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HEADER      ISOMERASE                               02-JUL-92   1FKB
TITLE      ATOMIC STRUCTURE OF THE RAPAMYCIN HUMAN IMMUNOPHILIN FKBP-
TITLE      2 12 COMPLEX
COMPND     MOL_ID: 1;
COMPND     2 MOLECULE: FK506 BINDING PROTEIN;
COMPND     3 CHAIN: A;
COMPND     4 ENGINEERED: YES
SOURCE     MOL_ID: 1;
SOURCE     2 ORGANISM_SCIENTIFIC: HOMO SAPIENS;
SOURCE     3 ORGANISM_COMMON: HUMAN;
SOURCE     4 ORGANISM_TAXID: 9606
KEYWDS     ISOMERASE
EXPDTA     X-RAY DIFFRACTION
AUTHOR     G.D.VAN DUYN, R.F.STANDAERT, S.L.SCHREIBER, J.C.CLARDY
REVDAT     2 24-FEB-09 1FKB 1 VERSN
REVDAT     1 31-OCT-93 1FKB 0
JRNL       AUTH  G.D.VAN DUYN, R.F.STANDAERT, S.L.SCHREIBER, J.C.CLARDY
JRNL       TITL  ATOMIC STRUCTURE OF THE RAPAMYCIN HUMAN
JRNL       TITL  2 IMMUNOPHILIN FKBP-12 COMPLEX
JRNL       REF   J.AM.CHEM.SOC.                      V. 113  7433 1991
JRNL       REFN                      ISSN 0002-7863
REMARK     1
REMARK     2
REMARK     2 RESOLUTION.      1.70 ANGSTROMS.
REMARK     3
REMARK     3 REFINEMENT.
REMARK     3 PROGRAM          : X-PLOR
REMARK     3 AUTHORS           : BRUNGER
REMARK     3
REMARK     3 DATA USED IN REFINEMENT.
REMARK     3 RESOLUTION RANGE HIGH (ANGSTROMS) : 1.70
REMARK     3 RESOLUTION RANGE LOW  (ANGSTROMS) : 10.00
REMARK     3 DATA CUTOFF              (SIGMA(F)) : NULL
REMARK     3 DATA CUTOFF HIGH          (ABS(F)) : NULL
REMARK     3 DATA CUTOFF LOW           (ABS(F)) : NULL
REMARK     3 COMPLETENESS (WORKING+TEST) (%) : NULL
REMARK     3 NUMBER OF REFLECTIONS          : NULL
REMARK     3
REMARK     3 FIT TO DATA USED IN REFINEMENT.
REMARK     3 CROSS-VALIDATION METHOD          : NULL
REMARK     3 FREE R VALUE TEST SET SELECTION : NULL
REMARK     3 R VALUE              (WORKING SET) : 0.165
REMARK     3 FREE R VALUE                          : NULL
REMARK     3 FREE R VALUE TEST SET SIZE (%) : NULL
REMARK     3 FREE R VALUE TEST SET COUNT        : NULL
REMARK     3 ESTIMATED ERROR OF FREE R VALUE    : NULL
REMARK     3
REMARK     3 FIT IN THE HIGHEST RESOLUTION BIN.
REMARK     3 TOTAL NUMBER OF BINS USED          : NULL
REMARK     3 BIN RESOLUTION RANGE HIGH          (A) : NULL
REMARK     3 BIN RESOLUTION RANGE LOW           (A) : NULL
REMARK     3 BIN COMPLETENESS (WORKING+TEST) (%) : NULL
REMARK     3 REFLECTIONS IN BIN (WORKING SET)   : NULL

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REMARK 3 BIN R VALUE (WORKING SET) : NULL
REMARK 3 BIN FREE R VALUE : NULL
REMARK 3 BIN FREE R VALUE TEST SET SIZE (%) : NULL
REMARK 3 BIN FREE R VALUE TEST SET COUNT : NULL
REMARK 3 ESTIMATED ERROR OF BIN FREE R VALUE : NULL
REMARK 3
REMARK 3 NUMBER OF NON-HYDROGEN ATOMS USED IN REFINEMENT.
REMARK 3 PROTEIN ATOMS : 1028
REMARK 3 NUCLEIC ACID ATOMS : 0
REMARK 3 HETEROGEN ATOMS : 68
REMARK 3 SOLVENT ATOMS : 133
REMARK 3
REMARK 3 B VALUES.
REMARK 3 FROM WILSON PLOT (A**2) : NULL
REMARK 3 MEAN B VALUE (OVERALL, A**2) : NULL
REMARK 3 OVERALL ANISOTROPIC B VALUE.
REMARK 3 B11 (A**2) : NULL
REMARK 3 B22 (A**2) : NULL
REMARK 3 B33 (A**2) : NULL
REMARK 3 B12 (A**2) : NULL
REMARK 3 B13 (A**2) : NULL
REMARK 3 B23 (A**2) : NULL
REMARK 3
REMARK 3 ESTIMATED COORDINATE ERROR.
REMARK 3 ESD FROM LUZZATI PLOT (A) : NULL
REMARK 3 ESD FROM SIGMAA (A) : NULL
REMARK 3 LOW RESOLUTION CUTOFF (A) : NULL
REMARK 3
REMARK 3 CROSS-VALIDATED ESTIMATED COORDINATE ERROR.
REMARK 3 ESD FROM C-V LUZZATI PLOT (A) : NULL
REMARK 3 ESD FROM C-V SIGMAA (A) : NULL
REMARK 3
REMARK 3 RMS DEVIATIONS FROM IDEAL VALUES.
REMARK 3 BOND LENGTHS (A) : 0.010
REMARK 3 BOND ANGLES (DEGREES) : 2.80
REMARK 3 DIHEDRAL ANGLES (DEGREES) : NULL
REMARK 3 IMPROPER ANGLES (DEGREES) : NULL
REMARK 3
REMARK 3 ISOTROPIC THERMAL MODEL : NULL
REMARK 3
REMARK 3 ISOTROPIC THERMAL FACTOR RESTRAINTS. RMS SIGMA
REMARK 3 MAIN-CHAIN BOND (A**2) : NULL ; NULL
REMARK 3 MAIN-CHAIN ANGLE (A**2) : NULL ; NULL
REMARK 3 SIDE-CHAIN BOND (A**2) : NULL ; NULL
REMARK 3 SIDE-CHAIN ANGLE (A**2) : NULL ; NULL
REMARK 3
REMARK 3 NCS MODEL : NULL
REMARK 3
REMARK 3 NCS RESTRAINTS. RMS SIGMA/WEIGHT
REMARK 3 GROUP 1 POSITIONAL (A) : NULL ; NULL
REMARK 3 GROUP 1 B-FACTOR (A**2) : NULL ; NULL
REMARK 3
REMARK 3 PARAMETER FILE 1 : NULL
REMARK 3 TOPOLOGY FILE 1 : NULL

REMARK 3
REMARK 3 OTHER REFINEMENT REMARKS: NULL
REMARK 4
REMARK 4 1FKB COMPLIES WITH FORMAT V. 3.15, 01-DEC-08
REMARK 100
REMARK 100 THIS ENTRY HAS BEEN PROCESSED BY BNL.
REMARK 200
REMARK 200 EXPERIMENTAL DETAILS
REMARK 200 EXPERIMENT TYPE : X-RAY DIFFRACTION
REMARK 200 DATE OF DATA COLLECTION : NULL
REMARK 200 TEMPERATURE (KELVIN) : NULL
REMARK 200 PH : NULL
REMARK 200 NUMBER OF CRYSTALS USED : NULL
REMARK 200
REMARK 200 SYNCHROTRON (Y/N) : NULL
REMARK 200 RADIATION SOURCE : NULL
REMARK 200 BEAMLINE : NULL
REMARK 200 X-RAY GENERATOR MODEL : NULL
REMARK 200 MONOCHROMATIC OR LAUE (M/L) : NULL
REMARK 200 WAVELENGTH OR RANGE (A) : NULL
REMARK 200 MONOCHROMATOR : NULL
REMARK 200 OPTICS : NULL
REMARK 200
REMARK 200 DETECTOR TYPE : NULL
REMARK 200 DETECTOR MANUFACTURER : NULL
REMARK 200 INTENSITY-INTEGRATION SOFTWARE : NULL
REMARK 200 DATA SCALING SOFTWARE : NULL
REMARK 200
REMARK 200 NUMBER OF UNIQUE REFLECTIONS : NULL
REMARK 200 RESOLUTION RANGE HIGH (A) : NULL
REMARK 200 RESOLUTION RANGE LOW (A) : NULL
REMARK 200 REJECTION CRITERIA (SIGMA(I)) : NULL
REMARK 200
REMARK 200 OVERALL.
REMARK 200 COMPLETENESS FOR RANGE (%) : NULL
REMARK 200 DATA REDUNDANCY : NULL
REMARK 200 R MERGE (I) : NULL
REMARK 200 R SYM (I) : NULL
REMARK 200 <I/SIGMA(I)> FOR THE DATA SET : NULL
REMARK 200
REMARK 200 IN THE HIGHEST RESOLUTION SHELL.
REMARK 200 HIGHEST RESOLUTION SHELL, RANGE HIGH (A) : NULL
REMARK 200 HIGHEST RESOLUTION SHELL, RANGE LOW (A) : NULL
REMARK 200 COMPLETENESS FOR SHELL (%) : NULL
REMARK 200 DATA REDUNDANCY IN SHELL : NULL
REMARK 200 R MERGE FOR SHELL (I) : NULL
REMARK 200 R SYM FOR SHELL (I) : NULL
REMARK 200 <I/SIGMA(I)> FOR SHELL : NULL
REMARK 200
REMARK 200 DIFFRACTION PROTOCOL: NULL
REMARK 200 METHOD USED TO DETERMINE THE STRUCTURE: NULL
REMARK 200 SOFTWARE USED: MERLOT, X-PLOR
REMARK 200 STARTING MODEL: NULL
REMARK 200

REMARK 200 REMARK: NULL
REMARK 280
REMARK 280 CRYSTAL
REMARK 280 SOLVENT CONTENT, VS (%): 52.33
REMARK 280 MATTHEWS COEFFICIENT, VM (ANGSTROMS**3/DA): 2.58
REMARK 280
REMARK 280 CRYSTALLIZATION CONDITIONS: NULL
REMARK 290
REMARK 290 CRYSTALLOGRAPHIC SYMMETRY
REMARK 290 SYMMETRY OPERATORS FOR SPACE GROUP: P 21 21 21
REMARK 290
REMARK 290 SYMOP SYMMETRY
REMARK 290 NNNMMM OPERATOR
REMARK 290 1555 X,Y,Z
REMARK 290 2555 -X+1/2,-Y,Z+1/2
REMARK 290 3555 -X,Y+1/2,-Z+1/2
REMARK 290 4555 X+1/2,-Y+1/2,-Z
REMARK 290
REMARK 290 WHERE NNN -> OPERATOR NUMBER
REMARK 290 MMM -> TRANSLATION VECTOR
REMARK 290
REMARK 290 CRYSTALLOGRAPHIC SYMMETRY TRANSFORMATIONS
REMARK 290 THE FOLLOWING TRANSFORMATIONS OPERATE ON THE ATOM/HETATM
REMARK 290 RECORDS IN THIS ENTRY TO PRODUCE CRYSTALLOGRAPHICALLY
REMARK 290 RELATED MOLECULES.
REMARK 290 SMTRY1 1 1.000000 0.000000 0.000000 0.000000
REMARK 290 SMTRY2 1 0.000000 1.000000 0.000000 0.000000
REMARK 290 SMTRY3 1 0.000000 0.000000 1.000000 0.000000
REMARK 290 SMTRY1 2 -1.000000 0.000000 0.000000 22.71000
REMARK 290 SMTRY2 2 0.000000 -1.000000 0.000000 0.000000
REMARK 290 SMTRY3 2 0.000000 0.000000 1.000000 27.37000
REMARK 290 SMTRY1 3 -1.000000 0.000000 0.000000 0.000000
REMARK 290 SMTRY2 3 0.000000 1.000000 0.000000 24.58000
REMARK 290 SMTRY3 3 0.000000 0.000000 -1.000000 27.37000
REMARK 290 SMTRY1 4 1.000000 0.000000 0.000000 22.71000
REMARK 290 SMTRY2 4 0.000000 -1.000000 0.000000 24.58000
REMARK 290 SMTRY3 4 0.000000 0.000000 -1.000000 0.000000
REMARK 290
REMARK 290 REMARK: NULL
REMARK 300
REMARK 300 BIOMOLECULE: 1
REMARK 300 SEE REMARK 350 FOR THE AUTHOR PROVIDED AND/OR PROGRAM
REMARK 300 GENERATED ASSEMBLY INFORMATION FOR THE STRUCTURE IN
REMARK 300 THIS ENTRY. THE REMARK MAY ALSO PROVIDE INFORMATION ON
REMARK 300 BURIED SURFACE AREA.
REMARK 350
REMARK 350 COORDINATES FOR A COMPLETE MULTIMER REPRESENTING THE KNOWN
REMARK 350 BIOLOGICALLY SIGNIFICANT OLIGOMERIZATION STATE OF THE
REMARK 350 MOLECULE CAN BE GENERATED BY APPLYING BIOMT TRANSFORMATIONS
REMARK 350 GIVEN BELOW. BOTH NON-CRYSTALLOGRAPHIC AND
REMARK 350 CRYSTALLOGRAPHIC OPERATIONS ARE GIVEN.
REMARK 350
REMARK 350 BIOMOLECULE: 1
REMARK 350 AUTHOR DETERMINED BIOLOGICAL UNIT: MONOMERIC

REMARK 350 APPLY THE FOLLOWING TO CHAINS: A
REMARK 350 BIOMT1 1 1.000000 0.000000 0.000000 0.000000
REMARK 350 BIOMT2 1 0.000000 1.000000 0.000000 0.000000
REMARK 350 BIOMT3 1 0.000000 0.000000 1.000000 0.000000
REMARK 500
REMARK 500 GEOMETRY AND STEREOCHEMISTRY
REMARK 500 SUBTOPIC: COVALENT BOND LENGTHS
REMARK 500
REMARK 500 THE STEREOCHEMICAL PARAMETERS OF THE FOLLOWING RESIDUES
REMARK 500 HAVE VALUES WHICH DEVIATE FROM EXPECTED VALUES BY MORE
REMARK 500 THAN 6*RMSD (M=MODEL NUMBER; RES=RESIDUE NAME; C=CHAIN
REMARK 500 IDENTIFIER; SSEQ=SEQUENCE NUMBER; I=INSERTION CODE).
REMARK 500
REMARK 500 STANDARD TABLE:
REMARK 500 FORMAT: (10X,I3,1X,2(A3,1X,A1,I4,A1,1X,A4,3X),1X,F6.3)
REMARK 500
REMARK 500 EXPECTED VALUES PROTEIN: ENGH AND HUBER, 1999
REMARK 500 EXPECTED VALUES NUCLEIC ACID: CLOWNEY ET AL 1996
REMARK 500
REMARK 500 M RES CSSEQI ATM1 RES CSSEQI ATM2 DEVIATION
REMARK 500 HIS A 87 NE2 HIS A 87 CD2 -0.075
REMARK 500
REMARK 500 REMARK: NULL
REMARK 500
REMARK 500 GEOMETRY AND STEREOCHEMISTRY
REMARK 500 SUBTOPIC: COVALENT BOND ANGLES
REMARK 500
REMARK 500 THE STEREOCHEMICAL PARAMETERS OF THE FOLLOWING RESIDUES
REMARK 500 HAVE VALUES WHICH DEVIATE FROM EXPECTED VALUES BY MORE
REMARK 500 THAN 6*RMSD (M=MODEL NUMBER; RES=RESIDUE NAME; C=CHAIN
REMARK 500 IDENTIFIER; SSEQ=SEQUENCE NUMBER; I=INSERTION CODE).
REMARK 500
REMARK 500 STANDARD TABLE:
REMARK 500 FORMAT: (10X,I3,1X,A3,1X,A1,I4,A1,3(1X,A4,2X),12X,F5.1)
REMARK 500
REMARK 500 EXPECTED VALUES PROTEIN: ENGH AND HUBER, 1999
REMARK 500 EXPECTED VALUES NUCLEIC ACID: CLOWNEY ET AL 1996
REMARK 500
REMARK 500 M RES CSSEQI ATM1 ATM2 ATM3
REMARK 500 TRP A 59 CD1 - CG - CD2 ANGL. DEV. = 5.7 DEGREES
REMARK 500
REMARK 500 REMARK: NULL
REMARK 500
REMARK 500 GEOMETRY AND STEREOCHEMISTRY
REMARK 500 SUBTOPIC: TORSION ANGLES
REMARK 500
REMARK 500 TORSION ANGLES OUTSIDE THE EXPECTED RAMACHANDRAN REGIONS:
REMARK 500 (M=MODEL NUMBER; RES=RESIDUE NAME; C=CHAIN IDENTIFIER;
REMARK 500 SSEQ=SEQUENCE NUMBER; I=INSERTION CODE).
REMARK 500
REMARK 500 STANDARD TABLE:
REMARK 500 FORMAT: (10X,I3,1X,A3,1X,A1,I4,A1,4X,F7.2,3X,F7.2)
REMARK 500
REMARK 500 EXPECTED VALUES: GJ KLEYWEGT AND TA JONES (1996). PHI/PSI-

REMARK 500 CHOLOGY: RAMACHANDRAN REVISITED. STRUCTURE 4, 1395 - 1400

REMARK 500

REMARK 500	M RES	CSSEQI	PSI	PHI
REMARK 500	ARG A	13	-42.57	-135.16
REMARK 500	ASN A	43	13.54	60.00
REMARK 500	ALA A	81	-117.61	-131.57
REMARK 500	ILE A	90	-56.84	-125.78

REMARK 500

REMARK 500 REMARK: NULL

REMARK 525

REMARK 525 SOLVENT

REMARK 525

REMARK 525 THE SOLVENT MOLECULES HAVE CHAIN IDENTIFIERS THAT
 REMARK 525 INDICATE THE POLYMER CHAIN WITH WHICH THEY ARE MOST
 REMARK 525 CLOSELY ASSOCIATED. THE REMARK LISTS ALL THE SOLVENT
 REMARK 525 MOLECULES WHICH ARE MORE THAN 5A AWAY FROM THE
 REMARK 525 NEAREST POLYMER CHAIN (M = MODEL NUMBER;
 REMARK 525 RES=RESIDUE NAME; C=CHAIN IDENTIFIER; SSEQ=SEQUENCE
 REMARK 525 NUMBER; I=INSERTION CODE):

