



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 06:23 pm GMT

PDB ID : 4RDH  
Title : Crystal structure of E. coli tRNA N6-threonylcarbamoyladenosine dehydratase, TcdA  
Authors : Park, S.Y.; Kim, S.; Lee, H.  
Deposited on : 2014-09-19  
Resolution : 2.10 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

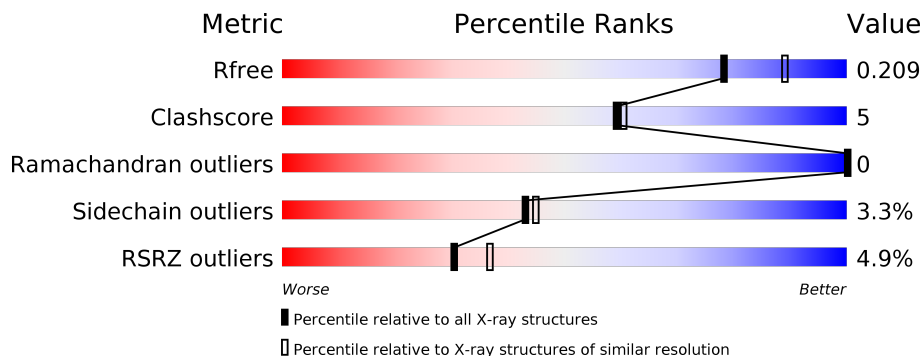
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	100719	4243 (2.10-2.10)
Clashscore	112137	4788 (2.10-2.10)
Ramachandran outliers	110173	4740 (2.10-2.10)
Sidechain outliers	110143	4741 (2.10-2.10)
RSRZ outliers	101464	4275 (2.10-2.10)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	288	<div> <div>%</div> <div> <div></div> <div>75%</div> <div>10%</div> <div>15%</div> </div> </div>
1	B	288	<div> <div>5%</div> <div> <div></div> <div>73%</div> <div>10%</div> <div>16%</div> </div> </div>
1	C	288	<div> <div>5%</div> <div> <div></div> <div>76%</div> <div>8%</div> <div>16%</div> </div> </div>
1	D	288	<div> <div>5%</div> <div> <div></div> <div>73%</div> <div>10%</div> <div>17%</div> </div> </div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7846 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called tRNA threonylcarbamoyladenosine dehydratase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	245	Total	C	N	O	S	Se	0	1	0
			1843	1160	329	342	6	6			
1	B	243	Total	C	N	O	S	Se	0	1	0
			1828	1152	326	338	6	6			
1	C	243	Total	C	N	O	S	Se	0	0	0
			1825	1150	326	338	5	6			
1	D	240	Total	C	N	O	S	Se	0	1	0
			1803	1135	323	333	6	6			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MSE	-	EXPRESSION TAG	UNP Q46927
A	-18	GLY	-	EXPRESSION TAG	UNP Q46927
A	-17	SER	-	EXPRESSION TAG	UNP Q46927
A	-16	SER	-	EXPRESSION TAG	UNP Q46927
A	-15	HIS	-	EXPRESSION TAG	UNP Q46927
A	-14	HIS	-	EXPRESSION TAG	UNP Q46927
A	-13	HIS	-	EXPRESSION TAG	UNP Q46927
A	-12	HIS	-	EXPRESSION TAG	UNP Q46927
A	-11	HIS	-	EXPRESSION TAG	UNP Q46927
A	-10	HIS	-	EXPRESSION TAG	UNP Q46927
A	-9	SER	-	EXPRESSION TAG	UNP Q46927
A	-8	SER	-	EXPRESSION TAG	UNP Q46927
A	-7	GLY	-	EXPRESSION TAG	UNP Q46927
A	-6	LEU	-	EXPRESSION TAG	UNP Q46927
A	-5	VAL	-	EXPRESSION TAG	UNP Q46927
A	-4	PRO	-	EXPRESSION TAG	UNP Q46927
A	-3	ARG	-	EXPRESSION TAG	UNP Q46927
A	-2	GLY	-	EXPRESSION TAG	UNP Q46927
A	-1	SER	-	EXPRESSION TAG	UNP Q46927
A	0	HIS	-	EXPRESSION TAG	UNP Q46927
B	-19	MSE	-	EXPRESSION TAG	UNP Q46927

