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(71) Applicant (for all designated States except US): **REGENTS OF THE UNIVERSITY OF COLORADO** [US/US]; 1800 Grant Street, 8th Floor, Denver, CO 80203 (US).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **BATEY, Robert, T.** [US/US]; 4939 Noble Park Place, Boulder, CO 80301 (US).
GILBERT, Sunny [US/US]; 1310 Lehigh Street, Boulder, CO 80305 (US).

(74) Agents: **HOXIE, Thomas** et al.; Hoxie & Associates LLC, 75 Main Street, Suite 301, Millburn, NJ 07041 (US).

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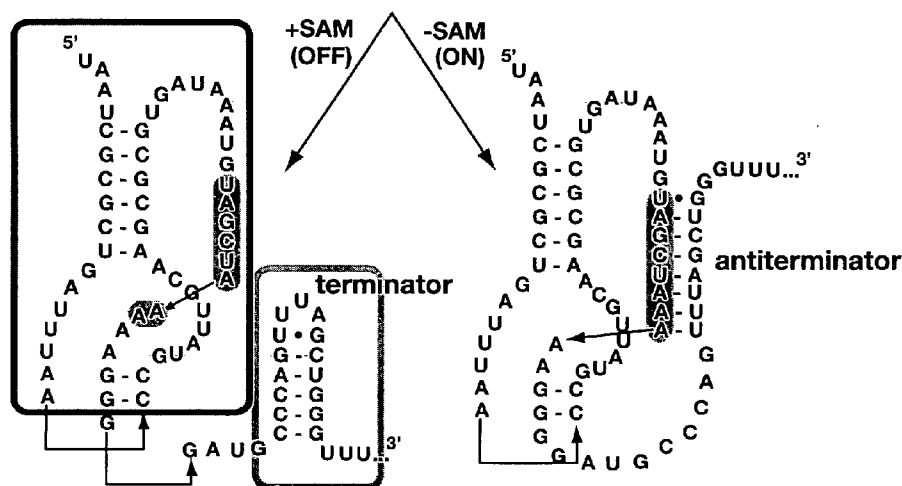
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Fig. 1



(57) Abstract: Embodiments of the present invention provide for SAM-II riboswitches and analogs thereof, and methods for using the same. In certain embodiments of the present invention, test compounds are identified that associate with SAM-II riboswitches. In other embodiments, test compounds found to associate with SAM II can be used to increase or decrease gene expression of Gram-negative bacterial organisms.

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SAM-II RIBOSWITCH AND USES THEREOF

[0001] This application claims priority from US provisional application 60/967,603, filed September 6, 2007, the contents of which are herein incorporated by reference.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH

[0002] The U.S. Government has a paid-up license in this invention and the right in limited circumstances to require the patent owner to license others on reasonable terms as provided for by the terms of Grant No. R-01 GM073850-01 awarded by the National Institutes of Health.

FIELD OF THE INVENTION

[0003] The present invention relates to compositions and methods of use thereof related to SAM-II riboswitch.

BACKGROUND OF THE INVENTION

[0004] Riboswitches are regulatory elements found within the 5'-untranslated regions (5'-UTRs) of many bacterial mRNAs. Riboswitches control gene expression in a cis-fashion through their ability to directly bind a specific small molecule metabolite. Ligand recognition is effected by the first domain of the riboswitch, termed the aptamer domain while the second, the expression platform, transduces the binding event into a regulatory switch. The switch includes an RNA element that can adapt to one of two mutually exclusive secondary structures. One of these structures is a signal for gene expression to be "on" and the other conformation turns the gene "off" (example in Fig. 1).). In *Bacillus subtilis* and other gram positive bacteria, it is believed riboswitches control greater than 2% of all genes, many of which are important for key pathways controlling the amino acid, nucleotide and cofactor metabolism.

[0005] Riboswitch aptamer domains are controlled by a diverse set of metabolites. In one example bacteria, amino acid metabolism in various *Bacillus* species is controlled by three known riboswitches: glycine, lysine and S-adenosylmethionine (SAM). Each has a distinct aptamer domain that has evolved to specifically recognize a specific ligand. Currently, there are three known distinct SAM riboswitches, one of which is dominant in gram positive bacteria, SAM-I, and one dominant in gram negative alpha-proteobacteria, SAM-II, and the third in lactobacteria, SAM-III. The SAM-II riboswitch is a cis-regulatory element found

predominantly in alpha-proteobacteria that binds S-adenosyl methionine (SAM). Its structure and sequence appear to be unrelated to the SAM I riboswitch found in Gram-positive bacteria. This SAM II riboswitch is located upstream of the metA and metC genes in *Agrobacterium tumefaciens*, and other methionine and SAM biosynthesis genes in other alpha-proteobacteria. The SAM-II riboswitch is short with less than 70 nucleotides and is structurally relatively simple being composed of a single hairpin and a pseudoknot.

[0006] A need exist to better control bacterial growth, such as Gram negative bacterial growth, and generate effective treatments against bacterial infections. Embodiments of the present invention fulfill this need.

SUMMARY OF THE INVENTION

[0007] One aspect of the present invention provides for methods of identifying a compound that associates with a SAM-II riboswitch including modeling at least a portion of the atomic structure depicted in Fig. 4A and 4B with a test compound; and determining the interaction between the test compound and the SAM-II riboswitch structure.

[0008] Certain embodiments herein concern crystalline atomic structures of SAM-II riboswitches. In accordance with the methods, the structures may also be used for modeling and assessing the interaction of a riboswitch with a binding ligand.

[0009] In other embodiments herein, a compound may be identified that associates with the SAM-II riboswitch and reduces bacterial gene expression or associates with the SAM-II riboswitch and induces bacterial gene expression. In a more particular embodiment, a bacteria can be a gram negative bacteria. In accordance with these embodiments, atomic coordinates of the atomic structure can include at least a portion of the atomic coordinates listed in Table 1 for atoms depicted in Fig. 4A and 4B wherein said association determination step can include determining a minimum interaction energy, a binding constant, a dissociation constant, or a combination thereof, for the test compound in the model of the SAM-II riboswitch. In some particular embodiments, an association determination step can include determining the interaction of the test compound with a nucleotide of SAM-II riboswitch including U10, U11, U12, U20, U21, G22, U44, A45, A46, A47 or a combination thereof. In other embodiments, an association determination step can include determining the interaction of the test compound with an S-adenosyl-methionine moiety including a ribose sugar, a methionine side chain, a sulfur moiety, an adenine moiety or combination thereof.

Alternatively, in a more particular embodiment, the association determination step can include determining the interaction of the test compound with a nucleotide of SAM-II riboswitch depicted in Fig. 4A and 4B including U10, U12, U20, G22, U44, A46, A47 or a combination thereof. Other embodiments contemplated herein include an association determination step of determining the interaction of the test compound with a P2b helix region of the SAM-II riboswitch. Yet other embodiments contemplated herein can include an association determination step including determining the interaction of the test compound within a pocket created in a major groove of the SAM-II riboswitch. Further embodiments concern an association determination step including determining the interaction of the test compound with a major groove of a P2b helix of the SAM-II riboswitch.

[0010] Bacterial cells contemplated of use in the methods and compositions herein include, but are not limited to, Gram negative species, for example, proteobacteria including *Escherichia coli*, *Salmonella*, and other Enterobacteriaceae, *Pseudomonas*, *Moraxella*, *Helicobacter*, *Stenotrophomonas*, *Bdellovibrio*, acetic acid bacteria, *Legionella* and many others. Other groups of Gram-negative bacteria include the cyanobacteria, spirochaetes, green sulfur and green non-sulfur bacteria. Medically relevant Gram-negative cocci include three organisms, which cause a sexually transmitted disease (*Neisseria gonorrhoeae*), a meningitis (*Neisseria meningitidis*), and respiratory symptoms (*Moraxella catarrhalis*). Medically relevant Gram-negative bacilli include, but are not limited to those that primarily cause respiratory problems (*Hemophilus influenzae*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Pseudomonas aeruginosa*), principally urinary problems (*Escherichia coli*, *Proteus mirabilis*, *Enterobacter cloacae*, *Serratia marcescens*), and usually gastrointestinal problems (*Helicobacter pylori*, *Salmonella enteritidis*, *Salmonella typhi*). Nosocomial gram negative bacteria can include *Acinetobacter baumannii*, which cause bacteremia, secondary meningitis, and ventilator-associated pneumonia. Medically relevant coccoid bacteria known to contain the SAM-II riboswitch include, but are not limited to, *Bordetella pertussis* and *Bordetella bronchiseptica* that causes whooping cough. In one embodiment, a bacterial organism can be medically relevant facultative intracellular bacteria known to contain the SAM-II riboswitch include, but are not limited to, *Brucella melitensis*, which causes brucellosis in many areas of the world, and has been classified by the U.S. Center for Disease Control and Prevention as a potential agent in biological warfare. A related organism, *Brucella suis*, that also contains a SAM-II riboswitch, was the first pathogenic organism to be

weaponized by the U.S. military in the 1950's, and thus represents a potential bioterrorism threat.

[0011] In certain embodiments, a SAM-II riboswitch disclosed herein can include one or more of the nucleotides listed in "Tertiary contacts" section of Table 2 where the nucleotide can be modified. In certain embodiments, the one or more modified nucleotides are selected from the group consisting of U10, U12, U20, G22, U44, A46, A47 or a combination thereof. In particular embodiments, the modified nucleotide of the SAM-II riboswitch can increase gene expression in a bacterial cell. For example, a test compound that contains a modified nucleotide may induce expression of a gene that is deleterious to a bacterial cell. In other embodiments, the modified nucleotide can decrease gene expression in a cell. For example, a test compound that contains a modified nucleotide may reduce expression of a gene that is necessary for survival of a bacterial cell. In certain particular embodiments, the modified nucleotide decreases sulfur production in a cell.

[0012] Embodiments of the present invention concern a test compound that associates with at least a portion of the SAM-II riboswitch atomic structure depicted in at least one of Fig. 4A or Fig. 4B. In accordance with these embodiments, the association can include association with at least one of nucleotides U10, U12, U20, G22, U44, A46, A47 or a combination thereof, wherein the composition is capable of modifying the SAM-II riboswitch activity of a bacterial organism by either inducing or reducing gene expression.

[0013] Certain embodiments concern compositions including, all of the 80 percent or more conserved nucleotides of the SAM-II riboswitch depicted in Fig. 1 (left) and 80% or greater, or 90% or greater or 95% or greater of the nucleotides depicted outside of the conserved region. One particular embodiment includes a composition of all 80 percent or more conserved nucleotides of the SAM-II riboswitch depicted in Fig. 1 (left) and all of the nucleotides depicted outside of the conserved region.

[0014] In one embodiment, the atomic coordinates of the atomic structure comprise the atomic coordinates listed in Table 1 for atoms depicted in Fig. 4A and 4B.

[0015] Yet in another embodiment, the interaction determination step can include determining a minimum interaction energy, a binding constant, a dissociation constant, or a combination thereof, for the test compound in the model of the SAM-II riboswitch.

[0016] Still in other embodiments, the interaction determination step and test compound identification can include determining the interaction of the test compound with a nucleotide of SAM-II riboswitch comprising U10, U12, U20, G22, U44, A46, A47 or a combination thereof. Within this embodiment, the interaction determination step can include determining the interaction of the test compound with a nucleotide of SAM-II riboswitch comprising U10, U12, U20, G22, U44, A46, A47 or a combination thereof. In addition, the test compound that effectively interacts with one or more of the above mentioned nucleotides can be identified and expanded for use in targeting bacterial organisms disclosed herein.

[0017] Another aspect of the present invention provides, a method of regulating a gene in a cell by modulating an mRNA, said method comprising administering a SAM-II riboswitch modulating compound to the cell to modulate the SAM-II riboswitch activity of the mRNA. In certain embodiments, the gene expression is stimulated, while in other embodiments the gene expression is inhibited. Within certain embodiments where the gene expression is inhibited, the SAM-II riboswitch modulating compound forms a complex with the SAM-II riboswitch, thereby preventing the mRNA from forming an antiterminator element.

[0018] Certain embodiments include a compound that associates with one or more of the contact nucleotides and modulates the activity of the SAM-II riboswitch. In one particular embodiment, a compound capable of associating with one or more of the contact nucleotides may be capable of reducing sulfur metabolism in an organism having a SAM-II or SAM-II like riboswitch. In accordance with these embodiments, compounds of the present invention may be used to reduce infection caused by, or as a treatment for infection caused by an organism contemplated herein. In certain embodiments target organisms include bacteria. Bacteria contemplated herein include, but are not limited to Gram-negative bacterial organisms.

BRIEF DESCRIPTION OF THE DRAWINGS

[0019] The following drawings form part of the present specification and are included to further demonstrate certain embodiments of the present invention. The embodiments may be better understood by reference to one or more of these drawings in combination with the detailed description of specific embodiments presented herein.

[0020] Fig. 1 represents a schematic of a secondary structural switching in the Env12 *metX* mRNA (SEQ ID NO:1). In high intracellular concentrations of SAM, the effector ligand

binds to the aptamer domain (dark grey box, left) incorporating a switching sequence (grey shaded area) into this domain, forcing the formation of a downstream rho-independent transcriptional terminator stem-loop in the expression platform (light grey box, middle). In the absence of SAM, the switching sequence is free to be incorporated into a more stable antiterminator element, allowing for transcription to proceed (SEQ ID NO: 2).

[0021] Figs. 2A-2C represents an exemplary schematic of (A) secondary structure of the Env12 metX SAM-2 riboswitch with base pairing reflecting the tertiary structure of the SAM-bound RNA (SEQ ID NO:5); (B) an exemplary schematic of the global structure of the RNA; and (C) 90° rotation of the perspective shown in (B).

[0022] Fig. 3A-3E represents a schematic of (3A) details of the interactions between L3 (magenta) and the P1 helix (blue) emphasizing the role of four stacked adenosine residues in cementing the loop to the minor groove. Fig. 3B represents a schematic of a binding pocket of SAM (salmon) with the P2b helix. Fig. 3C represents a schematic of a hydrogen bonding interactions involving the adenine moiety of SAM. Fig. 3D represents a schematic of hydrogen bonding and electrostatic interactions involving the positively charged sulfur moiety and the methyl group of SAM. Fig. 3E represents a schematic of interactions between the RNA and the main chain atoms of the methionine residue of SAM.

[0023] Figs. 4A (SEQ ID NO:6) and 4B (SEQ ID NO:7) represent schematics of exemplary sequences and secondary structures of the SAM-binding mRNA pseudoknot from Env12 and an exemplary sequence of the crystallized RNA construct with changes made to the sequence shaded in grey.

[0024] Figs. 5A and 5B represent a schematic of electron density maps around the SAM binding site promoter A of the SAM-II riboswitch contoured at 1σ (orange cage). The final model is superimposed upon the density (green, RNA; magenta, SAM). (A) Solvent flattened experimental electron density map. (B) Final $2F_o - F_c$ electron density map.

[0025] Figs. 6A and 6B. represent a schematic of superposition of the three protomers in the asymmetric unit that were built and refined individually. The standard pairwise r.m.s.d. for all atoms in the RNA and SAM is 1.26 Å and the maximum likelihood r.m.s.d. for all atoms is 0.19 Å, as calculated using the program THESEUS. The two perspectives correspond to (A) Fig.4A and (B) Fig.4B (Fig. 4B). Colors correspond to: red, molecule A; blue, molecule B; defined in the PDB coordinate file.

[0026] Figs. 7 represents a schematic of a side-by-side comparisons of the pseudoknot from human telomerase RNA (hTR, left) and SAM-II/SAM complex (right). The colors reflect the secondary structures of the RNA (blue, P1; green, P2; orange, L1; magenta, L3); the coloring pattern of SAM-II is slightly different from Figs. 4A and 4B to make a clearer comparison between the two RNAs. The hTR structure shown is model 1 from the family of structures derived from NMR constraints (PDB ID 1YMO).

Definitions

[0027] As used herein, “a” or “an” may mean one or more than one of an item.

DETAILED DESCRIPTION

[0028] In the following sections, various exemplary compositions and methods are described in order to detail various embodiments of the invention. It will be obvious to one skilled in the art that practicing the various embodiments does not require the employment of all or even some of the specific details outlined herein, but rather that molecules, test compounds, samples, concentrations, times and other specific details may be modified through routine experimentation. In some cases, well known methods or components have not been included in the description.

[0029] Embodiments of the present invention provide for compositions and methods concerning SAM-II riboswitch and SAM-II riboswitch-like molecules.

[0030] Riboswitch aptamer domains are controlled by a diverse set of metabolites. Amino acid metabolism in various *Bacillus* species is controlled by three known riboswitches: glycine, lysine and S-adenosylmethionine (SAM). Each has a distinct aptamer domain that has evolved to specifically recognize a specific ligand. Currently, there are three distinct SAM riboswitches, one of which is dominant in gram positive bacteria, SAM-I, and one dominant in gram negative alpha-proteobacteria, SAM-II, and the third in lactobacteria, SAM-III. Characterization of the binding of SAM analogs has indicated that this RNA recognizes every feature of the ligand, although the reactive methyl group indirectly. To further understand how this extreme degree of discrimination between SAM and closely related compounds can be achieved by this mRNA element, a crystal structure in complex with SAM has been solved.

[0031] Certain embodiments herein concern compositions and methods for selecting and identifying compounds that can activate, deactivate or block SAM-II riboswitch. Activation or deactivation of a SAM-II riboswitch refers to the change in state of the riboswitch upon binding of the compound of interest, a test compound. The term trigger molecule is used herein to refer to molecules and compounds that can activate the SAM-II riboswitch.

[0032] Deactivation of a riboswitch refers to the change in state of the riboswitch when the trigger molecule is not bound. A riboswitch can be deactivated by binding of compounds other than the trigger molecule and in ways other than removal of the trigger molecule. Blocking of a riboswitch refers to a condition or state of the riboswitch where the presence of the trigger molecule does not activate the riboswitch.

[0033] In certain particular embodiments, methods of identifying a compound that interact with a SAM-II riboswitch include modeling the atomic structure of the SAM-II riboswitch with a test compound and determining if the test compound interacts with the SAM-II riboswitch. In accordance with these embodiments, the atomic contacts of the SAM-II riboswitch and test compound can be determined by means known in the art. Further, analogs of a compound known to interact with a SAM-II riboswitch can be generated by analyzing the atomic contacts for example the contacts that interact with ligand binding, then optimizing the atomic structure of the analog to maximize interaction. In certain embodiments, these methods can be used in a high throughput screen.

[0034] Other embodiments concern methods for identifying compounds that block a riboswitch. For example, an assay can be performed for assessing the induction or inhibition of SAM-II riboswitch in the presence of a test compound.

[0035] Some embodiments herein concern compositions and methods for identifying a test compound for significantly reducing the activity or inactivating a SAM-II riboswitch by binding the test compound to at least a portion of the atomic structure represented in Figs. 4A and 4B. In accordance with these embodiments, activity of the SAM-II riboswitch can be measured by any methods known in the art. For example, the activity of the riboswitch can be measured in the presence or absence of a test compound in order to identify the efficiency of the test compound to reduce the activity of or inactivate the SAM-II riboswitch. Inactivation of a riboswitch in this manner can result from, for example, an alteration that prevents an S-adenosylmethionine molecule from binding; that prevents the change in state of

the SAM-II riboswitch upon binding of S-adenosylmethionine; or the binding of the test compound interferes with ligand interaction or prevents the change in state of the SAM riboswitch.

[0036] In other embodiments, a test compound that activates a SAM-II riboswitch can be identified. For example, test compounds that activate a riboswitch can be identified by bringing into contact a test compound and a SAM-II riboswitch including at least a portion of the SAM-II riboswitch of Fig. 4A and Fig. 4B and assessing activation of the riboswitch. Activation of a SAM-II riboswitch can be assessed in any suitable manner. For example, activation of the SAM-II riboswitch can be measured by expression level of or modification of the expression level of a reporter gene in the presence or absence of the test compound. Examples of a reporter gene include, but are not limited to, beta-galactosidase, luciferase or green-fluorescence protein.

[0037] The SAM-II riboswitch is known to regulate multiple operons in a number of bacteria. Example bacteria contemplated herein include, but are not limited to, Gram negative species, for example, proteobacteria including *Escherichia coli*, *Salmonella*, and other Enterobacteriaceae, *Pseudomonas*, *Moraxella*, *Helicobacter*, *Stenotrophomonas*, *Bdellovibrio*, acetic acid bacteria, *Legionella* and many others. Other groups of Gram-negative bacteria include the cyanobacteria, spirochaetes, green sulfur and green non-sulfur bacteria. Medically relevant Gram-negative cocci include three organisms, which cause a sexually transmitted disease (*Neisseria gonorrhoeae*), a meningitis (*Neisseria meningitidis*), and respiratory symptoms (*Moraxella catarrhalis*). Medically relevant Gram-negative bacilli include, but are not limited to those that primarily cause respiratory problems (*Hemophilus influenzae*, *Klebsiella pneumoniae*, *Legionella pneumophila*, *Pseudomonas aeruginosa*), principally urinary problems (*Escherichia coli*, *Proteus mirabilis*, *Enterobacter cloacae*, *Serratia marcescens*), and usually gastrointestinal problems (*Helicobacter pylori*, *Salmonella enteritidis*, *Salmonella typhi*). Nosocomial gram negative bacteria can include *Acinetobacter baumannii*, which cause bacteremia, secondary meningitis, and ventilator-associated pneumonia. Other medically relevant coccoid bacteria known to contain the SAM-II riboswitch include, but are not limited to, *Bordetella pertussis* and *Bordetella bronchiseptica* that causes whooping cough. In other embodiments, medically relevant facultative intracellular bacteria known to contain the SAM-II riboswitch include *Brucella melitensis*, which causes brucellosis in many areas of the world, and has been classified by the US

Center for Disease Control and Prevention as a potential agent in biological warfare. In addition, contemplated in methods herein, a related organism, *Brucella suis*, that also contains a SAM-II riboswitch, was the first pathogenic organism to be weaponized by the U.S. military in the 1950's, and thus represents a potential bioterrorism threat.

Organization of Riboswitch RNAs

[0038] Structural probing studies demonstrate that bacterial riboswitch elements are composed of two domains: a natural aptamer that serves as the ligand-binding domain, and an 'expression platform' that interfaces with RNA elements that are involved in gene expression. Structural probing investigations suggest that the aptamer domain of most riboswitches adopts a particular secondary- and tertiary-structure fold when examined independently, that is essentially identical to the aptamer structure when examined in the context of the entire 5' leader RNA. This implies that, in many cases, the aptamer domain is a modular unit that folds independently of the expression platform.

[0039] The ligand-bound or unbound status of the aptamer domain is interpreted through the expression platform, which is responsible for exerting an influence upon gene expression. The aptamer domains are highly conserved amongst various organisms, whereas the expression platform varies in sequence, structure, and in the mechanism by which expression of the appended open reading frame is controlled.

[0040] Aptamer domains for riboswitch RNAs typically range from ~70 to 170 nucleotides in length. Some aptamer domains, when isolated from the appended expression platform, exhibit improved affinity for the target ligand over that of the intact riboswitch. (~10 to 100-fold). Presumably, there is an energetic cost in sampling the multiple distinct RNA conformations required by a fully intact riboswitch RNA, which is reflected by a loss in ligand affinity. Since the aptamer domain must serve as a molecular switch, this might also add to the functional demands on natural aptamers that might help rationalize their more sophisticated structures.

Riboswitch Regulation

[0041] Bacteria primarily use two methods for termination of transcription. Certain genes incorporate a termination signal that is dependent upon the Rho protein, while others make use of Rho-independent terminators (intrinsic terminators) to destabilize the transcription

elongation complex. The latter RNA elements are composed of a GC-rich stem-loop followed by a stretch of 6-9 uridyl residues. Intrinsic terminators are widespread throughout bacterial genomes, and are typically located at the 3'-termini of genes or operons. Interestingly, an increasing number of examples are being observed for intrinsic terminators located within 5'-UTRs.

[0042] In certain examples, RNA polymerase responds to a termination signal within the 5'-UTR in a regulated fashion. Under certain conditions, the RNA polymerase complex is directed by external signals either to perceive or to ignore the termination signal. Although transcription initiation might occur without regulation, control over mRNA synthesis (and of gene expression) is ultimately dictated by regulation of the intrinsic terminator. Presumably, one of at least two mutually exclusive mRNA conformations results in the formation or disruption of the RNA structure that signals transcription termination. A trans-acting factor, which in some instances an RNA is generally required for receiving a particular intracellular signal and subsequently stabilizing one of the RNA conformations. Riboswitches offer a direct link between RNA structure modulation and the metabolite signals that are interpreted by the genetic control machinery.

[0043] Certain mRNAs involved in thiamine biosynthesis bind to thiamine (vitamin B₁) or its bioactive pyrophosphate derivative (TPP) without the participation of protein factors. The mRNA-effector complex adopts a distinct structure that sequesters the ribosome-binding site and leads to a reduction in gene expression. This metabolite-sensing mRNA system provides an example of a genetic "riboswitch" (referred to herein as a riboswitch) whose origin might predate the evolutionary emergence of proteins. It has been discovered that the mRNA leader sequence of the *btuB* gene of *Escherichia coli* can bind coenzyme B₁₂ selectively, and that this binding event brings about a structural change in the RNA that is important for genetic control. It was also discovered that mRNAs that encode thiamine biosynthetic proteins also employ a riboswitch mechanism.

[0044] Although certain specific natural riboswitches such as SAM-I riboswitch was one of the first examples of mRNA elements that control genetic expression by metabolite binding, it is suspected that this genetic control strategy may be widespread in biology. If these metabolites were being biosynthesized and used before the advent of proteins, then certain riboswitches might be modern examples of the most ancient form of genetic control. A search of genomic sequence databases has revealed that sequences corresponding to the TPP

aptamer exist in organisms from bacteria, archaea and eukarya—largely without major alteration. Although new metabolite-binding mRNAs are likely to emerge as evolution progresses, it is possible that the known riboswitches are molecular fossils from the RNA world.

[0045] In certain embodiments, it is contemplated that a SAM-II Reporter system can be used to assess whether a test compound activates or inactivates the SAM-II riboswitch. In certain particular embodiments, an *in vitro* selection protocol can be designed for example to assess whether a test compound activates or deactivates the SAM-II riboswitch. In one particular embodiment, binding of the ligand can be monitored by a mobility-shift assay, known in the art, to discern free and bound RNA, providing a basis for selection of binding-competent RNAs. Ligand binding to the RNA can cause a conformational and/or secondary structural change in the RNA that can result in a change in its migration in a native polyacrylamide gel.

[0046] In certain embodiments, a detectible tag can be incorporated into the SAM-II riboswitch. In accordance with these embodiments, a test compound can be placed in contact with the SAM-II riboswitch and the interaction of the test compound and the SAM-II riboswitch assessed by measuring the presence or absence of a detectible tag. In certain particular examples, a detectible tag may be undetectable in the presence of a test compound thereby quenching the signal. This mechanism can be adapted to existing SAM-II riboswitches, as this method can take advantage of assessing a ligand-mediated interaction of the SAM-II riboswitch. In certain particular embodiments, a detectible tag can be placed within the ligand interaction region. In more particular embodiments, a detectible tag can be placed on any one of ligand binding nucleic acids, including but not limited to, U10, U11, U12, U20, U21, G22, U44, A45, A46, A47, or a combination thereof of Fig. 4A or Fig. 4B of the SAM-II riboswitch. In these examples, a test compound can be combined with a SAM-II riboswitch depicted Fig. 4A or Fig. 4B and a detectible signal on the SAM-II riboswitch quenched when the test compound binds to at least one of the ligand-binding nucleic acids indicated above. In one particular example, a florescent tag molecule can be positioned in RNA adjacent to the binding site of SAM and binding can be monitored via a change in fluorescence of a reporter gene.

[0047] In other embodiments, control compounds can be used to assess interaction of the test compound compared to a known compound that interacts with a SAM-II riboswitch. To use riboswitches to report ligand binding by analyzing for a detectible tag, the appropriate

construct can be determined empirically. The optimum length and composition of a test compound and its binding site on the riboswitch can be assessed systematically to result in the highest ligand binding region interaction possible. The validity of the assay can be determined by comparing apparent relative binding affinities of different SAM-II analogs, SAM-II antibodies or other SAM-II binding agents to a particular test compound (determined by the presence or level of detectible signal generation of the tag) to the binding constants determined by standard in-line probing.

[0048] In other embodiments, interaction of a test compound with at least a portion of the atomic structures depicted in Fig. 4A or Fig. 4B may be assessed by measuring uptake and/or synthesis of methionine and/or synthesis of SAM in a bacterial test cell system (*e.g.*, cultures of *B. subtilis*). In accordance with these embodiments, a test compound confirmed to interact with at least a portion of the atomic structures depicted in Fig. 4A or 4B can be synthesized and/or purified for future use. In one example use, the test compound may be placed in contact with SAM-II riboswitch and the uptake and/or synthesis of methionine and/or synthesis of SAM can be measured. If a test compound is found to effectively block these functions, the test compound may be a candidate for use in inhibiting bacterial expansion or eliminating bacteria within a subject or a system.

[0049] In one example method, the structure depicted in Fig. 4A or 4B indicates that the RNA does not recognize the methyl group attached to the sulfur moiety, providing a place to build additional functionality that would be recognized by the RNA. Additionally, the positive charge on the sulfur is also recognized but not the sulfur atom itself, indicating that this region can be altered to ensure stability of the compound. Potential compounds could be computationally built and fit into the structure in place of SAM to determine if they would fit in the binding pocket of the riboswitch. Novel compounds can be synthesized by established chemistries and tested using a fluorescence or foot printing type assay to ensure that they are recognized by the RNA.

[0050] It is contemplated herein that test compounds capable of associating with the atomic structures depicted in Fig 4A or 4B may be a nucleic acid molecule, a small molecule, an antibody, a pharmaceutical agent, small peptide, peptide mimetic, nucleic acid mimetic, modified saccharide or aminoglycoside. Preferred test compound compositions would be small molecule mimetics of SAM or nucleic acid mimetics that build off of the adenosine moiety of SAM.

Kits

[0051] In still further embodiments, kits for methods and compositions described herein are contemplated. In one embodiment, the kits have a point-of care application, for example, the kits may have portability for use at a site of suspected bacterial outbreak. In another embodiment, a kit for treatment of a subject having a bacterial-induced infection is contemplated. In accordance with this embodiment, the kit may be used to reduce the bacterial infection of a subject.

[0052] The kits may include a container means. Any of the kits will generally include at least one vial, test tube, flask, bottle, syringe or other container means, into which the testing agent, may be preferably and/or suitably aliquoted. Kits herein may also include a means for comparing the results such as a suitable control sample such as a positive and/or negative control.

Nucleic Acids

[0053] In various embodiments, isolated nucleic acids may be used as test compounds for binding the atomic structure depicted in Fig. 4A or 4B. The isolated nucleic acid may be derived from genomic RNA or complementary DNA (cDNA). In other embodiments, isolated nucleic acids, such as chemically or enzymatically synthesized DNA, may be of use for capture probes, primers and/or labeled detection oligonucleotides.

[0054] A “nucleic acid” includes single-stranded and double-stranded molecules, as well as DNA, RNA, chemically modified nucleic acids and nucleic acid analogs. It is contemplated that a nucleic acid may be of 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, about 110, about 120, about 130, about 140, about 150, about 160, about 170, about 180, about 190, about 200, about 210, about 220, about 230, about 240, about 250, about 275, about 300, about 325, about 350, about 375, about 400, about 425, about 450, about 475, about 500, about 525, about 550, about 575, about 600, about 625, about 650, about 675, about 700, about 725, about 750, about 775, about 800, about 825, about 850, about 875, about 900, about 925, about 950, about 975, about 1000, about 1100, about 1200,

about 1300, about 1400, about 1500, about 1750, about 2000 or greater nucleotide residues in length, up to a full length protein encoding or regulatory genetic element.

Construction of Nucleic Acids

[0055] Isolated nucleic acids may be made by any method known in the art, for example using standard recombinant methods, synthetic techniques, or combinations thereof. In some embodiments, the nucleic acids may be cloned, amplified, or otherwise constructed.

[0056] The nucleic acids may conveniently comprise sequences in addition to a portion of a SAM-II riboswitch. For example, a multi-cloning site comprising one or more endonuclease restriction sites may be added. A nucleic acid may be attached to a vector, adapter, or linker for cloning of a nucleic acid. Additional sequences may be added to such cloning and sequences to optimize their function, to aid in isolation of the nucleic acid, or to improve the introduction of the nucleic acid into a cell. Use of cloning vectors, expression vectors, adapters, and linkers is well known in the art.

Recombinant Methods for Constructing Nucleic Acids

[0057] Isolated nucleic acids may be obtained from bacterial or other sources using any number of cloning methodologies known in the art. In some embodiments, oligonucleotide probes which selectively hybridize, under stringent conditions, to the nucleic acids of a bacterial organism. Methods for construction of nucleic acid libraries are known and any such known methods may be used.

Nucleic Acid Screening and Isolation

[0058] Bacterial RNA or cDNA may be screened for the presence of an identified genetic element of interest using a probe based upon one or more sequences. Various degrees of stringency of hybridization may be employed in the assay. As the conditions for hybridization become more stringent, there must be a greater degree of complementarity between the probe and the target for duplex formation to occur. The degree of stringency may be controlled by temperature, ionic strength, pH and/or the presence of a partially denaturing solvent such as formamide. For example, the stringency of hybridization is conveniently varied by changing the concentration of formamide within the range up to and about 50%. The degree of complementarity (sequence identity) required for detectable

binding will vary in accordance with the stringency of the hybridization medium and/or wash medium. In certain embodiments, the degree of complementarity can optimally be about 100 percent; but in other embodiments, sequence variations in the RNA may result in <100% complementarity, <90% complementarity probes, <80% complementarity probes, <70% complementarity probes or lower depending upon the conditions. In certain examples, primers may be compensated for by reducing the stringency of the hybridization and/or wash medium.

[0059] High stringency conditions for nucleic acid hybridization are well known in the art. For example, conditions may comprise low salt and/or high temperature conditions, such as provided by about 0.02 M to about 0.15 M NaCl at temperatures of about 50°C to about 70°C. Other exemplary conditions are disclosed in the following Examples. It is understood that the temperature and ionic strength of a desired stringency are determined in part by the length of the particular nucleic acid(s), the length and nucleotide content of the target sequence(s), the charge composition of the nucleic acid(s), and by the presence or concentration of formamide, tetramethylammonium chloride or other solvent(s) in a hybridization mixture. Nucleic acids may be completely complementary to a target sequence or may exhibit one or more mismatches.

Nucleic Acid Amplification

[0060] Nucleic acids of interest may also be amplified using a variety of known amplification techniques. For instance, polymerase chain reaction (PCR) technology may be used to amplify target sequences directly from bacterial RNA or cDNA. PCR and other in vitro amplification methods may also be useful, for example, to clone nucleic acid sequences, to make nucleic acids to use as probes for detecting the presence of a target nucleic acid in samples, for nucleic acid sequencing, or for other purposes.

Synthetic Methods for Constructing Nucleic Acids

[0061] Isolated nucleic acids may be prepared by direct chemical synthesis by methods such as the phosphotriester method, or using an automated synthesizer. Chemical synthesis generally produces a single stranded oligonucleotide. This may be converted into double stranded DNA by hybridization with a complementary sequence or by polymerization with a DNA polymerase using the single strand as a template. While chemical synthesis of DNA is

best employed for sequences of about 100 bases or less, longer sequences may be obtained by the ligation of shorter sequences.

Covalent Modification of Nucleic Acids

[0062] A variety of cross-linking agents, alkylating agents and radical generating species may be used to bind, label, detect, and/or cleave nucleic acids. In addition, covalent crosslinking to a target nucleotide using an alkylating agent complementary to the single-stranded target nucleotide sequence can be used. A photoactivated crosslinking to single-stranded oligonucleotides mediated by psoralen can be used. Use of N⁴, N⁴-ethanocytosine as an alkylating agent to crosslink to single-stranded oligonucleotides has also been disclosed. Various compounds to bind, detect, label, and/or cleave nucleic acids are known in the art.

Nucleic Acid Labeling

[0063] In various embodiments, tag nucleic acids may be labeled with one or more detectable labels to facilitate identification of a target nucleic acid sequence bound to a capture probe on the surface of a microchip. A number of different labels may be used, such as fluorophores, chromophores, radio-isotopes, enzymatic tags, antibodies, chemiluminescent, electroluminescent, affinity labels, *etc.* One of skill in the art will recognize that these and other label moieties not mentioned herein can be used. Examples of enzymatic tags include urease, alkaline phosphatase or peroxidase. Colorimetric indicator substrates can be employed with such enzymes to provide a detection means visible to the human eye or spectrophotometrically. A well-known example of a chemiluminescent label is the luciferin/luciferase combination.

[0064] In preferred embodiments, the label may be a fluorescent, phosphorescent or chemiluminescent label. Exemplary photodetectable labels may be selected from the group consisting of Alexa 350, Alexa 430, AMCA, aminoacridine, BODIPY 630/650, BODIPY 650/665, BODIPY-FL, BODIPY-R6G, BODIPY-TMR, BODIPY-TRX, 5-carboxy-4', 5'-dichloro-2',7'-dimethoxy fluorescein, 5-carboxy-2',4',5',7'-tetrachlorofluorescein, 5-carboxyfluorescein, 5-carboxyrhodamine, 6-carboxyrhodamine, 6-carboxytetramethyl amino, Cascade Blue, Cy2, Cy3, Cy5,6-FAM, dansyl chloride, Fluorescein, HEX, 6-JOE, NBD (7-nitrobenz-2-oxa-1,3-diazole), Oregon Green 488, Oregon Green 500, Oregon Green 514, Pacific Blue, phthalic acid, terephthalic acid, isophthalic acid, cresyl fast violet, cresyl blue

violet, brilliant cresyl blue, para-aminobenzoic acid, erythrosine, phthalocyanines, azomethines, cyanines, xanthenes, succinylfluoresceins, rare earth metal cryptates, europium trisbipyridine diamine, a europium cryptate or chelate, diamine, dicyanins, La Jolla blue dye, allopheophorbate, allophycocyanin B, phycoerythrin R, phycoerythrin, phycoerythrin R, REG, Rhodamine Green, rhodamine isothiocyanate, Rhodamine Red, ROX, TAMRA, TET, TRIT (tetramethyl rhodamine isothiol), Tetramethylrhodamine, and Texas Red. These and other labels are available from commercial sources, such as Molecular Probes (Eugene, OR).

Solid Supports

[0065] Solid supports are solid-state substrates or supports with which molecules (such as trigger molecules, *e.g.*, SAM) and riboswitches (or other components used in, or produced by, the disclosed methods) can be associated. Riboswitches and other molecules can be associated with solid supports directly or indirectly. For example, analytes (*e.g.*, trigger molecules, test compounds) can be bound to the surface of a solid support or associated with capture agents (*e.g.*, compounds or molecules that bind an analyte) immobilized on solid supports. As another example, riboswitches can be bound to the surface of a solid support or associated with probes immobilized on solid supports. An array is a solid support to which multiple riboswitches, probes or other molecules have been associated in an array, grid, or other organized pattern.

[0066] In some embodiments, a solid-state substrate may be used. Solid supports contemplated of use can include any solid material with which components can be associated, directly or indirectly. These materials include but are not limited to acrylamide, agarose, cellulose, nitrocellulose, glass, gold, polystyrene, polyethylene vinyl acetate, polypropylene, polymethacrylate, polyethylene, polyethylene oxide, polysilicates, polycarbonates, teflon, fluorocarbons, nylon, silicon rubber, polyanhydrides, polyglycolic acid, polylactic acid, polyorthoesters, functionalized silane, polypropylfumerate, collagen, glycosaminoglycans, and polyamino acids. Solid-state substrates can have any useful form including thin film, membrane, bottles, dishes, fibers, woven fibers, shaped polymers, particles, beads, microparticles, or a combination. Solid-state substrates and solid supports can be porous or non-porous. A chip is a rectangular or square small piece of material. Preferred forms for solid-state substrates are thin films, beads, or chips. A useful form for a solid-state substrate is a microtiter dish. In some embodiments, a multi-well glass slide can be employed.

[0067] In certain embodiments, an array can include a plurality of riboswitches, trigger molecules, other molecules, compounds or probes immobilized at identified or predefined locations on the solid support. Each predefined location on the solid support generally has one type of component (that is, all the components at that location are the same). Alternatively, multiple types of components can be immobilized in the same predefined location on a solid support. Each location will have multiple copies of the given components. The spatial separation of different components on the solid support allows separate detection and identification.

[0068] Although useful, it is not required that the solid support be a single unit or structure. A set of riboswitches, trigger molecules, other molecules, compounds and/or probes can be distributed over any number of solid supports. For example, in some embodiments, each component can be immobilized in a separate reaction tube or container, or on separate beads or microparticles.

[0069] Methods for immobilization of oligonucleotides to solid-state substrates are well established. Oligonucleotides, including address probes and detection probes, can be coupled to substrates using established coupling methods. For example, suitable attachment methods are described by Pease *et al.*, *Proc. Natl. Acad. Sci. USA* 91(11):5022-5026 (1994), and Khrapko *et al.*, *Mol Biol (Mosk) (USSR)* 25:718-730 (1991). A method for immobilization of 3'-amine oligonucleotides on casein-coated slides is described by Stimpson *et al.*, *Proc. Natl. Acad. Sci. USA* 92:6379-6383 (1995). A useful method of attaching oligonucleotides to solid-state substrates is described by Guo *et al.*, *Nucleic Acids Res.* 22:5456-5465 (1994).

[0070] Each of the components (for example, riboswitches, trigger molecules, or other molecules) immobilized on the solid support can be located in a different predefined region of the solid support. The different locations can be different reaction chambers. Each of the different predefined regions can be physically separated from each other of the different regions. The distance between the different predefined regions of the solid support can be either fixed or variable. For example, in an array, each of the components can be arranged at fixed distances from each other, while components associated with beads will not be in a fixed spatial relationship. In particular, the use of multiple solid support units (for example, multiple beads) will result in variable distances. In accordance with these examples, components can be associated or immobilized on a solid support at any density. Components can be immobilized to the solid support at a density exceeding 400 different components per

cubic centimeter. Arrays of components can have any number of components depending on the circumstances.

Pharmaceutical Compositions

[0071] In certain embodiments, compositions of identified test compounds may be generated for use in a subject having a bacterial infection in order to reduce or eliminate the infection in the subject. In accordance with these embodiments, the compositions can be administered in a subject in a biologically compatible form suitable for pharmaceutical administration *in vivo*. By "biologically compatible form suitable for administration *in vivo*" is meant a form of the active agent (*e.g.*, pharmaceutical chemical, protein, gene, antibody etc of the embodiments) to be administered in which any toxic effects are outweighed by the therapeutic effects of the active agent. Administration of a therapeutically active amount of the therapeutic compositions is defined as an amount effective, at dosages and for periods of time necessary to achieve the desired result. For example, a therapeutically effective amount of an antibody or nucleic acid molecule reactive with at least a portion of SAM-II riboswitch depicted in Fig. 4A or Fig. 4B may vary according to factors such as the disease state, age, sex, and weight of the individual, and the ability of antibody to elicit a desired response in the individual. Dosage regimens may be adjusted to provide the optimum therapeutic response. For example, several divided doses may be administered daily or the dose may be proportionally reduced as indicated by the exigencies of the therapeutic situation.

[0072] In one embodiment, the compound (*e.g.*, pharmaceutical chemical, nucleic acid molecule, gene, protein, antibody etc of the embodiments) may be administered in a convenient manner such as by injection such as subcutaneous, intravenous, by oral administration, inhalation, transdermal application, intravaginal application, topical application, intranasal or rectal administration. Depending on the route of administration, the active compound may be coated in a material to protect the compound from the degradation by enzymes, acids and other natural conditions that may inactivate the compound. In a preferred embodiment, the compound may be orally administered. In another preferred embodiment, the compound may be inhaled in order to make the compound bioavailable to the lung.

[0073] A compound may be administered to a subject in an appropriate carrier or diluent, co-administered with enzyme inhibitors or in an appropriate carrier such as liposomes. The term

"pharmaceutically acceptable carrier" as used herein is intended to include diluents such as saline and aqueous buffer solutions. To administer a compound that stimulates or inhibits a SAM-II riboswitch by other than parenteral administration, it may be necessary to coat the compound with, or co-administer the compound with, a material to prevent its inactivation. Enzyme inhibitors include pancreatic trypsin inhibitor, diisopropylfluorophosphate (DEP) and trasylol. Liposomes include water-in-oil-in-water emulsions as well as conventional liposomes. The active agent may also be administered parenterally or intraperitoneally. Dispersions can also be prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations may contain a preservative to prevent the growth of microorganisms.

[0074] Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. In all cases, the composition must be sterile and must be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The pharmaceutically acceptable carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of microorganisms can be achieved by various antibacterial and antifungal agents (*i.e.*, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like). In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. A compound such as aluminum monostearate and gelatin can be included to prolong absorption of the injectable compositions.

[0075] Sterile injectable solutions can be prepared by incorporating active compound (*e.g.*, a chemical that modulates the SAM-II riboswitch) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a dispersion medium and other required ingredients from those enumerated above. In the case of sterile powders for the preparation

of sterile injectable solutions, the preferred methods of preparation are vacuum drying and freeze-drying which yields a powder of the active ingredient (*i.e.*, a chemical agent, antibody etc.) plus any additional desired ingredient from a previously sterile-filtered solution thereof.

[0076] When the active agent is suitably protected, as described above, the composition may be orally administered (or otherwise indicated), for example, with an inert diluent or an assimilable edible carrier. It is especially advantageous to formulate parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the mammalian subjects to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms are dictated by and directly dependent on (a) the unique characteristics of the active agent and the particular therapeutic effect to be achieved, and (b) the limitations inherent an active agent for the therapeutic treatment of individuals.

EXAMPLES

[0077] The following examples are included to illustrate various embodiments. It should be appreciated by those of skill in the art that the techniques disclosed in the examples which follow represent techniques discovered to function well in the practice of the claimed methods, compositions and apparatus. However, those of skill in the art should, in light of the present disclosure, appreciate that many changes may be made in the specific embodiments which are disclosed and still obtain a like or similar result without departing from the spirit and scope of the invention.

[0078] Riboswitches act as genetic regulatory elements through the interplay of two distinct domains in the 5'-untranslated region (5'-UTR) of an mRNA: the aptamer domain that directly binds a specific cellular metabolite and a downstream expression platform containing a secondary structural switch that determines whether the gene will be expressed. Among the known mRNA elements that specifically bind small molecules *in vivo*, there are now at least three characterized S-adenosylmethionine (SAM)-responsive riboswitches: SAM-I, SAM-II (SAM- α), and SAM-III (SAM-MK), underscoring the importance of riboregulation of sulfur metabolism by SAM. Each riboswitch is unique in its primary or secondary structure and

appears to be exclusive within a particular bacterial genome. SAM-I, the only SAM riboswitch whose tertiary structure has been solved.

[0079] In one exemplary method, to further illuminate how mRNAs respond to SAM, the structure of a second class of SAM-responsive RNA: SAM-II was determined. To find a SAM-II mRNA that yielded diffraction-quality crystals, 13 phylogenetic variants were examined that differed in the lengths of its two primary helices in the predicted secondary structure. Crystals that diffracted X-rays to 2.8 Å resolution were obtained in the presence of SAM of an RNA derived from a Sargasso Sea environmental sequence (Env12) upstream of the metX gene (homoserine acetyltransferase). Phasing by SIRAS was achieved using a cesium atom bound to a G•U phasing module engineered into a non-conserved region of the P1 helix. All of the nucleotides in the RNA as well as SAM were found in three slightly different RNA-ligand complexes in the asymmetric unit were built and refined without NCS constraints to yield a final model with R_{xtal}=20.6 % and R_{free}=26.3 % (Table 1).

[0080] The global architecture of the SAM-II riboswitch comprises a classic (H-type) pseudoknot⁸ (Fig. 4A and 4B). The secondary structure consists of two Watson-Crick paired helices (P1 and P2a) and two loop regions (L1 and L3). A third helical element, not predicted from sequence alignment, is formed from highly conserved sequences in L2 and L3 to form P2b (Fig. 4, Fig 4A). The loops L1 and L3 interact with the major and minor grooves of P2a/b and P1, respectively, to form an intricate tertiary structure with the SAM binding pocket located in the center of P2b (Fig. 4B). Each of the helical segments stack upon the others without distortions creating a nearly straight structure.

[0081] Consistent with the sequence conservation patterns of classic pseudoknots, L1 is uracil rich while L3 is adenine rich. Bases in L3 do not form planar triples with the minor groove of P1, but rather are skewed at an ~70° angle with respect to P1 forming hydrogen bonding interactions with two successive base pairs (Fig. 5A). A stack of four adenosines in L3 (A33, A35-37) rotate clockwise (as viewed from A33) along P1, such that A33 interacts via its Hoogsteen face, while A37 uses its sugar face in a fashion akin to a type-I A-minor groove triple⁹. As a result, residues of L3 form extensive hydrogen bonding interactions with the minor groove side of every base pair of P1 except the C2-G30 base pair at the very top (Fig. 5A).

[0082] The SAM binding pocket is created by the formation of an extended triplex between L1 and the major groove of P2b. The beginning of the P2b-L1 interaction is defined by a single minor groove triple between A24-U40•A41 (Fig. 4A), followed by a series of major groove triples formed by nucleotides G8-U12 in L1 with the face of P2b. The Watson-Crick face of each nucleotide in L1 interacts with the Hoogsteen face of nucleotides in 3'-strand of the P2b helix (nucleotides 42-46). This near-perfect triplex is terminated by a sheared A19•A47 pair. Below this pair, the P2b triplex transitions into the P2a helix, defining the lower boundary of the SAM binding pocket. An isolated A13•(U18-A48) triple and a sheared G17•A49 pair comprise this transition. The final nucleotide of L1, which is not conserved in phylogeny, is flipped out and makes no contacts with the two-base-pair helix of P2a that corresponds to the second helix of the classic pseudoknot fold.

[0083] SAM binds in an extended trans-configuration along the major groove face of the P2b/L1 triplex forming direct contacts with five successive base pairs and triples (Fig 3B, C). The adenine moiety of SAM (ASAM) participates in a base triple between U10 and U44 using its Hoogsteen face to pair with U44 (Fig. 5A and 5B) similar to that observed in the SAM-I structure. Interestingly, this site appears to be created by the deletion of a single residue between U21 and G22; this "hole" thus requires adenine to be threaded through the helix sideways such that its Watson-Crick face is solvent exposed on the minor groove face of the triplex. The positively charged sulfur moiety and activated methyl group are recognized by the carbonyl oxygens of U11 and U21 (Fig. 3D) explaining the ability of SAM-II to discriminate between SAM and S-adenosylhomocysteine (SAH). Again, this is strikingly similar to discrimination by SAM-I, which uses the minor groove carbonyl moieties of two universally conserved A-U pairs to interact electrostatically with the positive charge. The main chain atoms of methionine (carboxylate and amino groups) are positioned in the major groove adjacent to the sheared A19•A47 pair (Fig. 3E). However, these groups are in different configurations in the three protomers in the asymmetric unit (Fig. 6A and 6B). Molecules A and C place the amino and carboxylate groups along the Watson-Crick face of A47 (Fig. 3E), while molecule B does not place the amino group in hydrogen bonding contact with the RNA. Recognition of the main chain atoms by the Watson-Crick face of an adenine base is similar to that observed in SAM-I, in which the Watson-Crick face of a guanine forms a salt bridge with the carboxylate moiety. Thus, all of the available functional groups in SAM appear to be directly or indirectly recognized by the mRNA, consistent with an investigation of the binding of SAM analogs to the SAM-II riboswitch. Despite the

extensive recognition of SAM, the ligand is not nearly as extensively buried within the RNA (64% solvent inaccessible) as observed in other riboswitch-small molecule complexes.

[0084] RNA pseudoknot motifs are ubiquitous throughout all classes of structured RNAs stabilizing local tertiary structure and acting as protein recognition elements. They function in diverse pathways from translational regulation like those found in viral genomes to their role in telomerase RNA (hTR) as a key element of TERT repeat addition processivity. SAM-II has an architecture consistent with other H-type pseudoknots, most notably the hTR pseudoknot core that is involved in protein recognition (Fig. 7A and 7B). Both the hTR RNA and SAM-II contain triplexes at the junction between P1 and P2a/b that have a strong preference for A•U base pairs in this region. The hTR core is a five-base-pair triplex broken only by a non-canonical A•U Hoogsteen base pair in the center. Similarly, the SAM-II core is a five-base-pair triplex, containing the ASAM motif in the center that forms a Hoogsteen base pair with U44. Thus, the SAM-II riboswitch employs a ligand-independent structure with which to scaffold the binding pocket; deletion of a single critical residue in the middle of the triplex destabilizes the tertiary structure such that SAM is required to fully form the pseudoknot.

[0085] Most riboswitches contain a switching sequence within the 3'-side of the P1 helix that is either incorporated within the aptamer domain or forms part of a secondary structure in the expression platform, depending upon whether the aptamer domain is ligand-bound¹⁴. Typically, the tertiary architecture of the aptamer domain in the presence of ligand stabilizes formation of the P1 helix. The SAM-II riboswitch differs from most other riboswitches in that its pseudoknot architecture prevents pairing of the 5'- and 3'-ends of the aptamer domain (Fig. 1). Despite this difference, the switching sequence (nucleotides 40-47) remains localized to the 3'-side of the aptamer domain, residing in P2b. In-line probing of the riboswitch in the absence and presence of SAM reveals strong ligand-dependent protections corresponding to nucleotides G8-U12 in L14. SAM binding to P2b, stabilizes the formation of key tertiary interactions between L1 and the 3'-side of P2b that serve to cement the switching sequence into the aptamer domain and thereby fating the secondary structure of the downstream expression platform. Thus, this structure lends support to a general mechanism of riboswitch action in which ligand binding is communicated to the expression platform via ligand-induced tertiary interactions with a switching sequence.

Methods and Materials.

[0086] RNA library synthesis and purification. A series of RNAs corresponding to secondary structure and sequence variations of the SAM-II RNA observed across phylogeny was constructed according to the length of the P1 and P2 helices of the minimal riboswitch (Fig. 4). These helices vary between 5-8 base pairs and 2-6 base pairs, respectively. Combinations of different helix length resulted in an initial library containing 13 representative RNAs that included the *metA* RNA previously characterized. RNAs were constructed by standard PCR methods using overlapping DNA oligonucleotides (Integrated DNA Technologies). The resulting DNA fragment, which contained *EcoRI* and *NcoI* restriction sites at the 5' and 3' ends, respectively, as well as sequences coding for a T7 RNA polymerase promoter and an 3' HδV ribozyme was ligated into pRAV12. The resulting plasmid was verified by sequence analysis. Template DNA for in vitro transcription was generated by PCR from each individual plasmid using primers directed against the T7 RNA polymerase promoter at the 5' end and the 3' side HδV ribozyme (5'GCGCGCGAATTCTAATACGACTCACTATAG (SEQ ID NO: 3); 3'GCACAGTCTAGAGGTCCCATTCGCCATGCCGAAGCATGTTG (SEQ ID NO: 4)). RNA was transcribed in a 12.5 mL reactions containing 30 mM Tris-HCl (pH 8.0), 10 mM DTT, 0.1 % Triton X-100, 0.1 mM spermidine-HCl, 6 mM of both ATP and GTP, 4 mM of both UTP and CTP, 36 mM MgCl₂, 25 mg/mL T7 RNA polymerase, 1 mL of ~0.5 mM template³, and 1 unit/mL inorganic pyrophosphatase. The reaction was incubated for 2 hr at 37 °C. RNA was precipitated in 70% EtOH, pelleted, and resuspended in load buffer containing 4 M urea, 100 mM Na-EDTA, pH 8.0, 25% formamide, xylene cyanol, and bromophenol blue, and purified by denaturing 12% PAGE. Gel slices containing target RNA were excised from the gel, electroeluted in 1x TBE buffer, collected, exchanged against 3 x 15 ml aliquots of buffer containing 10 mM K⁺-HEPES, pH 7.5 using a 10,000 MWCO centrifugal filter device (Amicon, Ultra-15), and concentrated to ~500 μL. RNA concentrations were determined from the magnitude of the UV absorbance at 260 nm and the calculated extinction coefficient (556,400 M⁻¹ cm⁻¹) of the individual RNA's base composition.