REMARK 525

REMARK 525 M RES CSSEQI

REMARK 525	HOH A	191	DISTANCE =	5.54	ANGSTROMS
REMARK 525	HOH A	219	DISTANCE =	6.83	ANGSTROMS
REMARK 525	HOH A	223	DISTANCE =	5.65	ANGSTROMS
REMARK 525	HOH A	233	DISTANCE =	5.82	ANGSTROMS

REMARK 800

REMARK 800 SITE

REMARK 800 SITE_IDENTIFIER: BP

REMARK 800 EVIDENCE_CODE: UNKNOWN

REMARK 800 SITE_DESCRIPTION: NULL

REMARK 800 SITE_IDENTIFIER: AC1

REMARK 800 EVIDENCE_CODE: SOFTWARE

REMARK 800 SITE_DESCRIPTION: BINDING SITE FOR RESIDUE RAP A 108

DBREF 1FKB A 1 107 UNP P62942 FKB1A_HUMAN 1 107

SEQRES 1 A 107 GLY VAL GLN VAL GLU THR ILE SER PRO GLY ASP GLY ARG

SEQRES 2 A 107 THR PHE PRO LYS ARG GLY GLN THR CYS VAL VAL HIS TYR

SEQRES 3 A 107 THR GLY MET LEU GLU ASP GLY LYS LYS PHE ASP SER SER

SEQRES 4 A 107 ARG ASP ARG ASN LYS PRO PHE LYS PHE MET LEU GLY LYS

SEQRES 5 A 107 GLN GLU VAL ILE ARG GLY TRP GLU GLU GLY VAL ALA GLN

SEQRES 6 A 107 MET SER VAL GLY GLN ARG ALA LYS LEU THR ILE SER PRO

SEQRES 7 A 107 ASP TYR ALA TYR GLY ALA THR GLY HIS PRO GLY ILE ILE

SEQRES 8 A 107 PRO PRO HIS ALA THR LEU VAL PHE ASP VAL GLU LEU LEU

SEQRES 9 A 107 LYS LEU GLU

HET RAP A 108 68

HETNAM RAP RAPAMYCIN IMMUNOSUPPRESSANT DRUG

FORMUL 2 RAP C51 H79 N 013

FORMUL 3 HOH *133(H2 O)

HELIX 1 A ARG A 57 VAL A 63 1

7

SHEET 1 A1 5 VAL A 2 SER A 8 0

SHEET 2 A1 5 ARG A 71 ILE A 76 -1 0 THR A 75 N GLN A 3

SHEET 3 A1 5 LEU A 97 LEU A 106 -1 N LEU A 97 0 ILE A 76

SHEET 4 A1 5 THR A 21 LEU A 30 -1 N VAL A 23 0 LYS A 105

SHEET 5 A1 5 LYS A 35 SER A 38 -1 N PHE A 36 0 GLY A 28

SHEET 1 A2 5 VAL A 2 SER A 8 0

SHEET	2	A2	5	ARG	A	71	ILE	A	76	-1	N	THR	A	75	0	GLN	A	3
SHEET	3	A2	5	LEU	A	97	LEU	A	106	-1	N	LEU	A	97	0	ILE	A	76
SHEET	4	A2	5	THR	A	21	LEU	A	30	-1	N	VAL	A	23	0	LYS	A	105
SHEET	5	A2	5	PHE	A	46	MET	A	49	-1	N	PHE	A	46	0	VAL	A	24
SITE	1	BP	6	TYR	A	26	PHE	A	46	VAL	A	55	ILE	A	56			
SITE	2	BP	6	TRP	A	59	PHE	A	99									
SITE	1	AC1	20	THR	A	6	TYR	A	26	THR	A	27	MET	A	29			
SITE	2	AC1	20	PHE	A	36	ASP	A	37	PHE	A	46	GLN	A	53			
SITE	3	AC1	20	GLU	A	54	VAL	A	55	ILE	A	56	TRP	A	59			
SITE	4	AC1	20	TYR	A	82	PHE	A	99	ASP	A	100	HOH	A	126			
SITE	5	AC1	20	HOH	A	127	HOH	A	145	HOH	A	189	HOH	A	197			
CRYST1	45.420	49.160	54.740	90.00	90.00	90.00	P	21	21	21							4	
ORIGX1	1.000000	0.000000	0.000000															
ORIGX2	0.000000	1.000000	0.000000															
ORIGX3	0.000000	0.000000	1.000000															
SCALE1	0.022017	0.000000	0.000000															
SCALE2	0.000000	0.020342	0.000000															
SCALE3	0.000000	0.000000	0.018268															
ATOM	1	N	GLY	A	1	15.915	-2.029	8.513	1.00	11.28								N
ATOM	2	CA	GLY	A	1	14.978	-1.665	7.474	1.00	14.35								C
ATOM	3	C	GLY	A	1	13.558	-1.877	7.981	1.00	15.91								C
ATOM	4	O	GLY	A	1	13.306	-1.692	9.187	1.00	16.11								O
ATOM	5	H1	GLY	A	1	15.621	-1.498	9.359	1.00	13.77								H
ATOM	6	H2	GLY	A	1	15.806	-3.035	8.734	1.00	13.77								H
ATOM	7	H3	GLY	A	1	16.887	-1.796	8.245	1.00	10.73								H
ATOM	8	N	VAL	A	2	12.677	-2.258	7.058	1.00	11.40								N
ATOM	9	CA	VAL	A	2	11.288	-2.572	7.337	1.00	7.65								C
ATOM	10	C	VAL	A	2	10.997	-3.900	6.634	1.00	18.43								C
ATOM	11	O	VAL	A	2	11.349	-4.131	5.471	1.00	15.55								O
ATOM	12	CB	VAL	A	2	10.348	-1.404	6.904	1.00	14.21								C
ATOM	13	CG1	VAL	A	2	10.467	-1.021	5.431	1.00	16.55								C
ATOM	14	CG2	VAL	A	2	8.887	-1.700	7.235	1.00	15.47								C
ATOM	15	H	VAL	A	2	12.943	-2.422	6.127	1.00	9.02								H
ATOM	16	N	GLN	A	3	10.439	-4.825	7.387	1.00	9.33								N
ATOM	17	CA	GLN	A	3	10.028	-6.109	6.837	1.00	10.30								C
ATOM	18	C	GLN	A	3	8.506	-6.047	6.705	1.00	10.81								C
ATOM	19	O	GLN	A	3	7.858	-5.607	7.648	1.00	11.33								O
ATOM	20	CB	GLN	A	3	10.455	-7.166	7.821	1.00	13.36								C
ATOM	21	CG	GLN	A	3	10.169	-8.570	7.309	1.00	55.99								C
ATOM	22	CD	GLN	A	3	10.506	-9.683	8.292	1.00	68.84								C
ATOM	23	OE1	GLN	A	3	11.212	-9.503	9.275	1.00	72.87								O
ATOM	24	NE2	GLN	A	3	10.044	-10.909	8.101	1.00	57.49								N
ATOM	25	H	GLN	A	3	10.217	-4.614	8.319	1.00	9.00								H
ATOM	26	HE21	GLN	A	3	10.307	-11.549	8.795	1.00	36.45								H
ATOM	27	HE22	GLN	A	3	9.485	-11.129	7.332	1.00	36.45								H
ATOM	28	N	VAL	A	4	7.878	-6.429	5.593	1.00	14.73								N
ATOM	29	CA	VAL	A	4	6.430	-6.364	5.422	1.00	15.13								C
ATOM	30	C	VAL	A	4	5.972	-7.817	5.319	1.00	14.25								C
ATOM	31	O	VAL	A	4	6.386	-8.538	4.411	1.00	16.89								O
ATOM	32	CB	VAL	A	4	6.069	-5.557	4.135	1.00	11.91								C
ATOM	33	CG1	VAL	A	4	4.574	-5.482	3.905	1.00	13.25								C
ATOM	34	CG2	VAL	A	4	6.644	-4.148	4.195	1.00	9.78								C
ATOM	35	H	VAL	A	4	8.374	-6.815	4.853	1.00	13.59								H
ATOM	36	N	GLU	A	5	5.174	-8.303	6.249	1.00	8.60								N

ATOM	37	CA	GLU	A	5	4.637	-9.657	6.191	1.00	9.41	C
ATOM	38	C	GLU	A	5	3.122	-9.577	6.038	1.00	7.91	C
ATOM	39	O	GLU	A	5	2.492	-8.892	6.835	1.00	14.55	O
ATOM	40	CB	GLU	A	5	4.958	-10.352	7.479	1.00	9.26	C
ATOM	41	CG	GLU	A	5	6.429	-10.624	7.556	1.00	7.92	C
ATOM	42	CD	GLU	A	5	6.796	-11.234	8.891	1.00	28.31	C
ATOM	43	OE1	GLU	A	5	7.086	-10.482	9.814	1.00	26.39	O
ATOM	44	OE2	GLU	A	5	6.797	-12.460	9.003	1.00	39.66	O
ATOM	45	H	GLU	A	5	4.883	-7.720	6.981	1.00	5.83	H
ATOM	46	N	THR	A	6	2.483	-10.198	5.049	1.00	11.40	N
ATOM	47	CA	THR	A	6	1.050	-10.065	4.801	1.00	9.56	C
ATOM	48	C	THR	A	6	0.135	-10.732	5.817	1.00	11.24	C
ATOM	49	O	THR	A	6	0.355	-11.888	6.159	1.00	13.61	O
ATOM	50	CB	THR	A	6	0.786	-10.568	3.404	1.00	14.22	C
ATOM	51	OG1	THR	A	6	1.470	-9.646	2.578	1.00	18.55	O
ATOM	52	CG2	THR	A	6	-0.674	-10.584	3.000	1.00	18.19	C
ATOM	53	H	THR	A	6	2.987	-10.761	4.441	1.00	7.55	H
ATOM	54	HG1	THR	A	6	1.637	-10.053	1.722	1.00	14.49	H
ATOM	55	N	ILE	A	7	-0.850	-10.012	6.359	1.00	10.07	N
ATOM	56	CA	ILE	A	7	-1.896	-10.635	7.149	1.00	9.55	C
ATOM	57	C	ILE	A	7	-3.054	-10.999	6.213	1.00	14.31	C
ATOM	58	O	ILE	A	7	-3.600	-12.093	6.327	1.00	15.11	O
ATOM	59	CB	ILE	A	7	-2.288	-9.703	8.324	1.00	15.34	C
ATOM	60	CG1	ILE	A	7	-1.088	-9.498	9.248	1.00	8.63	C
ATOM	61	CG2	ILE	A	7	-3.508	-10.227	9.092	1.00	4.62	C
ATOM	62	CD1	ILE	A	7	-1.211	-8.308	10.228	1.00	11.85	C
ATOM	63	H	ILE	A	7	-0.835	-9.044	6.238	1.00	5.00	H
ATOM	64	N	SER	A	8	-3.465	-10.137	5.280	1.00	16.77	N
ATOM	65	CA	SER	A	8	-4.521	-10.403	4.303	1.00	22.81	C
ATOM	66	C	SER	A	8	-4.096	-9.684	3.023	1.00	16.94	C
ATOM	67	O	SER	A	8	-3.584	-8.557	3.080	1.00	11.53	O
ATOM	68	CB	SER	A	8	-5.868	-9.853	4.740	1.00	16.46	C
ATOM	69	OG	SER	A	8	-6.033	-9.995	6.140	1.00	42.67	O
ATOM	70	H	SER	A	8	-3.009	-9.270	5.208	1.00	10.34	H
ATOM	71	HG	SER	A	8	-5.936	-9.106	6.499	1.00	39.81	H
ATOM	72	N	PRO	A	9	-4.201	-10.303	1.861	1.00	14.85	N
ATOM	73	CA	PRO	A	9	-3.773	-9.717	0.615	1.00	16.28	C
ATOM	74	C	PRO	A	9	-4.625	-8.548	0.137	1.00	15.80	C
ATOM	75	O	PRO	A	9	-5.822	-8.466	0.374	1.00	16.79	O
ATOM	76	CB	PRO	A	9	-3.781	-10.908	-0.331	1.00	17.69	C
ATOM	77	CG	PRO	A	9	-4.908	-11.757	0.188	1.00	20.98	C
ATOM	78	CD	PRO	A	9	-4.668	-11.683	1.687	1.00	13.76	C
ATOM	79	N	GLY	A	10	-3.971	-7.584	-0.490	1.00	11.05	N
ATOM	80	CA	GLY	A	10	-4.670	-6.518	-1.160	1.00	12.34	C
ATOM	81	C	GLY	A	10	-4.996	-6.956	-2.571	1.00	16.73	C
ATOM	82	O	GLY	A	10	-4.919	-8.134	-2.922	1.00	24.91	O
ATOM	83	H	GLY	A	10	-3.004	-7.640	-0.556	1.00	8.18	H
ATOM	84	N	ASP	A	11	-5.303	-6.001	-3.430	1.00	14.36	N
ATOM	85	CA	ASP	A	11	-5.633	-6.357	-4.802	1.00	28.85	C
ATOM	86	C	ASP	A	11	-4.434	-6.674	-5.692	1.00	27.10	C
ATOM	87	O	ASP	A	11	-4.615	-7.013	-6.860	1.00	20.65	O
ATOM	88	CB	ASP	A	11	-6.515	-5.278	-5.442	1.00	23.16	C
ATOM	89	CG	ASP	A	11	-5.875	-3.943	-5.797	1.00	17.74	C
ATOM	90	OD1	ASP	A	11	-4.693	-3.728	-5.552	1.00	15.46	O

ATOM	91	OD2	ASP	A	11	-6.586	-3.101	-6.329	1.00	19.20	O
ATOM	92	H	ASP	A	11	-5.412	-5.082	-3.102	1.00	14.04	H
ATOM	93	N	GLY	A	12	-3.211	-6.420	-5.217	1.00	15.02	N
ATOM	94	CA	GLY	A	12	-1.994	-6.703	-5.971	1.00	19.67	C
ATOM	95	C	GLY	A	12	-1.805	-5.836	-7.210	1.00	16.55	C
ATOM	96	O	GLY	A	12	-0.980	-6.150	-8.056	1.00	15.65	O
ATOM	97	H	GLY	A	12	-3.125	-6.046	-4.317	1.00	14.44	H
ATOM	98	N	ARG	A	13	-2.527	-4.729	-7.349	1.00	11.39	N
ATOM	99	CA	ARG	A	13	-2.502	-3.910	-8.541	1.00	11.95	C
ATOM	100	C	ARG	A	13	-2.408	-2.438	-8.220	1.00	10.82	C
ATOM	101	O	ARG	A	13	-1.685	-1.701	-8.893	1.00	19.47	O
ATOM	102	CB	ARG	A	13	-3.768	-4.076	-9.383	1.00	25.46	C
ATOM	103	CG	ARG	A	13	-3.946	-5.441	-10.001	1.00	42.88	C
ATOM	104	CD	ARG	A	13	-4.558	-5.218	-11.364	1.00	67.90	C
ATOM	105	NE	ARG	A	13	-4.520	-6.435	-12.166	1.00	80.80	N
ATOM	106	CZ	ARG	A	13	-3.611	-6.646	-13.138	1.00	94.75	C
ATOM	107	NH1	ARG	A	13	-2.600	-5.798	-13.398	1.00	98.27	N
ATOM	108	NH2	ARG	A	13	-3.707	-7.756	-13.879	1.00	90.34	N
ATOM	109	H	ARG	A	13	-3.092	-4.480	-6.604	1.00	10.19	H
ATOM	110	HE	ARG	A	13	-5.181	-7.136	-11.990	1.00	50.00	H
ATOM	111	HH11	ARG	A	13	-2.481	-4.953	-12.875	1.00	50.00	H
ATOM	112	HH12	ARG	A	13	-1.963	-6.006	-14.144	1.00	50.00	H
ATOM	113	HH21	ARG	A	13	-4.443	-8.411	-13.713	1.00	50.00	H
ATOM	114	HH22	ARG	A	13	-3.044	-7.923	-14.613	1.00	50.00	H
ATOM	115	N	THR	A	14	-3.160	-1.969	-7.223	1.00	16.37	N
ATOM	116	CA	THR	A	14	-3.242	-0.567	-6.846	1.00	20.68	C
ATOM	117	C	THR	A	14	-2.342	-0.232	-5.671	1.00	14.00	C
ATOM	118	O	THR	A	14	-2.668	-0.503	-4.509	1.00	12.73	O
ATOM	119	CB	THR	A	14	-4.728	-0.226	-6.500	1.00	17.19	C
ATOM	120	OG1	THR	A	14	-5.539	-0.798	-7.518	1.00	20.12	O
ATOM	121	CG2	THR	A	14	-4.956	1.250	-6.453	1.00	14.89	C
ATOM	122	H	THR	A	14	-3.858	-2.541	-6.881	1.00	8.83	H
ATOM	123	HG1	THR	A	14	-6.394	-0.358	-7.606	1.00	17.77	H
ATOM	124	N	PHE	A	15	-1.234	0.407	-5.994	1.00	12.81	N
ATOM	125	CA	PHE	A	15	-0.211	0.731	-5.024	1.00	7.88	C
ATOM	126	C	PHE	A	15	-0.157	2.235	-4.870	1.00	18.25	C
ATOM	127	O	PHE	A	15	-0.427	2.887	-5.885	1.00	22.03	O
ATOM	128	CB	PHE	A	15	1.156	0.231	-5.529	1.00	11.94	C
ATOM	129	CG	PHE	A	15	1.295	-1.284	-5.530	1.00	11.45	C
ATOM	130	CD1	PHE	A	15	0.868	-2.038	-6.622	1.00	9.87	C
ATOM	131	CD2	PHE	A	15	1.850	-1.917	-4.432	1.00	11.12	C
ATOM	132	CE1	PHE	A	15	0.975	-3.411	-6.611	1.00	7.22	C
ATOM	133	CE2	PHE	A	15	1.925	-3.302	-4.421	1.00	10.85	C
ATOM	134	CZ	PHE	A	15	1.482	-4.046	-5.501	1.00	10.98	C
ATOM	135	H	PHE	A	15	-1.154	0.805	-6.884	1.00	12.28	H
ATOM	136	N	PRO	A	16	0.175	2.836	-3.714	1.00	13.24	N
ATOM	137	CA	PRO	A	16	0.267	4.278	-3.551	1.00	16.94	C
ATOM	138	C	PRO	A	16	1.341	4.869	-4.454	1.00	27.68	C
ATOM	139	O	PRO	A	16	2.370	4.252	-4.765	1.00	18.36	O
ATOM	140	CB	PRO	A	16	0.646	4.454	-2.094	1.00	11.36	C
ATOM	141	CG	PRO	A	16	0.354	3.156	-1.405	1.00	13.31	C
ATOM	142	CD	PRO	A	16	0.627	2.156	-2.501	1.00	17.07	C
ATOM	143	N	LYS	A	17	1.062	6.076	-4.919	1.00	17.83	N
ATOM	144	CA	LYS	A	17	2.014	6.903	-5.619	1.00	24.33	C