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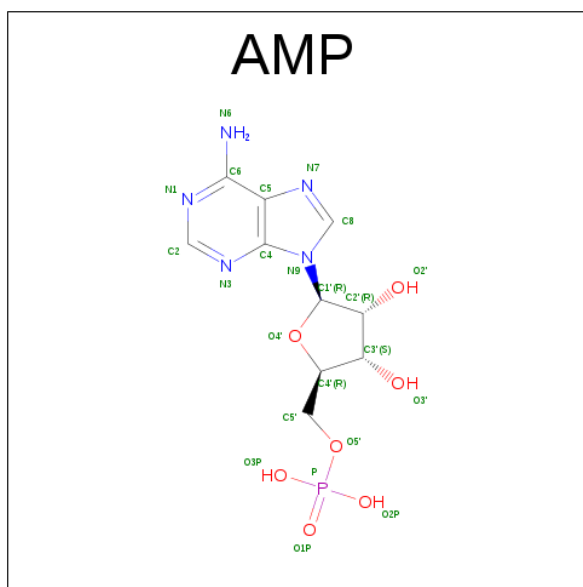
Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	EXPRESSION TAG	UNP Q46927
B	-17	SER	-	EXPRESSION TAG	UNP Q46927
B	-16	SER	-	EXPRESSION TAG	UNP Q46927
B	-15	HIS	-	EXPRESSION TAG	UNP Q46927
B	-14	HIS	-	EXPRESSION TAG	UNP Q46927
B	-13	HIS	-	EXPRESSION TAG	UNP Q46927
B	-12	HIS	-	EXPRESSION TAG	UNP Q46927
B	-11	HIS	-	EXPRESSION TAG	UNP Q46927
B	-10	HIS	-	EXPRESSION TAG	UNP Q46927
B	-9	SER	-	EXPRESSION TAG	UNP Q46927
B	-8	SER	-	EXPRESSION TAG	UNP Q46927
B	-7	GLY	-	EXPRESSION TAG	UNP Q46927
B	-6	LEU	-	EXPRESSION TAG	UNP Q46927
B	-5	VAL	-	EXPRESSION TAG	UNP Q46927
B	-4	PRO	-	EXPRESSION TAG	UNP Q46927
B	-3	ARG	-	EXPRESSION TAG	UNP Q46927
B	-2	GLY	-	EXPRESSION TAG	UNP Q46927
B	-1	SER	-	EXPRESSION TAG	UNP Q46927
B	0	HIS	-	EXPRESSION TAG	UNP Q46927
C	-19	MSE	-	EXPRESSION TAG	UNP Q46927
C	-18	GLY	-	EXPRESSION TAG	UNP Q46927
C	-17	SER	-	EXPRESSION TAG	UNP Q46927
C	-16	SER	-	EXPRESSION TAG	UNP Q46927
C	-15	HIS	-	EXPRESSION TAG	UNP Q46927
C	-14	HIS	-	EXPRESSION TAG	UNP Q46927
C	-13	HIS	-	EXPRESSION TAG	UNP Q46927
C	-12	HIS	-	EXPRESSION TAG	UNP Q46927
C	-11	HIS	-	EXPRESSION TAG	UNP Q46927
C	-10	HIS	-	EXPRESSION TAG	UNP Q46927
C	-9	SER	-	EXPRESSION TAG	UNP Q46927
C	-8	SER	-	EXPRESSION TAG	UNP Q46927
C	-7	GLY	-	EXPRESSION TAG	UNP Q46927
C	-6	LEU	-	EXPRESSION TAG	UNP Q46927
C	-5	VAL	-	EXPRESSION TAG	UNP Q46927
C	-4	PRO	-	EXPRESSION TAG	UNP Q46927
C	-3	ARG	-	EXPRESSION TAG	UNP Q46927
C	-2	GLY	-	EXPRESSION TAG	UNP Q46927
C	-1	SER	-	EXPRESSION TAG	UNP Q46927
C	0	HIS	-	EXPRESSION TAG	UNP Q46927
D	-19	MSE	-	EXPRESSION TAG	UNP Q46927
D	-18	GLY	-	EXPRESSION TAG	UNP Q46927
D	-17	SER	-	EXPRESSION TAG	UNP Q46927

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	SER	-	EXPRESSION TAG	UNP Q46927
D	-15	HIS	-	EXPRESSION TAG	UNP Q46927
D	-14	HIS	-	EXPRESSION TAG	UNP Q46927
D	-13	HIS	-	EXPRESSION TAG	UNP Q46927
D	-12	HIS	-	EXPRESSION TAG	UNP Q46927
D	-11	HIS	-	EXPRESSION TAG	UNP Q46927
D	-10	HIS	-	EXPRESSION TAG	UNP Q46927
D	-9	SER	-	EXPRESSION TAG	UNP Q46927
D	-8	SER	-	EXPRESSION TAG	UNP Q46927
D	-7	GLY	-	EXPRESSION TAG	UNP Q46927
D	-6	LEU	-	EXPRESSION TAG	UNP Q46927
D	-5	VAL	-	EXPRESSION TAG	UNP Q46927
D	-4	PRO	-	EXPRESSION TAG	UNP Q46927
D	-3	ARG	-	EXPRESSION TAG	UNP Q46927
D	-2	GLY	-	EXPRESSION TAG	UNP Q46927
D	-1	SER	-	EXPRESSION TAG	UNP Q46927
D	0	HIS	-	EXPRESSION TAG	UNP Q46927

