376 -31.155 -17.565 -38.273 1.00 25.13 C
ATOM 13953 OD1 ASN B 376 -30.491 -16.590 -38.601 1.00 25.53 O
ATOM 13954 ND2 ASN B 376 -31.389 -17.874 -37.013 1.00 24.64 N
ATOM 13957 C ASN B 376 -33.126 -18.824 -41.332 1.00 26.04 C
ATOM 13958 O ASN B 376 -32.343 -19.644 -41.807 1.00 26.36 O
ATOM 13960 N LYS B 377 -34.428 -18.824 -41.632 1.00 26.16 N
ATOM 13961 CA LYS B 377 -35.012 -19.811 -42.552 1.00 26.27 C
ATOM 13963 CB LYS B 377 -34.575 -19.538 -44.010 1.00 26.51 C
ATOM 13966 CG LYS B 377 -35.470 -18.561 -44.802 1.00 28.01 C
ATOM 13969 CD LYS B 377 -34.629 -17.592 -45.667 1.00 29.99 C
ATOM 13972 CE LYS B 377 -35.493 -16.605 -46.465 1.00 31.02 C
ATOM 13975 NZ LYS B 377 -36.420 -15.819 -45.589 1.00 32.17 N
ATOM 13979 C LYS B 377 -34.647 -21.243 -42.150 1.00 25.93 C
ATOM 13980 O LYS B 377 -34.380 -22.084 -43.003 1.00 25.82 O
ATOM 13982 N SER B 378 -34.637 -21.522 -40.852 1.00 25.65 N
ATOM 13983 CA SER B 378 -34.324 -22.860 -40.385 1.00 25.54 C
ATOM 13985 CB SER B 378 -34.132 -22.877 -38.882 1.00 25.41 C
ATOM 13988 OG SER B 378 -32.905 -22.269 -38.570 1.00 25.67 O
ATOM 13990 C SER B 378 -35.412 -23.838 -40.790 1.00 25.62 C
ATOM 13991 O SER B 378 -36.495 -23.435 -41.199 1.00 25.70 O
ATOM 13993 N THR B 379 -35.108 -25.129 -40.690 1.00 25.66 N
ATOM 13994 CA THR B 379 -36.038 -26.175 -41.097 1.00 25.55 C
ATOM 13996 CB THR B 379 -35.788 -26.635 -42.546 1.00 25.59 C
ATOM 13998 OG1 THR B 379 -34.391 -26.899 -42.736 1.00 25.46 O
ATOM 14000 CG2 THR B 379 -36.255 -25.574 -43.528 1.00 25.88 C
ATOM 14004 C THR B 379 -35.886 -27.348 -40.160 1.00 25.45 C
ATOM 14005 O THR B 379 -35.372 -28.393 -40.548 1.00 25.70 O
ATOM 14007 N PRO B 380 -36.335 -27.179 -38.915 1.00 25.37 N
ATOM 14008 CA PRO B 380 -36.144 -28.182 -37.876 1.00 25.22 C
ATOM 14010 CB PRO B 380 -36.500 -27.437 -36.583 1.00 25.19 C
ATOM 14013 CG PRO B 380 -36.643 -26.021 -36.955 1.00 25.83 C

ATOM 14016 CD PRO B 380 -37.025 -25.998 -38.390 1.00 25.71 C
ATOM 14019 C PRO B 380 -37.052 -29.379 -38.009 1.00 24.82 C
ATOM 14020 O PRO B 380 -38.143 -29.280 -38.575 1.00 24.84 O
ATOM 14021 N THR B 381 -36.607 -30.493 -37.436 1.00 24.42 N
ATOM 14022 CA THR B 381 -37.386 -31.712 -37.429 1.00 23.99 C
ATOM 14024 CB THR B 381 -36.614 -32.873 -36.789 1.00 23.99 C
ATOM 14026 OG1 THR B 381 -36.339 -32.575 -35.418 1.00 24.02 O
ATOM 14028 CG2 THR B 381 -35.302 -33.117 -37.524 1.00 23.76 C
ATOM 14032 C THR B 381 -38.649 -31.461 -36.636 1.00 23.78 C
ATOM 14033 O THR B 381 -38.700 -30.548 -35.813 1.00 23.89 O
ATOM 14035 N PHE B 382 -39.672 -32.267 -36.889 1.00 23.53 N
ATOM 14036 CA PHE B 382 -40.905 -32.204 -36.105 1.00 22.97 C
ATOM 14038 CB PHE B 382 -41.870 -33.305 -36.527 1.00 22.89 C
ATOM 14041 CG PHE B 382 -43.079 -33.394 -35.655 1.00 22.26 C
ATOM 14042 CD1 PHE B 382 -44.189 -32.601 -35.910 1.00 21.65 C
ATOM 14044 CE1 PHE B 382 -45.300 -32.672 -35.099 1.00 20.87 C
ATOM 14046 CZ PHE B 382 -45.310 -33.534 -34.016 1.00 20.36 C
ATOM 14048 CE2 PHE B 382 -44.204 -34.317 -33.744 1.00 20.52 C
ATOM 14050 CD2 PHE B 382 -43.098 -34.243 -34.556 1.00 21.17 C
ATOM 14052 C PHE B 382 -40.677 -32.329 -34.605 1.00 22.69 C
ATOM 14053 O PHE B 382 -41.341 -31.657 -33.834 1.00 22.44 O
ATOM 14055 N ASP B 383 -39.764 -33.205 -34.191 1.00 22.52 N
ATOM 14056 CA ASP B 383 -39.491 -33.375 -32.765 1.00 22.50 C
ATOM 14058 CB ASP B 383 -38.531 -34.525 -32.527 1.00 22.43 C
ATOM 14061 CG ASP B 383 -39.174 -35.863 -32.711 1.00 22.71 C
ATOM 14062 OD1 ASP B 383 -40.359 -35.945 -33.074 1.00 22.89 O
ATOM 14063 OD2 ASP B 383 -38.470 -36.856 -32.492 1.00 25.17 O
ATOM 14064 C ASP B 383 -38.954 -32.116 -32.091 1.00 22.43 C
ATOM 14065 O ASP B 383 -39.438 -31.758 -31.014 1.00 22.40 O
ATOM 14067 N ASP B 384 -37.966 -31.464 -32.713 1.00 22.37 N
ATOM 14068 CA ASP B 384 -37.422 -30.191 -32.213 1.00 22.61 C
ATOM 14070 CB ASP B 384 -36.317 -29.648 -33.124 1.00 22.82 C
ATOM 14073 CG ASP B 384 -34.963 -30.208 -32.807 1.00 23.40 C
ATOM 14074 OD1 ASP B 384 -34.847 -30.973 -31.832 1.00 25.33 O
ATOM 14075 OD2 ASP B 384 -34.009 -29.891 -33.545 1.00 24.26 O
ATOM 14076 C ASP B 384 -38.482 -29.113 -32.130 1.00 22.56 C
ATOM 14077 O ASP B 384 -38.598 -28.429 -31.108 1.00 22.48 O
ATOM 14079 N TYR B 385 -39.227 -28.963 -33.227 1.00 22.36 N
ATOM 14080 CA TYR B 385 -40.170 -27.870 -33.402 1.00 22.18 C
ATOM 14082 CB TYR B 385 -40.738 -27.867 -34.812 1.00 22.05 C
ATOM 14085 CG TYR B 385 -41.818 -26.834 -35.019 1.00 22.60 C
ATOM 14086 CD1 TYR B 385 -41.493 -25.553 -35.437 1.00 23.64 C
ATOM 14088 CE1 TYR B 385 -42.462 -24.580 -35.630 1.00 25.00 C
ATOM 14090 CZ TYR B 385 -43.788 -24.882 -35.410 1.00 26.86 C
ATOM 14091 OH TYR B 385 -44.734 -23.883 -35.622 1.00 28.48 O
ATOM 14093 CE2 TYR B 385 -44.149 -26.171 -34.980 1.00 25.95 C
ATOM 14095 CD2 TYR B 385 -43.158 -27.133 -34.790 1.00 23.94 C
ATOM 14097 C TYR B 385 -41.319 -27.986 -32.446 1.00 22.13 C
ATOM 14098 O TYR B 385 -41.703 -27.017 -31.808 1.00 22.95 O
ATOM 14100 N PHE B 386 -41.899 -29.169 -32.380 1.00 21.80 N
ATOM 14101 CA PHE B 386 -43.048 -29.394 -31.525 1.00 21.62 C
ATOM 14103 CB PHE B 386 -43.624 -30.795 -31.768 1.00 21.73 C
ATOM 14106 CG PHE B 386 -44.834 -31.104 -30.952 1.00 21.27 C
ATOM 14107 CD1 PHE B 386 -46.034 -30.447 -31.196 1.00 22.55 C
ATOM 14109 CE1 PHE B 386 -47.164 -30.732 -30.448 1.00 23.14 C
ATOM 14111 CZ PHE B 386 -47.095 -31.699 -29.446 1.00 23.20 C
ATOM 14113 CE2 PHE B 386 -45.896 -32.358 -29.208 1.00 21.57 C
ATOM 14115 CD2 PHE B 386 -44.781 -32.057 -29.959 1.00 20.29 C
ATOM 14117 C PHE B 386 -42.630 -29.226 -30.073 1.00 21.34 C
ATOM 14118 O PHE B 386 -43.353 -28.639 -29.284 1.00 21.44 O

ATOM 14120 N GLY B 387 -41.447 -29.725 -29.736 1.00 20.84 N
ATOM 14121 CA GLY B 387 -40.935 -29.618 -28.387 1.00 20.57 C
ATOM 14124 C GLY B 387 -40.854 -28.186 -27.916 1.00 20.26 C
ATOM 14125 O GLY B 387 -40.930 -27.908 -26.724 1.00 20.86 O
ATOM 14127 N ASN B 388 -40.691 -27.268 -28.852 1.00 19.81 N
ATOM 14128 CA ASN B 388 -40.758 -25.853 -28.536 1.00 19.51 C
ATOM 14130 CB ASN B 388 -39.877 -25.086 -29.508 1.00 19.42 C
ATOM 14133 CG ASN B 388 -39.593 -23.700 -29.045 1.00 19.26 C
ATOM 14134 OD1 ASN B 388 -38.916 -23.513 -28.038 1.00 18.93 O
ATOM 14135 ND2 ASN B 388 -40.105 -22.709 -29.774 1.00 17.99 N
ATOM 14138 C ASN B 388 -42.200 -25.320 -28.604 1.00 19.41 C
ATOM 14139 O ASN B 388 -42.591 -24.447 -27.833 1.00 19.58 O
ATOM 14141 N ALA B 389 -42.989 -25.848 -29.532 1.00 19.11 N
ATOM 14142 CA ALA B 389 -44.313 -25.307 -29.808 1.00 18.87 C
ATOM 14144 CB ALA B 389 -44.897 -25.949 -31.060 1.00 18.87 C
ATOM 14148 C ALA B 389 -45.264 -25.460 -28.634 1.00 18.51 C
ATOM 14149 O ALA B 389 -45.916 -24.511 -28.262 1.00 18.33 O
ATOM 14151 N TRP B 390 -45.344 -26.652 -28.054 1.00 18.73 N
ATOM 14152 CA TRP B 390 -46.258 -26.887 -26.935 1.00 18.74 C
ATOM 14154 CB TRP B 390 -46.389 -28.377 -26.569 1.00 18.75 C
ATOM 14157 CG TRP B 390 -45.166 -29.122 -26.019 1.00 18.46 C
ATOM 14158 CD1 TRP B 390 -44.390 -30.001 -26.705 1.00 18.75 C
ATOM 14160 NE1 TRP B 390 -43.417 -30.519 -25.897 1.00 17.56 N
ATOM 14162 CE2 TRP B 390 -43.559 -30.005 -24.642 1.00 16.67 C
ATOM 14163 CD2 TRP B 390 -44.661 -29.124 -24.674 1.00 17.50 C
ATOM 14164 CE3 TRP B 390 -45.008 -28.448 -23.505 1.00 18.38 C
ATOM 14166 CZ3 TRP B 390 -44.251 -28.685 -22.347 1.00 18.34 C
ATOM 14168 CH2 TRP B 390 -43.164 -29.573 -22.361 1.00 16.75 C
ATOM 14170 CZ2 TRP B 390 -42.805 -30.234 -23.495 1.00 15.75 C
ATOM 14172 C TRP B 390 -45.861 -26.066 -25.727 1.00 18.91 C
ATOM 14173 O TRP B 390 -46.707 -25.691 -24.919 1.00 19.02 O
ATOM 14175 N LYS B 391 -44.570 -25.787 -25.612 1.00 18.95 N
ATOM 14176 CA LYS B 391 -44.085 -24.810 -24.643 1.00 18.85 C
ATOM 14178 CB LYS B 391 -42.544 -24.888 -24.508 1.00 19.52 C
ATOM 14181 CG LYS B 391 -42.023 -25.373 -23.143 1.00 21.17 C
ATOM 14184 CD LYS B 391 -40.516 -25.689 -23.191 1.00 22.87 C
ATOM 14187 CE LYS B 391 -40.251 -27.159 -23.508 1.00 23.91 C
ATOM 14190 NZ LYS B 391 -38.938 -27.354 -24.191 1.00 25.44 N
ATOM 14194 C LYS B 391 -44.537 -23.400 -25.032 1.00 17.57 C
ATOM 14195 O LYS B 391 -44.937 -22.629 -24.180 1.00 17.66 O
ATOM 14197 N SER B 392 -44.490 -23.068 -26.314 1.00 16.65 N
ATOM 14198 CA SER B 392 -44.879 -21.718 -26.764 1.00 16.27 C
ATOM 14200 CB SER B 392 -44.241 -21.375 -28.119 1.00 16.22 C
ATOM 14203 OG SER B 392 -44.937 -21.969 -29.207 1.00 15.94 O
ATOM 14205 C SER B 392 -46.384 -21.504 -26.866 1.00 15.87 C
ATOM 14206 O SER B 392 -46.825 -20.395 -27.093 1.00 15.56 O
ATOM 14208 N SER B 393 -47.167 -22.568 -26.724 1.00 15.92 N
ATOM 14209 CA SER B 393 -48.629 -22.474 -26.718 1.00 15.80 C
ATOM 14211 CB SER B 393 -49.240 -23.867 -26.630 1.00 15.78 C
ATOM 14214 OG SER B 393 -49.025 -24.426 -25.348 1.00 15.00 O
ATOM 14216 C SER B 393 -49.097 -21.646 -25.533 1.00 15.94 C
ATOM 14217 O SER B 393 -50.115 -20.948 -25.599 1.00 15.60 O
ATOM 14219 N SER B 394 -48.296 -21.740 -24.471 1.00 16.14 N
ATOM 14220 CA SER B 394 -48.487 -21.091 -23.177 1.00 16.31 C
ATOM 14222 CB SER B 394 -49.062 -19.662 -23.271 1.00 16.18 C
ATOM 14225 OG SER B 394 -50.472 -19.649 -23.358 1.00 16.57 O
ATOM 14227 C SER B 394 -49.316 -22.006 -22.297 1.00 16.34 C
ATOM 14228 O SER B 394 -49.822 -21.595 -21.261 1.00 16.47 O
ATOM 14230 N GLY B 395 -49.403 -23.268 -22.702 1.00 16.55 N
ATOM 14231 CA GLY B 395 -50.103 -24.282 -21.927 1.00 16.79 C