ATOM	145	C	LYS	A	17	2.442	7.991	-4.619	1.00	27.42	C
ATOM	146	O	LYS	A	17	1.749	8.343	-3.654	1.00	25.81	O
ATOM	147	CB	LYS	A	17	1.294	7.482	-6.842	1.00	20.44	C
ATOM	148	CG	LYS	A	17	2.171	8.205	-7.839	1.00	73.40	C
ATOM	149	CD	LYS	A	17	1.368	8.988	-8.878	1.00	83.60	C
ATOM	150	CE	LYS	A	17	2.349	9.860	-9.675	1.00	79.68	C
ATOM	151	NZ	LYS	A	17	1.746	10.467	-10.851	1.00	88.66	N
ATOM	152	H	LYS	A	17	0.162	6.437	-4.763	1.00	17.77	H
ATOM	153	HZ1	LYS	A	17	1.340	9.722	-11.454	1.00	50.00	H
ATOM	154	HZ2	LYS	A	17	1.000	11.132	-10.568	1.00	50.00	H
ATOM	155	HZ3	LYS	A	17	2.478	10.970	-11.394	1.00	50.00	H
ATOM	156	N	ARG	A	18	3.659	8.501	-4.815	1.00	23.19	N
ATOM	157	CA	ARG	A	18	4.168	9.657	-4.102	1.00	25.30	C
ATOM	158	C	ARG	A	18	3.181	10.797	-4.283	1.00	20.31	C
ATOM	159	O	ARG	A	18	2.682	11.050	-5.389	1.00	26.79	O
ATOM	160	CB	ARG	A	18	5.484	10.053	-4.758	1.00	36.42	C
ATOM	161	CG	ARG	A	18	6.671	10.236	-3.828	1.00	61.98	C
ATOM	162	CD	ARG	A	18	7.174	8.920	-3.251	1.00	70.36	C
ATOM	163	NE	ARG	A	18	7.663	7.999	-4.274	1.00	91.69	N
ATOM	164	CZ	ARG	A	18	7.783	6.682	-4.033	1.00	99.06	C
ATOM	165	NH1	ARG	A	18	7.391	6.136	-2.874	1.00	87.08	N
ATOM	166	NH2	ARG	A	18	8.287	5.879	-4.974	1.00	91.74	N
ATOM	167	H	ARG	A	18	4.208	8.111	-5.521	1.00	22.37	H
ATOM	168	HE	ARG	A	18	7.895	8.344	-5.160	1.00	50.00	H
ATOM	169	HH11	ARG	A	18	6.990	6.706	-2.155	1.00	45.39	H
ATOM	170	HH12	ARG	A	18	7.505	5.155	-2.715	1.00	45.39	H
ATOM	171	HH21	ARG	A	18	8.577	6.257	-5.851	1.00	50.00	H
ATOM	172	HH22	ARG	A	18	8.390	4.902	-4.783	1.00	50.00	H
ATOM	173	N	GLY	A	19	2.864	11.439	-3.175	1.00	28.49	N
ATOM	174	CA	GLY	A	19	1.926	12.537	-3.206	1.00	22.19	C
ATOM	175	C	GLY	A	19	0.489	12.085	-2.986	1.00	24.43	C
ATOM	176	O	GLY	A	19	-0.358	12.934	-2.706	1.00	27.40	O
ATOM	177	H	GLY	A	19	3.239	11.160	-2.322	1.00	29.31	H
ATOM	178	N	GLN	A	20	0.150	10.799	-3.069	1.00	20.21	N
ATOM	179	CA	GLN	A	20	-1.208	10.390	-2.756	1.00	22.26	C
ATOM	180	C	GLN	A	20	-1.385	10.310	-1.259	1.00	19.19	C
ATOM	181	O	GLN	A	20	-0.426	10.014	-0.529	1.00	24.35	O
ATOM	182	CB	GLN	A	20	-1.546	9.019	-3.285	1.00	16.69	C
ATOM	183	CG	GLN	A	20	-1.718	9.040	-4.765	1.00	32.77	C
ATOM	184	CD	GLN	A	20	-2.345	7.753	-5.235	1.00	32.00	C
ATOM	185	OE1	GLN	A	20	-1.695	6.716	-5.369	1.00	30.66	O
ATOM	186	NE2	GLN	A	20	-3.645	7.793	-5.467	1.00	35.54	N
ATOM	187	H	GLN	A	20	0.818	10.113	-3.267	1.00	25.04	H
ATOM	188	HE21	GLN	A	20	-4.074	7.000	-5.838	1.00	33.30	H
ATOM	189	HE22	GLN	A	20	-4.128	8.625	-5.251	1.00	33.30	H
ATOM	190	N	THR	A	21	-2.626	10.531	-0.844	1.00	12.61	N
ATOM	191	CA	THR	A	21	-3.061	10.316	0.523	1.00	14.09	C
ATOM	192	C	THR	A	21	-3.416	8.850	0.708	1.00	12.40	C
ATOM	193	O	THR	A	21	-4.296	8.296	0.039	1.00	17.06	O
ATOM	194	CB	THR	A	21	-4.299	11.210	0.824	1.00	17.25	C
ATOM	195	OG1	THR	A	21	-3.788	12.529	0.655	1.00	23.17	O
ATOM	196	CG2	THR	A	21	-4.896	11.052	2.231	1.00	11.48	C
ATOM	197	H	THR	A	21	-3.316	10.769	-1.506	1.00	10.21	H
ATOM	198	HG1	THR	A	21	-3.998	12.779	-0.257	1.00	21.91	H

ATOM	199	N	CYS	A	22	-2.727	8.204	1.629	1.00	13.20	N
ATOM	200	CA	CYS	A	22	-3.072	6.841	2.021	1.00	13.95	C
ATOM	201	C	CYS	A	22	-3.990	6.926	3.232	1.00	13.08	C
ATOM	202	O	CYS	A	22	-3.723	7.718	4.170	1.00	15.66	O
ATOM	203	CB	CYS	A	22	-1.800	6.115	2.412	1.00	10.31	C
ATOM	204	SG	CYS	A	22	-0.631	6.186	1.042	1.00	17.72	S
ATOM	205	H	CYS	A	22	-1.985	8.661	2.079	1.00	13.00	H
ATOM	206	N	VAL	A	23	-5.066	6.127	3.208	1.00	11.74	N
ATOM	207	CA	VAL	A	23	-6.009	6.048	4.324	1.00	8.67	C
ATOM	208	C	VAL	A	23	-5.829	4.665	4.944	1.00	9.34	C
ATOM	209	O	VAL	A	23	-6.007	3.652	4.263	1.00	13.93	O
ATOM	210	CB	VAL	A	23	-7.470	6.229	3.853	1.00	12.47	C
ATOM	211	CG1	VAL	A	23	-8.395	6.418	5.051	1.00	14.36	C
ATOM	212	CG2	VAL	A	23	-7.576	7.428	2.952	1.00	13.59	C
ATOM	213	H	VAL	A	23	-5.224	5.548	2.433	1.00	9.07	H
ATOM	214	N	VAL	A	24	-5.428	4.593	6.217	1.00	9.59	N
ATOM	215	CA	VAL	A	24	-5.040	3.333	6.843	1.00	9.14	C
ATOM	216	C	VAL	A	24	-5.674	3.153	8.211	1.00	10.95	C
ATOM	217	O	VAL	A	24	-6.064	4.134	8.852	1.00	11.27	O
ATOM	218	CB	VAL	A	24	-3.513	3.204	7.057	1.00	8.47	C
ATOM	219	CG1	VAL	A	24	-2.770	3.323	5.732	1.00	9.52	C
ATOM	220	CG2	VAL	A	24	-2.957	4.172	8.102	1.00	8.56	C
ATOM	221	H	VAL	A	24	-5.407	5.406	6.771	1.00	8.97	H
ATOM	222	N	HIS	A	25	-5.791	1.917	8.686	1.00	9.36	N
ATOM	223	CA	HIS	A	25	-5.944	1.680	10.114	1.00	9.60	C
ATOM	224	C	HIS	A	25	-4.667	1.066	10.631	1.00	5.10	C
ATOM	225	O	HIS	A	25	-4.039	0.296	9.902	1.00	9.82	O
ATOM	226	CB	HIS	A	25	-7.097	0.749	10.449	1.00	10.47	C
ATOM	227	CG	HIS	A	25	-8.341	1.527	10.841	1.00	16.45	C
ATOM	228	ND1	HIS	A	25	-8.305	2.502	11.741	1.00	14.62	N
ATOM	229	CD2	HIS	A	25	-9.594	1.265	10.371	1.00	17.08	C
ATOM	230	CE1	HIS	A	25	-9.570	2.856	11.861	1.00	20.93	C
ATOM	231	NE2	HIS	A	25	-10.318	2.113	11.060	1.00	20.18	N
ATOM	232	H	HIS	A	25	-5.652	1.157	8.076	1.00	6.37	H
ATOM	233	HE2	HIS	A	25	-11.295	2.175	11.006	1.00	20.07	H
ATOM	234	N	TYR	A	26	-4.255	1.400	11.855	1.00	8.15	N
ATOM	235	CA	TYR	A	26	-3.055	0.828	12.426	1.00	5.33	C
ATOM	236	C	TYR	A	26	-3.187	0.576	13.922	1.00	10.06	C
ATOM	237	O	TYR	A	26	-4.009	1.188	14.609	1.00	9.71	O
ATOM	238	CB	TYR	A	26	-1.812	1.698	12.127	1.00	6.71	C
ATOM	239	CG	TYR	A	26	-1.729	2.985	12.947	1.00	6.72	C
ATOM	240	CD1	TYR	A	26	-2.330	4.116	12.436	1.00	14.55	C
ATOM	241	CD2	TYR	A	26	-1.089	3.009	14.183	1.00	5.79	C
ATOM	242	CE1	TYR	A	26	-2.307	5.281	13.168	1.00	8.62	C
ATOM	243	CE2	TYR	A	26	-1.064	4.170	14.924	1.00	13.96	C
ATOM	244	CZ	TYR	A	26	-1.688	5.298	14.401	1.00	13.12	C
ATOM	245	OH	TYR	A	26	-1.706	6.470	15.111	1.00	11.19	O
ATOM	246	H	TYR	A	26	-4.791	2.005	12.411	1.00	7.26	H
ATOM	247	HH	TYR	A	26	-2.285	7.105	14.682	1.00	10.85	H
ATOM	248	N	THR	A	27	-2.375	-0.377	14.389	1.00	12.99	N
ATOM	249	CA	THR	A	27	-2.069	-0.647	15.794	1.00	7.71	C
ATOM	250	C	THR	A	27	-0.546	-0.688	15.842	1.00	11.95	C
ATOM	251	O	THR	A	27	0.081	-1.324	14.988	1.00	11.60	O
ATOM	252	CB	THR	A	27	-2.668	-2.003	16.259	1.00	11.34	C

ATOM	253	OG1	THR	A	27	-4.065	-1.808	16.133	1.00	14.19	O
ATOM	254	CG2	THR	A	27	-2.234	-2.460	17.644	1.00	11.50	C
ATOM	255	H	THR	A	27	-1.885	-0.911	13.721	1.00	10.32	H
ATOM	256	HG1	THR	A	27	-4.242	-1.481	15.247	1.00	9.41	H
ATOM	257	N	GLY	A	28	0.060	0.004	16.796	1.00	8.64	N
ATOM	258	CA	GLY	A	28	1.493	-0.004	16.981	1.00	9.01	C
ATOM	259	C	GLY	A	28	1.850	-0.583	18.345	1.00	15.91	C
ATOM	260	O	GLY	A	28	1.187	-0.318	19.344	1.00	10.99	O
ATOM	261	H	GLY	A	28	-0.476	0.470	17.464	1.00	7.88	H
ATOM	262	N	MET	A	29	2.929	-1.348	18.403	1.00	12.93	N
ATOM	263	CA	MET	A	29	3.462	-1.861	19.655	1.00	11.46	C
ATOM	264	C	MET	A	29	4.979	-1.943	19.563	1.00	8.02	C
ATOM	265	O	MET	A	29	5.574	-1.915	18.473	1.00	12.78	O
ATOM	266	CB	MET	A	29	2.849	-3.235	20.000	1.00	12.38	C
ATOM	267	CG	MET	A	29	3.291	-4.355	19.114	1.00	17.40	C
ATOM	268	SD	MET	A	29	2.503	-5.953	19.399	1.00	21.98	S
ATOM	269	CE	MET	A	29	3.979	-6.652	20.063	1.00	33.26	C
ATOM	270	H	MET	A	29	3.419	-1.578	17.577	1.00	13.04	H
ATOM	271	N	LEU	A	30	5.617	-1.935	20.729	1.00	16.97	N
ATOM	272	CA	LEU	A	30	7.060	-2.152	20.818	1.00	14.92	C
ATOM	273	C	LEU	A	30	7.310	-3.646	20.595	1.00	20.11	C
ATOM	274	O	LEU	A	30	6.464	-4.433	21.034	1.00	15.50	O
ATOM	275	CB	LEU	A	30	7.517	-1.726	22.205	1.00	16.10	C
ATOM	276	CG	LEU	A	30	7.312	-0.272	22.669	1.00	20.40	C
ATOM	277	CD1	LEU	A	30	7.744	-0.157	24.122	1.00	36.95	C
ATOM	278	CD2	LEU	A	30	8.157	0.663	21.839	1.00	22.00	C
ATOM	279	H	LEU	A	30	5.081	-1.867	21.547	1.00	16.28	H
ATOM	280	N	GLU	A	31	8.384	-4.066	19.904	1.00	19.84	N
ATOM	281	CA	GLU	A	31	8.657	-5.481	19.648	1.00	30.77	C
ATOM	282	C	GLU	A	31	8.701	-6.234	20.964	1.00	23.77	C
ATOM	283	O	GLU	A	31	9.466	-5.871	21.849	1.00	40.64	O
ATOM	284	CB	GLU	A	31	9.986	-5.716	18.950	1.00	21.80	C
ATOM	285	CG	GLU	A	31	10.127	-7.196	18.569	1.00	32.10	C
ATOM	286	CD	GLU	A	31	11.094	-7.512	17.428	1.00	69.47	C
ATOM	287	OE1	GLU	A	31	12.309	-7.462	17.595	1.00	72.56	O
ATOM	288	OE2	GLU	A	31	10.619	-7.758	16.323	1.00	61.02	O
ATOM	289	H	GLU	A	31	8.999	-3.375	19.585	1.00	18.53	H
ATOM	290	N	ASP	A	32	7.800	-7.216	21.077	1.00	31.32	N
ATOM	291	CA	ASP	A	32	7.557	-7.960	22.312	1.00	55.76	C
ATOM	292	C	ASP	A	32	7.350	-7.114	23.565	1.00	36.62	C
ATOM	293	O	ASP	A	32	7.855	-7.359	24.666	1.00	49.81	O
ATOM	294	CB	ASP	A	32	8.596	-9.076	22.500	1.00	57.01	C
ATOM	295	CG	ASP	A	32	8.544	-10.107	21.374	1.00	64.95	C
ATOM	296	OD1	ASP	A	32	7.451	-10.455	20.913	1.00	71.74	O
ATOM	297	OD2	ASP	A	32	9.608	-10.558	20.949	1.00	71.59	O
ATOM	298	H	ASP	A	32	7.217	-7.390	20.317	1.00	29.65	H
ATOM	299	N	GLY	A	33	6.522	-6.101	23.343	1.00	48.70	N
ATOM	300	CA	GLY	A	33	6.247	-5.113	24.351	1.00	34.41	C
ATOM	301	C	GLY	A	33	4.833	-4.565	24.207	1.00	34.23	C
ATOM	302	O	GLY	A	33	3.914	-5.167	23.633	1.00	27.91	O
ATOM	303	H	GLY	A	33	6.064	-6.003	22.481	1.00	38.22	H
ATOM	304	N	LYS	A	34	4.738	-3.348	24.740	1.00	30.73	N
ATOM	305	CA	LYS	A	34	3.482	-2.662	24.973	1.00	29.07	C
ATOM	306	C	LYS	A	34	2.884	-2.167	23.656	1.00	15.38	C