[0087] RNA crystallization. SAM-II riboswitch crystals were obtained by the hanging drop/vapor diffusion method in which the RNA solution was mixed in a 1:1 ratio with mother liquor. The initial library of RNAs was screened versus the PEG-Ion, Crystal Screen, Natrix, and Nucleic Acid Mini-screen (Hampton Research). RNAs and promising conditions were further refined based on crystal morphology and size, as well as diffraction quality and space

group. The final RNA construct was further refined to contain a heavy-ion binding phasing module in the P1 helix that did not alter any of the residues that are conserved across phylogeny (Fig. 4). The final conditions that yielded diffractions quality crystals contained 8 mM cobalt hexammine chloride, 640 mM ammonium acetate, 10% PEG 1K, 10 mM barium chloride, 50 mM Na⁺-cacodylate, pH 6.0, 25 °C. Single crystal growth required cat whisker micro-seeding from a solution containing microcrystals from previously grown, but polymorphic, SAM-II crystals suspended in mother liquor plus 8% (2*R*,3*R*) –(–)-2,3-butanediol. Crystals reached their maximum size (~200 μm, cube-like) in 3-5 days, and were subsequently backsoaked in 30 μl one of two heavy-atom derivative solutions. Crystals designated for isomorphous replacement were backsoaked in mother liquor containing 2 mM magnesium chloride, 10 mM SAM, and 200 mM cesium chloride for ~10 minutes. Crystals designated as native were backsoaked in mother liquor that only contained 320 mM ammonium acetate (all other components remaining the same) with the addition of 2 mM magnesium chloride, 10 mM SAM, and 600 mM lithium chloride also for ~10 minutes. This was followed by a 10 minute exchange into the same solutions containing the addition of 8 % (2*R*,3*R*) –(–)-2,3-butanediol. Crystals were looped and flash-frozen in liquid nitrogen. Diffraction data was collected on a home X-ray source (Rigaku MSC) using CuK_α radiation. Anomalous diffraction data was collected by an inverse-beam experiment and was integrated, indexed, and scaled using HKL2000.

[0088] Phasing and structure determination. Phases were determined using a single wavelength isomorphous replacement with anomalous scattering (SIRAS) experiment and diffraction data extending to 2.5 Å resolution for that native data set and 2.8 Å resolution for the derivative set. In this experiment, cesium was treated as the heavy atom derivative, yielding anomalous signal at CuK_α wavelength ($f' = 1.16$, $f'' = 8.80$), while a lithium backsoaked crystal was treated as the native data set. A phasing solution containing four heavy atoms (FOM = 0.27, Z-score = 17) was generated in SOLVE. Following density modification in CNS, the figure of merit improved to 0.35. An experimental electron density map was of sufficient quality to follow the trace of the phosphate backbone and identify regions of base-pairing for two of the three molecules in the asymmetric unit. Using a combination of model and experimental phases, a final density modified electron density map was calculated (FOM = 0.74) and the location of the third protomer was identified. All nucleotides in the three RNAs, as well as the locations of SAM, and three Cs atoms were eventually built through subsequent rounds of iterative model building in Pymol and

refinement in CNS while following the improvement of R_{free} . Solvent molecules were added using two rounds of the water-picking in CNS. The 5'- and 3'- ends of the RNAs contained functional groups that required additional refinement at the end of the building process. The addition of a 5'ppGTP and a 2'-3'-cyclic phosphate at the RNA termini were supported by the electron density in these regions. A Mg^{2+} ion was also identified in the region where protomers A and B stack 5' to 5' and 3' to 3' causing the two 5'-diphosphate groups to come into close proximity. The final R and R_{free} are 20.6% and 26.3%, respectively.

[0089] Fig 1 represents an exemplary schematic of secondary structural switching in the Env12 *metX* mRNA. In high intracellular concentrations of SAM, the effector ligand binds to the aptamer domain (dark grey box, left) incorporating a switching sequence (grey shaded area) into this domain, forcing the formation of a downstream rho-independent transcriptional terminator stem-loop in the expression platform (light grey box). In the absence of SAM, the switching sequence is free to be incorporated into a more stable antiterminator element, allowing for transcription to proceed.

[0090] Fig 2. represents an exemplary schematic of (A) secondary structure of the Env12 *metX* SAM-2 riboswitch with base pairing reflects the tertiary structure of the SAM-bound RNA. Base interactions are shown using the notation of Neocoles and Westhof. Circles indicate an interaction involving the Watson-Crick face, squares the Hoogsteen face, and triangles the sugar edge; black symbols denote a parallel arrangement while open symbols denote an antiparallel arrangement. Dashed lines denote hydrogen bonding interactions that cannot be described as one of the standard pairing interactions. Colors of the bases reflect their position in the tertiary structure (blue, P1 or P2a; green, P2b; magenta, L3; orange, L1). (B) represents an exemplary schematic of the global structure of the RNA; colors are consistent with the secondary structure. The red dots represent the van der Waals surface of S-adenosylmethionine. (C) 90° rotation of the perspective shown in (B).

[0091] Fig. 3A-3E represents in (A) details of the interactions between L3 (magenta) and the P1 helix (blue) emphasizing the role of four stacked adenosine residues in cementing the loop to the minor groove. (B) represents a schematic of a binding pocket of SAM (salmon) with the P2b helix. The adenine base of SAM is accommodated by an opening in the 5'-strand of P2b between U21 and G22, while the ribose sugar and methionine residue reside in the narrow major groove of the triplex. (C) represents hydrogen bonding interactions involving the adenine moiety of SAM. (D) represents hydrogen bonding and electrostatic interactions

involving the positively charged sulfur moiety and the methyl group of SAM. (E) represents interactions between the RNA and the main chain atoms of the methionine residue of SAM.

[0092] Fig. 4 represents in (A) Sequence and secondary structure of the SAM-binding mRNA pseudoknot from Env12. The nomenclature for the stems and loops (P1-P2 and L1-L3, respectively) is derived from standard naming of H-type pseudoknots. Light grey nucleotides are those whose identity is >95% conserved and dark grey nucleotides corresponds to >80% conservation of identity. (B) represents a schematic of sequence of the crystallized RNA construct with changes made to the sequence shaded in grey. Each change was made for a specific purpose: U1G for efficient transcriptional initiation by T7 RNA polymerase, G52A for efficient 3'-end processing by a 3'-H δ V ribozyme, and (C6G,U7C,A25G,G26U) to add a cesium/iridium hexammine ion binding site for phasing.

[0093] Fig. 5 represents electron density maps around the SAM binding site protomer A of the SAM-II riboswitch contoured at 1 σ (orange cage). The final model is superimposed upon the density (green, RNA; magenta, SAM). (A) Solvent flattened experimental electron density map. (B) Final 2F_o-F_c electron density map.

[0094] Fig. 6 represents an exemplary schematic of superposition of the three protomers in the asymmetric unit that were built and refined individually. The standard pairwise r.m.s.d. for all atoms in the RNA and SAM is 1.26 Å and the maximum likelihood r.m.s.d. for all atoms is 0.19 Å, as calculated using in one example, the program THESEUS. The two perspectives correspond to (A) Fig. 6B and (b) Fig. 6C (Fig. 6B and C represent protomer A). Colors correspond to: red, molecule A; blue, molecule B; green, molecule C, as defined in the PDB coordinate file.

[0095] Fig. 7 represents an exemplary schematic of side-by-side comparisons of the pseudoknot from human telomerase RNA (hTR, left) and SAM-II/SAM complex (right). The colors reflect secondary structures of the RNA (blue, P1; green, P2; orange, L1; magenta, L3); the coloring pattern of SAM-II is slightly different from Fig. 4 to make a clearer comparison between the two RNAs. The hTR structure shown is model 1 from the family of structures derived from NMR constraints (PDB ID 1YMO).

Table 1 Data collection, phasing, and refinement statistics (SIRAS)

Native	Derivative
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Data collection

Space group	C2	C2
Cell dimensions		
a, b, c (Å)	115.26, 48.10, 109.62	115.64, 48.29, 109.51
α, β, γ (°)	90, 108.26, 90	90, 108.20, 90
Resolution (Å)	20-2.6 (2.69-2.60)	20-2.8 (2.90-2.80) ¹
R_{merge}	0.053 (0.368)	0.061 (0.349)
$I / \sigma I$	28.5(2.5)	31.9 (5.0)
Completeness (%)	89.6 (54.4)	97.9 (94.7)
Redundancy	3.6 (2.8)	7.8 (7.7)

Refinement

Resolution (Å)	20-2.8
No. reflections	26,866
$R_{\text{work}} / R_{\text{free}}$	20.6/26.3
No. atoms	
RNA	3,375
Ligand/ion	84
Water	154
B -factors	
RNA	64.90
Ligand/ion	64.87
Water	45.50
R.m.s. deviations	
Bond lengths (Å)	0.0059
Bond angles (°)	1.017

¹Reflections obtained from a single crystal. Values in parentheses are for highest-resolution shell.

Table 2

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REMARK 3
REMARK 3 REFINEMENT.
REMARK 3   PROGRAM       : CNS 1.2
REMARK 3   AUTHORS      : BRUNGER, ADAMS, CLORE, DELANO,
REMARK 3                   GROS, GROSSE-KUNSTLEVE, JIANG,
REMARK 3                   KUSZEWSKI, NILGES, PANNU, READ,
REMARK 3                   RICE, SIMONSON, WARREN
REMARK 3
REMARK 3 DATA USED IN REFINEMENT.
REMARK 3   RESOLUTION RANGE HIGH (ANGSTROMS) : 2.80
REMARK 3   RESOLUTION RANGE LOW  (ANGSTROMS) : 19.90
REMARK 3   DATA CUTOFF             (SIGMA(F)) : 0.0
REMARK 3   DATA CUTOFF HIGH      (ABS(F))    : 1022121.53
REMARK 3   DATA CUTOFF LOW      (ABS(F))    : 0.000000
REMARK 3   COMPLETENESS (WORKING+TEST) (%)    : 97.9
REMARK 3   NUMBER OF REFLECTIONS              : 26866
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 SET) : 0.206
REMARK 3   FREE R VALUE                      : 0.263
REMARK 3   FREE R VALUE TEST SET SIZE (%)     : 7.2
REMARK 3   FREE R VALUE TEST SET COUNT       : 1924
REMARK 3   ESTIMATED ERROR OF FREE R VALUE   : 0.006
REMARK 3
REMARK 3 FIT IN THE HIGHEST RESOLUTION BIN.
REMARK 3   TOTAL NUMBER OF BINS USED            : 6
REMARK 3   BIN RESOLUTION RANGE HIGH (A)        : 2.80
REMARK 3   BIN RESOLUTION RANGE LOW  (A)        : 2.97
REMARK 3   BIN COMPLETENESS (WORKING+TEST) (%)   : 94.8
REMARK 3   REFLECTIONS IN BIN (WORKING SET)     : 4033
REMARK 3   BIN R VALUE                      (WORKING SET) : 0.407
REMARK 3   BIN FREE R VALUE                      : 0.408
REMARK 3   BIN FREE R VALUE TEST SET SIZE (%)   : 7.4
REMARK 3   BIN FREE R VALUE TEST SET COUNT     : 324
REMARK 3   ESTIMATED ERROR OF BIN FREE R VALUE : 0.023
REMARK 3
REMARK 3 NUMBER OF NON-HYDROGEN ATOMS USED IN REFINEMENT.
REMARK 3   PROTEIN ATOMS                      : 0
REMARK 3   NUCLEIC ACID ATOMS                  : 1050
REMARK 3   HETEROGEN ATOMS                     : 81
REMARK 3   SOLVENT ATOMS                      : 154
REMARK 3
REMARK 3 B VALUES.
REMARK 3   FROM WILSON PLOT (A**2) :129.5
REMARK 3   MEAN B VALUE (OVERALL, A**2) : 65.6
REMARK 3   OVERALL ANISOTROPIC B VALUE.
REMARK 3   B11 (A**2) : 34.88
REMARK 3   B22 (A**2) : -5.03
REMARK 3   B33 (A**2) : -29.85
REMARK 3   B12 (A**2) : 0.00
REMARK 3   B13 (A**2) : 23.73
REMARK 3   B23 (A**2) : 0.00
REMARK 3
REMARK 3 BULK SOLVENT MODELING.
REMARK 3   METHOD USED : FLAT MODEL
REMARK 3   KSOL       : 0.25
REMARK 3   BSOL       : 9.21319 (A**2)