ATOM 14234 C GLY B 395 -49.543 -24.391 -20.534 1.00 16.80 C
ATOM 14235 O GLY B 395 -50.222 -24.083 -19.556 1.00 16.74 O
ATOM 14237 N PRO B 396 -48.291 -24.824 -20.430 1.00 17.07 N
ATOM 14238 CA PRO B 396 -47.698 -24.930 -19.103 1.00 17.18 C
ATOM 14240 CB PRO B 396 -46.273 -25.399 -19.386 1.00 17.09 C
ATOM 14243 CG PRO B 396 -46.087 -25.237 -20.874 1.00 17.77 C
ATOM 14246 CD PRO B 396 -47.424 -25.390 -21.470 1.00 17.20 C
ATOM 14249 C PRO B 396 -47.707 -23.615 -18.313 1.00 17.17 C
ATOM 14250 O PRO B 396 -47.921 -23.644 -17.089 1.00 17.10 O
ATOM 14251 N LEU B 397 -47.499 -22.475 -18.983 1.00 17.04 N
ATOM 14252 CA LEU B 397 -47.513 -21.183 -18.261 1.00 16.77 C
ATOM 14254 CB LEU B 397 -47.116 -19.969 -19.135 1.00 16.84 C
ATOM 14257 CG LEU B 397 -47.145 -18.576 -18.458 1.00 16.91 C
ATOM 14259 CD1 LEU B 397 -46.577 -18.641 -17.096 1.00 18.36 C
ATOM 14263 CD2 LEU B 397 -46.373 -17.515 -19.196 1.00 16.88 C
ATOM 14267 C LEU B 397 -48.894 -20.988 -17.682 1.00 16.24 C
ATOM 14268 O LEU B 397 -49.051 -20.710 -16.494 1.00 16.09 O
ATOM 14270 N GLN B 398 -49.902 -21.173 -18.515 1.00 15.72 N
ATOM 14271 CA GLN B 398 -51.262 -21.093 -18.024 1.00 15.49 C
ATOM 14273 CB GLN B 398 -52.267 -21.387 -19.120 1.00 15.51 C
ATOM 14276 CG GLN B 398 -52.371 -20.275 -20.118 1.00 16.12 C
ATOM 14279 CD GLN B 398 -53.436 -20.545 -21.114 1.00 17.86 C
ATOM 14280 OE1 GLN B 398 -54.509 -21.028 -20.757 1.00 20.99 O
ATOM 14281 NE2 GLN B 398 -53.170 -20.239 -22.374 1.00 18.31 N
ATOM 14284 C GLN B 398 -51.471 -22.040 -16.873 1.00 15.03 C
ATOM 14285 O GLN B 398 -51.974 -21.638 -15.843 1.00 15.21 O
ATOM 14287 N LEU B 399 -51.065 -23.291 -17.022 1.00 14.72 N
ATOM 14288 CA LEU B 399 -51.361 -24.254 -15.978 1.00 14.65 C
ATOM 14290 CB LEU B 399 -51.201 -25.688 -16.475 1.00 14.44 C
ATOM 14293 CG LEU B 399 -52.250 -26.191 -17.478 1.00 14.28 C
ATOM 14295 CD1 LEU B 399 -51.907 -27.633 -17.846 1.00 15.50 C
ATOM 14299 CD2 LEU B 399 -53.713 -26.077 -16.986 1.00 10.96 C
ATOM 14303 C LEU B 399 -50.554 -23.995 -14.704 1.00 14.88 C
ATOM 14304 O LEU B 399 -51.100 -24.161 -13.618 1.00 15.21 O
ATOM 14306 N ILE B 400 -49.291 -23.562 -14.810 1.00 14.91 N
ATOM 14307 CA ILE B 400 -48.532 -23.174 -13.607 1.00 14.89 C
ATOM 14309 CB ILE B 400 -47.158 -22.574 -13.907 1.00 15.19 C
ATOM 14311 CG1 ILE B 400 -46.189 -23.674 -14.353 1.00 16.76 C
ATOM 14314 CD1 ILE B 400 -44.777 -23.162 -14.716 1.00 18.19 C
ATOM 14318 CG2 ILE B 400 -46.603 -21.906 -12.665 1.00 13.65 C
ATOM 14322 C ILE B 400 -49.288 -22.137 -12.819 1.00 14.77 C
ATOM 14323 O ILE B 400 -49.485 -22.302 -11.632 1.00 15.36 O
ATOM 14325 N PHE B 401 -49.717 -21.071 -13.486 1.00 14.59 N
ATOM 14326 CA PHE B 401 -50.491 -20.001 -12.844 1.00 14.22 C
ATOM 14328 CB PHE B 401 -50.825 -18.900 -13.845 1.00 14.12 C
ATOM 14331 CG PHE B 401 -49.803 -17.790 -13.872 1.00 13.83 C
ATOM 14332 CD1 PHE B 401 -50.012 -16.623 -13.173 1.00 12.77 C
ATOM 14334 CE1 PHE B 401 -49.074 -15.629 -13.189 1.00 13.09 C
ATOM 14336 CZ PHE B 401 -47.906 -15.781 -13.902 1.00 12.96 C
ATOM 14338 CE2 PHE B 401 -47.684 -16.928 -14.592 1.00 12.86 C
ATOM 14340 CD2 PHE B 401 -48.622 -17.932 -14.574 1.00 13.30 C
ATOM 14342 C PHE B 401 -51.765 -20.478 -12.212 1.00 14.26 C
ATOM 14343 O PHE B 401 -52.184 -19.944 -11.207 1.00 13.90 O
ATOM 14345 N ALA B 402 -52.377 -21.480 -12.828 1.00 15.09 N
ATOM 14346 CA ALA B 402 -53.641 -22.054 -12.364 1.00 15.76 C
ATOM 14348 CB ALA B 402 -54.264 -22.899 -13.454 1.00 15.57 C
ATOM 14352 C ALA B 402 -53.417 -22.896 -11.129 1.00 16.63 C
ATOM 14353 O ALA B 402 -54.284 -22.970 -10.259 1.00 17.00 O
ATOM 14355 N TYR B 403 -52.253 -23.544 -11.060 1.00 17.50 N
ATOM 14356 CA TYR B 403 -51.885 -24.317 -9.894 1.00 17.86 C

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ATOM  14358  CB  TYR B 403     -50.486 -24.911 -10.038  1.00 17.73      C
ATOM  14361  CG  TYR B 403     -50.006 -25.576  -8.764  1.00 18.24      C
ATOM  14362  CD1 TYR B 403     -50.401 -26.867  -8.436  1.00 18.12      C
ATOM  14364  CE1 TYR B 403     -49.971 -27.476  -7.273  1.00 18.07      C
ATOM  14366  CZ  TYR B 403     -49.145 -26.790  -6.409  1.00 18.62      C
ATOM  14367  OH  TYR B 403     -48.727 -27.383  -5.244  1.00 17.70      O
ATOM  14369  CE2 TYR B 403     -48.748 -25.499  -6.703  1.00 18.93      C
ATOM  14371  CD2 TYR B 403     -49.177 -24.901  -7.876  1.00 18.88      C
ATOM  14373  C   TYR B 403     -51.966 -23.461  -8.630  1.00 18.48      C
ATOM  14374  O   TYR B 403     -52.494 -23.908  -7.616  1.00 18.66      O
ATOM  14376  N   PHE B 404     -51.468 -22.232  -8.682  1.00 18.91      N
ATOM  14377  CA  PHE B 404     -51.400 -21.430  -7.468  1.00 19.53      C
ATOM  14379  CB  PHE B 404     -50.395 -20.325  -7.644  1.00 19.35      C
ATOM  14382  CG  PHE B 404     -49.014 -20.808  -7.799  1.00 18.79      C
ATOM  14383  CD1 PHE B 404     -48.311 -21.246  -6.701  1.00 17.67      C
ATOM  14385  CE1 PHE B 404     -47.001 -21.683  -6.832  1.00 18.44      C
ATOM  14387  CZ  PHE B 404     -46.384 -21.688  -8.078  1.00 18.44      C
ATOM  14389  CE2 PHE B 404     -47.083 -21.245  -9.190  1.00 18.79      C
ATOM  14391  CD2 PHE B 404     -48.396 -20.805  -9.047  1.00 18.90      C
ATOM  14393  C   PHE B 404     -52.733 -20.817  -7.072  1.00 20.49      C
ATOM  14394  O   PHE B 404     -52.925 -20.389  -5.924  1.00 19.95      O
ATOM  14396  N   ALA B 405     -53.636 -20.756  -8.043  1.00 21.92      N
ATOM  14397  CA  ALA B 405     -54.918 -20.106  -7.872  1.00 23.09      C
ATOM  14399  CB  ALA B 405     -55.333 -19.426  -9.167  1.00 23.15      C
ATOM  14403  C   ALA B 405     -55.959 -21.113  -7.446  1.00 24.23      C
ATOM  14404  O   ALA B 405     -57.003 -20.726  -6.925  1.00 24.33      O
ATOM  14406  N   VAL B 406     -55.657 -22.399  -7.662  1.00 25.80      N
ATOM  14407  CA  VAL B 406     -56.569 -23.511  -7.355  1.00 26.88      C
ATOM  14409  CB  VAL B 406     -56.640 -24.514  -8.512  1.00 26.64      C
ATOM  14411  CG1 VAL B 406     -57.132 -25.854  -8.012  1.00 27.24      C
ATOM  14415  CG2 VAL B 406     -57.547 -23.986  -9.593  1.00 26.45      C
ATOM  14419  C   VAL B 406     -56.161 -24.266  -6.094  1.00 27.91      C
ATOM  14420  O   VAL B 406     -56.932 -24.345  -5.155  1.00 28.28      O
ATOM  14422  N   VAL B 407     -54.954 -24.825  -6.087  1.00 29.25      N
ATOM  14423  CA  VAL B 407     -54.443 -25.573  -4.941  1.00 30.16      C
ATOM  14425  CB  VAL B 407     -53.128 -26.276  -5.279  1.00 30.04      C
ATOM  14427  CG1 VAL B 407     -52.482 -26.831  -4.032  1.00 30.42      C
ATOM  14431  CG2 VAL B 407     -53.378 -27.376  -6.280  1.00 30.14      C
ATOM  14435  C   VAL B 407     -54.208 -24.646  -3.755  1.00 31.34      C
ATOM  14436  O   VAL B 407     -53.535 -23.618  -3.876  1.00 31.46      O
ATOM  14438  N   GLN B 408     -54.753 -25.032  -2.604  1.00 32.63      N
ATOM  14439  CA  GLN B 408     -54.727 -24.191  -1.417  1.00 33.51      C
ATOM  14441  CB  GLN B 408     -55.891 -24.572   -.514  1.00 33.84      C
ATOM  14444  CG  GLN B 408     -56.161 -23.548    .577  1.00 35.49      C
ATOM  14447  CD  GLN B 408     -57.623 -23.161    .656  1.00 37.61      C
ATOM  14448  OE1 GLN B 408     -58.519 -24.006    .501  1.00 38.23      O
ATOM  14449  NE2 GLN B 408     -57.876 -21.874    .893  1.00 38.64      N
ATOM  14452  C   GLN B 408     -53.399 -24.274   -.647  1.00 33.72      C
ATOM  14453  O   GLN B 408     -52.852 -23.253   -.204  1.00 33.52      O
ATOM  14455  N   ASN B 409     -52.889 -25.491   -.490  1.00 33.95      N
ATOM  14456  CA  ASN B 409     -51.642 -25.707    .226  1.00 34.16      C
ATOM  14458  CB  ASN B 409     -51.865 -26.665   1.391  1.00 34.25      C
ATOM  14461  CG  ASN B 409     -52.756 -26.069   2.459  1.00 34.39      C
ATOM  14462  OD1 ASN B 409     -52.269 -25.577   3.480  1.00 34.40      O
ATOM  14463  ND2 ASN B 409     -54.070 -26.089   2.222  1.00 34.12      N
ATOM  14466  C   ASN B 409     -50.582 -26.244   -.709  1.00 34.12      C
ATOM  14467  O   ASN B 409     -50.578 -27.422  -1.046  1.00 34.41      O
ATOM  14469  N   ILE B 410     -49.681 -25.369  -1.127  1.00 34.07      N
ATOM  14470  CA  ILE B 410     -48.699 -25.718  -2.138  1.00 34.08      C
ATOM  14472  CB  ILE B 410     -48.138 -24.455  -2.840  1.00 34.15      C
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ATOM 14474 CG1 ILE B 410 -47.274 -23.610 -1.891 1.00 34.26 C
ATOM 14477 CD1 ILE B 410 -47.216 -22.139 -2.249 1.00 34.10 C
ATOM 14481 CG2 ILE B 410 -49.290 -23.634 -3.404 1.00 34.49 C
ATOM 14485 C ILE B 410 -47.586 -26.553 -1.533 1.00 33.93 C
ATOM 14486 O ILE B 410 -47.181 -26.317 -.405 1.00 33.80 O
ATOM 14488 N LYS B 411 -47.123 -27.546 -2.285 1.00 34.12 N
ATOM 14489 CA LYS B 411 -46.012 -28.395 -1.874 1.00 34.45 C
ATOM 14491 CB LYS B 411 -46.414 -29.873 -1.907 1.00 34.67 C
ATOM 14494 CG LYS B 411 -47.850 -30.130 -1.460 1.00 35.79 C
ATOM 14497 CD LYS B 411 -48.102 -31.586 -1.052 1.00 37.60 C
ATOM 14500 CE LYS B 411 -49.450 -31.728 -.309 1.00 38.80 C
ATOM 14503 NZ LYS B 411 -49.568 -32.992 .488 1.00 39.20 N
ATOM 14507 C LYS B 411 -44.843 -28.132 -2.810 1.00 34.33 C
ATOM 14508 O LYS B 411 -45.038 -27.956 -4.006 1.00 34.14 O
ATOM 14510 N LYS B 412 -43.631 -28.102 -2.265 1.00 34.50 N
ATOM 14511 CA LYS B 412 -42.460 -27.688 -3.042 1.00 34.69 C
ATOM 14513 CB LYS B 412 -41.242 -27.398 -2.154 1.00 35.13 C
ATOM 14516 CG LYS B 412 -41.205 -25.960 -1.613 1.00 36.90 C
ATOM 14519 CD LYS B 412 -40.079 -25.749 -.588 1.00 38.57 C
ATOM 14522 CE LYS B 412 -40.546 -24.852 .555 1.00 39.55 C
ATOM 14525 NZ LYS B 412 -39.491 -24.644 1.587 1.00 40.83 N
ATOM 14529 C LYS B 412 -42.075 -28.687 -4.103 1.00 34.13 C
ATOM 14530 O LYS B 412 -41.468 -28.308 -5.093 1.00 34.21 O
ATOM 14532 N GLU B 413 -42.408 -29.958 -3.910 1.00 33.54 N
ATOM 14533 CA GLU B 413 -42.095 -30.949 -4.933 1.00 33.19 C
ATOM 14535 CB GLU B 413 -41.886 -32.335 -4.330 1.00 33.44 C
ATOM 14538 CG GLU B 413 -43.127 -33.037 -3.807 1.00 34.37 C
ATOM 14541 CD GLU B 413 -42.834 -34.490 -3.499 1.00 35.56 C
ATOM 14542 OE1 GLU B 413 -42.662 -35.264 -4.471 1.00 35.30 O
ATOM 14543 OE2 GLU B 413 -42.751 -34.847 -2.297 1.00 36.69 O
ATOM 14544 C GLU B 413 -43.157 -30.965 -6.029 1.00 32.47 C
ATOM 14545 O GLU B 413 -42.846 -31.232 -7.193 1.00 32.28 O
ATOM 14547 N GLU B 414 -44.403 -30.676 -5.652 1.00 31.58 N
ATOM 14548 CA GLU B 414 -45.482 -30.512 -6.614 1.00 30.99 C
ATOM 14550 CB GLU B 414 -46.781 -30.101 -5.927 1.00 30.98 C
ATOM 14553 CG GLU B 414 -47.732 -31.245 -5.642 1.00 31.82 C
ATOM 14556 CD GLU B 414 -49.100 -30.774 -5.138 1.00 34.29 C
ATOM 14557 OE1 GLU B 414 -49.258 -29.581 -4.777 1.00 35.53 O
ATOM 14558 OE2 GLU B 414 -50.036 -31.603 -5.101 1.00 36.44 O
ATOM 14559 C GLU B 414 -45.104 -29.455 -7.628 1.00 30.59 C
ATOM 14560 O GLU B 414 -45.169 -29.687 -8.828 1.00 30.37 O
ATOM 14562 N ILE B 415 -44.684 -28.295 -7.140 1.00 30.49 N
ATOM 14563 CA ILE B 415 -44.367 -27.177 -8.028 1.00 30.40 C
ATOM 14565 CB ILE B 415 -44.412 -25.797 -7.320 1.00 30.40 C
ATOM 14567 CG1 ILE B 415 -43.235 -25.589 -6.388 1.00 30.36 C
ATOM 14570 CD1 ILE B 415 -43.373 -24.313 -5.611 1.00 31.01 C
ATOM 14574 CG2 ILE B 415 -45.686 -25.644 -6.523 1.00 30.85 C
ATOM 14578 C ILE B 415 -43.037 -27.347 -8.730 1.00 30.12 C
ATOM 14579 O ILE B 415 -42.870 -26.865 -9.840 1.00 30.42 O
ATOM 14581 N GLU B 416 -42.095 -28.030 -8.099 1.00 29.75 N
ATOM 14582 CA GLU B 416 -40.799 -28.249 -8.719 1.00 29.70 C
ATOM 14584 CB GLU B 416 -39.825 -28.777 -7.690 1.00 30.02 C
ATOM 14587 CG GLU B 416 -38.386 -28.426 -7.948 1.00 31.20 C
ATOM 14590 CD GLU B 416 -37.523 -28.839 -6.776 1.00 32.91 C
ATOM 14591 OE1 GLU B 416 -38.008 -28.723 -5.632 1.00 32.37 O
ATOM 14592 OE2 GLU B 416 -36.377 -29.294 -6.994 1.00 35.31 O
ATOM 14593 C GLU B 416 -40.917 -29.222 -9.890 1.00 29.24 C
ATOM 14594 O GLU B 416 -40.121 -29.177 -10.835 1.00 28.86 O
ATOM 14596 N ASN B 417 -41.915 -30.097 -9.819 1.00 28.81 N
ATOM 14597 CA ASN B 417 -42.252 -30.960 -10.941 1.00 28.66 C