ATOM	307	O	LYS	A	34	3.623	-1.666	22.797	1.00	17.31	O
ATOM	308	CB	LYS	A	34	3.847	-1.499	25.893	1.00	28.79	C
ATOM	309	CG	LYS	A	34	2.778	-0.999	26.841	1.00	59.76	C
ATOM	310	CD	LYS	A	34	3.514	-0.163	27.871	1.00	72.83	C
ATOM	311	CE	LYS	A	34	2.560	0.475	28.874	1.00	77.19	C
ATOM	312	NZ	LYS	A	34	3.291	1.313	29.816	1.00	83.47	N
ATOM	313	H	LYS	A	34	5.568	-2.875	24.936	1.00	25.42	H
ATOM	314	HZ1	LYS	A	34	3.921	1.957	29.293	1.00	50.00	H
ATOM	315	HZ2	LYS	A	34	2.625	1.880	30.379	1.00	50.00	H
ATOM	316	HZ3	LYS	A	34	3.859	0.711	30.444	1.00	50.00	H
ATOM	317	N	LYS	A	35	1.577	-2.352	23.450	1.00	19.66	N
ATOM	318	CA	LYS	A	35	0.845	-1.563	22.462	1.00	18.14	C
ATOM	319	C	LYS	A	35	0.808	-0.117	22.936	1.00	23.43	C
ATOM	320	O	LYS	A	35	0.490	0.167	24.089	1.00	34.44	O
ATOM	321	CB	LYS	A	35	-0.549	-2.100	22.290	1.00	14.74	C
ATOM	322	CG	LYS	A	35	-1.477	-1.178	21.503	1.00	41.82	C
ATOM	323	CD	LYS	A	35	-2.919	-1.567	21.823	1.00	73.09	C
ATOM	324	CE	LYS	A	35	-3.964	-0.642	21.227	1.00	53.04	C
ATOM	325	NZ	LYS	A	35	-4.072	0.542	22.051	1.00	53.35	N
ATOM	326	H	LYS	A	35	1.096	-3.007	23.995	1.00	22.19	H
ATOM	327	HZ1	LYS	A	35	-4.322	0.223	23.009	1.00	50.00	H
ATOM	328	HZ2	LYS	A	35	-3.158	1.033	22.056	1.00	50.00	H
ATOM	329	HZ3	LYS	A	35	-4.821	1.159	21.679	1.00	50.00	H
ATOM	330	N	PHE	A	36	1.185	0.793	22.049	1.00	20.64	N
ATOM	331	CA	PHE	A	36	1.237	2.187	22.414	1.00	13.73	C
ATOM	332	C	PHE	A	36	0.196	2.995	21.645	1.00	20.97	C
ATOM	333	O	PHE	A	36	-0.093	4.119	22.052	1.00	19.29	O
ATOM	334	CB	PHE	A	36	2.670	2.766	22.244	1.00	11.07	C
ATOM	335	CG	PHE	A	36	3.260	2.688	20.848	1.00	14.52	C
ATOM	336	CD1	PHE	A	36	2.861	3.563	19.847	1.00	14.79	C
ATOM	337	CD2	PHE	A	36	4.183	1.694	20.578	1.00	15.57	C
ATOM	338	CE1	PHE	A	36	3.365	3.401	18.567	1.00	9.39	C
ATOM	339	CE2	PHE	A	36	4.688	1.555	19.302	1.00	12.97	C
ATOM	340	CZ	PHE	A	36	4.269	2.393	18.294	1.00	9.22	C
ATOM	341	H	PHE	A	36	1.433	0.506	21.145	1.00	16.81	H
ATOM	342	N	ASP	A	37	-0.377	2.524	20.520	1.00	16.37	N
ATOM	343	CA	ASP	A	37	-1.368	3.313	19.782	1.00	22.26	C
ATOM	344	C	ASP	A	37	-2.206	2.481	18.816	1.00	19.09	C
ATOM	345	O	ASP	A	37	-1.748	1.434	18.362	1.00	11.13	O
ATOM	346	CB	ASP	A	37	-0.679	4.456	19.026	1.00	10.58	C
ATOM	347	CG	ASP	A	37	-1.605	5.543	18.500	1.00	13.87	C
ATOM	348	OD1	ASP	A	37	-2.731	5.671	18.959	1.00	20.82	O
ATOM	349	OD2	ASP	A	37	-1.200	6.279	17.616	1.00	16.84	O
ATOM	350	H	ASP	A	37	-0.146	1.637	20.172	1.00	14.61	H
ATOM	351	N	SER	A	38	-3.446	2.869	18.520	1.00	12.66	N
ATOM	352	CA	SER	A	38	-4.246	2.209	17.530	1.00	17.76	C
ATOM	353	C	SER	A	38	-5.268	3.214	17.063	1.00	19.03	C
ATOM	354	O	SER	A	38	-5.996	3.775	17.879	1.00	23.31	O
ATOM	355	CB	SER	A	38	-5.006	1.063	18.146	1.00	15.16	C
ATOM	356	OG	SER	A	38	-5.843	0.424	17.203	1.00	19.65	O
ATOM	357	H	SER	A	38	-3.850	3.629	18.992	1.00	16.25	H
ATOM	358	HG	SER	A	38	-5.364	-0.372	16.920	1.00	20.60	H
ATOM	359	N	SER	A	39	-5.378	3.398	15.757	1.00	12.37	N
ATOM	360	CA	SER	A	39	-6.440	4.219	15.226	1.00	14.57	C

ATOM	361	C	SER	A	39	-7.785	3.510	15.317	1.00	15.72	C
ATOM	362	O	SER	A	39	-8.837	4.139	15.252	1.00	19.07	O
ATOM	363	CB	SER	A	39	-6.101	4.576	13.793	1.00	10.13	C
ATOM	364	OG	SER	A	39	-5.997	3.425	12.980	1.00	13.17	O
ATOM	365	H	SER	A	39	-4.798	2.915	15.128	1.00	19.30	H
ATOM	366	HG	SER	A	39	-6.783	3.433	12.415	1.00	11.96	H
ATOM	367	N	ARG	A	40	-7.792	2.183	15.454	1.00	18.89	N
ATOM	368	CA	ARG	A	40	-9.025	1.414	15.499	1.00	15.31	C
ATOM	369	C	ARG	A	40	-9.842	1.769	16.728	1.00	31.13	C
ATOM	370	O	ARG	A	40	-11.041	1.982	16.606	1.00	36.87	O
ATOM	371	CB	ARG	A	40	-8.735	-0.088	15.440	1.00	30.45	C
ATOM	372	CG	ARG	A	40	-8.214	-0.516	14.075	1.00	26.49	C
ATOM	373	CD	ARG	A	40	-7.845	-2.005	14.000	1.00	36.88	C
ATOM	374	NE	ARG	A	40	-7.282	-2.329	12.691	1.00	30.75	N
ATOM	375	CZ	ARG	A	40	-8.049	-2.663	11.642	1.00	50.14	C
ATOM	376	NH1	ARG	A	40	-9.381	-2.694	11.718	1.00	35.76	N
ATOM	377	NH2	ARG	A	40	-7.484	-2.936	10.466	1.00	25.34	N
ATOM	378	H	ARG	A	40	-6.936	1.710	15.517	1.00	21.59	H
ATOM	379	HE	ARG	A	40	-6.329	-2.206	12.530	1.00	33.35	H
ATOM	380	HH11	ARG	A	40	-9.838	-2.457	12.574	1.00	17.34	H
ATOM	381	HH12	ARG	A	40	-9.914	-2.949	10.915	1.00	17.34	H
ATOM	382	HH21	ARG	A	40	-6.496	-2.877	10.346	1.00	16.23	H
ATOM	383	HH22	ARG	A	40	-8.062	-3.199	9.701	1.00	16.23	H
ATOM	384	N	ASP	A	41	-9.168	1.932	17.876	1.00	32.90	N
ATOM	385	CA	ASP	A	41	-9.753	2.382	19.150	1.00	42.46	C
ATOM	386	C	ASP	A	41	-10.553	3.670	18.998	1.00	49.35	C
ATOM	387	O	ASP	A	41	-11.604	3.909	19.597	1.00	52.42	O
ATOM	388	CB	ASP	A	41	-8.668	2.761	20.201	1.00	58.24	C
ATOM	389	CG	ASP	A	41	-7.759	1.709	20.846	1.00	77.12	C
ATOM	390	OD1	ASP	A	41	-8.072	0.513	20.824	1.00	72.34	O
ATOM	391	OD2	ASP	A	41	-6.727	2.113	21.395	1.00	77.19	O
ATOM	392	H	ASP	A	41	-8.212	1.717	17.853	1.00	30.00	H
ATOM	393	N	ARG	A	42	-9.936	4.531	18.200	1.00	55.02	N
ATOM	394	CA	ARG	A	42	-10.429	5.864	17.980	1.00	31.32	C
ATOM	395	C	ARG	A	42	-11.542	5.911	16.952	1.00	32.97	C
ATOM	396	O	ARG	A	42	-12.118	6.975	16.702	1.00	39.40	O
ATOM	397	CB	ARG	A	42	-9.284	6.726	17.500	1.00	33.76	C
ATOM	398	CG	ARG	A	42	-8.390	7.201	18.609	1.00	43.44	C
ATOM	399	CD	ARG	A	42	-7.599	8.365	18.026	1.00	55.11	C
ATOM	400	NE	ARG	A	42	-6.641	7.928	17.021	1.00	68.77	N
ATOM	401	CZ	ARG	A	42	-5.501	7.312	17.363	1.00	34.61	C
ATOM	402	NH1	ARG	A	42	-5.250	6.978	18.633	1.00	29.77	N
ATOM	403	NH2	ARG	A	42	-4.604	7.027	16.419	1.00	50.73	N
ATOM	404	H	ARG	A	42	-9.159	4.236	17.684	1.00	49.11	H
ATOM	405	HE	ARG	A	42	-6.831	8.092	16.074	1.00	39.69	H
ATOM	406	HH11	ARG	A	42	-5.907	7.195	19.355	1.00	24.47	H
ATOM	407	HH12	ARG	A	42	-4.397	6.527	18.872	1.00	24.47	H
ATOM	408	HH21	ARG	A	42	-4.790	7.268	15.467	1.00	44.70	H
ATOM	409	HH22	ARG	A	42	-3.753	6.563	16.666	1.00	44.70	H
ATOM	410	N	ASN	A	43	-11.797	4.777	16.288	1.00	23.56	N
ATOM	411	CA	ASN	A	43	-12.825	4.649	15.268	1.00	42.03	C
ATOM	412	C	ASN	A	43	-12.577	5.608	14.099	1.00	70.45	C
ATOM	413	O	ASN	A	43	-13.453	5.786	13.246	1.00	92.53	O
ATOM	414	CB	ASN	A	43	-14.251	4.842	15.863	1.00	61.12	C

ATOM	415	CG	ASN	A	43	-14.624	3.954	17.056	1.00	61.70	C
ATOM	416	OD1	ASN	A	43	-14.630	2.729	16.997	1.00	55.55	O
ATOM	417	ND2	ASN	A	43	-14.967	4.509	18.211	1.00	33.11	N
ATOM	418	H	ASN	A	43	-11.275	3.973	16.489	1.00	22.60	H
ATOM	419	HD21	ASN	A	43	-15.134	3.883	18.941	1.00	43.61	H
ATOM	420	HD22	ASN	A	43	-14.998	5.483	18.285	1.00	43.61	H
ATOM	421	N	LYS	A	44	-11.384	6.218	13.984	1.00	58.24	N
ATOM	422	CA	LYS	A	44	-11.083	7.162	12.914	1.00	52.71	C
ATOM	423	C	LYS	A	44	-9.813	6.678	12.190	1.00	19.74	C
ATOM	424	O	LYS	A	44	-8.837	6.310	12.860	1.00	30.95	O
ATOM	425	CB	LYS	A	44	-10.906	8.591	13.467	1.00	56.69	C
ATOM	426	CG	LYS	A	44	-10.823	9.607	12.323	1.00	79.88	C
ATOM	427	CD	LYS	A	44	-10.478	11.054	12.671	1.00	81.56	C
ATOM	428	CE	LYS	A	44	-10.280	11.723	11.308	1.00	84.21	C
ATOM	429	NZ	LYS	A	44	-9.964	13.136	11.408	1.00	86.18	N
ATOM	430	H	LYS	A	44	-10.652	5.977	14.587	1.00	50.00	H
ATOM	431	HZ1	LYS	A	44	-9.103	13.264	11.974	1.00	50.00	H
ATOM	432	HZ2	LYS	A	44	-9.811	13.521	10.452	1.00	50.00	H
ATOM	433	HZ3	LYS	A	44	-10.760	13.637	11.852	1.00	50.00	H
ATOM	434	N	PRO	A	45	-9.793	6.558	10.845	1.00	32.57	N
ATOM	435	CA	PRO	A	45	-8.622	6.152	10.091	1.00	16.22	C
ATOM	436	C	PRO	A	45	-7.668	7.325	10.053	1.00	14.54	C
ATOM	437	O	PRO	A	45	-8.069	8.500	10.083	1.00	16.32	O
ATOM	438	CB	PRO	A	45	-9.166	5.844	8.692	1.00	14.02	C
ATOM	439	CG	PRO	A	45	-10.632	5.615	8.923	1.00	31.07	C
ATOM	440	CD	PRO	A	45	-10.924	6.706	9.937	1.00	32.99	C
ATOM	441	N	PHE	A	46	-6.401	6.936	9.931	1.00	10.29	N
ATOM	442	CA	PHE	A	46	-5.294	7.853	9.877	1.00	9.03	C
ATOM	443	C	PHE	A	46	-5.006	8.087	8.408	1.00	8.52	C
ATOM	444	O	PHE	A	46	-5.061	7.159	7.594	1.00	11.40	O
ATOM	445	CB	PHE	A	46	-4.078	7.243	10.593	1.00	8.19	C
ATOM	446	CG	PHE	A	46	-2.762	8.005	10.471	1.00	9.99	C
ATOM	447	CD1	PHE	A	46	-2.512	9.093	11.283	1.00	20.12	C
ATOM	448	CD2	PHE	A	46	-1.783	7.575	9.584	1.00	13.29	C
ATOM	449	CE1	PHE	A	46	-1.286	9.739	11.208	1.00	21.39	C
ATOM	450	CE2	PHE	A	46	-0.562	8.229	9.529	1.00	10.10	C
ATOM	451	CZ	PHE	A	46	-0.317	9.312	10.328	1.00	10.55	C
ATOM	452	H	PHE	A	46	-6.219	5.988	9.740	1.00	13.49	H
ATOM	453	N	LYS	A	47	-4.686	9.329	8.045	1.00	9.33	N
ATOM	454	CA	LYS	A	47	-4.357	9.639	6.671	1.00	7.21	C
ATOM	455	C	LYS	A	47	-3.020	10.347	6.698	1.00	12.96	C
ATOM	456	O	LYS	A	47	-2.716	11.128	7.616	1.00	14.92	O
ATOM	457	CB	LYS	A	47	-5.375	10.584	6.066	1.00	12.42	C
ATOM	458	CG	LYS	A	47	-6.777	10.063	6.134	1.00	15.45	C
ATOM	459	CD	LYS	A	47	-7.658	10.992	5.357	1.00	22.52	C
ATOM	460	CE	LYS	A	47	-9.069	10.523	5.624	1.00	20.02	C
ATOM	461	NZ	LYS	A	47	-9.974	11.333	4.838	1.00	31.31	N
ATOM	462	H	LYS	A	47	-4.545	10.027	8.710	1.00	8.09	H
ATOM	463	HZ1	LYS	A	47	-9.871	12.333	5.099	1.00	37.20	H
ATOM	464	HZ2	LYS	A	47	-9.750	11.212	3.829	1.00	37.20	H
ATOM	465	HZ3	LYS	A	47	-10.949	11.022	5.014	1.00	37.20	H
ATOM	466	N	PHE	A	48	-2.199	10.029	5.710	1.00	18.97	N
ATOM	467	CA	PHE	A	48	-0.949	10.741	5.518	1.00	24.29	C
ATOM	468	C	PHE	A	48	-0.628	10.760	4.031	1.00	15.17	C

ATOM	469	O	PHE	A	48	-1.079	9.910	3.248	1.00	14.27	O
ATOM	470	CB	PHE	A	48	0.201	10.117	6.312	1.00	8.79	C
ATOM	471	CG	PHE	A	48	0.690	8.803	5.717	1.00	8.83	C
ATOM	472	CD1	PHE	A	48	-0.012	7.636	5.941	1.00	12.25	C
ATOM	473	CD2	PHE	A	48	1.872	8.797	4.981	1.00	15.63	C
ATOM	474	CE1	PHE	A	48	0.494	6.452	5.434	1.00	16.62	C
ATOM	475	CE2	PHE	A	48	2.356	7.621	4.465	1.00	15.50	C
ATOM	476	CZ	PHE	A	48	1.666	6.440	4.694	1.00	14.07	C
ATOM	477	H	PHE	A	48	-2.457	9.335	5.059	1.00	14.35	H
ATOM	478	N	MET	A	49	0.207	11.707	3.639	1.00	11.11	N
ATOM	479	CA	MET	A	49	0.577	11.826	2.242	1.00	13.52	C
ATOM	480	C	MET	A	49	1.934	11.179	2.050	1.00	17.48	C
ATOM	481	O	MET	A	49	2.930	11.506	2.721	1.00	14.22	O
ATOM	482	CB	MET	A	49	0.619	13.297	1.884	1.00	15.86	C
ATOM	483	CG	MET	A	49	0.328	13.504	0.426	1.00	52.57	C
ATOM	484	SD	MET	A	49	0.381	15.258	0.020	1.00	50.59	S
ATOM	485	CE	MET	A	49	-1.045	15.719	0.957	1.00	35.23	C
ATOM	486	H	MET	A	49	0.619	12.298	4.295	1.00	10.91	H
ATOM	487	N	LEU	A	50	1.952	10.225	1.129	1.00	12.57	N
ATOM	488	CA	LEU	A	50	3.136	9.450	0.882	1.00	14.16	C
ATOM	489	C	LEU	A	50	4.170	10.346	0.236	1.00	18.48	C
ATOM	490	O	LEU	A	50	3.852	11.195	-0.587	1.00	23.65	O
ATOM	491	CB	LEU	A	50	2.839	8.264	-0.015	1.00	11.95	C
ATOM	492	CG	LEU	A	50	3.980	7.264	-0.161	1.00	23.71	C
ATOM	493	CD1	LEU	A	50	4.115	6.383	1.057	1.00	21.03	C
ATOM	494	CD2	LEU	A	50	3.739	6.394	-1.348	1.00	23.88	C
ATOM	495	H	LEU	A	50	1.148	10.074	0.584	1.00	14.70	H
ATOM	496	N	GLY	A	51	5.409	10.218	0.693	1.00	16.43	N
ATOM	497	CA	GLY	A	51	6.523	10.908	0.085	1.00	25.36	C
ATOM	498	C	GLY	A	51	6.812	12.284	0.664	1.00	37.86	C
ATOM	499	O	GLY	A	51	7.845	12.847	0.309	1.00	41.17	O
ATOM	500	H	GLY	A	51	5.564	9.643	1.466	1.00	17.23	H
ATOM	501	N	LYS	A	52	6.008	12.837	1.580	1.00	23.52	N
ATOM	502	CA	LYS	A	52	6.246	14.174	2.133	1.00	16.40	C
ATOM	503	C	LYS	A	52	7.053	14.205	3.423	1.00	17.66	C
ATOM	504	O	LYS	A	52	7.093	15.225	4.100	1.00	25.35	O
ATOM	505	CB	LYS	A	52	4.903	14.813	2.443	1.00	17.13	C
ATOM	506	CG	LYS	A	52	3.982	14.851	1.242	1.00	34.16	C
ATOM	507	CD	LYS	A	52	4.528	15.656	0.068	1.00	39.60	C
ATOM	508	CE	LYS	A	52	3.987	17.087	0.051	1.00	79.21	C
ATOM	509	NZ	LYS	A	52	4.352	17.800	-1.168	1.00	68.49	N
ATOM	510	H	LYS	A	52	5.194	12.362	1.852	1.00	24.55	H
ATOM	511	HZ1	LYS	A	52	4.033	17.261	-1.998	1.00	50.00	H
ATOM	512	HZ2	LYS	A	52	3.899	18.736	-1.168	1.00	50.00	H
ATOM	513	HZ3	LYS	A	52	5.385	17.914	-1.200	1.00	50.00	H
ATOM	514	N	GLN	A	53	7.643	13.068	3.832	1.00	25.80	N
ATOM	515	CA	GLN	A	53	8.286	12.911	5.139	1.00	26.19	C
ATOM	516	C	GLN	A	53	7.455	13.308	6.375	1.00	17.56	C
ATOM	517	O	GLN	A	53	7.939	13.755	7.411	1.00	17.09	O
ATOM	518	CB	GLN	A	53	9.651	13.589	5.158	1.00	41.87	C
ATOM	519	CG	GLN	A	53	10.720	12.906	4.332	1.00	26.68	C
ATOM	520	CD	GLN	A	53	12.054	13.629	4.498	1.00	64.57	C
ATOM	521	OE1	GLN	A	53	12.146	14.857	4.445	1.00	59.44	O
ATOM	522	NE2	GLN	A	53	13.118	12.873	4.721	1.00	66.86	N