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REMARK      3
REMARK      3 ESTIMATED COORDINATE ERROR.
REMARK      3 ESD FROM LUZZATI PLOT (A) : 0.40
REMARK      3 ESD FROM SIGMAA (A) : 0.62
REMARK      3 LOW RESOLUTION CUTOFF (A) : 5.00
REMARK      3
REMARK      3 CROSS-VALIDATED ESTIMATED COORDINATE ERROR.
REMARK      3 ESD FROM C-V LUZZATI PLOT (A) : 0.50
REMARK      3 ESD FROM C-V SIGMAA (A) : 0.62
REMARK      3
REMARK      3 RMS DEVIATIONS FROM IDEAL VALUES.
REMARK      3 BOND LENGTHS (A) : 0.006
REMARK      3 BOND ANGLES (DEGREES) : 1.0
REMARK      3 DIHEDRAL ANGLES (DEGREES) : 21.5
REMARK      3 IMPROPER ANGLES (DEGREES) : 1.40
REMARK      3
REMARK      3 ISOTROPIC THERMAL MODEL : RESTRAINED
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 : NONE
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 : CNS_TOPPAR/protein_rep.param
REMARK      3 PARAMETER FILE 2 : dna-rna_rep_revise4.param
REMARK      3 PARAMETER FILE 3 : CNS_TOPPAR/water_rep.param
REMARK      3 PARAMETER FILE 4 : CNS_TOPPAR/ion.param
REMARK      3 PARAMETER FILE 5 : sam7.param
REMARK      3 TOPOLOGY FILE 1 : CNS_TOPPAR/protein.top
REMARK      3 TOPOLOGY FILE 2 : dna-rna_rep_revise4.top
REMARK      3 TOPOLOGY FILE 3 : CNS_TOPPAR/water_rep.top
REMARK      3 TOPOLOGY FILE 4 : CNS_TOPPAR/ion.top
REMARK      3 TOPOLOGY FILE 5 : sam7.top
REMARK      3
REMARK      3 OTHER REFINEMENT REMARKS: BULK SOLVENT MODEL USED
SEQRES      1 A 52 GUA CYT GUA CYT GUA GUA CYT GUA ADE URI URI URI ADE
SEQRES      2 A 52 ADE CYT CYT GUA URI ADE URI URI GUA CYT ADE GUA URI
SEQRES      3 A 52 CYT GUA CYT GUA URI GUA ADE URI ADE ADE ADE URI GUA
SEQRES      4 A 52 URI ADE GUA CYT URI ADE ADE ADE ADE ADE GUA GUA ADE
SEQRES      1 B 52 GUA CYT GUA CYT GUA GUA CYT GUA ADE URI URI URI ADE
SEQRES      2 B 52 ADE CYT CYT GUA URI ADE URI URI GUA CYT ADE GUA URI
SEQRES      3 B 52 CYT GUA CYT GUA URI GUA ADE ADE ADE ADE ADE GUA URI GUA
SEQRES      4 B 52 URI ADE GUA CYT GUA URI ADE ADE ADE ADE ADE GUA GUA ADE
SEQRES      1 C 52 GUA CYT GUA CYT GUA GUA CYT GUA ADE URI URI URI ADE
SEQRES      2 C 52 ADE CYT CYT GUA URI ADE URI URI GUA CYT ADE GUA URI
SEQRES      3 C 52 CYT GUA CYT GUA URI GUA ADE URI ADE ADE ADE URI GUA
SEQRES      4 C 52 URI ADE GUA CYT URI ADE ADE ADE ADE ADE GUA GUA ADE
CRYST1      115.258 48.095 109.617 90.00 108.25 90.00 C 2 12
ORIGX1      1.000000 0.000000 0.000000 0.000000
ORIGX2      0.000000 1.000000 0.000000 0.000000
ORIGX3      0.000000 0.000000 1.000000 0.000000
SCALE1      0.008676 0.000000 0.002862 0.000000
SCALE2      0.000000 0.020792 0.000000 0.000000
SCALE3      0.000000 0.000000 0.009606 0.000000

```

ATOM	1	O6P	GUA	A	1	-3.122	22.893	35.812	1.00	79.01	A
ATOM	2	O3P	GUA	A	1	-2.183	21.111	37.439	1.00	75.49	A
ATOM	3	O4P	GUA	A	1	-1.328	21.287	35.020	1.00	77.61	A
ATOM	4	O5P	GUA	A	1	-0.763	23.120	36.591	1.00	81.95	A
ATOM	5	P2	GUA	A	1	-1.851	22.131	36.189	1.00	81.46	A
ATOM	6	P	GUA	A	1	-0.796	20.349	37.787	1.00	70.43	A
ATOM	7	O1P	GUA	A	1	0.242	21.364	38.237	1.00	69.31	A
ATOM	8	O2P	GUA	A	1	-0.373	19.586	36.525	1.00	67.03	A
ATOM	9	O5'	GUA	A	1	-0.900	19.278	39.005	1.00	62.45	A
ATOM	10	C5'	GUA	A	1	0.300	18.834	39.669	1.00	58.69	A
ATOM	11	C4'	GUA	A	1	0.890	17.581	39.014	1.00	53.75	A
ATOM	12	O4'	GUA	A	1	1.235	17.789	37.609	1.00	53.70	A
ATOM	13	C1'	GUA	A	1	2.550	17.294	37.340	1.00	52.22	A
ATOM	14	N9	GUA	A	1	3.421	18.451	37.118	1.00	53.59	A
ATOM	15	C4	GUA	A	1	4.803	18.541	37.218	1.00	53.64	A
ATOM	16	N3	GUA	A	1	5.653	17.553	37.565	1.00	53.63	A
ATOM	17	C2	GUA	A	1	6.917	17.975	37.595	1.00	53.12	A
ATOM	18	N2	GUA	A	1	7.905	17.149	37.950	1.00	51.55	A
ATOM	19	N1	GUA	A	1	7.309	19.248	37.290	1.00	53.64	A
ATOM	20	C6	GUA	A	1	6.459	20.280	36.926	1.00	53.32	A
ATOM	21	O6	GUA	A	1	6.922	21.401	36.675	1.00	50.63	A
ATOM	22	C5	GUA	A	1	5.104	19.855	36.904	1.00	54.13	A
ATOM	23	N7	GUA	A	1	3.951	20.571	36.615	1.00	54.92	A
ATOM	24	C8	GUA	A	1	2.986	19.704	36.753	1.00	55.27	A
ATOM	25	C2'	GUA	A	1	2.921	16.420	38.535	1.00	51.79	A
ATOM	26	O2'	GUA	A	1	2.437	15.113	38.346	1.00	51.21	A
ATOM	27	C3'	GUA	A	1	2.199	17.146	39.660	1.00	51.46	A
ATOM	28	O3'	GUA	A	1	1.933	16.312	40.761	1.00	46.95	A
ATOM	29	P	CYT	A	2	2.157	16.875	42.244	1.00	48.57	A
ATOM	30	O1P	CYT	A	2	1.929	18.348	42.278	1.00	42.96	A
ATOM	31	O2P	CYT	A	2	1.391	15.995	43.167	1.00	46.56	A
ATOM	32	O5'	CYT	A	2	3.706	16.597	42.479	1.00	47.77	A
ATOM	33	C5'	CYT	A	2	4.204	15.277	42.381	1.00	45.44	A
ATOM	34	C4'	CYT	A	2	5.702	15.280	42.403	1.00	45.59	A
ATOM	35	O4'	CYT	A	2	6.215	15.773	41.143	1.00	46.82	A
ATOM	36	C1'	CYT	A	2	7.449	16.434	41.369	1.00	47.01	A
ATOM	37	N1	CYT	A	2	7.263	17.843	41.054	1.00	47.95	A
ATOM	38	C6	CYT	A	2	6.035	18.339	40.736	1.00	47.93	A
ATOM	39	C2	CYT	A	2	8.361	18.671	41.107	1.00	48.84	A
ATOM	40	O2	CYT	A	2	9.458	18.170	41.388	1.00	52.02	A
ATOM	41	N3	CYT	A	2	8.215	19.990	40.851	1.00	48.53	A
ATOM	42	C4	CYT	A	2	7.016	20.470	40.531	1.00	48.44	A
ATOM	43	N4	CYT	A	2	6.913	21.769	40.247	1.00	48.35	A
ATOM	44	C5	CYT	A	2	5.868	19.636	40.471	1.00	49.66	A
ATOM	45	C2'	CYT	A	2	7.763	16.289	42.859	1.00	46.37	A
ATOM	46	O2'	CYT	A	2	8.562	15.149	43.091	1.00	45.81	A
ATOM	47	C3'	CYT	A	2	6.364	16.166	43.439	1.00	44.45	A
ATOM	48	O3'	CYT	A	2	6.412	15.484	44.675	1.00	41.89	A
ATOM	49	P	GUA	A	3	6.252	16.299	46.043	1.00	42.10	A
ATOM	50	O1P	GUA	A	3	5.280	17.407	45.892	1.00	40.61	A
ATOM	51	O2P	GUA	A	3	6.050	15.280	47.092	1.00	39.17	A
ATOM	52	O5'	GUA	A	3	7.692	16.926	46.261	1.00	44.58	A
ATOM	53	C5'	GUA	A	3	8.831	16.078	46.324	1.00	42.59	A
ATOM	54	C4'	GUA	A	3	10.078	16.903	46.297	1.00	42.78	A
ATOM	55	O4'	GUA	A	3	10.222	17.528	44.995	1.00	44.47	A
ATOM	56	C1'	GUA	A	3	10.876	18.778	45.148	1.00	45.39	A
ATOM	57	N9	GUA	A	3	9.983	19.828	44.670	1.00	48.03	A
ATOM	58	C4	GUA	A	3	10.288	21.163	44.574	1.00	49.13	A
ATOM	59	N3	GUA	A	3	11.468	21.727	44.896	1.00	50.26	A
ATOM	60	C2	GUA	A	3	11.459	23.035	44.705	1.00	51.54	A
ATOM	61	N2	GUA	A	3	12.545	23.757	44.991	1.00	54.67	A

ATOM	62	N1	GUA	A	3	10.385	23.732	44.223	1.00	51.22	A
ATOM	63	C6	GUA	A	3	9.162	23.176	43.880	1.00	50.02	A
ATOM	64	O6	GUA	A	3	8.267	23.902	43.447	1.00	50.31	A
ATOM	65	C5	GUA	A	3	9.148	21.767	44.095	1.00	49.23	A
ATOM	66	N7	GUA	A	3	8.143	20.830	43.893	1.00	48.38	A
ATOM	67	C8	GUA	A	3	8.683	19.694	44.245	1.00	47.42	A
ATOM	68	C2'	GUA	A	3	11.186	18.924	46.639	1.00	43.47	A
ATOM	69	O2'	GUA	A	3	12.459	18.377	46.910	1.00	45.99	A
ATOM	70	C3'	GUA	A	3	10.077	18.083	47.243	1.00	42.30	A
ATOM	71	O3'	GUA	A	3	10.414	17.644	48.543	1.00	43.04	A
ATOM	72	P	CYT	A	4	9.640	18.244	49.810	1.00	45.36	A
ATOM	73	O1P	CYT	A	4	8.240	18.530	49.414	1.00	46.28	A
ATOM	74	O2P	CYT	A	4	9.919	17.323	50.937	1.00	43.82	A
ATOM	75	O5'	CYT	A	4	10.345	19.649	50.068	1.00	43.71	A
ATOM	76	C5'	CYT	A	4	11.712	19.831	49.737	1.00	42.38	A
ATOM	77	C4'	CYT	A	4	12.118	21.257	49.960	1.00	40.12	A
ATOM	78	O4'	CYT	A	4	12.112	21.977	48.706	1.00	40.61	A
ATOM	79	C1'	CYT	A	4	11.708	23.313	48.930	1.00	41.97	A
ATOM	80	N1	CYT	A	4	10.437	23.527	48.227	1.00	44.61	A
ATOM	81	C6	CYT	A	4	9.659	22.471	47.856	1.00	46.63	A
ATOM	82	C2	CYT	A	4	10.033	24.820	47.950	1.00	44.55	A
ATOM	83	O2	CYT	A	4	10.754	25.743	48.291	1.00	46.38	A
ATOM	84	N3	CYT	A	4	8.862	25.031	47.319	1.00	45.19	A
ATOM	85	C4	CYT	A	4	8.102	23.996	46.969	1.00	44.95	A
ATOM	86	N4	CYT	A	4	6.953	24.242	46.367	1.00	45.12	A
ATOM	87	C5	CYT	A	4	8.491	22.662	47.228	1.00	47.16	A
ATOM	88	C2'	CYT	A	4	11.590	23.475	50.444	1.00	40.74	A
ATOM	89	O2'	CYT	A	4	12.850	23.840	50.938	1.00	42.41	A
ATOM	90	C3'	CYT	A	4	11.217	22.064	50.867	1.00	39.44	A
ATOM	91	O3'	CYT	A	4	11.634	21.823	52.196	1.00	39.48	A
ATOM	92	P	GUA	A	5	10.570	21.822	53.397	1.00	40.65	A
ATOM	93	O1P	GUA	A	5	9.225	22.097	52.851	1.00	41.86	A
ATOM	94	O2P	GUA	A	5	10.792	20.615	54.220	1.00	38.51	A
ATOM	95	O5'	GUA	A	5	11.010	23.078	54.260	1.00	40.18	A
ATOM	96	C5'	GUA	A	5	10.119	24.153	54.485	1.00	39.67	A
ATOM	97	C4'	GUA	A	5	10.754	25.446	54.064	1.00	38.08	A
ATOM	98	O4'	GUA	A	5	11.037	25.373	52.646	1.00	38.21	A
ATOM	99	C1'	GUA	A	5	10.629	26.579	52.018	1.00	41.62	A
ATOM	100	N9	GUA	A	5	9.439	26.289	51.222	1.00	42.26	A
ATOM	101	C4	GUA	A	5	8.684	27.173	50.489	1.00	43.07	A
ATOM	102	N3	GUA	A	5	8.883	28.501	50.392	1.00	45.16	A
ATOM	103	C2	GUA	A	5	7.985	29.083	49.613	1.00	43.59	A
ATOM	104	N2	GUA	A	5	8.014	30.407	49.437	1.00	39.55	A
ATOM	105	N1	GUA	A	5	6.993	28.408	48.963	1.00	44.54	A
ATOM	106	C6	GUA	A	5	6.782	27.037	49.043	1.00	46.16	A
ATOM	107	O6	GUA	A	5	5.867	26.515	48.401	1.00	51.42	A
ATOM	108	C5	GUA	A	5	7.713	26.413	49.892	1.00	43.96	A
ATOM	109	N7	GUA	A	5	7.838	25.086	50.251	1.00	44.24	A
ATOM	110	C8	GUA	A	5	8.868	25.061	51.044	1.00	43.14	A
ATOM	111	C2'	GUA	A	5	10.392	27.578	53.146	1.00	40.55	A
ATOM	112	O2'	GUA	A	5	11.615	28.116	53.575	1.00	40.58	A
ATOM	113	C3'	GUA	A	5	9.859	26.661	54.221	1.00	39.47	A
ATOM	114	O3'	GUA	A	5	10.051	27.260	55.484	1.00	39.23	A
ATOM	115	P	GUA	A	6	8.814	27.981	56.202	1.00	39.81	A
ATOM	116	O1P	GUA	A	6	7.644	27.061	56.084	1.00	34.66	A
ATOM	117	O2P	GUA	A	6	9.244	28.441	57.539	1.00	38.23	A
ATOM	118	O5'	GUA	A	6	8.606	29.286	55.316	1.00	37.57	A
ATOM	119	C5'	GUA	A	6	9.549	30.343	55.374	1.00	35.30	A
ATOM	120	C4'	GUA	A	6	9.070	31.533	54.575	1.00	35.94	A
ATOM	121	O4'	GUA	A	6	8.934	31.175	53.178	1.00	36.31	A
ATOM	122	C1'	GUA	A	6	7.826	31.865	52.619	1.00	37.34	A

ATOM	123	N9	GUA	A	6	6.814	30.888	52.222	1.00	38.69	A
ATOM	124	C4	GUA	A	6	5.667	31.157	51.531	1.00	39.43	A
ATOM	125	N3	GUA	A	6	5.244	32.379	51.154	1.00	39.49	A
ATOM	126	C2	GUA	A	6	4.118	32.327	50.467	1.00	39.64	A
ATOM	127	N2	GUA	A	6	3.564	33.461	50.032	1.00	38.79	A
ATOM	128	N1	GUA	A	6	3.456	31.160	50.161	1.00	39.77	A
ATOM	129	C6	GUA	A	6	3.864	29.881	50.541	1.00	40.75	A
ATOM	130	O6	GUA	A	6	3.190	28.886	50.209	1.00	36.84	A
ATOM	131	C5	GUA	A	6	5.079	29.929	51.300	1.00	41.36	A
ATOM	132	N7	GUA	A	6	5.824	28.910	51.883	1.00	38.94	A
ATOM	133	C8	GUA	A	6	6.836	29.527	52.427	1.00	38.93	A
ATOM	134	C2'	GUA	A	6	7.332	32.845	53.679	1.00	35.62	A
ATOM	135	O2'	GUA	A	6	8.027	34.065	53.563	1.00	35.89	A
ATOM	136	C3'	GUA	A	6	7.718	32.115	54.948	1.00	34.49	A
ATOM	137	O3'	GUA	A	6	7.848	33.067	55.974	1.00	33.17	A
ATOM	138	P	CYT	A	7	6.760	33.100	57.135	1.00	36.95	A
ATOM	139	O1P	CYT	A	7	6.435	31.689	57.467	1.00	36.80	A
ATOM	140	O2P	CYT	A	7	7.223	34.013	58.202	1.00	37.25	A
ATOM	141	O5'	CYT	A	7	5.510	33.776	56.427	1.00	37.87	A
ATOM	142	C5'	CYT	A	7	5.579	35.130	56.015	1.00	39.08	A
ATOM	143	C4'	CYT	A	7	4.321	35.514	55.296	1.00	41.04	A
ATOM	144	O4'	CYT	A	7	4.262	34.828	54.017	1.00	41.75	A
ATOM	145	C1'	CYT	A	7	2.927	34.445	53.751	1.00	42.97	A
ATOM	146	N1	CYT	A	7	2.856	32.986	53.794	1.00	44.72	A
ATOM	147	C6	CYT	A	7	3.633	32.261	54.651	1.00	45.48	A
ATOM	148	C2	CYT	A	7	1.986	32.351	52.935	1.00	44.06	A
ATOM	149	O2	CYT	A	7	1.282	33.047	52.206	1.00	46.39	A
ATOM	150	N3	CYT	A	7	1.923	31.003	52.920	1.00	42.20	A
ATOM	151	C4	CYT	A	7	2.679	30.299	53.754	1.00	43.31	A
ATOM	152	N4	CYT	A	7	2.577	28.971	53.721	1.00	43.90	A
ATOM	153	C5	CYT	A	7	3.574	30.926	54.666	1.00	46.03	A
ATOM	154	C2'	CYT	A	7	2.076	35.118	54.820	1.00	43.20	A
ATOM	155	O2'	CYT	A	7	1.826	36.454	54.434	1.00	47.51	A
ATOM	156	C3'	CYT	A	7	3.038	35.108	55.987	1.00	40.73	A
ATOM	157	O3'	CYT	A	7	2.664	36.118	56.886	1.00	38.58	A
ATOM	158	P	GUA	A	8	1.936	35.720	58.247	1.00	42.00	A
ATOM	159	O1P	GUA	A	8	2.563	34.485	58.780	1.00	41.25	A
ATOM	160	O2P	GUA	A	8	1.927	36.956	59.061	1.00	38.47	A
ATOM	161	O5'	GUA	A	8	0.458	35.310	57.814	1.00	43.41	A
ATOM	162	C5'	GUA	A	8	-0.427	36.243	57.189	1.00	45.59	A
ATOM	163	C4'	GUA	A	8	-1.864	35.893	57.503	1.00	47.15	A
ATOM	164	O4'	GUA	A	8	-2.222	34.610	56.904	1.00	46.35	A
ATOM	165	C1'	GUA	A	8	-2.960	33.871	57.845	1.00	47.37	A
ATOM	166	N9	GUA	A	8	-2.819	32.449	57.568	1.00	50.30	A
ATOM	167	C4	GUA	A	8	-3.739	31.651	56.951	1.00	52.71	A
ATOM	168	N3	GUA	A	8	-4.914	32.058	56.430	1.00	53.07	A
ATOM	169	C2	GUA	A	8	-5.611	31.051	55.942	1.00	53.51	A
ATOM	170	N2	GUA	A	8	-6.804	31.279	55.392	1.00	55.21	A
ATOM	171	N1	GUA	A	8	-5.189	29.744	55.960	1.00	55.13	A
ATOM	172	C6	GUA	A	8	-3.975	29.298	56.485	1.00	55.81	A
ATOM	173	O6	GUA	A	8	-3.683	28.085	56.453	1.00	56.49	A
ATOM	174	C5	GUA	A	8	-3.216	30.374	57.012	1.00	53.87	A
ATOM	175	N7	GUA	A	8	-1.969	30.380	57.615	1.00	51.04	A
ATOM	176	C8	GUA	A	8	-1.770	31.633	57.919	1.00	52.05	A
ATOM	177	C2'	GUA	A	8	-2.329	34.255	59.174	1.00	46.97	A
ATOM	178	O2'	GUA	A	8	-3.150	33.861	60.245	1.00	43.61	A
ATOM	179	C3'	GUA	A	8	-2.172	35.760	58.994	1.00	48.46	A
ATOM	180	O3'	GUA	A	8	-3.372	36.455	59.313	1.00	51.14	A
ATOM	181	P	ADE	A	9	-3.597	37.012	60.803	1.00	54.42	A
ATOM	182	O1P	ADE	A	9	-3.394	38.489	60.798	1.00	52.70	A
ATOM	183	O2P	ADE	A	9	-2.835	36.144	61.759	1.00	51.84	A

ATOM	184	O5'	ADE	A	9	-5.147	36.795	61.060	1.00	55.36	A
ATOM	185	C5'	ADE	A	9	-5.675	35.492	61.258	1.00	54.25	A
ATOM	186	C4'	ADE	A	9	-7.003	35.374	60.562	1.00	52.00	A
ATOM	187	O4'	ADE	A	9	-6.781	34.888	59.210	1.00	49.91	A
ATOM	188	C1'	ADE	A	9	-7.716	33.866	58.919	1.00	49.59	A
ATOM	189	N9	ADE	A	9	-7.032	32.582	59.020	1.00	46.92	A
ATOM	190	C4	ADE	A	9	-7.519	31.391	58.552	1.00	46.44	A
ATOM	191	N3	ADE	A	9	-8.686	31.187	57.925	1.00	45.85	A
ATOM	192	C2	ADE	A	9	-8.834	29.901	57.630	1.00	46.76	A
ATOM	193	N1	ADE	A	9	-8.009	28.877	57.867	1.00	46.92	A
ATOM	194	C6	ADE	A	9	-6.837	29.122	58.492	1.00	46.05	A
ATOM	195	N6	ADE	A	9	-6.009	28.100	58.715	1.00	46.20	A
ATOM	196	C5	ADE	A	9	-6.565	30.444	58.865	1.00	44.50	A
ATOM	197	N7	ADE	A	9	-5.493	31.028	59.515	1.00	44.66	A
ATOM	198	C8	ADE	A	9	-5.818	32.296	59.582	1.00	45.49	A
ATOM	199	C2'	ADE	A	9	-8.808	34.000	59.975	1.00	51.40	A
ATOM	200	O2'	ADE	A	9	-9.692	35.040	59.615	1.00	54.37	A
ATOM	201	C3'	ADE	A	9	-7.974	34.382	61.182	1.00	51.00	A
ATOM	202	O3'	ADE	A	9	-8.768	35.020	62.172	1.00	49.06	A
ATOM	203	P	URI	A	10	-9.231	34.196	63.471	1.00	51.70	A
ATOM	204	O1P	URI	A	10	-8.107	33.313	63.874	1.00	50.55	A
ATOM	205	O2P	URI	A	10	-9.786	35.166	64.454	1.00	48.53	A
ATOM	206	O5'	URI	A	10	-10.403	33.261	62.918	1.00	51.67	A
ATOM	207	C5'	URI	A	10	-11.358	33.775	61.994	1.00	52.81	A
ATOM	208	C4'	URI	A	10	-12.176	32.661	61.394	1.00	54.72	A
ATOM	209	O4'	URI	A	10	-11.443	31.990	60.339	1.00	54.38	A
ATOM	210	C1'	URI	A	10	-11.921	30.661	60.223	1.00	54.28	A
ATOM	211	N1	URI	A	10	-10.816	29.747	60.502	1.00	54.62	A
ATOM	212	C6	URI	A	10	-9.672	30.161	61.130	1.00	54.70	A
ATOM	213	C2	URI	A	10	-10.988	28.448	60.125	1.00	55.57	A
ATOM	214	O2	URI	A	10	-11.989	28.064	59.553	1.00	55.75	A
ATOM	215	N3	URI	A	10	-9.951	27.613	60.440	1.00	56.18	A
ATOM	216	C4	URI	A	10	-8.785	27.952	61.079	1.00	55.37	A
ATOM	217	O4	URI	A	10	-7.964	27.073	61.337	1.00	58.05	A
ATOM	218	C5	URI	A	10	-8.676	29.330	61.425	1.00	54.29	A
ATOM	219	C2'	URI	A	10	-12.991	30.472	61.295	1.00	54.86	A
ATOM	220	O2'	URI	A	10	-14.268	30.721	60.757	1.00	56.63	A
ATOM	221	C3'	URI	A	10	-12.577	31.521	62.312	1.00	55.55	A
ATOM	222	O3'	URI	A	10	-13.695	31.899	63.096	1.00	58.29	A
ATOM	223	P	URI	A	11	-14.115	31.020	64.373	1.00	59.94	A
ATOM	224	O1P	URI	A	11	-12.956	30.853	65.283	1.00	59.36	A
ATOM	225	O2P	URI	A	11	-15.352	31.662	64.888	1.00	60.92	A
ATOM	226	O5'	URI	A	11	-14.431	29.576	63.768	1.00	59.83	A
ATOM	227	C5'	URI	A	11	-15.507	29.360	62.854	1.00	59.21	A
ATOM	228	C4'	URI	A	11	-15.684	27.878	62.593	1.00	59.51	A
ATOM	229	O4'	URI	A	11	-14.571	27.380	61.805	1.00	59.78	A
ATOM	230	C1'	URI	A	11	-14.284	26.036	62.175	1.00	59.78	A
ATOM	231	N1	URI	A	11	-12.899	25.949	62.662	1.00	59.00	A
ATOM	232	C6	URI	A	11	-12.236	27.040	63.169	1.00	57.75	A
ATOM	233	C2	URI	A	11	-12.291	24.707	62.615	1.00	58.51	A
ATOM	234	O2	URI	A	11	-12.834	23.726	62.144	1.00	59.28	A
ATOM	235	N3	URI	A	11	-11.027	24.658	63.137	1.00	56.77	A
ATOM	236	C4	URI	A	11	-10.319	25.699	63.680	1.00	57.51	A
ATOM	237	O4	URI	A	11	-9.224	25.475	64.189	1.00	58.27	A
ATOM	238	C5	URI	A	11	-11.000	26.961	63.666	1.00	57.92	A
ATOM	239	C2'	URI	A	11	-15.266	25.639	63.276	1.00	59.82	A
ATOM	240	O2'	URI	A	11	-16.313	24.858	62.743	1.00	58.65	A
ATOM	241	C3'	URI	A	11	-15.673	27.001	63.833	1.00	60.24	A
ATOM	242	O3'	URI	A	11	-16.953	26.967	64.437	1.00	63.21	A
ATOM	243	P	URI	A	12	-17.085	26.618	65.999	1.00	66.40	A
ATOM	244	O1P	URI	A	12	-16.143	27.477	66.754	1.00	66.07	A

ATOM	245	O2P	URI	A	12	-18.527	26.661	66.331	1.00	68.45	A
ATOM	246	O5'	URI	A	12	-16.586	25.107	66.094	1.00	65.97	A
ATOM	247	C5'	URI	A	12	-17.182	24.093	65.296	1.00	67.36	A
ATOM	248	C4'	URI	A	12	-16.479	22.772	65.505	1.00	69.81	A
ATOM	249	O4'	URI	A	12	-15.173	22.795	64.879	1.00	70.39	A
ATOM	250	C1'	URI	A	12	-14.329	21.861	65.529	1.00	69.88	A
ATOM	251	N1	URI	A	12	-13.093	22.547	65.926	1.00	70.58	A
ATOM	252	C6	URI	A	12	-13.009	23.915	65.928	1.00	70.52	A
ATOM	253	C2	URI	A	12	-12.019	21.765	66.322	1.00	70.85	A
ATOM	254	O2	URI	A	12	-12.042	20.550	66.310	1.00	72.51	A
ATOM	255	N3	URI	A	12	-10.916	22.462	66.734	1.00	69.65	A
ATOM	256	C4	URI	A	12	-10.779	23.828	66.789	1.00	70.03	A
ATOM	257	O4	URI	A	12	-9.773	24.304	67.296	1.00	70.62	A
ATOM	258	C5	URI	A	12	-11.917	24.566	66.335	1.00	70.95	A
ATOM	259	C2'	URI	A	12	-15.089	21.334	66.747	1.00	70.55	A
ATOM	260	O2'	URI	A	12	-15.628	20.071	66.444	1.00	71.94	A
ATOM	261	C3'	URI	A	12	-16.158	22.402	66.939	1.00	70.69	A
ATOM	262	O3'	URI	A	12	-17.305	21.860	67.579	1.00	72.76	A
ATOM	263	P	ADE	A	13	-17.510	22.068	69.158	1.00	74.36	A
ATOM	264	O1P	ADE	A	13	-18.547	21.100	69.565	1.00	73.45	A
ATOM	265	O2P	ADE	A	13	-17.701	23.513	69.441	1.00	72.68	A
ATOM	266	O5'	ADE	A	13	-16.133	21.590	69.797	1.00	76.15	A
ATOM	267	C5'	ADE	A	13	-15.971	20.254	70.263	1.00	80.22	A
ATOM	268	C4'	ADE	A	13	-15.731	20.261	71.749	1.00	83.46	A
ATOM	269	O4'	ADE	A	13	-14.414	20.806	71.974	1.00	83.69	A
ATOM	270	C1'	ADE	A	13	-14.387	21.437	73.233	1.00	84.72	A
ATOM	271	N9	ADE	A	13	-13.487	22.587	73.160	1.00	83.53	A
ATOM	272	C4	ADE	A	13	-12.161	22.593	73.518	1.00	83.42	A
ATOM	273	N3	ADE	A	13	-11.430	21.552	73.955	1.00	83.67	A
ATOM	274	C2	ADE	A	13	-10.186	21.936	74.234	1.00	83.32	A
ATOM	275	N1	ADE	A	13	-9.634	23.151	74.139	1.00	83.45	A
ATOM	276	C6	ADE	A	13	-10.399	24.177	73.701	1.00	84.07	A
ATOM	277	N6	ADE	A	13	-9.855	25.395	73.624	1.00	85.24	A
ATOM	278	C5	ADE	A	13	-11.735	23.898	73.358	1.00	83.50	A
ATOM	279	N7	ADE	A	13	-12.765	24.696	72.874	1.00	82.37	A
ATOM	280	C8	ADE	A	13	-13.776	23.872	72.768	1.00	82.92	A
ATOM	281	C2'	ADE	A	13	-15.818	21.829	73.620	1.00	85.51	A
ATOM	282	O2'	ADE	A	13	-16.107	21.444	74.949	1.00	86.56	A
ATOM	283	C3'	ADE	A	13	-16.675	21.184	72.518	1.00	85.91	A
ATOM	284	O3'	ADE	A	13	-17.914	20.556	72.906	1.00	87.87	A
ATOM	285	P	ADE	A	14	-17.976	19.507	74.134	1.00	88.89	A
ATOM	286	O1P	ADE	A	14	-16.620	19.050	74.536	1.00	88.89	A
ATOM	287	O2P	ADE	A	14	-18.998	18.501	73.756	1.00	89.39	A
ATOM	288	O5'	ADE	A	14	-18.566	20.387	75.314	1.00	88.88	A
ATOM	289	C5'	ADE	A	14	-18.936	21.735	75.070	1.00	91.70	A
ATOM	290	C4'	ADE	A	14	-20.142	22.101	75.891	1.00	94.04	A
ATOM	291	O4'	ADE	A	14	-21.326	22.017	75.082	1.00	95.65	A
ATOM	292	C1'	ADE	A	14	-22.438	21.956	75.937	1.00	97.65	A
ATOM	293	N9	ADE	A	14	-23.456	21.153	75.272	1.00	101.14	A
ATOM	294	C4	ADE	A	14	-24.067	21.476	74.086	1.00	103.55	A
ATOM	295	N3	ADE	A	14	-23.868	22.580	73.342	1.00	104.35	A
ATOM	296	C2	ADE	A	14	-24.625	22.549	72.244	1.00	104.89	A
ATOM	297	N1	ADE	A	14	-25.490	21.609	71.836	1.00	104.95	A
ATOM	298	C6	ADE	A	14	-25.664	20.510	72.608	1.00	104.89	A
ATOM	299	N6	ADE	A	14	-26.516	19.566	72.198	1.00	104.41	A
ATOM	300	C5	ADE	A	14	-24.924	20.428	73.805	1.00	104.57	A
ATOM	301	N7	ADE	A	14	-24.871	19.469	74.808	1.00	104.45	A
ATOM	302	C8	ADE	A	14	-23.990	19.947	75.654	1.00	103.05	A
ATOM	303	C2'	ADE	A	14	-21.959	21.406	77.289	1.00	95.73	A
ATOM	304	O2'	ADE	A	14	-22.285	22.320	78.317	1.00	96.76	A
ATOM	305	C3'	ADE	A	14	-20.450	21.191	77.068	1.00	93.55	A

ATOM	306	O3'	ADE	A	14	-19.615	21.602	78.153	1.00	89.70	A
ATOM	307	P	CYT	A	15	-19.810	20.980	79.624	1.00	85.69	A
ATOM	308	O1P	CYT	A	15	-18.605	20.172	79.932	1.00	84.11	A
ATOM	309	O2P	CYT	A	15	-21.155	20.352	79.716	1.00	86.79	A
ATOM	310	O5'	CYT	A	15	-19.795	22.277	80.554	1.00	83.02	A
ATOM	311	C5'	CYT	A	15	-20.789	23.293	80.395	1.00	78.80	A
ATOM	312	C4'	CYT	A	15	-20.213	24.670	80.663	1.00	75.64	A
ATOM	313	O4'	CYT	A	15	-19.728	24.752	82.029	1.00	75.02	A
ATOM	314	C1'	CYT	A	15	-18.542	25.525	82.071	1.00	72.30	A
ATOM	315	N1	CYT	A	15	-17.419	24.625	82.362	1.00	71.80	A
ATOM	316	C6	CYT	A	15	-17.508	23.282	82.117	1.00	70.65	A
ATOM	317	C2	CYT	A	15	-16.246	25.171	82.878	1.00	71.69	A
ATOM	318	O2	CYT	A	15	-16.209	26.387	83.120	1.00	72.35	A
ATOM	319	N3	CYT	A	15	-15.185	24.364	83.102	1.00	70.96	A
ATOM	320	C4	CYT	A	15	-15.272	23.060	82.838	1.00	69.95	A
ATOM	321	N4	CYT	A	15	-14.194	22.315	83.047	1.00	68.69	A
ATOM	322	C5	CYT	A	15	-16.467	22.470	82.339	1.00	70.20	A
ATOM	323	C2'	CYT	A	15	-18.407	26.168	80.696	1.00	72.73	A
ATOM	324	O2'	CYT	A	15	-19.148	27.365	80.658	1.00	71.72	A
ATOM	325	C3'	CYT	A	15	-19.026	25.095	79.821	1.00	73.99	A
ATOM	326	O3'	CYT	A	15	-19.470	25.667	78.607	1.00	74.25	A
ATOM	327	P	CYT	A	16	-18.436	25.845	77.399	1.00	72.99	A
ATOM	328	O1P	CYT	A	16	-17.774	24.535	77.181	1.00	72.15	A
ATOM	329	O2P	CYT	A	16	-19.150	26.508	76.283	1.00	73.64	A
ATOM	330	O5'	CYT	A	16	-17.369	26.872	77.971	1.00	71.54	A
ATOM	331	C5'	CYT	A	16	-17.678	28.252	78.047	1.00	70.37	A
ATOM	332	C4'	CYT	A	16	-16.510	29.015	78.622	1.00	70.94	A
ATOM	333	O4'	CYT	A	16	-16.071	28.393	79.858	1.00	70.27	A
ATOM	334	C1'	CYT	A	16	-14.679	28.598	80.016	1.00	69.83	A
ATOM	335	N1	CYT	A	16	-14.026	27.287	80.081	1.00	70.24	A
ATOM	336	C6	CYT	A	16	-14.719	26.140	79.812	1.00	70.01	A
ATOM	337	C2	CYT	A	16	-12.676	27.232	80.424	1.00	70.90	A
ATOM	338	O2	CYT	A	16	-12.073	28.290	80.649	1.00	71.93	A
ATOM	339	N3	CYT	A	16	-12.061	26.033	80.502	1.00	71.06	A
ATOM	340	C4	CYT	A	16	-12.745	24.918	80.250	1.00	71.12	A
ATOM	341	N4	CYT	A	16	-12.098	23.759	80.356	1.00	72.78	A
ATOM	342	C5	CYT	A	16	-14.123	24.944	79.883	1.00	70.62	A
ATOM	343	C2'	CYT	A	16	-14.212	29.422	78.815	1.00	70.28	A
ATOM	344	O2'	CYT	A	16	-14.284	30.798	79.118	1.00	72.82	A
ATOM	345	C3'	CYT	A	16	-15.249	29.041	77.777	1.00	70.11	A
ATOM	346	O3'	CYT	A	16	-15.331	30.049	76.783	1.00	68.85	A
ATOM	347	P	GUA	A	17	-14.822	29.729	75.302	1.00	70.04	A
ATOM	348	O1P	GUA	A	17	-15.539	28.515	74.834	1.00	68.06	A
ATOM	349	O2P	GUA	A	17	-14.890	30.975	74.499	1.00	68.97	A
ATOM	350	O5'	GUA	A	17	-13.292	29.349	75.528	1.00	70.16	A
ATOM	351	C5'	GUA	A	17	-12.336	30.346	75.879	1.00	69.19	A
ATOM	352	C4'	GUA	A	17	-11.021	29.706	76.258	1.00	69.17	A
ATOM	353	O4'	GUA	A	17	-11.239	28.790	77.365	1.00	69.13	A
ATOM	354	C1'	GUA	A	17	-10.382	27.666	77.235	1.00	69.09	A
ATOM	355	N9	GUA	A	17	-11.205	26.467	77.085	1.00	67.10	A
ATOM	356	C4	GUA	A	17	-10.803	25.158	77.245	1.00	65.67	A
ATOM	357	N3	GUA	A	17	-9.569	24.740	77.593	1.00	66.51	A
ATOM	358	C2	GUA	A	17	-9.485	23.415	77.633	1.00	66.53	A
ATOM	359	N2	GUA	A	17	-8.323	22.819	77.952	1.00	66.24	A
ATOM	360	N1	GUA	A	17	-10.530	22.577	77.359	1.00	65.61	A
ATOM	361	C6	GUA	A	17	-11.810	22.988	77.003	1.00	66.05	A
ATOM	362	O6	GUA	A	17	-12.686	22.143	76.771	1.00	67.69	A
ATOM	363	C5	GUA	A	17	-11.913	24.399	76.955	1.00	65.35	A
ATOM	364	N7	GUA	A	17	-12.996	25.207	76.645	1.00	65.91	A
ATOM	365	C8	GUA	A	17	-12.532	26.422	76.738	1.00	66.71	A
ATOM	366	C2'	GUA	A	17	-9.467	27.952	76.040	1.00	69.82	A

ATOM	367	O2'	GUA	A	17	-8.322	28.647	76.492	1.00	68.53	A
ATOM	368	C3'	GUA	A	17	-10.351	28.854	75.190	1.00	69.79	A
ATOM	369	O3'	GUA	A	17	-9.536	29.659	74.347	1.00	71.64	A
ATOM	370	P	URI	A	18	-9.841	29.732	72.773	1.00	75.29	A
ATOM	371	O1P	URI	A	18	-10.045	28.347	72.291	1.00	75.45	A
ATOM	372	O2P	URI	A	18	-10.896	30.747	72.545	1.00	74.13	A
ATOM	373	O5'	URI	A	18	-8.478	30.266	72.138	1.00	78.88	A
ATOM	374	C5'	URI	A	18	-8.001	31.590	72.399	1.00	84.21	A
ATOM	375	C4'	URI	A	18	-6.671	31.537	73.125	1.00	87.36	A
ATOM	376	O4'	URI	A	18	-6.874	30.864	74.406	1.00	92.07	A
ATOM	377	C1'	URI	A	18	-5.734	30.059	74.718	1.00	94.03	A
ATOM	378	N1	URI	A	18	-6.098	28.632	74.613	1.00	98.01	A
ATOM	379	C6	URI	A	18	-6.878	28.149	73.574	1.00	99.76	A
ATOM	380	C2	URI	A	18	-5.611	27.772	75.590	1.00	99.81	A
ATOM	381	O2	URI	A	18	-4.936	28.154	76.531	1.00	99.86	A
ATOM	382	N3	URI	A	18	-5.946	26.447	75.423	1.00	101.21	A
ATOM	383	C4	URI	A	18	-6.707	25.898	74.406	1.00	101.59	A
ATOM	384	O4	URI	A	18	-6.922	24.682	74.399	1.00	101.64	A
ATOM	385	C5	URI	A	18	-7.186	26.848	73.439	1.00	101.34	A
ATOM	386	C2'	URI	A	18	-4.684	30.427	73.679	1.00	90.65	A
ATOM	387	O2'	URI	A	18	-3.971	31.589	74.065	1.00	91.21	A
ATOM	388	C3'	URI	A	18	-5.588	30.677	72.493	1.00	87.49	A
ATOM	389	O3'	URI	A	18	-4.851	31.276	71.460	1.00	83.08	A
ATOM	390	P	ADE	A	19	-3.932	30.345	70.538	1.00	81.25	A
ATOM	391	O1P	ADE	A	19	-3.088	31.243	69.704	1.00	80.29	A
ATOM	392	O2P	ADE	A	19	-4.832	29.356	69.885	1.00	80.09	A
ATOM	393	O5'	ADE	A	19	-2.994	29.564	71.567	1.00	79.28	A
ATOM	394	C5'	ADE	A	19	-1.630	29.937	71.742	1.00	77.82	A
ATOM	395	C4'	ADE	A	19	-0.795	28.745	72.158	1.00	77.72	A
ATOM	396	O4'	ADE	A	19	-1.556	27.877	73.031	1.00	77.57	A
ATOM	397	C1'	ADE	A	19	-1.016	26.564	72.971	1.00	77.68	A
ATOM	398	N9	ADE	A	19	-2.106	25.618	72.713	1.00	78.65	A
ATOM	399	C4	ADE	A	19	-2.044	24.245	72.774	1.00	78.79	A
ATOM	400	N3	ADE	A	19	-0.979	23.488	73.085	1.00	79.18	A
ATOM	401	C2	ADE	A	19	-1.292	22.193	73.032	1.00	79.24	A
ATOM	402	N1	ADE	A	19	-2.462	21.612	72.727	1.00	78.75	A
ATOM	403	C6	ADE	A	19	-3.515	22.399	72.424	1.00	78.55	A
ATOM	404	N6	ADE	A	19	-4.681	21.818	72.123	1.00	76.43	A
ATOM	405	C5	ADE	A	19	-3.313	23.793	72.444	1.00	79.04	A
ATOM	406	N7	ADE	A	19	-4.162	24.861	72.185	1.00	79.73	A
ATOM	407	C8	ADE	A	19	-3.401	25.916	72.359	1.00	80.36	A
ATOM	408	C2'	ADE	A	19	0.063	26.576	71.886	1.00	77.49	A
ATOM	409	O2'	ADE	A	19	1.327	26.762	72.486	1.00	76.48	A
ATOM	410	C3'	ADE	A	19	-0.343	27.792	71.064	1.00	78.16	A
ATOM	411	O3'	ADE	A	19	0.795	28.312	70.379	1.00	79.19	A
ATOM	412	P	URI	A	20	1.119	27.836	68.871	1.00	79.14	A
ATOM	413	O1P	URI	A	20	0.046	28.324	67.964	1.00	76.77	A
ATOM	414	O2P	URI	A	20	2.536	28.205	68.611	1.00	78.22	A
ATOM	415	O5'	URI	A	20	1.015	26.249	68.908	1.00	75.01	A
ATOM	416	C5'	URI	A	20	2.060	25.466	69.454	1.00	72.40	A
ATOM	417	C4'	URI	A	20	1.807	24.016	69.163	1.00	71.99	A
ATOM	418	O4'	URI	A	20	0.764	23.525	70.046	1.00	71.40	A
ATOM	419	C1'	URI	A	20	-0.064	22.610	69.348	1.00	70.50	A
ATOM	420	N1	URI	A	20	-1.419	23.173	69.278	1.00	69.99	A
ATOM	421	C6	URI	A	20	-1.641	24.526	69.396	1.00	69.65	A
ATOM	422	C2	URI	A	20	-2.470	22.296	69.079	1.00	69.79	A
ATOM	423	O2	URI	A	20	-2.315	21.091	68.976	1.00	69.83	A
ATOM	424	N3	URI	A	20	-3.711	22.883	69.006	1.00	68.93	A
ATOM	425	C4	URI	A	20	-4.003	24.223	69.116	1.00	68.00	A
ATOM	426	O4	URI	A	20	-5.179	24.586	69.103	1.00	66.76	A
ATOM	427	C5	URI	A	20	-2.863	25.066	69.320	1.00	68.94	A

ATOM	428	C2'	URI	A	20	0.552	22.421	67.960	1.00	71.39	A
ATOM	429	O2'	URI	A	20	1.424	21.310	67.946	1.00	69.58	A
ATOM	430	C3'	URI	A	20	1.267	23.750	67.771	1.00	72.13	A
ATOM	431	O3'	URI	A	20	2.338	23.633	66.851	1.00	74.59	A
ATOM	432	P	URI	A	21	2.098	23.975	65.301	1.00	75.64	A
ATOM	433	O1P	URI	A	21	3.447	24.101	64.692	1.00	75.59	A
ATOM	434	O2P	URI	A	21	1.146	25.116	65.209	1.00	76.07	A
ATOM	435	O5'	URI	A	21	1.388	22.660	64.745	1.00	72.90	A
ATOM	436	C5'	URI	A	21	2.021	21.390	64.850	1.00	69.19	A
ATOM	437	C4'	URI	A	21	1.095	20.303	64.371	1.00	67.68	A
ATOM	438	O4'	URI	A	21	0.085	20.078	65.387	1.00	67.43	A
ATOM	439	C1'	URI	A	21	-1.146	19.748	64.772	1.00	68.79	A
ATOM	440	N1	URI	A	21	-2.134	20.782	65.113	1.00	70.91	A
ATOM	441	C6	URI	A	21	-1.751	22.047	65.500	1.00	70.89	A
ATOM	442	C2	URI	A	21	-3.479	20.439	65.021	1.00	72.02	A
ATOM	443	O2	URI	A	21	-3.860	19.327	64.684	1.00	72.32	A
ATOM	444	N3	URI	A	21	-4.362	21.450	65.333	1.00	72.47	A
ATOM	445	C4	URI	A	21	-4.048	22.740	65.716	1.00	72.29	A
ATOM	446	O4	URI	A	21	-4.958	23.549	65.917	1.00	70.84	A
ATOM	447	C5	URI	A	21	-2.637	23.013	65.796	1.00	71.91	A
ATOM	448	C2'	URI	A	21	-0.888	19.673	63.267	1.00	68.38	A
ATOM	449	O2'	URI	A	21	-0.583	18.348	62.893	1.00	67.60	A
ATOM	450	C3'	URI	A	21	0.293	20.617	63.119	1.00	67.38	A
ATOM	451	O3'	URI	A	21	1.015	20.314	61.935	1.00	66.83	A
ATOM	452	P	GUA	A	22	0.452	20.816	60.513	1.00	69.29	A
ATOM	453	O1P	GUA	A	22	-0.119	22.178	60.708	1.00	67.61	A
ATOM	454	O2P	GUA	A	22	1.497	20.595	59.478	1.00	66.54	A
ATOM	455	O5'	GUA	A	22	-0.771	19.845	60.199	1.00	67.90	A
ATOM	456	C5'	GUA	A	22	-0.616	18.743	59.316	1.00	67.34	A
ATOM	457	C4'	GUA	A	22	-1.951	18.338	58.728	1.00	67.34	A
ATOM	458	O4'	GUA	A	22	-3.052	18.853	59.524	1.00	67.07	A
ATOM	459	C1'	GUA	A	22	-4.156	19.137	58.674	1.00	65.78	A
ATOM	460	N9	GUA	A	22	-4.409	20.570	58.714	1.00	63.69	A
ATOM	461	C4	GUA	A	22	-5.519	21.196	58.234	1.00	64.17	A
ATOM	462	N3	GUA	A	22	-6.578	20.590	57.669	1.00	66.48	A
ATOM	463	C2	GUA	A	22	-7.508	21.456	57.316	1.00	66.72	A
ATOM	464	N2	GUA	A	22	-8.640	21.019	56.741	1.00	67.37	A
ATOM	465	N1	GUA	A	22	-7.400	22.810	57.504	1.00	64.80	A
ATOM	466	C6	GUA	A	22	-6.319	23.449	58.092	1.00	62.77	A
ATOM	467	O6	GUA	A	22	-6.336	24.670	58.235	1.00	63.28	A
ATOM	468	C5	GUA	A	22	-5.317	22.535	58.467	1.00	63.01	A
ATOM	469	N7	GUA	A	22	-4.098	22.745	59.086	1.00	62.71	A
ATOM	470	C8	GUA	A	22	-3.594	21.551	59.213	1.00	62.98	A
ATOM	471	C2'	GUA	A	22	-3.750	18.723	57.262	1.00	67.09	A
ATOM	472	O2'	GUA	A	22	-4.164	17.403	56.976	1.00	66.74	A
ATOM	473	C3'	GUA	A	22	-2.242	18.887	57.346	1.00	67.87	A
ATOM	474	O3'	GUA	A	22	-1.577	18.129	56.355	1.00	68.73	A
ATOM	475	P	CYT	A	23	-0.934	18.878	55.097	1.00	69.00	A
ATOM	476	O1P	CYT	A	23	-0.475	20.227	55.551	1.00	66.88	A
ATOM	477	O2P	CYT	A	23	0.034	17.929	54.486	1.00	69.69	A
ATOM	478	O5'	CYT	A	23	-2.168	19.061	54.112	1.00	66.23	A
ATOM	479	C5'	CYT	A	23	-3.205	18.095	54.073	1.00	61.77	A
ATOM	480	C4'	CYT	A	23	-4.466	18.709	53.528	1.00	59.16	A
ATOM	481	O4'	CYT	A	23	-5.143	19.424	54.589	1.00	57.70	A
ATOM	482	C1'	CYT	A	23	-5.882	20.493	54.027	1.00	57.19	A
ATOM	483	N1	CYT	A	23	-5.376	21.740	54.583	1.00	55.24	A
ATOM	484	C6	CYT	A	23	-4.177	21.791	55.232	1.00	54.51	A
ATOM	485	C2	CYT	A	23	-6.128	22.881	54.404	1.00	55.15	A
ATOM	486	O2	CYT	A	23	-7.221	22.783	53.826	1.00	53.58	A
ATOM	487	N3	CYT	A	23	-5.652	24.063	54.851	1.00	55.42	A
ATOM	488	C4	CYT	A	23	-4.464	24.116	55.450	1.00	54.64	A

ATOM	489	N4	CYT	A	23	-4.011	25.308	55.831	1.00	55.93	A
ATOM	490	C5	CYT	A	23	-3.683	22.951	55.672	1.00	54.66	A
ATOM	491	C2'	CYT	A	23	-5.636	20.472	52.517	1.00	57.73	A
ATOM	492	O2'	CYT	A	23	-6.674	19.773	51.861	1.00	58.26	A
ATOM	493	C3'	CYT	A	23	-4.292	19.765	52.451	1.00	57.38	A
ATOM	494	O3'	CYT	A	23	-4.104	19.165	51.181	1.00	57.87	A
ATOM	495	P	ADE	A	24	-3.341	19.973	50.014	1.00	61.30	A
ATOM	496	O1P	ADE	A	24	-3.432	19.164	48.772	1.00	59.15	A
ATOM	497	O2P	ADE	A	24	-2.010	20.417	50.511	1.00	60.39	A
ATOM	498	O5'	ADE	A	24	-4.235	21.263	49.770	1.00	58.67	A
ATOM	499	C5'	ADE	A	24	-5.394	21.182	48.973	1.00	55.21	A
ATOM	500	C4'	ADE	A	24	-6.204	22.429	49.134	1.00	54.44	A
ATOM	501	O4'	ADE	A	24	-6.327	22.758	50.543	1.00	55.41	A
ATOM	502	C1'	ADE	A	24	-6.383	24.170	50.691	1.00	54.19	A
ATOM	503	N9	ADE	A	24	-5.209	24.575	51.446	1.00	54.73	A
ATOM	504	C4	ADE	A	24	-4.890	25.849	51.828	1.00	55.04	A
ATOM	505	N3	ADE	A	24	-5.585	26.968	51.577	1.00	55.11	A
ATOM	506	C2	ADE	A	24	-4.980	28.021	52.120	1.00	56.89	A
ATOM	507	N1	ADE	A	24	-3.843	28.074	52.836	1.00	56.19	A
ATOM	508	C6	ADE	A	24	-3.176	26.924	53.069	1.00	56.00	A
ATOM	509	N6	ADE	A	24	-2.056	26.967	53.791	1.00	57.98	A
ATOM	510	C5	ADE	A	24	-3.710	25.744	52.541	1.00	55.31	A
ATOM	511	N7	ADE	A	24	-3.287	24.425	52.596	1.00	55.37	A
ATOM	512	C8	ADE	A	24	-4.207	23.774	51.929	1.00	55.10	A
ATOM	513	C2'	ADE	A	24	-6.361	24.744	49.279	1.00	53.40	A
ATOM	514	O2'	ADE	A	24	-7.683	24.807	48.799	1.00	53.18	A
ATOM	515	C3'	ADE	A	24	-5.562	23.671	48.570	1.00	52.64	A
ATOM	516	O3'	ADE	A	24	-5.743	23.711	47.178	1.00	50.69	A
ATOM	517	P	GUA	A	25	-4.634	24.416	46.271	1.00	51.67	A
ATOM	518	O1P	GUA	A	25	-3.300	23.875	46.655	1.00	47.23	A
ATOM	519	O2P	GUA	A	25	-5.078	24.335	44.861	1.00	49.51	A
ATOM	520	O5'	GUA	A	25	-4.740	25.936	46.718	1.00	48.34	A
ATOM	521	C5'	GUA	A	25	-5.596	26.822	46.023	1.00	46.65	A
ATOM	522	C4'	GUA	A	25	-5.610	28.158	46.701	1.00	45.25	A
ATOM	523	O4'	GUA	A	25	-5.440	27.968	48.132	1.00	46.00	A
ATOM	524	C1'	GUA	A	25	-4.661	29.028	48.666	1.00	46.72	A
ATOM	525	N9	GUA	A	25	-3.430	28.456	49.219	1.00	49.02	A
ATOM	526	C4	GUA	A	25	-2.443	29.116	49.914	1.00	47.40	A
ATOM	527	N3	GUA	A	25	-2.422	30.427	50.202	1.00	47.74	A
ATOM	528	C2	GUA	A	25	-1.357	30.759	50.909	1.00	48.49	A
ATOM	529	N2	GUA	A	25	-1.178	32.029	51.298	1.00	48.42	A
ATOM	530	N1	GUA	A	25	-0.387	29.875	51.290	1.00	48.24	A
ATOM	531	C6	GUA	A	25	-0.384	28.520	50.998	1.00	49.17	A
ATOM	532	O6	GUA	A	25	0.547	27.806	51.392	1.00	51.70	A
ATOM	533	C5	GUA	A	25	-1.522	28.149	50.251	1.00	48.43	A
ATOM	534	N7	GUA	A	25	-1.910	26.908	49.770	1.00	48.09	A
ATOM	535	C8	GUA	A	25	-3.040	27.138	49.160	1.00	49.59	A
ATOM	536	C2'	GUA	A	25	-4.446	30.015	47.517	1.00	45.58	A
ATOM	537	O2'	GUA	A	25	-5.520	30.921	47.503	1.00	45.79	A
ATOM	538	C3'	GUA	A	25	-4.475	29.081	46.318	1.00	43.20	A
ATOM	539	O3'	GUA	A	25	-4.781	29.760	45.115	1.00	40.74	A
ATOM	540	P	URI	A	26	-3.717	29.749	43.908	1.00	43.39	A
ATOM	541	O1P	URI	A	26	-3.032	28.438	43.967	1.00	39.68	A
ATOM	542	O2P	URI	A	26	-4.351	30.177	42.633	1.00	40.27	A
ATOM	543	O5'	URI	A	26	-2.687	30.886	44.340	1.00	42.45	A
ATOM	544	C5'	URI	A	26	-3.136	32.211	44.602	1.00	42.90	A
ATOM	545	C4'	URI	A	26	-2.187	32.935	45.546	1.00	43.91	A
ATOM	546	O4'	URI	A	26	-2.250	32.368	46.882	1.00	43.17	A
ATOM	547	C1'	URI	A	26	-0.958	32.404	47.469	1.00	42.74	A
ATOM	548	N1	URI	A	26	-0.447	31.033	47.527	1.00	41.76	A
ATOM	549	C6	URI	A	26	-1.034	30.006	46.830	1.00	40.65	A

ATOM	550	C2	URI	A	26	0.645	30.820	48.319	1.00	38.14	A
ATOM	551	O2	URI	A	26	1.221	31.726	48.877	1.00	34.19	A
ATOM	552	N3	URI	A	26	1.050	29.517	48.409	1.00	36.80	A
ATOM	553	C4	URI	A	26	0.507	28.443	47.754	1.00	37.46	A
ATOM	554	O4	URI	A	26	0.959	27.329	47.962	1.00	38.00	A
ATOM	555	C5	URI	A	26	-0.597	28.753	46.905	1.00	39.39	A
ATOM	556	C2'	URI	A	26	-0.083	33.246	46.551	1.00	43.16	A
ATOM	557	O2'	URI	A	26	-0.193	34.611	46.897	1.00	43.72	A
ATOM	558	C3'	URI	A	26	-0.705	32.916	45.209	1.00	43.08	A
ATOM	559	O3'	URI	A	26	-0.386	33.922	44.284	1.00	42.91	A
ATOM	560	P	CYT	A	27	0.781	33.656	43.243	1.00	47.08	A
ATOM	561	O1P	CYT	A	27	0.666	32.223	42.869	1.00	43.13	A
ATOM	562	O2P	CYT	A	27	0.747	34.699	42.184	1.00	45.54	A
ATOM	563	O5'	CYT	A	27	2.092	33.854	44.129	1.00	49.14	A
ATOM	564	C5'	CYT	A	27	2.469	35.144	44.602	1.00	47.17	A
ATOM	565	C4'	CYT	A	27	3.765	35.055	45.362	1.00	46.81	A
ATOM	566	O4'	CYT	A	27	3.558	34.217	46.522	1.00	48.01	A
ATOM	567	C1'	CYT	A	27	4.764	33.560	46.856	1.00	46.91	A
ATOM	568	N1	CYT	A	27	4.514	32.118	46.875	1.00	46.48	A
ATOM	569	C6	CYT	A	27	3.504	31.568	46.147	1.00	45.80	A
ATOM	570	C2	CYT	A	27	5.331	31.320	47.646	1.00	47.12	A
ATOM	571	O2	CYT	A	27	6.233	31.854	48.289	1.00	49.30	A
ATOM	572	N3	CYT	A	27	5.127	29.990	47.676	1.00	46.54	A
ATOM	573	C4	CYT	A	27	4.144	29.458	46.961	1.00	44.47	A
ATOM	574	N4	CYT	A	27	3.979	28.144	47.013	1.00	44.09	A
ATOM	575	C5	CYT	A	27	3.287	30.251	46.159	1.00	45.18	A
ATOM	576	C2'	CYT	A	27	5.794	33.956	45.803	1.00	48.09	A
ATOM	577	O2'	CYT	A	27	6.562	35.031	46.282	1.00	49.01	A
ATOM	578	C3'	CYT	A	27	4.900	34.362	44.643	1.00	46.40	A
ATOM	579	O3'	CYT	A	27	5.589	35.277	43.816	1.00	46.57	A
ATOM	580	P	GUA	A	28	5.737	34.965	42.253	1.00	47.65	A
ATOM	581	O1P	GUA	A	28	4.565	34.146	41.873	1.00	48.71	A
ATOM	582	O2P	GUA	A	28	6.029	36.244	41.550	1.00	44.75	A
ATOM	583	O5'	GUA	A	28	6.988	33.995	42.133	1.00	48.15	A
ATOM	584	C5'	GUA	A	28	8.304	34.513	42.003	1.00	45.36	A
ATOM	585	C4'	GUA	A	28	9.135	34.087	43.181	1.00	42.58	A
ATOM	586	O4'	GUA	A	28	8.258	33.510	44.180	1.00	40.98	A
ATOM	587	C1'	GUA	A	28	8.963	32.528	44.906	1.00	40.82	A
ATOM	588	N9	GUA	A	28	8.238	31.274	44.785	1.00	41.22	A
ATOM	589	C4	GUA	A	28	8.577	30.088	45.376	1.00	42.88	A
ATOM	590	N3	GUA	A	28	9.650	29.876	46.163	1.00	42.86	A
ATOM	591	C2	GUA	A	28	9.701	28.629	46.600	1.00	44.96	A
ATOM	592	N2	GUA	A	28	10.691	28.242	47.405	1.00	44.64	A
ATOM	593	N1	GUA	A	28	8.780	27.666	46.283	1.00	45.93	A
ATOM	594	C6	GUA	A	28	7.674	27.859	45.470	1.00	43.79	A
ATOM	595	O6	GUA	A	28	6.918	26.919	45.245	1.00	44.25	A
ATOM	596	C5	GUA	A	28	7.599	29.197	44.999	1.00	43.04	A
ATOM	597	N7	GUA	A	28	6.667	29.812	44.180	1.00	42.58	A
ATOM	598	C8	GUA	A	28	7.091	31.044	44.078	1.00	40.68	A
ATOM	599	C2'	GUA	A	28	10.374	32.465	44.326	1.00	40.07	A
ATOM	600	O2'	GUA	A	28	11.213	33.316	45.079	1.00	37.21	A