ATOM 14599 CB ASN B 417 -43.165 -32.105 -10.503 1.00 28.72 C
ATOM 14602 CG ASN B 417 -42.379 -33.285 -9.973 1.00 29.78 C
ATOM 14603 OD1 ASN B 417 -41.887 -34.108 -10.744 1.00 30.39 O
ATOM 14604 ND2 ASN B 417 -42.223 -33.358 -8.653 1.00 31.45 N
ATOM 14607 C ASN B 417 -42.888 -30.183 -12.067 1.00 28.32 C
ATOM 14608 O ASN B 417 -42.611 -30.456 -13.232 1.00 27.95 O
ATOM 14610 N LEU B 418 -43.740 -29.217 -11.713 1.00 28.23 N
ATOM 14611 CA LEU B 418 -44.349 -28.313 -12.697 1.00 27.92 C
ATOM 14613 CB LEU B 418 -45.298 -27.320 -12.023 1.00 27.48 C
ATOM 14616 CG LEU B 418 -46.636 -27.896 -11.553 1.00 27.02 C
ATOM 14618 CD1 LEU B 418 -47.393 -26.882 -10.691 1.00 26.70 C
ATOM 14622 CD2 LEU B 418 -47.499 -28.355 -12.720 1.00 25.90 C
ATOM 14626 C LEU B 418 -43.275 -27.567 -13.491 1.00 28.20 C
ATOM 14627 O LEU B 418 -43.310 -27.541 -14.733 1.00 27.90 O
ATOM 14629 N GLN B 419 -42.308 -26.995 -12.770 1.00 28.43 N
ATOM 14630 CA GLN B 419 -41.170 -26.315 -13.395 1.00 28.72 C
ATOM 14632 CB GLN B 419 -40.223 -25.746 -12.347 1.00 28.81 C
ATOM 14635 CG GLN B 419 -40.592 -24.332 -11.946 1.00 30.14 C
ATOM 14638 CD GLN B 419 -39.535 -23.671 -11.092 1.00 32.05 C
ATOM 14639 OE1 GLN B 419 -39.246 -22.477 -11.257 1.00 33.88 O
ATOM 14640 NE2 GLN B 419 -38.948 -24.437 -10.170 1.00 31.84 N
ATOM 14643 C GLN B 419 -40.390 -27.179 -14.370 1.00 28.83 C
ATOM 14644 O GLN B 419 -39.922 -26.668 -15.386 1.00 28.72 O
ATOM 14646 N LYS B 420 -40.265 -28.475 -14.067 1.00 29.21 N
ATOM 14647 CA LYS B 420 -39.613 -29.451 -14.968 1.00 29.26 C
ATOM 14649 CB LYS B 420 -38.924 -30.555 -14.143 1.00 29.42 C
ATOM 14652 CG LYS B 420 -37.800 -30.052 -13.207 1.00 30.58 C
ATOM 14655 CD LYS B 420 -37.373 -31.113 -12.151 1.00 32.35 C
ATOM 14658 CE LYS B 420 -36.572 -30.506 -10.955 1.00 33.05 C
ATOM 14661 NZ LYS B 420 -36.520 -31.368 -9.702 1.00 32.62 N
ATOM 14665 C LYS B 420 -40.579 -30.057 -16.021 1.00 28.96 C
ATOM 14666 O LYS B 420 -40.216 -30.965 -16.753 1.00 28.66 O
ATOM 14668 N TYR B 421 -41.804 -29.543 -16.088 1.00 29.01 N
ATOM 14669 CA TYR B 421 -42.777 -29.893 -17.134 1.00 29.16 C
ATOM 14671 CB TYR B 421 -42.209 -29.602 -18.534 1.00 29.48 C
ATOM 14674 CG TYR B 421 -41.968 -28.127 -18.773 1.00 31.04 C
ATOM 14675 CD1 TYR B 421 -43.018 -27.219 -18.716 1.00 32.54 C
ATOM 14677 CE1 TYR B 421 -42.815 -25.878 -18.914 1.00 33.35 C
ATOM 14679 CZ TYR B 421 -41.556 -25.413 -19.193 1.00 34.56 C
ATOM 14680 OH TYR B 421 -41.377 -24.066 -19.384 1.00 37.99 O
ATOM 14682 CE2 TYR B 421 -40.490 -26.278 -19.267 1.00 33.56 C
ATOM 14684 CD2 TYR B 421 -40.702 -27.638 -19.051 1.00 32.75 C
ATOM 14686 C TYR B 421 -43.345 -31.311 -17.042 1.00 28.60 C
ATOM 14687 O TYR B 421 -43.395 -32.046 -18.025 1.00 28.49 O
ATOM 14689 N HIS B 422 -43.808 -31.662 -15.846 1.00 28.18 N
ATOM 14690 CA HIS B 422 -44.507 -32.919 -15.594 1.00 27.66 C
ATOM 14692 CB HIS B 422 -45.082 -32.914 -14.180 1.00 27.73 C
ATOM 14695 CG HIS B 422 -45.500 -34.264 -13.685 1.00 28.14 C
ATOM 14696 ND1 HIS B 422 -44.597 -35.195 -13.217 1.00 29.15 N
ATOM 14698 CE1 HIS B 422 -45.247 -36.277 -12.829 1.00 29.50 C
ATOM 14700 NE2 HIS B 422 -46.539 -36.078 -13.022 1.00 28.69 N
ATOM 14702 CD2 HIS B 422 -46.724 -34.827 -13.552 1.00 27.24 C
ATOM 14704 C HIS B 422 -45.650 -33.164 -16.575 1.00 27.29 C
ATOM 14705 O HIS B 422 -46.463 -32.269 -16.853 1.00 26.86 O
ATOM 14707 N ASP B 423 -45.712 -34.402 -17.060 1.00 26.96 N
ATOM 14708 CA ASP B 423 -46.772 -34.883 -17.952 1.00 26.78 C
ATOM 14710 CB ASP B 423 -46.792 -36.413 -17.939 1.00 27.01 C
ATOM 14713 CG ASP B 423 -45.594 -37.018 -18.646 1.00 28.21 C
ATOM 14714 OD1 ASP B 423 -45.100 -36.378 -19.602 1.00 31.33 O
ATOM 14715 OD2 ASP B 423 -45.153 -38.130 -18.262 1.00 28.39 O

ATOM 14716 C ASP B 423 -48.187 -34.383 -17.651 1.00 26.21 C
ATOM 14717 O ASP B 423 -49.015 -34.336 -18.556 1.00 26.75 O
ATOM 14719 N ILE B 424 -48.463 -34.042 -16.391 1.00 25.11 N
ATOM 14720 CA ILE B 424 -49.773 -33.553 -15.956 1.00 23.82 C
ATOM 14722 CB ILE B 424 -49.798 -33.310 -14.439 1.00 23.67 C
ATOM 14724 CG1 ILE B 424 -51.196 -32.990 -13.938 1.00 22.97 C
ATOM 14727 CD1 ILE B 424 -51.220 -32.693 -12.465 1.00 22.06 C
ATOM 14731 CG2 ILE B 424 -48.859 -32.171 -14.065 1.00 24.35 C
ATOM 14735 C ILE B 424 -50.102 -32.265 -16.669 1.00 23.08 C
ATOM 14736 O ILE B 424 -51.265 -32.025 -17.023 1.00 22.99 O
ATOM 14738 N ILE B 425 -49.082 -31.436 -16.886 1.00 22.22 N
ATOM 14739 CA ILE B 425 -49.282 -30.199 -17.633 1.00 21.61 C
ATOM 14741 CB ILE B 425 -48.796 -28.959 -16.848 1.00 21.18 C
ATOM 14743 CG1 ILE B 425 -47.279 -28.853 -16.804 1.00 19.47 C
ATOM 14746 CD1 ILE B 425 -46.850 -27.581 -16.140 1.00 18.00 C
ATOM 14750 CG2 ILE B 425 -49.357 -28.977 -15.428 1.00 20.75 C
ATOM 14754 C ILE B 425 -48.665 -30.255 -19.033 1.00 21.73 C
ATOM 14755 O ILE B 425 -49.100 -29.523 -19.912 1.00 21.75 O
ATOM 14757 N SER B 426 -47.686 -31.134 -19.258 1.00 21.74 N
ATOM 14758 CA SER B 426 -47.016 -31.174 -20.560 1.00 21.53 C
ATOM 14760 CB SER B 426 -45.639 -31.876 -20.516 1.00 21.66 C
ATOM 14763 OG SER B 426 -45.724 -33.281 -20.405 1.00 22.19 O
ATOM 14765 C SER B 426 -47.922 -31.798 -21.582 1.00 21.19 C
ATOM 14766 O SER B 426 -47.950 -31.358 -22.721 1.00 21.37 O
ATOM 14768 N ARG B 427 -48.692 -32.800 -21.177 1.00 20.91 N
ATOM 14769 CA ARG B 427 -49.532 -33.504 -22.143 1.00 20.78 C
ATOM 14771 CB ARG B 427 -50.038 -34.840 -21.616 1.00 20.94 C
ATOM 14774 CG ARG B 427 -49.006 -35.887 -21.874 1.00 22.76 C
ATOM 14777 CD ARG B 427 -49.158 -37.101 -21.025 1.00 26.75 C
ATOM 14780 NE ARG B 427 -47.960 -37.927 -21.185 1.00 29.36 N
ATOM 14782 CZ ARG B 427 -47.574 -38.887 -20.352 1.00 30.25 C
ATOM 14783 NH1 ARG B 427 -48.293 -39.179 -19.266 1.00 30.27 N
ATOM 14786 NH2 ARG B 427 -46.447 -39.547 -20.611 1.00 31.25 N
ATOM 14789 C ARG B 427 -50.646 -32.650 -22.668 1.00 20.07 C
ATOM 14790 O ARG B 427 -50.724 -32.466 -23.866 1.00 20.13 O
ATOM 14792 N PRO B 428 -51.482 -32.091 -21.786 1.00 19.38 N
ATOM 14793 CA PRO B 428 -52.533 -31.202 -22.264 1.00 19.05 C
ATOM 14795 CB PRO B 428 -53.046 -30.547 -20.990 1.00 19.13 C
ATOM 14798 CG PRO B 428 -52.696 -31.476 -19.918 1.00 19.55 C
ATOM 14801 CD PRO B 428 -51.443 -32.161 -20.319 1.00 19.20 C
ATOM 14804 C PRO B 428 -52.016 -30.135 -23.227 1.00 18.84 C
ATOM 14805 O PRO B 428 -52.688 -29.802 -24.205 1.00 18.73 O
ATOM 14806 N SER B 429 -50.828 -29.608 -22.964 1.00 18.57 N
ATOM 14807 CA SER B 429 -50.208 -28.679 -23.899 1.00 18.64 C
ATOM 14809 CB SER B 429 -48.960 -28.086 -23.291 1.00 18.46 C
ATOM 14812 OG SER B 429 -49.141 -27.980 -21.911 1.00 19.08 O
ATOM 14814 C SER B 429 -49.877 -29.315 -25.260 1.00 18.52 C
ATOM 14815 O SER B 429 -49.886 -28.633 -26.276 1.00 19.02 O
ATOM 14817 N HIS B 430 -49.579 -30.606 -25.297 1.00 18.29 N
ATOM 14818 CA HIS B 430 -49.457 -31.273 -26.583 1.00 18.25 C
ATOM 14820 CB HIS B 430 -49.085 -32.765 -26.467 1.00 18.40 C
ATOM 14823 CG HIS B 430 -47.753 -33.024 -25.806 1.00 19.41 C
ATOM 14824 ND1 HIS B 430 -46.776 -32.055 -25.657 1.00 19.55 N
ATOM 14826 CE1 HIS B 430 -45.729 -32.576 -25.043 1.00 17.77 C
ATOM 14828 NE2 HIS B 430 -45.981 -33.849 -24.800 1.00 18.52 N
ATOM 14830 CD2 HIS B 430 -47.232 -34.160 -25.277 1.00 19.19 C
ATOM 14832 C HIS B 430 -50.789 -31.105 -27.306 1.00 17.93 C
ATOM 14833 O HIS B 430 -50.816 -30.599 -28.417 1.00 18.54 O
ATOM 14835 N ILE B 431 -51.897 -31.479 -26.665 1.00 17.34 N
ATOM 14836 CA ILE B 431 -53.217 -31.372 -27.301 1.00 16.58 C

ATOM 14838 CB ILE B 431 -54.400 -31.738 -26.375 1.00 16.53 C
ATOM 14840 CG1 ILE B 431 -54.225 -33.123 -25.728 1.00 16.06 C
ATOM 14843 CD1 ILE B 431 -54.069 -34.212 -26.698 1.00 16.05 C
ATOM 14847 CG2 ILE B 431 -55.701 -31.666 -27.149 1.00 15.49 C
ATOM 14851 C ILE B 431 -53.431 -29.949 -27.748 1.00 16.35 C
ATOM 14852 O ILE B 431 -53.856 -29.712 -28.860 1.00 16.74 O
ATOM 14854 N PHE B 432 -53.110 -29.003 -26.881 1.00 16.15 N
ATOM 14855 CA PHE B 432 -53.353 -27.577 -27.145 1.00 16.19 C
ATOM 14857 CB PHE B 432 -52.811 -26.776 -25.956 1.00 16.36 C
ATOM 14860 CG PHE B 432 -53.007 -25.295 -26.043 1.00 16.54 C
ATOM 14861 CD1 PHE B 432 -53.869 -24.708 -26.946 1.00 16.55 C
ATOM 14863 CE1 PHE B 432 -54.007 -23.334 -26.974 1.00 17.89 C
ATOM 14865 CZ PHE B 432 -53.305 -22.538 -26.080 1.00 17.96 C
ATOM 14867 CE2 PHE B 432 -52.461 -23.114 -25.169 1.00 17.30 C
ATOM 14869 CD2 PHE B 432 -52.323 -24.482 -25.151 1.00 17.54 C
ATOM 14871 C PHE B 432 -52.726 -27.104 -28.452 1.00 15.93 C
ATOM 14872 O PHE B 432 -53.398 -26.525 -29.303 1.00 15.63 O
ATOM 14874 N ARG B 433 -51.438 -27.387 -28.594 1.00 15.79 N
ATOM 14875 CA ARG B 433 -50.674 -27.044 -29.778 1.00 15.74 C
ATOM 14877 CB ARG B 433 -49.196 -27.279 -29.470 1.00 15.68 C
ATOM 14880 CG ARG B 433 -48.259 -27.218 -30.665 1.00 16.39 C
ATOM 14883 CD ARG B 433 -48.348 -25.919 -31.388 1.00 16.27 C
ATOM 14886 NE ARG B 433 -47.969 -24.850 -30.492 1.00 17.34 N
ATOM 14888 CZ ARG B 433 -48.210 -23.565 -30.703 1.00 17.89 C
ATOM 14889 NH1 ARG B 433 -48.834 -23.142 -31.803 1.00 16.79 N
ATOM 14892 NH2 ARG B 433 -47.805 -22.701 -29.792 1.00 18.53 N
ATOM 14895 C ARG B 433 -51.114 -27.852 -31.011 1.00 15.85 C
ATOM 14896 O ARG B 433 -51.197 -27.328 -32.120 1.00 15.40 O
ATOM 14898 N LEU B 434 -51.381 -29.134 -30.813 1.00 16.18 N
ATOM 14899 CA LEU B 434 -51.794 -29.986 -31.902 1.00 16.58 C
ATOM 14901 CB LEU B 434 -51.802 -31.453 -31.468 1.00 16.79 C
ATOM 14904 CG LEU B 434 -50.408 -32.055 -31.232 1.00 17.49 C
ATOM 14906 CD1 LEU B 434 -50.486 -33.548 -30.864 1.00 16.63 C
ATOM 14910 CD2 LEU B 434 -49.511 -31.836 -32.467 1.00 18.00 C
ATOM 14914 C LEU B 434 -53.158 -29.559 -32.423 1.00 17.07 C
ATOM 14915 O LEU B 434 -53.333 -29.442 -33.633 1.00 17.44 O
ATOM 14917 N CYS B 435 -54.118 -29.308 -31.532 1.00 17.23 N
ATOM 14918 CA CYS B 435 -55.419 -28.778 -31.947 1.00 17.44 C
ATOM 14920 CB CYS B 435 -56.301 -28.529 -30.746 1.00 17.38 C
ATOM 14923 SG CYS B 435 -56.825 -29.993 -29.971 1.00 17.90 S
ATOM 14925 C CYS B 435 -55.295 -27.460 -32.696 1.00 17.78 C
ATOM 14926 O CYS B 435 -55.978 -27.232 -33.701 1.00 17.44 O
ATOM 14928 N ASN B 436 -54.442 -26.585 -32.178 1.00 18.31 N
ATOM 14929 CA ASN B 436 -54.248 -25.267 -32.769 1.00 19.14 C
ATOM 14931 CB ASN B 436 -53.392 -24.394 -31.844 1.00 19.31 C
ATOM 14934 CG ASN B 436 -52.984 -23.068 -32.478 1.00 20.07 C
ATOM 14935 OD1 ASN B 436 -53.456 -22.686 -33.555 1.00 22.72 O
ATOM 14936 ND2 ASN B 436 -52.099 -22.356 -31.800 1.00 20.90 N
ATOM 14939 C ASN B 436 -53.615 -25.345 -34.157 1.00 19.51 C
ATOM 14940 O ASN B 436 -54.173 -24.840 -35.131 1.00 19.79 O
ATOM 14942 N ASP B 437 -52.446 -25.965 -34.245 1.00 19.85 N
ATOM 14943 CA ASP B 437 -51.754 -26.058 -35.517 1.00 20.01 C
ATOM 14945 CB ASP B 437 -50.340 -26.638 -35.331 1.00 20.00 C
ATOM 14948 CG ASP B 437 -49.397 -25.675 -34.557 1.00 21.23 C
ATOM 14949 OD1 ASP B 437 -49.902 -24.749 -33.877 1.00 22.90 O
ATOM 14950 OD2 ASP B 437 -48.149 -25.821 -34.632 1.00 22.18 O
ATOM 14951 C ASP B 437 -52.629 -26.838 -36.512 1.00 20.00 C
ATOM 14952 O ASP B 437 -52.678 -26.491 -37.695 1.00 20.02 O
ATOM 14954 N LEU B 438 -53.372 -27.836 -36.021 1.00 20.02 N
ATOM 14955 CA LEU B 438 -54.352 -28.558 -36.858 1.00 20.18 C