ATOM	523	H	GLN	A	53	7.733	12.356	3.172	1.00	20.07	H
ATOM	524	HE21	GLN	A	53	14.011	13.287	4.763	1.00	48.95	H
ATOM	525	HE22	GLN	A	53	12.985	11.913	4.790	1.00	48.95	H
ATOM	526	N	GLU	A	54	6.150	13.067	6.283	1.00	12.54	N
ATOM	527	CA	GLU	A	54	5.266	13.265	7.417	1.00	13.97	C
ATOM	528	C	GLU	A	54	5.419	12.178	8.471	1.00	12.18	C
ATOM	529	O	GLU	A	54	5.185	12.417	9.655	1.00	12.93	O
ATOM	530	CB	GLU	A	54	3.843	13.293	6.925	1.00	13.36	C
ATOM	531	CG	GLU	A	54	3.575	14.437	5.960	1.00	13.00	C
ATOM	532	CD	GLU	A	54	2.128	14.544	5.492	1.00	21.07	C
ATOM	533	OE1	GLU	A	54	1.303	13.667	5.760	1.00	22.75	O
ATOM	534	OE2	GLU	A	54	1.803	15.524	4.844	1.00	26.18	O
ATOM	535	H	GLU	A	54	5.783	12.846	5.410	1.00	11.96	H
ATOM	536	N	VAL	A	55	5.792	10.964	8.039	1.00	11.28	N
ATOM	537	CA	VAL	A	55	5.866	9.820	8.929	1.00	5.68	C
ATOM	538	C	VAL	A	55	7.259	9.193	8.880	1.00	9.59	C
ATOM	539	O	VAL	A	55	8.072	9.481	7.993	1.00	13.30	O
ATOM	540	CB	VAL	A	55	4.749	8.801	8.577	1.00	8.42	C
ATOM	541	CG1	VAL	A	55	3.370	9.373	8.930	1.00	5.29	C
ATOM	542	CG2	VAL	A	55	4.865	8.327	7.100	1.00	10.91	C
ATOM	543	H	VAL	A	55	6.195	10.871	7.157	1.00	10.12	H
ATOM	544	N	ILE	A	56	7.539	8.306	9.827	1.00	6.13	N
ATOM	545	CA	ILE	A	56	8.812	7.611	9.893	1.00	11.35	C
ATOM	546	C	ILE	A	56	9.121	6.836	8.626	1.00	11.05	C
ATOM	547	O	ILE	A	56	8.226	6.388	7.895	1.00	10.94	O
ATOM	548	CB	ILE	A	56	8.912	6.698	11.145	1.00	9.45	C
ATOM	549	CG1	ILE	A	56	7.807	5.617	11.167	1.00	5.31	C
ATOM	550	CG2	ILE	A	56	8.933	7.580	12.397	1.00	8.84	C
ATOM	551	CD1	ILE	A	56	7.892	4.605	12.297	1.00	7.74	C
ATOM	552	H	ILE	A	56	6.858	8.156	10.512	1.00	6.00	H
ATOM	553	N	ARG	A	57	10.413	6.641	8.372	1.00	8.31	N
ATOM	554	CA	ARG	A	57	10.883	6.046	7.139	1.00	9.12	C
ATOM	555	C	ARG	A	57	10.329	4.657	6.830	1.00	9.73	C
ATOM	556	O	ARG	A	57	10.001	4.310	5.688	1.00	11.55	O
ATOM	557	CB	ARG	A	57	12.390	6.009	7.226	1.00	13.65	C
ATOM	558	CG	ARG	A	57	13.025	5.548	5.952	1.00	13.35	C
ATOM	559	CD	ARG	A	57	14.540	5.650	6.054	1.00	27.70	C
ATOM	560	NE	ARG	A	57	15.067	5.173	4.782	1.00	32.60	N
ATOM	561	CZ	ARG	A	57	16.373	5.108	4.477	1.00	63.58	C
ATOM	562	NH1	ARG	A	57	17.328	5.506	5.317	1.00	64.64	N
ATOM	563	NH2	ARG	A	57	16.740	4.674	3.272	1.00	55.48	N
ATOM	564	H	ARG	A	57	11.064	6.900	9.055	1.00	10.24	H
ATOM	565	HE	ARG	A	57	14.430	4.872	4.100	1.00	33.42	H
ATOM	566	HH11	ARG	A	57	17.095	5.933	6.185	1.00	48.07	H
ATOM	567	HH12	ARG	A	57	18.290	5.387	5.086	1.00	48.07	H
ATOM	568	HH21	ARG	A	57	16.057	4.414	2.590	1.00	40.69	H
ATOM	569	HH22	ARG	A	57	17.712	4.620	3.037	1.00	40.69	H
ATOM	570	N	GLY	A	58	10.196	3.847	7.877	1.00	9.85	N
ATOM	571	CA	GLY	A	58	9.639	2.519	7.752	1.00	11.31	C
ATOM	572	C	GLY	A	58	8.208	2.498	7.242	1.00	11.34	C
ATOM	573	O	GLY	A	58	7.827	1.531	6.578	1.00	12.57	O
ATOM	574	H	GLY	A	58	10.497	4.159	8.757	1.00	7.54	H
ATOM	575	N	TRP	A	59	7.418	3.536	7.565	1.00	9.25	N
ATOM	576	CA	TRP	A	59	6.084	3.662	7.036	1.00	5.89	C

ATOM	577	C	TRP	A	59	6.173	4.115	5.604	1.00	11.62	C
ATOM	578	O	TRP	A	59	5.462	3.562	4.776	1.00	10.65	O
ATOM	579	CB	TRP	A	59	5.212	4.650	7.798	1.00	2.00	C
ATOM	580	CG	TRP	A	59	4.390	3.977	8.883	1.00	7.15	C
ATOM	581	CD1	TRP	A	59	4.957	3.282	9.922	1.00	9.09	C
ATOM	582	CD2	TRP	A	59	3.022	4.024	8.981	1.00	12.44	C
ATOM	583	NE1	TRP	A	59	3.938	2.910	10.664	1.00	14.82	N
ATOM	584	CE2	TRP	A	59	2.776	3.338	10.155	1.00	9.06	C
ATOM	585	CE3	TRP	A	59	1.976	4.592	8.280	1.00	10.43	C
ATOM	586	CZ2	TRP	A	59	1.492	3.225	10.673	1.00	6.28	C
ATOM	587	CZ3	TRP	A	59	0.701	4.489	8.796	1.00	12.15	C
ATOM	588	CH2	TRP	A	59	0.456	3.812	9.975	1.00	8.16	C
ATOM	589	H	TRP	A	59	7.774	4.261	8.120	1.00	7.13	H
ATOM	590	HE1	TRP	A	59	4.020	2.358	11.470	1.00	13.77	H
ATOM	591	N	GLU	A	60	7.038	5.084	5.269	1.00	10.64	N
ATOM	592	CA	GLU	A	60	7.183	5.548	3.898	1.00	10.98	C
ATOM	593	C	GLU	A	60	7.543	4.411	2.943	1.00	15.13	C
ATOM	594	O	GLU	A	60	6.959	4.255	1.870	1.00	18.15	O
ATOM	595	CB	GLU	A	60	8.260	6.631	3.809	1.00	10.74	C
ATOM	596	CG	GLU	A	60	8.012	7.965	4.510	1.00	19.92	C
ATOM	597	CD	GLU	A	60	7.200	8.970	3.705	1.00	18.76	C
ATOM	598	OE1	GLU	A	60	6.054	8.703	3.381	1.00	32.83	O
ATOM	599	OE2	GLU	A	60	7.729	10.028	3.398	1.00	44.50	O
ATOM	600	H	GLU	A	60	7.589	5.487	5.974	1.00	9.88	H
ATOM	601	N	GLU	A	61	8.496	3.579	3.335	1.00	9.75	N
ATOM	602	CA	GLU	A	61	8.879	2.443	2.520	1.00	11.54	C
ATOM	603	C	GLU	A	61	7.951	1.256	2.638	1.00	8.40	C
ATOM	604	O	GLU	A	61	7.754	0.522	1.668	1.00	11.35	O
ATOM	605	CB	GLU	A	61	10.292	2.007	2.872	1.00	11.79	C
ATOM	606	CG	GLU	A	61	11.215	3.062	2.265	1.00	44.46	C
ATOM	607	CD	GLU	A	61	12.709	2.945	2.517	1.00	52.63	C
ATOM	608	OE1	GLU	A	61	13.235	1.867	2.791	1.00	26.54	O
ATOM	609	OE2	GLU	A	61	13.367	3.969	2.403	1.00	28.84	O
ATOM	610	H	GLU	A	61	8.966	3.757	4.173	1.00	8.57	H
ATOM	611	N	GLY	A	62	7.393	1.043	3.819	1.00	6.34	N
ATOM	612	CA	GLY	A	62	6.525	-0.089	4.072	1.00	11.76	C
ATOM	613	C	GLY	A	62	5.216	0.039	3.329	1.00	14.21	C
ATOM	614	O	GLY	A	62	4.843	-0.847	2.556	1.00	11.00	O
ATOM	615	H	GLY	A	62	7.581	1.656	4.558	1.00	5.00	H
ATOM	616	N	VAL	A	63	4.532	1.176	3.508	1.00	12.36	N
ATOM	617	CA	VAL	A	63	3.231	1.383	2.893	1.00	8.38	C
ATOM	618	C	VAL	A	63	3.316	1.490	1.369	1.00	10.73	C
ATOM	619	O	VAL	A	63	2.426	1.004	0.671	1.00	11.09	O
ATOM	620	CB	VAL	A	63	2.477	2.554	3.586	1.00	10.46	C
ATOM	621	CG1	VAL	A	63	1.152	2.864	2.892	1.00	7.10	C
ATOM	622	CG2	VAL	A	63	2.236	2.219	5.070	1.00	13.30	C
ATOM	623	H	VAL	A	63	4.916	1.884	4.063	1.00	9.81	H
ATOM	624	N	ALA	A	64	4.406	2.049	0.822	1.00	8.64	N
ATOM	625	CA	ALA	A	64	4.603	2.091	-0.611	1.00	5.07	C
ATOM	626	C	ALA	A	64	4.567	0.745	-1.337	1.00	10.97	C
ATOM	627	O	ALA	A	64	4.244	0.673	-2.531	1.00	11.35	O
ATOM	628	CB	ALA	A	64	5.946	2.736	-0.902	1.00	9.58	C
ATOM	629	H	ALA	A	64	5.071	2.477	1.402	1.00	7.42	H
ATOM	630	N	GLN	A	65	4.866	-0.363	-0.648	1.00	8.60	N

ATOM	631	CA	GLN	A	65	4.817	-1.649	-1.328	1.00	3.86	C
ATOM	632	C	GLN	A	65	3.521	-2.390	-1.037	1.00	7.84	C
ATOM	633	O	GLN	A	65	3.405	-3.585	-1.318	1.00	13.14	O
ATOM	634	CB	GLN	A	65	6.063	-2.460	-1.029	1.00	14.43	C
ATOM	635	CG	GLN	A	65	6.304	-2.643	0.436	1.00	9.21	C
ATOM	636	CD	GLN	A	65	7.655	-3.240	0.752	1.00	18.89	C
ATOM	637	OE1	GLN	A	65	7.850	-4.456	0.694	1.00	16.81	O
ATOM	638	NE2	GLN	A	65	8.622	-2.417	1.129	1.00	16.04	N
ATOM	639	H	GLN	A	65	5.042	-0.323	0.315	1.00	6.02	H
ATOM	640	HE21	GLN	A	65	9.494	-2.809	1.330	1.00	13.74	H
ATOM	641	HE22	GLN	A	65	8.401	-1.460	1.188	1.00	13.74	H
ATOM	642	N	MET	A	66	2.526	-1.708	-0.469	1.00	12.58	N
ATOM	643	CA	MET	A	66	1.278	-2.360	-0.162	1.00	9.01	C
ATOM	644	C	MET	A	66	0.279	-1.954	-1.229	1.00	5.22	C
ATOM	645	O	MET	A	66	0.324	-0.856	-1.779	1.00	11.06	O
ATOM	646	CB	MET	A	66	0.795	-1.977	1.233	1.00	8.72	C
ATOM	647	CG	MET	A	66	1.586	-2.584	2.396	1.00	14.13	C
ATOM	648	SD	MET	A	66	1.010	-1.927	3.979	1.00	13.76	S
ATOM	649	CE	MET	A	66	-0.513	-2.835	4.016	1.00	11.06	C
ATOM	650	H	MET	A	66	2.587	-0.736	-0.357	1.00	7.87	H
ATOM	651	N	SER	A	67	-0.624	-2.870	-1.551	1.00	8.79	N
ATOM	652	CA	SER	A	67	-1.719	-2.517	-2.428	1.00	11.09	C
ATOM	653	C	SER	A	67	-3.022	-2.272	-1.664	1.00	15.47	C
ATOM	654	O	SER	A	67	-3.145	-2.711	-0.508	1.00	12.61	O
ATOM	655	CB	SER	A	67	-1.871	-3.548	-3.519	1.00	8.47	C
ATOM	656	OG	SER	A	67	-2.072	-4.887	-3.109	1.00	11.08	O
ATOM	657	H	SER	A	67	-0.598	-3.730	-1.081	1.00	5.60	H
ATOM	658	HG	SER	A	67	-1.404	-5.088	-2.439	1.00	11.49	H
ATOM	659	N	VAL	A	68	-4.015	-1.616	-2.286	1.00	13.66	N
ATOM	660	CA	VAL	A	68	-5.265	-1.301	-1.624	1.00	10.45	C
ATOM	661	C	VAL	A	68	-5.930	-2.574	-1.150	1.00	6.70	C
ATOM	662	O	VAL	A	68	-5.995	-3.535	-1.918	1.00	10.56	O
ATOM	663	CB	VAL	A	68	-6.183	-0.467	-2.550	1.00	22.97	C
ATOM	664	CG1	VAL	A	68	-7.561	-0.162	-1.944	1.00	11.78	C
ATOM	665	CG2	VAL	A	68	-5.511	0.851	-2.829	1.00	13.49	C
ATOM	666	H	VAL	A	68	-3.845	-1.276	-3.185	1.00	10.34	H
ATOM	667	N	GLY	A	69	-6.344	-2.591	0.112	1.00	12.27	N
ATOM	668	CA	GLY	A	69	-7.019	-3.716	0.737	1.00	12.60	C
ATOM	669	C	GLY	A	69	-6.084	-4.587	1.575	1.00	16.68	C
ATOM	670	O	GLY	A	69	-6.540	-5.404	2.375	1.00	12.60	O
ATOM	671	H	GLY	A	69	-6.171	-1.805	0.665	1.00	9.34	H
ATOM	672	N	GLN	A	70	-4.767	-4.425	1.407	1.00	9.90	N
ATOM	673	CA	GLN	A	70	-3.837	-5.290	2.065	1.00	5.02	C
ATOM	674	C	GLN	A	70	-3.777	-4.939	3.543	1.00	8.32	C
ATOM	675	O	GLN	A	70	-3.816	-3.767	3.911	1.00	13.62	O
ATOM	676	CB	GLN	A	70	-2.479	-5.108	1.444	1.00	2.98	C
ATOM	677	CG	GLN	A	70	-1.464	-6.150	1.926	1.00	6.45	C
ATOM	678	CD	GLN	A	70	-0.145	-6.045	1.200	1.00	11.80	C
ATOM	679	OE1	GLN	A	70	-0.071	-5.465	0.116	1.00	16.00	O
ATOM	680	NE2	GLN	A	70	0.943	-6.614	1.680	1.00	12.64	N
ATOM	681	H	GLN	A	70	-4.433	-3.674	0.873	1.00	8.31	H
ATOM	682	HE21	GLN	A	70	1.766	-6.470	1.167	1.00	12.73	H
ATOM	683	HE22	GLN	A	70	0.903	-7.147	2.502	1.00	12.73	H
ATOM	684	N	ARG	A	71	-3.610	-5.952	4.386	1.00	8.72	N