ATOM	601	C3'	GUA	A	28	10.128	32.974	42.917	1.00	40.00	A
ATOM	602	O3'	GUA	A	28	11.306	33.508	42.343	1.00	38.81	A
ATOM	603	P	CYT	A	29	11.983	32.776	41.088	1.00	40.37	A
ATOM	604	O1P	CYT	A	29	10.945	32.136	40.247	1.00	43.72	A
ATOM	605	O2P	CYT	A	29	12.870	33.786	40.482	1.00	38.14	A
ATOM	606	O5'	CYT	A	29	12.817	31.590	41.759	1.00	38.45	A
ATOM	607	C5'	CYT	A	29	13.936	31.870	42.589	1.00	36.61	A
ATOM	608	C4'	CYT	A	29	14.295	30.674	43.441	1.00	36.86	A
ATOM	609	O4'	CYT	A	29	13.190	30.316	44.311	1.00	37.88	A
ATOM	610	C1'	CYT	A	29	13.239	28.917	44.576	1.00	40.99	A

ATOM	611	N1	CYT	A	29	12.051	28.285	43.971	1.00	44.33	A
ATOM	612	C6	CYT	A	29	11.208	28.999	43.167	1.00	46.13	A
ATOM	613	C2	CYT	A	29	11.796	26.930	44.233	1.00	47.42	A
ATOM	614	O2	CYT	A	29	12.582	26.302	44.964	1.00	48.50	A
ATOM	615	N3	CYT	A	29	10.698	26.342	43.682	1.00	48.76	A
ATOM	616	C4	CYT	A	29	9.877	27.059	42.908	1.00	47.66	A
ATOM	617	N4	CYT	A	29	8.802	26.457	42.403	1.00	47.18	A
ATOM	618	C5	CYT	A	29	10.121	28.431	42.622	1.00	47.63	A
ATOM	619	C2'	CYT	A	29	14.525	28.412	43.923	1.00	38.38	A
ATOM	620	O2'	CYT	A	29	15.633	28.573	44.781	1.00	36.10	A
ATOM	621	C3'	CYT	A	29	14.615	29.359	42.752	1.00	36.23	A
ATOM	622	O3'	CYT	A	29	15.919	29.304	42.233	1.00	34.41	A
ATOM	623	P	GUA	A	30	16.152	28.661	40.790	1.00	38.05	A
ATOM	624	O1P	GUA	A	30	14.826	28.589	40.130	1.00	39.90	A
ATOM	625	O2P	GUA	A	30	17.252	29.385	40.126	1.00	33.67	A
ATOM	626	O5'	GUA	A	30	16.582	27.160	41.107	1.00	38.02	A
ATOM	627	C5'	GUA	A	30	16.835	26.749	42.437	1.00	40.68	A
ATOM	628	C4'	GUA	A	30	16.851	25.248	42.523	1.00	43.03	A
ATOM	629	O4'	GUA	A	30	15.496	24.779	42.704	1.00	45.49	A
ATOM	630	C1'	GUA	A	30	15.149	23.912	41.646	1.00	46.19	A
ATOM	631	N9	GUA	A	30	13.761	24.171	41.287	1.00	46.68	A
ATOM	632	C4	GUA	A	30	12.741	23.263	41.260	1.00	46.15	A
ATOM	633	N3	GUA	A	30	12.830	21.966	41.595	1.00	46.81	A
ATOM	634	C2	GUA	A	30	11.677	21.337	41.433	1.00	47.98	A
ATOM	635	N2	GUA	A	30	11.573	20.030	41.724	1.00	47.46	A
ATOM	636	N1	GUA	A	30	10.537	21.940	40.974	1.00	48.25	A
ATOM	637	C6	GUA	A	30	10.430	23.278	40.624	1.00	48.04	A
ATOM	638	O6	GUA	A	30	9.359	23.723	40.214	1.00	48.66	A
ATOM	639	C5	GUA	A	30	11.648	23.958	40.801	1.00	47.58	A
ATOM	640	N7	GUA	A	30	11.967	25.283	40.575	1.00	48.54	A
ATOM	641	C8	GUA	A	30	13.230	25.365	40.881	1.00	47.36	A
ATOM	642	C2'	GUA	A	30	16.131	24.219	40.514	1.00	45.05	A
ATOM	643	O2'	GUA	A	30	16.324	23.065	39.711	1.00	42.26	A
ATOM	644	C3'	GUA	A	30	17.387	24.513	41.306	1.00	44.67	A
ATOM	645	O3'	GUA	A	30	17.875	23.241	41.698	1.00	47.60	A
ATOM	646	P	URI	A	31	19.368	23.092	42.242	1.00	46.90	A
ATOM	647	O1P	URI	A	31	19.788	21.707	41.922	1.00	43.72	A
ATOM	648	O2P	URI	A	31	20.164	24.243	41.749	1.00	42.41	A
ATOM	649	O5'	URI	A	31	19.165	23.178	43.810	1.00	44.16	A
ATOM	650	C5'	URI	A	31	18.437	22.169	44.475	1.00	47.25	A
ATOM	651	C4'	URI	A	31	19.073	21.875	45.800	1.00	50.83	A
ATOM	652	O4'	URI	A	31	19.933	20.714	45.670	1.00	51.79	A
ATOM	653	C1'	URI	A	31	21.260	21.063	46.011	1.00	53.42	A
ATOM	654	N1	URI	A	31	22.159	20.294	45.141	1.00	54.61	A
ATOM	655	C6	URI	A	31	22.280	20.580	43.797	1.00	55.01	A
ATOM	656	C2	URI	A	31	22.864	19.255	45.711	1.00	53.45	A
ATOM	657	O2	URI	A	31	22.796	18.992	46.901	1.00	54.06	A
ATOM	658	N3	URI	A	31	23.644	18.533	44.834	1.00	51.58	A
ATOM	659	C4	URI	A	31	23.787	18.749	43.473	1.00	51.47	A
ATOM	660	O4	URI	A	31	24.429	17.943	42.792	1.00	52.23	A
ATOM	661	C5	URI	A	31	23.050	19.861	42.969	1.00	52.57	A
ATOM	662	C2'	URI	A	31	21.341	22.579	45.844	1.00	53.16	A
ATOM	663	O2'	URI	A	31	22.354	23.115	46.667	1.00	55.10	A
ATOM	664	C3'	URI	A	31	19.958	22.995	46.323	1.00	51.91	A
ATOM	665	O3'	URI	A	31	19.921	22.992	47.737	1.00	51.68	A
ATOM	666	P	GUA	A	32	19.570	24.336	48.516	1.00	52.63	A
ATOM	667	O1P	GUA	A	32	20.544	24.456	49.629	1.00	52.90	A
ATOM	668	O2P	GUA	A	32	19.402	25.444	47.546	1.00	54.44	A
ATOM	669	O5'	GUA	A	32	18.151	24.043	49.147	1.00	52.92	A
ATOM	670	C5'	GUA	A	32	18.056	23.544	50.461	1.00	50.79	A
ATOM	671	C4'	GUA	A	32	16.887	22.616	50.572	1.00	49.82	A

ATOM	672	O4 '	GUA	A	32	16.685	21.897	49.326	1.00	46.72	A
ATOM	673	C1 '	GUA	A	32	16.347	20.554	49.606	1.00	48.10	A
ATOM	674	N9	GUA	A	32	17.438	19.710	49.133	1.00	49.09	A
ATOM	675	C4	GUA	A	32	17.638	19.232	47.851	1.00	49.10	A
ATOM	676	N3	GUA	A	32	16.845	19.452	46.782	1.00	49.00	A
ATOM	677	C2	GUA	A	32	17.325	18.878	45.688	1.00	48.99	A
ATOM	678	N2	GUA	A	32	16.690	19.006	44.518	1.00	48.27	A
ATOM	679	N1	GUA	A	32	18.473	18.136	45.653	1.00	50.19	A
ATOM	680	C6	GUA	A	32	19.297	17.892	46.740	1.00	48.64	A
ATOM	681	O6	GUA	A	32	20.311	17.205	46.595	1.00	49.28	A
ATOM	682	C5	GUA	A	32	18.808	18.510	47.913	1.00	48.50	A
ATOM	683	N7	GUA	A	32	19.324	18.518	49.197	1.00	50.10	A
ATOM	684	C8	GUA	A	32	18.481	19.238	49.884	1.00	49.69	A
ATOM	685	C2 '	GUA	A	32	16.142	20.468	51.120	1.00	48.46	A
ATOM	686	O2 '	GUA	A	32	14.815	20.805	51.432	1.00	50.02	A
ATOM	687	C3 '	GUA	A	32	17.087	21.547	51.615	1.00	49.56	A
ATOM	688	O3 '	GUA	A	32	16.674	22.088	52.855	1.00	51.72	A
ATOM	689	P	ADE	A	33	17.734	22.865	53.778	1.00	54.75	A
ATOM	690	O1P	ADE	A	33	17.193	22.727	55.153	1.00	53.71	A
ATOM	691	O2P	ADE	A	33	19.089	22.361	53.463	1.00	54.42	A
ATOM	692	O5 '	ADE	A	33	17.655	24.403	53.346	1.00	54.90	A
ATOM	693	C5 '	ADE	A	33	18.840	25.165	53.082	1.00	56.73	A
ATOM	694	C4 '	ADE	A	33	18.598	26.656	53.296	1.00	58.69	A
ATOM	695	O4 '	ADE	A	33	18.004	27.270	52.123	1.00	55.47	A
ATOM	696	C1 '	ADE	A	33	16.732	27.800	52.448	1.00	57.59	A
ATOM	697	N9	ADE	A	33	15.796	27.377	51.407	1.00	55.80	A
ATOM	698	C4	ADE	A	33	15.851	27.674	50.066	1.00	54.67	A
ATOM	699	N3	ADE	A	33	16.754	28.443	49.434	1.00	54.07	A
ATOM	700	C2	ADE	A	33	16.509	28.473	48.126	1.00	53.39	A
ATOM	701	N1	ADE	A	33	15.532	27.875	47.435	1.00	54.37	A
ATOM	702	C6	ADE	A	33	14.636	27.117	48.107	1.00	53.78	A
ATOM	703	N6	ADE	A	33	13.654	26.522	47.427	1.00	52.21	A
ATOM	704	C5	ADE	A	33	14.790	26.999	49.490	1.00	53.97	A
ATOM	705	N7	ADE	A	33	14.066	26.310	50.450	1.00	54.45	A
ATOM	706	C8	ADE	A	33	14.693	26.573	51.567	1.00	54.16	A
ATOM	707	C2 '	ADE	A	33	16.349	27.215	53.810	1.00	60.60	A
ATOM	708	O2 '	ADE	A	33	15.509	28.085	54.546	1.00	61.50	A
ATOM	709	C3 '	ADE	A	33	17.706	27.046	54.462	1.00	61.94	A
ATOM	710	O3 '	ADE	A	33	18.122	28.286	55.015	1.00	68.98	A
ATOM	711	P	URI	A	34	19.075	28.289	56.309	1.00	74.21	A
ATOM	712	O1P	URI	A	34	18.592	27.226	57.235	1.00	71.88	A
ATOM	713	O2P	URI	A	34	20.478	28.258	55.795	1.00	72.15	A
ATOM	714	O5 '	URI	A	34	18.811	29.688	57.024	1.00	73.89	A
ATOM	715	C5 '	URI	A	34	17.508	30.253	57.099	1.00	74.78	A
ATOM	716	C4 '	URI	A	34	17.553	31.691	56.640	1.00	76.05	A
ATOM	717	O4 '	URI	A	34	18.494	32.435	57.460	1.00	78.89	A
ATOM	718	C1 '	URI	A	34	19.610	32.847	56.688	1.00	81.15	A
ATOM	719	N1	URI	A	34	20.836	32.426	57.390	1.00	87.35	A
ATOM	720	C6	URI	A	34	20.975	31.133	57.855	1.00	89.21	A
ATOM	721	C2	URI	A	34	21.849	33.365	57.573	1.00	89.29	A
ATOM	722	O2	URI	A	34	21.775	34.523	57.169	1.00	89.92	A
ATOM	723	N3	URI	A	34	22.955	32.893	58.245	1.00	91.09	A
ATOM	724	C4	URI	A	34	23.152	31.608	58.734	1.00	92.28	A
ATOM	725	O4	URI	A	34	24.214	31.326	59.303	1.00	93.85	A
ATOM	726	C5	URI	A	34	22.064	30.705	58.500	1.00	91.36	A
ATOM	727	C2 '	URI	A	34	19.489	32.244	55.289	1.00	76.83	A
ATOM	728	O2 '	URI	A	34	20.020	33.134	54.327	1.00	73.41	A
ATOM	729	C3 '	URI	A	34	17.996	31.874	55.196	1.00	75.09	A
ATOM	730	O3 '	URI	A	34	17.057	32.711	54.511	1.00	68.53	A
ATOM	731	P	ADE	A	35	17.398	34.241	54.188	1.00	64.01	A
ATOM	732	O1P	ADE	A	35	16.110	34.964	54.265	1.00	63.53	A

ATOM	733	O2P	ADE	A	35	18.545	34.712	54.999	1.00	66.80	A
ATOM	734	O5'	ADE	A	35	17.868	34.190	52.667	1.00	59.77	A
ATOM	735	C5'	ADE	A	35	18.506	33.031	52.150	1.00	53.12	A
ATOM	736	C4'	ADE	A	35	18.690	33.158	50.666	1.00	50.24	A
ATOM	737	O4'	ADE	A	35	18.497	31.850	50.068	1.00	50.66	A
ATOM	738	C1'	ADE	A	35	17.427	31.904	49.149	1.00	48.04	A
ATOM	739	N9	ADE	A	35	16.228	31.385	49.815	1.00	47.05	A
ATOM	740	C4	ADE	A	35	15.054	30.994	49.220	1.00	46.40	A
ATOM	741	N3	ADE	A	35	14.750	31.027	47.914	1.00	47.60	A
ATOM	742	C2	ADE	A	35	13.540	30.532	47.707	1.00	44.79	A
ATOM	743	N1	ADE	A	35	12.664	30.052	48.586	1.00	43.36	A
ATOM	744	C6	ADE	A	35	12.993	30.042	49.887	1.00	43.86	A
ATOM	745	N6	ADE	A	35	12.105	29.577	50.766	1.00	42.72	A
ATOM	746	C5	ADE	A	35	14.251	30.529	50.241	1.00	45.10	A
ATOM	747	N7	ADE	A	35	14.892	30.643	51.461	1.00	45.15	A
ATOM	748	C8	ADE	A	35	16.055	31.161	51.154	1.00	47.04	A
ATOM	749	C2'	ADE	A	35	17.350	33.361	48.702	1.00	46.80	A
ATOM	750	O2'	ADE	A	35	18.306	33.616	47.701	1.00	41.13	A
ATOM	751	C3'	ADE	A	35	17.699	34.097	49.989	1.00	47.70	A
ATOM	752	O3'	ADE	A	35	18.352	35.324	49.695	1.00	46.15	A
ATOM	753	P	ADE	A	36	17.500	36.579	49.176	1.00	44.91	A
ATOM	754	O1P	ADE	A	36	18.409	37.475	48.418	1.00	45.54	A
ATOM	755	O2P	ADE	A	36	16.717	37.121	50.316	1.00	42.81	A
ATOM	756	O5'	ADE	A	36	16.511	35.947	48.103	1.00	44.04	A
ATOM	757	C5'	ADE	A	36	16.849	35.905	46.722	1.00	39.76	A
ATOM	758	C4'	ADE	A	36	15.618	35.594	45.904	1.00	40.10	A
ATOM	759	O4'	ADE	A	36	15.126	34.280	46.278	1.00	38.85	A
ATOM	760	C1'	ADE	A	36	13.731	34.317	46.453	1.00	38.26	A
ATOM	761	N9	ADE	A	36	13.432	34.093	47.861	1.00	39.33	A
ATOM	762	C4	ADE	A	36	12.309	33.474	48.356	1.00	41.34	A
ATOM	763	N3	ADE	A	36	11.279	32.972	47.655	1.00	41.49	A
ATOM	764	C2	ADE	A	36	10.382	32.433	48.467	1.00	40.53	A
ATOM	765	N1	ADE	A	36	10.390	32.345	49.796	1.00	39.89	A
ATOM	766	C6	ADE	A	36	11.432	32.860	50.471	1.00	40.76	A
ATOM	767	N6	ADE	A	36	11.428	32.775	51.804	1.00	41.52	A
ATOM	768	C5	ADE	A	36	12.459	33.458	49.724	1.00	40.32	A
ATOM	769	N7	ADE	A	36	13.650	34.057	50.086	1.00	41.48	A
ATOM	770	C8	ADE	A	36	14.183	34.421	48.944	1.00	39.27	A
ATOM	771	C2'	ADE	A	36	13.248	35.653	45.919	1.00	38.75	A
ATOM	772	O2'	ADE	A	36	13.033	35.501	44.544	1.00	42.97	A
ATOM	773	C3'	ADE	A	36	14.455	36.537	46.164	1.00	40.00	A
ATOM	774	O3'	ADE	A	36	14.470	37.597	45.220	1.00	37.24	A
ATOM	775	P	ADE	A	37	13.703	38.959	45.564	1.00	40.82	A
ATOM	776	O1P	ADE	A	37	14.010	39.984	44.531	1.00	36.22	A
ATOM	777	O2P	ADE	A	37	13.933	39.254	47.005	1.00	36.06	A
ATOM	778	O5'	ADE	A	37	12.162	38.587	45.420	1.00	42.41	A
ATOM	779	C5'	ADE	A	37	11.607	38.229	44.170	1.00	43.07	A
ATOM	780	C4'	ADE	A	37	10.234	37.659	44.380	1.00	45.84	A
ATOM	781	O4'	ADE	A	37	10.341	36.414	45.126	1.00	47.43	A
ATOM	782	C1'	ADE	A	37	9.225	36.284	45.991	1.00	47.98	A
ATOM	783	N9	ADE	A	37	9.703	36.337	47.369	1.00	48.10	A
ATOM	784	C4	ADE	A	37	9.166	35.679	48.446	1.00	48.11	A
ATOM	785	N3	ADE	A	37	8.126	34.837	48.446	1.00	47.34	A
ATOM	786	C2	ADE	A	37	7.867	34.417	49.683	1.00	48.62	A
ATOM	787	N1	ADE	A	37	8.485	34.719	50.832	1.00	47.87	A
ATOM	788	C6	ADE	A	37	9.528	35.569	50.794	1.00	48.60	A
ATOM	789	N6	ADE	A	37	10.138	35.876	51.934	1.00	48.53	A
ATOM	790	C5	ADE	A	37	9.904	36.084	49.544	1.00	48.72	A
ATOM	791	N7	ADE	A	37	10.904	36.961	49.163	1.00	49.65	A
ATOM	792	C8	ADE	A	37	10.748	37.071	47.865	1.00	50.20	A
ATOM	793	C2'	ADE	A	37	8.299	37.459	45.667	1.00	47.59	A

ATOM	794	O2'	ADE	A	37	7.452	37.118	44.584	1.00	51.37	A
ATOM	795	C3'	ADE	A	37	9.306	38.505	45.235	1.00	45.40	A
ATOM	796	O3'	ADE	A	37	8.660	39.477	44.430	1.00	42.84	A
ATOM	797	P	URI	A	38	7.845	40.673	45.122	1.00	42.60	A
ATOM	798	O1P	URI	A	38	8.528	41.081	46.379	1.00	42.82	A
ATOM	799	O2P	URI	A	38	7.641	41.675	44.052	1.00	36.14	A
ATOM	800	O5'	URI	A	38	6.462	39.999	45.548	1.00	42.36	A
ATOM	801	C5'	URI	A	38	5.891	40.240	46.841	1.00	44.35	A
ATOM	802	C4'	URI	A	38	4.952	39.115	47.235	1.00	46.75	A
ATOM	803	O4'	URI	A	38	5.725	37.988	47.741	1.00	47.80	A
ATOM	804	C1'	URI	A	38	4.998	37.325	48.765	1.00	48.04	A
ATOM	805	N1	URI	A	38	5.771	37.389	50.011	1.00	47.05	A
ATOM	806	C6	URI	A	38	6.835	38.239	50.144	1.00	46.72	A
ATOM	807	C2	URI	A	38	5.371	36.579	51.062	1.00	46.91	A
ATOM	808	O2	URI	A	38	4.473	35.766	50.969	1.00	46.67	A
ATOM	809	N3	URI	A	38	6.078	36.747	52.224	1.00	46.31	A
ATOM	810	C4	URI	A	38	7.142	37.594	52.429	1.00	46.35	A
ATOM	811	O4	URI	A	38	7.685	37.627	53.533	1.00	45.78	A
ATOM	812	C5	URI	A	38	7.518	38.365	51.285	1.00	47.05	A
ATOM	813	C2'	URI	A	38	3.660	38.050	48.911	1.00	48.80	A
ATOM	814	O2'	URI	A	38	2.661	37.414	48.141	1.00	52.16	A
ATOM	815	C3'	URI	A	38	4.004	39.434	48.383	1.00	48.58	A
ATOM	816	O3'	URI	A	38	2.825	40.090	47.936	1.00	48.56	A
ATOM	817	P	GUA	A	39	2.254	41.336	48.767	1.00	48.44	A
ATOM	818	O1P	GUA	A	39	3.327	42.356	48.824	1.00	43.94	A
ATOM	819	O2P	GUA	A	39	0.950	41.673	48.150	1.00	50.57	A
ATOM	820	O5'	GUA	A	39	2.001	40.763	50.237	1.00	49.08	A
ATOM	821	C5'	GUA	A	39	0.842	39.975	50.537	1.00	52.34	A
ATOM	822	C4'	GUA	A	39	0.884	39.493	51.974	1.00	52.64	A
ATOM	823	O4'	GUA	A	39	2.200	38.950	52.198	1.00	53.74	A
ATOM	824	C1'	GUA	A	39	2.677	39.322	53.472	1.00	55.12	A
ATOM	825	N9	GUA	A	39	4.040	39.832	53.331	1.00	53.40	A
ATOM	826	C4	GUA	A	39	5.030	39.793	54.280	1.00	53.51	A
ATOM	827	N3	GUA	A	39	4.921	39.272	55.521	1.00	55.12	A
ATOM	828	C2	GUA	A	39	6.055	39.368	56.203	1.00	56.07	A
ATOM	829	N2	GUA	A	39	6.133	38.880	57.444	1.00	55.26	A
ATOM	830	N1	GUA	A	39	7.198	39.945	55.713	1.00	57.90	A
ATOM	831	C6	GUA	A	39	7.329	40.498	54.442	1.00	57.91	A
ATOM	832	O6	GUA	A	39	8.405	41.009	54.100	1.00	61.79	A
ATOM	833	C5	GUA	A	39	6.122	40.385	53.693	1.00	55.10	A
ATOM	834	N7	GUA	A	39	5.827	40.789	52.403	1.00	53.11	A
ATOM	835	C8	GUA	A	39	4.584	40.441	52.233	1.00	52.96	A
ATOM	836	C2'	GUA	A	39	1.702	40.302	54.127	1.00	54.78	A
ATOM	837	O2'	GUA	A	39	1.187	39.738	55.314	1.00	54.03	A
ATOM	838	C3'	GUA	A	39	0.674	40.577	53.025	1.00	55.19	A
ATOM	839	O3'	GUA	A	39	-0.706	40.787	53.445	1.00	59.20	A
ATOM	840	P	URI	A	40	-1.599	39.602	54.126	1.00	56.47	A
ATOM	841	O1P	URI	A	40	-1.160	39.317	55.525	1.00	54.80	A
ATOM	842	O2P	URI	A	40	-3.004	39.999	53.874	1.00	58.19	A
ATOM	843	O5'	URI	A	40	-1.371	38.302	53.245	1.00	55.95	A
ATOM	844	C5'	URI	A	40	-1.812	37.034	53.718	1.00	55.43	A
ATOM	845	C4'	URI	A	40	-2.982	36.549	52.905	1.00	54.71	A
ATOM	846	O4'	URI	A	40	-2.742	35.169	52.519	1.00	54.93	A
ATOM	847	C1'	URI	A	40	-3.665	34.317	53.174	1.00	54.07	A
ATOM	848	N1	URI	A	40	-2.937	33.133	53.656	1.00	54.14	A
ATOM	849	C6	URI	A	40	-1.741	33.250	54.316	1.00	53.97	A
ATOM	850	C2	URI	A	40	-3.485	31.892	53.401	1.00	51.99	A
ATOM	851	O2	URI	A	40	-4.562	31.753	52.881	1.00	52.24	A
ATOM	852	N3	URI	A	40	-2.724	30.824	53.795	1.00	51.15	A
ATOM	853	C4	URI	A	40	-1.504	30.871	54.432	1.00	52.19	A
ATOM	854	O4	URI	A	40	-0.904	29.822	54.676	1.00	52.40	A

ATOM	855	C5	URI	A	40	-1.028	32.190	54.706	1.00	52.91	A
ATOM	856	C2'	URI	A	40	-4.307	35.144	54.280	1.00	53.49	A
ATOM	857	O2'	URI	A	40	-5.602	34.648	54.520	1.00	53.75	A
ATOM	858	C3'	URI	A	40	-4.307	36.529	53.647	1.00	54.99	A
ATOM	859	O3'	URI	A	40	-5.363	36.652	52.705	1.00	57.21	A
ATOM	860	P	ADE	A	41	-6.710	37.431	53.104	1.00	58.89	A
ATOM	861	O1P	ADE	A	41	-6.562	38.826	52.614	1.00	58.50	A
ATOM	862	O2P	ADE	A	41	-7.038	37.180	54.546	1.00	55.76	A
ATOM	863	O5'	ADE	A	41	-7.800	36.713	52.199	1.00	58.92	A
ATOM	864	C5'	ADE	A	41	-7.650	35.342	51.838	1.00	60.17	A
ATOM	865	C4'	ADE	A	41	-8.829	34.888	51.014	1.00	59.95	A
ATOM	866	O4'	ADE	A	41	-8.375	34.035	49.934	1.00	60.38	A
ATOM	867	C1'	ADE	A	41	-9.373	33.076	49.636	1.00	61.63	A
ATOM	868	N9	ADE	A	41	-8.821	31.756	49.905	1.00	62.90	A
ATOM	869	C4	ADE	A	41	-9.190	30.583	49.294	1.00	64.74	A
ATOM	870	N3	ADE	A	41	-10.063	30.430	48.284	1.00	65.58	A
ATOM	871	C2	ADE	A	41	-10.204	29.139	47.975	1.00	66.23	A
ATOM	872	N1	ADE	A	41	-9.627	28.066	48.531	1.00	66.78	A
ATOM	873	C6	ADE	A	41	-8.763	28.256	49.556	1.00	66.47	A
ATOM	874	N6	ADE	A	41	-8.218	27.183	50.141	1.00	66.76	A
ATOM	875	C5	ADE	A	41	-8.503	29.583	49.957	1.00	65.70	A
ATOM	876	N7	ADE	A	41	-7.669	30.123	50.926	1.00	65.96	A
ATOM	877	C8	ADE	A	41	-7.888	31.414	50.846	1.00	63.92	A
ATOM	878	C2'	ADE	A	41	-10.552	33.358	50.573	1.00	60.59	A
ATOM	879	O2'	ADE	A	41	-11.506	34.185	49.940	1.00	59.58	A
ATOM	880	C3'	ADE	A	41	-9.840	34.027	51.741	1.00	60.33	A
ATOM	881	O3'	ADE	A	41	-10.708	34.839	52.517	1.00	60.73	A
ATOM	882	P	GUA	A	42	-11.635	34.165	53.642	1.00	63.04	A
ATOM	883	O1P	GUA	A	42	-10.778	33.611	54.722	1.00	60.30	A
ATOM	884	O2P	GUA	A	42	-12.698	35.154	53.979	1.00	61.99	A
ATOM	885	O5'	GUA	A	42	-12.294	32.926	52.888	1.00	60.43	A
ATOM	886	C5'	GUA	A	42	-12.827	31.843	53.623	1.00	58.01	A
ATOM	887	C4'	GUA	A	42	-13.024	30.658	52.724	1.00	57.39	A
ATOM	888	O4'	GUA	A	42	-11.830	30.476	51.921	1.00	56.25	A
ATOM	889	C1'	GUA	A	42	-11.422	29.117	51.969	1.00	57.45	A
ATOM	890	N9	GUA	A	42	-10.237	29.022	52.821	1.00	55.08	A
ATOM	891	C4	GUA	A	42	-9.535	27.884	53.138	1.00	53.31	A
ATOM	892	N3	GUA	A	42	-9.812	26.635	52.714	1.00	53.57	A
ATOM	893	C2	GUA	A	42	-8.959	25.742	53.213	1.00	55.55	A
ATOM	894	N2	GUA	A	42	-9.082	24.441	52.911	1.00	56.87	A
ATOM	895	N1	GUA	A	42	-7.920	26.055	54.047	1.00	55.96	A
ATOM	896	C6	GUA	A	42	-7.606	27.335	54.486	1.00	55.98	A
ATOM	897	O6	GUA	A	42	-6.626	27.508	55.224	1.00	56.71	A
ATOM	898	C5	GUA	A	42	-8.520	28.301	53.973	1.00	54.30	A
ATOM	899	N7	GUA	A	42	-8.581	29.671	54.173	1.00	53.33	A
ATOM	900	C8	GUA	A	42	-9.610	30.056	53.472	1.00	53.69	A
ATOM	901	C2'	GUA	A	42	-12.616	28.332	52.510	1.00	58.44	A
ATOM	902	O2'	GUA	A	42	-13.472	27.964	51.450	1.00	58.26	A
ATOM	903	C3'	GUA	A	42	-13.221	29.349	53.470	1.00	58.81	A
ATOM	904	O3'	GUA	A	42	-14.605	29.138	53.722	1.00	61.50	A
ATOM	905	P	CYT	A	43	-15.070	28.243	54.977	1.00	64.98	A
ATOM	906	O1P	CYT	A	43	-14.485	28.761	56.250	1.00	59.74	A
ATOM	907	O2P	CYT	A	43	-16.546	28.116	54.851	1.00	64.87	A
ATOM	908	O5'	CYT	A	43	-14.458	26.811	54.652	1.00	64.07	A
ATOM	909	C5'	CYT	A	43	-14.898	26.095	53.506	1.00	65.62	A
ATOM	910	C4'	CYT	A	43	-14.456	24.660	53.584	1.00	65.98	A
ATOM	911	O4'	CYT	A	43	-13.029	24.599	53.330	1.00	65.81	A
ATOM	912	C1'	CYT	A	43	-12.432	23.669	54.211	1.00	65.26	A
ATOM	913	N1	CYT	A	43	-11.549	24.400	55.135	1.00	63.82	A
ATOM	914	C6	CYT	A	43	-11.704	25.739	55.352	1.00	62.45	A
ATOM	915	C2	CYT	A	43	-10.531	23.698	55.780	1.00	64.02	A

ATOM	916	O2	CYT	A	43	-10.427	22.480	55.576	1.00	65.38	A
ATOM	917	N3	CYT	A	43	-9.688	24.356	56.604	1.00	62.61	A
ATOM	918	C4	CYT	A	43	-9.831	25.666	56.793	1.00	62.22	A
ATOM	919	N4	CYT	A	43	-8.954	26.279	57.593	1.00	60.19	A
ATOM	920	C5	CYT	A	43	-10.874	26.407	56.164	1.00	62.02	A
ATOM	921	C2'	CYT	A	43	-13.573	22.913	54.890	1.00	65.89	A
ATOM	922	O2'	CYT	A	43	-13.956	21.825	54.071	1.00	66.59	A
ATOM	923	C3'	CYT	A	43	-14.649	23.987	54.935	1.00	66.04	A
ATOM	924	O3'	CYT	A	43	-15.946	23.395	55.000	1.00	66.73	A
ATOM	925	P	URI	A	44	-16.711	23.269	56.415	1.00	65.82	A
ATOM	926	O1P	URI	A	44	-16.592	24.556	57.157	1.00	63.68	A
ATOM	927	O2P	URI	A	44	-18.052	22.723	56.105	1.00	66.14	A
ATOM	928	O5'	URI	A	44	-15.917	22.137	57.199	1.00	63.62	A
ATOM	929	C5'	URI	A	44	-16.200	20.773	56.957	1.00	63.38	A
ATOM	930	C4'	URI	A	44	-15.136	19.904	57.572	1.00	65.62	A
ATOM	931	O4'	URI	A	44	-13.825	20.362	57.151	1.00	65.65	A
ATOM	932	C1'	URI	A	44	-12.880	20.075	58.172	1.00	65.84	A
ATOM	933	N1	URI	A	44	-12.292	21.338	58.638	1.00	66.30	A
ATOM	934	C6	URI	A	44	-12.758	22.562	58.215	1.00	65.36	A
ATOM	935	C2	URI	A	44	-11.233	21.246	59.514	1.00	65.77	A
ATOM	936	O2	URI	A	44	-10.826	20.185	59.927	1.00	67.70	A
ATOM	937	N3	URI	A	44	-10.678	22.438	59.891	1.00	64.76	A
ATOM	938	C4	URI	A	44	-11.075	23.692	59.494	1.00	66.40	A
ATOM	939	O4	URI	A	44	-10.453	24.674	59.898	1.00	67.76	A
ATOM	940	C5	URI	A	44	-12.201	23.713	58.602	1.00	65.92	A
ATOM	941	C2'	URI	A	44	-13.638	19.357	59.285	1.00	66.12	A
ATOM	942	O2'	URI	A	44	-13.566	17.958	59.087	1.00	66.69	A
ATOM	943	C3'	URI	A	44	-15.032	19.932	59.086	1.00	65.90	A
ATOM	944	O3'	URI	A	44	-16.017	19.111	59.690	1.00	67.53	A
ATOM	945	P	ADE	A	45	-16.217	19.151	61.284	1.00	68.53	A
ATOM	946	O1P	ADE	A	45	-16.924	17.900	61.656	1.00	68.32	A
ATOM	947	O2P	ADE	A	45	-16.789	20.469	61.673	1.00	67.51	A
ATOM	948	O5'	ADE	A	45	-14.740	19.052	61.865	1.00	69.08	A
ATOM	949	C5'	ADE	A	45	-14.502	18.673	63.214	1.00	68.01	A
ATOM	950	C4'	ADE	A	45	-13.284	17.797	63.283	1.00	68.82	A
ATOM	951	O4'	ADE	A	45	-12.273	18.326	62.385	1.00	70.13	A
ATOM	952	C1'	ADE	A	45	-10.995	18.206	62.981	1.00	71.44	A
ATOM	953	N9	ADE	A	45	-10.492	19.550	63.260	1.00	73.11	A
ATOM	954	C4	ADE	A	45	-9.264	19.852	63.792	1.00	73.86	A
ATOM	955	N3	ADE	A	45	-8.291	18.988	64.129	1.00	74.54	A
ATOM	956	C2	ADE	A	45	-7.241	19.638	64.619	1.00	75.77	A
ATOM	957	N1	ADE	A	45	-7.066	20.955	64.797	1.00	75.85	A
ATOM	958	C6	ADE	A	45	-8.063	21.795	64.441	1.00	74.73	A
ATOM	959	N6	ADE	A	45	-7.881	23.107	64.606	1.00	74.84	A
ATOM	960	C5	ADE	A	45	-9.231	21.230	63.910	1.00	73.92	A
ATOM	961	N7	ADE	A	45	-10.412	21.791	63.448	1.00	73.89	A
ATOM	962	C8	ADE	A	45	-11.124	20.756	63.070	1.00	73.73	A
ATOM	963	C2'	ADE	A	45	-11.175	17.369	64.249	1.00	71.14	A
ATOM	964	O2'	ADE	A	45	-11.023	16.000	63.944	1.00	71.70	A
ATOM	965	C3'	ADE	A	45	-12.606	17.709	64.638	1.00	69.95	A
ATOM	966	O3'	ADE	A	45	-13.179	16.632	65.359	1.00	71.13	A
ATOM	967	P	ADE	A	46	-13.171	16.646	66.961	1.00	72.38	A
ATOM	968	O1P	ADE	A	46	-13.939	15.447	67.395	1.00	70.63	A
ATOM	969	O2P	ADE	A	46	-13.583	17.997	67.434	1.00	71.11	A
ATOM	970	O5'	ADE	A	46	-11.638	16.438	67.330	1.00	71.76	A
ATOM	971	C5'	ADE	A	46	-10.956	15.253	66.964	1.00	72.17	A
ATOM	972	C4'	ADE	A	46	-9.555	15.292	67.496	1.00	73.44	A
ATOM	973	O4'	ADE	A	46	-8.795	16.246	66.714	1.00	73.28	A
ATOM	974	C1'	ADE	A	46	-7.798	16.844	67.532	1.00	73.77	A
ATOM	975	N9	ADE	A	46	-7.983	18.292	67.495	1.00	71.50	A
ATOM	976	C4	ADE	A	46	-7.068	19.231	67.896	1.00	70.59	A

ATOM	977	N3	ADE	A	46	-5.832	19.010	68.365	1.00	70.30	A
ATOM	978	C2	ADE	A	46	-5.240	20.156	68.673	1.00	70.11	A
ATOM	979	N1	ADE	A	46	-5.708	21.403	68.574	1.00	70.07	A
ATOM	980	C6	ADE	A	46	-6.954	21.589	68.100	1.00	69.89	A
ATOM	981	N6	ADE	A	46	-7.423	22.831	68.011	1.00	69.62	A
ATOM	982	C5	ADE	A	46	-7.685	20.455	67.732	1.00	70.34	A
ATOM	983	N7	ADE	A	46	-8.961	20.295	67.217	1.00	70.99	A
ATOM	984	C8	ADE	A	46	-9.087	18.996	67.092	1.00	71.76	A
ATOM	985	C2'	ADE	A	46	-7.983	16.299	68.952	1.00	75.60	A
ATOM	986	O2'	ADE	A	46	-7.045	15.278	69.248	1.00	76.78	A
ATOM	987	C3'	ADE	A	46	-9.434	15.830	68.910	1.00	75.50	A
ATOM	988	O3'	ADE	A	46	-9.700	14.831	69.883	1.00	77.29	A
ATOM	989	P	ADE	A	47	-10.668	15.174	71.117	1.00	79.69	A
ATOM	990	O1P	ADE	A	47	-10.647	14.026	72.061	1.00	79.57	A
ATOM	991	O2P	ADE	A	47	-11.959	15.634	70.546	1.00	78.48	A
ATOM	992	O5'	ADE	A	47	-9.939	16.386	71.851	1.00	79.12	A
ATOM	993	C5'	ADE	A	47	-8.813	16.148	72.694	1.00	79.56	A
ATOM	994	C4'	ADE	A	47	-7.789	17.251	72.536	1.00	79.57	A
ATOM	995	O4'	ADE	A	47	-8.054	17.996	71.320	1.00	78.89	A
ATOM	996	C1'	ADE	A	47	-7.612	19.336	71.482	1.00	76.86	A
ATOM	997	N9	ADE	A	47	-8.699	20.239	71.089	1.00	73.28	A
ATOM	998	C4	ADE	A	47	-8.651	21.616	71.042	1.00	70.83	A
ATOM	999	N3	ADE	A	47	-7.618	22.412	71.369	1.00	69.61	A
ATOM	1000	C2	ADE	A	47	-7.935	23.696	71.184	1.00	68.39	A
ATOM	1001	N1	ADE	A	47	-9.075	24.231	70.734	1.00	66.31	A
ATOM	1002	C6	ADE	A	47	-10.090	23.404	70.403	1.00	67.06	A
ATOM	1003	N6	ADE	A	47	-11.218	23.937	69.931	1.00	65.64	A
ATOM	1004	C5	ADE	A	47	-9.889	22.020	70.569	1.00	68.98	A
ATOM	1005	N7	ADE	A	47	-10.710	20.923	70.341	1.00	69.48	A
ATOM	1006	C8	ADE	A	47	-9.963	19.896	70.669	1.00	71.21	A
ATOM	1007	C2'	ADE	A	47	-7.133	19.498	72.928	1.00	79.08	A
ATOM	1008	O2'	ADE	A	47	-5.720	19.415	72.987	1.00	79.49	A
ATOM	1009	C3'	ADE	A	47	-7.810	18.318	73.619	1.00	79.92	A
ATOM	1010	O3'	ADE	A	47	-7.040	17.900	74.735	1.00	81.30	A
ATOM	1011	P	ADE	A	48	-7.584	18.174	76.218	1.00	82.37	A
ATOM	1012	O1P	ADE	A	48	-8.374	16.983	76.624	1.00	81.64	A
ATOM	1013	O2P	ADE	A	48	-8.214	19.516	76.241	1.00	81.56	A
ATOM	1014	O5'	ADE	A	48	-6.260	18.214	77.095	1.00	82.32	A
ATOM	1015	C5'	ADE	A	48	-5.365	17.113	77.094	1.00	83.46	A
ATOM	1016	C4'	ADE	A	48	-3.960	17.594	77.326	1.00	85.20	A
ATOM	1017	O4'	ADE	A	48	-3.499	18.305	76.143	1.00	84.90	A
ATOM	1018	C1'	ADE	A	48	-2.600	19.334	76.533	1.00	85.40	A
ATOM	1019	N9	ADE	A	48	-3.174	20.620	76.142	1.00	85.75	A
ATOM	1020	C4	ADE	A	48	-2.527	21.834	76.201	1.00	85.93	A
ATOM	1021	N3	ADE	A	48	-1.253	22.065	76.574	1.00	85.58	A
ATOM	1022	C2	ADE	A	48	-0.984	23.367	76.546	1.00	85.50	A
ATOM	1023	N1	ADE	A	48	-1.783	24.390	76.216	1.00	85.56	A
ATOM	1024	C6	ADE	A	48	-3.055	24.125	75.843	1.00	84.69	A
ATOM	1025	N6	ADE	A	48	-3.849	25.145	75.523	1.00	83.49	A
ATOM	1026	C5	ADE	A	48	-3.464	22.779	75.821	1.00	84.98	A
ATOM	1027	N7	ADE	A	48	-4.669	22.171	75.491	1.00	84.83	A
ATOM	1028	C8	ADE	A	48	-4.442	20.892	75.691	1.00	85.38	A
ATOM	1029	C2'	ADE	A	48	-2.463	19.256	78.059	1.00	85.92	A
ATOM	1030	O2'	ADE	A	48	-1.327	18.501	78.444	1.00	84.47	A
ATOM	1031	C3'	ADE	A	48	-3.796	18.622	78.435	1.00	85.80	A
ATOM	1032	O3'	ADE	A	48	-3.766	18.027	79.729	1.00	86.27	A
ATOM	1033	P	ADE	A	49	-4.373	18.832	80.986	1.00	88.05	A
ATOM	1034	O1P	ADE	A	49	-4.142	18.025	82.212	1.00	87.72	A
ATOM	1035	O2P	ADE	A	49	-5.755	19.264	80.647	1.00	88.03	A
ATOM	1036	O5'	ADE	A	49	-3.455	20.131	81.084	1.00	85.69	A
ATOM	1037	C5'	ADE	A	49	-2.071	20.026	81.397	1.00	82.44	A

ATOM	1038	C4'	ADE	A	49	-1.389	21.358	81.192	1.00	81.27	A
ATOM	1039	O4'	ADE	A	49	-1.679	21.845	79.853	1.00	80.07	A
ATOM	1040	C1'	ADE	A	49	-1.745	23.264	79.861	1.00	77.99	A
ATOM	1041	N9	ADE	A	49	-3.084	23.658	79.430	1.00	76.14	A
ATOM	1042	C4	ADE	A	49	-3.522	24.942	79.227	1.00	75.30	A
ATOM	1043	N3	ADE	A	49	-2.812	26.072	79.362	1.00	74.58	A
ATOM	1044	C2	ADE	A	49	-3.569	27.135	79.106	1.00	74.96	A
ATOM	1045	N1	ADE	A	49	-4.860	27.192	78.758	1.00	75.05	A
ATOM	1046	C6	ADE	A	49	-5.546	26.036	78.631	1.00	75.57	A
ATOM	1047	N6	ADE	A	49	-6.834	26.093	78.292	1.00	75.44	A
ATOM	1048	C5	ADE	A	49	-4.853	24.836	78.871	1.00	75.74	A
ATOM	1049	N7	ADE	A	49	-5.247	23.506	78.834	1.00	75.97	A
ATOM	1050	C8	ADE	A	49	-4.162	22.849	79.167	1.00	76.26	A
ATOM	1051	C2'	ADE	A	49	-1.442	23.720	81.289	1.00	79.04	A
ATOM	1052	O2'	ADE	A	49	-0.075	24.059	81.411	1.00	77.88	A
ATOM	1053	C3'	ADE	A	49	-1.862	22.490	82.087	1.00	80.35	A
ATOM	1054	O3'	ADE	A	49	-1.261	22.428	83.375	1.00	80.33	A
ATOM	1055	P	GUA	A	50	-2.185	22.582	84.679	1.00	81.00	A
ATOM	1056	O1P	GUA	A	50	-3.300	21.604	84.529	1.00	80.20	A
ATOM	1057	O2P	GUA	A	50	-1.341	22.560	85.906	1.00	79.72	A
ATOM	1058	O5'	GUA	A	50	-2.784	24.050	84.525	1.00	79.65	A
ATOM	1059	C5'	GUA	A	50	-1.921	25.173	84.372	1.00	77.16	A
ATOM	1060	C4'	GUA	A	50	-2.719	26.402	84.007	1.00	75.00	A
ATOM	1061	O4'	GUA	A	50	-3.208	26.286	82.638	1.00	73.43	A
ATOM	1062	C1'	GUA	A	50	-4.541	26.770	82.564	1.00	72.01	A
ATOM	1063	N9	GUA	A	50	-5.433	25.623	82.411	1.00	70.22	A
ATOM	1064	C4	GUA	A	50	-6.724	25.655	81.960	1.00	67.92	A
ATOM	1065	N3	GUA	A	50	-7.402	26.758	81.590	1.00	66.32	A
ATOM	1066	C2	GUA	A	50	-8.637	26.476	81.219	1.00	66.81	A
ATOM	1067	N2	GUA	A	50	-9.463	27.461	80.851	1.00	65.04	A
ATOM	1068	N1	GUA	A	50	-9.158	25.205	81.191	1.00	68.08	A
ATOM	1069	C6	GUA	A	50	-8.473	24.051	81.564	1.00	69.44	A
ATOM	1070	O6	GUA	A	50	-9.037	22.946	81.506	1.00	70.39	A
ATOM	1071	C5	GUA	A	50	-7.153	24.344	81.981	1.00	68.58	A
ATOM	1072	N7	GUA	A	50	-6.150	23.503	82.441	1.00	68.42	A
ATOM	1073	C8	GUA	A	50	-5.149	24.303	82.685	1.00	69.29	A
ATOM	1074	C2'	GUA	A	50	-4.770	27.520	83.872	1.00	72.81	A
ATOM	1075	O2'	GUA	A	50	-4.222	28.817	83.756	1.00	71.66	A
ATOM	1076	C3'	GUA	A	50	-3.977	26.639	84.822	1.00	73.60	A
ATOM	1077	O3'	GUA	A	50	-3.684	27.280	86.054	1.00	73.95	A
ATOM	1078	P	GUA	A	51	-4.694	27.112	87.294	1.00	74.38	A
ATOM	1079	O1P	GUA	A	51	-5.138	25.695	87.343	1.00	73.33	A
ATOM	1080	O2P	GUA	A	51	-4.067	27.727	88.487	1.00	72.68	A
ATOM	1081	O5'	GUA	A	51	-5.952	27.991	86.870	1.00	74.71	A
ATOM	1082	C5'	GUA	A	51	-5.783	29.325	86.397	1.00	73.94	A
ATOM	1083	C4'	GUA	A	51	-7.125	29.948	86.118	1.00	73.27	A
ATOM	1084	O4'	GUA	A	51	-7.656	29.393	84.888	1.00	72.61	A
ATOM	1085	C1'	GUA	A	51	-9.060	29.227	85.005	1.00	72.51	A
ATOM	1086	N9	GUA	A	51	-9.354	27.805	84.898	1.00	71.49	A
ATOM	1087	C4	GUA	A	51	-10.535	27.252	84.485	1.00	69.81	A
ATOM	1088	N3	GUA	A	51	-11.648	27.931	84.147	1.00	68.51	A
ATOM	1089	C2	GUA	A	51	-12.622	27.123	83.780	1.00	68.74	A
ATOM	1090	N2	GUA	A	51	-13.810	27.628	83.424	1.00	68.49	A
ATOM	1091	N1	GUA	A	51	-12.505	25.757	83.737	1.00	69.64	A
ATOM	1092	C6	GUA	A	51	-11.365	25.039	84.076	1.00	70.00	A
ATOM	1093	O6	GUA	A	51	-11.362	23.804	83.990	1.00	71.28	A
ATOM	1094	C5	GUA	A	51	-10.322	25.892	84.486	1.00	69.35	A
ATOM	1095	N7	GUA	A	51	-9.040	25.595	84.918	1.00	70.02	A
ATOM	1096	C8	GUA	A	51	-8.505	26.759	85.160	1.00	70.88	A
ATOM	1097	C2'	GUA	A	51	-9.475	29.821	86.347	1.00	73.56	A
ATOM	1098	O2'	GUA	A	51	-9.867	31.166	86.164	1.00	74.00	A

ATOM	1099	C3'	GUA	A	51	-8.194	29.643	87.150	1.00	73.77	A
ATOM	1100	O3'	GUA	A	51	-8.114	30.545	88.238	1.00	74.52	A
ATOM	1101	P	ADE	A	52	-8.773	30.142	89.642	1.00	76.30	A
ATOM	1102	O1P	ADE	A	52	-8.331	28.768	90.007	1.00	73.86	A
ATOM	1103	O2P	ADE	A	52	-8.551	31.261	90.586	1.00	76.17	A
ATOM	1104	O5'	ADE	A	52	-10.323	30.090	89.311	1.00	78.15	A
ATOM	1105	PC	ADE	A	52	-13.399	30.333	93.693	1.00	89.30	A
ATOM	1106	O1C	ADE	A	52	-12.966	29.470	94.833	1.00	88.46	A
ATOM	1107	O2C	ADE	A	52	-13.966	31.592	94.237	1.00	89.76	A
ATOM	1108	O3'	ADE	A	52	-12.135	30.667	92.749	1.00	88.47	A
ATOM	1109	C5'	ADE	A	52	-11.120	29.037	89.802	1.00	82.75	A
ATOM	1110	C4'	ADE	A	52	-12.297	29.587	90.555	1.00	85.33	A
ATOM	1111	O4'	ADE	A	52	-13.454	28.844	90.104	1.00	86.70	A
ATOM	1112	C1'	ADE	A	52	-13.899	28.008	91.146	1.00	88.21	A
ATOM	1113	N9	ADE	A	52	-13.256	26.699	91.016	1.00	87.28	A
ATOM	1114	C4	ADE	A	52	-13.874	25.553	90.585	1.00	85.99	A
ATOM	1115	N3	ADE	A	52	-15.152	25.418	90.189	1.00	84.73	A
ATOM	1116	C2	ADE	A	52	-15.402	24.160	89.845	1.00	84.82	A
ATOM	1117	N1	ADE	A	52	-14.580	23.101	89.854	1.00	85.66	A
ATOM	1118	C6	ADE	A	52	-13.299	23.276	90.261	1.00	86.47	A
ATOM	1119	N6	ADE	A	52	-12.472	22.225	90.275	1.00	87.46	A
ATOM	1120	C5	ADE	A	52	-12.910	24.561	90.648	1.00	86.01	A
ATOM	1121	N7	ADE	A	52	-11.702	25.071	91.102	1.00	85.88	A
ATOM	1122	C8	ADE	A	52	-11.956	26.339	91.305	1.00	87.01	A
ATOM	1123	C2'	ADE	A	52	-13.529	28.719	92.445	1.00	88.72	A
ATOM	1124	O2'	ADE	A	52	-14.557	29.604	92.858	1.00	89.03	A
ATOM	1125	C3'	ADE	A	52	-12.218	29.415	92.075	1.00	86.83	A
TER											
ATOM	1126	O6P	GUA	B	201	0.475	29.070	36.643	1.00	78.07	B
ATOM	1127	O3P	GUA	B	201	2.504	29.382	35.176	1.00	72.28	B
ATOM	1128	O4P	GUA	B	201	1.151	27.209	35.096	1.00	78.40	B
ATOM	1129	O5P	GUA	B	201	0.153	29.309	34.172	1.00	77.17	B
ATOM	1130	P2	GUA	B	201	1.035	28.724	35.273	1.00	78.53	B
ATOM	1131	P	GUA	B	201	3.207	29.078	33.730	1.00	67.30	B
ATOM	1132	O1P	GUA	B	201	2.397	29.678	32.604	1.00	68.58	B
ATOM	1133	O2P	GUA	B	201	3.397	27.584	33.493	1.00	65.14	B
ATOM	1134	O5'	GUA	B	201	4.661	29.812	33.757	1.00	65.23	B
ATOM	1135	C5'	GUA	B	201	4.779	31.168	34.260	1.00	59.17	B
ATOM	1136	C4'	GUA	B	201	6.020	31.321	35.109	1.00	54.52	B
ATOM	1137	O4'	GUA	B	201	5.753	30.983	36.494	1.00	52.68	B
ATOM	1138	C1'	GUA	B	201	6.913	30.394	37.065	1.00	52.45	B
ATOM	1139	N9	GUA	B	201	6.599	29.022	37.436	1.00	51.23	B
ATOM	1140	C4	GUA	B	201	7.438	28.136	38.073	1.00	50.83	B
ATOM	1141	N3	GUA	B	201	8.698	28.388	38.480	1.00	50.53	B
ATOM	1142	C2	GUA	B	201	9.253	27.328	39.046	1.00	50.31	B
ATOM	1143	N2	GUA	B	201	10.512	27.380	39.486	1.00	48.27	B
ATOM	1144	N1	GUA	B	201	8.615	26.133	39.216	1.00	51.41	B
ATOM	1145	C6	GUA	B	201	7.317	25.855	38.814	1.00	51.48	B
ATOM	1146	O6	GUA	B	201	6.835	24.742	39.029	1.00	53.50	B
ATOM	1147	C5	GUA	B	201	6.717	26.970	38.189	1.00	51.05	B
ATOM	1148	N7	GUA	B	201	5.452	27.117	37.639	1.00	51.16	B
ATOM	1149	C8	GUA	B	201	5.426	28.351	37.209	1.00	50.70	B
ATOM	1150	C2'	GUA	B	201	7.999	30.409	35.993	1.00	52.40	B
ATOM	1151	O2'	GUA	B	201	8.806	31.555	36.121	1.00	52.70	B
ATOM	1152	C3'	GUA	B	201	7.161	30.406	34.729	1.00	52.42	B
ATOM	1153	O3'	GUA	B	201	7.874	30.965	33.658	1.00	50.70	B
ATOM	1154	P	CYT	B	202	8.761	30.015	32.732	1.00	54.04	B
ATOM	1155	O1P	CYT	B	202	7.936	28.821	32.381	1.00	53.07	B
ATOM	1156	O2P	CYT	B	202	9.316	30.881	31.657	1.00	49.44	B
ATOM	1157	O5'	CYT	B	202	9.943	29.532	33.689	1.00	51.35	B
ATOM	1158	C5'	CYT	B	202	10.766	30.485	34.352	1.00	47.88	B

ATOM	1159	C4'	CYT	B	202	11.962	29.817	34.972	1.00	44.57	B
ATOM	1160	O4'	CYT	B	202	11.589	29.271	36.260	1.00	42.31	B
ATOM	1161	C1'	CYT	B	202	12.237	28.030	36.451	1.00	41.89	B
ATOM	1162	N1	CYT	B	202	11.233	26.976	36.380	1.00	41.10	B
ATOM	1163	C6	CYT	B	202	9.994	27.211	35.848	1.00	43.60	B
ATOM	1164	C2	CYT	B	202	11.570	25.720	36.840	1.00	40.20	B
ATOM	1165	O2	CYT	B	202	12.674	25.559	37.350	1.00	38.30	B
ATOM	1166	N3	CYT	B	202	10.680	24.708	36.725	1.00	43.53	B
ATOM	1167	C4	CYT	B	202	9.477	24.934	36.194	1.00	43.15	B
ATOM	1168	N4	CYT	B	202	8.637	23.907	36.097	1.00	43.58	B
ATOM	1169	C5	CYT	B	202	9.090	26.225	35.740	1.00	43.56	B
ATOM	1170	C2'	CYT	B	202	13.247	27.874	35.317	1.00	42.94	B
ATOM	1171	O2'	CYT	B	202	14.469	28.448	35.705	1.00	43.96	B
ATOM	1172	C3'	CYT	B	202	12.565	28.653	34.202	1.00	43.70	B
ATOM	1173	O3'	CYT	B	202	13.531	29.144	33.290	1.00	43.33	B
ATOM	1174	P	GUA	B	203	13.858	28.332	31.949	1.00	46.72	B
ATOM	1175	O1P	GUA	B	203	12.593	27.844	31.370	1.00	48.52	B
ATOM	1176	O2P	GUA	B	203	14.725	29.223	31.147	1.00	46.78	B
ATOM	1177	O5'	GUA	B	203	14.709	27.082	32.448	1.00	46.96	B
ATOM	1178	C5'	GUA	B	203	15.833	27.282	33.296	1.00	46.67	B
ATOM	1179	C4'	GUA	B	203	16.366	25.968	33.800	1.00	46.87	B
ATOM	1180	O4'	GUA	B	203	15.544	25.479	34.885	1.00	46.06	B
ATOM	1181	C1'	GUA	B	203	15.525	24.059	34.853	1.00	49.05	B
ATOM	1182	N9	GUA	B	203	14.176	23.616	34.536	1.00	50.83	B
ATOM	1183	C4	GUA	B	203	13.697	22.350	34.693	1.00	51.60	B
ATOM	1184	N3	GUA	B	203	14.391	21.306	35.180	1.00	52.97	B
ATOM	1185	C2	GUA	B	203	13.677	20.193	35.173	1.00	55.12	B
ATOM	1186	N2	GUA	B	203	14.227	19.044	35.596	1.00	55.46	B
ATOM	1187	N1	GUA	B	203	12.373	20.120	34.741	1.00	55.24	B
ATOM	1188	C6	GUA	B	203	11.638	21.187	34.236	1.00	54.21	B
ATOM	1189	O6	GUA	B	203	10.471	21.008	33.857	1.00	55.53	B
ATOM	1190	C5	GUA	B	203	12.400	22.385	34.228	1.00	52.79	B
ATOM	1191	N7	GUA	B	203	12.065	23.661	33.803	1.00	52.05	B
ATOM	1192	C8	GUA	B	203	13.147	24.360	34.008	1.00	52.06	B
ATOM	1193	C2'	GUA	B	203	16.491	23.627	33.754	1.00	49.39	B
ATOM	1194	O2'	GUA	B	203	17.774	23.426	34.320	1.00	50.70	B
ATOM	1195	C3'	GUA	B	203	16.394	24.818	32.813	1.00	48.50	B
ATOM	1196	O3'	GUA	B	203	17.540	24.916	31.986	1.00	51.54	B
ATOM	1197	P	CYT	B	204	17.445	24.511	30.436	1.00	53.75	B
ATOM	1198	O1P	CYT	B	204	16.121	24.953	29.937	1.00	55.60	B
ATOM	1199	O2P	CYT	B	204	18.682	25.001	29.770	1.00	53.17	B
ATOM	1200	O5'	CYT	B	204	17.457	22.922	30.460	1.00	51.80	B
ATOM	1201	C5'	CYT	B	204	18.473	22.229	31.158	1.00	51.55	B
ATOM	1202	C4'	CYT	B	204	18.146	20.765	31.227	1.00	52.80	B
ATOM	1203	O4'	CYT	B	204	17.050	20.563	32.153	1.00	53.65	B
ATOM	1204	C1'	CYT	B	204	16.323	19.404	31.769	1.00	51.69	B
ATOM	1205	N1	CYT	B	204	14.946	19.803	31.490	1.00	50.29	B
ATOM	1206	C6	CYT	B	204	14.635	21.098	31.189	1.00	51.07	B
ATOM	1207	C2	CYT	B	204	13.956	18.837	31.544	1.00	51.03	B
ATOM	1208	O2	CYT	B	204	14.279	17.677	31.819	1.00	50.84	B
ATOM	1209	N3	CYT	B	204	12.671	19.187	31.302	1.00	51.56	B
ATOM	1210	C4	CYT	B	204	12.370	20.456	31.026	1.00	51.67	B
ATOM	1211	N4	CYT	B	204	11.091	20.764	30.824	1.00	51.58	B
ATOM	1212	C5	CYT	B	204	13.369	21.467	30.953	1.00	51.72	B
ATOM	1213	C2'	CYT	B	204	17.028	18.840	30.538	1.00	52.66	B
ATOM	1214	O2'	CYT	B	204	18.028	17.937	30.975	1.00	50.99	B
ATOM	1215	C3'	CYT	B	204	17.615	20.117	29.960	1.00	54.04	B
ATOM	1216	O3'	CYT	B	204	18.650	19.862	29.017	1.00	57.06	B
ATOM	1217	P	GUA	B	205	18.527	20.459	27.539	1.00	57.66	B
ATOM	1218	O1P	GUA	B	205	17.497	21.519	27.638	1.00	59.12	B
ATOM	1219	O2P	GUA	B	205	19.878	20.793	27.025	1.00	55.89	B

ATOM	1220	O5'	GUA	B	205	17.899	19.260	26.700	1.00	58.91	B
ATOM	1221	C5'	GUA	B	205	18.625	18.050	26.478	1.00	58.65	B
ATOM	1222	C4'	GUA	B	205	17.775	16.846	26.835	1.00	57.77	B
ATOM	1223	O4'	GUA	B	205	17.003	17.156	28.024	1.00	58.08	B
ATOM	1224	C1'	GUA	B	205	15.757	16.478	27.976	1.00	58.15	B
ATOM	1225	N9	GUA	B	205	14.689	17.469	27.941	1.00	57.22	B
ATOM	1226	C4	GUA	B	205	13.342	17.211	27.974	1.00	55.21	B
ATOM	1227	N3	GUA	B	205	12.771	15.997	28.063	1.00	54.66	B
ATOM	1228	C2	GUA	B	205	11.452	16.071	28.036	1.00	54.04	B
ATOM	1229	N2	GUA	B	205	10.719	14.963	28.091	1.00	53.92	B
ATOM	1230	N1	GUA	B	205	10.756	17.238	27.942	1.00	54.33	B
ATOM	1231	C6	GUA	B	205	11.323	18.497	27.838	1.00	55.11	B
ATOM	1232	O6	GUA	B	205	10.599	19.484	27.714	1.00	57.19	B
ATOM	1233	C5	GUA	B	205	12.733	18.437	27.872	1.00	55.05	B