ATOM 14957 CB LEU B 438 -55.144 -29.593 -36.049 1.00 19.88 C
ATOM 14960 CG LEU B 438 -54.699 -31.050 -36.142 1.00 18.97 C
ATOM 14962 CD1 LEU B 438 -55.537 -31.869 -35.200 1.00 18.86 C
ATOM 14966 CD2 LEU B 438 -54.818 -31.585 -37.550 1.00 16.23 C
ATOM 14970 C LEU B 438 -55.358 -27.644 -37.564 1.00 20.60 C
ATOM 14971 O LEU B 438 -55.717 -27.889 -38.712 1.00 20.30 O
ATOM 14973 N ALA B 439 -55.825 -26.620 -36.853 1.00 21.39 N
ATOM 14974 CA ALA B 439 -56.802 -25.654 -37.377 1.00 21.96 C
ATOM 14976 CB ALA B 439 -57.306 -24.741 -36.242 1.00 21.77 C
ATOM 14980 C ALA B 439 -56.214 -24.805 -38.494 1.00 22.47 C
ATOM 14981 O ALA B 439 -56.850 -24.559 -39.517 1.00 22.13 O
ATOM 14983 N SER B 440 -54.983 -24.370 -38.282 1.00 23.40 N
ATOM 14984 CA SER B 440 -54.337 -23.428 -39.169 1.00 24.40 C
ATOM 14986 CB SER B 440 -53.423 -22.529 -38.342 1.00 24.44 C
ATOM 14989 OG SER B 440 -52.994 -23.206 -37.166 1.00 25.19 O
ATOM 14991 C SER B 440 -53.544 -24.103 -40.289 1.00 25.15 C
ATOM 14992 O SER B 440 -53.093 -23.424 -41.210 1.00 25.24 O
ATOM 14994 N ALA B 441 -53.392 -25.428 -40.222 1.00 25.99 N
ATOM 14995 CA ALA B 441 -52.488 -26.160 -41.119 1.00 26.53 C
ATOM 14997 CB ALA B 441 -52.532 -27.655 -40.830 1.00 26.26 C
ATOM 15001 C ALA B 441 -52.726 -25.903 -42.608 1.00 27.31 C
ATOM 15002 O ALA B 441 -51.811 -25.489 -43.310 1.00 27.26 O
ATOM 15004 N SER B 442 -53.940 -26.134 -43.098 1.00 28.45 N
ATOM 15005 CA SER B 442 -54.138 -26.138 -44.545 1.00 29.47 C
ATOM 15007 CB SER B 442 -55.477 -26.769 -44.936 1.00 29.40 C
ATOM 15010 OG SER B 442 -56.454 -25.784 -45.181 1.00 30.36 O
ATOM 15012 C SER B 442 -53.966 -24.731 -45.125 1.00 30.22 C
ATOM 15013 O SER B 442 -53.304 -24.562 -46.139 1.00 30.26 O
ATOM 15015 N ALA B 443 -54.537 -23.729 -44.467 1.00 31.38 N
ATOM 15016 CA ALA B 443 -54.308 -22.333 -44.835 1.00 32.22 C
ATOM 15018 CB ALA B 443 -55.057 -21.410 -43.893 1.00 32.28 C
ATOM 15022 C ALA B 443 -52.820 -21.992 -44.818 1.00 33.12 C
ATOM 15023 O ALA B 443 -52.302 -21.419 -45.766 1.00 33.24 O
ATOM 15025 N GLU B 444 -52.136 -22.351 -43.736 1.00 34.43 N
ATOM 15026 CA GLU B 444 -50.711 -22.033 -43.582 1.00 35.35 C
ATOM 15028 CB GLU B 444 -50.237 -22.271 -42.134 1.00 35.46 C
ATOM 15031 CG GLU B 444 -50.757 -21.227 -41.126 1.00 36.42 C
ATOM 15034 CD GLU B 444 -50.178 -21.376 -39.708 1.00 37.82 C
ATOM 15035 OE1 GLU B 444 -49.965 -22.506 -39.224 1.00 37.92 O
ATOM 15036 OE2 GLU B 444 -49.955 -20.344 -39.049 1.00 40.09 O
ATOM 15037 C GLU B 444 -49.840 -22.794 -44.594 1.00 35.87 C
ATOM 15038 O GLU B 444 -48.870 -22.239 -45.107 1.00 35.85 O
ATOM 15040 N ILE B 445 -50.193 -24.048 -44.883 1.00 36.63 N
ATOM 15041 CA ILE B 445 -49.517 -24.837 -45.928 1.00 37.21 C
ATOM 15043 CB ILE B 445 -49.854 -26.366 -45.832 1.00 37.15 C
ATOM 15045 CG1 ILE B 445 -49.181 -26.991 -44.609 1.00 36.85 C
ATOM 15048 CD1 ILE B 445 -49.867 -28.244 -44.102 1.00 36.62 C
ATOM 15052 CG2 ILE B 445 -49.416 -27.120 -47.093 1.00 36.66 C
ATOM 15056 C ILE B 445 -49.933 -24.289 -47.290 1.00 37.88 C
ATOM 15057 O ILE B 445 -50.926 -24.733 -47.874 1.00 38.20 O
ATOM 15059 N ALA B 446 -49.175 -23.314 -47.785 1.00 38.56 N
ATOM 15060 CA ALA B 446 -49.544 -22.575 -48.992 1.00 39.03 C
ATOM 15062 CB ALA B 446 -49.833 -23.522 -50.169 1.00 39.19 C
ATOM 15066 C ALA B 446 -50.768 -21.740 -48.685 1.00 39.42 C
ATOM 15067 O ALA B 446 -51.866 -22.288 -48.742 1.00 39.26 O
ATOM 15069 N ARG B 447 -50.650 -20.443 -48.361 1.00 40.06 N
ATOM 15070 CA ARG B 447 -49.426 -19.589 -48.361 1.00 40.54 C
ATOM 15072 CB ARG B 447 -49.276 -18.901 -46.986 1.00 40.70 C
ATOM 15075 CG ARG B 447 -50.121 -17.634 -46.836 1.00 41.82 C
ATOM 15078 CD ARG B 447 -50.292 -17.234 -45.377 1.00 42.99 C

ATOM 15081 NE ARG B 447 -51.628 -17.546 -44.864 1.00 44.22 N
ATOM 15083 CZ ARG B 447 -51.924 -17.766 -43.580 1.00 46.00 C
ATOM 15084 NH1 ARG B 447 -50.977 -17.730 -42.633 1.00 46.34 N
ATOM 15087 NH2 ARG B 447 -53.184 -18.039 -43.236 1.00 46.39 N
ATOM 15090 C ARG B 447 -48.095 -20.208 -48.837 1.00 40.35 C
ATOM 15091 O ARG B 447 -47.897 -20.403 -50.038 1.00 40.95 O
ATOM 15093 N GLY B 448 -47.170 -20.442 -47.918 1.00 39.87 N
ATOM 15094 CA GLY B 448 -46.020 -21.306 -48.162 1.00 39.52 C
ATOM 15097 C GLY B 448 -45.258 -21.517 -46.865 1.00 39.26 C
ATOM 15098 O GLY B 448 -44.071 -21.842 -46.885 1.00 39.15 O
ATOM 15100 N GLU B 449 -45.966 -21.344 -45.742 1.00 38.85 N
ATOM 15101 CA GLU B 449 -45.365 -21.215 -44.426 1.00 38.45 C
ATOM 15103 CB GLU B 449 -46.288 -20.472 -43.444 1.00 38.76 C
ATOM 15106 CG GLU B 449 -46.346 -18.943 -43.636 1.00 40.34 C
ATOM 15109 CD GLU B 449 -47.486 -18.257 -42.839 1.00 42.09 C
ATOM 15110 OE1 GLU B 449 -47.897 -18.787 -41.780 1.00 43.23 O
ATOM 15111 OE2 GLU B 449 -47.972 -17.184 -43.274 1.00 42.13 O
ATOM 15112 C GLU B 449 -45.073 -22.600 -43.906 1.00 37.54 C
ATOM 15113 O GLU B 449 -45.810 -23.553 -44.167 1.00 37.34 O
ATOM 15115 N THR B 450 -43.986 -22.688 -43.159 1.00 36.47 N
ATOM 15116 CA THR B 450 -43.459 -23.950 -42.702 1.00 35.65 C
ATOM 15118 CB THR B 450 -42.017 -24.105 -43.245 1.00 35.81 C
ATOM 15120 OG1 THR B 450 -41.593 -25.465 -43.109 1.00 37.67 O
ATOM 15122 CG2 THR B 450 -41.029 -23.152 -42.538 1.00 36.21 C
ATOM 15126 C THR B 450 -43.528 -24.084 -41.166 1.00 34.22 C
ATOM 15127 O THR B 450 -43.165 -25.127 -40.619 1.00 34.00 O
ATOM 15129 N ALA B 451 -44.024 -23.034 -40.495 1.00 32.69 N
ATOM 15130 CA ALA B 451 -44.144 -22.974 -39.026 1.00 31.28 C
ATOM 15132 CB ALA B 451 -43.952 -21.546 -38.545 1.00 31.06 C
ATOM 15136 C ALA B 451 -45.495 -23.500 -38.547 1.00 29.97 C
ATOM 15137 O ALA B 451 -46.337 -22.735 -38.082 1.00 30.08 O
ATOM 15139 N ASN B 452 -45.690 -24.809 -38.656 1.00 28.19 N
ATOM 15140 CA ASN B 452 -46.935 -25.444 -38.272 1.00 26.73 C
ATOM 15142 CB ASN B 452 -47.929 -25.339 -39.422 1.00 26.45 C
ATOM 15145 CG ASN B 452 -49.311 -25.832 -39.057 1.00 25.38 C
ATOM 15146 OD1 ASN B 452 -49.608 -27.004 -39.195 1.00 24.57 O
ATOM 15147 ND2 ASN B 452 -50.171 -24.928 -38.618 1.00 24.44 N
ATOM 15150 C ASN B 452 -46.631 -26.889 -37.952 1.00 26.05 C
ATOM 15151 O ASN B 452 -45.930 -27.544 -38.695 1.00 26.21 O
ATOM 15153 N SER B 453 -47.131 -27.388 -36.834 1.00 25.30 N
ATOM 15154 CA SER B 453 -46.843 -28.760 -36.432 1.00 24.72 C
ATOM 15156 CB SER B 453 -47.638 -29.139 -35.174 1.00 24.81 C
ATOM 15159 OG SER B 453 -47.143 -28.455 -34.031 1.00 24.36 O
ATOM 15161 C SER B 453 -47.111 -29.770 -37.543 1.00 24.12 C
ATOM 15162 O SER B 453 -46.325 -30.679 -37.743 1.00 24.33 O
ATOM 15164 N VAL B 454 -48.202 -29.606 -38.272 1.00 23.57 N
ATOM 15165 CA VAL B 454 -48.546 -30.541 -39.328 1.00 23.27 C
ATOM 15167 CB VAL B 454 -50.001 -30.361 -39.795 1.00 23.06 C
ATOM 15169 CG1 VAL B 454 -50.363 -31.385 -40.829 1.00 22.41 C
ATOM 15173 CG2 VAL B 454 -50.946 -30.489 -38.622 1.00 22.80 C
ATOM 15177 C VAL B 454 -47.581 -30.473 -40.521 1.00 23.83 C
ATOM 15178 O VAL B 454 -47.370 -31.493 -41.175 1.00 24.48 O
ATOM 15180 N SER B 455 -46.981 -29.309 -40.803 1.00 23.99 N
ATOM 15181 CA SER B 455 -45.978 -29.198 -41.881 1.00 24.22 C
ATOM 15183 CB SER B 455 -45.577 -27.767 -42.111 1.00 24.02 C
ATOM 15186 OG SER B 455 -46.655 -27.098 -42.689 1.00 25.57 O
ATOM 15188 C SER B 455 -44.708 -29.949 -41.582 1.00 24.65 C
ATOM 15189 O SER B 455 -44.211 -30.700 -42.417 1.00 25.23 O
ATOM 15191 N CYS B 456 -44.151 -29.700 -40.405 1.00 24.82 N
ATOM 15192 CA CYS B 456 -43.024 -30.462 -39.935 1.00 24.81 C

ATOM 15194 CB CYS B 456 -42.765 -30.170 -38.470 1.00 24.92 C
ATOM 15197 SG CYS B 456 -42.139 -28.541 -38.190 1.00 25.18 S
ATOM 15199 C CYS B 456 -43.304 -31.938 -40.124 1.00 24.84 C
ATOM 15200 O CYS B 456 -42.507 -32.634 -40.728 1.00 25.34 O
ATOM 15202 N TYR B 457 -44.442 -32.421 -39.644 1.00 24.75 N
ATOM 15203 CA TYR B 457 -44.735 -33.838 -39.778 1.00 24.85 C
ATOM 15205 CB TYR B 457 -46.069 -34.197 -39.142 1.00 24.64 C
ATOM 15208 CG TYR B 457 -46.057 -35.537 -38.451 1.00 24.00 C
ATOM 15209 CD1 TYR B 457 -45.846 -35.635 -37.083 1.00 24.19 C
ATOM 15211 CE1 TYR B 457 -45.848 -36.873 -36.436 1.00 23.72 C
ATOM 15213 CZ TYR B 457 -46.059 -38.025 -37.170 1.00 23.27 C
ATOM 15214 OH TYR B 457 -46.063 -39.244 -36.554 1.00 22.94 O
ATOM 15216 CE2 TYR B 457 -46.268 -37.961 -38.528 1.00 23.68 C
ATOM 15218 CD2 TYR B 457 -46.265 -36.711 -39.163 1.00 24.16 C
ATOM 15220 C TYR B 457 -44.676 -34.267 -41.251 1.00 25.30 C
ATOM 15221 O TYR B 457 -43.965 -35.208 -41.584 1.00 24.94 O
ATOM 15223 N MET B 458 -45.388 -33.569 -42.134 1.00 26.02 N
ATOM 15224 CA MET B 458 -45.207 -33.775 -43.585 1.00 26.76 C
ATOM 15226 CB MET B 458 -45.913 -32.685 -44.407 1.00 26.84 C
ATOM 15229 CG MET B 458 -47.419 -32.720 -44.429 1.00 27.32 C
ATOM 15232 SD MET B 458 -48.092 -31.238 -45.229 1.00 27.76 S
ATOM 15233 CE MET B 458 -47.283 -31.311 -46.830 1.00 26.95 C
ATOM 15237 C MET B 458 -43.723 -33.759 -43.996 1.00 27.06 C
ATOM 15238 O MET B 458 -43.192 -34.746 -44.485 1.00 26.94 O
ATOM 15240 N ARG B 459 -43.069 -32.624 -43.800 1.00 27.58 N
ATOM 15241 CA ARG B 459 -41.720 -32.419 -44.289 1.00 28.38 C
ATOM 15243 CB ARG B 459 -41.313 -30.965 -44.041 1.00 28.96 C
ATOM 15246 CG ARG B 459 -39.862 -30.642 -44.328 1.00 31.93 C
ATOM 15249 CD ARG B 459 -39.656 -29.139 -44.480 1.00 36.88 C
ATOM 15252 NE ARG B 459 -40.318 -28.349 -43.427 1.00 41.70 N
ATOM 15254 CZ ARG B 459 -39.890 -28.241 -42.161 1.00 45.68 C
ATOM 15255 NH1 ARG B 459 -38.795 -28.899 -41.751 1.00 48.08 N
ATOM 15258 NH2 ARG B 459 -40.566 -27.489 -41.284 1.00 45.92 N
ATOM 15261 C ARG B 459 -40.717 -33.401 -43.672 1.00 28.03 C
ATOM 15262 O ARG B 459 -39.829 -33.881 -44.356 1.00 28.13 O
ATOM 15264 N THR B 460 -40.882 -33.711 -42.393 1.00 27.88 N
ATOM 15265 CA THR B 460 -40.002 -34.635 -41.664 1.00 27.75 C
ATOM 15267 CB THR B 460 -40.240 -34.502 -40.134 1.00 27.79 C
ATOM 15269 OG1 THR B 460 -39.805 -33.209 -39.689 1.00 27.98 O
ATOM 15271 CG2 THR B 460 -39.519 -35.589 -39.356 1.00 27.46 C
ATOM 15275 C THR B 460 -40.171 -36.114 -42.045 1.00 27.72 C
ATOM 15276 O THR B 460 -39.211 -36.857 -42.069 1.00 27.60 O
ATOM 15278 N LYS B 461 -41.398 -36.538 -42.313 1.00 28.05 N
ATOM 15279 CA LYS B 461 -41.701 -37.929 -42.649 1.00 28.25 C
ATOM 15281 CB LYS B 461 -42.972 -38.381 -41.914 1.00 28.32 C
ATOM 15284 CG LYS B 461 -42.767 -38.763 -40.453 1.00 28.57 C
ATOM 15287 CD LYS B 461 -42.569 -40.271 -40.299 1.00 29.79 C
ATOM 15290 CE LYS B 461 -41.913 -40.651 -38.970 1.00 30.32 C
ATOM 15293 NZ LYS B 461 -42.651 -40.184 -37.749 1.00 30.60 N
ATOM 15297 C LYS B 461 -41.876 -38.139 -44.155 1.00 28.50 C
ATOM 15298 O LYS B 461 -42.071 -39.269 -44.598 1.00 28.58 O
ATOM 15300 N GLY B 462 -41.818 -37.057 -44.933 1.00 28.79 N
ATOM 15301 CA GLY B 462 -41.978 -37.114 -46.385 1.00 29.04 C
ATOM 15304 C GLY B 462 -43.333 -37.610 -46.853 1.00 29.39 C
ATOM 15305 O GLY B 462 -43.410 -38.452 -47.738 1.00 29.53 O
ATOM 15307 N ILE B 463 -44.406 -37.081 -46.270 1.00 29.91 N
ATOM 15308 CA ILE B 463 -45.764 -37.552 -46.572 1.00 30.27 C
ATOM 15310 CB ILE B 463 -46.333 -38.444 -45.433 1.00 30.13 C
ATOM 15312 CG1 ILE B 463 -46.308 -37.706 -44.092 1.00 30.22 C
ATOM 15315 CD1 ILE B 463 -46.983 -38.462 -42.965 1.00 30.14 C