ATOM	685	CA	ARG	A	71	-3.298	-5.763	5.789	1.00	6.13	C
ATOM	686	C	ARG	A	71	-1.942	-6.416	6.008	1.00	11.97	C
ATOM	687	O	ARG	A	71	-1.748	-7.566	5.592	1.00	9.70	O
ATOM	688	CB	ARG	A	71	-4.398	-6.389	6.650	1.00	4.08	C
ATOM	689	CG	ARG	A	71	-4.161	-6.112	8.095	1.00	5.95	C
ATOM	690	CD	ARG	A	71	-5.408	-6.513	8.869	1.00	15.19	C
ATOM	691	NE	ARG	A	71	-5.181	-6.428	10.310	1.00	14.21	N
ATOM	692	CZ	ARG	A	71	-6.097	-6.771	11.224	1.00	19.71	C
ATOM	693	NH1	ARG	A	71	-7.273	-7.277	10.883	1.00	19.34	N
ATOM	694	NH2	ARG	A	71	-5.842	-6.612	12.514	1.00	14.73	N
ATOM	695	H	ARG	A	71	-3.640	-6.864	4.024	1.00	9.72	H
ATOM	696	HE	ARG	A	71	-4.288	-6.214	10.622	1.00	15.80	H
ATOM	697	HH11	ARG	A	71	-7.504	-7.415	9.920	1.00	23.16	H
ATOM	698	HH12	ARG	A	71	-7.931	-7.520	11.596	1.00	23.16	H
ATOM	699	HH21	ARG	A	71	-4.980	-6.219	12.806	1.00	12.53	H
ATOM	700	HH22	ARG	A	71	-6.520	-6.884	13.196	1.00	12.53	H
ATOM	701	N	ALA	A	72	-0.987	-5.740	6.640	1.00	7.24	N
ATOM	702	CA	ALA	A	72	0.354	-6.268	6.821	1.00	11.91	C
ATOM	703	C	ALA	A	72	0.958	-5.948	8.187	1.00	8.84	C
ATOM	704	O	ALA	A	72	0.586	-4.995	8.862	1.00	8.80	O
ATOM	705	CB	ALA	A	72	1.255	-5.702	5.728	1.00	10.80	C
ATOM	706	H	ALA	A	72	-1.181	-4.852	7.016	1.00	5.52	H
ATOM	707	N	LYS	A	73	1.848	-6.815	8.647	1.00	7.18	N
ATOM	708	CA	LYS	A	73	2.652	-6.581	9.821	1.00	6.47	C
ATOM	709	C	LYS	A	73	3.945	-5.968	9.276	1.00	8.25	C
ATOM	710	O	LYS	A	73	4.612	-6.541	8.407	1.00	10.41	O
ATOM	711	CB	LYS	A	73	2.933	-7.910	10.482	1.00	7.24	C
ATOM	712	CG	LYS	A	73	3.850	-7.802	11.652	1.00	10.08	C
ATOM	713	CD	LYS	A	73	4.298	-9.215	11.830	1.00	20.02	C
ATOM	714	CE	LYS	A	73	5.555	-9.246	12.640	1.00	40.73	C
ATOM	715	NZ	LYS	A	73	5.263	-9.663	13.984	1.00	23.83	N
ATOM	716	H	LYS	A	73	2.019	-7.630	8.133	1.00	5.00	H
ATOM	717	HZ1	LYS	A	73	4.823	-10.604	13.963	1.00	22.87	H
ATOM	718	HZ2	LYS	A	73	6.144	-9.695	14.535	1.00	22.87	H
ATOM	719	HZ3	LYS	A	73	4.607	-8.980	14.414	1.00	22.87	H
ATOM	720	N	LEU	A	74	4.261	-4.765	9.749	1.00	7.63	N
ATOM	721	CA	LEU	A	74	5.503	-4.073	9.414	1.00	6.00	C
ATOM	722	C	LEU	A	74	6.433	-4.158	10.600	1.00	8.48	C
ATOM	723	O	LEU	A	74	6.048	-3.694	11.666	1.00	11.64	O
ATOM	724	CB	LEU	A	74	5.252	-2.594	9.077	1.00	7.28	C
ATOM	725	CG	LEU	A	74	4.823	-2.163	7.690	1.00	10.30	C
ATOM	726	CD1	LEU	A	74	3.492	-2.735	7.286	1.00	26.74	C
ATOM	727	CD2	LEU	A	74	4.673	-0.655	7.703	1.00	11.53	C
ATOM	728	H	LEU	A	74	3.662	-4.334	10.384	1.00	6.31	H
ATOM	729	N	THR	A	75	7.622	-4.744	10.507	1.00	8.68	N
ATOM	730	CA	THR	A	75	8.595	-4.703	11.598	1.00	12.38	C
ATOM	731	C	THR	A	75	9.671	-3.694	11.212	1.00	12.11	C
ATOM	732	O	THR	A	75	10.273	-3.804	10.139	1.00	11.11	O
ATOM	733	CB	THR	A	75	9.245	-6.062	11.812	1.00	10.07	C
ATOM	734	OG1	THR	A	75	8.156	-6.961	11.983	1.00	11.55	O
ATOM	735	CG2	THR	A	75	10.174	-6.048	13.032	1.00	13.86	C
ATOM	736	H	THR	A	75	7.879	-5.144	9.646	1.00	7.78	H
ATOM	737	HG1	THR	A	75	7.394	-6.668	11.476	1.00	10.83	H
ATOM	738	N	ILE	A	76	9.916	-2.689	12.042	1.00	8.14	N

ATOM	739	CA	ILE	A	76	10.710	-1.548	11.658	1.00	7.06	C
ATOM	740	C	ILE	A	76	11.859	-1.432	12.660	1.00	9.06	C
ATOM	741	O	ILE	A	76	11.692	-1.294	13.880	1.00	11.09	O
ATOM	742	CB	ILE	A	76	9.796	-0.291	11.673	1.00	8.36	C
ATOM	743	CG1	ILE	A	76	8.618	-0.412	10.733	1.00	10.32	C
ATOM	744	CG2	ILE	A	76	10.605	0.942	11.331	1.00	7.99	C
ATOM	745	CD1	ILE	A	76	7.546	0.672	10.920	1.00	10.56	C
ATOM	746	H	ILE	A	76	9.555	-2.717	12.954	1.00	6.76	H
ATOM	747	N	SER	A	77	13.068	-1.411	12.113	1.00	8.81	N
ATOM	748	CA	SER	A	77	14.250	-1.311	12.952	1.00	7.83	C
ATOM	749	C	SER	A	77	14.345	0.106	13.479	1.00	7.30	C
ATOM	750	O	SER	A	77	13.849	0.992	12.789	1.00	11.14	O
ATOM	751	CB	SER	A	77	15.497	-1.685	12.137	1.00	8.20	C
ATOM	752	OG	SER	A	77	15.654	-0.913	10.938	1.00	15.98	O
ATOM	753	H	SER	A	77	13.138	-1.429	11.140	1.00	5.58	H
ATOM	754	HG	SER	A	77	15.238	-0.057	11.127	1.00	16.20	H
ATOM	755	N	PRO	A	78	15.036	0.422	14.569	1.00	11.54	N
ATOM	756	CA	PRO	A	78	15.088	1.750	15.171	1.00	7.44	C
ATOM	757	C	PRO	A	78	15.574	2.803	14.213	1.00	8.77	C
ATOM	758	O	PRO	A	78	15.087	3.921	14.275	1.00	14.50	O
ATOM	759	CB	PRO	A	78	16.115	1.632	16.249	1.00	14.11	C
ATOM	760	CG	PRO	A	78	16.041	0.202	16.644	1.00	16.36	C
ATOM	761	CD	PRO	A	78	15.821	-0.524	15.340	1.00	16.21	C
ATOM	762	N	ASP	A	79	16.521	2.494	13.334	1.00	10.39	N
ATOM	763	CA	ASP	A	79	16.994	3.458	12.367	1.00	11.10	C
ATOM	764	C	ASP	A	79	15.969	3.832	11.306	1.00	20.89	C
ATOM	765	O	ASP	A	79	16.142	4.825	10.614	1.00	18.96	O
ATOM	766	CB	ASP	A	79	18.304	3.017	11.724	1.00	10.92	C
ATOM	767	CG	ASP	A	79	18.248	1.750	10.895	1.00	22.06	C
ATOM	768	OD1	ASP	A	79	17.790	0.743	11.413	1.00	22.96	O
ATOM	769	OD2	ASP	A	79	18.672	1.770	9.743	1.00	25.87	O
ATOM	770	H	ASP	A	79	16.933	1.613	13.373	1.00	13.50	H
ATOM	771	N	TYR	A	80	14.892	3.062	11.156	1.00	15.31	N
ATOM	772	CA	TYR	A	80	13.797	3.412	10.251	1.00	10.00	C
ATOM	773	C	TYR	A	80	12.598	3.956	11.020	1.00	10.44	C
ATOM	774	O	TYR	A	80	11.528	4.195	10.453	1.00	9.56	O
ATOM	775	CB	TYR	A	80	13.396	2.189	9.444	1.00	12.34	C
ATOM	776	CG	TYR	A	80	14.202	2.043	8.172	1.00	12.21	C
ATOM	777	CD1	TYR	A	80	15.574	2.049	8.242	1.00	19.81	C
ATOM	778	CD2	TYR	A	80	13.558	1.947	6.952	1.00	9.98	C
ATOM	779	CE1	TYR	A	80	16.319	1.955	7.090	1.00	32.48	C
ATOM	780	CE2	TYR	A	80	14.302	1.828	5.795	1.00	13.63	C
ATOM	781	CZ	TYR	A	80	15.678	1.808	5.880	1.00	40.19	C
ATOM	782	OH	TYR	A	80	16.439	1.587	4.751	1.00	35.14	O
ATOM	783	H	TYR	A	80	14.747	2.327	11.773	1.00	11.31	H
ATOM	784	HH	TYR	A	80	15.972	1.898	3.968	1.00	37.08	H
ATOM	785	N	ALA	A	81	12.765	4.168	12.326	1.00	9.86	N
ATOM	786	CA	ALA	A	81	11.712	4.569	13.230	1.00	6.99	C
ATOM	787	C	ALA	A	81	12.286	5.753	14.032	1.00	13.78	C
ATOM	788	O	ALA	A	81	12.649	6.757	13.432	1.00	14.63	O
ATOM	789	CB	ALA	A	81	11.424	3.384	14.120	1.00	4.72	C
ATOM	790	H	ALA	A	81	13.672	4.168	12.693	1.00	7.46	H
ATOM	791	N	TYR	A	82	12.463	5.740	15.343	1.00	10.57	N
ATOM	792	CA	TYR	A	82	12.896	6.895	16.115	1.00	7.88	C

ATOM	793	C	TYR	A	82	14.326	6.832	16.605	1.00	9.94	C
ATOM	794	O	TYR	A	82	14.759	7.711	17.359	1.00	11.53	O
ATOM	795	CB	TYR	A	82	11.927	7.081	17.303	1.00	8.60	C
ATOM	796	CG	TYR	A	82	10.480	7.353	16.885	1.00	11.16	C
ATOM	797	CD1	TYR	A	82	10.118	8.604	16.401	1.00	10.94	C
ATOM	798	CD2	TYR	A	82	9.557	6.324	16.916	1.00	6.14	C
ATOM	799	CE1	TYR	A	82	8.842	8.820	15.897	1.00	14.49	C
ATOM	800	CE2	TYR	A	82	8.275	6.533	16.422	1.00	13.98	C
ATOM	801	CZ	TYR	A	82	7.934	7.781	15.919	1.00	14.00	C
ATOM	802	OH	TYR	A	82	6.668	7.997	15.452	1.00	10.90	O
ATOM	803	H	TYR	A	82	12.259	4.924	15.823	1.00	7.19	H
ATOM	804	HH	TYR	A	82	6.175	7.165	15.497	1.00	9.22	H
ATOM	805	N	GLY	A	83	15.077	5.781	16.257	1.00	8.29	N
ATOM	806	CA	GLY	A	83	16.521	5.780	16.424	1.00	13.72	C
ATOM	807	C	GLY	A	83	17.007	5.856	17.852	1.00	9.49	C
ATOM	808	O	GLY	A	83	16.369	5.371	18.777	1.00	10.37	O
ATOM	809	H	GLY	A	83	14.644	5.029	15.809	1.00	8.74	H
ATOM	810	N	ALA	A	84	18.142	6.510	18.054	1.00	11.50	N
ATOM	811	CA	ALA	A	84	18.739	6.468	19.371	1.00	14.29	C
ATOM	812	C	ALA	A	84	18.082	7.446	20.325	1.00	19.90	C
ATOM	813	O	ALA	A	84	18.271	7.385	21.525	1.00	19.35	O
ATOM	814	CB	ALA	A	84	20.213	6.768	19.254	1.00	13.93	C
ATOM	815	H	ALA	A	84	18.565	7.022	17.334	1.00	11.82	H
ATOM	816	N	THR	A	85	17.247	8.337	19.838	1.00	11.93	N
ATOM	817	CA	THR	A	85	16.613	9.331	20.683	1.00	26.11	C
ATOM	818	C	THR	A	85	15.247	8.879	21.166	1.00	19.04	C
ATOM	819	O	THR	A	85	14.824	9.266	22.257	1.00	18.38	O
ATOM	820	CB	THR	A	85	16.600	10.722	19.972	1.00	18.88	C
ATOM	821	OG1	THR	A	85	15.321	11.318	20.063	1.00	46.16	O
ATOM	822	CG2	THR	A	85	17.090	10.721	18.526	1.00	35.65	C
ATOM	823	H	THR	A	85	16.961	8.277	18.907	1.00	11.01	H
ATOM	824	HG1	THR	A	85	15.009	11.278	20.976	1.00	38.30	H
ATOM	825	N	GLY	A	86	14.535	8.115	20.331	1.00	14.37	N
ATOM	826	CA	GLY	A	86	13.198	7.678	20.663	1.00	8.67	C
ATOM	827	C	GLY	A	86	12.228	8.842	20.429	1.00	8.93	C
ATOM	828	O	GLY	A	86	12.537	9.865	19.804	1.00	15.03	O
ATOM	829	H	GLY	A	86	14.855	7.964	19.418	1.00	13.44	H
ATOM	830	N	HIS	A	87	11.001	8.657	20.894	1.00	11.92	N
ATOM	831	CA	HIS	A	87	9.984	9.667	20.776	1.00	13.18	C
ATOM	832	C	HIS	A	87	9.610	9.972	22.211	1.00	8.36	C
ATOM	833	O	HIS	A	87	9.003	9.127	22.884	1.00	12.76	O
ATOM	834	CB	HIS	A	87	8.783	9.118	20.021	1.00	12.71	C
ATOM	835	CG	HIS	A	87	7.728	10.207	19.827	1.00	10.84	C
ATOM	836	ND1	HIS	A	87	7.793	11.283	19.044	1.00	16.17	N
ATOM	837	CD2	HIS	A	87	6.543	10.244	20.513	1.00	11.90	C
ATOM	838	CE1	HIS	A	87	6.693	11.981	19.247	1.00	10.11	C
ATOM	839	NE2	HIS	A	87	5.957	11.333	20.120	1.00	16.02	N
ATOM	840	H	HIS	A	87	10.833	7.861	21.439	1.00	8.36	H
ATOM	841	HD1	HIS	A	87	8.474	11.468	18.369	1.00	15.87	H
ATOM	842	HE2	HIS	A	87	5.093	11.653	20.461	1.00	13.02	H
ATOM	843	N	PRO	A	88	9.957	11.157	22.713	1.00	20.43	N
ATOM	844	CA	PRO	A	88	9.857	11.525	24.124	1.00	40.00	C
ATOM	845	C	PRO	A	88	8.530	11.195	24.776	1.00	16.70	C
ATOM	846	O	PRO	A	88	7.461	11.464	24.228	1.00	31.15	O