ATOM	1234	N7	GUA	B	205	13.677	19.450	27.805	1.00	57.05	B
ATOM	1235	C8	GUA	B	205	14.823	18.830	27.850	1.00	56.48	B
ATOM	1236	C2'	GUA	B	205	15.775	15.615	26.718	1.00	57.78	B
ATOM	1237	O2'	GUA	B	205	16.279	14.348	27.071	1.00	60.51	B
ATOM	1238	C3'	GUA	B	205	16.720	16.411	25.828	1.00	57.96	B
ATOM	1239	O3'	GUA	B	205	17.269	15.591	24.793	1.00	59.77	B
ATOM	1240	P	GUA	B	206	16.445	15.362	23.419	1.00	61.50	B
ATOM	1241	O1P	GUA	B	206	15.949	16.687	22.956	1.00	59.32	B
ATOM	1242	O2P	GUA	B	206	17.276	14.536	22.510	1.00	60.35	B
ATOM	1243	O5'	GUA	B	206	15.191	14.472	23.844	1.00	60.21	B
ATOM	1244	C5'	GUA	B	206	15.360	13.112	24.241	1.00	60.08	B
ATOM	1245	C4'	GUA	B	206	14.035	12.378	24.209	1.00	60.45	B
ATOM	1246	O4'	GUA	B	206	13.174	12.848	25.287	1.00	61.47	B
ATOM	1247	C1'	GUA	B	206	11.829	12.928	24.835	1.00	61.03	B
ATOM	1248	N9	GUA	B	206	11.441	14.339	24.794	1.00	59.51	B
ATOM	1249	C4	GUA	B	206	10.167	14.845	24.683	1.00	57.68	B
ATOM	1250	N3	GUA	B	206	9.038	14.124	24.594	1.00	57.86	B
ATOM	1251	C2	GUA	B	206	7.973	14.892	24.488	1.00	57.96	B
ATOM	1252	N2	GUA	B	206	6.762	14.332	24.390	1.00	60.81	B
ATOM	1253	N1	GUA	B	206	8.010	16.265	24.470	1.00	57.03	B
ATOM	1254	C6	GUA	B	206	9.161	17.035	24.555	1.00	55.93	B
ATOM	1255	O6	GUA	B	206	9.083	18.275	24.518	1.00	49.77	B
ATOM	1256	C5	GUA	B	206	10.316	16.219	24.673	1.00	57.07	B
ATOM	1257	N7	GUA	B	206	11.651	16.568	24.781	1.00	58.68	B
ATOM	1258	C8	GUA	B	206	12.280	15.425	24.851	1.00	60.02	B
ATOM	1259	C2'	GUA	B	206	11.807	12.242	23.467	1.00	61.82	B
ATOM	1260	O2'	GUA	B	206	11.614	10.848	23.619	1.00	63.71	B
ATOM	1261	C3'	GUA	B	206	13.201	12.569	22.956	1.00	61.23	B
ATOM	1262	O3'	GUA	B	206	13.593	11.654	21.946	1.00	60.82	B
ATOM	1263	P	CYT	B	207	13.254	11.977	20.411	1.00	62.09	B
ATOM	1264	O1P	CYT	B	207	13.802	13.316	20.065	1.00	59.83	B
ATOM	1265	O2P	CYT	B	207	13.687	10.794	19.646	1.00	62.58	B
ATOM	1266	O5'	CYT	B	207	11.666	12.035	20.365	1.00	60.49	B
ATOM	1267	C5'	CYT	B	207	10.910	10.862	20.580	1.00	61.91	B
ATOM	1268	C4'	CYT	B	207	9.470	11.104	20.236	1.00	63.97	B
ATOM	1269	O4'	CYT	B	207	8.838	11.868	21.297	1.00	64.87	B
ATOM	1270	C1'	CYT	B	207	7.926	12.791	20.734	1.00	63.80	B
ATOM	1271	N1	CYT	B	207	8.496	14.125	20.900	1.00	63.17	B
ATOM	1272	C6	CYT	B	207	9.847	14.323	20.840	1.00	62.47	B
ATOM	1273	C2	CYT	B	207	7.640	15.188	21.116	1.00	62.29	B
ATOM	1274	O2	CYT	B	207	6.419	14.973	21.138	1.00	62.58	B
ATOM	1275	N3	CYT	B	207	8.153	16.423	21.288	1.00	62.17	B
ATOM	1276	C4	CYT	B	207	9.472	16.610	21.235	1.00	61.91	B
ATOM	1277	N4	CYT	B	207	9.936	17.844	21.422	1.00	62.98	B
ATOM	1278	C5	CYT	B	207	10.372	15.539	20.994	1.00	61.76	B
ATOM	1279	C2'	CYT	B	207	7.802	12.407	19.263	1.00	64.14	B
ATOM	1280	O2'	CYT	B	207	6.858	11.364	19.158	1.00	64.99	B

ATOM	1281	C3'	CYT	B	207	9.217	11.932	18.996	1.00	64.31	B
ATOM	1282	O3'	CYT	B	207	9.304	11.120	17.845	1.00	68.01	B
ATOM	1283	P	GUA	B	208	10.039	11.681	16.530	1.00	71.50	B
ATOM	1284	O1P	GUA	B	208	10.903	12.834	16.895	1.00	71.03	B
ATOM	1285	O2P	GUA	B	208	10.630	10.512	15.838	1.00	70.19	B
ATOM	1286	O5'	GUA	B	208	8.831	12.216	15.654	1.00	71.24	B
ATOM	1287	C5'	GUA	B	208	7.619	11.488	15.626	1.00	75.00	B
ATOM	1288	C4'	GUA	B	208	6.593	12.222	14.819	1.00	77.63	B
ATOM	1289	O4'	GUA	B	208	6.258	13.454	15.502	1.00	78.81	B
ATOM	1290	C1'	GUA	B	208	5.958	14.454	14.546	1.00	77.89	B
ATOM	1291	N9	GUA	B	208	6.908	15.543	14.725	1.00	76.63	B
ATOM	1292	C4	GUA	B	208	6.596	16.873	14.757	1.00	76.06	B
ATOM	1293	N3	GUA	B	208	5.363	17.394	14.605	1.00	75.43	B
ATOM	1294	C2	GUA	B	208	5.371	18.710	14.688	1.00	75.88	B
ATOM	1295	N2	GUA	B	208	4.225	19.386	14.555	1.00	76.45	B
ATOM	1296	N1	GUA	B	208	6.503	19.462	14.907	1.00	75.46	B
ATOM	1297	C6	GUA	B	208	7.786	18.948	15.071	1.00	76.04	B
ATOM	1298	O6	GUA	B	208	8.739	19.716	15.276	1.00	75.23	B
ATOM	1299	C5	GUA	B	208	7.792	17.526	14.976	1.00	76.48	B
ATOM	1300	N7	GUA	B	208	8.839	16.616	15.068	1.00	75.92	B
ATOM	1301	C8	GUA	B	208	8.268	15.453	14.909	1.00	75.95	B
ATOM	1302	C2'	GUA	B	208	6.023	13.790	13.170	1.00	79.19	B
ATOM	1303	O2'	GUA	B	208	4.734	13.291	12.840	1.00	80.56	B
ATOM	1304	C3'	GUA	B	208	7.025	12.675	13.434	1.00	78.39	B
ATOM	1305	O3'	GUA	B	208	6.853	11.614	12.505	1.00	78.55	B
ATOM	1306	P	ADE	B	209	7.557	11.694	11.066	1.00	79.91	B
ATOM	1307	O1P	ADE	B	209	7.729	10.295	10.601	1.00	79.05	B
ATOM	1308	O2P	ADE	B	209	8.743	12.592	11.172	1.00	79.16	B
ATOM	1309	O5'	ADE	B	209	6.461	12.386	10.137	1.00	78.24	B
ATOM	1310	C5'	ADE	B	209	6.714	13.641	9.507	1.00	75.75	B
ATOM	1311	C4'	ADE	B	209	5.411	14.354	9.221	1.00	73.21	B
ATOM	1312	O4'	ADE	B	209	4.873	14.899	10.460	1.00	73.62	B
ATOM	1313	C1'	ADE	B	209	4.502	16.256	10.270	1.00	72.82	B
ATOM	1314	N9	ADE	B	209	5.575	17.095	10.804	1.00	72.74	B
ATOM	1315	C4	ADE	B	209	5.493	18.434	11.097	1.00	71.79	B
ATOM	1316	N3	ADE	B	209	4.414	19.226	10.987	1.00	70.98	B
ATOM	1317	C2	ADE	B	209	4.715	20.472	11.336	1.00	71.75	B
ATOM	1318	N1	ADE	B	209	5.885	20.981	11.746	1.00	72.10	B
ATOM	1319	C6	ADE	B	209	6.952	20.154	11.837	1.00	72.26	B
ATOM	1320	N6	ADE	B	209	8.129	20.658	12.223	1.00	71.78	B
ATOM	1321	C5	ADE	B	209	6.760	18.807	11.508	1.00	71.85	B
ATOM	1322	N7	ADE	B	209	7.621	17.720	11.501	1.00	72.48	B
ATOM	1323	C8	ADE	B	209	6.872	16.730	11.085	1.00	72.58	B
ATOM	1324	C2'	ADE	B	209	4.371	16.428	8.758	1.00	72.33	B
ATOM	1325	O2'	ADE	B	209	3.104	16.003	8.293	1.00	72.90	B
ATOM	1326	C3'	ADE	B	209	5.512	15.544	8.279	1.00	71.38	B
ATOM	1327	O3'	ADE	B	209	5.308	15.134	6.943	1.00	69.22	B
ATOM	1328	P	URI	B	210	5.948	15.987	5.751	1.00	68.62	B
ATOM	1329	O1P	URI	B	210	7.386	16.234	6.026	1.00	66.35	B
ATOM	1330	O2P	URI	B	210	5.552	15.310	4.493	1.00	70.59	B
ATOM	1331	O5'	URI	B	210	5.184	17.379	5.847	1.00	67.97	B
ATOM	1332	C5'	URI	B	210	3.784	17.451	5.619	1.00	65.59	B
ATOM	1333	C4'	URI	B	210	3.285	18.867	5.806	1.00	64.54	B
ATOM	1334	O4'	URI	B	210	3.438	19.289	7.190	1.00	63.95	B
ATOM	1335	C1'	URI	B	210	3.513	20.706	7.236	1.00	63.40	B
ATOM	1336	N1	URI	B	210	4.820	21.090	7.786	1.00	62.33	B
ATOM	1337	C6	URI	B	210	5.885	20.236	7.750	1.00	60.71	B
ATOM	1338	C2	URI	B	210	4.952	22.366	8.301	1.00	61.50	B
ATOM	1339	O2	URI	B	210	4.010	23.134	8.428	1.00	62.05	B
ATOM	1340	N3	URI	B	210	6.224	22.709	8.673	1.00	59.69	B
ATOM	1341	C4	URI	B	210	7.342	21.919	8.613	1.00	59.43	B

ATOM	1342	O4	URI	B	210	8.440	22.411	8.868	1.00	60.44	B
ATOM	1343	C5	URI	B	210	7.109	20.596	8.138	1.00	60.21	B
ATOM	1344	C2'	URI	B	210	3.400	21.181	5.782	1.00	63.67	B
ATOM	1345	O2'	URI	B	210	2.047	21.387	5.433	1.00	64.63	B
ATOM	1346	C3'	URI	B	210	3.980	19.986	5.050	1.00	63.00	B
ATOM	1347	O3'	URI	B	210	3.613	20.025	3.674	1.00	61.87	B
ATOM	1348	P	URI	B	211	4.552	20.791	2.619	1.00	62.14	B
ATOM	1349	O1P	URI	B	211	5.953	20.288	2.709	1.00	62.97	B
ATOM	1350	O2P	URI	B	211	3.861	20.762	1.316	1.00	64.45	B
ATOM	1351	O5'	URI	B	211	4.552	22.292	3.144	1.00	64.09	B
ATOM	1352	C5'	URI	B	211	3.352	23.055	3.188	1.00	63.77	B
ATOM	1353	C4'	URI	B	211	3.648	24.477	3.606	1.00	64.74	B
ATOM	1354	O4'	URI	B	211	4.134	24.496	4.975	1.00	64.83	B
ATOM	1355	C1'	URI	B	211	5.030	25.586	5.145	1.00	66.00	B
ATOM	1356	N1	URI	B	211	6.350	25.066	5.527	1.00	64.36	B
ATOM	1357	C6	URI	B	211	6.708	23.768	5.295	1.00	63.97	B
ATOM	1358	C2	URI	B	211	7.224	25.947	6.111	1.00	63.57	B
ATOM	1359	O2	URI	B	211	6.921	27.098	6.359	1.00	65.32	B
ATOM	1360	N3	URI	B	211	8.463	25.434	6.399	1.00	62.40	B
ATOM	1361	C4	URI	B	211	8.896	24.151	6.173	1.00	62.58	B
ATOM	1362	O4	URI	B	211	10.061	23.851	6.424	1.00	61.65	B
ATOM	1363	C5	URI	B	211	7.920	23.291	5.591	1.00	64.22	B
ATOM	1364	C2'	URI	B	211	5.096	26.322	3.806	1.00	66.91	B
ATOM	1365	O2'	URI	B	211	4.175	27.396	3.821	1.00	67.58	B
ATOM	1366	C3'	URI	B	211	4.746	25.196	2.836	1.00	66.05	B
ATOM	1367	O3'	URI	B	211	4.266	25.680	1.582	1.00	67.10	B
ATOM	1368	P	URI	B	212	5.296	25.943	0.371	1.00	68.24	B
ATOM	1369	O1P	URI	B	212	6.124	24.732	0.127	1.00	66.86	B
ATOM	1370	O2P	URI	B	212	4.515	26.535	-0.748	1.00	67.34	B
ATOM	1371	O5'	URI	B	212	6.262	27.074	0.935	1.00	66.78	B
ATOM	1372	C5'	URI	B	212	5.753	28.356	1.279	1.00	63.87	B
ATOM	1373	C4'	URI	B	212	6.880	29.264	1.683	1.00	61.99	B
ATOM	1374	O4'	URI	B	212	7.431	28.817	2.944	1.00	61.09	B
ATOM	1375	C1'	URI	B	212	8.789	29.201	3.012	1.00	60.91	B
ATOM	1376	N1	URI	B	212	9.596	28.017	3.306	1.00	62.64	B
ATOM	1377	C6	URI	B	212	9.116	26.742	3.141	1.00	63.07	B
ATOM	1378	C2	URI	B	212	10.872	28.244	3.744	1.00	64.10	B
ATOM	1379	O2	URI	B	212	11.315	29.368	3.896	1.00	65.97	B
ATOM	1380	N3	URI	B	212	11.613	27.116	3.992	1.00	64.01	B
ATOM	1381	C4	URI	B	212	11.204	25.814	3.841	1.00	62.96	B
ATOM	1382	O4	URI	B	212	11.991	24.909	4.086	1.00	62.78	B
ATOM	1383	C5	URI	B	212	9.858	25.659	3.384	1.00	62.88	B
ATOM	1384	C2'	URI	B	212	9.179	29.779	1.655	1.00	60.05	B
ATOM	1385	O2'	URI	B	212	9.195	31.180	1.725	1.00	60.00	B
ATOM	1386	C3'	URI	B	212	8.079	29.232	0.760	1.00	60.82	B
ATOM	1387	O3'	URI	B	212	7.861	30.082	-0.345	1.00	62.32	B
ATOM	1388	P	ADE	B	213	8.786	29.945	-1.642	1.00	64.19	B
ATOM	1389	O1P	ADE	B	213	8.514	31.129	-2.486	1.00	62.11	B
ATOM	1390	O2P	ADE	B	213	8.592	28.580	-2.199	1.00	64.56	B
ATOM	1391	O5'	ADE	B	213	10.270	30.084	-1.086	1.00	64.30	B
ATOM	1392	C5'	ADE	B	213	10.903	31.352	-1.037	1.00	66.56	B
ATOM	1393	C4'	ADE	B	213	11.967	31.424	-2.091	1.00	68.08	B
ATOM	1394	O4'	ADE	B	213	12.985	30.491	-1.693	1.00	67.73	B
ATOM	1395	C1'	ADE	B	213	13.593	29.941	-2.834	1.00	69.20	B
ATOM	1396	N9	ADE	B	213	13.824	28.534	-2.557	1.00	68.20	B
ATOM	1397	C4	ADE	B	213	15.013	28.009	-2.132	1.00	68.22	B
ATOM	1398	N3	ADE	B	213	16.161	28.672	-1.919	1.00	67.53	B
ATOM	1399	C2	ADE	B	213	17.102	27.846	-1.484	1.00	67.81	B
ATOM	1400	N1	ADE	B	213	17.034	26.532	-1.260	1.00	67.62	B
ATOM	1401	C6	ADE	B	213	15.868	25.897	-1.495	1.00	67.62	B
ATOM	1402	N6	ADE	B	213	15.808	24.586	-1.284	1.00	68.78	B

ATOM	1403	C5	ADE	B	213	14.788	26.663	-1.952	1.00	67.89	B
ATOM	1404	N7	ADE	B	213	13.478	26.340	-2.274	1.00	68.10	B
ATOM	1405	C8	ADE	B	213	12.952	27.485	-2.631	1.00	68.29	B
ATOM	1406	C2'	ADE	B	213	12.708	30.196	-4.054	1.00	70.12	B
ATOM	1407	O2'	ADE	B	213	13.432	30.890	-5.056	1.00	72.73	B
ATOM	1408	C3'	ADE	B	213	11.508	30.945	-3.462	1.00	69.63	B
ATOM	1409	O3'	ADE	B	213	10.942	31.982	-4.285	1.00	70.47	B
ATOM	1410	P	ADE	B	214	11.773	33.329	-4.649	1.00	69.36	B
ATOM	1411	O1P	ADE	B	214	13.241	33.164	-4.465	1.00	68.13	B
ATOM	1412	O2P	ADE	B	214	11.068	34.439	-3.965	1.00	67.30	B
ATOM	1413	O5'	ADE	B	214	11.486	33.476	-6.204	1.00	67.59	B
ATOM	1414	C5'	ADE	B	214	10.417	32.740	-6.774	1.00	69.16	B
ATOM	1415	C4'	ADE	B	214	10.411	32.875	-8.268	1.00	70.01	B
ATOM	1416	O4'	ADE	B	214	10.089	34.245	-8.615	1.00	69.71	B
ATOM	1417	C1'	ADE	B	214	10.711	34.566	-9.849	1.00	69.81	B
ATOM	1418	N9	ADE	B	214	11.758	35.547	-9.587	1.00	67.72	B
ATOM	1419	C4	ADE	B	214	11.965	36.718	-10.265	1.00	66.16	B
ATOM	1420	N3	ADE	B	214	11.225	37.218	-11.267	1.00	63.36	B
ATOM	1421	C2	ADE	B	214	11.738	38.363	-11.693	1.00	64.58	B
ATOM	1422	N1	ADE	B	214	12.832	39.016	-11.266	1.00	66.51	B
ATOM	1423	C6	ADE	B	214	13.554	38.478	-10.257	1.00	66.22	B
ATOM	1424	N6	ADE	B	214	14.648	39.116	-9.833	1.00	65.04	B
ATOM	1425	C5	ADE	B	214	13.107	37.272	-9.715	1.00	66.42	B
ATOM	1426	N7	ADE	B	214	13.594	36.479	-8.691	1.00	67.11	B
ATOM	1427	C8	ADE	B	214	12.756	35.475	-8.649	1.00	67.96	B
ATOM	1428	C2'	ADE	B	214	11.324	33.259	-10.351	1.00	70.77	B
ATOM	1429	O2'	ADE	B	214	10.339	32.494	-11.025	1.00	70.42	B
ATOM	1430	C3'	ADE	B	214	11.708	32.637	-9.024	1.00	71.72	B
ATOM	1431	O3'	ADE	B	214	12.024	31.255	-9.166	1.00	76.39	B
ATOM	1432	P	CYT	B	215	13.418	30.800	-9.864	1.00	79.37	B
ATOM	1433	O1P	CYT	B	215	14.341	30.359	-8.769	1.00	77.34	B
ATOM	1434	O2P	CYT	B	215	13.884	31.829	-10.846	1.00	79.33	B
ATOM	1435	O5'	CYT	B	215	12.976	29.515	-10.704	1.00	76.94	B
ATOM	1436	C5'	CYT	B	215	11.607	29.327	-11.086	1.00	71.33	B
ATOM	1437	C4'	CYT	B	215	11.448	28.061	-11.897	1.00	67.39	B
ATOM	1438	O4'	CYT	B	215	12.392	28.049	-13.007	1.00	65.08	B
ATOM	1439	C1'	CYT	B	215	13.043	26.801	-13.057	1.00	61.70	B
ATOM	1440	N1	CYT	B	215	14.359	26.971	-12.449	1.00	59.95	B
ATOM	1441	C6	CYT	B	215	14.792	28.206	-12.062	1.00	58.65	B
ATOM	1442	C2	CYT	B	215	15.160	25.851	-12.258	1.00	60.14	B
ATOM	1443	O2	CYT	B	215	14.750	24.747	-12.652	1.00	60.89	B
ATOM	1444	N3	CYT	B	215	16.362	25.995	-11.656	1.00	58.69	B
ATOM	1445	C4	CYT	B	215	16.768	27.205	-11.264	1.00	57.84	B
ATOM	1446	N4	CYT	B	215	17.953	27.302	-10.663	1.00	57.51	B
ATOM	1447	C5	CYT	B	215	15.975	28.367	-11.469	1.00	57.82	B
ATOM	1448	C2'	CYT	B	215	12.156	25.844	-12.265	1.00	63.48	B
ATOM	1449	O2'	CYT	B	215	11.095	25.406	-13.089	1.00	64.98	B
ATOM	1450	C3'	CYT	B	215	11.667	26.754	-11.151	1.00	64.05	B
ATOM	1451	O3'	CYT	B	215	10.410	26.296	-10.690	1.00	63.08	B
ATOM	1452	P	CYT	B	216	10.197	25.977	-9.135	1.00	64.12	B
ATOM	1453	O1P	CYT	B	216	11.047	26.891	-8.322	1.00	63.64	B
ATOM	1454	O2P	CYT	B	216	8.729	25.920	-8.889	1.00	62.19	B
ATOM	1455	O5'	CYT	B	216	10.802	24.517	-8.988	1.00	61.93	B
ATOM	1456	C5'	CYT	B	216	10.525	23.517	-9.957	1.00	58.67	B
ATOM	1457	C4'	CYT	B	216	11.344	22.282	-9.675	1.00	56.94	B
ATOM	1458	O4'	CYT	B	216	12.646	22.445	-10.283	1.00	58.42	B
ATOM	1459	C1'	CYT	B	216	13.623	21.798	-9.496	1.00	55.98	B
ATOM	1460	N1	CYT	B	216	14.576	22.800	-9.063	1.00	56.15	B
ATOM	1461	C6	CYT	B	216	14.295	24.130	-9.178	1.00	56.50	B
ATOM	1462	C2	CYT	B	216	15.772	22.374	-8.527	1.00	57.23	B
ATOM	1463	O2	CYT	B	216	15.970	21.157	-8.420	1.00	56.87	B

ATOM	1464	N3	CYT	B	216	16.682	23.290	-8.130	1.00	57.99	B
ATOM	1465	C4	CYT	B	216	16.406	24.591	-8.247	1.00	58.03	B
ATOM	1466	N4	CYT	B	216	17.326	25.466	-7.844	1.00	58.87	B
ATOM	1467	C5	CYT	B	216	15.172	25.051	-8.784	1.00	58.58	B
ATOM	1468	C2'	CYT	B	216	12.920	21.181	-8.296	1.00	55.14	B
ATOM	1469	O2'	CYT	B	216	12.635	19.837	-8.575	1.00	58.96	B
ATOM	1470	C3'	CYT	B	216	11.653	22.012	-8.212	1.00	54.62	B
ATOM	1471	O3'	CYT	B	216	10.641	21.211	-7.651	1.00	51.22	B
ATOM	1472	P	GUA	B	217	10.195	21.454	-6.141	1.00	51.46	B
ATOM	1473	O1P	GUA	B	217	9.903	22.898	-6.028	1.00	51.75	B
ATOM	1474	O2P	GUA	B	217	9.140	20.468	-5.804	1.00	52.33	B
ATOM	1475	O5'	GUA	B	217	11.506	21.148	-5.295	1.00	50.74	B
ATOM	1476	C5'	GUA	B	217	12.249	19.952	-5.488	1.00	53.55	B
ATOM	1477	C4'	GUA	B	217	13.474	19.959	-4.605	1.00	56.25	B
ATOM	1478	O4'	GUA	B	217	14.391	20.990	-5.056	1.00	59.75	B
ATOM	1479	C1'	GUA	B	217	14.472	22.021	-4.090	1.00	61.77	B
ATOM	1480	N9	GUA	B	217	14.188	23.291	-4.738	1.00	66.26	B
ATOM	1481	C4	GUA	B	217	15.045	24.339	-4.873	1.00	68.16	B
ATOM	1482	N3	GUA	B	217	16.327	24.364	-4.461	1.00	69.17	B
ATOM	1483	C2	GUA	B	217	16.896	25.533	-4.714	1.00	73.15	B
ATOM	1484	N2	GUA	B	217	18.191	25.746	-4.372	1.00	73.91	B
ATOM	1485	N1	GUA	B	217	16.242	26.585	-5.323	1.00	73.30	B
ATOM	1486	C6	GUA	B	217	14.916	26.566	-5.752	1.00	72.06	B
ATOM	1487	O6	GUA	B	217	14.419	27.562	-6.288	1.00	74.99	B
ATOM	1488	C5	GUA	B	217	14.310	25.335	-5.491	1.00	69.90	B
ATOM	1489	N7	GUA	B	217	13.019	24.908	-5.754	1.00	68.66	B
ATOM	1490	C8	GUA	B	217	12.993	23.687	-5.297	1.00	68.05	B
ATOM	1491	C2'	GUA	B	217	13.388	21.772	-3.047	1.00	59.42	B
ATOM	1492	O2'	GUA	B	217	13.837	22.202	-1.779	1.00	59.88	B
ATOM	1493	C3'	GUA	B	217	13.179	20.270	-3.147	1.00	56.41	B
ATOM	1494	O3'	GUA	B	217	14.074	19.609	-2.290	1.00	50.70	B
ATOM	1495	P	URI	B	218	13.502	18.644	-1.157	1.00	49.79	B
ATOM	1496	O1P	URI	B	218	13.606	19.315	0.155	1.00	46.50	B
ATOM	1497	O2P	URI	B	218	12.181	18.143	-1.602	1.00	49.67	B
ATOM	1498	O5'	URI	B	218	14.553	17.455	-1.218	1.00	50.09	B
ATOM	1499	C5'	URI	B	218	15.031	16.855	-0.037	1.00	54.12	B
ATOM	1500	C4'	URI	B	218	16.493	16.552	-0.168	1.00	57.01	B
ATOM	1501	O4'	URI	B	218	17.078	17.324	-1.248	1.00	58.97	B
ATOM	1502	C1'	URI	B	218	18.380	17.762	-0.867	1.00	60.00	B
ATOM	1503	N1	URI	B	218	18.354	19.226	-0.735	1.00	60.71	B
ATOM	1504	C6	URI	B	218	17.184	19.929	-0.865	1.00	60.31	B
ATOM	1505	C2	URI	B	218	19.547	19.876	-0.483	1.00	60.85	B
ATOM	1506	O2	URI	B	218	20.601	19.291	-0.346	1.00	62.32	B
ATOM	1507	N3	URI	B	218	19.457	21.241	-0.392	1.00	60.77	B
ATOM	1508	C4	URI	B	218	18.322	22.006	-0.522	1.00	60.53	B
ATOM	1509	O4	URI	B	218	18.402	23.232	-0.437	1.00	58.93	B
ATOM	1510	C5	URI	B	218	17.128	21.260	-0.769	1.00	61.10	B
ATOM	1511	C2'	URI	B	218	18.693	17.057	0.450	1.00	59.40	B
ATOM	1512	O2'	URI	B	218	19.214	15.781	0.165	1.00	61.50	B
ATOM	1513	C3'	URI	B	218	17.301	16.966	1.040	1.00	59.18	B
ATOM	1514	O3'	URI	B	218	17.185	15.965	2.016	1.00	60.42	B
ATOM	1515	P	ADE	B	219	16.564	16.333	3.438	1.00	64.24	B
ATOM	1516	O1P	ADE	B	219	15.728	15.179	3.852	1.00	62.72	B
ATOM	1517	O2P	ADE	B	219	15.965	17.690	3.380	1.00	62.59	B
ATOM	1518	O5'	ADE	B	219	17.862	16.379	4.350	1.00	66.08	B
ATOM	1519	C5'	ADE	B	219	19.022	15.656	3.956	1.00	68.19	B
ATOM	1520	C4'	ADE	B	219	20.261	16.406	4.352	1.00	69.24	B
ATOM	1521	O4'	ADE	B	219	20.575	17.422	3.373	1.00	70.00	B
ATOM	1522	C1'	ADE	B	219	21.308	18.458	4.006	1.00	71.78	B
ATOM	1523	N9	ADE	B	219	20.667	19.735	3.704	1.00	74.23	B
ATOM	1524	C4	ADE	B	219	21.235	20.970	3.866	1.00	74.89	B

ATOM	1525	N3	ADE B 219	22.460	21.238	4.335	1.00	75.81	B
ATOM	1526	C2	ADE B 219	22.677	22.547	4.342	1.00	76.38	B
ATOM	1527	N1	ADE B 219	21.871	23.542	3.959	1.00	76.67	B
ATOM	1528	C6	ADE B 219	20.643	23.237	3.491	1.00	76.42	B
ATOM	1529	N6	ADE B 219	19.839	24.234	3.103	1.00	77.15	B
ATOM	1530	C5	ADE B 219	20.288	21.882	3.439	1.00	75.79	B
ATOM	1531	N7	ADE B 219	19.135	21.235	3.022	1.00	75.71	B
ATOM	1532	C8	ADE B 219	19.408	19.965	3.201	1.00	76.30	B
ATOM	1533	C2'	ADE B 219	21.328	18.143	5.503	1.00	70.95	B
ATOM	1534	O2'	ADE B 219	22.542	17.496	5.822	1.00	71.79	B
ATOM	1535	C3'	ADE B 219	20.135	17.209	5.625	1.00	69.63	B
ATOM	1536	O3'	ADE B 219	20.258	16.343	6.735	1.00	69.76	B
ATOM	1537	P	URI B 220	19.453	16.666	8.079	1.00	70.71	B
ATOM	1538	O1P	URI B 220	18.008	16.748	7.750	1.00	69.47	B
ATOM	1539	O2P	URI B 220	19.918	15.701	9.099	1.00	70.74	B
ATOM	1540	O5'	URI B 220	19.976	18.115	8.483	1.00	70.85	B
ATOM	1541	C5'	URI B 220	21.273	18.291	9.050	1.00	71.86	B
ATOM	1542	C4'	URI B 220	21.498	19.742	9.400	1.00	73.26	B
ATOM	1543	O4'	URI B 220	21.577	20.510	8.172	1.00	73.76	B
ATOM	1544	C1'	URI B 220	20.934	21.761	8.345	1.00	74.30	B
ATOM	1545	N1	URI B 220	19.789	21.822	7.429	1.00	73.87	B
ATOM	1546	C6	URI B 220	19.072	20.700	7.101	1.00	73.82	B
ATOM	1547	C2	URI B 220	19.456	23.051	6.921	1.00	74.08	B
ATOM	1548	O2	URI B 220	20.068	24.066	7.200	1.00	74.27	B
ATOM	1549	N3	URI B 220	18.372	23.056	6.083	1.00	74.62	B
ATOM	1550	C4	URI B 220	17.597	21.978	5.723	1.00	74.41	B
ATOM	1551	O4	URI B 220	16.595	22.158	5.027	1.00	74.63	B
ATOM	1552	C5	URI B 220	18.014	20.734	6.290	1.00	74.26	B
ATOM	1553	C2'	URI B 220	20.503	21.863	9.808	1.00	74.65	B
ATOM	1554	O2'	URI B 220	21.466	22.564	10.564	1.00	74.96	B
ATOM	1555	C3'	URI B 220	20.375	20.394	10.192	1.00	74.77	B
ATOM	1556	O3'	URI B 220	20.548	20.202	11.590	1.00	75.28	B
ATOM	1557	P	URI B 221	19.260	20.164	12.547	1.00	76.37	B
ATOM	1558	O1P	URI B 221	19.697	19.545	13.817	1.00	76.58	B
ATOM	1559	O2P	URI B 221	18.112	19.576	11.804	1.00	76.32	B
ATOM	1560	O5'	URI B 221	18.939	21.702	12.808	1.00	75.73	B
ATOM	1561	C5'	URI B 221	19.977	22.607	13.156	1.00	75.43	B
ATOM	1562	C4'	URI B 221	19.425	24.000	13.335	1.00	76.00	B
ATOM	1563	O4'	URI B 221	19.468	24.701	12.064	1.00	75.92	B
ATOM	1564	C1'	URI B 221	18.376	25.602	11.983	1.00	77.20	B
ATOM	1565	N1	URI B 221	17.537	25.194	10.850	1.00	78.74	B
ATOM	1566	C6	URI B 221	17.445	23.872	10.481	1.00	80.55	B
ATOM	1567	C2	URI B 221	16.831	26.171	10.178	1.00	78.55	B
ATOM	1568	O2	URI B 221	16.907	27.352	10.459	1.00	78.21	B
ATOM	1569	N3	URI B 221	16.032	25.709	9.161	1.00	78.98	B
ATOM	1570	C4	URI B 221	15.880	24.395	8.754	1.00	79.57	B
ATOM	1571	O4	URI B 221	15.102	24.127	7.839	1.00	79.33	B
ATOM	1572	C5	URI B 221	16.661	23.451	9.486	1.00	80.16	B
ATOM	1573	C2'	URI B 221	17.616	25.510	13.311	1.00	76.85	B
ATOM	1574	O2'	URI B 221	18.051	26.492	14.233	1.00	76.78	B
ATOM	1575	C3'	URI B 221	17.972	24.104	13.770	1.00	76.38	B
ATOM	1576	O3'	URI B 221	17.846	24.017	15.185	1.00	76.55	B
ATOM	1577	P	GUA B 222	16.386	23.883	15.847	1.00	76.67	B
ATOM	1578	O1P	GUA B 222	15.693	22.756	15.175	1.00	74.54	B
ATOM	1579	O2P	GUA B 222	16.530	23.877	17.321	1.00	76.48	B
ATOM	1580	O5'	GUA B 222	15.650	25.238	15.450	1.00	76.37	B
ATOM	1581	C5'	GUA B 222	15.906	26.441	16.164	1.00	75.09	B
ATOM	1582	C4'	GUA B 222	14.740	27.398	16.029	1.00	75.06	B
ATOM	1583	O4'	GUA B 222	14.095	27.260	14.733	1.00	74.11	B
ATOM	1584	C1'	GUA B 222	12.733	27.669	14.841	1.00	73.06	B
ATOM	1585	N9	GUA B 222	11.874	26.564	14.434	1.00	71.60	B

ATOM	1586	C4	GUA	B	222	10.550	26.653	14.082	1.00	70.04	B
ATOM	1587	N3	GUA	B	222	9.820	27.782	14.028	1.00	68.98	B
ATOM	1588	C2	GUA	B	222	8.580	27.545	13.656	1.00	68.24	B
ATOM	1589	N2	GUA	B	222	7.710	28.556	13.555	1.00	69.22	B
ATOM	1590	N1	GUA	B	222	8.099	26.302	13.355	1.00	67.50	B
ATOM	1591	C6	GUA	B	222	8.833	25.129	13.400	1.00	67.30	B
ATOM	1592	O6	GUA	B	222	8.303	24.061	13.100	1.00	66.59	B
ATOM	1593	C5	GUA	B	222	10.160	25.365	13.804	1.00	69.14	B
ATOM	1594	N7	GUA	B	222	11.216	24.482	13.974	1.00	70.34	B
ATOM	1595	C8	GUA	B	222	12.211	25.238	14.346	1.00	70.99	B
ATOM	1596	C2'	GUA	B	222	12.499	28.021	16.306	1.00	74.21	B
ATOM	1597	O2'	GUA	B	222	12.671	29.412	16.469	1.00	74.59	B
ATOM	1598	C3'	GUA	B	222	13.578	27.179	16.975	1.00	75.13	B
ATOM	1599	O3'	GUA	B	222	13.873	27.625	18.287	1.00	76.50	B
ATOM	1600	P	CYT	B	223	13.005	27.071	19.515	1.00	78.32	B
ATOM	1601	O1P	CYT	B	223	12.973	25.587	19.411	1.00	77.82	B
ATOM	1602	O2P	CYT	B	223	13.492	27.714	20.761	1.00	77.45	B
ATOM	1603	O5'	CYT	B	223	11.543	27.615	19.213	1.00	76.19	B
ATOM	1604	C5'	CYT	B	223	11.321	29.006	19.055	1.00	75.87	B
ATOM	1605	C4'	CYT	B	223	9.864	29.272	18.814	1.00	74.71	B
ATOM	1606	O4'	CYT	B	223	9.508	28.903	17.458	1.00	75.35	B
ATOM	1607	C1'	CYT	B	223	8.192	28.376	17.444	1.00	73.35	B
ATOM	1608	N1	CYT	B	223	8.273	26.965	17.054	1.00	71.88	B
ATOM	1609	C6	CYT	B	223	9.418	26.242	17.238	1.00	70.84	B
ATOM	1610	C2	CYT	B	223	7.148	26.371	16.507	1.00	71.26	B
ATOM	1611	O2	CYT	B	223	6.145	27.071	16.321	1.00	71.83	B
ATOM	1612	N3	CYT	B	223	7.178	25.056	16.189	1.00	70.51	B
ATOM	1613	C4	CYT	B	223	8.292	24.350	16.390	1.00	70.31	B
ATOM	1614	N4	CYT	B	223	8.276	23.054	16.075	1.00	69.46	B
ATOM	1615	C5	CYT	B	223	9.471	24.943	16.924	1.00	70.47	B
ATOM	1616	C2'	CYT	B	223	7.638	28.551	18.859	1.00	72.90	B
ATOM	1617	O2'	CYT	B	223	7.013	29.811	18.962	1.00	71.35	B
ATOM	1618	C3'	CYT	B	223	8.919	28.459	19.674	1.00	73.63	B
ATOM	1619	O3'	CYT	B	223	8.828	29.085	20.942	1.00	73.42	B
ATOM	1620	P	ADE	B	224	7.950	28.421	22.107	1.00	72.93	B
ATOM	1621	O1P	ADE	B	224	8.161	29.304	23.283	1.00	72.84	B
ATOM	1622	O2P	ADE	B	224	8.213	26.961	22.222	1.00	71.45	B
ATOM	1623	O5'	ADE	B	224	6.463	28.609	21.589	1.00	71.28	B
ATOM	1624	C5'	ADE	B	224	5.421	27.807	22.102	1.00	70.45	B
ATOM	1625	C4'	ADE	B	224	4.399	27.548	21.033	1.00	69.38	B
ATOM	1626	O4'	ADE	B	224	5.056	27.306	19.759	1.00	69.07	B
ATOM	1627	C1'	ADE	B	224	4.415	26.231	19.092	1.00	68.77	B
ATOM	1628	N9	ADE	B	224	5.324	25.083	19.084	1.00	68.39	B
ATOM	1629	C4	ADE	B	224	4.975	23.793	18.763	1.00	67.71	B
ATOM	1630	N3	ADE	B	224	3.757	23.343	18.403	1.00	66.60	B
ATOM	1631	C2	ADE	B	224	3.797	22.038	18.169	1.00	66.24	B
ATOM	1632	N1	ADE	B	224	4.837	21.193	18.249	1.00	65.92	B
ATOM	1633	C6	ADE	B	224	6.042	21.680	18.615	1.00	65.51	B
ATOM	1634	N6	ADE	B	224	7.072	20.842	18.698	1.00	66.29	B
ATOM	1635	C5	ADE	B	224	6.135	23.047	18.887	1.00	66.23	B
ATOM	1636	N7	ADE	B	224	7.198	23.848	19.278	1.00	65.86	B
ATOM	1637	C8	ADE	B	224	6.667	25.043	19.383	1.00	67.75	B
ATOM	1638	C2'	ADE	B	224	3.134	25.942	19.871	1.00	69.52	B
ATOM	1639	O2'	ADE	B	224	2.086	26.764	19.407	1.00	71.88	B
ATOM	1640	C3'	ADE	B	224	3.571	26.305	21.278	1.00	69.39	B
ATOM	1641	O3'	ADE	B	224	2.483	26.645	22.114	1.00	68.87	B
ATOM	1642	P	GUA	B	225	2.437	26.080	23.611	1.00	67.84	B
ATOM	1643	O1P	GUA	B	225	3.847	25.967	24.070	1.00	65.04	B
ATOM	1644	O2P	GUA	B	225	1.460	26.894	24.385	1.00	66.71	B
ATOM	1645	O5'	GUA	B	225	1.822	24.626	23.424	1.00	66.33	B
ATOM	1646	C5'	GUA	B	225	0.601	24.455	22.717	1.00	65.13	B

ATOM	1647	C4'	GUA	B	225	0.505	23.057	22.173	1.00	63.34	B
ATOM	1648	O4'	GUA	B	225	1.584	22.835	21.228	1.00	63.06	B
ATOM	1649	C1'	GUA	B	225	1.949	21.463	21.246	1.00	62.23	B
ATOM	1650	N9	GUA	B	225	3.374	21.380	21.544	1.00	61.82	B
ATOM	1651	C4	GUA	B	225	4.182	20.265	21.447	1.00	61.57	B
ATOM	1652	N3	GUA	B	225	3.794	19.022	21.072	1.00	60.26	B
ATOM	1653	C2	GUA	B	225	4.812	18.170	21.062	1.00	60.24	B
ATOM	1654	N2	GUA	B	225	4.624	16.893	20.707	1.00	59.34	B
ATOM	1655	N1	GUA	B	225	6.097	18.509	21.402	1.00	61.02	B
ATOM	1656	C6	GUA	B	225	6.512	19.773	21.806	1.00	61.71	B
ATOM	1657	O6	GUA	B	225	7.694	19.962	22.120	1.00	65.20	B
ATOM	1658	C5	GUA	B	225	5.441	20.699	21.806	1.00	61.15	B
ATOM	1659	N7	GUA	B	225	5.423	22.045	22.135	1.00	61.04	B
ATOM	1660	C8	GUA	B	225	4.181	22.406	21.967	1.00	61.37	B
ATOM	1661	C2'	GUA	B	225	1.058	20.787	22.291	1.00	62.66	B
ATOM	1662	O2'	GUA	B	225	-0.092	20.267	21.662	1.00	63.62	B
ATOM	1663	C3'	GUA	B	225	0.733	21.964	23.192	1.00	62.60	B
ATOM	1664	O3'	GUA	B	225	-0.413	21.752	23.998	1.00	61.67	B
ATOM	1665	P	URI	B	226	-0.221	21.412	25.560	1.00	64.35	B
ATOM	1666	O1P	URI	B	226	0.847	22.297	26.105	1.00	62.52	B
ATOM	1667	O2P	URI	B	226	-1.550	21.373	26.227	1.00	62.13	B
ATOM	1668	O5'	URI	B	226	0.377	19.940	25.549	1.00	61.29	B
ATOM	1669	C5'	URI	B	226	-0.341	18.874	24.963	1.00	59.62	B
ATOM	1670	C4'	URI	B	226	0.582	17.718	24.726	1.00	59.37	B
ATOM	1671	O4'	URI	B	226	1.675	18.167	23.892	1.00	60.60	B
ATOM	1672	C1'	URI	B	226	2.834	17.419	24.200	1.00	59.54	B
ATOM	1673	N1	URI	B	226	3.915	18.354	24.521	1.00	59.11	B
ATOM	1674	C6	URI	B	226	3.694	19.697	24.700	1.00	59.62	B
ATOM	1675	C2	URI	B	226	5.168	17.823	24.616	1.00	59.24	B
ATOM	1676	O2	URI	B	226	5.371	16.632	24.511	1.00	59.59	B
ATOM	1677	N3	URI	B	226	6.175	18.728	24.844	1.00	60.64	B
ATOM	1678	C4	URI	B	226	6.044	20.091	25.000	1.00	60.95	B
ATOM	1679	O4	URI	B	226	7.060	20.794	25.038	1.00	61.49	B
ATOM	1680	C5	URI	B	226	4.689	20.565	24.935	1.00	61.22	B
ATOM	1681	C2'	URI	B	226	2.488	16.492	25.363	1.00	59.58	B
ATOM	1682	O2'	URI	B	226	2.192	15.200	24.876	1.00	58.65	B
ATOM	1683	C3'	URI	B	226	1.290	17.209	25.964	1.00	57.85	B
ATOM	1684	O3'	URI	B	226	0.465	16.313	26.675	1.00	56.69	B
ATOM	1685	P	CYT	B	227	0.658	16.159	28.251	1.00	57.65	B
ATOM	1686	O1P	CYT	B	227	0.953	17.503	28.816	1.00	56.13	B
ATOM	1687	O2P	CYT	B	227	-0.457	15.353	28.811	1.00	56.22	B
ATOM	1688	O5'	CYT	B	227	1.971	15.279	28.349	1.00	57.28	B
ATOM	1689	C5'	CYT	B	227	1.877	13.870	28.337	1.00	55.41	B
ATOM	1690	C4'	CYT	B	227	3.244	13.264	28.279	1.00	53.68	B
ATOM	1691	O4'	CYT	B	227	4.029	13.948	27.268	1.00	52.41	B
ATOM	1692	C1'	CYT	B	227	5.398	13.840	27.599	1.00	50.88	B
ATOM	1693	N1	CYT	B	227	5.955	15.185	27.709	1.00	50.59	B
ATOM	1694	C6	CYT	B	227	5.158	16.293	27.758	1.00	51.57	B
ATOM	1695	C2	CYT	B	227	7.318	15.307	27.771	1.00	51.15	B
ATOM	1696	O2	CYT	B	227	7.992	14.281	27.735	1.00	54.89	B
ATOM	1697	N3	CYT	B	227	7.881	16.526	27.873	1.00	50.46	B
ATOM	1698	C4	CYT	B	227	7.113	17.605	27.915	1.00	49.35	B
ATOM	1699	N4	CYT	B	227	7.714	18.782	28.001	1.00	48.12	B
ATOM	1700	C5	CYT	B	227	5.692	17.518	27.865	1.00	51.06	B
ATOM	1701	C2'	CYT	B	227	5.469	13.096	28.934	1.00	52.88	B
ATOM	1702	O2'	CYT	B	227	5.667	11.713	28.694	1.00	50.84	B
ATOM	1703	C3'	CYT	B	227	4.101	13.428	29.516	1.00	52.37	B
ATOM	1704	O3'	CYT	B	227	3.707	12.532	30.547	1.00	53.39	B
ATOM	1705	P	GUA	B	228	2.977	13.107	31.856	1.00	58.66	B
ATOM	1706	O1P	GUA	B	228	2.593	14.499	31.527	1.00	58.56	B
ATOM	1707	O2P	GUA	B	228	1.946	12.152	32.350	1.00	57.37	B

ATOM	1708	O5'	GUA	B	228	4.121	13.179	32.958	1.00	57.02	B
ATOM	1709	C5'	GUA	B	228	4.727	11.996	33.453	1.00	55.04	B
ATOM	1710	C4'	GUA	B	228	6.155	11.907	32.973	1.00	53.26	B
ATOM	1711	O4'	GUA	B	228	6.327	12.734	31.799	1.00	53.28	B
ATOM	1712	C1'	GUA	B	228	7.670	13.187	31.733	1.00	53.19	B
ATOM	1713	N9	GUA	B	228	7.665	14.646	31.617	1.00	53.81	B
ATOM	1714	C4	GUA	B	228	8.769	15.465	31.480	1.00	53.76	B
ATOM	1715	N3	GUA	B	228	10.056	15.062	31.408	1.00	53.36	B
ATOM	1716	C2	GUA	B	228	10.888	16.083	31.303	1.00	51.84	B
ATOM	1717	N2	GUA	B	228	12.197	15.867	31.210	1.00	48.75	B
ATOM	1718	N1	GUA	B	228	10.494	17.391	31.283	1.00	52.85	B
ATOM	1719	C6	GUA	B	228	9.181	17.832	31.371	1.00	53.04	B
ATOM	1720	O6	GUA	B	228	8.941	19.044	31.379	1.00	54.64	B
ATOM	1721	C5	GUA	B	228	8.270	16.748	31.461	1.00	53.49	B
ATOM	1722	N7	GUA	B	228	6.884	16.741	31.554	1.00	54.44	B
ATOM	1723	C8	GUA	B	228	6.571	15.475	31.643	1.00	53.87	B
ATOM	1724	C2'	GUA	B	228	8.376	12.685	32.995	1.00	51.78	B
ATOM	1725	O2'	GUA	B	228	9.059	11.488	32.715	1.00	50.97	B
ATOM	1726	C3'	GUA	B	228	7.203	12.443	33.928	1.00	51.60	B
ATOM	1727	O3'	GUA	B	228	7.537	11.436	34.862	1.00	49.14	B
ATOM	1728	P	CYT	B	229	7.620	11.796	36.417	1.00	50.14	B
ATOM	1729	O1P	CYT	B	229	6.710	12.935	36.705	1.00	47.87	B
ATOM	1730	O2P	CYT	B	229	7.440	10.515	37.145	1.00	46.49	B
ATOM	1731	O5'	CYT	B	229	9.129	12.286	36.571	1.00	49.59	B
ATOM	1732	C5'	CYT	B	229	10.191	11.415	36.193	1.00	49.36	B
ATOM	1733	C4'	CYT	B	229	11.493	12.164	36.075	1.00	48.50	B
ATOM	1734	O4'	CYT	B	229	11.513	12.942	34.849	1.00	49.47	B
ATOM	1735	C1'	CYT	B	229	12.233	14.144	35.061	1.00	48.55	B
ATOM	1736	N1	CYT	B	229	11.286	15.263	34.997	1.00	49.12	B
ATOM	1737	C6	CYT	B	229	9.957	15.064	35.225	1.00	49.46	B
ATOM	1738	C2	CYT	B	229	11.767	16.539	34.704	1.00	48.95	B
ATOM	1739	O2	CYT	B	229	12.978	16.692	34.508	1.00	49.05	B
ATOM	1740	N3	CYT	B	229	10.904	17.571	34.639	1.00	48.91	B
ATOM	1741	C4	CYT	B	229	9.607	17.366	34.849	1.00	49.64	B
ATOM	1742	N4	CYT	B	229	8.782	18.413	34.749	1.00	50.11	B
ATOM	1743	C5	CYT	B	229	9.091	16.078	35.164	1.00	50.66	B
ATOM	1744	C2'	CYT	B	229	12.851	14.011	36.449	1.00	48.95	B
ATOM	1745	O2'	CYT	B	229	14.059	13.294	36.360	1.00	50.48	B
ATOM	1746	C3'	CYT	B	229	11.785	13.190	37.145	1.00	48.46	B
ATOM	1747	O3'	CYT	B	229	12.322	12.584	38.306	1.00	48.74	B
ATOM	1748	P	GUA	B	230	12.075	13.265	39.739	1.00	49.49	B
ATOM	1749	O1P	GUA	B	230	10.667	13.756	39.761	1.00	50.64	B
ATOM	1750	O2P	GUA	B	230	12.531	12.304	40.772	1.00	50.34	B
ATOM	1751	O5'	GUA	B	230	13.046	14.531	39.748	1.00	49.69	B
ATOM	1752	C5'	GUA	B	230	14.427	14.394	39.426	1.00	49.57	B
ATOM	1753	C4'	GUA	B	230	15.145	15.706	39.621	1.00	51.51	B
ATOM	1754	O4'	GUA	B	230	14.571	16.710	38.741	1.00	50.73	B
ATOM	1755	C1'	GUA	B	230	14.206	17.841	39.496	1.00	51.22	B
ATOM	1756	N9	GUA	B	230	12.995	18.399	38.911	1.00	52.23	B
ATOM	1757	C4	GUA	B	230	12.803	19.701	38.511	1.00	52.74	B
ATOM	1758	N3	GUA	B	230	13.715	20.692	38.570	1.00	52.74	B
ATOM	1759	C2	GUA	B	230	13.224	21.838	38.141	1.00	52.25	B
ATOM	1760	N2	GUA	B	230	13.984	22.930	38.134	1.00	52.25	B
ATOM	1761	N1	GUA	B	230	11.947	22.000	37.689	1.00	54.49	B
ATOM	1762	C6	GUA	B	230	10.988	21.001	37.622	1.00	53.15	B
ATOM	1763	O6	GUA	B	230	9.858	21.269	37.217	1.00	54.25	B
ATOM	1764	C5	GUA	B	230	11.498	19.759	38.071	1.00	53.53	B
ATOM	1765	N7	GUA	B	230	10.889	18.515	38.169	1.00	54.01	B
ATOM	1766	C8	GUA	B	230	11.816	17.740	38.669	1.00	53.29	B
ATOM	1767	C2'	GUA	B	230	13.988	17.331	40.921	1.00	52.69	B
ATOM	1768	O2'	GUA	B	230	14.157	18.372	41.864	1.00	50.69	B

ATOM	1769	C3'	GUA	B	230	15.087	16.285	41.031	1.00	52.14	B
ATOM	1770	O3'	GUA	B	230	16.296	16.965	41.337	1.00	54.91	B
ATOM	1771	P	URI	B	231	17.564	16.146	41.868	1.00	55.02	B
ATOM	1772	O1P	URI	B	231	18.266	17.052	42.816	1.00	52.02	B
ATOM	1773	O2P	URI	B	231	17.113	14.812	42.330	1.00	53.85	B
ATOM	1774	O5'	URI	B	231	18.437	15.930	40.553	1.00	55.40	B
ATOM	1775	C5'	URI	B	231	18.892	17.033	39.779	1.00	58.23	B
ATOM	1776	C4'	URI	B	231	20.114	16.640	38.978	1.00	62.66	B
ATOM	1777	O4'	URI	B	231	21.297	16.816	39.804	1.00	62.63	B
ATOM	1778	C1'	URI	B	231	21.910	15.562	40.032	1.00	62.26	B
ATOM	1779	N1	URI	B	231	22.357	15.523	41.428	1.00	61.38	B
ATOM	1780	C6	URI	B	231	21.550	15.957	42.452	1.00	60.83	B
ATOM	1781	C2	URI	B	231	23.620	15.042	41.669	1.00	61.54	B
ATOM	1782	O2	URI	B	231	24.344	14.639	40.770	1.00	62.29	B
ATOM	1783	N3	URI	B	231	24.004	15.046	42.994	1.00	61.42	B
ATOM	1784	C4	URI	B	231	23.245	15.466	44.082	1.00	62.36	B
ATOM	1785	O4	URI	B	231	23.705	15.380	45.230	1.00	61.50	B
ATOM	1786	C5	URI	B	231	21.938	15.944	43.737	1.00	62.52	B
ATOM	1787	C2'	URI	B	231	20.865	14.510	39.681	1.00	63.79	B
ATOM	1788	O2'	URI	B	231	21.499	13.302	39.319	1.00	63.87	B
ATOM	1789	C3'	URI	B	231	20.174	15.189	38.510	1.00	65.22	B
ATOM	1790	O3'	URI	B	231	21.013	15.093	37.361	1.00	70.38	B
ATOM	1791	P	GUA	B	232	20.580	14.153	36.129	1.00	74.73	B
ATOM	1792	O1P	GUA	B	232	21.816	13.664	35.458	1.00	74.60	B
ATOM	1793	O2P	GUA	B	232	19.583	13.168	36.633	1.00	74.73	B
ATOM	1794	O5'	GUA	B	232	19.843	15.167	35.143	1.00	74.06	B
ATOM	1795	C5'	GUA	B	232	20.363	15.429	33.850	1.00	72.97	B
ATOM	1796	C4'	GUA	B	232	20.387	16.911	33.587	1.00	72.59	B
ATOM	1797	O4'	GUA	B	232	20.097	17.653	34.800	1.00	71.37	B
ATOM	1798	C1'	GUA	B	232	20.742	18.918	34.738	1.00	72.27	B
ATOM	1799	N9	GUA	B	232	21.585	19.057	35.920	1.00	74.07	B
ATOM	1800	C4	GUA	B	232	21.247	19.648	37.115	1.00	74.59	B
ATOM	1801	N3	GUA	B	232	20.058	20.216	37.415	1.00	74.20	B
ATOM	1802	C2	GUA	B	232	20.036	20.686	38.651	1.00	73.75	B
ATOM	1803	N2	GUA	B	232	18.936	21.287	39.118	1.00	74.62	B
ATOM	1804	N1	GUA	B	232	21.093	20.604	39.522	1.00	74.18	B
ATOM	1805	C6	GUA	B	232	22.326	20.027	39.236	1.00	73.75	B
ATOM	1806	O6	GUA	B	232	23.213	20.004	40.097	1.00	72.28	B
ATOM	1807	C5	GUA	B	232	22.366	19.522	37.914	1.00	74.36	B
ATOM	1808	N7	GUA	B	232	23.388	18.877	37.231	1.00	74.62	B
ATOM	1809	C8	GUA	B	232	22.880	18.621	36.057	1.00	74.00	B
ATOM	1810	C2'	GUA	B	232	21.583	18.938	33.459	1.00	71.92	B
ATOM	1811	O2'	GUA	B	232	20.918	19.654	32.445	1.00	69.55	B
ATOM	1812	C3'	GUA	B	232	21.741	17.448	33.177	1.00	72.97	B
ATOM	1813	O3'	GUA	B	232	21.999	17.156	31.808	1.00	75.27	B
ATOM	1814	P	ADE	B	233	23.030	15.978	31.426	1.00	76.87	B
ATOM	1815	O1P	ADE	B	233	23.450	16.242	30.030	1.00	74.87	B
ATOM	1816	O2P	ADE	B	233	24.054	15.871	32.501	1.00	75.85	B
ATOM	1817	O5'	ADE	B	233	22.153	14.648	31.448	1.00	76.78	B
ATOM	1818	C5'	ADE	B	233	22.695	13.427	31.937	1.00	79.21	B
ATOM	1819	C4'	ADE	B	233	21.916	12.252	31.394	1.00	81.95	B
ATOM	1820	O4'	ADE	B	233	20.571	12.264	31.942	1.00	82.72	B
ATOM	1821	C1'	ADE	B	233	19.624	12.348	30.893	1.00	83.95	B
ATOM	1822	N9	ADE	B	233	18.556	13.252	31.322	1.00	84.20	B
ATOM	1823	C4	ADE	B	233	17.675	13.035	32.354	1.00	84.30	B
ATOM	1824	N3	ADE	B	233	17.600	11.956	33.152	1.00	84.48	B
ATOM	1825	C2	ADE	B	233	16.645	12.111	34.060	1.00	82.93	B
ATOM	1826	N1	ADE	B	233	15.824	13.142	34.252	1.00	82.81	B
ATOM	1827	C6	ADE	B	233	15.928	14.213	33.439	1.00	83.48	B
ATOM	1828	N6	ADE	B	233	15.124	15.256	33.649	1.00	83.96	B
ATOM	1829	C5	ADE	B	233	16.891	14.169	32.424	1.00	83.94	B

ATOM	1830	N7	ADE B 233	17.246	15.074	31.434	1.00	84.28	B
ATOM	1831	C8	ADE B 233	18.234	14.484	30.809	1.00	84.16	B
ATOM	1832	C2'	ADE B 233	20.386	12.855	29.669	1.00	84.22	B
ATOM	1833	O2'	ADE B 233	19.747	12.438	28.476	1.00	85.53	B
ATOM	1834	C3'	ADE B 233	21.752	12.215	29.881	1.00	83.72	B
ATOM	1835	O3'	ADE B 233	21.764	10.871	29.415	1.00	84.83	B
ATOM	1836	P	URI B 234	22.914	10.397	28.401	1.00	86.34	B
ATOM	1837	O1P	URI B 234	23.017	11.423	27.324	1.00	84.26	B
ATOM	1838	O2P	URI B 234	24.114	10.047	29.213	1.00	85.14	B
ATOM	1839	O5'	URI B 234	22.334	9.072	27.744	1.00	85.10	B
ATOM	1840	C5'	URI B 234	21.216	9.128	26.873	1.00	86.55	B
ATOM	1841	C4'	URI B 234	20.265	8.015	27.203	1.00	87.02	B
ATOM	1842	O4'	URI B 234	20.923	6.767	26.879	1.00	88.52	B
ATOM	1843	C1'	URI B 234	21.153	6.018	28.050	1.00	89.34	B
ATOM	1844	N1	URI B 234	22.532	5.514	28.019	1.00	90.55	B
ATOM	1845	C6	URI B 234	23.609	6.374	28.072	1.00	91.32	B
ATOM	1846	C2	URI B 234	22.717	4.140	27.963	1.00	91.37	B
ATOM	1847	O2	URI B 234	21.793	3.343	27.862	1.00	91.49	B
ATOM	1848	N3	URI B 234	24.027	3.732	28.025	1.00	91.61	B
ATOM	1849	C4	URI B 234	25.146	4.536	28.125	1.00	91.41	B
ATOM	1850	O4	URI B 234	26.232	4.014	28.352	1.00	89.82	B
ATOM	1851	C5	URI B 234	24.876	5.944	28.124	1.00	91.21	B
ATOM	1852	C2'	URI B 234	20.862	6.909	29.257	1.00	89.26	B
ATOM	1853	O2'	URI B 234	20.314	6.159	30.326	1.00	90.70	B
ATOM	1854	C3'	URI B 234	19.908	7.950	28.677	1.00	87.78	B
ATOM	1855	O3'	URI B 234	18.518	7.722	28.903	1.00	86.95	B
ATOM	1856	P	ADE B 235	17.817	6.342	28.445	1.00	85.44	B
ATOM	1857	O1P	ADE B 235	16.896	6.684	27.332	1.00	85.69	B
ATOM	1858	O2P	ADE B 235	18.801	5.257	28.260	1.00	85.00	B