ATOM 15319 CG2 ILE B 463 -45.558 -39.740 -45.340 1.00 29.85 C
ATOM 15323 C ILE B 463 -46.775 -36.429 -46.881 1.00 30.75 C
ATOM 15324 O ILE B 463 -46.595 -35.270 -46.495 1.00 30.52 O
ATOM 15326 N SER B 464 -47.842 -36.822 -47.581 1.00 31.33 N
ATOM 15327 CA SER B 464 -48.951 -35.944 -47.952 1.00 31.68 C
ATOM 15329 CB SER B 464 -49.948 -36.709 -48.830 1.00 32.02 C
ATOM 15332 OG SER B 464 -50.547 -37.793 -48.123 1.00 32.84 O
ATOM 15334 C SER B 464 -49.705 -35.396 -46.747 1.00 31.62 C
ATOM 15335 O SER B 464 -49.897 -36.097 -45.747 1.00 31.69 O
ATOM 15337 N GLU B 465 -50.165 -34.153 -46.874 1.00 31.42 N
ATOM 15338 CA GLU B 465 -50.881 -33.466 -45.803 1.00 31.20 C
ATOM 15340 CB GLU B 465 -51.465 -32.141 -46.324 1.00 31.33 C
ATOM 15343 CG GLU B 465 -52.441 -31.455 -45.359 1.00 31.42 C
ATOM 15346 CD GLU B 465 -52.768 -30.006 -45.712 1.00 31.30 C
ATOM 15347 OE1 GLU B 465 -52.325 -29.490 -46.765 1.00 30.56 O
ATOM 15348 OE2 GLU B 465 -53.487 -29.380 -44.906 1.00 31.84 O
ATOM 15349 C GLU B 465 -51.985 -34.325 -45.202 1.00 30.97 C
ATOM 15350 O GLU B 465 -52.175 -34.327 -43.992 1.00 30.72 O
ATOM 15352 N GLU B 466 -52.709 -35.052 -46.055 1.00 30.98 N
ATOM 15353 CA GLU B 466 -53.865 -35.833 -45.618 1.00 30.65 C
ATOM 15355 CB GLU B 466 -54.553 -36.541 -46.788 1.00 30.62 C
ATOM 15358 CG GLU B 466 -55.733 -37.401 -46.336 1.00 31.50 C
ATOM 15361 CD GLU B 466 -56.353 -38.240 -47.446 1.00 33.14 C
ATOM 15362 OE1 GLU B 466 -56.512 -37.736 -48.581 1.00 34.40 O
ATOM 15363 OE2 GLU B 466 -56.699 -39.413 -47.173 1.00 33.21 O
ATOM 15364 C GLU B 466 -53.477 -36.851 -44.564 1.00 30.17 C
ATOM 15365 O GLU B 466 -54.215 -37.049 -43.606 1.00 30.46 O
ATOM 15367 N LEU B 467 -52.333 -37.506 -44.726 1.00 29.59 N
ATOM 15368 CA LEU B 467 -51.953 -38.540 -43.769 1.00 29.19 C
ATOM 15370 CB LEU B 467 -51.640 -39.869 -44.476 1.00 29.27 C
ATOM 15373 CG LEU B 467 -50.356 -40.081 -45.268 1.00 29.84 C
ATOM 15375 CD1 LEU B 467 -49.341 -40.761 -44.357 1.00 31.06 C
ATOM 15379 CD2 LEU B 467 -50.589 -40.920 -46.523 1.00 29.47 C
ATOM 15383 C LEU B 467 -50.865 -38.092 -42.794 1.00 28.54 C
ATOM 15384 O LEU B 467 -50.490 -38.834 -41.894 1.00 28.28 O
ATOM 15386 N ALA B 468 -50.388 -36.862 -42.962 1.00 28.04 N
ATOM 15387 CA ALA B 468 -49.682 -36.158 -41.893 1.00 27.54 C
ATOM 15389 CB ALA B 468 -48.922 -34.970 -42.435 1.00 27.34 C
ATOM 15393 C ALA B 468 -50.711 -35.698 -40.865 1.00 27.17 C
ATOM 15394 O ALA B 468 -50.482 -35.801 -39.662 1.00 27.40 O
ATOM 15396 N THR B 469 -51.841 -35.182 -41.349 1.00 26.57 N
ATOM 15397 CA THR B 469 -52.957 -34.795 -40.490 1.00 25.87 C
ATOM 15399 CB THR B 469 -54.130 -34.297 -41.328 1.00 25.53 C
ATOM 15401 OG1 THR B 469 -53.737 -33.111 -42.025 1.00 24.99 O
ATOM 15403 CG2 THR B 469 -55.316 -33.993 -40.453 1.00 24.62 C
ATOM 15407 C THR B 469 -53.412 -35.988 -39.669 1.00 25.95 C
ATOM 15408 O THR B 469 -53.551 -35.925 -38.450 1.00 25.80 O
ATOM 15410 N GLU B 470 -53.618 -37.091 -40.367 1.00 26.06 N
ATOM 15411 CA GLU B 470 -54.043 -38.344 -39.756 1.00 26.10 C
ATOM 15413 CB GLU B 470 -54.057 -39.436 -40.848 1.00 26.60 C
ATOM 15416 CG GLU B 470 -55.038 -40.587 -40.646 1.00 28.01 C
ATOM 15419 CD GLU B 470 -54.553 -41.897 -41.286 1.00 29.05 C
ATOM 15420 OE1 GLU B 470 -54.298 -41.930 -42.515 1.00 27.96 O
ATOM 15421 OE2 GLU B 470 -54.435 -42.892 -40.536 1.00 30.42 O
ATOM 15422 C GLU B 470 -53.148 -38.746 -38.557 1.00 25.28 C
ATOM 15423 O GLU B 470 -53.629 -39.266 -37.556 1.00 25.08 O
ATOM 15425 N SER B 471 -51.850 -38.497 -38.654 1.00 24.70 N
ATOM 15426 CA SER B 471 -50.930 -38.906 -37.599 1.00 24.26 C
ATOM 15428 CB SER B 471 -49.494 -38.842 -38.085 1.00 24.11 C
ATOM 15431 OG SER B 471 -49.315 -39.693 -39.186 1.00 23.98 O

ATOM 15433 C SER B 471 -51.085 -38.029 -36.377 1.00 23.92 C
ATOM 15434 O SER B 471 -51.240 -38.530 -35.270 1.00 24.09 O
ATOM 15436 N VAL B 472 -51.032 -36.719 -36.582 1.00 23.48 N
ATOM 15437 CA VAL B 472 -51.279 -35.774 -35.510 1.00 23.15 C
ATOM 15439 CB VAL B 472 -51.377 -34.332 -36.045 1.00 23.03 C
ATOM 15441 CG1 VAL B 472 -51.739 -33.347 -34.929 1.00 21.74 C
ATOM 15445 CG2 VAL B 472 -50.067 -33.945 -36.728 1.00 22.27 C
ATOM 15449 C VAL B 472 -52.572 -36.192 -34.830 1.00 23.49 C
ATOM 15450 O VAL B 472 -52.663 -36.276 -33.614 1.00 23.29 O
ATOM 15452 N MET B 473 -53.573 -36.508 -35.626 1.00 24.34 N
ATOM 15453 CA MET B 473 -54.850 -36.901 -35.070 1.00 24.93 C
ATOM 15455 CB MET B 473 -55.816 -37.266 -36.190 1.00 25.09 C
ATOM 15458 CG MET B 473 -57.191 -36.788 -35.912 1.00 26.94 C
ATOM 15461 SD MET B 473 -57.328 -35.035 -36.251 1.00 29.69 S
ATOM 15462 CE MET B 473 -58.316 -35.080 -37.775 1.00 29.12 C
ATOM 15466 C MET B 473 -54.668 -38.072 -34.100 1.00 25.00 C
ATOM 15467 O MET B 473 -55.135 -38.018 -32.963 1.00 24.78 O
ATOM 15469 N ASN B 474 -53.965 -39.110 -34.556 1.00 25.30 N
ATOM 15470 CA ASN B 474 -53.681 -40.293 -33.738 1.00 25.55 C
ATOM 15472 CB ASN B 474 -53.143 -41.439 -34.601 1.00 25.82 C
ATOM 15475 CG ASN B 474 -54.243 -42.137 -35.402 1.00 27.62 C
ATOM 15476 OD1 ASN B 474 -54.238 -42.102 -36.638 1.00 29.33 O
ATOM 15477 ND2 ASN B 474 -55.196 -42.780 -34.697 1.00 28.58 N
ATOM 15480 C ASN B 474 -52.711 -40.034 -32.592 1.00 25.20 C
ATOM 15481 O ASN B 474 -52.711 -40.773 -31.621 1.00 25.71 O
ATOM 15483 N LEU B 475 -51.883 -38.999 -32.704 1.00 24.65 N
ATOM 15484 CA LEU B 475 -50.987 -38.595 -31.614 1.00 24.04 C
ATOM 15486 CB LEU B 475 -49.939 -37.626 -32.142 1.00 23.88 C
ATOM 15489 CG LEU B 475 -48.837 -37.285 -31.164 1.00 23.70 C
ATOM 15491 CD1 LEU B 475 -47.936 -38.471 -31.004 1.00 23.97 C
ATOM 15495 CD2 LEU B 475 -48.088 -36.104 -31.679 1.00 23.99 C
ATOM 15499 C LEU B 475 -51.747 -37.940 -30.453 1.00 23.65 C
ATOM 15500 O LEU B 475 -51.323 -38.014 -29.299 1.00 23.74 O
ATOM 15502 N ILE B 476 -52.858 -37.282 -30.766 1.00 23.15 N
ATOM 15503 CA ILE B 476 -53.728 -36.711 -29.742 1.00 22.50 C
ATOM 15505 CB ILE B 476 -54.779 -35.755 -30.359 1.00 22.27 C
ATOM 15507 CG1 ILE B 476 -54.099 -34.508 -30.910 1.00 20.55 C
ATOM 15510 CD1 ILE B 476 -55.000 -33.671 -31.693 1.00 19.19 C
ATOM 15514 CG2 ILE B 476 -55.817 -35.363 -29.336 1.00 22.15 C
ATOM 15518 C ILE B 476 -54.398 -37.849 -28.985 1.00 22.40 C
ATOM 15519 O ILE B 476 -54.316 -37.900 -27.767 1.00 22.32 O
ATOM 15521 N ASP B 477 -55.023 -38.777 -29.708 1.00 22.37 N
ATOM 15522 CA ASP B 477 -55.616 -39.975 -29.090 1.00 22.55 C
ATOM 15524 CB ASP B 477 -55.996 -41.007 -30.151 1.00 22.67 C
ATOM 15527 CG ASP B 477 -57.262 -40.636 -30.892 1.00 24.93 C
ATOM 15528 OD1 ASP B 477 -57.690 -39.458 -30.818 1.00 28.87 O
ATOM 15529 OD2 ASP B 477 -57.847 -41.523 -31.549 1.00 27.92 O
ATOM 15530 C ASP B 477 -54.675 -40.622 -28.083 1.00 22.10 C
ATOM 15531 O ASP B 477 -55.048 -40.877 -26.938 1.00 21.83 O
ATOM 15533 N GLU B 478 -53.444 -40.867 -28.510 1.00 21.73 N
ATOM 15534 CA GLU B 478 -52.472 -41.506 -27.645 1.00 21.69 C
ATOM 15536 CB GLU B 478 -51.233 -41.920 -28.437 1.00 21.97 C
ATOM 15539 CG GLU B 478 -50.786 -43.360 -28.150 1.00 24.18 C
ATOM 15542 CD GLU B 478 -51.793 -44.429 -28.618 1.00 27.03 C
ATOM 15543 OE1 GLU B 478 -51.599 -45.627 -28.285 1.00 29.15 O
ATOM 15544 OE2 GLU B 478 -52.770 -44.080 -29.323 1.00 28.37 O
ATOM 15545 C GLU B 478 -52.107 -40.608 -26.449 1.00 20.97 C
ATOM 15546 O GLU B 478 -51.928 -41.110 -25.316 1.00 21.15 O
ATOM 15548 N THR B 479 -52.031 -39.291 -26.687 1.00 19.82 N
ATOM 15549 CA THR B 479 -51.787 -38.319 -25.604 1.00 18.59 C

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ATOM  15551  CB  THR B 479     -51.587 -36.897 -26.129  1.00 17.95           C
ATOM  15553  OG1 THR B 479     -50.291 -36.779 -26.712  1.00 17.43           O
ATOM  15555  CG2 THR B 479     -51.654 -35.938 -25.009  1.00 17.90           C
ATOM  15559  C   THR B 479     -52.927 -38.342 -24.580  1.00 18.16           C
ATOM  15560  O   THR B 479     -52.695 -38.339 -23.383  1.00 18.06           O
ATOM  15562  N   TRP B 480     -54.160 -38.390 -25.057  1.00 17.77           N
ATOM  15563  CA  TRP B 480     -55.301 -38.493 -24.169  1.00 17.54           C
ATOM  15565  CB  TRP B 480     -56.605 -38.464 -24.970  1.00 17.49           C
ATOM  15568  CG  TRP B 480     -57.239 -37.099 -25.028  1.00 17.53           C
ATOM  15569  CD1 TRP B 480     -57.150 -36.186 -26.041  1.00 17.04           C
ATOM  15571  NE1 TRP B 480     -57.857 -35.067 -25.721  1.00 16.57           N
ATOM  15573  CE2 TRP B 480     -58.423 -35.236 -24.484  1.00 16.41           C
ATOM  15574  CD2 TRP B 480     -58.055 -36.498 -24.020  1.00 16.68           C
ATOM  15575  CE3 TRP B 480     -58.507 -36.914 -22.765  1.00 16.92           C
ATOM  15577  CZ3 TRP B 480     -59.300 -36.076 -22.039  1.00 16.97           C
ATOM  15579  CH2 TRP B 480     -59.654 -34.823 -22.524  1.00 16.91           C
ATOM  15581  CZ2 TRP B 480     -59.223 -34.383 -23.742  1.00 16.89           C
ATOM  15583  C   TRP B 480     -55.232 -39.760 -23.334  1.00 17.75           C
ATOM  15584  O   TRP B 480     -55.582 -39.747 -22.164  1.00 17.74           O
ATOM  15586  N   LYS B 481     -54.784 -40.861 -23.933  1.00 18.09           N
ATOM  15587  CA  LYS B 481     -54.721 -42.124 -23.210  1.00 18.10           C
ATOM  15589  CB  LYS B 481     -54.277 -43.282 -24.115  1.00 18.01           C
ATOM  15592  CG  LYS B 481     -55.311 -43.803 -25.114  1.00 16.89           C
ATOM  15595  CD  LYS B 481     -54.613 -44.663 -26.199  1.00 15.83           C
ATOM  15598  CE  LYS B 481     -55.587 -45.500 -27.025  1.00 14.74           C
ATOM  15601  NZ  LYS B 481     -55.119 -45.725 -28.413  1.00 12.34           N
ATOM  15605  C   LYS B 481     -53.750 -41.970 -22.054  1.00 18.46           C
ATOM  15606  O   LYS B 481     -53.976 -42.494 -20.969  1.00 18.44           O
ATOM  15608  N   LYS B 482     -52.662 -41.252 -22.279  1.00 18.80           N
ATOM  15609  CA  LYS B 482     -51.727 -41.019 -21.192  1.00 19.58           C
ATOM  15611  CB  LYS B 482     -50.425 -40.424 -21.727  1.00 20.03           C
ATOM  15614  CG  LYS B 482     -49.499 -41.500 -22.277  1.00 22.03           C
ATOM  15617  CD  LYS B 482     -48.706 -41.063 -23.506  1.00 24.87           C
ATOM  15620  CE  LYS B 482     -47.908 -42.268 -24.066  1.00 26.65           C
ATOM  15623  NZ  LYS B 482     -47.287 -41.996 -25.408  1.00 28.80           N
ATOM  15627  C   LYS B 482     -52.363 -40.156 -20.096  1.00 19.56           C
ATOM  15628  O   LYS B 482     -52.367 -40.537 -18.926  1.00 19.19           O
ATOM  15630  N   MET B 483     -52.922 -39.013 -20.483  1.00 20.00           N
ATOM  15631  CA  MET B 483     -53.677 -38.165 -19.552  1.00 20.37           C
ATOM  15633  CB  MET B 483     -54.426 -37.057 -20.295  1.00 20.25           C
ATOM  15636  CG  MET B 483     -53.529 -35.951 -20.807  1.00 20.52           C
ATOM  15639  SD  MET B 483     -54.461 -34.483 -21.225  1.00 20.47           S
ATOM  15640  CE  MET B 483     -55.361 -35.084 -22.649  1.00 22.07           C
ATOM  15644  C   MET B 483     -54.668 -38.981 -18.741  1.00 20.72           C
ATOM  15645  O   MET B 483     -54.809 -38.779 -17.543  1.00 20.37           O
ATOM  15647  N   ASN B 484     -55.345 -39.910 -19.403  1.00 21.57           N
ATOM  15648  CA  ASN B 484     -56.339 -40.731 -18.744  1.00 22.46           C
ATOM  15650  CB  ASN B 484     -57.042 -41.631 -19.765  1.00 22.23           C
ATOM  15653  CG  ASN B 484     -58.118 -40.900 -20.576  1.00 21.61           C
ATOM  15654  OD1 ASN B 484     -58.412 -39.722 -20.362  1.00 20.25           O
ATOM  15655  ND2 ASN B 484     -58.720 -41.622 -21.510  1.00 20.80           N
ATOM  15658  C   ASN B 484     -55.723 -41.555 -17.598  1.00 23.83           C
ATOM  15659  O   ASN B 484     -56.262 -41.591 -16.484  1.00 23.76           O
ATOM  15661  N   LYS B 485     -54.585 -42.190 -17.868  1.00 25.69           N
ATOM  15662  CA  LYS B 485     -53.854 -42.937 -16.843  1.00 27.11           C
ATOM  15664  CB  LYS B 485     -52.679 -43.712 -17.447  1.00 27.13           C
ATOM  15667  CG  LYS B 485     -52.073 -44.755 -16.489  1.00 28.85           C
ATOM  15670  CD  LYS B 485     -51.643 -46.082 -17.187  1.00 31.17           C
ATOM  15673  CE  LYS B 485     -50.150 -46.132 -17.555  1.00 32.11           C
ATOM  15676  NZ  LYS B 485     -49.291 -46.282 -16.344  1.00 33.08           N
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ATOM 15680 C LYS B 485 -53.370 -42.035 -15.701 1.00 28.37 C
ATOM 15681 O LYS B 485 -53.288 -42.481 -14.563 1.00 28.59 O
ATOM 15683 N GLU B 486 -53.083 -40.766 -15.980 1.00 29.89 N
ATOM 15684 CA GLU B 486 -52.683 -39.849 -14.910 1.00 31.09 C
ATOM 15686 CB GLU B 486 -52.174 -38.511 -15.470 1.00 31.55 C
ATOM 15689 CG GLU B 486 -51.059 -37.851 -14.643 1.00 32.69 C
ATOM 15692 CD GLU B 486 -49.785 -38.689 -14.605 1.00 34.51 C
ATOM 15693 OE1 GLU B 486 -49.104 -38.682 -13.557 1.00 36.35 O
ATOM 15694 OE2 GLU B 486 -49.476 -39.368 -15.611 1.00 34.55 O
ATOM 15695 C GLU B 486 -53.836 -39.615 -13.939 1.00 31.70 C
ATOM 15696 O GLU B 486 -53.684 -39.868 -12.750 1.00 31.90 O
ATOM 15698 N LYS B 487 -54.983 -39.164 -14.453 1.00 32.71 N
ATOM 15699 CA LYS B 487 -56.177 -38.856 -13.629 1.00 33.57 C
ATOM 15701 CB LYS B 487 -57.343 -38.402 -14.519 1.00 33.54 C
ATOM 15704 CG LYS B 487 -58.703 -38.196 -13.823 1.00 33.45 C
ATOM 15707 CD LYS B 487 -58.686 -37.024 -12.866 1.00 33.71 C
ATOM 15710 CE LYS B 487 -59.906 -36.996 -11.931 1.00 34.48 C
ATOM 15713 NZ LYS B 487 -61.123 -36.378 -12.526 1.00 35.03 N
ATOM 15717 C LYS B 487 -56.626 -40.046 -12.802 1.00 34.60 C
ATOM 15718 O LYS B 487 -57.126 -39.892 -11.681 1.00 34.55 O
ATOM 15720 N LEU B 488 -56.453 -41.233 -13.371 1.00 35.94 N
ATOM 15721 CA LEU B 488 -56.878 -42.451 -12.723 1.00 37.00 C
ATOM 15723 CB LEU B 488 -57.280 -43.489 -13.778 1.00 36.90 C
ATOM 15726 CG LEU B 488 -58.081 -44.714 -13.312 1.00 37.52 C
ATOM 15728 CD1 LEU B 488 -58.758 -44.536 -11.946 1.00 38.76 C
ATOM 15732 CD2 LEU B 488 -59.121 -45.084 -14.346 1.00 38.42 C
ATOM 15736 C LEU B 488 -55.786 -42.980 -11.803 1.00 38.02 C
ATOM 15737 O LEU B 488 -56.063 -43.315 -10.653 1.00 38.19 O
ATOM 15739 N GLY B 489 -54.550 -43.016 -12.298 1.00 39.44 N
ATOM 15740 CA GLY B 489 -53.441 -43.710 -11.621 1.00 40.62 C
ATOM 15743 C GLY B 489 -52.563 -42.837 -10.740 1.00 41.76 C
ATOM 15744 O GLY B 489 -51.357 -42.703 -10.988 1.00 41.83 O
ATOM 15746 N GLY B 490 -53.183 -42.230 -9.726 1.00 43.10 N
ATOM 15747 CA GLY B 490 -52.481 -41.538 -8.636 1.00 43.82 C
ATOM 15750 C GLY B 490 -51.131 -40.924 -8.967 1.00 44.31 C
ATOM 15751 O GLY B 490 -50.084 -41.560 -8.831 1.00 44.25 O
ATOM 15753 N SER B 491 -51.161 -39.672 -9.396 1.00 44.87 N
ATOM 15754 CA SER B 491 -49.939 -38.892 -9.575 1.00 45.22 C
ATOM 15756 CB SER B 491 -50.224 -37.723 -10.537 1.00 45.34 C
ATOM 15759 OG SER B 491 -51.411 -37.032 -10.166 1.00 45.38 O
ATOM 15761 C SER B 491 -49.419 -38.389 -8.203 1.00 45.14 C
ATOM 15762 O SER B 491 -49.896 -38.824 -7.140 1.00 45.11 O
ATOM 15764 N LEU B 492 -48.429 -37.491 -8.227 1.00 44.77 N
ATOM 15765 CA LEU B 492 -48.046 -36.752 -7.018 1.00 44.31 C
ATOM 15767 CB LEU B 492 -46.726 -35.971 -7.188 1.00 44.55 C
ATOM 15770 CG LEU B 492 -45.530 -36.546 -7.972 1.00 45.73 C
ATOM 15772 CD1 LEU B 492 -44.373 -35.556 -7.859 1.00 46.25 C
ATOM 15776 CD2 LEU B 492 -45.084 -37.972 -7.530 1.00 46.14 C
ATOM 15780 C LEU B 492 -49.151 -35.760 -6.703 1.00 43.30 C
ATOM 15781 O LEU B 492 -49.315 -35.370 -5.555 1.00 43.49 O
ATOM 15783 N PHE B 493 -49.903 -35.367 -7.735 1.00 42.05 N
ATOM 15784 CA PHE B 493 -50.822 -34.239 -7.668 1.00 41.03 C
ATOM 15786 CB PHE B 493 -50.913 -33.549 -9.028 1.00 40.81 C
ATOM 15789 CG PHE B 493 -49.696 -32.771 -9.408 1.00 38.96 C
ATOM 15790 CD1 PHE B 493 -49.651 -31.408 -9.233 1.00 37.06 C
ATOM 15792 CE1 PHE B 493 -48.543 -30.697 -9.603 1.00 36.41 C
ATOM 15794 CZ PHE B 493 -47.471 -31.341 -10.158 1.00 35.87 C
ATOM 15796 CE2 PHE B 493 -47.507 -32.690 -10.343 1.00 36.39 C
ATOM 15798 CD2 PHE B 493 -48.612 -33.400 -9.977 1.00 37.36 C
ATOM 15800 C PHE B 493 -52.240 -34.603 -7.268 1.00 40.76 C