ATOM	847	CB	PRO	A	88	10.101	13.013	24.098	1.00	47.23	C
ATOM	848	CG	PRO	A	88	9.769	13.445	22.687	1.00	43.23	C
ATOM	849	CD	PRO	A	88	10.394	12.300	21.918	1.00	45.60	C
ATOM	850	N	GLY	A	89	8.635	10.487	25.885	1.00	17.71	N
ATOM	851	CA	GLY	A	89	7.477	10.104	26.645	1.00	14.18	C
ATOM	852	C	GLY	A	89	6.884	8.800	26.184	1.00	19.36	C
ATOM	853	O	GLY	A	89	6.171	8.171	26.951	1.00	25.36	O
ATOM	854	H	GLY	A	89	9.514	10.195	26.194	1.00	16.99	H
ATOM	855	N	ILE	A	90	7.139	8.328	24.961	1.00	19.64	N
ATOM	856	CA	ILE	A	90	6.369	7.223	24.404	1.00	16.74	C
ATOM	857	C	ILE	A	90	7.332	6.117	23.957	1.00	14.30	C
ATOM	858	O	ILE	A	90	7.232	4.980	24.409	1.00	16.09	O
ATOM	859	CB	AILE	A	90	5.468	7.723	23.227	0.50	18.90	C
ATOM	860	CB	BILE	A	90	5.525	7.697	23.180	0.50	22.58	C
ATOM	861	CG1AILE	A	90	4.597	8.930	23.621	0.50	20.70	C	
ATOM	862	CG1BILE	A	90	4.731	8.994	23.409	0.50	26.06	C	
ATOM	863	CG2AILE	A	90	4.603	6.573	22.728	0.50	14.95	C	
ATOM	864	CG2BILE	A	90	4.617	6.567	22.707	0.50	14.82	C	
ATOM	865	CD1AILE	A	90	3.777	9.621	22.505	0.50	13.02	C	
ATOM	866	CD1BILE	A	90	3.699	8.977	24.553	0.50	27.61	C	
ATOM	867	H	ILE	A	90	7.858	8.722	24.434	1.00	14.01	H
ATOM	868	N	ILE	A	91	8.302	6.386	23.074	1.00	20.63	N
ATOM	869	CA	ILE	A	91	9.112	5.319	22.478	1.00	9.02	C
ATOM	870	C	ILE	A	91	10.518	5.518	23.031	1.00	10.99	C
ATOM	871	O	ILE	A	91	11.048	6.622	22.882	1.00	8.91	O
ATOM	872	CB	ILE	A	91	9.112	5.420	20.926	1.00	13.49	C
ATOM	873	CG1	ILE	A	91	7.726	5.403	20.279	1.00	15.53	C
ATOM	874	CG2	ILE	A	91	9.999	4.380	20.291	1.00	11.43	C
ATOM	875	CD1	ILE	A	91	6.855	4.203	20.549	1.00	11.48	C
ATOM	876	H	ILE	A	91	8.573	7.308	22.924	1.00	15.61	H
ATOM	877	N	PRO	A	92	11.137	4.511	23.669	1.00	14.31	N
ATOM	878	CA	PRO	A	92	12.512	4.569	24.185	1.00	8.63	C
ATOM	879	C	PRO	A	92	13.561	4.595	23.054	1.00	11.44	C
ATOM	880	O	PRO	A	92	13.250	4.212	21.910	1.00	9.68	O
ATOM	881	CB	PRO	A	92	12.640	3.226	24.953	1.00	13.25	C
ATOM	882	CG	PRO	A	92	11.294	2.557	24.973	1.00	14.48	C
ATOM	883	CD	PRO	A	92	10.605	3.142	23.767	1.00	23.63	C
ATOM	884	N	PRO	A	93	14.827	4.991	23.322	1.00	17.49	N
ATOM	885	CA	PRO	A	93	15.940	4.825	22.401	1.00	10.43	C
ATOM	886	C	PRO	A	93	16.043	3.372	21.956	1.00	8.59	C
ATOM	887	O	PRO	A	93	15.801	2.417	22.705	1.00	9.95	O
ATOM	888	CB	PRO	A	93	17.138	5.192	23.264	1.00	9.89	C
ATOM	889	CG	PRO	A	93	16.617	6.269	24.167	1.00	12.29	C
ATOM	890	CD	PRO	A	93	15.290	5.628	24.560	1.00	16.81	C
ATOM	891	N	HIS	A	94	16.398	3.247	20.674	1.00	7.49	N
ATOM	892	CA	HIS	A	94	16.720	1.961	20.078	1.00	11.47	C
ATOM	893	C	HIS	A	94	15.547	0.984	20.149	1.00	10.68	C
ATOM	894	O	HIS	A	94	15.782	-0.213	20.308	1.00	12.00	O
ATOM	895	CB	HIS	A	94	17.976	1.374	20.767	1.00	13.33	C
ATOM	896	CG	HIS	A	94	18.600	0.239	19.990	1.00	12.75	C
ATOM	897	ND1	HIS	A	94	18.608	-1.059	20.281	1.00	23.48	N
ATOM	898	CD2	HIS	A	94	19.281	0.418	18.810	1.00	20.24	C
ATOM	899	CE1	HIS	A	94	19.282	-1.681	19.339	1.00	16.30	C
ATOM	900	NE2	HIS	A	94	19.679	-0.778	18.464	1.00	28.26	N

ATOM	901	H	HIS	A	94	16.375	4.054	20.124	1.00	6.99	H
ATOM	902	HD1	HIS	A	94	18.062	-1.490	20.978	1.00	17.79	H
ATOM	903	HE2	HIS	A	94	20.205	-0.979	17.659	1.00	17.68	H
ATOM	904	N	ALA	A	95	14.295	1.424	19.985	1.00	5.88	N
ATOM	905	CA	ALA	A	95	13.196	0.485	19.964	1.00	6.75	C
ATOM	906	C	ALA	A	95	12.853	0.009	18.548	1.00	16.10	C
ATOM	907	O	ALA	A	95	12.811	0.800	17.590	1.00	13.72	O
ATOM	908	CB	ALA	A	95	11.935	1.098	20.567	1.00	7.08	C
ATOM	909	H	ALA	A	95	14.102	2.382	19.903	1.00	5.00	H
ATOM	910	N	THR	A	96	12.679	-1.316	18.404	1.00	11.69	N
ATOM	911	CA	THR	A	96	12.098	-1.931	17.217	1.00	10.07	C
ATOM	912	C	THR	A	96	10.557	-1.838	17.339	1.00	7.93	C
ATOM	913	O	THR	A	96	9.998	-2.132	18.406	1.00	13.22	O
ATOM	914	CB	THR	A	96	12.599	-3.419	17.057	1.00	15.74	C
ATOM	915	OG1	THR	A	96	14.021	-3.381	16.899	1.00	14.12	O
ATOM	916	CG2	THR	A	96	11.974	-4.155	15.861	1.00	11.48	C
ATOM	917	H	THR	A	96	12.900	-1.900	19.149	1.00	13.93	H
ATOM	918	HG1	THR	A	96	14.366	-4.209	17.248	1.00	13.94	H
ATOM	919	N	LEU	A	97	9.866	-1.408	16.273	1.00	11.13	N
ATOM	920	CA	LEU	A	97	8.430	-1.167	16.316	1.00	12.13	C
ATOM	921	C	LEU	A	97	7.766	-2.178	15.408	1.00	8.98	C
ATOM	922	O	LEU	A	97	8.268	-2.498	14.331	1.00	7.48	O
ATOM	923	CB	LEU	A	97	8.035	0.267	15.842	1.00	5.98	C
ATOM	924	CG	LEU	A	97	8.713	1.455	16.513	1.00	14.61	C
ATOM	925	CD1	LEU	A	97	8.154	2.783	15.998	1.00	10.49	C
ATOM	926	CD2	LEU	A	97	8.609	1.342	18.027	1.00	10.50	C
ATOM	927	H	LEU	A	97	10.345	-1.277	15.423	1.00	9.23	H
ATOM	928	N	VAL	A	98	6.635	-2.694	15.854	1.00	9.66	N
ATOM	929	CA	VAL	A	98	5.812	-3.488	14.970	1.00	9.32	C
ATOM	930	C	VAL	A	98	4.443	-2.824	14.832	1.00	8.48	C
ATOM	931	O	VAL	A	98	3.830	-2.387	15.800	1.00	8.62	O
ATOM	932	CB	AVAL	A	98	5.780	-5.019	15.309	0.50	9.81	C
ATOM	933	CB	BVAL	A	98	5.766	-5.013	15.350	0.50	8.56	C
ATOM	934	CG1AVAL	A	98	7.134	-5.518	15.794	0.50	2.00	C	
ATOM	935	CG1BVAL	A	98	5.842	-5.274	16.826	0.50	21.38	C	
ATOM	936	CG2AVAL	A	98	4.687	-5.488	16.208	0.50	14.46	C	
ATOM	937	CG2BVAL	A	98	4.578	-5.764	14.748	0.50	2.00	C	
ATOM	938	H	VAL	A	98	6.283	-2.461	16.742	1.00	7.57	H
ATOM	939	N	PHE	A	99	4.039	-2.628	13.579	1.00	12.47	N
ATOM	940	CA	PHE	A	99	2.739	-2.065	13.257	1.00	11.83	C
ATOM	941	C	PHE	A	99	1.895	-3.058	12.471	1.00	11.96	C
ATOM	942	O	PHE	A	99	2.383	-3.742	11.569	1.00	14.60	O
ATOM	943	CB	PHE	A	99	2.843	-0.764	12.443	1.00	9.84	C
ATOM	944	CG	PHE	A	99	3.321	0.444	13.238	1.00	12.64	C
ATOM	945	CD1	PHE	A	99	4.687	0.685	13.377	1.00	11.18	C
ATOM	946	CD2	PHE	A	99	2.387	1.353	13.754	1.00	9.23	C
ATOM	947	CE1	PHE	A	99	5.118	1.852	13.988	1.00	9.63	C
ATOM	948	CE2	PHE	A	99	2.841	2.499	14.372	1.00	8.47	C
ATOM	949	CZ	PHE	A	99	4.197	2.754	14.488	1.00	10.83	C
ATOM	950	H	PHE	A	99	4.615	-2.934	12.841	1.00	9.67	H
ATOM	951	N	ASP	A	100	0.614	-3.105	12.792	1.00	6.70	N
ATOM	952	CA	ASP	A	100	-0.379	-3.770	11.956	1.00	7.98	C
ATOM	953	C	ASP	A	100	-1.039	-2.659	11.134	1.00	7.35	C
ATOM	954	O	ASP	A	100	-1.632	-1.764	11.724	1.00	12.17	O

ATOM	955	CB	ASP	A	100	-1.324	-4.481	12.930	1.00	10.14	C
ATOM	956	CG	ASP	A	100	-2.605	-5.090	12.425	1.00	9.95	C
ATOM	957	OD1	ASP	A	100	-2.950	-4.951	11.258	1.00	11.11	O
ATOM	958	OD2	ASP	A	100	-3.285	-5.677	13.249	1.00	15.34	O
ATOM	959	H	ASP	A	100	0.312	-2.608	13.579	1.00	7.14	H
ATOM	960	N	VAL	A	101	-0.931	-2.646	9.808	1.00	5.55	N
ATOM	961	CA	VAL	A	101	-1.390	-1.566	8.975	1.00	7.61	C
ATOM	962	C	VAL	A	101	-2.294	-2.156	7.914	1.00	8.52	C
ATOM	963	O	VAL	A	101	-1.958	-3.138	7.247	1.00	9.25	O
ATOM	964	CB	VAL	A	101	-0.219	-0.822	8.287	1.00	7.15	C
ATOM	965	CG1	VAL	A	101	-0.756	0.324	7.443	1.00	15.13	C
ATOM	966	CG2	VAL	A	101	0.747	-0.254	9.298	1.00	7.68	C
ATOM	967	H	VAL	A	101	-0.521	-3.420	9.361	1.00	6.45	H
ATOM	968	N	GLU	A	102	-3.461	-1.547	7.760	1.00	7.96	N
ATOM	969	CA	GLU	A	102	-4.403	-1.955	6.737	1.00	9.92	C
ATOM	970	C	GLU	A	102	-4.604	-0.785	5.781	1.00	13.06	C
ATOM	971	O	GLU	A	102	-5.052	0.294	6.203	1.00	12.50	O
ATOM	972	CB	GLU	A	102	-5.695	-2.390	7.379	1.00	5.36	C
ATOM	973	CG	GLU	A	102	-6.606	-2.921	6.277	1.00	13.32	C
ATOM	974	CD	GLU	A	102	-8.027	-3.374	6.662	1.00	26.98	C
ATOM	975	OE1	GLU	A	102	-8.444	-3.183	7.801	1.00	18.82	O
ATOM	976	OE2	GLU	A	102	-8.726	-3.911	5.797	1.00	35.49	O
ATOM	977	H	GLU	A	102	-3.672	-0.769	8.321	1.00	7.09	H
ATOM	978	N	LEU	A	103	-4.264	-0.934	4.499	1.00	10.24	N
ATOM	979	CA	LEU	A	103	-4.412	0.162	3.545	1.00	17.35	C
ATOM	980	C	LEU	A	103	-5.842	0.131	2.996	1.00	16.77	C
ATOM	981	O	LEU	A	103	-6.218	-0.674	2.131	1.00	10.58	O
ATOM	982	CB	LEU	A	103	-3.383	0.101	2.396	1.00	6.83	C
ATOM	983	CG	LEU	A	103	-3.420	1.173	1.322	1.00	6.78	C
ATOM	984	CD1	LEU	A	103	-3.355	2.593	1.903	1.00	9.81	C
ATOM	985	CD2	LEU	A	103	-2.305	0.884	0.336	1.00	7.93	C
ATOM	986	H	LEU	A	103	-3.985	-1.823	4.179	1.00	5.61	H
ATOM	987	N	LEU	A	104	-6.632	1.054	3.534	1.00	12.27	N
ATOM	988	CA	LEU	A	104	-8.049	1.135	3.206	1.00	19.13	C
ATOM	989	C	LEU	A	104	-8.359	1.714	1.814	1.00	26.84	C
ATOM	990	O	LEU	A	104	-9.183	1.175	1.064	1.00	20.98	O
ATOM	991	CB	LEU	A	104	-8.760	1.959	4.286	1.00	11.01	C
ATOM	992	CG	LEU	A	104	-8.697	1.550	5.741	1.00	13.52	C
ATOM	993	CD1	LEU	A	104	-9.264	2.663	6.620	1.00	15.82	C
ATOM	994	CD2	LEU	A	104	-9.395	0.223	5.923	1.00	17.08	C
ATOM	995	H	LEU	A	104	-6.243	1.701	4.162	1.00	8.40	H
ATOM	996	N	LYS	A	105	-7.714	2.825	1.437	1.00	17.27	N
ATOM	997	CA	LYS	A	105	-8.164	3.660	0.330	1.00	22.31	C
ATOM	998	C	LYS	A	105	-7.044	4.641	0.029	1.00	15.60	C
ATOM	999	O	LYS	A	105	-6.223	4.973	0.895	1.00	15.20	O
ATOM	1000	CB	LYS	A	105	-9.399	4.418	0.867	1.00	19.05	C
ATOM	1001	CG	LYS	A	105	-10.040	5.538	0.110	1.00	31.96	C
ATOM	1002	CD	LYS	A	105	-11.223	5.999	0.948	1.00	34.16	C
ATOM	1003	CE	LYS	A	105	-12.030	7.009	0.125	1.00	71.57	C
ATOM	1004	NZ	LYS	A	105	-13.268	7.398	0.781	1.00	74.94	N
ATOM	1005	H	LYS	A	105	-6.934	3.132	1.952	1.00	14.54	H
ATOM	1006	HZ1	LYS	A	105	-13.049	7.778	1.724	1.00	50.00	H
ATOM	1007	HZ2	LYS	A	105	-13.743	8.131	0.215	1.00	50.00	H
ATOM	1008	HZ3	LYS	A	105	-13.889	6.570	0.873	1.00	50.00	H

ATOM	1009	N	LEU	A	106	-7.008	5.096	-1.213	1.00	14.99	N
ATOM	1010	CA	LEU	A	106	-6.121	6.152	-1.629	1.00	11.65	C
ATOM	1011	C	LEU	A	106	-6.996	7.338	-2.035	1.00	14.03	C
ATOM	1012	O	LEU	A	106	-8.065	7.137	-2.605	1.00	28.26	O
ATOM	1013	CB	LEU	A	106	-5.295	5.656	-2.810	1.00	18.89	C
ATOM	1014	CG	LEU	A	106	-4.296	4.535	-2.575	1.00	13.45	C
ATOM	1015	CD1	LEU	A	106	-3.659	4.162	-3.895	1.00	18.28	C
ATOM	1016	CD2	LEU	A	106	-3.206	4.994	-1.580	1.00	27.57	C
ATOM	1017	H	LEU	A	106	-7.703	4.847	-1.855	1.00	13.04	H
ATOM	1018	N	GLU	A	107	-6.585	8.553	-1.697	1.00	20.68	N
ATOM	1019	CA	GLU	A	107	-7.208	9.779	-2.162	1.00	17.07	C
ATOM	1020	C	GLU	A	107	-6.108	10.687	-2.745	1.00	21.33	C
ATOM	1021	O	GLU	A	107	-4.930	10.316	-2.752	1.00	47.95	O
ATOM	1022	CB	GLU	A	107	-7.864	10.477	-1.003	1.00	24.97	C
ATOM	1023	CG	GLU	A	107	-8.835	9.575	-0.288	1.00	20.19	C
ATOM	1024	CD	GLU	A	107	-9.421	10.133	0.990	1.00	30.01	C
ATOM	1025	OE1	GLU	A	107	-8.949	11.142	1.525	1.00	31.02	O
ATOM	1026	OE2	GLU	A	107	-10.372	9.522	1.466	1.00	46.48	O
ATOM	1027	OXT	GLU	A	107	-6.431	11.768	-3.232	1.00	62.18	O
ATOM	1028	H	GLU	A	107	-5.744	8.663	-1.209	1.00	17.46	H
TER	1029		GLU	A	107						
HETATM	1030	C1	RAP	A	108	4.633	8.500	12.847	1.00	5.98	C
HETATM	1031	O1	RAP	A	108	4.264	9.593	13.679	1.00	9.08	O
HETATM	1032	O2	RAP	A	108	5.367	8.726	11.888	1.00	14.08	O
HETATM	1033	C2	RAP	A	108	4.177	7.070	13.135	1.00	6.42	C
HETATM	1034	C3	RAP	A	108	3.720	6.374	11.862	1.00	5.50	C
HETATM	1035	C4	RAP	A	108	2.354	6.832	11.372	1.00	4.49	C
HETATM	1036	C5	RAP	A	108	1.360	6.653	12.505	1.00	4.19	C
HETATM	1037	C6	RAP	A	108	1.783	7.430	13.713	1.00	3.25	C
HETATM	1038	N7	RAP	A	108	3.105	6.934	14.127	1.00	8.46	N
HETATM	1039	C8	RAP	A	108	3.385	6.549	15.382	1.00	10.06	C
HETATM	1040	O3	RAP	A	108	4.552	6.237	15.654	1.00	10.38	O
HETATM	1041	C9	RAP	A	108	2.397	6.409	16.381	1.00	11.13	C
HETATM	1042	O4	RAP	A	108	1.783	5.339	16.474	1.00	10.60	O
HETATM	1043	C10	RAP	A	108	2.056	7.541	17.368	1.00	16.59	C
HETATM	1044	O5	RAP	A	108	1.280	8.457	16.631	1.00	10.76	O
HETATM	1045	O6	RAP	A	108	1.310	6.992	18.458	1.00	14.16	O
HETATM	1046	C11	RAP	A	108	3.332	8.282	17.940	1.00	10.40	C
HETATM	1047	C12	RAP	A	108	2.942	9.591	18.664	1.00	12.17	C
HETATM	1048	C13	RAP	A	108	2.010	10.423	17.795	1.00	12.80	C
HETATM	1049	C14	RAP	A	108	0.842	9.628	17.221	1.00	10.37	C
HETATM	1050	C15	RAP	A	108	0.193	10.413	16.094	1.00	5.94	C
HETATM	1051	C16	RAP	A	108	-0.582	11.664	16.490	1.00	9.79	C
HETATM	1052	O7	RAP	A	108	-1.627	11.272	17.324	1.00	20.17	O
HETATM	1053	C17	RAP	A	108	-1.145	12.371	15.276	1.00	15.52	C
HETATM	1054	C18	RAP	A	108	-0.672	13.571	14.967	1.00	14.38	C
HETATM	1055	C19	RAP	A	108	-1.096	14.367	13.807	1.00	9.73	C
HETATM	1056	C20	RAP	A	108	-0.586	15.578	13.634	1.00	10.26	C
HETATM	1057	C21	RAP	A	108	-0.900	16.377	12.435	1.00	11.40	C
HETATM	1058	C22	RAP	A	108	-0.248	17.488	12.149	1.00	17.77	C
HETATM	1059	C23	RAP	A	108	-0.450	18.289	10.881	1.00	15.64	C
HETATM	1060	C24	RAP	A	108	0.911	18.401	10.216	1.00	14.68	C
HETATM	1061	C25	RAP	A	108	1.674	17.112	9.975	1.00	11.87	C
HETATM	1062	C26	RAP	A	108	3.157	17.391	9.771	1.00	11.65	C