ATOM	1859	O5'	ADE B 235	16.940	5.955	29.723	1.00	83.93	B
ATOM	1860	C5'	ADE B 235	17.569	5.536	30.939	1.00	78.89	B
ATOM	1861	C4'	ADE B 235	17.097	6.374	32.112	1.00	75.23	B
ATOM	1862	O4'	ADE B 235	17.610	7.722	32.010	1.00	73.86	B
ATOM	1863	C1'	ADE B 235	16.680	8.625	32.585	1.00	72.80	B
ATOM	1864	N9	ADE B 235	16.308	9.611	31.570	1.00	72.57	B
ATOM	1865	C4	ADE B 235	15.277	10.511	31.650	1.00	70.87	B
ATOM	1866	N3	ADE B 235	14.391	10.645	32.650	1.00	70.49	B
ATOM	1867	C2	ADE B 235	13.561	11.645	32.402	1.00	69.46	B
ATOM	1868	N1	ADE B 235	13.518	12.466	31.347	1.00	69.42	B
ATOM	1869	C6	ADE B 235	14.423	12.301	30.360	1.00	70.02	B
ATOM	1870	N6	ADE B 235	14.388	13.125	29.309	1.00	69.14	B
ATOM	1871	C5	ADE B 235	15.351	11.271	30.500	1.00	70.73	B
ATOM	1872	N7	ADE B 235	16.388	10.837	29.687	1.00	72.05	B
ATOM	1873	C8	ADE B 235	16.920	9.851	30.362	1.00	73.00	B
ATOM	1874	C2'	ADE B 235	15.490	7.812	33.092	1.00	72.76	B
ATOM	1875	O2'	ADE B 235	15.621	7.556	34.472	1.00	72.46	B
ATOM	1876	C3'	ADE B 235	15.598	6.553	32.249	1.00	73.17	B
ATOM	1877	O3'	ADE B 235	15.059	5.455	32.949	1.00	72.86	B
ATOM	1878	P	ADE B 236	13.960	4.541	32.236	1.00	74.90	B
ATOM	1879	O1P	ADE B 236	13.971	3.192	32.860	1.00	74.45	B
ATOM	1880	O2P	ADE B 236	14.181	4.677	30.771	1.00	75.24	B
ATOM	1881	O5'	ADE B 236	12.590	5.251	32.625	1.00	72.45	B
ATOM	1882	C5'	ADE B 236	12.365	5.699	33.953	1.00	68.86	B
ATOM	1883	C4'	ADE B 236	11.428	6.869	33.942	1.00	66.95	B
ATOM	1884	O4'	ADE B 236	12.138	8.049	33.482	1.00	66.04	B
ATOM	1885	C1'	ADE B 236	11.263	8.863	32.724	1.00	64.52	B
ATOM	1886	N9	ADE B 236	11.860	9.062	31.406	1.00	63.45	B
ATOM	1887	C4	ADE B 236	11.669	10.123	30.554	1.00	62.72	B
ATOM	1888	N3	ADE B 236	10.874	11.186	30.739	1.00	62.70	B
ATOM	1889	C2	ADE B 236	10.977	12.031	29.717	1.00	62.13	B
ATOM	1890	N1	ADE B 236	11.730	11.942	28.615	1.00	61.58	B

ATOM	1891	C6	ADE B 236	12.519	10.860	28.464	1.00	62.43	B
ATOM	1892	N6	ADE B 236	13.283	10.775	27.376	1.00	62.70	B
ATOM	1893	C5	ADE B 236	12.494	9.890	29.472	1.00	62.23	B
ATOM	1894	N7	ADE B 236	13.169	8.695	29.623	1.00	64.68	B
ATOM	1895	C8	ADE B 236	12.754	8.242	30.781	1.00	64.90	B
ATOM	1896	C2'	ADE B 236	9.897	8.178	32.720	1.00	65.12	B
ATOM	1897	O2'	ADE B 236	9.114	8.717	33.769	1.00	64.29	B
ATOM	1898	C3'	ADE B 236	10.287	6.724	32.959	1.00	66.25	B
ATOM	1899	O3'	ADE B 236	9.240	5.963	33.556	1.00	67.09	B
ATOM	1900	P	ADE B 237	8.247	5.102	32.626	1.00	67.47	B
ATOM	1901	O1P	ADE B 237	7.456	4.214	33.517	1.00	66.06	B
ATOM	1902	O2P	ADE B 237	9.027	4.525	31.498	1.00	66.74	B
ATOM	1903	O5'	ADE B 237	7.246	6.171	32.000	1.00	68.64	B
ATOM	1904	C5'	ADE B 237	6.265	6.819	32.800	1.00	67.38	B
ATOM	1905	C4'	ADE B 237	5.743	8.032	32.078	1.00	68.03	B
ATOM	1906	O4'	ADE B 237	6.855	8.925	31.800	1.00	66.67	B
ATOM	1907	C1'	ADE B 237	6.721	9.468	30.501	1.00	66.14	B
ATOM	1908	N9	ADE B 237	7.805	8.942	29.684	1.00	63.47	B
ATOM	1909	C4	ADE B 237	8.462	9.597	28.671	1.00	63.64	B
ATOM	1910	N3	ADE B 237	8.243	10.847	28.229	1.00	62.98	B
ATOM	1911	C2	ADE B 237	9.062	11.139	27.214	1.00	63.10	B
ATOM	1912	N1	ADE B 237	10.009	10.380	26.642	1.00	63.59	B
ATOM	1913	C6	ADE B 237	10.208	9.129	27.121	1.00	64.56	B
ATOM	1914	N6	ADE B 237	11.163	8.372	26.566	1.00	65.06	B
ATOM	1915	C5	ADE B 237	9.395	8.698	28.187	1.00	64.20	B
ATOM	1916	N7	ADE B 237	9.328	7.501	28.884	1.00	64.99	B
ATOM	1917	C8	ADE B 237	8.373	7.700	29.759	1.00	63.91	B
ATOM	1918	C2'	ADE B 237	5.343	9.059	29.982	1.00	67.57	B
ATOM	1919	O2'	ADE B 237	4.385	10.037	30.334	1.00	67.19	B
ATOM	1920	C3'	ADE B 237	5.121	7.745	30.719	1.00	68.79	B
ATOM	1921	O3'	ADE B 237	3.729	7.493	30.869	1.00	71.20	B
ATOM	1922	P	URI B 238	2.956	6.603	29.778	1.00	74.04	B
ATOM	1923	O1P	URI B 238	3.699	5.327	29.602	1.00	71.72	B
ATOM	1924	O2P	URI B 238	1.516	6.576	30.161	1.00	73.12	B
ATOM	1925	O5'	URI B 238	3.110	7.429	28.426	1.00	74.17	B
ATOM	1926	C5'	URI B 238	2.071	8.280	27.968	1.00	75.65	B
ATOM	1927	C4'	URI B 238	2.636	9.338	27.061	1.00	77.79	B
ATOM	1928	O4'	URI B 238	4.078	9.354	27.176	1.00	78.47	B
ATOM	1929	C1'	URI B 238	4.599	10.049	26.060	1.00	78.56	B
ATOM	1930	N1	URI B 238	5.849	9.413	25.623	1.00	77.53	B
ATOM	1931	C6	URI B 238	6.286	8.214	26.139	1.00	77.02	B
ATOM	1932	C2	URI B 238	6.582	10.081	24.656	1.00	77.77	B
ATOM	1933	O2	URI B 238	6.228	11.146	24.181	1.00	77.80	B
ATOM	1934	N3	URI B 238	7.743	9.461	24.267	1.00	77.99	B
ATOM	1935	C4	URI B 238	8.242	8.267	24.736	1.00	78.47	B
ATOM	1936	O4	URI B 238	9.287	7.818	24.248	1.00	79.15	B
ATOM	1937	C5	URI B 238	7.430	7.632	25.744	1.00	77.52	B
ATOM	1938	C2'	URI B 238	3.504	10.061	24.988	1.00	79.64	B
ATOM	1939	O2'	URI B 238	2.993	11.371	24.840	1.00	79.89	B
ATOM	1940	C3'	URI B 238	2.483	9.088	25.574	1.00	80.64	B
ATOM	1941	O3'	URI B 238	1.159	9.356	25.120	1.00	83.61	B
ATOM	1942	P	GUA B 239	0.479	8.386	24.021	1.00	85.15	B
ATOM	1943	O1P	GUA B 239	0.691	6.974	24.448	1.00	83.25	B
ATOM	1944	O2P	GUA B 239	-0.903	8.895	23.802	1.00	83.34	B
ATOM	1945	O5'	GUA B 239	1.346	8.601	22.697	1.00	84.02	B
ATOM	1946	C5'	GUA B 239	0.951	9.532	21.690	1.00	83.77	B
ATOM	1947	C4'	GUA B 239	2.166	10.049	20.965	1.00	84.35	B
ATOM	1948	O4'	GUA B 239	3.330	9.793	21.785	1.00	84.90	B
ATOM	1949	C1'	GUA B 239	4.285	9.050	21.062	1.00	85.92	B
ATOM	1950	N9	GUA B 239	4.778	7.985	21.933	1.00	87.13	B
ATOM	1951	C4	GUA B 239	6.051	7.456	21.941	1.00	87.25	B

ATOM	1952	N3	GUA B 239	7.077	7.839	21.144	1.00	87.13	B
ATOM	1953	C2	GUA B 239	8.180	7.132	21.381	1.00	88.19	B
ATOM	1954	N2	GUA B 239	9.298	7.367	20.668	1.00	88.31	B
ATOM	1955	N1	GUA B 239	8.272	6.139	22.331	1.00	87.85	B
ATOM	1956	C6	GUA B 239	7.235	5.731	23.168	1.00	87.29	B
ATOM	1957	O6	GUA B 239	7.434	4.834	24.001	1.00	86.46	B
ATOM	1958	C5	GUA B 239	6.033	6.473	22.918	1.00	87.33	B
ATOM	1959	N7	GUA B 239	4.775	6.391	23.514	1.00	85.92	B
ATOM	1960	C8	GUA B 239	4.067	7.304	22.903	1.00	86.41	B
ATOM	1961	C2'	GUA B 239	3.623	8.504	19.797	1.00	85.49	B
ATOM	1962	O2'	GUA B 239	4.541	8.533	18.723	1.00	84.99	B
ATOM	1963	C3'	GUA B 239	2.427	9.436	19.596	1.00	85.70	B
ATOM	1964	O3'	GUA B 239	2.688	10.452	18.636	1.00	87.60	B
ATOM	1965	P	URI B 240	1.613	10.740	17.474	1.00	88.74	B
ATOM	1966	O1P	URI B 240	2.153	10.101	16.246	1.00	88.37	B
ATOM	1967	O2P	URI B 240	0.261	10.358	17.977	1.00	87.64	B
ATOM	1968	O5'	URI B 240	1.646	12.324	17.273	1.00	87.55	B
ATOM	1969	C5'	URI B 240	0.919	13.196	18.146	1.00	86.34	B
ATOM	1970	C4'	URI B 240	0.733	14.555	17.503	1.00	84.94	B
ATOM	1971	O4'	URI B 240	1.698	15.501	18.037	1.00	82.31	B
ATOM	1972	C1'	URI B 240	2.250	16.239	16.974	1.00	80.29	B
ATOM	1973	N1	URI B 240	3.592	16.675	17.364	1.00	77.74	B
ATOM	1974	C6	URI B 240	4.588	15.774	17.632	1.00	76.62	B
ATOM	1975	C2	URI B 240	3.815	18.027	17.440	1.00	76.37	B
ATOM	1976	O2	URI B 240	2.945	18.846	17.226	1.00	75.50	B
ATOM	1977	N3	URI B 240	5.092	18.384	17.778	1.00	75.78	B
ATOM	1978	C4	URI B 240	6.145	17.536	18.044	1.00	76.60	B
ATOM	1979	O4	URI B 240	7.260	18.008	18.270	1.00	76.78	B
ATOM	1980	C5	URI B 240	5.824	16.146	17.961	1.00	76.69	B
ATOM	1981	C2'	URI B 240	2.248	15.272	15.797	1.00	82.64	B
ATOM	1982	O2'	URI B 240	2.361	15.966	14.569	1.00	80.34	B
ATOM	1983	C3'	URI B 240	0.893	14.605	15.985	1.00	85.43	B
ATOM	1984	O3'	URI B 240	-0.116	15.438	15.448	1.00	90.12	B
ATOM	1985	P	ADE B 241	-1.384	14.778	14.732	1.00	93.02	B
ATOM	1986	O1P	ADE B 241	-1.786	13.583	15.518	1.00	92.58	B
ATOM	1987	O2P	ADE B 241	-1.052	14.636	13.293	1.00	93.42	B
ATOM	1988	O5'	ADE B 241	-2.504	15.892	14.882	1.00	94.43	B
ATOM	1989	C5'	ADE B 241	-2.321	17.164	14.290	1.00	98.62	B
ATOM	1990	C4'	ADE B 241	-3.623	17.918	14.270	1.00	101.48	B
ATOM	1991	O4'	ADE B 241	-4.073	18.103	15.643	1.00	104.39	B
ATOM	1992	C1'	ADE B 241	-4.272	19.481	15.893	1.00	106.54	B
ATOM	1993	N9	ADE B 241	-3.081	19.989	16.588	1.00	110.86	B
ATOM	1994	C4	ADE B 241	-3.062	20.942	17.584	1.00	113.37	B
ATOM	1995	N3	ADE B 241	-4.118	21.576	18.131	1.00	113.96	B
ATOM	1996	C2	ADE B 241	-3.717	22.446	19.062	1.00	114.64	B
ATOM	1997	N1	ADE B 241	-2.472	22.739	19.474	1.00	115.18	B
ATOM	1998	C6	ADE B 241	-1.430	22.093	18.899	1.00	115.28	B
ATOM	1999	N6	ADE B 241	-0.191	22.407	19.290	1.00	115.87	B
ATOM	2000	C5	ADE B 241	-1.722	21.128	17.905	1.00	114.44	B
ATOM	2001	N7	ADE B 241	-0.912	20.294	17.142	1.00	113.34	B
ATOM	2002	C8	ADE B 241	-1.760	19.639	16.383	1.00	111.93	B
ATOM	2003	C2'	ADE B 241	-4.500	20.115	14.516	1.00	103.51	B
ATOM	2004	O2'	ADE B 241	-5.835	19.954	14.076	1.00	102.72	B
ATOM	2005	C3'	ADE B 241	-3.522	19.316	13.673	1.00	101.05	B
ATOM	2006	O3'	ADE B 241	-3.853	19.293	12.295	1.00	96.50	B
ATOM	2007	P	GUA B 242	-2.673	19.182	11.212	1.00	94.24	B
ATOM	2008	O1P	GUA B 242	-1.663	18.220	11.733	1.00	93.59	B
ATOM	2009	O2P	GUA B 242	-3.265	18.957	9.870	1.00	95.12	B
ATOM	2010	O5'	GUA B 242	-2.028	20.638	11.239	1.00	91.69	B
ATOM	2011	C5'	GUA B 242	-1.297	21.089	12.377	1.00	86.38	B
ATOM	2012	C4'	GUA B 242	-1.773	22.460	12.811	1.00	81.63	B

ATOM	2013	O4'	GUA	B	242	-1.631	22.555	14.259	1.00	80.15	B
ATOM	2014	C1'	GUA	B	242	-0.711	23.581	14.575	1.00	78.46	B
ATOM	2015	N9	GUA	B	242	0.627	22.994	14.628	1.00	77.67	B
ATOM	2016	C4	GUA	B	242	1.808	23.664	14.862	1.00	77.32	B
ATOM	2017	N3	GUA	B	242	1.936	24.983	15.111	1.00	77.22	B
ATOM	2018	C2	GUA	B	242	3.201	25.332	15.287	1.00	76.26	B
ATOM	2019	N2	GUA	B	242	3.508	26.613	15.545	1.00	76.47	B
ATOM	2020	N1	GUA	B	242	4.255	24.455	15.223	1.00	74.74	B
ATOM	2021	C6	GUA	B	242	4.147	23.096	14.967	1.00	74.67	B
ATOM	2022	O6	GUA	B	242	5.159	22.401	14.926	1.00	73.56	B
ATOM	2023	C5	GUA	B	242	2.795	22.705	14.778	1.00	76.45	B
ATOM	2024	N7	GUA	B	242	2.248	21.457	14.511	1.00	76.62	B
ATOM	2025	C8	GUA	B	242	0.963	21.675	14.437	1.00	77.01	B
ATOM	2026	C2'	GUA	B	242	-0.855	24.575	13.428	1.00	78.62	B
ATOM	2027	O2'	GUA	B	242	-2.017	25.361	13.596	1.00	78.37	B
ATOM	2028	C3'	GUA	B	242	-0.963	23.625	12.241	1.00	78.98	B
ATOM	2029	O3'	GUA	B	242	-1.642	24.238	11.153	1.00	75.65	B
ATOM	2030	P	CYT	B	243	-0.826	25.160	10.121	1.00	73.97	B
ATOM	2031	O1P	CYT	B	243	0.183	24.313	9.425	1.00	71.15	B
ATOM	2032	O2P	CYT	B	243	-1.840	25.894	9.323	1.00	73.99	B
ATOM	2033	O5'	CYT	B	243	-0.071	26.213	11.050	1.00	70.50	B
ATOM	2034	C5'	CYT	B	243	-0.772	27.305	11.636	1.00	67.12	B
ATOM	2035	C4'	CYT	B	243	0.185	28.422	11.972	1.00	65.60	B
ATOM	2036	O4'	CYT	B	243	1.082	27.971	13.020	1.00	65.34	B
ATOM	2037	C1'	CYT	B	243	2.391	28.452	12.778	1.00	62.94	B
ATOM	2038	N1	CYT	B	243	3.265	27.302	12.537	1.00	59.80	B
ATOM	2039	C6	CYT	B	243	2.747	26.090	12.183	1.00	58.51	B
ATOM	2040	C2	CYT	B	243	4.637	27.466	12.679	1.00	58.89	B
ATOM	2041	O2	CYT	B	243	5.072	28.582	12.996	1.00	59.23	B
ATOM	2042	N3	CYT	B	243	5.454	26.410	12.471	1.00	57.13	B
ATOM	2043	C4	CYT	B	243	4.937	25.226	12.144	1.00	56.84	B
ATOM	2044	N4	CYT	B	243	5.771	24.202	11.982	1.00	55.44	B
ATOM	2045	C5	CYT	B	243	3.539	25.036	11.978	1.00	57.53	B
ATOM	2046	C2'	CYT	B	243	2.319	29.390	11.577	1.00	65.14	B
ATOM	2047	O2'	CYT	B	243	2.176	30.720	12.026	1.00	67.49	B
ATOM	2048	C3'	CYT	B	243	1.096	28.858	10.838	1.00	65.51	B
ATOM	2049	O3'	CYT	B	243	0.485	29.886	10.070	1.00	66.47	B
ATOM	2050	P	URI	B	244	1.011	30.180	8.578	1.00	67.88	B
ATOM	2051	O1P	URI	B	244	1.033	28.866	7.888	1.00	68.52	B
ATOM	2052	O2P	URI	B	244	0.249	31.306	7.986	1.00	67.85	B
ATOM	2053	O5'	URI	B	244	2.512	30.663	8.781	1.00	65.45	B
ATOM	2054	C5'	URI	B	244	2.797	32.001	9.150	1.00	64.15	B
ATOM	2055	C4'	URI	B	244	4.286	32.210	9.234	1.00	63.22	B
ATOM	2056	O4'	URI	B	244	4.831	31.277	10.202	1.00	63.70	B
ATOM	2057	C1'	URI	B	244	6.142	30.901	9.812	1.00	64.16	B
ATOM	2058	N1	URI	B	244	6.167	29.445	9.642	1.00	65.13	B
ATOM	2059	C6	URI	B	244	5.021	28.735	9.364	1.00	65.67	B
ATOM	2060	C2	URI	B	244	7.386	28.811	9.762	1.00	65.43	B
ATOM	2061	O2	URI	B	244	8.413	29.407	10.018	1.00	64.90	B
ATOM	2062	N3	URI	B	244	7.357	27.452	9.571	1.00	65.48	B
ATOM	2063	C4	URI	B	244	6.254	26.680	9.283	1.00	66.10	B
ATOM	2064	O4	URI	B	244	6.395	25.473	9.111	1.00	66.74	B
ATOM	2065	C5	URI	B	244	5.022	27.408	9.184	1.00	66.64	B
ATOM	2066	C2'	URI	B	244	6.460	31.632	8.507	1.00	63.91	B
ATOM	2067	O2'	URI	B	244	7.219	32.795	8.762	1.00	63.56	B
ATOM	2068	C3'	URI	B	244	5.058	31.895	7.965	1.00	63.41	B
ATOM	2069	O3'	URI	B	244	5.008	32.959	7.018	1.00	61.34	B
ATOM	2070	P	ADE	B	245	5.762	32.802	5.605	1.00	60.75	B
ATOM	2071	O1P	ADE	B	245	5.276	33.892	4.731	1.00	60.89	B
ATOM	2072	O2P	ADE	B	245	5.658	31.404	5.142	1.00	61.86	B
ATOM	2073	O5'	ADE	B	245	7.284	33.065	5.989	1.00	61.11	B

ATOM	2074	C5'	ADE B 245	8.355	32.596	5.182	1.00	61.47	B
ATOM	2075	C4'	ADE B 245	9.642	32.754	5.941	1.00	63.53	B
ATOM	2076	O4'	ADE B 245	9.548	31.926	7.129	1.00	64.13	B
ATOM	2077	C1'	ADE B 245	10.835	31.458	7.482	1.00	64.97	B
ATOM	2078	N9	ADE B 245	10.828	30.001	7.449	1.00	65.17	B
ATOM	2079	C4	ADE B 245	11.902	29.220	7.783	1.00	66.29	B
ATOM	2080	N3	ADE B 245	13.100	29.638	8.220	1.00	67.68	B
ATOM	2081	C2	ADE B 245	13.910	28.603	8.430	1.00	68.28	B
ATOM	2082	N1	ADE B 245	13.678	27.298	8.259	1.00	67.73	B
ATOM	2083	C6	ADE B 245	12.463	26.911	7.812	1.00	67.75	B
ATOM	2084	N6	ADE B 245	12.240	25.606	7.633	1.00	68.72	B
ATOM	2085	C5	ADE B 245	11.506	27.918	7.561	1.00	66.45	B
ATOM	2086	N7	ADE B 245	10.191	27.876	7.118	1.00	64.62	B
ATOM	2087	C8	ADE B 245	9.835	29.136	7.073	1.00	64.32	B
ATOM	2088	C2'	ADE B 245	11.829	32.017	6.462	1.00	65.52	B
ATOM	2089	O2'	ADE B 245	12.446	33.165	6.996	1.00	66.76	B
ATOM	2090	C3'	ADE B 245	10.929	32.305	5.262	1.00	65.07	B
ATOM	2091	O3'	ADE B 245	11.483	33.339	4.441	1.00	65.59	B
ATOM	2092	P	ADE B 246	12.649	32.985	3.381	1.00	68.47	B
ATOM	2093	O1P	ADE B 246	13.185	34.225	2.771	1.00	66.95	B
ATOM	2094	O2P	ADE B 246	12.164	31.892	2.496	1.00	68.82	B
ATOM	2095	O5'	ADE B 246	13.818	32.421	4.292	1.00	66.81	B
ATOM	2096	C5'	ADE B 246	14.494	33.274	5.189	1.00	66.99	B
ATOM	2097	C4'	ADE B 246	15.813	32.676	5.539	1.00	68.35	B
ATOM	2098	O4'	ADE B 246	15.615	31.599	6.489	1.00	68.88	B
ATOM	2099	C1'	ADE B 246	16.508	30.539	6.198	1.00	69.64	B
ATOM	2100	N9	ADE B 246	15.709	29.386	5.804	1.00	70.53	B
ATOM	2101	C4	ADE B 246	16.123	28.081	5.802	1.00	70.88	B
ATOM	2102	N3	ADE B 246	17.327	27.613	6.165	1.00	70.57	B
ATOM	2103	C2	ADE B 246	17.369	26.292	6.037	1.00	72.08	B
ATOM	2104	N1	ADE B 246	16.417	25.452	5.616	1.00	73.37	B
ATOM	2105	C6	ADE B 246	15.219	25.966	5.250	1.00	73.57	B
ATOM	2106	N6	ADE B 246	14.269	25.139	4.810	1.00	75.70	B
ATOM	2107	C5	ADE B 246	15.047	27.345	5.348	1.00	71.37	B
ATOM	2108	N7	ADE B 246	13.969	28.168	5.071	1.00	70.32	B
ATOM	2109	C8	ADE B 246	14.412	29.368	5.356	1.00	70.83	B
ATOM	2110	C2'	ADE B 246	17.394	31.015	5.046	1.00	69.74	B
ATOM	2111	O2'	ADE B 246	18.583	31.628	5.501	1.00	68.86	B
ATOM	2112	C3'	ADE B 246	16.463	31.993	4.360	1.00	69.45	B
ATOM	2113	O3'	ADE B 246	17.170	32.940	3.595	1.00	71.42	B
ATOM	2114	P	ADE B 247	17.302	32.725	2.018	1.00	74.08	B
ATOM	2115	O1P	ADE B 247	18.211	33.790	1.522	1.00	72.22	B
ATOM	2116	O2P	ADE B 247	15.927	32.594	1.449	1.00	71.77	B
ATOM	2117	O5'	ADE B 247	18.077	31.338	1.916	1.00	73.67	B
ATOM	2118	C5'	ADE B 247	19.313	31.159	2.597	1.00	73.69	B
ATOM	2119	C4'	ADE B 247	19.699	29.702	2.626	1.00	74.19	B
ATOM	2120	O4'	ADE B 247	18.730	28.929	3.380	1.00	74.62	B
ATOM	2121	C1'	ADE B 247	18.643	27.623	2.836	1.00	72.69	B
ATOM	2122	N9	ADE B 247	17.276	27.432	2.363	1.00	70.73	B
ATOM	2123	C4	ADE B 247	16.635	26.234	2.170	1.00	69.33	B
ATOM	2124	N3	ADE B 247	17.137	25.003	2.361	1.00	68.40	B
ATOM	2125	C2	ADE B 247	16.219	24.079	2.093	1.00	67.91	B
ATOM	2126	N1	ADE B 247	14.950	24.236	1.690	1.00	67.46	B
ATOM	2127	C6	ADE B 247	14.478	25.487	1.511	1.00	67.48	B
ATOM	2128	N6	ADE B 247	13.212	25.643	1.122	1.00	66.56	B
ATOM	2129	C5	ADE B 247	15.356	26.554	1.753	1.00	68.54	B
ATOM	2130	N7	ADE B 247	15.199	27.929	1.665	1.00	69.46	B
ATOM	2131	C8	ADE B 247	16.363	28.402	2.033	1.00	69.88	B
ATOM	2132	C2'	ADE B 247	19.687	27.545	1.721	1.00	74.57	B
ATOM	2133	O2'	ADE B 247	20.918	27.104	2.257	1.00	75.29	B
ATOM	2134	C3'	ADE B 247	19.759	29.000	1.285	1.00	74.55	B

ATOM	2135	O3'	ADE	B	247	21.008	29.282	0.681	1.00	76.68	B
ATOM	2136	P	ADE	B	248	21.113	29.431	-0.913	1.00	78.64	B
ATOM	2137	O1P	ADE	B	248	22.305	30.276	-1.169	1.00	79.02	B
ATOM	2138	O2P	ADE	B	248	19.800	29.822	-1.487	1.00	77.28	B
ATOM	2139	O5'	ADE	B	248	21.459	27.953	-1.387	1.00	80.68	B
ATOM	2140	C5'	ADE	B	248	22.772	27.608	-1.819	1.00	81.26	B
ATOM	2141	C4'	ADE	B	248	23.671	27.365	-0.630	1.00	81.73	B
ATOM	2142	O4'	ADE	B	248	22.939	26.704	0.436	1.00	81.21	B
ATOM	2143	C1'	ADE	B	248	23.827	25.861	1.159	1.00	82.59	B
ATOM	2144	N9	ADE	B	248	23.358	24.484	1.048	1.00	82.41	B
ATOM	2145	C4	ADE	B	248	24.067	23.360	1.389	1.00	82.27	B
ATOM	2146	N3	ADE	B	248	25.319	23.302	1.863	1.00	82.48	B
ATOM	2147	C2	ADE	B	248	25.670	22.041	2.111	1.00	82.79	B
ATOM	2148	N1	ADE	B	248	24.964	20.917	1.954	1.00	83.05	B
ATOM	2149	C6	ADE	B	248	23.706	21.011	1.475	1.00	83.89	B
ATOM	2150	N6	ADE	B	248	22.992	19.890	1.329	1.00	83.78	B
ATOM	2151	C5	ADE	B	248	23.219	22.295	1.164	1.00	83.22	B
ATOM	2152	N7	ADE	B	248	22.003	22.737	0.668	1.00	83.80	B
ATOM	2153	C8	ADE	B	248	22.140	24.039	0.613	1.00	83.41	B
ATOM	2154	C2'	ADE	B	248	25.209	26.036	0.536	1.00	83.45	B
ATOM	2155	O2'	ADE	B	248	25.901	27.065	1.212	1.00	85.26	B
ATOM	2156	C3'	ADE	B	248	24.827	26.415	-0.882	1.00	83.04	B
ATOM	2157	O3'	ADE	B	248	25.890	27.072	-1.550	1.00	84.14	B
ATOM	2158	P	ADE	B	249	26.230	26.683	-3.069	1.00	85.50	B
ATOM	2159	O1P	ADE	B	249	27.452	27.452	-3.406	1.00	84.72	B
ATOM	2160	O2P	ADE	B	249	25.009	26.835	-3.911	1.00	84.17	B
ATOM	2161	O5'	ADE	B	249	26.583	25.132	-2.986	1.00	85.53	B
ATOM	2162	C5'	ADE	B	249	27.427	24.630	-1.956	1.00	87.01	B
ATOM	2163	C4'	ADE	B	249	27.413	23.117	-1.958	1.00	89.05	B
ATOM	2164	O4'	ADE	B	249	26.309	22.642	-1.135	1.00	89.34	B
ATOM	2165	C1'	ADE	B	249	25.689	21.529	-1.761	1.00	87.86	B
ATOM	2166	N9	ADE	B	249	24.405	21.978	-2.284	1.00	86.17	B
ATOM	2167	C4	ADE	B	249	23.339	21.182	-2.615	1.00	85.23	B
ATOM	2168	N3	ADE	B	249	23.254	19.847	-2.499	1.00	84.97	B
ATOM	2169	C2	ADE	B	249	22.076	19.418	-2.932	1.00	84.39	B
ATOM	2170	N1	ADE	B	249	21.049	20.117	-3.427	1.00	83.82	B
ATOM	2171	C6	ADE	B	249	21.166	21.455	-3.527	1.00	83.86	B
ATOM	2172	N6	ADE	B	249	20.139	22.150	-4.016	1.00	83.30	B
ATOM	2173	C5	ADE	B	249	22.371	22.035	-3.105	1.00	84.70	B
ATOM	2174	N7	ADE	B	249	22.815	23.349	-3.073	1.00	85.43	B
ATOM	2175	C8	ADE	B	249	24.020	23.261	-2.572	1.00	85.15	B
ATOM	2176	C2'	ADE	B	249	26.616	21.102	-2.899	1.00	88.41	B
ATOM	2177	O2'	ADE	B	249	27.588	20.176	-2.454	1.00	87.62	B
ATOM	2178	C3'	ADE	B	249	27.192	22.450	-3.309	1.00	89.31	B
ATOM	2179	O3'	ADE	B	249	28.405	22.304	-4.033	1.00	91.31	B
ATOM	2180	P	GUA	B	250	28.374	22.328	-5.640	1.00	92.94	B
ATOM	2181	O1P	GUA	B	250	27.440	23.404	-6.075	1.00	91.54	B
ATOM	2182	O2P	GUA	B	250	29.774	22.320	-6.136	1.00	93.37	B
ATOM	2183	O5'	GUA	B	250	27.712	20.935	-6.024	1.00	91.73	B
ATOM	2184	C5'	GUA	B	250	26.822	20.839	-7.121	1.00	89.58	B
ATOM	2185	C4'	GUA	B	250	25.917	19.655	-6.941	1.00	88.31	B
ATOM	2186	O4'	GUA	B	250	25.089	19.860	-5.762	1.00	87.08	B
ATOM	2187	C1'	GUA	B	250	23.726	19.682	-6.102	1.00	86.14	B
ATOM	2188	N9	GUA	B	250	23.146	21.005	-6.315	1.00	84.76	B
ATOM	2189	C4	GUA	B	250	21.856	21.278	-6.690	1.00	83.37	B
ATOM	2190	N3	GUA	B	250	20.888	20.366	-6.902	1.00	82.60	B
ATOM	2191	C2	GUA	B	250	19.756	20.929	-7.278	1.00	81.86	B
ATOM	2192	N2	GUA	B	250	18.689	20.160	-7.531	1.00	81.52	B
ATOM	2193	N1	GUA	B	250	19.588	22.286	-7.433	1.00	81.35	B
ATOM	2194	C6	GUA	B	250	20.574	23.244	-7.219	1.00	81.91	B
ATOM	2195	O6	GUA	B	250	20.322	24.442	-7.397	1.00	81.19	B

ATOM	2196	C5	GUA	B	250	21.791	22.651	-6.811	1.00	82.53	B
ATOM	2197	N7	GUA	B	250	23.010	23.231	-6.498	1.00	82.75	B
ATOM	2198	C8	GUA	B	250	23.781	22.219	-6.205	1.00	84.50	B
ATOM	2199	C2'	GUA	B	250	23.740	18.841	-7.380	1.00	87.17	B
ATOM	2200	O2'	GUA	B	250	23.898	17.468	-7.079	1.00	86.01	B
ATOM	2201	C3'	GUA	B	250	24.948	19.437	-8.089	1.00	88.35	B
ATOM	2202	O3'	GUA	B	250	25.535	18.561	-9.039	1.00	89.61	B
ATOM	2203	P	GUA	B	251	25.721	19.050	-10.558	1.00	90.34	B
ATOM	2204	O1P	GUA	B	251	25.813	20.535	-10.570	1.00	88.07	B
ATOM	2205	O2P	GUA	B	251	26.809	18.240	-11.162	1.00	88.48	B
ATOM	2206	O5'	GUA	B	251	24.340	18.632	-11.230	1.00	89.75	B
ATOM	2207	C5'	GUA	B	251	23.603	17.524	-10.724	1.00	88.88	B
ATOM	2208	C4'	GUA	B	251	22.141	17.681	-11.048	1.00	88.40	B
ATOM	2209	O4'	GUA	B	251	21.513	18.539	-10.062	1.00	87.77	B
ATOM	2210	C1'	GUA	B	251	20.486	19.303	-10.681	1.00	86.45	B
ATOM	2211	N9	GUA	B	251	20.798	20.717	-10.503	1.00	83.86	B
ATOM	2212	C4	GUA	B	251	19.947	21.778	-10.691	1.00	81.12	B
ATOM	2213	N3	GUA	B	251	18.662	21.702	-11.096	1.00	78.40	B
ATOM	2214	C2	GUA	B	251	18.095	22.898	-11.166	1.00	78.93	B
ATOM	2215	N2	GUA	B	251	16.813	23.013	-11.541	1.00	76.86	B
ATOM	2216	N1	GUA	B	251	18.742	24.075	-10.867	1.00	79.94	B
ATOM	2217	C6	GUA	B	251	20.067	24.177	-10.441	1.00	81.36	B
ATOM	2218	O6	GUA	B	251	20.556	25.296	-10.172	1.00	80.76	B
ATOM	2219	C5	GUA	B	251	20.685	22.900	-10.367	1.00	81.39	B
ATOM	2220	N7	GUA	B	251	21.976	22.551	-9.999	1.00	82.18	B
ATOM	2221	C8	GUA	B	251	22.000	21.250	-10.098	1.00	83.36	B
ATOM	2222	C2'	GUA	B	251	20.428	18.880	-12.149	1.00	87.55	B
ATOM	2223	O2'	GUA	B	251	19.444	17.881	-12.316	1.00	87.74	B
ATOM	2224	C3'	GUA	B	251	21.848	18.371	-12.367	1.00	88.81	B
ATOM	2225	O3'	GUA	B	251	21.920	17.441	-13.436	1.00	90.30	B
ATOM	2226	P	ADE	B	252	22.780	17.800	-14.739	1.00	91.05	B
ATOM	2227	O1P	ADE	B	252	23.910	18.660	-14.296	1.00	90.39	B
ATOM	2228	O2P	ADE	B	252	23.054	16.533	-15.459	1.00	89.96	B
ATOM	2229	O5'	ADE	B	252	21.781	18.671	-15.620	1.00	91.95	B
ATOM	2230	PC	ADE	B	252	20.987	18.578	-20.533	1.00	104.90	B
ATOM	2231	O1C	ADE	B	252	22.147	19.251	-21.189	1.00	103.28	B
ATOM	2232	O2C	ADE	B	252	20.449	17.555	-21.467	1.00	104.27	B
ATOM	2233	O3'	ADE	B	252	21.484	17.850	-19.180	1.00	101.71	B
ATOM	2234	C5'	ADE	B	252	20.538	18.128	-16.046	1.00	94.48	B
ATOM	2235	C4'	ADE	B	252	20.126	18.735	-17.362	1.00	96.88	B
ATOM	2236	O4'	ADE	B	252	19.568	20.051	-17.110	1.00	97.25	B
ATOM	2237	C1'	ADE	B	252	19.932	20.933	-18.158	1.00	97.83	B
ATOM	2238	N9	ADE	B	252	20.812	21.964	-17.615	1.00	96.09	B
ATOM	2239	C4	ADE	B	252	20.556	23.312	-17.556	1.00	94.96	B
ATOM	2240	N3	ADE	B	252	19.437	23.947	-17.947	1.00	94.36	B
ATOM	2241	C2	ADE	B	252	19.555	25.259	-17.758	1.00	93.41	B
ATOM	2242	N1	ADE	B	252	20.587	25.953	-17.262	1.00	93.74	B
ATOM	2243	C6	ADE	B	252	21.697	25.278	-16.878	1.00	94.05	B
ATOM	2244	N6	ADE	B	252	22.733	25.964	-16.384	1.00	93.71	B
ATOM	2245	C5	ADE	B	252	21.696	23.887	-17.025	1.00	94.40	B
ATOM	2246	N7	ADE	B	252	22.647	22.920	-16.734	1.00	95.22	B
ATOM	2247	C8	ADE	B	252	22.074	21.799	-17.094	1.00	95.90	B
ATOM	2248	C2'	ADE	B	252	20.677	20.106	-19.204	1.00	99.30	B
ATOM	2249	O2'	ADE	B	252	19.816	19.648	-20.230	1.00	101.99	B
ATOM	2250	C3'	ADE	B	252	21.251	18.984	-18.355	1.00	98.41	B
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ATOM	2251	O6P	GUA	C	401	19.129	13.958	103.041	1.00	82.82	C
ATOM	2252	O3P	GUA	C	401	19.403	15.512	101.028	1.00	79.10	C
ATOM	2253	O4P	GUA	C	401	21.349	15.070	102.651	1.00	84.74	C
ATOM	2254	O5P	GUA	C	401	20.623	13.217	101.168	1.00	81.84	C
ATOM	2255	P2	GUA	C	401	20.137	14.411	101.990	1.00	84.24	C

ATOM	2256	P	GUA	C	401	20.421	16.053	99.862	1.00	74.41	C
ATOM	2257	O1P	GUA	C	401	20.862	14.926	98.946	1.00	74.15	C
ATOM	2258	O2P	GUA	C	401	21.628	16.722	100.495	1.00	73.92	C
ATOM	2259	O5'	GUA	C	401	19.661	17.160	98.943	1.00	70.87	C
ATOM	2260	C5'	GUA	C	401	18.262	17.037	98.648	1.00	65.12	C
ATOM	2261	C4'	GUA	C	401	17.543	18.329	98.955	1.00	61.77	C
ATOM	2262	O4'	GUA	C	401	17.378	18.484	100.385	1.00	61.70	C
ATOM	2263	C1'	GUA	C	401	17.296	19.867	100.708	1.00	61.13	C
ATOM	2264	N9	GUA	C	401	18.352	20.172	101.671	1.00	61.89	C
ATOM	2265	C4	GUA	C	401	18.674	21.411	102.173	1.00	62.05	C
ATOM	2266	N3	GUA	C	401	18.048	22.569	101.884	1.00	63.41	C
ATOM	2267	C2	GUA	C	401	18.613	23.598	102.490	1.00	63.99	C
ATOM	2268	N2	GUA	C	401	18.118	24.834	102.308	1.00	65.06	C
ATOM	2269	N1	GUA	C	401	19.703	23.495	103.315	1.00	62.94	C
ATOM	2270	C6	GUA	C	401	20.363	22.313	103.626	1.00	62.01	C
ATOM	2271	O6	GUA	C	401	21.352	22.334	104.371	1.00	61.22	C
ATOM	2272	C5	GUA	C	401	19.766	21.203	102.988	1.00	61.68	C
ATOM	2273	N7	GUA	C	401	20.106	19.860	103.023	1.00	60.80	C
ATOM	2274	C8	GUA	C	401	19.241	19.287	102.233	1.00	61.30	C
ATOM	2275	C2'	GUA	C	401	17.485	20.633	99.396	1.00	61.41	C
ATOM	2276	O2'	GUA	C	401	16.246	20.987	98.818	1.00	60.56	C
ATOM	2277	C3'	GUA	C	401	18.242	19.614	98.560	1.00	60.57	C
ATOM	2278	O3'	GUA	C	401	18.078	19.901	97.186	1.00	60.34	C
ATOM	2279	P	CYT	C	402	19.241	20.679	96.403	1.00	61.86	C
ATOM	2280	O1P	CYT	C	402	20.524	20.130	96.912	1.00	59.62	C
ATOM	2281	O2P	CYT	C	402	18.953	20.634	94.946	1.00	59.04	C
ATOM	2282	O5'	CYT	C	402	19.105	22.187	96.914	1.00	60.52	C
ATOM	2283	C5'	CYT	C	402	17.883	22.915	96.767	1.00	58.50	C
ATOM	2284	C4'	CYT	C	402	18.073	24.367	97.163	1.00	57.08	C
ATOM	2285	O4'	CYT	C	402	18.105	24.471	98.613	1.00	56.35	C
ATOM	2286	C1'	CYT	C	402	19.046	25.456	99.004	1.00	56.26	C
ATOM	2287	N1	CYT	C	402	20.152	24.804	99.712	1.00	54.77	C
ATOM	2288	C6	CYT	C	402	20.387	23.472	99.565	1.00	55.24	C
ATOM	2289	C2	CYT	C	402	20.968	25.572	100.529	1.00	55.02	C
ATOM	2290	O2	CYT	C	402	20.734	26.778	100.644	1.00	55.36	C
ATOM	2291	N3	CYT	C	402	21.999	24.986	101.173	1.00	56.15	C
ATOM	2292	C4	CYT	C	402	22.227	23.685	101.017	1.00	54.69	C
ATOM	2293	N4	CYT	C	402	23.260	23.146	101.663	1.00	53.49	C
ATOM	2294	C5	CYT	C	402	21.407	22.879	100.191	1.00	55.59	C
ATOM	2295	C2'	CYT	C	402	19.544	26.136	97.733	1.00	57.33	C
ATOM	2296	O2'	CYT	C	402	18.766	27.279	97.489	1.00	58.09	C
ATOM	2297	C3'	CYT	C	402	19.362	25.031	96.697	1.00	57.73	C
ATOM	2298	O3'	CYT	C	402	19.225	25.584	95.387	1.00	58.74	C
ATOM	2299	P	GUA	C	403	20.522	25.744	94.435	1.00	61.06	C
ATOM	2300	O1P	GUA	C	403	21.422	24.578	94.631	1.00	58.35	C
ATOM	2301	O2P	GUA	C	403	20.042	26.077	93.069	1.00	59.89	C
ATOM	2302	O5'	GUA	C	403	21.291	27.014	95.018	1.00	60.71	C
ATOM	2303	C5'	GUA	C	403	20.609	28.245	95.250	1.00	59.30	C
ATOM	2304	C4'	GUA	C	403	21.497	29.205	96.019	1.00	58.89	C
ATOM	2305	O4'	GUA	C	403	21.602	28.788	97.407	1.00	56.96	C
ATOM	2306	C1'	GUA	C	403	22.882	29.133	97.907	1.00	57.03	C
ATOM	2307	N9	GUA	C	403	23.580	27.909	98.280	1.00	56.30	C
ATOM	2308	C4	GUA	C	403	24.724	27.815	99.036	1.00	56.42	C
ATOM	2309	N3	GUA	C	403	25.397	28.845	99.594	1.00	57.34	C
ATOM	2310	C2	GUA	C	403	26.467	28.435	100.254	1.00	57.44	C
ATOM	2311	N2	GUA	C	403	27.242	29.308	100.887	1.00	57.79	C
ATOM	2312	N1	GUA	C	403	26.852	27.129	100.346	1.00	58.64	C
ATOM	2313	C6	GUA	C	403	26.177	26.054	99.782	1.00	58.04	C
ATOM	2314	O6	GUA	C	403	26.616	24.907	99.929	1.00	59.05	C
ATOM	2315	C5	GUA	C	403	25.020	26.474	99.083	1.00	56.53	C
ATOM	2316	N7	GUA	C	403	24.074	25.736	98.390	1.00	56.87	C

ATOM	2317	C8	GUA	C	403	23.240	26.628	97.934	1.00	56.90	C
ATOM	2318	C2'	GUA	C	403	23.602	29.888	96.793	1.00	57.48	C
ATOM	2319	O2'	GUA	C	403	23.309	31.256	96.911	1.00	58.00	C
ATOM	2320	C3'	GUA	C	403	22.943	29.297	95.563	1.00	58.20	C
ATOM	2321	O3'	GUA	C	403	23.064	30.206	94.483	1.00	59.54	C
ATOM	2322	P	CYT	C	404	24.252	30.020	93.414	1.00	62.17	C
ATOM	2323	O1P	CYT	C	404	24.328	28.585	93.021	1.00	60.43	C
ATOM	2324	O2P	CYT	C	404	24.071	31.055	92.367	1.00	60.24	C
ATOM	2325	O5'	CYT	C	404	25.561	30.375	94.245	1.00	59.69	C
ATOM	2326	C5'	CYT	C	404	25.812	31.702	94.657	1.00	58.57	C
ATOM	2327	C4'	CYT	C	404	27.087	31.757	95.437	1.00	58.59	C
ATOM	2328	O4'	CYT	C	404	26.953	30.922	96.612	1.00	58.87	C
ATOM	2329	C1'	CYT	C	404	28.217	30.366	96.943	1.00	60.79	C
ATOM	2330	N1	CYT	C	404	28.099	28.897	96.917	1.00	63.43	C
ATOM	2331	C6	CYT	C	404	26.989	28.297	96.391	1.00	64.17	C
ATOM	2332	C2	CYT	C	404	29.140	28.113	97.449	1.00	64.26	C
ATOM	2333	O2	CYT	C	404	30.148	28.671	97.898	1.00	65.75	C
ATOM	2334	N3	CYT	C	404	29.017	26.768	97.454	1.00	63.85	C
ATOM	2335	C4	CYT	C	404	27.921	26.198	96.948	1.00	63.56	C
ATOM	2336	N4	CYT	C	404	27.837	24.872	96.985	1.00	63.44	C
ATOM	2337	C5	CYT	C	404	26.861	26.964	96.384	1.00	63.47	C
ATOM	2338	C2'	CYT	C	404	29.213	30.917	95.922	1.00	60.30	C
ATOM	2339	O2'	CYT	C	404	29.788	32.110	96.419	1.00	59.22	C
ATOM	2340	C3'	CYT	C	404	28.298	31.176	94.737	1.00	59.12	C
ATOM	2341	O3'	CYT	C	404	28.874	32.138	93.870	1.00	60.41	C
ATOM	2342	P	GUA	C	405	29.058	31.800	92.313	1.00	61.74	C
ATOM	2343	O1P	GUA	C	405	27.858	31.061	91.852	1.00	62.51	C
ATOM	2344	O2P	GUA	C	405	29.451	33.057	91.636	1.00	62.92	C
ATOM	2345	O5'	GUA	C	405	30.300	30.809	92.261	1.00	59.83	C
ATOM	2346	C5'	GUA	C	405	31.594	31.286	91.938	1.00	55.90	C
ATOM	2347	C4'	GUA	C	405	32.500	31.127	93.120	1.00	55.47	C
ATOM	2348	O4'	GUA	C	405	31.704	30.707	94.256	1.00	56.80	C
ATOM	2349	C1'	GUA	C	405	32.410	29.728	95.004	1.00	57.76	C
ATOM	2350	N9	GUA	C	405	31.719	28.450	94.860	1.00	58.84	C
ATOM	2351	C4	GUA	C	405	32.102	27.246	95.395	1.00	58.87	C
ATOM	2352	N3	GUA	C	405	33.195	27.026	96.142	1.00	59.93	C
ATOM	2353	C2	GUA	C	405	33.291	25.767	96.511	1.00	59.79	C
ATOM	2354	N2	GUA	C	405	34.328	25.368	97.258	1.00	59.82	C
ATOM	2355	N1	GUA	C	405	32.381	24.806	96.176	1.00	59.90	C
ATOM	2356	C6	GUA	C	405	31.255	25.014	95.400	1.00	59.29	C
ATOM	2357	O6	GUA	C	405	30.510	24.076	95.143	1.00	61.07	C
ATOM	2358	C5	GUA	C	405	31.142	26.349	95.000	1.00	59.13	C
ATOM	2359	N7	GUA	C	405	30.178	26.969	94.225	1.00	60.31	C
ATOM	2360	C8	GUA	C	405	30.562	28.213	94.168	1.00	60.29	C
ATOM	2361	C2'	GUA	C	405	33.822	29.694	94.434	1.00	56.55	C
ATOM	2362	O2'	GUA	C	405	34.605	30.659	95.099	1.00	56.61	C
ATOM	2363	C3'	GUA	C	405	33.543	30.040	92.984	1.00	55.45	C
ATOM	2364	O3'	GUA	C	405	34.691	30.557	92.361	1.00	55.55	C
ATOM	2365	P	GUA	C	406	35.407	29.710	91.213	1.00	59.15	C
ATOM	2366	O1P	GUA	C	406	34.348	28.968	90.477	1.00	58.47	C
ATOM	2367	O2P	GUA	C	406	36.287	30.642	90.475	1.00	59.19	C
ATOM	2368	O5'	GUA	C	406	36.327	28.690	92.023	1.00	59.02	C
ATOM	2369	C5'	GUA	C	406	37.191	29.170	93.049	1.00	60.68	C
ATOM	2370	C4'	GUA	C	406	37.996	28.040	93.648	1.00	61.84	C
ATOM	2371	O4'	GUA	C	406	37.229	27.387	94.701	1.00	63.42	C
ATOM	2372	C1'	GUA	C	406	37.474	25.985	94.671	1.00	62.97	C
ATOM	2373	N9	GUA	C	406	36.247	25.298	94.264	1.00	63.61	C
ATOM	2374	C4	GUA	C	406	35.986	23.955	94.391	1.00	62.31	C
ATOM	2375	N3	GUA	C	406	36.819	23.036	94.915	1.00	62.46	C
ATOM	2376	C2	GUA	C	406	36.282	21.828	94.914	1.00	63.04	C
ATOM	2377	N2	GUA	C	406	36.972	20.790	95.410	1.00	63.23	C

ATOM	2378	N1	GUA	C	406	35.028	21.545	94.431	1.00	61.67	C
ATOM	2379	C6	GUA	C	406	34.152	22.475	93.891	1.00	60.40	C
ATOM	2380	O6	GUA	C	406	33.040	22.110	93.494	1.00	58.01	C
ATOM	2381	C5	GUA	C	406	34.714	23.778	93.887	1.00	61.21	C
ATOM	2382	N7	GUA	C	406	34.185	24.985	93.452	1.00	61.85	C
ATOM	2383	C8	GUA	C	406	35.127	25.855	93.690	1.00	63.00	C
ATOM	2384	C2'	GUA	C	406	38.643	25.785	93.709	1.00	61.67	C
ATOM	2385	O2'	GUA	C	406	39.842	25.986	94.423	1.00	61.44	C
ATOM	2386	C3'	GUA	C	406	38.391	26.908	92.714	1.00	61.32	C
ATOM	2387	O3'	GUA	C	406	39.575	27.226	91.992	1.00	61.04	C
ATOM	2388	P	CYT	C	407	39.696	26.813	90.441	1.00	62.09	C
ATOM	2389	O1P	CYT	C	407	38.390	27.100	89.786	1.00	60.46	C
ATOM	2390	O2P	CYT	C	407	40.938	27.411	89.900	1.00	61.54	C
ATOM	2391	O5'	CYT	C	407	39.905	25.237	90.475	1.00	62.16	C
ATOM	2392	C5'	CYT	C	407	40.898	24.665	91.310	1.00	64.28	C
ATOM	2393	C4'	CYT	C	407	40.632	23.197	91.503	1.00	65.55	C
ATOM	2394	O4'	CYT	C	407	39.418	23.007	92.269	1.00	65.83	C
ATOM	2395	C1'	CYT	C	407	38.826	21.770	91.907	1.00	65.87	C
ATOM	2396	N1	CYT	C	407	37.451	22.028	91.465	1.00	65.12	C
ATOM	2397	C6	CYT	C	407	37.117	23.212	90.878	1.00	65.22	C
ATOM	2398	C2	CYT	C	407	36.490	21.042	91.653	1.00	64.19	C
ATOM	2399	O2	CYT	C	407	36.823	19.981	92.188	1.00	64.69	C
ATOM	2400	N3	CYT	C	407	35.225	21.267	91.252	1.00	63.31	C
ATOM	2401	C4	CYT	C	407	34.906	22.425	90.680	1.00	63.47	C
ATOM	2402	N4	CYT	C	407	33.645	22.608	90.301	1.00	63.66	C
ATOM	2403	C5	CYT	C	407	35.866	23.449	90.473	1.00	64.34	C
ATOM	2404	C2'	CYT	C	407	39.701	21.163	90.810	1.00	67.10	C
ATOM	2405	O2'	CYT	C	407	40.644	20.291	91.403	1.00	68.84	C
ATOM	2406	C3'	CYT	C	407	40.360	22.410	90.238	1.00	66.94	C
ATOM	2407	O3'	CYT	C	407	41.586	22.095	89.599	1.00	68.23	C
ATOM	2408	P	GUA	C	408	41.689	22.166	88.002	1.00	70.32	C
ATOM	2409	O1P	GUA	C	408	40.649	23.080	87.472	1.00	68.95	C
ATOM	2410	O2P	GUA	C	408	43.111	22.392	87.664	1.00	70.47	C
ATOM	2411	O5'	GUA	C	408	41.345	20.690	87.551	1.00	70.99	C
ATOM	2412	C5'	GUA	C	408	42.147	19.625	88.008	1.00	73.91	C
ATOM	2413	C4'	GUA	C	408	41.779	18.368	87.287	1.00	75.11	C
ATOM	2414	O4'	GUA	C	408	40.379	18.115	87.519	1.00	75.66	C
ATOM	2415	C1'	GUA	C	408	39.857	17.389	86.431	1.00	74.76	C
ATOM	2416	N9	GUA	C	408	38.630	18.047	85.997	1.00	72.57	C
ATOM	2417	C4	GUA	C	408	37.432	17.423	85.774	1.00	71.47	C
ATOM	2418	N3	GUA	C	408	37.199	16.098	85.901	1.00	70.90	C
ATOM	2419	C2	GUA	C	408	35.948	15.786	85.611	1.00	70.55	C
ATOM	2420	N2	GUA	C	408	35.556	14.509	85.662	1.00	69.17	C
ATOM	2421	N1	GUA	C	408	34.994	16.703	85.241	1.00	70.87	C
ATOM	2422	C6	GUA	C	408	35.208	18.072	85.110	1.00	71.62	C
ATOM	2423	O6	GUA	C	408	34.271	18.811	84.776	1.00	73.46	C
ATOM	2424	C5	GUA	C	408	36.559	18.423	85.405	1.00	71.18	C
ATOM	2425	N7	GUA	C	408	37.200	19.656	85.391	1.00	70.33	C
ATOM	2426	C8	GUA	C	408	38.427	19.384	85.746	1.00	71.47	C
ATOM	2427	C2'	GUA	C	408	40.966	17.271	85.378	1.00	76.55	C
ATOM	2428	O2'	GUA	C	408	41.615	16.012	85.508	1.00	76.60	C
ATOM	2429	C3'	GUA	C	408	41.889	18.415	85.774	1.00	75.72	C
ATOM	2430	O3'	GUA	C	408	43.239	18.127	85.411	1.00	77.71	C
ATOM	2431	P	ADE	C	409	43.631	17.905	83.865	1.00	78.05	C
ATOM	2432	O1P	ADE	C	409	45.116	17.841	83.822	1.00	77.62	C
ATOM	2433	O2P	ADE	C	409	42.909	18.918	83.043	1.00	77.11	C
ATOM	2434	O5'	ADE	C	409	43.084	16.445	83.528	1.00	75.49	C
ATOM	2435	C5'	ADE	C	409	42.285	16.201	82.374	1.00	71.72	C
ATOM	2436	C4'	ADE	C	409	41.693	14.813	82.439	1.00	70.03	C
ATOM	2437	O4'	ADE	C	409	40.734	14.749	83.535	1.00	68.77	C
ATOM	2438	C1'	ADE	C	409	39.546	14.109	83.095	1.00	67.15	C

ATOM	2439	N9	ADE	C	409	38.538	15.134	82.827	1.00	63.77	C
ATOM	2440	C4	ADE	C	409	37.201	14.910	82.610	1.00	61.48	C
ATOM	2441	N3	ADE	C	409	36.566	13.727	82.597	1.00	60.86	C
ATOM	2442	C2	ADE	C	409	35.272	13.896	82.350	1.00	60.34	C
ATOM	2443	N1	ADE	C	409	34.590	15.026	82.133	1.00	59.77	C
ATOM	2444	C6	ADE	C	409	35.261	16.196	82.150	1.00	60.33	C
ATOM	2445	N6	ADE	C	409	34.584	17.323	81.924	1.00	60.45	C
ATOM	2446	C5	ADE	C	409	36.640	16.153	82.402	1.00	60.68	C
ATOM	2447	N7	ADE	C	409	37.604	17.146	82.484	1.00	61.47	C
ATOM	2448	C8	ADE	C	409	38.710	16.490	82.735	1.00	62.04	C
ATOM	2449	C2'	ADE	C	409	39.935	13.373	81.821	1.00	68.85	C
ATOM	2450	O2'	ADE	C	409	40.547	12.152	82.173	1.00	69.62	C
ATOM	2451	C3'	ADE	C	409	40.900	14.379	81.216	1.00	69.51	C
ATOM	2452	O3'	ADE	C	409	41.738	13.788	80.238	1.00	69.60	C
ATOM	2453	P	URI	C	410	41.499	14.124	78.685	1.00	71.45	C
ATOM	2454	O1P	URI	C	410	41.183	15.569	78.541	1.00	69.04	C
ATOM	2455	O2P	URI	C	410	42.648	13.542	77.940	1.00	70.39	C
ATOM	2456	O5'	URI	C	410	40.172	13.320	78.324	1.00	70.02	C
ATOM	2457	C5'	URI	C	410	40.097	11.929	78.575	1.00	70.01	C
ATOM	2458	C4'	URI	C	410	38.670	11.458	78.515	1.00	69.54	C
ATOM	2459	O4'	URI	C	410	37.849	12.157	79.484	1.00	69.30	C
ATOM	2460	C1'	URI	C	410	36.490	12.014	79.104	1.00	69.48	C
ATOM	2461	N1	URI	C	410	35.864	13.337	79.046	1.00	68.66	C
ATOM	2462	C6	URI	C	410	36.592	14.498	79.080	1.00	68.60	C
ATOM	2463	C2	URI	C	410	34.498	13.359	78.915	1.00	69.40	C
ATOM	2464	O2	URI	C	410	33.828	12.342	78.918	1.00	69.84	C
ATOM	2465	N3	URI	C	410	33.944	14.606	78.776	1.00	69.35	C
ATOM	2466	C4	URI	C	410	34.610	15.808	78.765	1.00	69.40	C
ATOM	2467	O4	URI	C	410	33.980	16.842	78.552	1.00	70.68	C
ATOM	2468	C5	URI	C	410	36.028	15.705	78.944	1.00	68.74	C
ATOM	2469	C2'	URI	C	410	36.492	11.412	77.694	1.00	70.35	C
ATOM	2470	O2'	URI	C	410	36.224	10.025	77.741	1.00	72.52	C
ATOM	2471	C3'	URI	C	410	37.907	11.736	77.240	1.00	68.80	C
ATOM	2472	O3'	URI	C	410	38.307	10.895	76.171	1.00	66.35	C
ATOM	2473	P	URI	C	411	37.802	11.224	74.683	1.00	66.37	C
ATOM	2474	O1P	URI	C	411	38.216	12.601	74.317	1.00	65.70	C
ATOM	2475	O2P	URI	C	411	38.191	10.095	73.816	1.00	67.37	C
ATOM	2476	O5'	URI	C	411	36.216	11.211	74.803	1.00	66.35	C
ATOM	2477	C5'	URI	C	411	35.502	9.992	74.705	1.00	65.04	C
ATOM	2478	C4'	URI	C	411	34.034	10.229	74.921	1.00	65.29	C
ATOM	2479	O4'	URI	C	411	33.822	11.266	75.909	1.00	64.72	C
ATOM	2480	C1'	URI	C	411	32.551	11.861	75.680	1.00	64.83	C