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ATOM  15801  O   PHE B 493     -52.686 -35.733  -7.419  1.00 40.35           O
ATOM  15803  N   ALA B 494     -52.943 -33.584  -6.790  1.00 40.72           N
ATOM  15804  CA  ALA B 494     -54.355 -33.658  -6.471  1.00 40.68           C
ATOM  15806  CB  ALA B 494     -54.786 -32.362  -5.770  1.00 40.70           C
ATOM  15810  C   ALA B 494     -55.175 -33.851  -7.744  1.00 40.59           C
ATOM  15811  O   ALA B 494     -55.013 -33.099  -8.716  1.00 40.95           O
ATOM  15813  N   LYS B 495     -56.071 -34.835  -7.733  1.00 40.12           N
ATOM  15814  CA  LYS B 495     -57.000 -35.047  -8.854  1.00 39.67           C
ATOM  15816  CB  LYS B 495     -58.008 -36.166  -8.520  1.00 39.98           C
ATOM  15819  CG  LYS B 495     -57.388 -37.590  -8.496  1.00 40.57           C
ATOM  15822  CD  LYS B 495     -58.468 -38.688  -8.419  1.00 41.18           C
ATOM  15825  CE  LYS B 495     -57.878 -40.065  -8.132  1.00 41.28           C
ATOM  15828  NZ  LYS B 495     -58.736 -41.159  -8.671  1.00 41.39           N
ATOM  15832  C   LYS B 495     -57.717 -33.752  -9.333  1.00 38.82           C
ATOM  15833  O   LYS B 495     -57.847 -33.535 -10.537  1.00 38.70           O
ATOM  15835  N   PRO B 496     -58.169 -32.890  -8.397  1.00 37.71           N
ATOM  15836  CA  PRO B 496     -58.701 -31.551  -8.687  1.00 36.80           C
ATOM  15838  CB  PRO B 496     -58.820 -30.937  -7.304  1.00 36.94           C
ATOM  15841  CG  PRO B 496     -59.255 -32.073  -6.483  1.00 37.90           C
ATOM  15844  CD  PRO B 496     -58.534 -33.294  -7.030  1.00 37.86           C
ATOM  15847  C   PRO B 496     -57.845 -30.625  -9.536  1.00 35.57           C
ATOM  15848  O   PRO B 496     -58.389 -29.693 -10.139  1.00 35.93           O
ATOM  15849  N   PHE B 497     -56.527 -30.836  -9.546  1.00 33.52           N
ATOM  15850  CA  PHE B 497     -55.654 -30.083 -10.439  1.00 31.34           C
ATOM  15852  CB  PHE B 497     -54.355 -29.710  -9.750  1.00 30.86           C
ATOM  15855  CG  PHE B 497     -53.394 -28.989 -10.634  1.00 29.04           C
ATOM  15856  CD1 PHE B 497     -53.639 -27.700 -11.022  1.00 27.89           C
ATOM  15858  CE1 PHE B 497     -52.752 -27.028 -11.834  1.00 27.39           C
ATOM  15860  CZ  PHE B 497     -51.599 -27.653 -12.259  1.00 27.40           C
ATOM  15862  CE2 PHE B 497     -51.341 -28.941 -11.877  1.00 27.44           C
ATOM  15864  CD2 PHE B 497     -52.236 -29.604 -11.074  1.00 28.18           C
ATOM  15866  C   PHE B 497     -55.390 -30.870 -11.714  1.00 30.24           C
ATOM  15867  O   PHE B 497     -55.301 -30.266 -12.786  1.00 30.39           O
ATOM  15869  N   VAL B 498     -55.295 -32.200 -11.630  1.00 28.50           N
ATOM  15870  CA  VAL B 498     -55.076 -32.983 -12.854  1.00 27.54           C
ATOM  15872  CB  VAL B 498     -54.778 -34.472 -12.611  1.00 27.34           C
ATOM  15874  CG1 VAL B 498     -56.027 -35.194 -12.262  1.00 28.14           C
ATOM  15878  CG2 VAL B 498     -53.731 -34.649 -11.530  1.00 27.04           C
ATOM  15882  C   VAL B 498     -56.277 -32.857 -13.784  1.00 26.60           C
ATOM  15883  O   VAL B 498     -56.129 -32.864 -14.995  1.00 26.33           O
ATOM  15885  N   GLU B 499     -57.468 -32.731 -13.214  1.00 25.87           N
ATOM  15886  CA  GLU B 499     -58.662 -32.484 -14.022  1.00 25.20           C
ATOM  15888  CB  GLU B 499     -59.975 -32.639 -13.206  1.00 25.26           C
ATOM  15891  CG  GLU B 499     -61.287 -32.694 -14.028  1.00 25.16           C
ATOM  15894  CD  GLU B 499     -61.422 -33.922 -14.973  1.00 26.79           C
ATOM  15895  OE1 GLU B 499     -60.607 -34.880 -14.928  1.00 26.39           O
ATOM  15896  OE2 GLU B 499     -62.379 -33.926 -15.785  1.00 27.83           O
ATOM  15897  C   GLU B 499     -58.542 -31.097 -14.641  1.00 24.27           C
ATOM  15898  O   GLU B 499     -58.819 -30.948 -15.832  1.00 24.32           O
ATOM  15900  N   THR B 500     -58.098 -30.093 -13.882  1.00 22.90           N
ATOM  15901  CA  THR B 500     -58.027 -28.764 -14.487  1.00 22.29           C
ATOM  15903  CB  THR B 500     -57.908 -27.592 -13.488  1.00 22.43           C
ATOM  15905  OG1 THR B 500     -56.536 -27.259 -13.274  1.00 22.65           O
ATOM  15907  CG2 THR B 500     -58.614 -27.899 -12.183  1.00 22.84           C
ATOM  15911  C   THR B 500     -56.940 -28.671 -15.565  1.00 21.20           C
ATOM  15912  O   THR B 500     -57.120 -27.939 -16.536  1.00 21.06           O
ATOM  15914  N   ALA B 501     -55.845 -29.414 -15.422  1.00 19.88           N
ATOM  15915  CA  ALA B 501     -54.906 -29.574 -16.537  1.00 19.24           C
ATOM  15917  CB  ALA B 501     -53.704 -30.393 -16.115  1.00 19.22           C
ATOM  15921  C   ALA B 501     -55.581 -30.226 -17.757  1.00 18.68           C
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ATOM 15922 O ALA B 501 -55.427 -29.768 -18.881 1.00 18.32 O
ATOM 15924 N ILE B 502 -56.324 -31.300 -17.523 1.00 18.11 N
ATOM 15925 CA ILE B 502 -57.023 -31.988 -18.591 1.00 17.68 C
ATOM 15927 CB ILE B 502 -57.750 -33.251 -18.059 1.00 17.63 C
ATOM 15929 CG1 ILE B 502 -56.713 -34.350 -17.769 1.00 18.16 C
ATOM 15932 CD1 ILE B 502 -57.253 -35.645 -17.115 1.00 17.02 C
ATOM 15936 CG2 ILE B 502 -58.756 -33.762 -19.063 1.00 16.93 C
ATOM 15940 C ILE B 502 -57.990 -31.030 -19.289 1.00 17.50 C
ATOM 15941 O ILE B 502 -58.153 -31.071 -20.512 1.00 17.62 O
ATOM 15943 N ASN B 503 -58.604 -30.139 -18.524 1.00 17.23 N
ATOM 15944 CA ASN B 503 -59.545 -29.184 -19.102 1.00 17.07 C
ATOM 15946 CB ASN B 503 -60.184 -28.327 -18.016 1.00 17.21 C
ATOM 15949 CG ASN B 503 -61.155 -29.094 -17.176 1.00 17.29 C
ATOM 15950 OD1 ASN B 503 -61.721 -30.097 -17.609 1.00 16.66 O
ATOM 15951 ND2 ASN B 503 -61.365 -28.621 -15.958 1.00 19.16 N
ATOM 15954 C ASN B 503 -58.920 -28.270 -20.149 1.00 16.59 C
ATOM 15955 O ASN B 503 -59.611 -27.811 -21.071 1.00 16.67 O
ATOM 15957 N LEU B 504 -57.629 -27.992 -20.014 1.00 15.79 N
ATOM 15958 CA LEU B 504 -56.948 -27.204 -21.031 1.00 15.44 C
ATOM 15960 CB LEU B 504 -55.530 -26.865 -20.609 1.00 15.07 C
ATOM 15963 CG LEU B 504 -54.933 -25.837 -21.552 1.00 14.21 C
ATOM 15965 CD1 LEU B 504 -54.246 -24.726 -20.800 1.00 14.21 C
ATOM 15969 CD2 LEU B 504 -54.000 -26.538 -22.462 1.00 14.27 C
ATOM 15973 C LEU B 504 -56.954 -27.933 -22.375 1.00 15.59 C
ATOM 15974 O LEU B 504 -57.177 -27.323 -23.414 1.00 15.30 O
ATOM 15976 N ALA B 505 -56.732 -29.242 -22.341 1.00 15.89 N
ATOM 15977 CA ALA B 505 -56.914 -30.073 -23.514 1.00 16.23 C
ATOM 15979 CB ALA B 505 -56.608 -31.483 -23.188 1.00 16.05 C
ATOM 15983 C ALA B 505 -58.352 -29.955 -24.010 1.00 16.69 C
ATOM 15984 O ALA B 505 -58.598 -29.738 -25.204 1.00 16.88 O
ATOM 15986 N ARG B 506 -59.300 -30.071 -23.090 1.00 16.88 N
ATOM 15987 CA ARG B 506 -60.709 -29.972 -23.457 1.00 17.20 C
ATOM 15989 CB ARG B 506 -61.630 -30.170 -22.248 1.00 17.34 C
ATOM 15992 CG ARG B 506 -61.549 -31.537 -21.614 1.00 17.46 C
ATOM 15995 CD ARG B 506 -62.837 -31.917 -20.962 1.00 17.48 C
ATOM 15998 NE ARG B 506 -62.783 -33.280 -20.435 1.00 18.37 N
ATOM 16000 CZ ARG B 506 -62.404 -33.613 -19.201 1.00 19.03 C
ATOM 16001 NH1 ARG B 506 -62.008 -32.690 -18.324 1.00 18.83 N
ATOM 16004 NH2 ARG B 506 -62.415 -34.892 -18.841 1.00 19.72 N
ATOM 16007 C ARG B 506 -61.038 -28.646 -24.114 1.00 17.32 C
ATOM 16008 O ARG B 506 -61.754 -28.622 -25.111 1.00 17.41 O
ATOM 16010 N GLN B 507 -60.540 -27.543 -23.564 1.00 17.59 N
ATOM 16011 CA GLN B 507 -60.864 -26.233 -24.139 1.00 18.05 C
ATOM 16013 CB GLN B 507 -60.382 -25.090 -23.258 1.00 18.16 C
ATOM 16016 CG GLN B 507 -60.798 -23.709 -23.764 1.00 17.57 C
ATOM 16019 CD GLN B 507 -62.291 -23.508 -23.723 1.00 17.42 C
ATOM 16020 OE1 GLN B 507 -62.953 -23.959 -22.800 1.00 17.55 O
ATOM 16021 NE2 GLN B 507 -62.832 -22.823 -24.722 1.00 17.56 N
ATOM 16024 C GLN B 507 -60.258 -26.060 -25.521 1.00 18.49 C
ATOM 16025 O GLN B 507 -60.855 -25.413 -26.380 1.00 18.73 O
ATOM 16027 N SER B 508 -59.066 -26.619 -25.724 1.00 18.85 N
ATOM 16028 CA SER B 508 -58.427 -26.621 -27.037 1.00 19.07 C
ATOM 16030 CB SER B 508 -57.108 -27.364 -26.969 1.00 19.04 C
ATOM 16033 OG SER B 508 -56.304 -26.772 -25.979 1.00 20.10 O
ATOM 16035 C SER B 508 -59.305 -27.296 -28.065 1.00 19.12 C
ATOM 16036 O SER B 508 -59.438 -26.827 -29.187 1.00 19.00 O
ATOM 16038 N HIS B 509 -59.905 -28.409 -27.674 1.00 19.26 N
ATOM 16039 CA HIS B 509 -60.814 -29.095 -28.559 1.00 19.33 C
ATOM 16041 CB HIS B 509 -61.275 -30.412 -27.959 1.00 19.30 C
ATOM 16044 CG HIS B 509 -60.263 -31.501 -28.067 1.00 18.71 C