HETATM	1063	08	RAP	A	108	3.611	17.669	8.663	1.00	18.31	O
HETATM	1064	C27	RAP	A	108	4.048	17.297	11.005	1.00	8.13	C
HETATM	1065	09	RAP	A	108	5.210	18.050	10.778	1.00	23.09	O
HETATM	1066	C28	RAP	A	108	4.513	15.841	11.329	1.00	10.80	C
HETATM	1067	010	RAP	A	108	4.824	15.200	10.084	1.00	12.16	O
HETATM	1068	C29	RAP	A	108	3.462	15.014	12.094	1.00	9.60	C
HETATM	1069	C30	RAP	A	108	2.808	13.989	11.549	1.00	8.55	C
HETATM	1070	C31	RAP	A	108	1.773	13.042	12.175	1.00	8.43	C
HETATM	1071	C32	RAP	A	108	2.433	11.701	12.495	1.00	10.69	C
HETATM	1072	011	RAP	A	108	2.264	10.701	11.791	1.00	9.49	O
HETATM	1073	C33	RAP	A	108	3.358	11.693	13.707	1.00	6.51	C
HETATM	1074	C34	RAP	A	108	4.630	10.909	13.455	1.00	9.62	C
HETATM	1075	C35	RAP	A	108	5.846	11.169	14.367	1.00	9.58	C
HETATM	1076	C36	RAP	A	108	6.551	12.480	14.027	1.00	10.31	C
HETATM	1077	C37	RAP	A	108	7.210	12.586	12.650	1.00	22.90	C
HETATM	1078	C38	RAP	A	108	7.812	13.983	12.461	1.00	14.17	C
HETATM	1079	C39	RAP	A	108	8.386	14.202	11.059	1.00	34.20	C
HETATM	1080	012	RAP	A	108	9.041	15.444	11.086	1.00	30.82	O
HETATM	1081	C40	RAP	A	108	9.399	13.057	10.711	1.00	38.24	C
HETATM	1082	013	RAP	A	108	9.803	13.189	9.349	1.00	28.84	O
HETATM	1083	C41	RAP	A	108	8.819	11.645	10.930	1.00	16.32	C
HETATM	1084	C42	RAP	A	108	8.243	11.505	12.332	1.00	14.05	C
HETATM	1085	C43	RAP	A	108	4.258	7.412	18.840	1.00	11.25	C
HETATM	1086	C44	RAP	A	108	-2.257	11.621	14.522	1.00	14.40	C
HETATM	1087	C45	RAP	A	108	-1.014	19.668	11.190	1.00	9.23	C
HETATM	1088	C46	RAP	A	108	1.099	16.327	8.793	1.00	15.99	C
HETATM	1089	C47	RAP	A	108	3.222	15.475	13.519	1.00	14.60	C
HETATM	1090	C48	RAP	A	108	0.625	12.830	11.175	1.00	9.37	C
HETATM	1091	C49	RAP	A	108	5.482	11.130	15.824	1.00	8.29	C
HETATM	1092	C50	RAP	A	108	-2.123	12.243	18.189	1.00	28.36	C
HETATM	1093	C51	RAP	A	108	5.134	19.387	11.130	1.00	19.04	C
HETATM	1094	C52	RAP	A	108	8.352	16.524	10.556	1.00	28.14	C
HETATM	1095	H06	RAP	A	108	1.193	6.051	18.296	1.00	13.32	H
HETATM	1096	H01	RAP	A	108	5.144	14.296	10.221	1.00	13.32	H
HETATM	1097	H03	RAP	A	108	9.118	13.653	8.851	1.00	13.32	H
HETATM	1098	O	HOH	A	109	13.711	4.614	19.317	1.00	10.44	O
HETATM	1099	O	HOH	A	110	12.370	3.552	17.185	1.00	10.27	O
HETATM	1100	O	HOH	A	111	-1.241	-8.284	-1.434	1.00	12.23	O
HETATM	1101	O	HOH	A	112	7.154	-7.826	9.801	1.00	13.23	O
HETATM	1102	O	HOH	A	113	14.014	-2.120	4.238	1.00	21.56	O
HETATM	1103	O	HOH	A	114	12.989	-4.988	10.267	0.88	14.72	O
HETATM	1104	O	HOH	A	115	14.742	0.139	23.855	1.00	20.97	O
HETATM	1105	O	HOH	A	116	-4.908	-2.760	13.811	1.00	20.45	O
HETATM	1106	O	HOH	A	117	3.308	-6.273	-0.446	1.00	19.05	O
HETATM	1107	O	HOH	A	118	15.723	-2.951	18.984	0.92	19.73	O
HETATM	1108	O	HOH	A	119	-4.683	-2.710	10.979	1.00	21.45	O
HETATM	1109	O	HOH	A	120	9.150	0.338	-0.871	1.00	21.75	O
HETATM	1110	O	HOH	A	121	12.319	7.586	10.611	0.89	16.22	O
HETATM	1111	O	HOH	A	122	4.956	11.211	4.410	1.00	20.92	O
HETATM	1112	O	HOH	A	123	0.223	-6.141	-2.826	1.00	19.78	O
HETATM	1113	O	HOH	A	124	4.496	2.494	-4.547	0.86	22.55	O
HETATM	1114	O	HOH	A	125	-8.981	15.116	13.622	0.93	29.61	O
HETATM	1115	O	HOH	A	126	-2.561	8.843	18.364	0.51	9.74	O
HETATM	1116	O	HOH	A	127	0.579	7.596	21.102	0.83	21.64	O

HETATM	1117	0	HOH	A	128	-1.361	15.053	5.335	0.97	27.18	0
HETATM	1118	0	HOH	A	129	9.868	12.384	17.361	0.99	26.41	0
HETATM	1119	0	HOH	A	130	13.021	-3.084	20.746	0.84	25.47	0
HETATM	1120	0	HOH	A	131	13.147	-6.244	19.809	1.00	33.69	0
HETATM	1121	0	HOH	A	132	19.691	7.330	15.401	1.00	34.12	0
HETATM	1122	0	HOH	A	133	4.131	-12.241	3.833	0.61	29.31	0
HETATM	1123	0	HOH	A	134	10.563	10.031	7.095	1.00	34.36	0
HETATM	1124	0	HOH	A	135	19.240	3.723	15.306	1.00	30.14	0
HETATM	1125	0	HOH	A	136	-7.944	-8.631	7.452	0.76	26.11	0
HETATM	1126	0	HOH	A	137	9.738	-7.426	3.673	0.77	29.04	0
HETATM	1127	0	HOH	A	138	19.287	3.331	18.119	1.00	29.46	0
HETATM	1128	0	HOH	A	139	15.311	-2.532	22.773	0.59	18.35	0
HETATM	1129	0	HOH	A	140	12.602	-7.831	10.522	0.70	26.37	0
HETATM	1130	0	HOH	A	141	20.311	7.632	23.452	0.88	32.87	0
HETATM	1131	0	HOH	A	142	-8.290	-6.594	13.906	1.00	37.66	0
HETATM	1132	0	HOH	A	143	6.000	-7.155	0.752	1.00	36.79	0
HETATM	1133	0	HOH	A	144	11.712	8.562	25.025	1.00	37.93	0
HETATM	1134	0	HOH	A	145	6.408	17.304	7.663	1.00	42.88	0
HETATM	1135	0	HOH	A	146	8.316	5.712	-0.315	0.89	35.11	0
HETATM	1136	0	HOH	A	147	-8.695	3.719	-3.268	0.41	27.28	0
HETATM	1137	0	HOH	A	148	-6.139	-2.153	17.988	0.79	28.45	0
HETATM	1138	0	HOH	A	149	0.610	-9.863	-0.440	0.99	38.91	0
HETATM	1139	0	HOH	A	150	15.715	9.985	24.770	1.00	42.21	0
HETATM	1140	0	HOH	A	151	-0.495	1.447	-8.979	0.64	30.72	0
HETATM	1141	0	HOH	A	152	4.285	-9.238	1.709	1.00	37.55	0
HETATM	1142	0	HOH	A	153	-11.723	-0.712	23.869	1.00	40.86	0
HETATM	1143	0	HOH	A	154	11.488	-3.074	2.350	0.72	41.01	0
HETATM	1144	0	HOH	A	155	15.120	7.199	9.581	0.59	20.76	0
HETATM	1145	0	HOH	A	156	9.795	11.399	-2.302	0.98	37.75	0
HETATM	1146	0	HOH	A	157	-8.735	-4.901	-2.370	0.50	33.79	0
HETATM	1147	0	HOH	A	158	-0.568	-3.277	25.728	0.85	51.27	0
HETATM	1148	0	HOH	A	159	19.373	8.856	25.776	1.00	38.05	0
HETATM	1149	0	HOH	A	160	-2.602	-9.850	-3.927	1.00	43.85	0
HETATM	1150	0	HOH	A	161	0.050	-14.393	2.288	1.00	40.23	0
HETATM	1151	0	HOH	A	162	1.610	-14.281	5.871	0.76	37.91	0
HETATM	1152	0	HOH	A	163	5.428	-14.217	6.653	0.80	37.24	0
HETATM	1153	0	HOH	A	164	-9.314	-2.214	-5.662	1.00	34.97	0
HETATM	1154	0	HOH	A	165	-2.162	4.552	-7.445	0.90	44.53	0
HETATM	1155	0	HOH	A	166	-7.983	-6.626	5.079	1.00	38.42	0
HETATM	1156	0	HOH	A	167	21.106	-2.754	16.088	0.82	44.40	0
HETATM	1157	0	HOH	A	168	8.565	-10.372	3.861	1.00	49.24	0
HETATM	1158	0	HOH	A	169	-8.100	-8.798	1.688	0.95	45.19	0
HETATM	1159	0	HOH	A	170	9.799	3.505	-1.518	1.00	39.70	0
HETATM	1160	0	HOH	A	171	0.503	-4.780	-10.227	0.92	41.96	0
HETATM	1161	0	HOH	A	172	19.059	-0.774	13.939	0.40	46.58	0
HETATM	1162	0	HOH	A	173	4.165	-11.485	2.776	0.68	46.57	0
HETATM	1163	0	HOH	A	174	6.724	-9.652	16.834	0.75	43.11	0
HETATM	1164	0	HOH	A	175	8.449	20.615	10.147	1.00	52.53	0
HETATM	1165	0	HOH	A	176	-6.246	8.458	13.805	0.99	43.67	0
HETATM	1166	0	HOH	A	177	18.565	-0.788	8.535	0.58	25.28	0
HETATM	1167	0	HOH	A	178	12.524	14.156	15.048	0.75	50.62	0
HETATM	1168	0	HOH	A	179	-7.361	4.286	-6.120	0.87	45.92	0
HETATM	1169	0	HOH	A	180	9.084	8.193	30.107	0.73	50.62	0
HETATM	1170	0	HOH	A	181	5.353	7.074	-7.617	1.00	45.14	0

HETATM	1171	0	HOH	A	182	7.071	14.671	-2.213	0.72	44.31	0
HETATM	1172	0	HOH	A	183	11.390	-5.548	2.903	1.00	45.24	0
HETATM	1173	0	HOH	A	184	3.705	-11.294	15.714	0.73	62.78	0
HETATM	1174	0	HOH	A	185	6.290	-12.577	11.834	0.91	63.29	0
HETATM	1175	0	HOH	A	186	15.724	7.740	12.569	0.84	43.78	0
HETATM	1176	0	HOH	A	187	15.320	3.814	-0.109	1.00	46.69	0
HETATM	1177	0	HOH	A	188	11.066	12.165	14.148	1.00	52.26	0
HETATM	1178	0	HOH	A	189	-2.305	13.015	10.396	0.69	48.40	0
HETATM	1179	0	HOH	A	190	10.289	15.215	2.271	1.00	49.99	0
HETATM	1180	0	HOH	A	191	-14.194	-3.824	4.927	0.56	46.37	0
HETATM	1181	0	HOH	A	192	15.576	-4.385	14.703	1.00	56.00	0
HETATM	1182	0	HOH	A	193	-4.948	11.515	9.936	0.75	45.07	0
HETATM	1183	0	HOH	A	194	11.767	-6.802	23.315	0.67	45.81	0
HETATM	1184	0	HOH	A	195	19.013	11.621	24.860	1.00	66.21	0
HETATM	1185	0	HOH	A	196	12.529	17.914	12.306	0.59	50.92	0
HETATM	1186	0	HOH	A	197	4.616	20.134	7.429	1.00	56.06	0
HETATM	1187	0	HOH	A	198	11.720	10.374	28.067	0.78	49.39	0
HETATM	1188	0	HOH	A	199	21.956	9.297	22.399	0.92	61.45	0
HETATM	1189	0	HOH	A	200	3.813	-10.487	21.876	1.00	60.11	0
HETATM	1190	0	HOH	A	201	-10.177	-5.766	1.941	0.89	47.46	0
HETATM	1191	0	HOH	A	202	12.912	11.341	17.471	0.72	29.24	0
HETATM	1192	0	HOH	A	203	-13.247	13.956	10.938	0.58	53.33	0
HETATM	1193	0	HOH	A	204	2.516	-14.263	2.186	0.72	45.69	0
HETATM	1194	0	HOH	A	205	11.923	-9.286	21.896	0.98	45.91	0
HETATM	1195	0	HOH	A	206	-5.617	14.450	1.733	1.00	50.10	0
HETATM	1196	0	HOH	A	207	13.176	-7.604	14.206	0.50	41.46	0
HETATM	1197	0	HOH	A	208	-5.817	10.729	11.860	1.00	44.20	0
HETATM	1198	0	HOH	A	209	2.093	-13.180	-0.045	0.68	49.74	0
HETATM	1199	0	HOH	A	210	11.679	-0.994	23.351	0.62	46.69	0
HETATM	1200	0	HOH	A	211	12.019	19.146	9.856	0.62	48.55	0
HETATM	1201	0	HOH	A	212	2.351	20.217	6.237	0.82	55.30	0
HETATM	1202	0	HOH	A	213	-0.468	-8.897	-8.871	0.60	43.26	0
HETATM	1203	0	HOH	A	214	12.074	6.391	1.989	0.68	42.25	0
HETATM	1204	0	HOH	A	215	-10.022	-8.902	11.765	0.97	59.16	0
HETATM	1205	0	HOH	A	216	17.246	5.567	7.897	0.96	72.72	0
HETATM	1206	0	HOH	A	217	10.220	-8.740	26.275	0.53	48.13	0
HETATM	1207	0	HOH	A	218	5.332	3.455	25.799	0.60	49.45	0
HETATM	1208	0	HOH	A	219	-14.447	-4.763	15.812	0.67	49.47	0
HETATM	1209	0	HOH	A	220	-11.952	-7.785	3.937	0.59	48.74	0
HETATM	1210	0	HOH	A	221	11.239	-2.520	21.226	0.59	41.21	0
HETATM	1211	0	HOH	A	222	19.871	7.101	2.737	0.70	54.57	0
HETATM	1212	0	HOH	A	223	-9.253	8.067	22.611	0.88	71.92	0
HETATM	1213	0	HOH	A	224	14.762	-9.286	11.495	0.43	54.93	0
HETATM	1214	0	HOH	A	225	8.516	18.025	4.379	0.71	53.38	0
HETATM	1215	0	HOH	A	226	13.793	-1.543	0.127	0.66	49.81	0
HETATM	1216	0	HOH	A	227	-12.297	6.615	5.037	0.61	48.14	0
HETATM	1217	0	HOH	A	228	11.923	8.740	4.379	0.71	46.89	0
HETATM	1218	0	HOH	A	229	10.123	-6.243	0.055	0.54	49.94	0
HETATM	1219	0	HOH	A	230	-10.759	-8.925	9.485	1.00	68.01	0
HETATM	1220	0	HOH	A	231	-10.487	14.161	-0.107	0.80	46.65	0
HETATM	1221	0	HOH	A	232	3.196	18.042	4.596	0.69	59.09	0
HETATM	1222	0	HOH	A	233	11.610	-14.657	3.936	0.44	80.48	0
HETATM	1223	0	HOH	A	234	12.491	-0.546	2.190	0.65	47.59	0
HETATM	1224	0	HOH	A	235	10.787	7.101	0.000	0.52	49.42	0

HETATM	1225	0	HOH	A	236	-9.426	-6.421	8.886	0.34	47.03	0
HETATM	1226	0	HOH	A	237	11.923	0.546	-0.547	0.89	45.99	0
HETATM	1227	0	HOH	A	238	-2.327	14.131	7.962	0.56	52.95	0
HETATM	1228	0	HOH	A	239	14.190	8.846	3.456	0.54	52.74	0
HETATM	1229	0	HOH	A	240	1.142	1.871	26.400	0.44	45.02	0
HETATM	1230	0	HOH	A	241	-10.179	-5.869	12.400	0.74	80.37	0
CONECT	1030	1031	1032	1033							
CONECT	1031	1030	1074								
CONECT	1032	1030									
CONECT	1033	1030	1034	1038							
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CONECT	1036	1035	1037								
CONECT	1037	1036	1038								
CONECT	1038	1033	1037	1039							
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CONECT	1066	1064	1067	1068							
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CONECT	1068	1066	1069	1089							
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CONECT	1071	1070	1072	1073							
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CONECT	1073	1071	1074								
CONECT	1074	1031	1073	1075							
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CONECT	1076	1075	1077								
CONECT	1077	1076	1078	1084							

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CONNECT 1097 1082
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