ATOM	2481	N1	URI	C	411	32.744	13.300	75.497	1.00	64.62	C
ATOM	2482	C6	URI	C	411	33.986	13.869	75.569	1.00	65.33	C
ATOM	2483	C2	URI	C	411	31.626	14.058	75.254	1.00	64.72	C
ATOM	2484	O2	URI	C	411	30.517	13.575	75.169	1.00	65.12	C
ATOM	2485	N3	URI	C	411	31.857	15.403	75.112	1.00	65.38	C
ATOM	2486	C4	URI	C	411	33.077	16.046	75.186	1.00	66.26	C
ATOM	2487	O4	URI	C	411	33.127	17.274	75.088	1.00	67.41	C
ATOM	2488	C5	URI	C	411	34.188	15.182	75.425	1.00	65.97	C
ATOM	2489	C2'	URI	C	411	31.982	11.214	74.419	1.00	65.19	C
ATOM	2490	O2'	URI	C	411	31.146	10.139	74.799	1.00	65.30	C
ATOM	2491	C3'	URI	C	411	33.264	10.769	73.737	1.00	65.47	C
ATOM	2492	O3'	URI	C	411	33.036	9.746	72.786	1.00	67.90	C
ATOM	2493	P	URI	C	412	33.458	9.981	71.256	1.00	69.75	C
ATOM	2494	O1P	URI	C	412	34.775	10.668	71.271	1.00	67.86	C
ATOM	2495	O2P	URI	C	412	33.316	8.688	70.542	1.00	69.18	C
ATOM	2496	O5'	URI	C	412	32.325	10.965	70.717	1.00	69.11	C
ATOM	2497	C5'	URI	C	412	30.975	10.520	70.646	1.00	67.01	C
ATOM	2498	C4'	URI	C	412	30.031	11.686	70.489	1.00	66.73	C
ATOM	2499	O4'	URI	C	412	30.184	12.623	71.575	1.00	65.01	C

ATOM	2500	C1'	URI	C	412	29.687	13.882	71.158	1.00	63.86	C
ATOM	2501	N1	URI	C	412	30.717	14.892	71.399	1.00	62.20	C
ATOM	2502	C6	URI	C	412	32.002	14.558	71.731	1.00	61.49	C
ATOM	2503	C2	URI	C	412	30.332	16.196	71.274	1.00	61.27	C
ATOM	2504	O2	URI	C	412	29.202	16.515	70.962	1.00	62.77	C
ATOM	2505	N3	URI	C	412	31.312	17.115	71.518	1.00	59.78	C
ATOM	2506	C4	URI	C	412	32.611	16.861	71.861	1.00	59.79	C
ATOM	2507	O4	URI	C	412	33.374	17.804	72.049	1.00	59.40	C
ATOM	2508	C5	URI	C	412	32.941	15.475	71.962	1.00	60.45	C
ATOM	2509	C2'	URI	C	412	29.380	13.779	69.665	1.00	66.11	C
ATOM	2510	O2'	URI	C	412	27.995	13.585	69.466	1.00	67.05	C
ATOM	2511	C3'	URI	C	412	30.221	12.574	69.276	1.00	67.25	C
ATOM	2512	O3'	URI	C	412	29.704	11.954	68.111	1.00	71.00	C
ATOM	2513	P	ADE	C	413	30.718	11.338	67.033	1.00	73.23	C
ATOM	2514	O1P	ADE	C	413	30.203	10.003	66.618	1.00	73.04	C
ATOM	2515	O2P	ADE	C	413	32.098	11.461	67.573	1.00	72.20	C
ATOM	2516	O5'	ADE	C	413	30.585	12.334	65.810	1.00	73.28	C
ATOM	2517	C5'	ADE	C	413	30.645	13.727	66.017	1.00	73.61	C
ATOM	2518	C4'	ADE	C	413	29.751	14.418	65.038	1.00	74.87	C
ATOM	2519	O4'	ADE	C	413	29.847	15.831	65.290	1.00	75.30	C
ATOM	2520	C1'	ADE	C	413	30.475	16.458	64.205	1.00	75.52	C
ATOM	2521	N9	ADE	C	413	31.805	16.884	64.637	1.00	72.95	C
ATOM	2522	C4	ADE	C	413	32.223	18.189	64.754	1.00	71.28	C
ATOM	2523	N3	ADE	C	413	31.532	19.298	64.439	1.00	69.94	C
ATOM	2524	C2	ADE	C	413	32.242	20.389	64.724	1.00	70.10	C
ATOM	2525	N1	ADE	C	413	33.467	20.488	65.256	1.00	69.99	C
ATOM	2526	C6	ADE	C	413	34.128	19.351	65.564	1.00	69.99	C
ATOM	2527	N6	ADE	C	413	35.337	19.444	66.113	1.00	69.89	C
ATOM	2528	C5	ADE	C	413	33.492	18.130	65.296	1.00	70.40	C
ATOM	2529	N7	ADE	C	413	33.887	16.814	65.474	1.00	70.94	C
ATOM	2530	C8	ADE	C	413	32.857	16.116	65.058	1.00	72.68	C
ATOM	2531	C2'	ADE	C	413	30.364	15.552	62.973	1.00	76.97	C
ATOM	2532	O2'	ADE	C	413	29.313	16.035	62.146	1.00	80.11	C
ATOM	2533	C3'	ADE	C	413	30.064	14.164	63.561	1.00	75.75	C
ATOM	2534	O3'	ADE	C	413	28.930	13.511	62.951	1.00	75.06	C
ATOM	2535	P	ADE	C	414	28.765	13.461	61.338	1.00	76.96	C
ATOM	2536	O1P	ADE	C	414	27.335	13.728	61.042	1.00	76.26	C
ATOM	2537	O2P	ADE	C	414	29.811	14.270	60.658	1.00	78.09	C
ATOM	2538	O5'	ADE	C	414	29.092	11.954	60.949	1.00	74.22	C
ATOM	2539	C5'	ADE	C	414	30.427	11.471	61.047	1.00	70.82	C
ATOM	2540	C4'	ADE	C	414	30.851	10.780	59.771	1.00	66.77	C
ATOM	2541	O4'	ADE	C	414	29.773	9.960	59.251	1.00	65.37	C
ATOM	2542	C1'	ADE	C	414	29.876	9.887	57.841	1.00	63.05	C
ATOM	2543	N9	ADE	C	414	28.710	10.543	57.255	1.00	61.54	C
ATOM	2544	C4	ADE	C	414	28.003	10.100	56.168	1.00	59.49	C
ATOM	2545	N3	ADE	C	414	28.217	8.979	55.466	1.00	58.27	C
ATOM	2546	C2	ADE	C	414	27.363	8.889	54.459	1.00	58.36	C
ATOM	2547	N1	ADE	C	414	26.395	9.731	54.090	1.00	60.36	C
ATOM	2548	C6	ADE	C	414	26.211	10.858	54.810	1.00	61.88	C
ATOM	2549	N6	ADE	C	414	25.261	11.719	54.421	1.00	62.50	C
ATOM	2550	C5	ADE	C	414	27.045	11.062	55.922	1.00	60.84	C
ATOM	2551	N7	ADE	C	414	27.123	12.083	56.858	1.00	61.16	C
ATOM	2552	C8	ADE	C	414	28.119	11.723	57.630	1.00	61.66	C
ATOM	2553	C2'	ADE	C	414	31.169	10.612	57.475	1.00	63.77	C
ATOM	2554	O2'	ADE	C	414	32.225	9.683	57.550	1.00	63.04	C
ATOM	2555	C3'	ADE	C	414	31.237	11.646	58.587	1.00	64.95	C
ATOM	2556	O3'	ADE	C	414	32.562	12.156	58.741	1.00	65.26	C
ATOM	2557	P	CYT	C	415	33.103	13.307	57.750	1.00	64.49	C
ATOM	2558	O1P	CYT	C	415	32.556	13.058	56.397	1.00	64.22	C
ATOM	2559	O2P	CYT	C	415	32.929	14.645	58.378	1.00	63.51	C
ATOM	2560	O5'	CYT	C	415	34.657	13.010	57.669	1.00	63.60	C

ATOM	2561	C5'	CYT	C	415	35.129	11.714	57.340	1.00	61.44	C
ATOM	2562	C4'	CYT	C	415	36.619	11.758	57.148	1.00	60.98	C
ATOM	2563	O4'	CYT	C	415	36.914	12.600	55.995	1.00	61.26	C
ATOM	2564	C1'	CYT	C	415	38.068	13.381	56.256	1.00	58.35	C
ATOM	2565	N1	CYT	C	415	37.666	14.787	56.333	1.00	57.21	C
ATOM	2566	C6	CYT	C	415	36.358	15.155	56.196	1.00	57.26	C
ATOM	2567	C2	CYT	C	415	38.647	15.747	56.549	1.00	57.02	C
ATOM	2568	O2	CYT	C	415	39.823	15.383	56.668	1.00	59.07	C
ATOM	2569	N3	CYT	C	415	38.298	17.046	56.625	1.00	55.70	C
ATOM	2570	C4	CYT	C	415	37.024	17.399	56.496	1.00	55.51	C
ATOM	2571	N4	CYT	C	415	36.730	18.693	56.588	1.00	56.00	C
ATOM	2572	C5	CYT	C	415	35.995	16.440	56.270	1.00	56.63	C
ATOM	2573	C2'	CYT	C	415	38.651	12.861	57.566	1.00	58.28	C
ATOM	2574	O2'	CYT	C	415	39.501	11.771	57.275	1.00	58.67	C
ATOM	2575	C3'	CYT	C	415	37.386	12.423	58.280	1.00	59.17	C
ATOM	2576	O3'	CYT	C	415	37.659	11.498	59.322	1.00	57.74	C
ATOM	2577	P	CYT	C	416	37.493	11.963	60.851	1.00	59.52	C
ATOM	2578	O1P	CYT	C	416	36.259	12.797	60.912	1.00	58.54	C
ATOM	2579	O2P	CYT	C	416	37.627	10.769	61.730	1.00	54.71	C
ATOM	2580	O5'	CYT	C	416	38.731	12.941	61.096	1.00	58.54	C
ATOM	2581	C5'	CYT	C	416	40.063	12.480	60.905	1.00	56.26	C
ATOM	2582	C4'	CYT	C	416	41.046	13.602	61.094	1.00	53.74	C
ATOM	2583	O4'	CYT	C	416	40.937	14.552	60.009	1.00	54.50	C
ATOM	2584	C1'	CYT	C	416	41.313	15.837	60.466	1.00	52.76	C
ATOM	2585	N1	CYT	C	416	40.191	16.738	60.245	1.00	52.47	C
ATOM	2586	C6	CYT	C	416	38.959	16.263	59.895	1.00	53.65	C
ATOM	2587	C2	CYT	C	416	40.398	18.085	60.416	1.00	52.84	C
ATOM	2588	O2	CYT	C	416	41.525	18.463	60.740	1.00	53.51	C
ATOM	2589	N3	CYT	C	416	39.366	18.949	60.236	1.00	53.73	C
ATOM	2590	C4	CYT	C	416	38.160	18.482	59.906	1.00	53.74	C
ATOM	2591	N4	CYT	C	416	37.164	19.358	59.753	1.00	53.22	C
ATOM	2592	C5	CYT	C	416	37.921	17.094	59.721	1.00	54.01	C
ATOM	2593	C2'	CYT	C	416	41.598	15.715	61.962	1.00	53.86	C
ATOM	2594	O2'	CYT	C	416	42.981	15.591	62.179	1.00	56.70	C
ATOM	2595	C3'	CYT	C	416	40.826	14.451	62.322	1.00	54.09	C
ATOM	2596	O3'	CYT	C	416	41.376	13.796	63.453	1.00	52.07	C
ATOM	2597	P	GUA	C	417	40.666	13.954	64.877	1.00	50.57	C
ATOM	2598	O1P	GUA	C	417	39.279	13.475	64.689	1.00	50.99	C
ATOM	2599	O2P	GUA	C	417	41.515	13.315	65.909	1.00	49.71	C
ATOM	2600	O5'	GUA	C	417	40.676	15.533	65.098	1.00	49.38	C
ATOM	2601	C5'	GUA	C	417	41.879	16.271	64.953	1.00	51.97	C
ATOM	2602	C4'	GUA	C	417	41.622	17.748	65.133	1.00	57.26	C
ATOM	2603	O4'	GUA	C	417	41.047	18.318	63.925	1.00	57.83	C
ATOM	2604	C1'	GUA	C	417	40.017	19.231	64.270	1.00	59.99	C
ATOM	2605	N9	GUA	C	417	38.746	18.618	63.896	1.00	61.24	C
ATOM	2606	C4	GUA	C	417	37.612	19.249	63.444	1.00	59.92	C
ATOM	2607	N3	GUA	C	417	37.455	20.576	63.273	1.00	59.88	C
ATOM	2608	C2	GUA	C	417	36.240	20.875	62.829	1.00	61.24	C
ATOM	2609	N2	GUA	C	417	35.894	22.158	62.613	1.00	59.68	C
ATOM	2610	N1	GUA	C	417	35.268	19.939	62.568	1.00	61.42	C
ATOM	2611	C6	GUA	C	417	35.416	18.565	62.736	1.00	62.16	C
ATOM	2612	O6	GUA	C	417	34.475	17.800	62.475	1.00	63.58	C
ATOM	2613	C5	GUA	C	417	36.703	18.237	63.214	1.00	61.70	C
ATOM	2614	N7	GUA	C	417	37.250	16.999	63.519	1.00	61.89	C
ATOM	2615	C8	GUA	C	417	38.457	17.272	63.921	1.00	62.05	C
ATOM	2616	C2'	GUA	C	417	40.144	19.478	65.776	1.00	60.59	C
ATOM	2617	O2'	GUA	C	417	41.060	20.524	66.020	1.00	60.70	C
ATOM	2618	C3'	GUA	C	417	40.675	18.134	66.259	1.00	60.19	C
ATOM	2619	O3'	GUA	C	417	41.418	18.282	67.467	1.00	63.36	C
ATOM	2620	P	URI	C	418	40.649	18.448	68.868	1.00	64.75	C
ATOM	2621	O1P	URI	C	418	39.195	18.308	68.586	1.00	64.68	C

ATOM	2622	O2P	URI	C	418	41.292	17.551	69.870	1.00	60.42	C
ATOM	2623	O5'	URI	C	418	40.941	19.967	69.252	1.00	63.59	C
ATOM	2624	C5'	URI	C	418	42.277	20.447	69.381	1.00	63.57	C
ATOM	2625	C4'	URI	C	418	42.293	21.952	69.332	1.00	64.03	C
ATOM	2626	O4'	URI	C	418	41.790	22.373	68.040	1.00	64.53	C
ATOM	2627	C1'	URI	C	418	41.029	23.558	68.183	1.00	64.27	C
ATOM	2628	N1	URI	C	418	39.654	23.276	67.757	1.00	64.25	C
ATOM	2629	C6	URI	C	418	39.136	21.998	67.775	1.00	64.17	C
ATOM	2630	C2	URI	C	418	38.900	24.342	67.338	1.00	63.52	C
ATOM	2631	O2	URI	C	418	39.319	25.477	67.342	1.00	63.70	C
ATOM	2632	N3	URI	C	418	37.630	24.032	66.922	1.00	63.65	C
ATOM	2633	C4	URI	C	418	37.048	22.782	66.896	1.00	63.02	C
ATOM	2634	O4	URI	C	418	35.904	22.659	66.450	1.00	62.11	C
ATOM	2635	C5	URI	C	418	37.892	21.721	67.372	1.00	63.38	C
ATOM	2636	C2'	URI	C	418	41.084	23.960	69.651	1.00	65.55	C
ATOM	2637	O2'	URI	C	418	42.113	24.892	69.868	1.00	67.22	C
ATOM	2638	C3'	URI	C	418	41.362	22.625	70.320	1.00	66.18	C
ATOM	2639	O3'	URI	C	418	42.000	22.835	71.564	1.00	68.22	C
ATOM	2640	P	ADE	C	419	41.108	23.135	72.859	1.00	69.94	C
ATOM	2641	O1P	ADE	C	419	42.038	23.210	74.017	1.00	69.40	C
ATOM	2642	O2P	ADE	C	419	39.974	22.169	72.868	1.00	68.19	C
ATOM	2643	O5'	ADE	C	419	40.535	24.595	72.609	1.00	68.67	C
ATOM	2644	C5'	ADE	C	419	41.334	25.731	72.889	1.00	69.84	C
ATOM	2645	C4'	ADE	C	419	40.592	26.984	72.518	1.00	71.36	C
ATOM	2646	O4'	ADE	C	419	39.995	26.802	71.212	1.00	71.02	C
ATOM	2647	C1'	ADE	C	419	38.859	27.640	71.099	1.00	71.24	C
ATOM	2648	N9	ADE	C	419	37.749	26.831	70.600	1.00	71.50	C
ATOM	2649	C4	ADE	C	419	36.570	27.309	70.086	1.00	71.60	C
ATOM	2650	N3	ADE	C	419	36.211	28.596	69.936	1.00	71.24	C
ATOM	2651	C2	ADE	C	419	34.998	28.680	69.398	1.00	71.83	C
ATOM	2652	N1	ADE	C	419	34.163	27.698	69.022	1.00	71.68	C
ATOM	2653	C6	ADE	C	419	34.554	26.417	69.193	1.00	71.81	C
ATOM	2654	N6	ADE	C	419	33.719	25.440	68.829	1.00	72.19	C
ATOM	2655	C5	ADE	C	419	35.826	26.192	69.751	1.00	71.46	C
ATOM	2656	N7	ADE	C	419	36.525	25.031	70.047	1.00	70.90	C
ATOM	2657	C8	ADE	C	419	37.657	25.463	70.544	1.00	71.01	C
ATOM	2658	C2'	ADE	C	419	38.597	28.251	72.480	1.00	71.58	C
ATOM	2659	O2'	ADE	C	419	39.053	29.588	72.523	1.00	70.81	C
ATOM	2660	C3'	ADE	C	419	39.391	27.314	73.384	1.00	71.75	C
ATOM	2661	O3'	ADE	C	419	39.783	27.926	74.606	1.00	72.07	C
ATOM	2662	P	URI	C	420	39.153	27.397	75.984	1.00	73.09	C
ATOM	2663	O1P	URI	C	420	39.251	25.913	75.945	1.00	72.17	C
ATOM	2664	O2P	URI	C	420	39.755	28.136	77.116	1.00	72.78	C
ATOM	2665	O5'	URI	C	420	37.623	27.829	75.875	1.00	72.35	C
ATOM	2666	C5'	URI	C	420	37.270	29.189	75.637	1.00	71.51	C
ATOM	2667	C4'	URI	C	420	35.856	29.286	75.113	1.00	71.76	C
ATOM	2668	O4'	URI	C	420	35.791	28.756	73.764	1.00	72.59	C
ATOM	2669	C1'	URI	C	420	34.534	28.135	73.556	1.00	72.66	C
ATOM	2670	N1	URI	C	420	34.769	26.717	73.253	1.00	73.83	C
ATOM	2671	C6	URI	C	420	35.983	26.127	73.498	1.00	73.89	C
ATOM	2672	C2	URI	C	420	33.722	25.997	72.708	1.00	74.56	C
ATOM	2673	O2	URI	C	420	32.618	26.482	72.506	1.00	74.87	C
ATOM	2674	N3	URI	C	420	34.012	24.685	72.420	1.00	74.69	C
ATOM	2675	C4	URI	C	420	35.209	24.033	72.635	1.00	75.13	C
ATOM	2676	O4	URI	C	420	35.320	22.846	72.320	1.00	75.68	C
ATOM	2677	C5	URI	C	420	36.231	24.844	73.221	1.00	75.12	C
ATOM	2678	C2'	URI	C	420	33.715	28.336	74.828	1.00	72.30	C
ATOM	2679	O2'	URI	C	420	32.894	29.473	74.680	1.00	71.57	C
ATOM	2680	C3'	URI	C	420	34.817	28.485	75.870	1.00	71.73	C
ATOM	2681	O3'	URI	C	420	34.385	29.203	77.013	1.00	72.72	C
ATOM	2682	P	URI	C	421	34.258	28.445	78.421	1.00	73.56	C

ATOM	2683	O1P	URI	C	421	34.493	29.419	79.518	1.00	71.63	C
ATOM	2684	O2P	URI	C	421	35.102	27.234	78.331	1.00	73.93	C
ATOM	2685	O5'	URI	C	421	32.734	27.986	78.454	1.00	72.57	C
ATOM	2686	C5'	URI	C	421	31.714	28.809	77.898	1.00	70.50	C
ATOM	2687	C4'	URI	C	421	30.450	28.009	77.697	1.00	70.66	C
ATOM	2688	O4'	URI	C	421	30.495	27.386	76.389	1.00	70.40	C
ATOM	2689	C1'	URI	C	421	29.731	26.190	76.413	1.00	70.60	C
ATOM	2690	N1	URI	C	421	30.585	25.074	75.982	1.00	69.64	C
ATOM	2691	C6	URI	C	421	31.945	25.095	76.161	1.00	69.33	C
ATOM	2692	C2	URI	C	421	29.966	23.990	75.404	1.00	69.60	C
ATOM	2693	O2	URI	C	421	28.765	23.939	75.223	1.00	70.36	C
ATOM	2694	N3	URI	C	421	30.802	22.963	75.053	1.00	69.02	C
ATOM	2695	C4	URI	C	421	32.165	22.911	75.222	1.00	68.95	C
ATOM	2696	O4	URI	C	421	32.772	21.881	74.924	1.00	69.29	C
ATOM	2697	C5	URI	C	421	32.734	24.077	75.813	1.00	68.62	C
ATOM	2698	C2'	URI	C	421	29.220	26.007	77.845	1.00	71.32	C
ATOM	2699	O2'	URI	C	421	27.907	26.514	77.977	1.00	72.51	C
ATOM	2700	C3'	URI	C	421	30.224	26.831	78.635	1.00	70.79	C
ATOM	2701	O3'	URI	C	421	29.629	27.235	79.860	1.00	70.56	C
ATOM	2702	P	GUA	C	422	29.852	26.353	81.188	1.00	72.90	C
ATOM	2703	O1P	GUA	C	422	31.224	25.778	81.143	1.00	71.16	C
ATOM	2704	O2P	GUA	C	422	29.449	27.203	82.343	1.00	71.02	C
ATOM	2705	O5'	GUA	C	422	28.807	25.155	81.054	1.00	68.77	C
ATOM	2706	C5'	GUA	C	422	27.420	25.393	81.250	1.00	66.08	C
ATOM	2707	C4'	GUA	C	422	26.633	24.104	81.165	1.00	64.53	C
ATOM	2708	O4'	GUA	C	422	27.229	23.176	80.219	1.00	64.44	C
ATOM	2709	C1'	GUA	C	422	26.859	21.846	80.570	1.00	62.29	C
ATOM	2710	N9	GUA	C	422	28.079	21.089	80.834	1.00	62.20	C
ATOM	2711	C4	GUA	C	422	28.208	19.719	80.893	1.00	61.30	C
ATOM	2712	N3	GUA	C	422	27.229	18.815	80.671	1.00	61.22	C
ATOM	2713	C2	GUA	C	422	27.663	17.569	80.819	1.00	60.68	C
ATOM	2714	N2	GUA	C	422	26.832	16.537	80.629	1.00	59.27	C
ATOM	2715	N1	GUA	C	422	28.947	17.241	81.161	1.00	60.17	C
ATOM	2716	C6	GUA	C	422	29.969	18.149	81.394	1.00	59.68	C
ATOM	2717	O6	GUA	C	422	31.092	17.738	81.696	1.00	59.79	C
ATOM	2718	C5	GUA	C	422	29.524	19.491	81.234	1.00	60.33	C
ATOM	2719	N7	GUA	C	422	30.214	20.688	81.359	1.00	61.18	C
ATOM	2720	C8	GUA	C	422	29.322	21.606	81.108	1.00	61.74	C
ATOM	2721	C2'	GUA	C	422	25.987	21.974	81.823	1.00	62.23	C
ATOM	2722	O2'	GUA	C	422	24.633	22.114	81.447	1.00	59.81	C
ATOM	2723	C3'	GUA	C	422	26.531	23.260	82.419	1.00	63.24	C
ATOM	2724	O3'	GUA	C	422	25.614	23.826	83.350	1.00	63.42	C
ATOM	2725	P	CYT	C	423	25.701	23.419	84.903	1.00	63.44	C
ATOM	2726	O1P	CYT	C	423	27.112	23.605	85.339	1.00	62.60	C
ATOM	2727	O2P	CYT	C	423	24.612	24.108	85.639	1.00	63.14	C
ATOM	2728	O5'	CYT	C	423	25.367	21.859	84.903	1.00	62.50	C
ATOM	2729	C5'	CYT	C	423	24.200	21.356	84.249	1.00	59.63	C
ATOM	2730	C4'	CYT	C	423	24.091	19.861	84.448	1.00	57.75	C
ATOM	2731	O4'	CYT	C	423	24.956	19.159	83.503	1.00	54.89	C
ATOM	2732	C1'	CYT	C	423	25.509	18.008	84.127	1.00	54.29	C
ATOM	2733	N1	CYT	C	423	26.964	18.198	84.267	1.00	53.29	C
ATOM	2734	C6	CYT	C	423	27.507	19.448	84.335	1.00	53.60	C
ATOM	2735	C2	CYT	C	423	27.786	17.075	84.331	1.00	53.88	C
ATOM	2736	O2	CYT	C	423	27.268	15.953	84.273	1.00	57.13	C
ATOM	2737	N3	CYT	C	423	29.122	17.235	84.456	1.00	52.34	C
ATOM	2738	C4	CYT	C	423	29.641	18.456	84.517	1.00	51.34	C
ATOM	2739	N4	CYT	C	423	30.960	18.566	84.632	1.00	51.69	C
ATOM	2740	C5	CYT	C	423	28.831	19.620	84.459	1.00	52.45	C
ATOM	2741	C2'	CYT	C	423	24.816	17.892	85.481	1.00	56.07	C
ATOM	2742	O2'	CYT	C	423	23.620	17.170	85.325	1.00	54.32	C
ATOM	2743	C3'	CYT	C	423	24.580	19.361	85.793	1.00	57.83	C

ATOM	2744	O3'	CYT	C	423	23.641	19.584	86.842	1.00	59.37	C
ATOM	2745	P	ADE	C	424	23.978	19.061	88.330	1.00	63.43	C
ATOM	2746	O1P	ADE	C	424	22.818	19.387	89.198	1.00	61.43	C
ATOM	2747	O2P	ADE	C	424	25.346	19.517	88.742	1.00	61.11	C
ATOM	2748	O5'	ADE	C	424	24.014	17.483	88.115	1.00	60.07	C
ATOM	2749	C5'	ADE	C	424	24.210	16.607	89.205	1.00	58.07	C
ATOM	2750	C4'	ADE	C	424	25.091	15.462	88.795	1.00	55.88	C
ATOM	2751	O4'	ADE	C	424	25.801	15.776	87.572	1.00	56.48	C
ATOM	2752	C1'	ADE	C	424	27.120	15.250	87.647	1.00	57.15	C
ATOM	2753	N9	ADE	C	424	28.055	16.370	87.707	1.00	59.22	C
ATOM	2754	C4	ADE	C	424	29.412	16.286	87.902	1.00	58.46	C
ATOM	2755	N3	ADE	C	424	30.138	15.179	88.114	1.00	57.20	C
ATOM	2756	C2	ADE	C	424	31.420	15.482	88.231	1.00	57.56	C
ATOM	2757	N1	ADE	C	424	32.018	16.672	88.157	1.00	57.82	C
ATOM	2758	C6	ADE	C	424	31.258	17.762	87.941	1.00	58.97	C
ATOM	2759	N6	ADE	C	424	31.852	18.953	87.845	1.00	60.54	C
ATOM	2760	C5	ADE	C	424	29.883	17.578	87.819	1.00	58.76	C
ATOM	2761	N7	ADE	C	424	28.841	18.468	87.613	1.00	61.16	C
ATOM	2762	C8	ADE	C	424	27.779	17.704	87.561	1.00	60.44	C
ATOM	2763	C2'	ADE	C	424	27.184	14.421	88.923	1.00	55.92	C
ATOM	2764	O2'	ADE	C	424	26.784	13.099	88.655	1.00	56.30	C
ATOM	2765	C3'	ADE	C	424	26.199	15.182	89.780	1.00	54.65	C
ATOM	2766	O3'	ADE	C	424	25.681	14.415	90.827	1.00	54.00	C
ATOM	2767	P	GUA	C	425	25.671	15.023	92.297	1.00	55.14	C
ATOM	2768	O1P	GUA	C	425	25.540	16.492	92.171	1.00	54.82	C
ATOM	2769	O2P	GUA	C	425	24.679	14.267	93.096	1.00	55.19	C
ATOM	2770	O5'	GUA	C	425	27.130	14.653	92.800	1.00	54.58	C
ATOM	2771	C5'	GUA	C	425	27.602	13.329	92.630	1.00	53.72	C
ATOM	2772	C4'	GUA	C	425	29.087	13.320	92.505	1.00	52.36	C
ATOM	2773	O4'	GUA	C	425	29.485	14.125	91.377	1.00	53.75	C
ATOM	2774	C1'	GUA	C	425	30.791	14.626	91.607	1.00	55.50	C
ATOM	2775	N9	GUA	C	425	30.774	16.076	91.399	1.00	57.33	C
ATOM	2776	C4	GUA	C	425	31.849	16.935	91.500	1.00	57.15	C
ATOM	2777	N3	GUA	C	425	33.115	16.592	91.812	1.00	57.47	C
ATOM	2778	C2	GUA	C	425	33.925	17.635	91.819	1.00	56.02	C
ATOM	2779	N2	GUA	C	425	35.219	17.469	92.092	1.00	55.54	C
ATOM	2780	N1	GUA	C	425	33.528	18.917	91.559	1.00	56.41	C
ATOM	2781	C6	GUA	C	425	32.232	19.303	91.247	1.00	57.54	C
ATOM	2782	O6	GUA	C	425	31.981	20.499	91.048	1.00	59.51	C
ATOM	2783	C5	GUA	C	425	31.345	18.187	91.216	1.00	57.41	C
ATOM	2784	N7	GUA	C	425	29.985	18.121	90.943	1.00	56.45	C
ATOM	2785	C8	GUA	C	425	29.690	16.854	91.065	1.00	57.56	C
ATOM	2786	C2'	GUA	C	425	31.178	14.194	93.027	1.00	54.96	C
ATOM	2787	O2'	GUA	C	425	31.884	12.977	92.972	1.00	55.11	C
ATOM	2788	C3'	GUA	C	425	29.814	13.975	93.652	1.00	53.91	C
ATOM	2789	O3'	GUA	C	425	29.879	13.068	94.743	1.00	55.10	C
ATOM	2790	P	URI	C	426	29.644	13.602	96.243	1.00	55.46	C
ATOM	2791	O1P	URI	C	426	28.622	14.689	96.184	1.00	54.09	C
ATOM	2792	O2P	URI	C	426	29.429	12.439	97.148	1.00	52.76	C
ATOM	2793	O5'	URI	C	426	31.064	14.214	96.588	1.00	53.38	C
ATOM	2794	C5'	URI	C	426	32.232	13.489	96.251	1.00	51.95	C
ATOM	2795	C4'	URI	C	426	33.440	14.328	96.507	1.00	51.33	C
ATOM	2796	O4'	URI	C	426	33.752	15.073	95.305	1.00	50.28	C
ATOM	2797	C1'	URI	C	426	34.131	16.385	95.647	1.00	49.45	C
ATOM	2798	N1	URI	C	426	33.084	17.280	95.148	1.00	48.32	C
ATOM	2799	C6	URI	C	426	31.803	16.839	95.002	1.00	46.72	C
ATOM	2800	C2	URI	C	426	33.435	18.569	94.830	1.00	47.83	C
ATOM	2801	O2	URI	C	426	34.564	19.001	94.955	1.00	47.66	C
ATOM	2802	N3	URI	C	426	32.413	19.340	94.358	1.00	47.12	C
ATOM	2803	C4	URI	C	426	31.117	18.960	94.182	1.00	47.17	C
ATOM	2804	O4	URI	C	426	30.342	19.736	93.635	1.00	50.31	C

ATOM	2805	C5	URI	C 426	30.833	17.614	94.547	1.00	47.19	C
ATOM	2806	C2'	URI	C 426	34.275	16.420	97.170	1.00	51.69	C
ATOM	2807	O2'	URI	C 426	35.583	16.059	97.573	1.00	52.95	C
ATOM	2808	C3'	URI	C 426	33.259	15.375	97.590	1.00	51.04	C
ATOM	2809	O3'	URI	C 426	33.625	14.817	98.839	1.00	52.74	C
ATOM	2810	P	CYT	C 427	33.377	15.647	100.187	1.00	55.80	C
ATOM	2811	O1P	CYT	C 427	31.930	15.990	100.242	1.00	53.06	C
ATOM	2812	O2P	CYT	C 427	34.005	14.909	101.317	1.00	54.75	C
ATOM	2813	O5'	CYT	C 427	34.224	16.977	99.972	1.00	54.34	C
ATOM	2814	C5'	CYT	C 427	35.518	17.108	100.541	1.00	53.79	C
ATOM	2815	C4'	CYT	C 427	36.034	18.508	100.340	1.00	52.68	C
ATOM	2816	O4'	CYT	C 427	35.823	18.895	98.961	1.00	51.71	C
ATOM	2817	C1'	CYT	C 427	35.651	20.299	98.886	1.00	52.92	C
ATOM	2818	N1	CYT	C 427	34.338	20.573	98.292	1.00	54.24	C
ATOM	2819	C6	CYT	C 427	33.402	19.583	98.172	1.00	55.08	C
ATOM	2820	C2	CYT	C 427	34.049	21.874	97.865	1.00	54.20	C
ATOM	2821	O2	CYT	C 427	34.929	22.740	97.950	1.00	53.16	C
ATOM	2822	N3	CYT	C 427	32.819	22.148	97.365	1.00	53.57	C
ATOM	2823	C4	CYT	C 427	31.909	21.178	97.272	1.00	54.42	C
ATOM	2824	N4	CYT	C 427	30.714	21.491	96.794	1.00	55.39	C
ATOM	2825	C5	CYT	C 427	32.186	19.839	97.671	1.00	55.03	C
ATOM	2826	C2'	CYT	C 427	35.748	20.827	100.317	1.00	53.24	C
ATOM	2827	O2'	CYT	C 427	37.085	21.179	100.595	1.00	55.47	C
ATOM	2828	C3'	CYT	C 427	35.320	19.605	101.106	1.00	52.83	C
ATOM	2829	O3'	CYT	C 427	35.781	19.690	102.445	1.00	53.08	C
ATOM	2830	P	GUA	C 428	34.819	19.224	103.637	1.00	56.16	C
ATOM	2831	O1P	GUA	C 428	33.772	18.364	103.013	1.00	56.05	C
ATOM	2832	O2P	GUA	C 428	35.649	18.690	104.747	1.00	56.57	C
ATOM	2833	O5'	GUA	C 428	34.122	20.566	104.140	1.00	56.07	C
ATOM	2834	C5'	GUA	C 428	34.815	21.494	104.971	1.00	55.18	C
ATOM	2835	C4'	GUA	C 428	35.171	22.736	104.186	1.00	54.66	C
ATOM	2836	O4'	GUA	C 428	34.976	22.483	102.774	1.00	55.76	C
ATOM	2837	C1'	GUA	C 428	34.557	23.666	102.128	1.00	55.37	C
ATOM	2838	N9	GUA	C 428	33.277	23.407	101.484	1.00	56.56	C
ATOM	2839	C4	GUA	C 428	32.555	24.276	100.713	1.00	57.44	C
ATOM	2840	N3	GUA	C 428	32.898	25.541	100.414	1.00	59.24	C
ATOM	2841	C2	GUA	C 428	32.000	26.121	99.635	1.00	60.77	C
ATOM	2842	N2	GUA	C 428	32.188	27.382	99.216	1.00	61.88	C
ATOM	2843	N1	GUA	C 428	30.855	25.507	99.203	1.00	59.95	C
ATOM	2844	C6	GUA	C 428	30.487	24.206	99.509	1.00	58.62	C
ATOM	2845	O6	GUA	C 428	29.436	23.747	99.075	1.00	61.20	C
ATOM	2846	C5	GUA	C 428	31.436	23.576	100.324	1.00	57.79	C
ATOM	2847	N7	GUA	C 428	31.452	22.295	100.842	1.00	58.66	C
ATOM	2848	C8	GUA	C 428	32.562	22.240	101.525	1.00	58.08	C
ATOM	2849	C2'	GUA	C 428	34.510	24.768	103.182	1.00	54.88	C
ATOM	2850	O2'	GUA	C 428	35.741	25.444	103.138	1.00	56.37	C
ATOM	2851	C3'	GUA	C 428	34.340	23.975	104.471	1.00	54.17	C
ATOM	2852	O3'	GUA	C 428	34.938	24.693	105.543	1.00	53.83	C
ATOM	2853	P	CYT	C 429	34.036	25.227	106.760	1.00	55.71	C
ATOM	2854	O1P	CYT	C 429	32.936	24.258	107.022	1.00	54.57	C
ATOM	2855	O2P	CYT	C 429	34.965	25.601	107.852	1.00	52.48	C
ATOM	2856	O5'	CYT	C 429	33.373	26.557	106.191	1.00	55.60	C
ATOM	2857	C5'	CYT	C 429	34.183	27.609	105.690	1.00	54.46	C
ATOM	2858	C4'	CYT	C 429	33.340	28.611	104.941	1.00	54.38	C
ATOM	2859	O4'	CYT	C 429	33.174	28.184	103.562	1.00	54.38	C
ATOM	2860	C1'	CYT	C 429	31.881	28.547	103.102	1.00	54.82	C
ATOM	2861	N1	CYT	C 429	31.095	27.318	102.934	1.00	55.41	C
ATOM	2862	C6	CYT	C 429	31.401	26.195	103.646	1.00	56.89	C
ATOM	2863	C2	CYT	C 429	30.018	27.318	102.047	1.00	55.74	C
ATOM	2864	O2	CYT	C 429	29.769	28.337	101.409	1.00	56.97	C
ATOM	2865	N3	CYT	C 429	29.273	26.207	101.910	1.00	57.40	C

ATOM	2866	C4	CYT	C 429	29.567	25.118	102.620	1.00	59.54	C
ATOM	2867	N4	CYT	C 429	28.789	24.038	102.465	1.00	59.89	C
ATOM	2868	C5	CYT	C 429	30.670	25.084	103.525	1.00	59.76	C
ATOM	2869	C2'	CYT	C 429	31.292	29.436	104.194	1.00	54.49	C
ATOM	2870	O2'	CYT	C 429	31.715	30.769	104.009	1.00	54.42	C
ATOM	2871	C3'	CYT	C 429	31.916	28.809	105.427	1.00	54.17	C
ATOM	2872	O3'	CYT	C 429	31.868	29.702	106.530	1.00	55.30	C
ATOM	2873	P	GUA	C 430	30.474	29.975	107.280	1.00	55.18	C
ATOM	2874	O1P	GUA	C 430	29.896	28.696	107.762	1.00	54.20	C
ATOM	2875	O2P	GUA	C 430	30.703	31.072	108.240	1.00	55.34	C
ATOM	2876	O5'	GUA	C 430	29.533	30.517	106.120	1.00	56.60	C
ATOM	2877	C5'	GUA	C 430	29.584	31.875	105.702	1.00	58.01	C
ATOM	2878	C4'	GUA	C 430	28.227	32.297	105.204	1.00	60.07	C
ATOM	2879	O4'	GUA	C 430	27.824	31.334	104.211	1.00	59.91	C
ATOM	2880	C1'	GUA	C 430	26.494	30.933	104.428	1.00	60.74	C
ATOM	2881	N9	GUA	C 430	26.421	29.482	104.266	1.00	60.14	C
ATOM	2882	C4	GUA	C 430	25.465	28.782	103.566	1.00	59.13	C
ATOM	2883	N3	GUA	C 430	24.429	29.315	102.889	1.00	59.30	C
ATOM	2884	C2	GUA	C 430	23.658	28.384	102.353	1.00	60.04	C
ATOM	2885	N2	GUA	C 430	22.564	28.731	101.664	1.00	60.31	C
ATOM	2886	N1	GUA	C 430	23.891	27.043	102.458	1.00	59.51	C
ATOM	2887	C6	GUA	C 430	24.948	26.470	103.141	1.00	59.46	C
ATOM	2888	O6	GUA	C 430	25.052	25.244	103.178	1.00	60.37	C
ATOM	2889	C5	GUA	C 430	25.788	27.456	103.730	1.00	59.42	C
ATOM	2890	N7	GUA	C 430	26.939	27.321	104.493	1.00	59.34	C
ATOM	2891	C8	GUA	C 430	27.279	28.547	104.787	1.00	59.75	C
ATOM	2892	C2'	GUA	C 430	26.012	31.435	105.789	1.00	60.81	C
ATOM	2893	O2'	GUA	C 430	24.775	32.101	105.631	1.00	63.49	C
ATOM	2894	C3'	GUA	C 430	27.162	32.318	106.291	1.00	61.67	C
ATOM	2895	O3'	GUA	C 430	26.835	33.650	106.732	1.00	66.15	C
ATOM	2896	P	URI	C 431	26.269	34.760	105.696	1.00	68.52	C
ATOM	2897	O1P	URI	C 431	25.470	34.098	104.634	1.00	71.17	C
ATOM	2898	O2P	URI	C 431	25.641	35.811	106.523	1.00	69.16	C
ATOM	2899	O5'	URI	C 431	27.553	35.410	105.010	1.00	71.54	C
ATOM	2900	C5'	URI	C 431	27.731	35.343	103.595	1.00	77.99	C
ATOM	2901	C4'	URI	C 431	27.963	36.722	103.013	1.00	82.63	C
ATOM	2902	O4'	URI	C 431	26.978	37.659	103.522	1.00	84.74	C
ATOM	2903	C1'	URI	C 431	27.617	38.881	103.806	1.00	84.92	C
ATOM	2904	N1	URI	C 431	26.808	39.608	104.793	1.00	84.31	C
ATOM	2905	C6	URI	C 431	26.189	38.950	105.829	1.00	84.61	C
ATOM	2906	C2	URI	C 431	26.681	40.977	104.640	1.00	84.06	C
ATOM	2907	O2	URI	C 431	27.224	41.598	103.736	1.00	83.22	C
ATOM	2908	N3	URI	C 431	25.894	41.593	105.583	1.00	84.06	C
ATOM	2909	C4	URI	C 431	25.238	40.990	106.641	1.00	84.44	C
ATOM	2910	O4	URI	C 431	24.541	41.674	107.393	1.00	84.73	C
ATOM	2911	C5	URI	C 431	25.428	39.576	106.733	1.00	84.34	C
ATOM	2912	C2'	URI	C 431	29.005	38.467	104.283	1.00	85.04	C
ATOM	2913	O2'	URI	C 431	29.904	39.548	104.148	1.00	87.61	C
ATOM	2914	C3'	URI	C 431	29.324	37.354	103.291	1.00	84.77	C
ATOM	2915	O3'	URI	C 431	29.813	37.934	102.097	1.00	86.28	C
ATOM	2916	P	GUA	C 432	31.210	37.441	101.497	1.00	90.42	C
ATOM	2917	O1P	GUA	C 432	31.952	38.646	101.053	1.00	90.72	C
ATOM	2918	O2P	GUA	C 432	31.839	36.515	102.472	1.00	89.74	C
ATOM	2919	O5'	GUA	C 432	30.782	36.625	100.200	1.00	90.83	C
ATOM	2920	C5'	GUA	C 432	30.313	37.303	99.043	1.00	92.43	C
ATOM	2921	C4'	GUA	C 432	29.470	36.381	98.201	1.00	94.35	C
ATOM	2922	O4'	GUA	C 432	28.357	35.893	99.001	1.00	95.57	C
ATOM	2923	C1'	GUA	C 432	27.137	36.278	98.401	1.00	97.09	C
ATOM	2924	N9	GUA	C 432	26.682	37.501	99.056	1.00	99.52	C
ATOM	2925	C4	GUA	C 432	25.840	37.572	100.135	1.00	100.59	C
ATOM	2926	N3	GUA	C 432	25.272	36.523	100.757	1.00	101.44	C

ATOM	2927	C2	GUA	C	432	24.518	36.902	101.774	1.00103.28	C
ATOM	2928	N2	GUA	C	432	23.868	35.971	102.501	1.00104.52	C
ATOM	2929	N1	GUA	C	432	24.340	38.217	102.155	1.00102.87	C
ATOM	2930	C6	GUA	C	432	24.916	39.317	101.527	1.00101.33	C
ATOM	2931	O6	GUA	C	432	24.694	40.461	101.953	1.00 99.83	C
ATOM	2932	C5	GUA	C	432	25.725	38.919	100.426	1.00101.00	C
ATOM	2933	N7	GUA	C	432	26.467	39.680	99.533	1.00100.89	C
ATOM	2934	C8	GUA	C	432	27.014	38.800	98.738	1.00100.42	C
ATOM	2935	C2'	GUA	C	432	27.453	36.453	96.918	1.00 96.55	C
ATOM	2936	O2'	GUA	C	432	27.415	35.208	96.248	1.00 97.29	C
ATOM	2937	C3'	GUA	C	432	28.852	37.056	96.983	1.00 95.20	C
ATOM	2938	O3'	GUA	C	432	29.616	36.775	95.821	1.00 94.28	C
ATOM	2939	P	ADE	C	433	30.860	37.719	95.454	1.00 93.89	C
ATOM	2940	O1P	ADE	C	433	31.273	37.434	94.053	1.00 93.02	C
ATOM	2941	O2P	ADE	C	433	30.498	39.108	95.848	1.00 92.98	C
ATOM	2942	O5'	ADE	C	433	32.011	37.212	96.427	1.00 91.05	C
ATOM	2943	C5'	ADE	C	433	32.764	38.132	97.209	1.00 85.17	C
ATOM	2944	C4'	ADE	C	433	34.017	37.471	97.711	1.00 80.49	C
ATOM	2945	O4'	ADE	C	433	33.648	36.316	98.506	1.00 77.74	C
ATOM	2946	C1'	ADE	C	433	34.344	35.184	98.048	1.00 74.83	C
ATOM	2947	N9	ADE	C	433	33.454	34.036	98.172	1.00 71.45	C
ATOM	2948	C4	ADE	C	433	33.173	33.345	99.322	1.00 69.90	C
ATOM	2949	N3	ADE	C	433	33.654	33.582	100.554	1.00 70.14	C
ATOM	2950	C2	ADE	C	433	33.152	32.710	101.426	1.00 69.09	C
ATOM	2951	N1	ADE	C	433	32.295	31.706	101.220	1.00 67.52	C
ATOM	2952	C6	ADE	C	433	31.836	31.498	99.969	1.00 67.36	C
ATOM	2953	N6	ADE	C	433	30.986	30.500	99.759	1.00 66.58	C
ATOM	2954	C5	ADE	C	433	32.286	32.353	98.957	1.00 68.74	C
ATOM	2955	N7	ADE	C	433	32.013	32.414	97.599	1.00 69.59	C
ATOM	2956	C8	ADE	C	433	32.728	33.426	97.181	1.00 70.82	C
ATOM	2957	C2'	ADE	C	433	34.731	35.467	96.600	1.00 76.41	C
ATOM	2958	O2'	ADE	C	433	35.919	34.775	96.295	1.00 77.66	C
ATOM	2959	C3'	ADE	C	433	34.946	36.973	96.613	1.00 77.91	C
ATOM	2960	O3'	ADE	C	433	36.287	37.288	96.938	1.00 78.38	C
ATOM	2961	P	URI	C	434	36.861	38.737	96.573	1.00 79.09	C
ATOM	2962	O1P	URI	C	434	36.931	38.805	95.093	1.00 79.39	C
ATOM	2963	O2P	URI	C	434	36.083	39.759	97.329	1.00 76.85	C
ATOM	2964	O5'	URI	C	434	38.352	38.733	97.122	1.00 77.52	C
ATOM	2965	C5'	URI	C	434	39.306	37.780	96.677	1.00 75.37	C
ATOM	2966	C4'	URI	C	434	40.437	37.713	97.670	1.00 76.23	C
ATOM	2967	O4'	URI	C	434	41.106	38.997	97.657	1.00 77.08	C
ATOM	2968	C1'	URI	C	434	41.570	39.311	98.957	1.00 77.57	C
ATOM	2969	N1	URI	C	434	41.269	40.727	99.224	1.00 78.74	C
ATOM	2970	C6	URI	C	434	40.067	41.285	98.853	1.00 79.58	C
ATOM	2971	C2	URI	C	434	42.238	41.486	99.858	1.00 78.34	C
ATOM	2972	O2	URI	C	434	43.312	41.027	100.204	1.00 79.04	C
ATOM	2973	N3	URI	C	434	41.899	42.804	100.067	1.00 77.66	C
ATOM	2974	C4	URI	C	434	40.716	43.428	99.715	1.00 78.36	C
ATOM	2975	O4	URI	C	434	40.557	44.627	99.965	1.00 79.03	C
ATOM	2976	C5	URI	C	434	39.766	42.576	99.070	1.00 79.25	C
ATOM	2977	C2'	URI	C	434	40.942	38.338	99.963	1.00 75.79	C
ATOM	2978	O2'	URI	C	434	41.926	37.552	100.609	1.00 75.86	C
ATOM	2979	C3'	URI	C	434	39.957	37.538	99.106	1.00 75.37	C
ATOM	2980	O3'	URI	C	434	39.822	36.165	99.498	1.00 73.16	C
ATOM	2981	P	ADE	C	435	40.896	35.055	99.030	1.00 70.07	C
ATOM	2982	O1P	ADE	C	435	40.489	34.541	97.697	1.00 67.84	C
ATOM	2983	O2P	ADE	C	435	42.289	35.524	99.248	1.00 69.36	C
ATOM	2984	O5'	ADE	C	435	40.663	33.927	100.113	1.00 69.65	C
ATOM	2985	C5'	ADE	C	435	40.828	34.244	101.483	1.00 70.14	C
ATOM	2986	C4'	ADE	C	435	39.571	33.936	102.246	1.00 69.70	C
ATOM	2987	O4'	ADE	C	435	38.403	34.134	101.418	1.00 71.18	C

ATOM	2988	C1'	ADE	C 435	37.383	33.234	101.823	1.00	70.22	C
ATOM	2989	N9	ADE	C 435	36.925	32.513	100.636	1.00	70.43	C
ATOM	2990	C4	ADE	C 435	36.083	31.428	100.598	1.00	69.40	C
ATOM	2991	N3	ADE	C 435	35.515	30.801	101.639	1.00	69.03	C
ATOM	2992	C2	ADE	C 435	34.747	29.800	101.219	1.00	68.55	C
ATOM	2993	N1	ADE	C 435	34.500	29.389	99.969	1.00	68.15	C
ATOM	2994	C6	ADE	C 435	35.083	30.044	98.947	1.00	68.35	C
ATOM	2995	N6	ADE	C 435	34.828	29.641	97.703	1.00	67.46	C
ATOM	2996	C5	ADE	C 435	35.925	31.121	99.259	1.00	69.18	C
ATOM	2997	N7	ADE	C 435	36.661	31.988	98.465	1.00	70.13	C
ATOM	2998	C8	ADE	C 435	37.237	32.790	99.327	1.00	70.31	C
ATOM	2999	C2'	ADE	C 435	37.973	32.339	102.916	1.00	69.38	C
ATOM	3000	O2'	ADE	C 435	37.591	32.838	104.176	1.00	68.95	C
ATOM	3001	C3'	ADE	C 435	39.465	32.487	102.646	1.00	69.55	C
ATOM	3002	O3'	ADE	C 435	40.295	32.301	103.774	1.00	68.77	C
ATOM	3003	P	ADE	C 436	41.552	31.314	103.666	1.00	69.41	C
ATOM	3004	O1P	ADE	C 436	42.557	31.779	104.656	1.00	67.75	C
ATOM	3005	O2P	ADE	C 436	41.938	31.161	102.236	1.00	66.39	C
ATOM	3006	O5'	ADE	C 436	40.930	29.948	104.192	1.00	68.62	C
ATOM	3007	C5'	ADE	C 436	39.961	29.978	105.237	1.00	67.50	C
ATOM	3008	C4'	ADE	C 436	39.062	28.778	105.153	1.00	66.76	C
ATOM	3009	O4'	ADE	C 436	37.955	29.042	104.253	1.00	65.84	C
ATOM	3010	C1'	ADE	C 436	37.673	27.878	103.500	1.00	64.84	C
ATOM	3011	N9	ADE	C 436	37.994	28.169	102.107	1.00	63.84	C
ATOM	3012	C4	ADE	C 436	37.339	27.711	100.988	1.00	63.55	C
ATOM	3013	N3	ADE	C 436	36.295	26.869	100.940	1.00	62.20	C
ATOM	3014	C2	ADE	C 436	35.910	26.673	99.678	1.00	63.29	C
ATOM	3015	N1	ADE	C 436	36.410	27.187	98.546	1.00	62.42	C
ATOM	3016	C6	ADE	C 436	37.456	28.030	98.631	1.00	62.84	C
ATOM	3017	N6	ADE	C 436	37.944	28.550	97.505	1.00	62.83	C
ATOM	3018	C5	ADE	C 436	37.964	28.314	99.912	1.00	63.58	C
ATOM	3019	N7	ADE	C 436	39.010	29.113	100.343	1.00	65.53	C
ATOM	3020	C8	ADE	C 436	38.989	28.986	101.649	1.00	64.55	C
ATOM	3021	C2'	ADE	C 436	38.503	26.756	104.120	1.00	65.24	C
ATOM	3022	O2'	ADE	C 436	37.804	26.224	105.227	1.00	66.40	C
ATOM	3023	C3'	ADE	C 436	39.715	27.531	104.595	1.00	66.18	C
ATOM	3024	O3'	ADE	C 436	40.368	26.843	105.646	1.00	66.58	C
ATOM	3025	P	ADE	C 437	41.651	25.943	105.318	1.00	67.89	C
ATOM	3026	O1P	ADE	C 437	42.351	25.674	106.598	1.00	67.81	C
ATOM	3027	O2P	ADE	C 437	42.384	26.565	104.182	1.00	67.40	C
ATOM	3028	O5'	ADE	C 437	41.023	24.572	104.831	1.00	66.73	C
ATOM	3029	C5'	ADE	C 437	40.025	23.933	105.603	1.00	67.55	C
ATOM	3030	C4'	ADE	C 437	39.313	22.918	104.762	1.00	68.47	C
ATOM	3031	O4'	ADE	C 437	38.419	23.610	103.845	1.00	68.30	C
ATOM	3032	C1'	ADE	C 437	38.485	23.002	102.567	1.00	67.40	C
ATOM	3033	N9	ADE	C 437	39.111	23.954	101.651	1.00	65.38	C
ATOM	3034	C4	ADE	C 437	38.823	24.112	100.320	1.00	64.64	C
ATOM	3035	N3	ADE	C 437	37.923	23.432	99.598	1.00	64.22	C
ATOM	3036	C2	ADE	C 437	37.920	23.852	98.335	1.00	65.30	C
ATOM	3037	N1	ADE	C 437	38.660	24.801	97.756	1.00	65.94	C
ATOM	3038	C6	ADE	C 437	39.558	25.467	98.512	1.00	65.81	C
ATOM	3039	N6	ADE	C 437	40.298	26.411	97.934	1.00	66.54	C
ATOM	3040	C5	ADE	C 437	39.656	25.118	99.870	1.00	65.25	C
ATOM	3041	N7	ADE	C 437	40.454	25.591	100.900	1.00	66.13	C
ATOM	3042	C8	ADE	C 437	40.092	24.869	101.932	1.00	66.12	C
ATOM	3043	C2'	ADE	C 437	39.272	21.703	102.755	1.00	67.83	C
ATOM	3044	O2'	ADE	C 437	38.406	20.672	103.193	1.00	66.91	C
ATOM	3045	C3'	ADE	C 437	40.231	22.118	103.857	1.00	68.95	C
ATOM	3046	O3'	ADE	C 437	40.751	21.005	104.565	1.00	71.12	C
ATOM	3047	P	URI	C 438	41.863	20.075	103.879	1.00	73.66	C
ATOM	3048	O1P	URI	C 438	42.506	20.826	102.769	1.00	71.57	C

ATOM	3049	O2P	URI	C	438	42.702	19.539	104.981	1.00	73.16	C
ATOM	3050	O5'	URI	C	438	41.002	18.886	103.258	1.00	74.03	C
ATOM	3051	C5'	URI	C	438	41.468	18.148	102.138	1.00	76.70	C
ATOM	3052	C4'	URI	C	438	40.353	17.964	101.141	1.00	78.88	C
ATOM	3053	O4'	URI	C	438	39.685	19.237	100.955	1.00	79.02	C
ATOM	3054	C1'	URI	C	438	39.506	19.493	99.575	1.00	78.40	C
ATOM	3055	N1	URI	C	438	40.353	20.638	99.206	1.00	76.81	C
ATOM	3056	C6	URI	C	438	41.213	21.205	100.120	1.00	77.28	C
ATOM	3057	C2	URI	C	438	40.249	21.142	97.920	1.00	75.94	C
ATOM	3058	O2	URI	C	438	39.522	20.654	97.072	1.00	75.16	C
ATOM	3059	N3	URI	C	438	41.033	22.243	97.666	1.00	75.22	C
ATOM	3060	C4	URI	C	438	41.892	22.877	98.545	1.00	75.03	C
ATOM	3061	O4	URI	C	438	42.431	23.931	98.208	1.00	73.84	C
ATOM	3062	C5	URI	C	438	41.966	22.278	99.840	1.00	76.07	C
ATOM	3063	C2'	URI	C	438	39.817	18.199	98.826	1.00	79.68	C
ATOM	3064	O2'	URI	C	438	38.650	17.426	98.641	1.00	80.05	C
ATOM	3065	C3'	URI	C	438	40.810	17.522	99.759	1.00	81.02	C
ATOM	3066	O3'	URI	C	438	40.687	16.114	99.641	1.00	85.73	C
ATOM	3067	P	GUA	C	439	41.958	15.243	99.201	1.00	89.61	C
ATOM	3068	O1P	GUA	C	439	43.063	15.595	100.137	1.00	86.65	C
ATOM	3069	O2P	GUA	C	439	41.487	13.839	99.104	1.00	88.33	C
ATOM	3070	O5'	GUA	C	439	42.317	15.776	97.734	1.00	94.00	C
ATOM	3071	C5'	GUA	C	439	41.454	15.520	96.617	1.00	101.35	C
ATOM	3072	C4'	GUA	C	439	41.385	16.731	95.698	1.00	106.66	C
ATOM	3073	O4'	GUA	C	439	41.296	17.935	96.498	1.00	109.59	C
ATOM	3074	C1'	GUA	C	439	42.080	18.963	95.920	1.00	111.32	C
ATOM	3075	N9	GUA	C	439	43.115	19.344	96.874	1.00	113.82	C
ATOM	3076	C4	GUA	C	439	43.905	20.462	96.810	1.00	115.05	C
ATOM	3077	N3	GUA	C	439	43.864	21.402	95.844	1.00	115.22	C
ATOM	3078	C2	GUA	C	439	44.748	22.363	96.054	1.00	116.16	C
ATOM	3079	N2	GUA	C	439	44.845	23.380	95.188	1.00	116.49	C
ATOM	3080	N1	GUA	C	439	45.605	22.397	97.130	1.00	117.15	C
ATOM	3081	C6	GUA	C	439	45.665	21.437	98.139	1.00	117.34	C
ATOM	3082	O6	GUA	C	439	46.480	21.561	99.069	1.00	118.17	C
ATOM	3083	C5	GUA	C	439	44.720	20.400	97.924	1.00	116.29	C
ATOM	3084	N7	GUA	C	439	44.448	19.263	98.672	1.00	115.53	C
ATOM	3085	C8	GUA	C	439	43.492	18.666	98.012	1.00	115.04	C
ATOM	3086	C2'	GUA	C	439	42.648	18.457	94.595	1.00	110.41	C
ATOM	3087	O2'	GUA	C	439	41.899	18.960	93.505	1.00	109.71	C
ATOM	3088	C3'	GUA	C	439	42.567	16.938	94.756	1.00	109.48	C
ATOM	3089	O3'	GUA	C	439	42.291	16.365	93.486	1.00	111.37	C
ATOM	3090	P	URI	C	440	41.819	14.834	93.390	1.00	113.61	C
ATOM	3091	O1P	URI	C	440	42.876	14.008	94.033	1.00	113.47	C
ATOM	3092	O2P	URI	C	440	40.423	14.748	93.891	1.00	113.46	C
ATOM	3093	O5'	URI	C	440	41.824	14.541	91.820	1.00	113.15	C
ATOM	3094	C5'	URI	C	440	41.126	15.393	90.908	1.00	112.76	C
ATOM	3095	C4'	URI	C	440	39.673	14.991	90.843	1.00	112.75	C