ATOM 16045 ND1 HIS B 509 -59.941 -32.089 -29.267 1.00 18.57 N
ATOM 16047 CE1 HIS B 509 -59.020 -33.012 -29.064 1.00 19.07 C
ATOM 16049 NE2 HIS B 509 -58.738 -33.044 -27.774 1.00 18.52 N
ATOM 16051 CD2 HIS B 509 -59.499 -32.105 -27.129 1.00 18.43 C
ATOM 16053 C HIS B 509 -62.017 -28.251 -28.878 1.00 19.60 C
ATOM 16054 O HIS B 509 -62.491 -28.286 -29.969 1.00 19.68 O
ATOM 16056 N CYS B 510 -62.540 -27.502 -27.932 1.00 20.12 N
ATOM 16057 CA CYS B 510 -63.748 -26.738 -28.216 1.00 20.63 C
ATOM 16059 CB CYS B 510 -64.493 -26.492 -26.915 1.00 20.70 C
ATOM 16062 SG CYS B 510 -64.856 -28.020 -26.065 1.00 22.93 S
ATOM 16064 C CYS B 510 -63.465 -25.422 -28.950 1.00 20.55 C
ATOM 16065 O CYS B 510 -64.338 -24.881 -29.622 1.00 20.16 O
ATOM 16067 N THR B 511 -62.236 -24.933 -28.827 1.00 20.89 N
ATOM 16068 CA THR B 511 -61.833 -23.654 -29.378 1.00 21.32 C
ATOM 16070 CB THR B 511 -60.682 -23.107 -28.550 1.00 20.76 C
ATOM 16072 OG1 THR B 511 -61.208 -22.619 -27.324 1.00 19.50 O
ATOM 16074 CG2 THR B 511 -59.961 -21.994 -29.253 1.00 19.79 C
ATOM 16078 C THR B 511 -61.417 -23.735 -30.851 1.00 23.11 C
ATOM 16079 O THR B 511 -61.910 -22.992 -31.694 1.00 22.75 O
ATOM 16081 N TYR B 512 -60.501 -24.646 -31.152 1.00 25.46 N
ATOM 16082 CA TYR B 512 -59.867 -24.704 -32.462 1.00 27.09 C
ATOM 16084 CB TYR B 512 -58.397 -25.107 -32.327 1.00 27.16 C
ATOM 16087 CG TYR B 512 -57.598 -24.056 -31.582 1.00 27.26 C
ATOM 16088 CD1 TYR B 512 -57.300 -22.834 -32.182 1.00 28.18 C
ATOM 16090 CE1 TYR B 512 -56.583 -21.844 -31.511 1.00 27.98 C
ATOM 16092 CZ TYR B 512 -56.164 -22.068 -30.226 1.00 27.72 C
ATOM 16093 OH TYR B 512 -55.462 -21.072 -29.584 1.00 27.09 O
ATOM 16095 CE2 TYR B 512 -56.453 -23.281 -29.602 1.00 27.52 C
ATOM 16097 CD2 TYR B 512 -57.171 -24.262 -30.278 1.00 26.68 C
ATOM 16099 C TYR B 512 -60.633 -25.623 -33.382 1.00 28.79 C
ATOM 16100 O TYR B 512 -61.050 -25.179 -34.444 1.00 28.98 O
ATOM 16102 N HIS B 513 -60.789 -26.893 -32.991 1.00 31.06 N
ATOM 16103 CA HIS B 513 -61.865 -27.800 -33.492 1.00 33.07 C
ATOM 16105 CB HIS B 513 -62.740 -28.208 -32.265 1.00 33.66 C
ATOM 16108 CG HIS B 513 -64.181 -28.602 -32.535 1.00 34.73 C
ATOM 16109 ND1 HIS B 513 -65.035 -27.903 -33.367 1.00 35.70 N
ATOM 16111 CE1 HIS B 513 -66.234 -28.464 -33.343 1.00 35.40 C
ATOM 16113 NE2 HIS B 513 -66.206 -29.469 -32.491 1.00 35.10 N
ATOM 16115 CD2 HIS B 513 -64.943 -29.565 -31.956 1.00 35.07 C
ATOM 16117 C HIS B 513 -62.692 -27.179 -34.623 1.00 34.03 C
ATOM 16118 O HIS B 513 -63.003 -27.848 -35.627 1.00 34.55 O
ATOM 16120 N ASN B 514 -63.047 -25.906 -34.444 1.00 34.65 N
ATOM 16121 CA ASN B 514 -63.713 -25.123 -35.483 1.00 35.15 C
ATOM 16123 CB ASN B 514 -63.845 -23.643 -35.070 1.00 35.01 C
ATOM 16126 CG ASN B 514 -64.704 -23.456 -33.820 1.00 33.48 C
ATOM 16127 OD1 ASN B 514 -64.787 -24.343 -32.968 1.00 30.92 O
ATOM 16128 ND2 ASN B 514 -65.327 -22.295 -33.703 1.00 32.16 N
ATOM 16131 C ASN B 514 -63.192 -25.274 -36.942 1.00 36.08 C
ATOM 16132 O ASN B 514 -62.010 -25.051 -37.254 1.00 35.69 O
ATOM 16134 N GLY B 515 -64.119 -25.765 -37.772 1.00 37.15 N
ATOM 16135 CA GLY B 515 -64.224 -25.493 -39.177 1.00 37.94 C
ATOM 16138 C GLY B 515 -65.269 -24.384 -39.284 1.00 39.01 C
ATOM 16139 O GLY B 515 -64.904 -23.286 -39.702 1.00 39.58 O
ATOM 16141 N ASP B 516 -66.550 -24.585 -38.909 1.00 39.95 N
ATOM 16142 CA ASP B 516 -67.167 -25.810 -38.349 1.00 40.65 C
ATOM 16144 CB ASP B 516 -67.296 -25.652 -36.836 1.00 41.09 C
ATOM 16147 CG ASP B 516 -66.318 -26.511 -36.063 1.00 43.63 C
ATOM 16148 OD1 ASP B 516 -65.697 -27.434 -36.662 1.00 45.83 O
ATOM 16149 OD2 ASP B 516 -66.152 -26.246 -34.843 1.00 47.12 O
ATOM 16150 C ASP B 516 -68.603 -26.067 -38.853 1.00 40.78 C

ATOM 16151 O ASP B 516 -69.134 -25.301 -39.660 1.00 41.28 O
ATOM 16153 N ALA B 517 -69.222 -27.141 -38.349 1.00 40.66 N
ATOM 16154 CA ALA B 517 -70.675 -27.396 -38.468 1.00 40.60 C
ATOM 16156 CB ALA B 517 -71.422 -26.622 -37.359 1.00 40.27 C
ATOM 16160 C ALA B 517 -71.295 -27.106 -39.862 1.00 40.79 C
ATOM 16161 O ALA B 517 -70.654 -27.296 -40.899 1.00 40.67 O
ATOM 16163 N HIS B 518 -72.562 -26.696 -39.874 1.00 41.13 N
ATOM 16164 CA HIS B 518 -73.162 -26.033 -41.039 1.00 41.60 C
ATOM 16166 CB HIS B 518 -74.446 -26.756 -41.480 1.00 42.24 C
ATOM 16169 CG HIS B 518 -74.207 -28.179 -41.910 1.00 45.54 C
ATOM 16170 ND1 HIS B 518 -73.441 -28.509 -43.012 1.00 48.51 N
ATOM 16172 CE1 HIS B 518 -73.392 -29.825 -43.140 1.00 48.79 C
ATOM 16174 NE2 HIS B 518 -74.092 -30.364 -42.156 1.00 49.12 N
ATOM 16176 CD2 HIS B 518 -74.608 -29.357 -41.369 1.00 48.28 C
ATOM 16178 C HIS B 518 -73.377 -24.545 -40.686 1.00 40.84 C
ATOM 16179 O HIS B 518 -74.487 -23.997 -40.769 1.00 40.60 O
ATOM 16181 N THR B 519 -72.261 -23.932 -40.275 1.00 40.10 N
ATOM 16182 CA THR B 519 -72.143 -22.521 -39.878 1.00 39.39 C
ATOM 16184 CB THR B 519 -72.561 -22.263 -38.393 1.00 39.40 C
ATOM 16186 OG1 THR B 519 -71.823 -23.131 -37.517 1.00 39.55 O
ATOM 16188 CG2 THR B 519 -74.074 -22.460 -38.178 1.00 38.98 C
ATOM 16192 C THR B 519 -70.654 -22.164 -40.059 1.00 38.81 C
ATOM 16193 O THR B 519 -69.800 -23.050 -40.067 1.00 38.48 O
ATOM 16195 N SER B 520 -70.338 -20.881 -40.199 1.00 38.19 N
ATOM 16196 CA SER B 520 -68.959 -20.453 -40.521 1.00 37.77 C
ATOM 16198 CB SER B 520 -68.983 -18.976 -40.960 1.00 37.76 C
ATOM 16201 OG SER B 520 -68.760 -18.106 -39.870 1.00 38.49 O
ATOM 16203 C SER B 520 -67.974 -20.724 -39.340 1.00 37.24 C
ATOM 16204 O SER B 520 -68.394 -21.267 -38.320 1.00 36.89 O
ATOM 16206 N PRO B 521 -66.671 -20.350 -39.472 1.00 36.96 N
ATOM 16207 CA PRO B 521 -65.692 -20.638 -38.396 1.00 36.80 C
ATOM 16209 CB PRO B 521 -64.320 -20.354 -39.041 1.00 36.68 C
ATOM 16212 CG PRO B 521 -64.599 -19.593 -40.309 1.00 37.19 C
ATOM 16215 CD PRO B 521 -66.091 -19.469 -40.507 1.00 37.10 C
ATOM 16218 C PRO B 521 -65.915 -19.763 -37.168 1.00 36.68 C
ATOM 16219 O PRO B 521 -66.233 -20.289 -36.105 1.00 36.90 O
ATOM 16220 N ASP B 522 -65.744 -18.445 -37.298 1.00 36.61 N
ATOM 16221 CA ASP B 522 -66.373 -17.528 -36.347 1.00 36.58 C
ATOM 16223 CB ASP B 522 -65.938 -16.070 -36.543 1.00 36.82 C
ATOM 16226 CG ASP B 522 -64.456 -15.846 -36.243 1.00 37.94 C
ATOM 16227 OD1 ASP B 522 -63.848 -16.627 -35.473 1.00 39.62 O
ATOM 16228 OD2 ASP B 522 -63.891 -14.876 -36.790 1.00 39.40 O
ATOM 16229 C ASP B 522 -67.836 -17.718 -36.681 1.00 36.12 C
ATOM 16230 O ASP B 522 -68.150 -18.306 -37.702 1.00 35.98 O
ATOM 16232 N GLU B 523 -68.732 -17.249 -35.830 1.00 35.69 N
ATOM 16233 CA GLU B 523 -70.152 -17.605 -35.927 1.00 35.46 C
ATOM 16235 CB GLU B 523 -70.703 -17.560 -37.379 1.00 35.51 C
ATOM 16238 CG GLU B 523 -70.535 -16.175 -38.061 1.00 36.11 C
ATOM 16241 CD GLU B 523 -70.854 -16.136 -39.572 1.00 36.72 C
ATOM 16242 OE1 GLU B 523 -71.848 -16.767 -40.013 1.00 37.20 O
ATOM 16243 OE2 GLU B 523 -70.101 -15.452 -40.314 1.00 35.53 O
ATOM 16244 C GLU B 523 -70.440 -18.943 -35.216 1.00 34.97 C
ATOM 16245 O GLU B 523 -71.557 -19.148 -34.765 1.00 35.02 O
ATOM 16247 N LEU B 524 -69.462 -19.846 -35.099 1.00 34.59 N
ATOM 16248 CA LEU B 524 -69.503 -20.832 -34.004 1.00 34.45 C
ATOM 16250 CB LEU B 524 -68.735 -22.136 -34.286 1.00 34.21 C
ATOM 16253 CG LEU B 524 -69.530 -23.434 -34.508 1.00 33.92 C
ATOM 16255 CD1 LEU B 524 -68.657 -24.627 -34.227 1.00 32.21 C
ATOM 16259 CD2 LEU B 524 -70.794 -23.520 -33.641 1.00 34.06 C
ATOM 16263 C LEU B 524 -68.901 -20.162 -32.791 1.00 34.38 C

ATOM 16264 O LEU B 524 -69.535 -20.067 -31.741 1.00 34.49 O
ATOM 16266 N THR B 525 -67.670 -19.688 -32.958 1.00 34.30 N
ATOM 16267 CA THR B 525 -66.913 -19.073 -31.874 1.00 34.23 C
ATOM 16269 CB THR B 525 -65.570 -18.524 -32.380 1.00 34.04 C
ATOM 16271 OG1 THR B 525 -64.894 -19.549 -33.112 1.00 33.83 O
ATOM 16273 CG2 THR B 525 -64.689 -18.087 -31.227 1.00 33.37 C
ATOM 16277 C THR B 525 -67.702 -17.960 -31.184 1.00 34.46 C
ATOM 16278 O THR B 525 -67.684 -17.858 -29.955 1.00 34.57 O
ATOM 16280 N ARG B 526 -68.401 -17.144 -31.969 1.00 34.54 N
ATOM 16281 CA ARG B 526 -69.200 -16.056 -31.418 1.00 34.60 C
ATOM 16283 CB ARG B 526 -69.571 -15.059 -32.513 1.00 35.04 C
ATOM 16286 CG ARG B 526 -70.256 -13.800 -32.013 1.00 37.13 C
ATOM 16289 CD ARG B 526 -70.143 -12.656 -33.026 1.00 39.87 C
ATOM 16292 NE ARG B 526 -70.353 -13.075 -34.420 1.00 42.28 N
ATOM 16294 CZ ARG B 526 -71.543 -13.292 -35.000 1.00 44.26 C
ATOM 16295 NH1 ARG B 526 -72.685 -13.159 -34.320 1.00 44.66 N
ATOM 16298 NH2 ARG B 526 -71.593 -13.658 -36.279 1.00 44.49 N
ATOM 16301 C ARG B 526 -70.448 -16.593 -30.735 1.00 33.91 C
ATOM 16302 O ARG B 526 -70.848 -16.074 -29.704 1.00 33.74 O
ATOM 16304 N LYS B 527 -71.048 -17.637 -31.306 1.00 33.39 N
ATOM 16305 CA LYS B 527 -72.240 -18.252 -30.722 1.00 33.15 C
ATOM 16307 CB LYS B 527 -72.837 -19.332 -31.639 1.00 33.42 C
ATOM 16310 CG LYS B 527 -73.898 -18.804 -32.609 1.00 34.55 C
ATOM 16313 CD LYS B 527 -74.643 -19.919 -33.358 1.00 35.43 C
ATOM 16316 CE LYS B 527 -75.230 -19.383 -34.667 1.00 36.11 C
ATOM 16319 NZ LYS B 527 -76.076 -20.372 -35.384 1.00 37.04 N
ATOM 16323 C LYS B 527 -71.925 -18.865 -29.378 1.00 32.36 C
ATOM 16324 O LYS B 527 -72.589 -18.584 -28.387 1.00 32.56 O
ATOM 16326 N ARG B 528 -70.909 -19.713 -29.358 1.00 31.53 N
ATOM 16327 CA ARG B 528 -70.502 -20.401 -28.138 1.00 30.77 C
ATOM 16329 CB ARG B 528 -69.283 -21.286 -28.414 1.00 30.55 C
ATOM 16332 CG ARG B 528 -69.624 -22.519 -29.252 1.00 29.48 C
ATOM 16335 CD ARG B 528 -68.418 -23.417 -29.493 1.00 28.05 C
ATOM 16338 NE ARG B 528 -68.811 -24.774 -29.880 1.00 26.55 N
ATOM 16340 CZ ARG B 528 -67.968 -25.719 -30.288 1.00 25.87 C
ATOM 16341 NH1 ARG B 528 -66.668 -25.472 -30.385 1.00 26.33 N
ATOM 16344 NH2 ARG B 528 -68.424 -26.920 -30.615 1.00 25.49 N
ATOM 16347 C ARG B 528 -70.225 -19.415 -27.004 1.00 30.42 C
ATOM 16348 O ARG B 528 -70.721 -19.582 -25.885 1.00 30.30 O
ATOM 16350 N VAL B 529 -69.455 -18.376 -27.307 1.00 29.96 N
ATOM 16351 CA VAL B 529 -69.194 -17.312 -26.342 1.00 29.47 C
ATOM 16353 CB VAL B 529 -68.261 -16.227 -26.932 1.00 29.40 C
ATOM 16355 CG1 VAL B 529 -68.269 -14.968 -26.081 1.00 29.18 C
ATOM 16359 CG2 VAL B 529 -66.845 -16.782 -27.062 1.00 28.90 C
ATOM 16363 C VAL B 529 -70.516 -16.723 -25.841 1.00 28.98 C
ATOM 16364 O VAL B 529 -70.759 -16.682 -24.641 1.00 28.97 O
ATOM 16366 N LEU B 530 -71.384 -16.308 -26.752 1.00 28.54 N
ATOM 16367 CA LEU B 530 -72.709 -15.824 -26.353 1.00 28.23 C
ATOM 16369 CB LEU B 530 -73.631 -15.604 -27.559 1.00 28.09 C
ATOM 16372 CG LEU B 530 -73.767 -14.150 -28.007 1.00 28.15 C
ATOM 16374 CD1 LEU B 530 -72.412 -13.570 -28.406 1.00 27.99 C
ATOM 16378 CD2 LEU B 530 -74.784 -14.034 -29.150 1.00 28.85 C
ATOM 16382 C LEU B 530 -73.389 -16.767 -25.367 1.00 27.88 C
ATOM 16383 O LEU B 530 -73.932 -16.319 -24.363 1.00 28.11 O
ATOM 16385 N SER B 531 -73.352 -18.066 -25.652 1.00 27.28 N
ATOM 16386 CA SER B 531 -74.081 -19.049 -24.849 1.00 26.68 C
ATOM 16388 CB SER B 531 -74.209 -20.363 -25.612 1.00 26.68 C
ATOM 16391 OG SER B 531 -72.970 -21.033 -25.681 1.00 26.67 O
ATOM 16393 C SER B 531 -73.410 -19.312 -23.514 1.00 26.20 C
ATOM 16394 O SER B 531 -74.076 -19.550 -22.511 1.00 25.86 O