- Molecule 2 is ADENOSINE MONOPHOSPHATE (three-letter code: AMP) (formula:  $C_{10}H_{14}N_5O_7P$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
2	B	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
2	C	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

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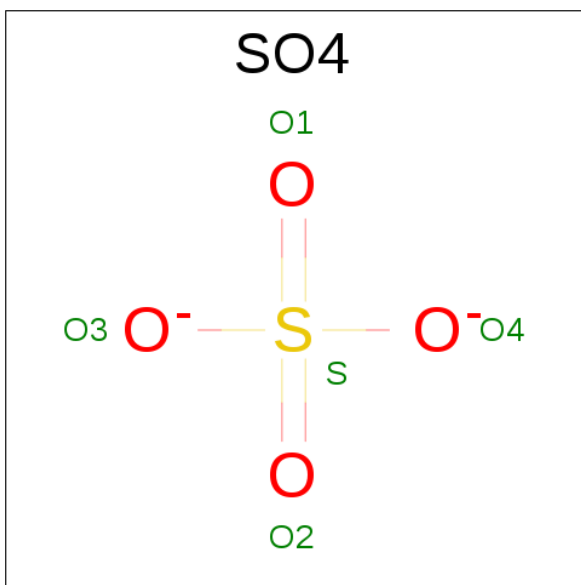
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	D	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula:  $C_3H_8O_3$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	C	1	Total	C	O	0	0
			6	3	3		
3	D	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula:  $O_4S$ ).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is water.

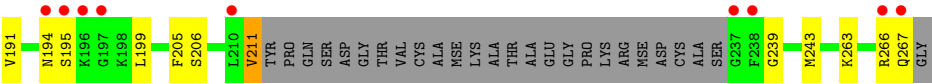
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	104	Total	O	0	0
			104	104		
5	B	114	Total	O	0	0
			114	114		
5	C	120	Total	O	0	0
			120	120		
5	D	88	Total	O	0	0
			88	88		



- Molecule 1: tRNA threonylcarbamoyladenosine dehydratase







## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	65.69Å 97.19Å 84.48Å 90.00° 112.04° 90.00°	Depositor
Resolution (Å)	50.00 – 2.10 29.94 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.6 (50.00-2.10) 99.6 (29.94-2.10)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	0.09	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	5.08 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, $R_{free}$	0.148 , 0.204 0.159 , 0.209	Depositor DCC
$R_{free}$ test set	2896 reflections (5.34%)	DCC
Wilson B-factor (Å <sup>2</sup> )	21.6	Xtriage
Anisotropy	0.578	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.41 , 53.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.025 for h,-k,-h-l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	7846	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.20% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, SO4, AMP

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.92	0/1866	0.94	1/2516 (0.0%)
1	B	0.90	1/1851 (0.1%)	0.97	6/2496 (0.2%)
1	C	0.81	0/1845	0.88	2/2488 (0.1%)
1	D	0.87	0/1824	0.88	2/2458 (0.1%)
All	All	0.88	1/7386 (0.0%)	0.92	11/9958 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	124	TYR	CE2-CZ	-5.08	1.31	1.38

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	72	ARG	NE-CZ-NH2	-5.86	117.37	120.30
1	D	144	ARG	NE-CZ-NH1	5.69	123.14	120.30
1	B	92	ARG	NE-CZ-NH2	-5.60	117.50	120.30
1	C	133	ARG	C-N-CD	5.59	140.15	128.40
1	B	72	ARG	NE-CZ-NH2	-5.58	117.51	120.30

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1843	0	1883	20	0
1	B	1828	0	1870	30	0
1	C	1825	0	1865	17	0
1	D	1803	0	1849	18	0
2	A	23	0	12	0	0
2	B	23	0	12	0	0
2	C	23	0	12	0	0
2	D	23	0	12	0	0
3	A	6	0	8	0	0
3	B	6	0	8	0	0
3	C	6	0	8	0	0
3	D	6	0	8	0	0
4	C	5	0	0	0	0
5	A	104	0	0	3	0
5	B	114	0	0	4	0
5	C	120	0	0	0	0
5	D	88	0	0	4	0
All	All	7846	0	7547	80	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 5.