ATOM	3096	O4'	URI	C	440	38.835	16.101	90.479	1.00	112.32	C
ATOM	3097	C1'	URI	C	440	37.587	15.567	90.130	1.00	111.52	C
ATOM	3098	N1	URI	C	440	36.778	16.612	89.482	1.00	109.39	C
ATOM	3099	C6	URI	C	440	37.282	17.876	89.285	1.00	109.63	C
ATOM	3100	C2	URI	C	440	35.484	16.296	89.108	1.00	107.64	C
ATOM	3101	O2	URI	C	440	35.011	15.182	89.229	1.00	105.80	C
ATOM	3102	N3	URI	C	440	34.764	17.338	88.584	1.00	107.65	C
ATOM	3103	C4	URI	C	440	35.198	18.634	88.389	1.00	108.72	C
ATOM	3104	O4	URI	C	440	34.416	19.477	87.948	1.00	109.01	C
ATOM	3105	C5	URI	C	440	36.556	18.871	88.768	1.00	109.19	C
ATOM	3106	C2'	URI	C	440	37.908	14.313	89.313	1.00	112.54	C
ATOM	3107	O2'	URI	C	440	36.925	13.323	89.561	1.00	112.81	C
ATOM	3108	C3'	URI	C	440	39.304	13.908	89.834	1.00	113.01	C
ATOM	3109	O3'	URI	C	440	39.263	12.650	90.501	1.00	113.21	C

ATOM	3110	P	ADE	C	441	40.229	11.459	90.017	1.00113.40	C
ATOM	3111	O1P	ADE	C	441	40.156	10.387	91.047	1.00113.55	C
ATOM	3112	O2P	ADE	C	441	41.553	12.033	89.643	1.00112.92	C
ATOM	3113	O5'	ADE	C	441	39.519	10.921	88.696	1.00110.64	C
ATOM	3114	C5'	ADE	C	441	38.116	11.095	88.499	1.00104.96	C
ATOM	3115	C4'	ADE	C	441	37.362	9.926	89.076	1.00100.67	C
ATOM	3116	O4'	ADE	C	441	36.506	10.381	90.160	1.00 99.35	C
ATOM	3117	C1'	ADE	C	441	35.350	9.551	90.222	1.00 99.29	C
ATOM	3118	N9	ADE	C	441	34.178	10.370	89.921	1.00 99.63	C
ATOM	3119	C4	ADE	C	441	32.866	9.986	90.077	1.00100.33	C
ATOM	3120	N3	ADE	C	441	32.409	8.815	90.560	1.00100.94	C
ATOM	3121	C2	ADE	C	441	31.076	8.787	90.543	1.00100.93	C
ATOM	3122	N1	ADE	C	441	30.214	9.724	90.127	1.00100.56	C
ATOM	3123	C6	ADE	C	441	30.706	10.889	89.647	1.00100.33	C
ATOM	3124	N6	ADE	C	441	29.847	11.819	89.224	1.00100.95	C
ATOM	3125	C5	ADE	C	441	32.106	11.047	89.618	1.00100.21	C
ATOM	3126	N7	ADE	C	441	32.922	12.092	89.202	1.00 99.64	C
ATOM	3127	C8	ADE	C	441	34.138	11.644	89.407	1.00 99.73	C
ATOM	3128	C2'	ADE	C	441	35.535	8.476	89.149	1.00 98.46	C
ATOM	3129	O2'	ADE	C	441	36.198	7.350	89.691	1.00 98.08	C
ATOM	3130	C3'	ADE	C	441	36.378	9.242	88.143	1.00 98.19	C
ATOM	3131	O3'	ADE	C	441	37.018	8.396	87.189	1.00 93.51	C
ATOM	3132	P	GUA	C	442	36.821	8.678	85.612	1.00 89.51	C
ATOM	3133	O1P	GUA	C	442	37.440	9.991	85.294	1.00 89.28	C
ATOM	3134	O2P	GUA	C	442	37.273	7.462	84.887	1.00 89.23	C
ATOM	3135	O5'	GUA	C	442	35.241	8.828	85.427	1.00 84.16	C
ATOM	3136	C5'	GUA	C	442	34.414	7.677	85.295	1.00 76.13	C
ATOM	3137	C4'	GUA	C	442	32.964	8.028	85.534	1.00 70.89	C
ATOM	3138	O4'	GUA	C	442	32.854	9.114	86.483	1.00 69.42	C
ATOM	3139	C1'	GUA	C	442	31.710	9.895	86.176	1.00 69.07	C
ATOM	3140	N9	GUA	C	442	32.148	11.239	85.830	1.00 69.99	C
ATOM	3141	C4	GUA	C	442	31.341	12.276	85.441	1.00 70.26	C
ATOM	3142	N3	GUA	C	442	30.001	12.225	85.304	1.00 70.70	C
ATOM	3143	C2	GUA	C	442	29.500	13.389	84.932	1.00 71.20	C
ATOM	3144	N2	GUA	C	442	28.181	13.513	84.739	1.00 72.00	C
ATOM	3145	N1	GUA	C	442	30.255	14.518	84.720	1.00 71.27	C
ATOM	3146	C6	GUA	C	442	31.638	14.595	84.866	1.00 71.01	C
ATOM	3147	O6	GUA	C	442	32.224	15.671	84.676	1.00 71.49	C
ATOM	3148	C5	GUA	C	442	32.188	13.348	85.248	1.00 70.44	C
ATOM	3149	N7	GUA	C	442	33.504	12.984	85.492	1.00 69.90	C
ATOM	3150	C8	GUA	C	442	33.433	11.726	85.833	1.00 70.15	C
ATOM	3151	C2'	GUA	C	442	31.029	9.239	84.983	1.00 68.98	C
ATOM	3152	O2'	GUA	C	442	30.049	8.342	85.438	1.00 69.32	C
ATOM	3153	C3'	GUA	C	442	32.207	8.541	84.327	1.00 69.32	C
ATOM	3154	O3'	GUA	C	442	31.757	7.461	83.538	1.00 67.22	C
ATOM	3155	P	CYT	C	443	31.675	7.628	81.951	1.00 66.82	C
ATOM	3156	O1P	CYT	C	443	32.780	8.543	81.568	1.00 65.40	C
ATOM	3157	O2P	CYT	C	443	31.602	6.273	81.351	1.00 66.64	C
ATOM	3158	O5'	CYT	C	443	30.280	8.362	81.719	1.00 64.23	C
ATOM	3159	C5'	CYT	C	443	29.212	8.179	82.632	1.00 60.44	C
ATOM	3160	C4'	CYT	C	443	28.034	9.028	82.237	1.00 60.42	C
ATOM	3161	O4'	CYT	C	443	28.120	10.311	82.901	1.00 60.75	C
ATOM	3162	C1'	CYT	C	443	27.632	11.325	82.043	1.00 59.94	C
ATOM	3163	N1	CYT	C	443	28.741	12.233	81.752	1.00 60.55	C
ATOM	3164	C6	CYT	C	443	30.034	11.807	81.851	1.00 61.41	C
ATOM	3165	C2	CYT	C	443	28.458	13.543	81.398	1.00 61.61	C
ATOM	3166	O2	CYT	C	443	27.281	13.879	81.264	1.00 62.93	C
ATOM	3167	N3	CYT	C	443	29.473	14.411	81.203	1.00 62.99	C
ATOM	3168	C4	CYT	C	443	30.736	13.998	81.338	1.00 63.16	C
ATOM	3169	N4	CYT	C	443	31.714	14.898	81.176	1.00 63.54	C
ATOM	3170	C5	CYT	C	443	31.054	12.648	81.655	1.00 62.50	C

ATOM	3171	C2'	CYT	C 443	27.071	10.626	80.811	1.00	60.08	C
ATOM	3172	O2'	CYT	C 443	25.713	10.318	81.032	1.00	58.31	C
ATOM	3173	C3'	CYT	C 443	27.939	9.382	80.770	1.00	60.24	C
ATOM	3174	O3'	CYT	C 443	27.290	8.353	80.052	1.00	61.43	C
ATOM	3175	P	URI	C 444	27.651	8.130	78.509	1.00	62.89	C
ATOM	3176	O1P	URI	C 444	29.135	8.146	78.411	1.00	62.11	C
ATOM	3177	O2P	URI	C 444	26.902	6.940	78.051	1.00	62.24	C
ATOM	3178	O5'	URI	C 444	27.049	9.422	77.789	1.00	62.10	C
ATOM	3179	C5'	URI	C 444	25.641	9.652	77.769	1.00	60.87	C
ATOM	3180	C4'	URI	C 444	25.324	11.023	77.207	1.00	61.87	C
ATOM	3181	O4'	URI	C 444	25.733	12.063	78.133	1.00	63.01	C
ATOM	3182	C1'	URI	C 444	26.046	13.248	77.410	1.00	62.90	C
ATOM	3183	N1	URI	C 444	27.444	13.612	77.690	1.00	64.77	C
ATOM	3184	C6	URI	C 444	28.354	12.674	78.113	1.00	65.25	C
ATOM	3185	C2	URI	C 444	27.826	14.936	77.505	1.00	64.97	C
ATOM	3186	O2	URI	C 444	27.060	15.803	77.139	1.00	66.12	C
ATOM	3187	N3	URI	C 444	29.144	15.204	77.763	1.00	65.12	C
ATOM	3188	C4	URI	C 444	30.105	14.311	78.170	1.00	65.52	C
ATOM	3189	O4	URI	C 444	31.270	14.694	78.287	1.00	66.32	C
ATOM	3190	C5	URI	C 444	29.637	12.970	78.351	1.00	66.21	C
ATOM	3191	C2'	URI	C 444	25.805	12.934	75.933	1.00	62.39	C
ATOM	3192	O2'	URI	C 444	24.491	13.306	75.581	1.00	60.13	C
ATOM	3193	C3'	URI	C 444	26.013	11.425	75.918	1.00	62.63	C
ATOM	3194	O3'	URI	C 444	25.383	10.827	74.793	1.00	64.64	C
ATOM	3195	P	ADE	C 445	25.916	11.155	73.308	1.00	66.28	C
ATOM	3196	O1P	ADE	C 445	25.219	10.211	72.397	1.00	64.73	C
ATOM	3197	O2P	ADE	C 445	27.409	11.194	73.325	1.00	66.33	C
ATOM	3198	O5'	ADE	C 445	25.378	12.631	73.036	1.00	62.89	C
ATOM	3199	C5'	ADE	C 445	26.059	13.503	72.143	1.00	62.04	C
ATOM	3200	C4'	ADE	C 445	25.576	14.918	72.337	1.00	61.54	C
ATOM	3201	O4'	ADE	C 445	26.035	15.392	73.628	1.00	61.02	C
ATOM	3202	C1'	ADE	C 445	26.237	16.797	73.573	1.00	59.77	C
ATOM	3203	N9	ADE	C 445	27.620	17.092	73.952	1.00	57.68	C
ATOM	3204	C4	ADE	C 445	28.145	18.350	74.089	1.00	57.02	C
ATOM	3205	N3	ADE	C 445	27.499	19.518	73.939	1.00	58.61	C
ATOM	3206	C2	ADE	C 445	28.333	20.541	74.126	1.00	60.44	C
ATOM	3207	N1	ADE	C 445	29.641	20.529	74.422	1.00	58.87	C
ATOM	3208	C6	ADE	C 445	30.256	19.337	74.571	1.00	57.61	C
ATOM	3209	N6	ADE	C 445	31.557	19.330	74.874	1.00	58.29	C
ATOM	3210	C5	ADE	C 445	29.477	18.172	74.399	1.00	56.54	C
ATOM	3211	N7	ADE	C 445	29.783	16.821	74.481	1.00	56.12	C
ATOM	3212	C8	ADE	C 445	28.649	16.225	74.213	1.00	56.67	C
ATOM	3213	C2'	ADE	C 445	25.940	17.243	72.139	1.00	60.70	C
ATOM	3214	O2'	ADE	C 445	24.631	17.755	72.031	1.00	58.79	C
ATOM	3215	C3'	ADE	C 445	26.135	15.946	71.368	1.00	61.36	C
ATOM	3216	O3'	ADE	C 445	25.406	15.987	70.150	1.00	63.54	C
ATOM	3217	P	ADE	C 446	26.082	16.646	68.855	1.00	65.43	C
ATOM	3218	O1P	ADE	C 446	25.161	16.539	67.699	1.00	64.30	C
ATOM	3219	O2P	ADE	C 446	27.449	16.070	68.762	1.00	64.89	C
ATOM	3220	O5'	ADE	C 446	26.212	18.185	69.236	1.00	65.58	C
ATOM	3221	C5'	ADE	C 446	25.061	18.980	69.484	1.00	67.19	C
ATOM	3222	C4'	ADE	C 446	25.449	20.438	69.609	1.00	69.70	C
ATOM	3223	O4'	ADE	C 446	26.117	20.673	70.881	1.00	69.91	C
ATOM	3224	C1'	ADE	C 446	27.070	21.719	70.732	1.00	68.88	C
ATOM	3225	N9	ADE	C 446	28.390	21.162	71.001	1.00	67.70	C
ATOM	3226	C4	ADE	C 446	29.535	21.876	71.246	1.00	66.81	C
ATOM	3227	N3	ADE	C 446	29.667	23.211	71.291	1.00	66.09	C
ATOM	3228	C2	ADE	C 446	30.929	23.545	71.544	1.00	65.77	C
ATOM	3229	N1	ADE	C 446	31.991	22.758	71.741	1.00	64.82	C
ATOM	3230	C6	ADE	C 446	31.821	21.422	71.690	1.00	65.47	C
ATOM	3231	N6	ADE	C 446	32.882	20.636	71.883	1.00	66.43	C

ATOM	3232	C5	ADE	C 446	30.532	20.938	71.431	1.00	66.11	C
ATOM	3233	N7	ADE	C 446	30.025	19.653	71.306	1.00	67.03	C
ATOM	3234	C8	ADE	C 446	28.753	19.840	71.051	1.00	67.08	C
ATOM	3235	C2'	ADE	C 446	26.974	22.201	69.284	1.00	70.69	C
ATOM	3236	O2'	ADE	C 446	26.100	23.309	69.172	1.00	71.01	C
ATOM	3237	C3'	ADE	C 446	26.462	20.944	68.599	1.00	70.64	C
ATOM	3238	O3'	ADE	C 446	25.863	21.222	67.346	1.00	72.10	C
ATOM	3239	P	ADE	C 447	26.629	20.801	66.002	1.00	74.80	C
ATOM	3240	O1P	ADE	C 447	25.726	21.123	64.867	1.00	74.26	C
ATOM	3241	O2P	ADE	C 447	27.136	19.409	66.164	1.00	73.67	C
ATOM	3242	O5'	ADE	C 447	27.877	21.791	65.965	1.00	73.64	C
ATOM	3243	C5'	ADE	C 447	27.703	23.182	66.193	1.00	73.27	C
ATOM	3244	C4'	ADE	C 447	29.010	23.806	66.603	1.00	73.72	C
ATOM	3245	O4'	ADE	C 447	29.479	23.193	67.826	1.00	72.33	C
ATOM	3246	C1'	ADE	C 447	30.894	23.188	67.843	1.00	72.82	C
ATOM	3247	N9	ADE	C 447	31.335	21.803	67.995	1.00	73.10	C
ATOM	3248	C4	ADE	C 447	32.552	21.369	68.464	1.00	72.15	C
ATOM	3249	N3	ADE	C 447	33.582	22.124	68.880	1.00	72.73	C
ATOM	3250	C2	ADE	C 447	34.600	21.352	69.276	1.00	72.40	C
ATOM	3251	N1	ADE	C 447	34.695	20.015	69.296	1.00	70.81	C
ATOM	3252	C6	ADE	C 447	33.642	19.290	68.867	1.00	70.89	C
ATOM	3253	N6	ADE	C 447	33.738	17.961	68.877	1.00	69.94	C
ATOM	3254	C5	ADE	C 447	32.500	19.987	68.428	1.00	71.53	C
ATOM	3255	N7	ADE	C 447	31.271	19.555	67.949	1.00	72.07	C
ATOM	3256	C8	ADE	C 447	30.620	20.667	67.706	1.00	72.94	C
ATOM	3257	C2'	ADE	C 447	31.359	23.840	66.541	1.00	73.60	C
ATOM	3258	O2'	ADE	C 447	31.584	25.213	66.757	1.00	72.67	C
ATOM	3259	C3'	ADE	C 447	30.158	23.597	65.639	1.00	74.90	C
ATOM	3260	O3'	ADE	C 447	30.084	24.566	64.603	1.00	79.87	C
ATOM	3261	P	ADE	C 448	30.492	24.163	63.098	1.00	83.67	C
ATOM	3262	O1P	ADE	C 448	29.899	25.203	62.213	1.00	82.49	C
ATOM	3263	O2P	ADE	C 448	30.178	22.725	62.860	1.00	80.82	C
ATOM	3264	O5'	ADE	C 448	32.077	24.339	63.091	1.00	84.13	C
ATOM	3265	C5'	ADE	C 448	32.699	25.406	62.374	1.00	84.08	C
ATOM	3266	C4'	ADE	C 448	32.454	26.728	63.066	1.00	83.97	C
ATOM	3267	O4'	ADE	C 448	32.636	26.595	64.504	1.00	83.19	C
ATOM	3268	C1'	ADE	C 448	33.134	27.821	65.033	1.00	83.31	C
ATOM	3269	N9	ADE	C 448	34.454	27.575	65.611	1.00	82.50	C
ATOM	3270	C4	ADE	C 448	35.292	28.540	66.112	1.00	81.82	C
ATOM	3271	N3	ADE	C 448	35.047	29.857	66.208	1.00	82.11	C
ATOM	3272	C2	ADE	C 448	36.095	30.491	66.727	1.00	82.15	C
ATOM	3273	N1	ADE	C 448	37.275	29.996	67.122	1.00	81.66	C
ATOM	3274	C6	ADE	C 448	37.492	28.671	67.003	1.00	80.57	C
ATOM	3275	N6	ADE	C 448	38.676	28.191	67.369	1.00	78.90	C
ATOM	3276	C5	ADE	C 448	36.449	27.882	66.484	1.00	81.08	C
ATOM	3277	N7	ADE	C 448	36.333	26.520	66.253	1.00	81.17	C
ATOM	3278	C8	ADE	C 448	35.131	26.388	65.742	1.00	82.13	C
ATOM	3279	C2'	ADE	C 448	33.242	28.796	63.858	1.00	83.95	C
ATOM	3280	O2'	ADE	C 448	32.075	29.588	63.742	1.00	84.45	C
ATOM	3281	C3'	ADE	C 448	33.436	27.827	62.704	1.00	84.49	C
ATOM	3282	O3'	ADE	C 448	33.142	28.405	61.440	1.00	86.19	C
ATOM	3283	P	ADE	C 449	34.210	28.275	60.245	1.00	87.99	C
ATOM	3284	O1P	ADE	C 449	33.853	29.283	59.215	1.00	87.00	C
ATOM	3285	O2P	ADE	C 449	34.307	26.840	59.863	1.00	86.93	C
ATOM	3286	O5'	ADE	C 449	35.588	28.715	60.919	1.00	86.55	C
ATOM	3287	C5'	ADE	C 449	35.750	30.027	61.447	1.00	85.31	C
ATOM	3288	C4'	ADE	C 449	37.078	30.154	62.154	1.00	85.28	C
ATOM	3289	O4'	ADE	C 449	37.082	29.328	63.350	1.00	85.85	C
ATOM	3290	C1'	ADE	C 449	38.410	28.880	63.611	1.00	84.64	C
ATOM	3291	N9	ADE	C 449	38.424	27.420	63.534	1.00	82.84	C
ATOM	3292	C4	ADE	C 449	39.426	26.589	63.976	1.00	81.56	C

ATOM	3293	N3	ADE	C	449	40.587	26.942	64.555	1.00	80.63	C
ATOM	3294	C2	ADE	C	449	41.310	25.864	64.858	1.00	79.78	C
ATOM	3295	N1	ADE	C	449	41.030	24.571	64.665	1.00	79.45	C
ATOM	3296	C6	ADE	C	449	39.856	24.249	64.080	1.00	81.05	C
ATOM	3297	N6	ADE	C	449	39.571	22.957	63.888	1.00	81.21	C
ATOM	3298	C5	ADE	C	449	38.996	25.305	63.706	1.00	81.23	C
ATOM	3299	N7	ADE	C	449	37.749	25.326	63.096	1.00	81.07	C
ATOM	3300	C8	ADE	C	449	37.456	26.600	63.017	1.00	80.87	C
ATOM	3301	C2'	ADE	C	449	39.302	29.513	62.544	1.00	84.95	C
ATOM	3302	O2'	ADE	C	449	39.817	30.743	63.022	1.00	84.38	C
ATOM	3303	C3'	ADE	C	449	38.305	29.666	61.403	1.00	85.19	C
ATOM	3304	O3'	ADE	C	449	38.751	30.611	60.443	1.00	84.91	C
ATOM	3305	P	GUA	C	450	39.413	30.095	59.074	1.00	84.58	C
ATOM	3306	O1P	GUA	C	450	38.369	29.339	58.332	1.00	83.17	C
ATOM	3307	O2P	GUA	C	450	40.085	31.251	58.427	1.00	84.98	C
ATOM	3308	O5'	GUA	C	450	40.556	29.094	59.551	1.00	83.16	C
ATOM	3309	C5'	GUA	C	450	41.783	29.595	60.073	1.00	81.52	C
ATOM	3310	C4'	GUA	C	450	42.628	28.459	60.594	1.00	81.00	C
ATOM	3311	O4'	GUA	C	450	41.834	27.654	61.508	1.00	80.06	C
ATOM	3312	C1'	GUA	C	450	42.197	26.286	61.380	1.00	79.33	C
ATOM	3313	N9	GUA	C	450	41.032	25.541	60.904	1.00	77.56	C
ATOM	3314	C4	GUA	C	450	40.926	24.175	60.809	1.00	74.96	C
ATOM	3315	N3	GUA	C	450	41.891	23.285	61.115	1.00	72.47	C
ATOM	3316	C2	GUA	C	450	41.486	22.042	60.933	1.00	72.36	C
ATOM	3317	N2	GUA	C	450	42.324	21.023	61.174	1.00	71.30	C
ATOM	3318	N1	GUA	C	450	40.227	21.701	60.498	1.00	72.99	C
ATOM	3319	C6	GUA	C	450	39.216	22.600	60.187	1.00	72.97	C
ATOM	3320	O6	GUA	C	450	38.113	22.183	59.828	1.00	72.47	C
ATOM	3321	C5	GUA	C	450	39.641	23.937	60.357	1.00	74.31	C
ATOM	3322	N7	GUA	C	450	38.963	25.129	60.146	1.00	75.07	C
ATOM	3323	C8	GUA	C	450	39.825	26.054	60.481	1.00	77.45	C
ATOM	3324	C2'	GUA	C	450	43.375	26.233	60.410	1.00	80.25	C
ATOM	3325	O2'	GUA	C	450	44.596	26.322	61.117	1.00	78.73	C
ATOM	3326	C3'	GUA	C	450	43.084	27.454	59.551	1.00	80.96	C
ATOM	3327	O3'	GUA	C	450	44.236	27.901	58.853	1.00	81.13	C
ATOM	3328	P	GUA	C	451	44.420	27.508	57.305	1.00	81.46	C
ATOM	3329	O1P	GUA	C	451	43.133	27.796	56.616	1.00	80.36	C
ATOM	3330	O2P	GUA	C	451	45.673	28.147	56.825	1.00	80.48	C
ATOM	3331	O5'	GUA	C	451	44.631	25.927	57.341	1.00	79.28	C
ATOM	3332	C5'	GUA	C	451	45.580	25.349	58.229	1.00	76.29	C
ATOM	3333	C4'	GUA	C	451	45.730	23.875	57.957	1.00	74.88	C
ATOM	3334	O4'	GUA	C	451	44.758	23.130	58.728	1.00	73.92	C
ATOM	3335	C1'	GUA	C	451	44.363	21.975	58.003	1.00	72.37	C
ATOM	3336	N9	GUA	C	451	42.947	22.106	57.687	1.00	69.07	C
ATOM	3337	C4	GUA	C	451	42.051	21.085	57.486	1.00	66.32	C
ATOM	3338	N3	GUA	C	451	42.325	19.763	57.546	1.00	63.40	C
ATOM	3339	C2	GUA	C	451	41.246	19.027	57.317	1.00	63.39	C
ATOM	3340	N2	GUA	C	451	41.323	17.683	57.356	1.00	60.65	C
ATOM	3341	N1	GUA	C	451	40.004	19.554	57.040	1.00	64.12	C
ATOM	3342	C6	GUA	C	451	39.703	20.914	56.975	1.00	64.33	C
ATOM	3343	O6	GUA	C	451	38.544	21.287	56.729	1.00	62.58	C
ATOM	3344	C5	GUA	C	451	40.846	21.707	57.222	1.00	65.72	C
ATOM	3345	N7	GUA	C	451	40.987	23.086	57.252	1.00	67.31	C
ATOM	3346	C8	GUA	C	451	42.247	23.277	57.530	1.00	67.97	C
ATOM	3347	C2'	GUA	C	451	45.215	21.935	56.736	1.00	73.66	C
ATOM	3348	O2'	GUA	C	451	46.375	21.162	56.966	1.00	72.93	C
ATOM	3349	C3'	GUA	C	451	45.501	23.414	56.529	1.00	74.10	C
ATOM	3350	O3'	GUA	C	451	46.695	23.571	55.791	1.00	76.92	C
ATOM	3351	P	ADE	C	452	46.646	23.622	54.191	1.00	79.92	C
ATOM	3352	O1P	ADE	C	452	45.749	24.737	53.778	1.00	77.97	C
ATOM	3353	O2P	ADE	C	452	48.062	23.622	53.752	1.00	80.27	C

ATOM	3354	O5'	ADE	C	452	46.002	22.225	53.768	1.00	81.04	C
ATOM	3355	PC	ADE	C	452	47.403	20.187	49.052	1.00	94.69	C
ATOM	3356	O1C	ADE	C	452	48.478	20.648	48.135	1.00	92.74	C
ATOM	3357	O2C	ADE	C	452	46.873	18.888	48.562	1.00	93.16	C
ATOM	3358	O3'	ADE	C	452	47.997	19.949	50.531	1.00	92.25	C
ATOM	3359	C5'	ADE	C	452	46.769	21.023	53.811	1.00	84.82	C
ATOM	3360	C4'	ADE	C	452	46.607	20.249	52.521	1.00	88.58	C
ATOM	3361	O4'	ADE	C	452	45.193	20.079	52.251	1.00	89.88	C
ATOM	3362	C1'	ADE	C	452	44.954	20.314	50.882	1.00	90.96	C
ATOM	3363	N9	ADE	C	452	43.567	20.751	50.722	1.00	90.40	C
ATOM	3364	C4	ADE	C	452	42.474	19.924	50.615	1.00	89.68	C
ATOM	3365	N3	ADE	C	452	42.462	18.579	50.648	1.00	89.15	C
ATOM	3366	C2	ADE	C	452	41.222	18.118	50.497	1.00	89.12	C
ATOM	3367	N1	ADE	C	452	40.076	18.797	50.332	1.00	88.58	C
ATOM	3368	C6	ADE	C	452	40.123	20.148	50.308	1.00	89.15	C
ATOM	3369	N6	ADE	C	452	38.982	20.827	50.148	1.00	88.59	C
ATOM	3370	C5	ADE	C	452	41.383	20.761	50.455	1.00	89.44	C
ATOM	3371	N7	ADE	C	452	41.779	22.092	50.468	1.00	89.57	C
ATOM	3372	C8	ADE	C	452	43.079	22.033	50.633	1.00	90.05	C
ATOM	3373	C2'	ADE	C	452	46.001	21.345	50.459	1.00	91.00	C
ATOM	3374	O2'	ADE	C	452	46.225	21.291	49.060	1.00	92.14	C
ATOM	3375	C3'	ADE	C	452	47.216	20.892	51.270	1.00	90.65	C
TER											
HETATM	3376	CS+1	CS1		101	2.853	25.764	50.394	1.00	98.04	D
HETATM	3377	CS+1	CS1		501	30.101	22.718	92.220	1.00	108.11	F
HETATM	3378	MG+2	MG2		102	2.352	24.068	36.432	1.00	50.96	E
HETATM	3379	N	SAM		100	-8.439	27.146	69.630	1.00	67.99	G
HETATM	3380	CA	SAM		100	-9.271	27.703	68.534	1.00	70.40	G
HETATM	3381	C	SAM		100	-10.749	27.414	68.789	1.00	71.30	G
HETATM	3382	O	SAM		100	-11.601	27.834	68.013	1.00	71.72	G
HETATM	3383	OXT	SAM		100	-11.093	26.708	69.727	1.00	72.44	G
HETATM	3384	CB	SAM		100	-8.870	27.061	67.190	1.00	70.62	G
HETATM	3385	CG	SAM		100	-7.645	27.736	66.544	1.00	71.18	G
HETATM	3386	SD	SAM		100	-6.617	26.445	65.764	1.00	69.00	G
HETATM	3387	CE	SAM		100	-5.148	26.604	66.812	1.00	70.58	G
HETATM	3388	C5'	SAM		100	-6.000	27.274	64.272	1.00	68.56	G
HETATM	3389	C4'	SAM		100	-5.124	26.274	63.522	1.00	67.11	G
HETATM	3390	O4'	SAM		100	-5.882	25.101	63.332	1.00	68.09	G
HETATM	3391	C3'	SAM		100	-4.748	26.782	62.126	1.00	67.21	G
HETATM	3392	O3'	SAM		100	-3.403	27.274	62.073	1.00	66.59	G
HETATM	3393	C2'	SAM		100	-4.914	25.524	61.221	1.00	68.03	G
HETATM	3394	O2'	SAM		100	-3.763	25.403	60.376	1.00	68.41	G
HETATM	3395	C1'	SAM		100	-5.287	24.402	62.250	1.00	67.94	G
HETATM	3396	N9	SAM		100	-6.236	23.412	61.722	1.00	68.51	G
HETATM	3397	C8	SAM		100	-7.480	23.661	61.200	1.00	69.21	G
HETATM	3398	N7	SAM		100	-8.049	22.542	60.827	1.00	70.09	G
HETATM	3399	C5	SAM		100	-7.217	21.507	61.086	1.00	69.15	G
HETATM	3400	C6	SAM		100	-7.270	20.099	60.911	1.00	68.58	G
HETATM	3401	N6	SAM		100	-8.373	19.508	60.350	1.00	69.87	G
HETATM	3402	N1	SAM		100	-6.223	19.349	61.301	1.00	68.53	G
HETATM	3403	C2	SAM		100	-5.144	19.895	61.859	1.00	69.32	G
HETATM	3404	N3	SAM		100	-5.039	21.218	62.023	1.00	69.30	G
HETATM	3405	C4	SAM		100	-6.039	22.051	61.667	1.00	69.21	G
HETATM	3406	N	SAM		300	10.237	21.648	2.816	1.00	60.97	H
HETATM	3407	CA	SAM		300	11.651	22.047	3.005	1.00	62.32	H
HETATM	3408	C	SAM		300	12.362	21.942	1.712	1.00	62.83	H
HETATM	3409	O	SAM		300	13.587	21.876	1.687	1.00	64.00	H
HETATM	3410	OXT	SAM		300	11.716	21.890	0.688	1.00	64.42	H
HETATM	3411	CB	SAM		300	12.377	21.174	4.031	1.00	60.97	H
HETATM	3412	CG	SAM		300	11.577	21.118	5.324	1.00	63.92	H
HETATM	3413	SD	SAM		300	12.498	21.859	6.693	1.00	63.71	H

HETATM	3414	CE	SAM	300	14.101	21.012	6.547	1.00	64.61	H
HETATM	3415	C5'	SAM	300	11.741	20.937	8.074	1.00	64.51	H
HETATM	3416	C4'	SAM	300	12.212	21.514	9.408	1.00	64.50	H
HETATM	3417	O4'	SAM	300	12.014	22.911	9.367	1.00	64.16	H
HETATM	3418	C3'	SAM	300	11.355	20.977	10.578	1.00	64.84	H
HETATM	3419	O3'	SAM	300	12.242	20.357	11.519	1.00	63.50	H
HETATM	3420	C2'	SAM	300	10.763	22.266	11.209	1.00	64.14	H
HETATM	3421	O2'	SAM	300	10.507	22.213	12.604	1.00	65.81	H
HETATM	3422	C1'	SAM	300	11.770	23.312	10.702	1.00	64.78	H
HETATM	3423	N9	SAM	300	11.276	24.678	10.695	1.00	66.74	H
HETATM	3424	C8	SAM	300	10.025	25.110	10.342	1.00	67.03	H
HETATM	3425	N7	SAM	300	9.961	26.407	10.437	1.00	68.42	H
HETATM	3426	C5	SAM	300	11.160	26.888	10.851	1.00	68.11	H
HETATM	3427	C6	SAM	300	11.695	28.174	11.120	1.00	68.47	H
HETATM	3428	N6	SAM	300	10.914	29.302	10.963	1.00	68.71	H
HETATM	3429	N1	SAM	300	12.984	28.276	11.521	1.00	68.18	H
HETATM	3430	C2	SAM	300	13.765	27.201	11.655	1.00	67.60	H
HETATM	3431	N3	SAM	300	13.296	25.977	11.432	1.00	67.44	H
HETATM	3432	C4	SAM	300	12.020	25.779	11.024	1.00	67.46	H
HETATM	3433	N	SAM	500	37.476	19.907	71.774	1.00	68.92	I
HETATM	3434	CA	SAM	500	37.189	18.545	72.257	1.00	67.92	I
HETATM	3435	C	SAM	500	36.755	17.664	71.104	1.00	68.27	I
HETATM	3436	O	SAM	500	36.488	16.474	71.300	1.00	67.81	I
HETATM	3437	OXT	SAM	500	36.602	18.151	69.994	1.00	68.25	I
HETATM	3438	CB	SAM	500	36.063	18.606	73.284	1.00	66.91	I
HETATM	3439	CG	SAM	500	36.585	19.106	74.614	1.00	65.20	I
HETATM	3440	SD	SAM	500	35.226	19.924	75.468	1.00	66.03	I
HETATM	3441	CE	SAM	500	35.742	21.645	75.216	1.00	64.78	I
HETATM	3442	C5'	SAM	500	35.723	19.678	77.207	1.00	63.31	I
HETATM	3443	C4'	SAM	500	34.701	20.362	78.111	1.00	61.48	I
HETATM	3444	O4'	SAM	500	33.419	20.080	77.600	1.00	60.13	I
HETATM	3445	C3'	SAM	500	34.729	19.784	79.530	1.00	61.39	I
HETATM	3446	O3'	SAM	500	35.604	20.343	80.522	1.00	60.89	I
HETATM	3447	C2'	SAM	500	33.217	19.729	79.929	1.00	61.21	I
HETATM	3448	O2'	SAM	500	33.076	20.298	81.242	1.00	62.97	I
HETATM	3449	C1'	SAM	500	32.495	20.295	78.655	1.00	59.83	I
HETATM	3450	N9	SAM	500	31.254	19.595	78.306	1.00	59.64	I
HETATM	3451	C8	SAM	500	31.073	18.238	78.197	1.00	59.28	I
HETATM	3452	N7	SAM	500	29.849	17.970	77.845	1.00	59.16	I
HETATM	3453	C5	SAM	500	29.164	19.128	77.702	1.00	59.32	I
HETATM	3454	C6	SAM	500	27.830	19.479	77.339	1.00	59.18	I
HETATM	3455	N6	SAM	500	26.899	18.506	77.027	1.00	58.09	I
HETATM	3456	N1	SAM	500	27.493	20.782	77.296	1.00	59.09	I
HETATM	3457	C2	SAM	500	28.380	21.745	77.571	1.00	58.95	I
HETATM	3458	N3	SAM	500	29.630	21.460	77.925	1.00	58.97	I
HETATM	3459	C4	SAM	500	30.062	20.188	77.999	1.00	59.11	I
HETATM	3460	O	HOH	1000	1.710	38.862	57.073	1.00	6.38	S
HETATM	3461	O	HOH	1002	9.109	30.706	-10.011	1.00	41.55	S
HETATM	3462	O	HOH	1003	10.672	39.117	54.293	1.00	13.45	S
HETATM	3463	O	HOH	1004	-1.136	27.508	33.730	1.00	37.86	S
HETATM	3464	O	HOH	1005	9.642	20.371	24.593	1.00	23.91	S
HETATM	3465	O	HOH	1006	24.182	12.968	37.659	1.00	29.49	S
HETATM	3466	O	HOH	1007	23.014	43.756	107.299	1.00	42.31	S
HETATM	3467	O	HOH	1008	1.203	10.487	33.970	1.00	19.01	S
HETATM	3468	O	HOH	1009	0.895	28.820	56.844	1.00	19.53	S
HETATM	3469	O	HOH	1011	-12.488	37.567	51.296	1.00	41.81	S
HETATM	3470	O	HOH	1012	30.364	42.530	104.047	1.00	38.54	S
HETATM	3471	O	HOH	1013	14.002	22.976	53.710	1.00	32.39	S
HETATM	3472	O	HOH	1014	10.679	28.362	-4.887	1.00	74.66	S
HETATM	3473	O	HOH	1015	8.558	21.534	-0.603	1.00	37.38	S
HETATM	3474	O	HOH	1016	6.242	38.900	42.266	1.00	33.46	S

HETATM	3475	O	HOH	1017	-15.226	17.903	65.737	1.00	45.33	S
HETATM	3476	O	HOH	1018	4.523	11.428	11.327	1.00	36.06	S
HETATM	3477	O	HOH	1020	18.196	24.026	37.816	1.00	57.02	S
HETATM	3478	O	HOH	1021	-1.012	36.439	45.147	1.00	32.47	S
HETATM	3479	O	HOH	1022	7.578	20.568	51.009	1.00	39.39	S
HETATM	3480	O	HOH	1023	-14.823	28.188	59.227	1.00	30.57	S
HETATM	3481	O	HOH	1024	36.985	17.198	95.795	1.00	52.06	S
HETATM	3482	O	HOH	1026	25.333	21.807	45.339	1.00	36.69	S
HETATM	3483	O	HOH	1027	15.473	28.282	57.160	1.00	49.29	S
HETATM	3484	O	HOH	1028	41.659	12.070	93.116	1.00	51.81	S
HETATM	3485	O	HOH	1029	37.830	24.077	56.753	1.00	56.04	S
HETATM	3486	O	HOH	1030	1.496	18.974	19.910	1.00	46.52	S
HETATM	3487	O	HOH	1031	-21.564	18.695	76.954	1.00	42.72	S
HETATM	3488	O	HOH	1032	5.632	6.369	28.271	1.00	54.24	S
HETATM	3489	O	HOH	1033	-12.164	20.042	54.326	1.00	37.69	S
HETATM	3490	O	HOH	1034	-9.635	21.741	83.667	1.00	28.64	S
HETATM	3491	O	HOH	1035	16.349	18.517	-10.014	1.00	32.54	S
HETATM	3492	O	HOH	1036	-19.165	22.912	60.859	1.00	40.83	S
HETATM	3493	O	HOH	1037	42.317	14.698	87.404	1.00	54.29	S
HETATM	3494	O	HOH	1038	5.305	30.972	14.298	1.00	45.65	S
HETATM	3495	O	HOH	1039	17.404	7.202	37.021	1.00	42.45	S
HETATM	3496	O	HOH	1040	9.144	11.513	24.225	1.00	119.44	S
HETATM	3497	O	HOH	1041	3.177	32.569	38.072	1.00	25.83	S
HETATM	3498	O	HOH	1042	29.325	17.646	67.611	1.00	53.76	S
HETATM	3499	O	HOH	1043	-11.046	32.302	57.055	1.00	47.80	S
HETATM	3500	O	HOH	1045	2.422	16.973	31.694	1.00	41.35	S
HETATM	3501	O	HOH	1046	-13.045	28.534	71.549	1.00	47.13	S
HETATM	3502	O	HOH	1047	8.497	31.635	16.931	1.00	50.64	S
HETATM	3503	O	HOH	1048	-0.041	28.567	59.602	1.00	32.18	S
HETATM	3504	O	HOH	1049	24.871	19.578	80.883	1.00	68.34	S
HETATM	3505	O	HOH	1050	-7.523	19.578	79.061	1.00	113.57	S
HETATM	3506	O	HOH	1051	32.273	17.481	60.997	1.00	41.48	S
HETATM	3507	O	HOH	1052	1.502	18.555	10.879	1.00	50.88	S
HETATM	3508	O	HOH	1053	-1.995	27.026	58.607	1.00	49.02	S
HETATM	3509	O	HOH	1054	-17.653	24.848	53.584	1.00	77.80	S
HETATM	3510	O	HOH	1055	40.398	23.070	95.424	1.00	51.36	S
HETATM	3511	O	HOH	1056	15.212	31.641	-13.652	1.00	63.71	S
HETATM	3512	O	HOH	1057	24.773	21.394	76.777	1.00	54.68	S
HETATM	3513	O	HOH	1058	16.892	31.552	45.517	1.00	36.41	S
HETATM	3514	O	HOH	1059	10.090	33.120	2.682	1.00	35.81	S
HETATM	3515	O	HOH	1060	40.562	32.813	61.039	1.00	58.14	S
HETATM	3516	O	HOH	1061	14.161	20.416	47.160	1.00	49.47	S
HETATM	3517	O	HOH	1062	16.854	25.674	45.737	1.00	63.64	S
HETATM	3518	O	HOH	1063	3.203	43.376	51.094	1.00	49.11	S
HETATM	3519	O	HOH	1064	10.256	14.418	12.230	1.00	47.72	S
HETATM	3520	O	HOH	1065	-11.321	23.776	50.912	1.00	41.32	S
HETATM	3521	O	HOH	1066	43.248	26.720	100.251	1.00	43.17	S
HETATM	3522	O	HOH	1067	6.827	22.199	53.781	1.00	44.26	S
HETATM	3523	O	HOH	1068	11.021	5.705	24.649	1.00	32.82	S
HETATM	3524	O	HOH	1069	-5.141	16.290	65.889	1.00	67.72	S
HETATM	3525	O	HOH	1070	37.653	20.345	106.218	1.00	43.17	S
HETATM	3526	O	HOH	1071	1.874	28.432	16.664	1.00	40.53	S
HETATM	3527	O	HOH	1072	-3.039	39.908	51.178	1.00	52.15	S
HETATM	3528	O	HOH	1073	1.616	35.304	49.349	1.00	31.83	S
HETATM	3529	O	HOH	1074	19.821	9.573	32.159	1.00	94.53	S
HETATM	3530	O	HOH	1075	21.624	32.806	94.159	1.00	47.85	S
HETATM	3531	O	HOH	1076	24.732	34.155	108.435	1.00	51.09	S
HETATM	3532	O	HOH	1077	44.822	15.942	65.700	1.00	67.94	S
HETATM	3533	O	HOH	1078	36.613	14.026	63.136	1.00	45.24	S
HETATM	3534	O	HOH	1079	6.121	30.417	-2.435	1.00	46.00	S
HETATM	3535	O	HOH	1080	-4.110	38.667	58.528	1.00	47.87	S

HETATM	3536	O	HOH	1081	12.209	22.292	-13.923	1.00	42.28	S
HETATM	3537	O	HOH	1082	0.899	35.587	51.902	1.00	26.89	S
HETATM	3538	O	HOH	1083	44.968	38.661	100.718	1.00	44.22	S
HETATM	3539	O	HOH	1084	-16.065	33.146	77.476	1.00	39.70	S
HETATM	3540	O	HOH	1085	5.667	23.312	50.094	1.00	54.65	S
HETATM	3541	O	HOH	1086	13.710	35.700	41.870	1.00	32.97	S
HETATM	3542	O	HOH	1087	12.259	28.157	57.075	1.00	58.60	S
HETATM	3543	O	HOH	1088	9.409	21.549	27.534	1.00	31.98	S
HETATM	3544	O	HOH	1089	10.012	36.290	54.703	1.00	31.08	S
HETATM	3545	O	HOH	1090	24.694	14.271	55.811	1.00	58.74	S
HETATM	3546	O	HOH	1091	21.329	17.967	85.737	1.00	52.06	S
HETATM	3547	O	HOH	1092	28.126	18.707	-4.949	1.00	56.14	S
HETATM	3548	O	HOH	1093	7.439	16.780	52.218	1.00	40.03	S
HETATM	3549	O	HOH	1094	23.184	15.715	36.268	1.00	74.82	S
HETATM	3550	O	HOH	1095	12.880	8.881	36.591	1.00	45.48	S
HETATM	3551	O	HOH	1096	32.397	14.748	68.336	1.00	66.46	S
HETATM	3552	O	HOH	1097	29.121	35.417	93.382	1.00	61.44	S
HETATM	3553	O	HOH	1098	38.004	11.531	92.474	1.00	48.19	S
HETATM	3554	O	HOH	1099	-22.649	19.849	71.095	1.00	64.38	S
HETATM	3555	O	HOH	1100	12.052	19.274	24.729	1.00	31.27	S
HETATM	3556	O	HOH	1102	0.090	13.188	35.366	1.00	32.03	S
HETATM	3557	O	HOH	1104	23.453	21.387	48.664	1.00	63.46	S
HETATM	3558	O	HOH	1105	1.388	17.977	33.901	1.00	23.04	S
HETATM	3559	O	HOH	1106	7.878	30.217	-11.732	1.00	37.04	S
HETATM	3560	O	HOH	1107	-24.804	23.927	75.393	1.00	49.59	S
HETATM	3561	O	HOH	1108	16.882	19.485	-12.274	1.00	44.73	S
HETATM	3562	O	HOH	1109	14.777	27.186	38.023	1.00	29.39	S
HETATM	3563	O	HOH	1110	10.347	22.869	25.228	1.00	25.02	S
HETATM	3564	O	HOH	1111	29.806	43.730	102.021	1.00	65.53	S
HETATM	3565	O	HOH	1112	24.539	44.456	105.464	1.00	47.15	S
HETATM	3566	O	HOH	1114	2.511	8.834	32.890	1.00	40.34	S
HETATM	3567	O	HOH	1115	0.302	44.186	52.911	1.00	35.43	S
HETATM	3568	O	HOH	1117	35.474	19.466	108.178	1.00	47.59	S
HETATM	3569	O	HOH	1118	9.046	17.460	7.452	1.00	52.67	S
HETATM	3570	O	HOH	1119	13.977	25.103	55.311	1.00	65.26	S
HETATM	3571	O	HOH	1120	35.407	36.186	102.048	1.00	50.73	S
HETATM	3572	O	HOH	1121	22.824	25.739	-8.232	1.00	37.73	S
HETATM	3573	O	HOH	1122	0.043	26.609	56.812	1.00	54.24	S
HETATM	3574	O	HOH	1123	-13.846	35.118	50.740	1.00	32.63	S
HETATM	3575	O	HOH	1125	11.978	33.811	55.449	1.00	51.87	S
HETATM	3576	O	HOH	1126	-9.343	19.524	53.426	1.00	46.19	S
HETATM	3577	O	HOH	1127	6.170	24.270	42.074	1.00	36.77	S
HETATM	3578	O	HOH	1128	-4.329	16.897	62.855	1.00	54.10	S
HETATM	3579	O	HOH	1129	14.894	23.528	19.116	1.00	54.16	S
HETATM	3580	O	HOH	1130	17.139	17.867	35.891	1.00	36.70	S
HETATM	3581	O	HOH	1131	24.693	13.072	28.311	1.00	43.09	S
HETATM	3582	O	HOH	1132	-9.732	23.050	48.641	1.00	59.37	S
HETATM	3583	O	HOH	1134	19.573	25.812	-1.906	1.00	60.33	S
HETATM	3584	O	HOH	1135	16.632	2.961	29.344	1.00	55.25	S
HETATM	3585	O	HOH	1136	14.928	18.328	-7.543	1.00	56.32	S
HETATM	3586	O	HOH	1137	0.639	23.943	84.616	1.00	72.67	S
HETATM	3587	O	HOH	1138	7.076	38.013	40.230	1.00	36.05	S
HETATM	3588	O	HOH	1139	5.349	21.667	44.278	1.00	35.31	S
HETATM	3589	O	HOH	1140	-10.726	18.421	55.747	1.00	39.21	S
HETATM	3590	O	HOH	1141	13.721	30.346	55.808	1.00	60.85	S
HETATM	3591	O	HOH	1142	15.808	12.052	20.001	1.00	38.62	S
HETATM	3592	O	HOH	1143	41.564	40.597	95.179	1.00	54.30	S
HETATM	3593	O	HOH	1144	28.387	35.762	107.518	1.00	41.34	S
HETATM	3594	O	HOH	1145	-7.803	17.872	56.940	1.00	50.33	S
HETATM	3595	O	HOH	1146	-0.206	16.169	9.275	1.00	45.70	S
HETATM	3596	O	HOH	1147	22.226	14.100	6.368	1.00	54.35	S

HETATM	3597	O	HOH	1148	-3.958	39.941	64.039	1.00	38.06	S
HETATM	3598	O	HOH	1149	-15.212	25.794	59.423	1.00	56.35	S
HETATM	3599	O	HOH	1150	-0.407	7.594	32.284	1.00	37.21	S
HETATM	3600	O	HOH	1151	42.733	12.142	57.515	1.00	37.02	S
HETATM	3601	O	HOH	1152	31.461	6.907	58.235	1.00	37.15	S
HETATM	3602	O	HOH	1153	5.446	26.093	52.566	1.00	51.35	S
HETATM	3603	O	HOH	1154	33.199	9.154	79.042	1.00	48.70	S
HETATM	3604	O	HOH	1155	-18.518	20.525	59.955	1.00	46.00	S
HETATM	3605	O	HOH	1156	-2.783	28.127	64.601	1.00	49.49	S
HETATM	3606	O	HOH	1157	10.260	2.953	24.931	1.00	35.76	S
HETATM	3607	O	HOH	1158	17.806	19.552	41.831	1.00	62.42	S
HETATM	3608	O	HOH	1159	34.865	16.077	59.910	1.00	77.33	S
HETATM	3609	O	HOH	1160	13.810	38.261	-7.058	1.00	40.41	S
HETATM	3610	O	HOH	1161	10.253	23.899	0.112	1.00	44.76	S
HETATM	3611	O	HOH	1162	-8.092	22.939	45.493	1.00	60.62	S
HETATM	3612	O	HOH	1163	12.939	42.444	43.941	1.00	47.94	S
HETATM	3613	O	HOH	1164	-7.966	16.660	61.300	1.00	56.65	S
END										

The foregoing discussion of the invention has been presented for purposes of illustration and description. The foregoing is not intended to limit the invention to the form or forms disclosed herein. Although the description of the invention has included description of one or more embodiments and certain variations and modifications, other variations and modifications are within the scope of the invention, *e.g.*, as may be within the skill and knowledge of those in the art, after understanding the present disclosure. It is intended to obtain rights which include alternative embodiments to the extent permitted, including alternate, interchangeable and/or equivalent structures, functions, ranges or steps to those claimed, whether or not such alternate, interchangeable and/or equivalent structures, functions, ranges or steps are disclosed herein, and without intending to publicly dedicate any patentable subject matter.

What is Claimed is:

1. A method for identifying a compound that associates with a SAM-II riboswitch comprising the steps of:
modeling at least one portion of the SAM-II riboswitch atomic structure depicted in at least one of Fig. 4A (SEQ IDNO:6) or Fig. 4B (SEQ ID NO:7) with a test compound; and
determining an association between the test compound and the SAM-II riboswitch atomic structure.
2. The method of Claim 1, further comprising determining that the test compound reduces bacterial gene expression.
3. The method of Claim 1, further comprising determining that the test compound induces bacterial gene expression.
4. The method of Claim 1, wherein the association determination step comprises determining at least one of a minimum interaction energy, a binding constant, a dissociation constant, or a combination thereof, for the test compound with the modeling of at least one portion of the SAM-II riboswitch atomic structure.
5. The method of Claim 1, wherein the association determination step comprises determining the interaction of the test compound with one or more nucleotides of the SAM-II riboswitch comprising U10, U11, U12, U20, U21, G22, U44, A45, A46, A47, or a combination thereof.
6. The method of Claim 1, wherein the association determination step further comprises determining an interaction of the test compound with a S-adenosyl-methionine moiety comprising a ribose sugar, a methionine side chain, a sulfur atom, an adenine moiety or combination thereof.
7. The method of Claim 1, wherein the association determination step further comprises determining an interaction of the test compound with a nucleotide of the SAM-II riboswitch atomic structure comprising U10, U12, U20, G22, U44, A46, A47 or a combination thereof.

8. The method of Claim 1, wherein the association determination step further comprises determining an interaction of the test compound with a P2b helix region of the SAM-II riboswitch atomic structure.

9. A method of regulating gene expression in a cell by modulating an mRNA, the method comprising the steps of administering a SAM-II riboswitch modulating compound to the cell to modulate the SAM-II riboswitch activity of the mRNA.

10. The method of Claim 9, wherein gene expression is stimulated.

11. The method of Claim 9, wherein gene expression is inhibited.

12. The method of Claim 9, wherein the SAM-II riboswitch modulating compound forms a complex with the SAM-II riboswitch decreasing the formation of an antiterminator element by the mRNA.

13. The method of Claim 10, wherein the cell is a bacterial cell.

14. The method of Claim 14, wherein the bacterial cell is a gram-negative bacterial cell.

15. A SAM-II riboswitch, wherein one or more of nucleotides U10, U11, U12, U20, U21, G22, U44, A45, A46, A47 are modified.

16. The method of Claim 15, wherein interaction with a SAM-II riboswitch having the one or more modified nucleotide causes an increase gene expression in a cell.

17. The method of Claim 15, wherein interaction with a SAM-II riboswitch having the one or more modified nucleotide causes a decrease gene expression in a cell.

18. The method of Claim 15, wherein interaction with a SAM-II riboswitch having the one or more modified nucleotide causes a decreases in sulfur production in a cell.

19. A composition comprising a compound that associates with at least a portion of the SAM-II riboswitch atomic structure depicted in at least one of Fig. 4A (SEQ ID NO:6) or Fig. 4B (SEQ ID NO:7), wherein the association includes compound interaction with at least one of nucleotides U10, U11, U12, U20, U21, G22, U44, A45, A46, or A47, and wherein the composition is capable of modifying SAM-II riboswitch activity in a bacterial organism.

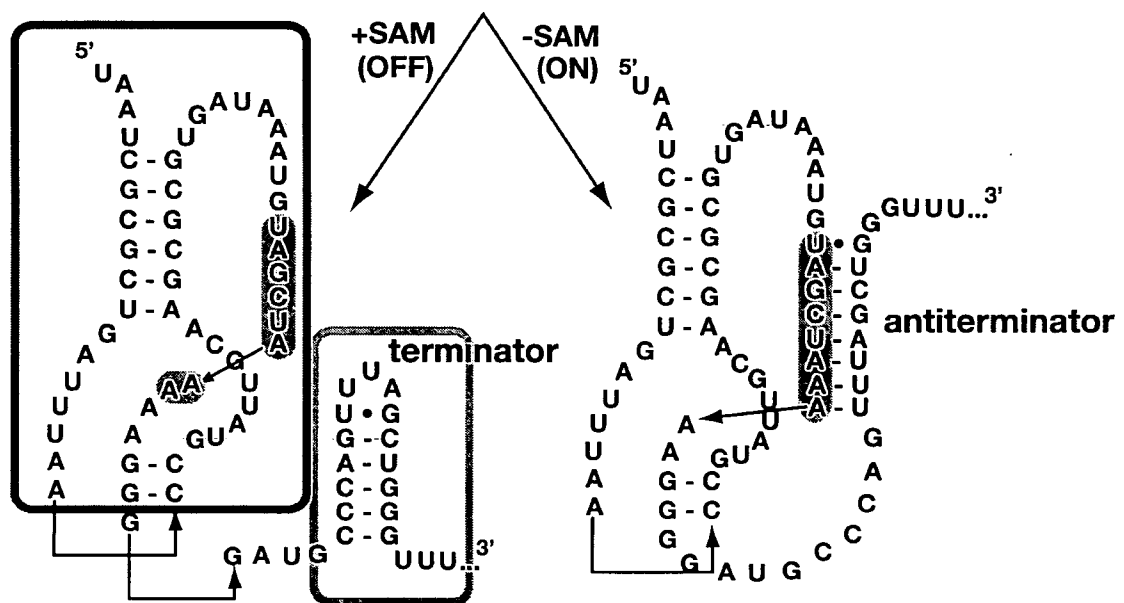
20. The composition of claim 19, wherein the composition further comprises a pharmaceutically acceptable excipient.

21. A composition comprising at least 80% of a conserved nucleotide sequence of a SAM-II riboswitch core depicted in Fig. 1 (SEQ ID NO:1) and 80% or more of nucleotides depicted outside of a conserved region depicted in Fig. 4A (SEQ ID NO:6) or 4B (SEQ ID NO:7).

22. The composition of claim 21, further comprising a nucleotide sequence depicted in Fig. 4A (SEQ ID NO:6) or 4B (SEQ ID NO:7).

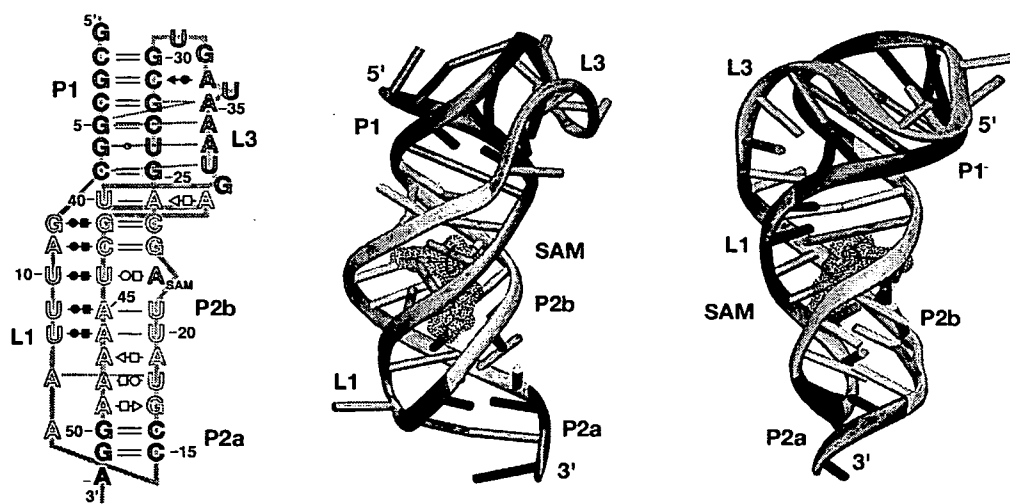
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Fig. 1



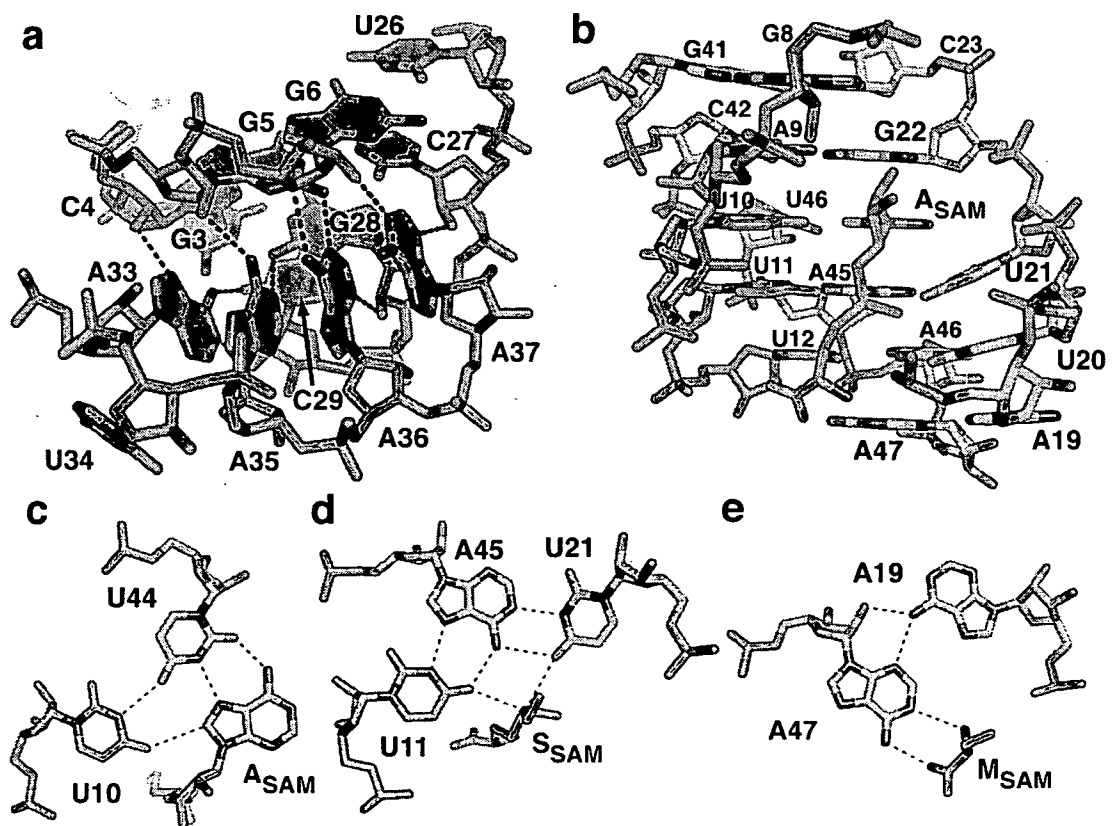
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Fig. 2



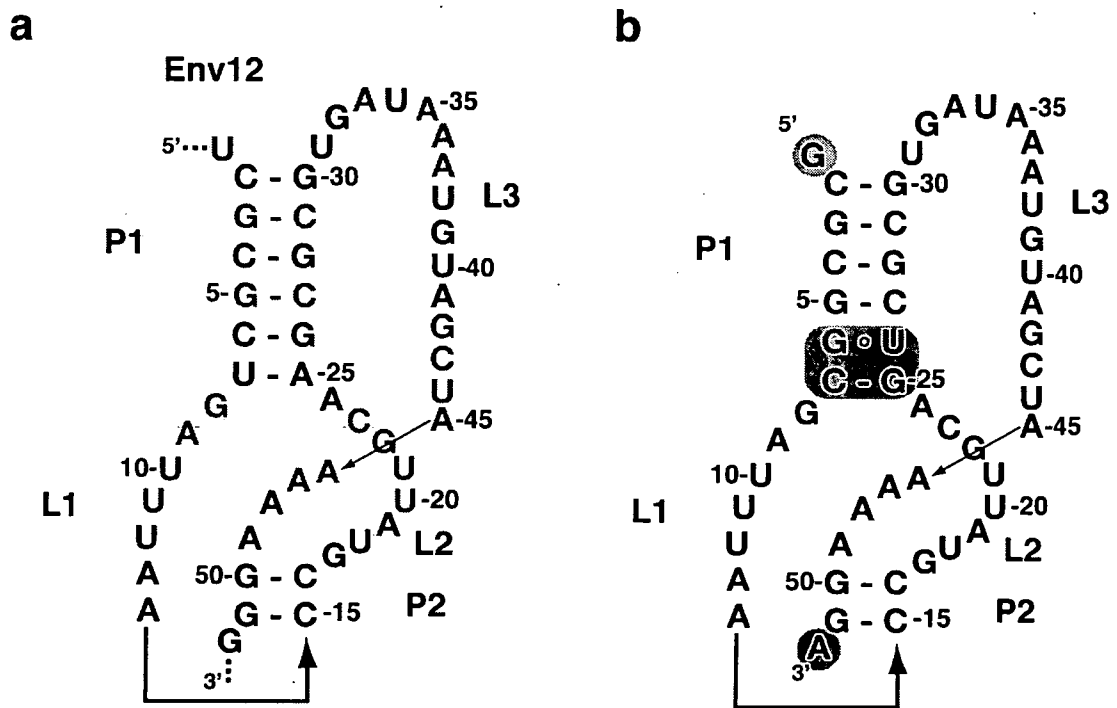
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Figs. 3a-3e



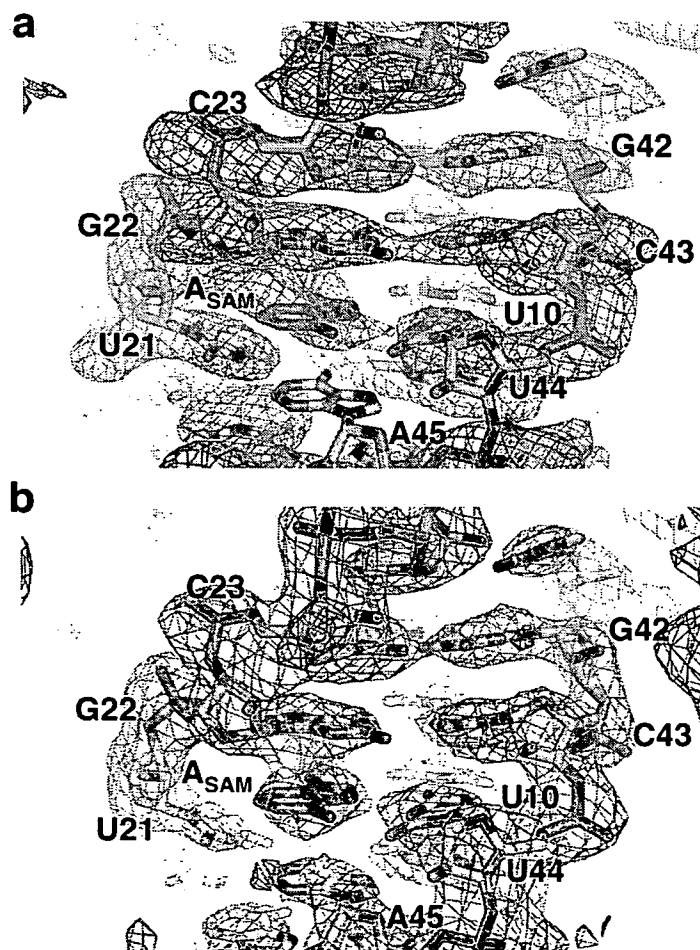
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Figs. 4a and 4b



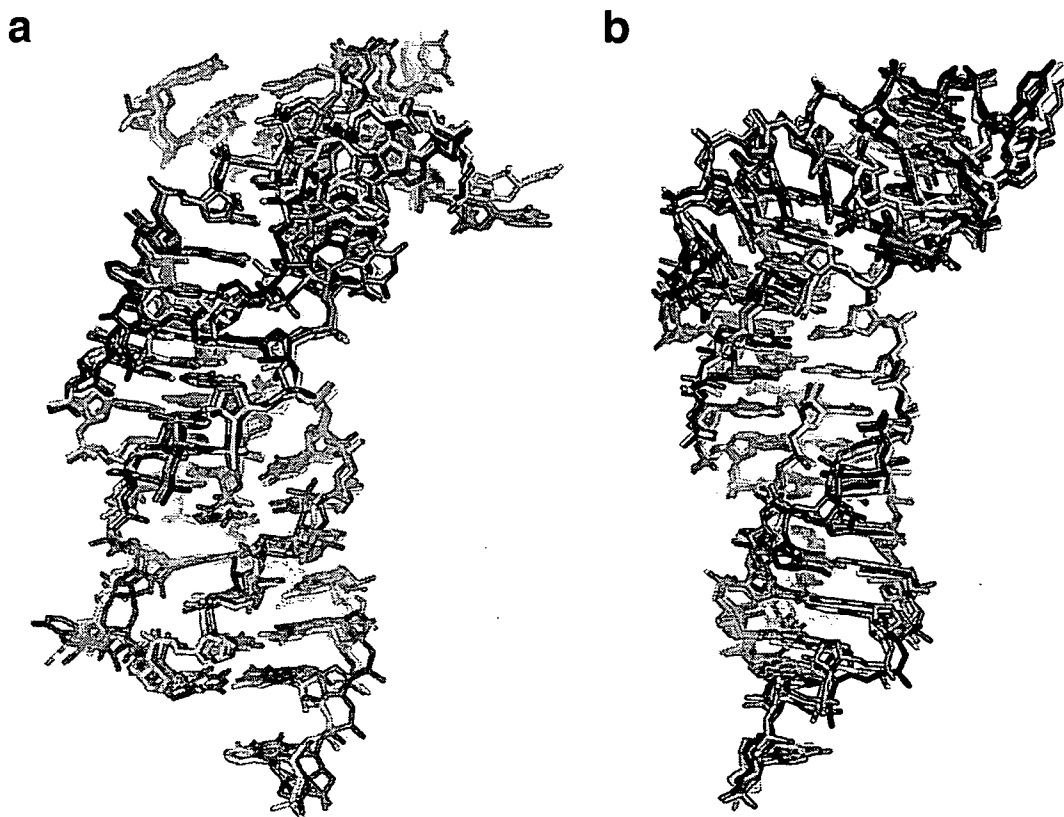
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Figs. 5a and 5b



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Figs. 6a and 6b



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Fig. 7