ATOM 16396 N VAL B 532 -72.085 -19.281 -23.512 1.00 25.86 N
ATOM 16397 CA VAL B 532 -71.320 -19.562 -22.306 1.00 25.51 C
ATOM 16399 CB VAL B 532 -69.891 -20.055 -22.651 1.00 25.34 C
ATOM 16401 CG1 VAL B 532 -68.955 -19.932 -21.460 1.00 24.01 C
ATOM 16405 CG2 VAL B 532 -69.950 -21.484 -23.158 1.00 24.95 C
ATOM 16409 C VAL B 532 -71.271 -18.357 -21.373 1.00 25.52 C
ATOM 16410 O VAL B 532 -71.377 -18.523 -20.164 1.00 25.82 O
ATOM 16412 N ILE B 533 -71.137 -17.158 -21.935 1.00 25.39 N
ATOM 16413 CA ILE B 533 -70.875 -15.954 -21.151 1.00 25.48 C
ATOM 16415 CB ILE B 533 -69.666 -15.185 -21.732 1.00 25.30 C
ATOM 16417 CG1 ILE B 533 -68.375 -15.928 -21.451 1.00 24.91 C
ATOM 16420 CD1 ILE B 533 -68.118 -16.120 -19.989 1.00 25.00 C
ATOM 16424 CG2 ILE B 533 -69.553 -13.797 -21.130 1.00 25.81 C
ATOM 16428 C ILE B 533 -72.065 -14.983 -21.030 1.00 25.77 C
ATOM 16429 O ILE B 533 -72.537 -14.707 -19.928 1.00 25.77 O
ATOM 16431 N THR B 534 -72.541 -14.442 -22.142 1.00 25.98 N
ATOM 16432 CA THR B 534 -73.446 -13.295 -22.064 1.00 26.31 C
ATOM 16434 CB THR B 534 -73.094 -12.253 -23.143 1.00 26.21 C
ATOM 16436 OG1 THR B 534 -72.914 -12.909 -24.397 1.00 26.72 O
ATOM 16438 CG2 THR B 534 -71.795 -11.535 -22.781 1.00 25.97 C
ATOM 16442 C THR B 534 -74.961 -13.621 -22.064 1.00 26.50 C
ATOM 16443 O THR B 534 -75.713 -12.974 -21.344 1.00 26.67 O
ATOM 16445 N GLU B 535 -75.410 -14.616 -22.829 1.00 26.55 N
ATOM 16446 CA GLU B 535 -76.851 -14.892 -22.961 1.00 26.50 C
ATOM 16448 CB GLU B 535 -77.197 -15.197 -24.426 1.00 26.68 C
ATOM 16451 CG GLU B 535 -77.226 -13.936 -25.296 1.00 27.68 C
ATOM 16454 CD GLU B 535 -78.193 -14.014 -26.475 1.00 28.75 C
ATOM 16455 OE1 GLU B 535 -79.370 -13.588 -26.330 1.00 27.72 O
ATOM 16456 OE2 GLU B 535 -77.762 -14.492 -27.549 1.00 30.06 O
ATOM 16457 C GLU B 535 -77.355 -16.019 -22.056 1.00 26.19 C
ATOM 16458 O GLU B 535 -77.021 -17.171 -22.279 1.00 26.15 O
ATOM 16460 N PRO B 536 -78.186 -15.697 -21.047 1.00 26.05 N
ATOM 16461 CA PRO B 536 -78.692 -16.763 -20.196 1.00 26.05 C
ATOM 16463 CB PRO B 536 -79.495 -16.018 -19.118 1.00 25.87 C
ATOM 16466 CG PRO B 536 -79.140 -14.621 -19.239 1.00 25.88 C
ATOM 16469 CD PRO B 536 -78.760 -14.402 -20.660 1.00 26.21 C
ATOM 16472 C PRO B 536 -79.608 -17.717 -20.943 1.00 26.14 C
ATOM 16473 O PRO B 536 -80.173 -17.359 -21.973 1.00 25.99 O
ATOM 16474 N ILE B 537 -79.746 -18.924 -20.411 1.00 26.38 N
ATOM 16475 CA ILE B 537 -80.662 -19.905 -20.960 1.00 26.58 C
ATOM 16477 CB ILE B 537 -80.443 -21.292 -20.333 1.00 26.47 C
ATOM 16479 CG1 ILE B 537 -79.023 -21.789 -20.600 1.00 26.38 C
ATOM 16482 CD1 ILE B 537 -78.709 -23.102 -19.907 1.00 26.40 C
ATOM 16486 CG2 ILE B 537 -81.430 -22.300 -20.890 1.00 26.71 C
ATOM 16490 C ILE B 537 -82.072 -19.420 -20.657 1.00 26.93 C
ATOM 16491 O ILE B 537 -82.347 -18.965 -19.545 1.00 26.81 O
ATOM 16493 N LEU B 538 -82.963 -19.491 -21.641 1.00 27.36 N
ATOM 16494 CA LEU B 538 -84.309 -18.984 -21.439 1.00 27.68 C
ATOM 16496 CB LEU B 538 -85.181 -19.094 -22.698 1.00 27.75 C
ATOM 16499 CG LEU B 538 -84.782 -18.291 -23.949 1.00 27.47 C
ATOM 16501 CD1 LEU B 538 -85.992 -18.109 -24.844 1.00 27.11 C
ATOM 16505 CD2 LEU B 538 -84.164 -16.933 -23.621 1.00 26.99 C
ATOM 16509 C LEU B 538 -84.919 -19.752 -20.288 1.00 28.01 C
ATOM 16512 N PRO B 539 -85.645 -19.046 -19.421 1.00 28.69 N
ATOM 16513 CA PRO B 539 -86.028 -19.631 -18.152 1.00 29.05 C
ATOM 16515 CB PRO B 539 -86.640 -18.452 -17.397 1.00 29.08 C
ATOM 16518 CG PRO B 539 -87.144 -17.548 -18.447 1.00 28.86 C
ATOM 16521 CD PRO B 539 -86.298 -17.748 -19.660 1.00 28.62 C
ATOM 16524 C PRO B 539 -87.035 -20.767 -18.259 1.00 29.51 C
ATOM 16525 O PRO B 539 -87.665 -20.970 -19.297 1.00 29.23 O

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ATOM  16526 N   PHE B 540    -87.164 -21.500 -17.159  1.00 30.25           N
ATOM  16527 CA  PHE B 540    -88.089 -22.613 -17.070  1.00 30.56           C
ATOM  16529 CB  PHE B 540    -87.971 -23.297 -15.708  1.00 30.73           C
ATOM  16532 CG  PHE B 540    -88.848 -24.499 -15.567  1.00 30.49           C
ATOM  16533 CD1 PHE B 540    -89.910 -24.505 -14.683  1.00 30.32           C
ATOM  16535 CE1 PHE B 540    -90.718 -25.614 -14.568  1.00 30.59           C
ATOM  16537 CZ  PHE B 540    -90.475 -26.722 -15.346  1.00 30.55           C
ATOM  16539 CE2 PHE B 540    -89.420 -26.720 -16.234  1.00 30.68           C
ATOM  16541 CD2 PHE B 540    -88.619 -25.617 -16.342  1.00 30.43           C
ATOM  16543 C   PHE B 540    -89.507 -22.120 -17.257  1.00 30.76           C
ATOM  16544 O   PHE B 540    -89.967 -21.257 -16.508  1.00 30.59           O
ATOM  16546 N   GLU B 541    -90.184 -22.677 -18.259  1.00 31.13           N
ATOM  16547 CA  GLU B 541    -91.553 -22.289 -18.608  1.00 31.45           C
ATOM  16549 CB  GLU B 541    -91.525 -21.186 -19.680  1.00 31.60           C
ATOM  16552 CG  GLU B 541    -92.860 -20.454 -19.911  1.00 32.56           C
ATOM  16555 CD  GLU B 541    -93.773 -21.133 -20.935  1.00 33.64           C
ATOM  16556 OE1 GLU B 541    -93.261 -21.922 -21.771  1.00 35.06           O
ATOM  16557 OE2 GLU B 541    -95.002 -20.868 -20.901  1.00 32.44           O
ATOM  16558 C   GLU B 541    -92.326 -23.510 -19.105  1.00 31.31           C
ATOM  16559 O   GLU B 541    -92.860 -24.286 -18.310  1.00 31.30           O
ATOM  16562 MG   MG C  1    -42.844  11.427  13.309  1.00 46.29          MG
ATOM  16561 MG   MG C  2    -46.615 -18.454 -33.231  1.00 48.45          MG
ATOM  16563 O   HOH E  1    -50.507  -5.408  -4.491  1.00 17.42           O
ATOM  16566 O   HOH E  2    -64.748 -36.007 -11.725  1.00  2.00           O
ATOM  16569 O   HOH E  3    -40.643  -2.220 -34.996  1.00  2.00           O
ATOM  16572 O   HOH E  4    -36.090  -9.757 -37.074  1.00 17.20           O
ATOM  16575 O   HOH E  5    -46.117 -37.662 -22.916  1.00 17.03           O
ATOM  16578 O   HOH E  6    -49.541  35.476   6.921  1.00 14.03           O
ATOM  16581 O   HOH E  7    -32.288  27.572  16.443  1.00 13.16           O
ATOM  16584 O   HOH E  8    -50.706  10.207 -15.061  1.00 18.73           O
ATOM  16587 O   HOH E  9    -77.188  36.767  -9.218  1.00  8.05           O
ATOM  16590 O   HOH E 10    -90.260 -31.248 -21.071  1.00  2.00           O
ATOM  16593 O   HOH E 11    -70.920 -33.414  -3.884  1.00  9.35           O
ATOM  16596 O   HOH E 12    -37.761 -21.294  -9.249  1.00 25.78           O
ATOM  16599 O   HOH E 13    -76.050  23.855 -18.293  1.00  2.00           O
ATOM  16602 O   HOH E 14    -76.876 -19.575 -22.856  1.00 19.25           O
ATOM  16605 O   HOH E 15    -40.936  11.629 -24.832  1.00 22.29           O
ATOM  16608 O   HOH E 16    -85.551  34.832   3.260  1.00 25.14           O
ATOM  16611 O   HOH E 17    -56.825  31.771  -7.464  1.00 17.27           O
ATOM  16614 O   HOH E 18    -76.222  39.261   -.613  1.00 25.47           O
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[0478] Various modifications and variations of the described method and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention, which are obvious to those skilled in the relevant fields, are intended to be within the scope of the following claims.

Claims:

1. An isoprene synthase variant comprising an amino acid substitution of the amino acid residue at amino acid position 507 with a serine, wherein each amino acid position is numbered by correspondence with an amino acid position in the poplar isoprene synthase sequence as shown SEQ ID NO: 120.

2. The isoprene synthase variant of claim 1, wherein the variant comprises the amino acid substitution G507S.

3. The isoprene synthase variant of claim 1, wherein the variant further comprises one or more amino acid substitutions selected from the group consisting of V10M, F12S, T15A, E18G, V58I, V58F, L70Q, L70R, L70V, L70T, T71P, V79L, E89D, G94A, S119F, F120L, G127R, E175V, T212I, S257A, R262G, A266G, F280L, N297K, F305L, L319M, E323K, A328T, D342E, A359T, K366N, E368D, L374M, S396T, V418S, K438N, H440R, T442I, T442A, I449V, A469S, K500R, K505Q, S509N, F511Y, and N532K.

4. The isoprene synthase variant of claim 1, wherein the variant further comprises one or more amino acid substitutions selected from the group consisting of G127R/F511Y, L70Q/G94A/R262G/F305L, F12S/ T15A/E18G/N297K, S396T/T442I, V10M/E323K, F120L/A266G, K438N/K500R, V79L/S509N, E175V/S257A/E368D/A469S, T71P/L374M, F280L/H440R, E89D/H440R, V58F/A328T/N532K, S119F/D342E/I449V, and K366N/G507S.

5. An isoprene synthase variant comprising an amino acid substitution of the amino acid residue at amino acid position 70 with arginine, wherein each amino acid position is numbered by correspondence with an amino acid position in the poplar isoprene synthase sequence as shown in SEQ ID NO: 120.

6. The isoprene synthase variant of claim 5, wherein the variant comprises the amino acid substitution L70R.

7. The isoprene synthase variant of claim 5, wherein the variant further comprises one or more amino acid substitutions selected from the group consisting of V10M, F12S, T15A, E18G, V58I, V58F, T71P, V79L, E89D, G94A, S119F, F120L, G127R, E175V, T212I, S257A, R262G, A266G, F280L, N297K, F305L, L319M, E323K, A328T, D342E, A359T, K366N, E368D, L374M, S396T, V418S, K438N, H440R, T442I, T442A, I449V, A469S, K500R, K505Q, S509N, F511Y, and N532K.

8. The isoprene synthase variant of claim 5, wherein the variant further comprises one or more amino acid substitutions selected from the group consisting of G127R/F511Y, L70R/G94A/R262G/F305L, F12S/ T15A/E18G/N297K, S396T/T442I, V10M/E323K, F120L/A266G, K438N/K500R, V79L/S509N, E175V/S257A/E368D/A469S, T71P/L374M, F280L/H440R, E89D/H440R, V58F/A328T/N532K, S119F/D342E/I449V, and K366N/G507S.

9. The isoprene synthase variant of any one of claims 1-8, wherein the variant has a N-terminal truncation.

10. The isoprene synthase variant of any one of claims 1-8, wherein the isoprene synthase variant is a variant of a plant isoprene synthase, such as poplar, kudzu, aspen or English oak isoprene synthase, said isoprene synthase variant comprising an amino acid substitution of the glycine residue at position 507 with a serine residue.

11. The isoprene synthase variant of any one of claims 1-8, wherein the variant comprises an amino acid sequence having at least 40% sequence identity to a wild-type isoprene synthase and having a substitution of the glycine at position 507 with a serine residue.

12. The isoprene synthase variant of any one of claims 1-8, wherein the isoprene synthase variant is a variant of a plant isoprene synthase, such as poplar, kudzu, aspen or English oak isoprene synthase, said isoprene synthase variant comprising an amino acid substitution of the leucine residue at position 70 with an arginine residue.

13. The isoprene synthase variant of any one of claims 1-8, wherein the variant comprises an amino acid sequence having at least 40% sequence identity to a wild-type

isoprene synthase and having a substitution of the leucine residue at position 70 with an arginine residue.

14. A host cell comprising a heterologous polynucleotide sequence encoding an isoprene synthase variant of any one of claims 1-13 in operable combination with a promoter.

15. The host cell of claim 14 wherein the polynucleotide sequence is contained within a plasmid, or wherein the polynucleotide sequence is integrated into a chromosome of the host cell.

16. The host cell of claim 14 wherein the host cell further comprises a heterologous or native nucleic acid encoding an IDI polypeptide and/or a heterologous or native nucleic acid encoding a DXS polypeptide, optionally in combination with the native DXP pathway.

17. The host cell of claim 14 wherein the host cell comprises one vector encoding the isoprene synthase variant, the IDI polypeptide, and the DXS polypeptide.

18. The host cell of claim 14 wherein the host cell further comprises a heterologous or native nucleic acid encoding an MVA pathway polypeptide, wherein the MVA pathway polypeptide is optionally selected from the group consisting of *Saccharomyces cerevisiae* and *Enterococcus faecalis*.

19. The host cell of claim 14 wherein the host cell further comprises one or more nucleic acids encoding an MVA pathway polypeptide and a DXS polypeptide and wherein one vector encodes the isoprene synthase variant, the MVA pathway polypeptide, and the DXS polypeptide.

20. A method of producing a host cell capable of producing isoprene, the method comprising introducing a heterologous polynucleotide sequence encoding an isoprene synthase variant of any one of claims 1-13 into the host cell.

21. A method of producing isoprene, comprising

(a) culturing the host cells of any of claims 14-19 under suitable culture conditions for production of isoprene; and

(b) producing the isoprene.

22. The host cell of claim 14 wherein the host cell is selected from the group consisting of gram-positive bacterial cells, gram-negative bacterial cells, filamentous fungal cells, yeast cells, Saccharomyces sp. (S. cerevisiae), Escherichia sp. (E. coli), Panteoa sp. (P. citrea), Bacillus sp. (B. subtilis), Yarrowia sp. (Y. lipolytica), and Trichoderma (T. reesei).

23. The host cell of claim 14 wherein the host cell is cultured in a medium comprising a carbon source selected from the group consisting of glucose, glycerol, glycerine, dihydroxyacetone, yeast extract, biomass, molasses, sucrose, and oil.

24. The host cell of claim 14 wherein the host cell further comprises one or more nucleic acids encoding a DXS polypeptide, an IDI polypeptide, one or more of the rest of the DXP pathway polypeptides, and/or a MVA pathway polypeptide.

25. The method of claim 21 further comprising (c) recovering the isoprene.

26. A method of producing isoprene comprising:

(a) providing: (i) a host cell; and (ii) a nucleic acid encoding an isoprene synthase variant of any one of claims 1-13 in operable combination with a promoter;

(b) contacting the host cell with the nucleic acid to produce a transformed host cell; and

(c) culturing the transformed host cells under suitable culture conditions for production of isoprene.

27. The method of claim 26 further comprising (c) recovering the isoprene.