The worst 5 of 80 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:194:ASN:OD1	1:D:195:SER:N	1.98	0.96
1:B:195:SER:HB2	1:B:196:LYS:HE3	1.46	0.94
1:D:194:ASN:OD1	1:D:195:SER:OG	1.86	0.92
1:B:195:SER:HB2	1:B:196:LYS:CE	2.03	0.89
1:B:195:SER:C	1:B:196:LYS:HE3	1.93	0.89

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	242/288 (84%)	236 (98%)	6 (2%)	0	100	100
1	B	240/288 (83%)	234 (98%)	6 (2%)	0	100	100
1	C	239/288 (83%)	236 (99%)	3 (1%)	0	100	100
1	D	237/288 (82%)	231 (98%)	6 (2%)	0	100	100
All	All	958/1152 (83%)	937 (98%)	21 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	193/215 (90%)	188 (97%)	5 (3%)	51	55
1	B	191/215 (89%)	182 (95%)	9 (5%)	30	28
1	C	190/215 (88%)	184 (97%)	6 (3%)	44	46
1	D	188/215 (87%)	183 (97%)	5 (3%)	50	54
All	All	762/860 (89%)	737 (97%)	25 (3%)	43	45

5 of 25 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	196	LYS
1	B	267	GLN
1	D	211	VAL
1	B	210	LEU
1	C	7	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	116	GLN
1	A	267	GLN
1	C	26	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

9 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	AMP	A	301	-	22,25,25	1.29	3 (13%)	24,38,38	1.92	6 (25%)
3	GOL	A	302	-	5,5,5	0.96	0	5,5,5	0.69	0
2	AMP	B	301	-	22,25,25	1.30	4 (18%)	24,38,38	2.15	9 (37%)
3	GOL	B	302	-	5,5,5	0.60	0	5,5,5	0.60	0
2	AMP	C	301	-	22,25,25	1.30	2 (9%)	24,38,38	1.87	6 (25%)
3	GOL	C	302	-	5,5,5	0.88	0	5,5,5	0.79	0
4	SO4	C	303	-	4,4,4	0.45	0	6,6,6	0.37	0
2	AMP	D	301	-	22,25,25	1.27	2 (9%)	24,38,38	2.43	7 (29%)
3	GOL	D	302	-	5,5,5	0.82	0	5,5,5	0.91	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	AMP	A	301	-	-	0/6/26/26	0/3/3/3
3	GOL	A	302	-	-	0/4/4/4	0/0/0/0
2	AMP	B	301	-	-	0/6/26/26	0/3/3/3
3	GOL	B	302	-	-	0/4/4/4	0/0/0/0
2	AMP	C	301	-	-	0/6/26/26	0/3/3/3
3	GOL	C	302	-	-	0/4/4/4	0/0/0/0
4	SO4	C	303	-	-	0/0/0/0	0/0/0/0
2	AMP	D	301	-	-	0/6/26/26	0/3/3/3
3	GOL	D	302	-	-	0/4/4/4	0/0/0/0

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	AMP	P-O3P	-2.54	1.44	1.54
2	A	301	AMP	C2-N3	2.04	1.35	1.32
2	B	301	AMP	O4'-C1'	2.23	1.44	1.41
2	B	301	AMP	C5-C4	2.27	1.45	1.40
2	C	301	AMP	C5-C4	2.50	1.46	1.40

The worst 5 of 28 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	301	AMP	N3-C2-N1	-7.81	122.06	128.86
2	B	301	AMP	N3-C2-N1	-6.91	122.84	128.86
2	A	301	AMP	N3-C2-N1	-5.37	124.18	128.86
2	C	301	AMP	N3-C2-N1	-4.75	124.72	128.86
2	D	301	AMP	O5'-P-O1P	-4.41	94.11	106.47

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.



## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	239/288 (82%)	-0.14	4 (1%) 70 75	11, 20, 42, 59	0
1	B	237/288 (82%)	0.14	14 (5%) 23 29	12, 22, 53, 77	0
1	C	237/288 (82%)	0.28	15 (6%) 21 26	15, 27, 49, 68	0
1	D	234/288 (81%)	0.13	13 (5%) 25 31	17, 26, 48, 73	0
All	All	947/1152 (82%)	0.10	46 (4%) 30 37	11, 24, 49, 77	0

The worst 5 of 46 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	267	GLN	7.3
1	A	267	GLN	7.0
1	C	267	GLN	6.4
1	D	267	GLN	6.3
1	B	195	SER	6.0

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors

of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	GOL	C	302	6/6	0.94	0.13	0.23	30,36,38,40	0
3	GOL	D	302	6/6	0.91	0.13	0.22	28,37,38,39	0
3	GOL	A	302	6/6	0.96	0.10	-0.13	21,24,25,27	0
3	GOL	B	302	6/6	0.95	0.08	-1.04	22,26,27,28	0
2	AMP	B	301	23/23	0.97	0.09	-1.11	16,20,23,27	0
2	AMP	D	301	23/23	0.97	0.08	-1.39	23,27,31,35	0
4	SO4	C	303	5/5	0.98	0.08	-1.40	40,40,47,52	0
2	AMP	C	301	23/23	0.98	0.08	-1.54	19,21,24,29	0
2	AMP	A	301	23/23	0.98	0.07	-1.54	18,19,26,28	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.