



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 10, 2026 – 12:50 AM UTC

PDB ID : 6K0K / pdb_00006k0k
Title : Crystal structure of Escherichia coli pyruvate kinase II
Authors : Zhao, C.H.; Zhang, Y.P.; Li, Y.
Deposited on : 2019-05-07
Resolution : 2.68 Å(reported)

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

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A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

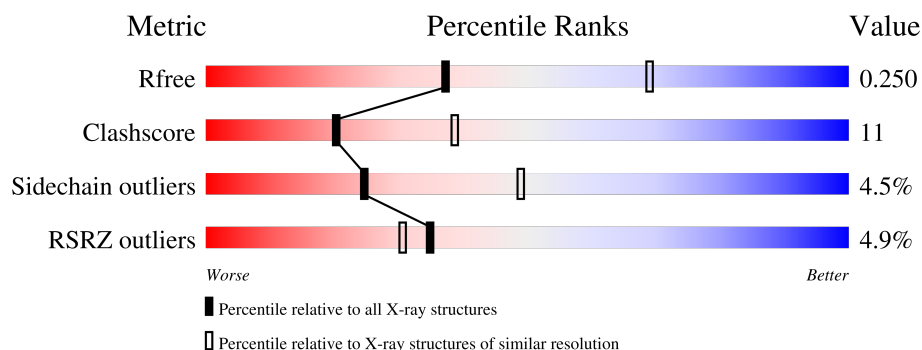
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.68 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}	180053	5070 (2.70-2.66)
Clashscore	190562	5409 (2.70-2.66)
Sidechain outliers	187428	5324 (2.70-2.66)
RSRZ outliers	180081	5070 (2.70-2.66)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	489	 4% 73% 23% . .
1	B	489	 5% 74% 21% . .
1	C	489	 3% 61% 19% . 19%
1	D	489	 5% 56% 23% . 20%

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 13318 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 Pyruvate kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	479	Total	C	N	O	S	0	0	0
			3579	2220	643	693	23			
1	B	478	Total	C	N	O	S	0	0	0
			3573	2217	642	691	23			
1	C	397	Total	C	N	O	S	0	0	0
			2955	1820	541	572	22			
1	D	392	Total	C	N	O	S	0	0	0
			2924	1801	536	565	22			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	481	ALA	-	expression tag	UNP C3T5U7
A	482	LEU	-	expression tag	UNP C3T5U7
A	483	GLY	-	expression tag	UNP C3T5U7
A	484	HIS	-	expression tag	UNP C3T5U7
A	485	HIS	-	expression tag	UNP C3T5U7
A	486	HIS	-	expression tag	UNP C3T5U7
A	487	HIS	-	expression tag	UNP C3T5U7
A	488	HIS	-	expression tag	UNP C3T5U7
A	489	HIS	-	expression tag	UNP C3T5U7
B	481	ALA	-	expression tag	UNP C3T5U7
B	482	LEU	-	expression tag	UNP C3T5U7
B	483	GLY	-	expression tag	UNP C3T5U7
B	484	HIS	-	expression tag	UNP C3T5U7
B	485	HIS	-	expression tag	UNP C3T5U7
B	486	HIS	-	expression tag	UNP C3T5U7
B	487	HIS	-	expression tag	UNP C3T5U7
B	488	HIS	-	expression tag	UNP C3T5U7
B	489	HIS	-	expression tag	UNP C3T5U7
C	481	ALA	-	expression tag	UNP C3T5U7
C	482	LEU	-	expression tag	UNP C3T5U7
C	483	GLY	-	expression tag	UNP C3T5U7

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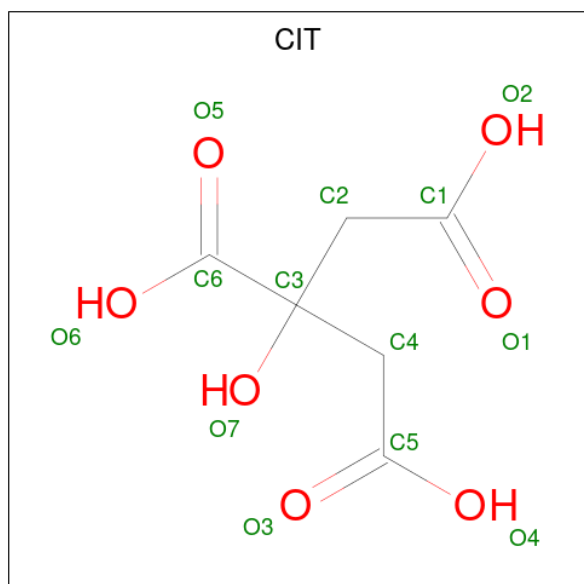
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Chain	Residue	Modelled	Actual	Comment	Reference
C	484	HIS	-	expression tag	UNP C3T5U7
C	485	HIS	-	expression tag	UNP C3T5U7
C	486	HIS	-	expression tag	UNP C3T5U7
C	487	HIS	-	expression tag	UNP C3T5U7
C	488	HIS	-	expression tag	UNP C3T5U7
C	489	HIS	-	expression tag	UNP C3T5U7
D	481	ALA	-	expression tag	UNP C3T5U7
D	482	LEU	-	expression tag	UNP C3T5U7
D	483	GLY	-	expression tag	UNP C3T5U7
D	484	HIS	-	expression tag	UNP C3T5U7
D	485	HIS	-	expression tag	UNP C3T5U7
D	486	HIS	-	expression tag	UNP C3T5U7
D	487	HIS	-	expression tag	UNP C3T5U7
D	488	HIS	-	expression tag	UNP C3T5U7
D	489	HIS	-	expression tag	UNP C3T5U7

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Mg 1 1	0	0
2	C	2	Total Mg 2 2	0	0
2	D	1	Total Mg 1 1	0	0

- Molecule 3 is CITRIC ACID (CCD ID: CIT) (formula: C₆H₈O₇).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	6	7		
3	C	1	Total	C	O	0	0
			13	6	7		
3	D	1	Total	C	O	0	0
			13	6	7		

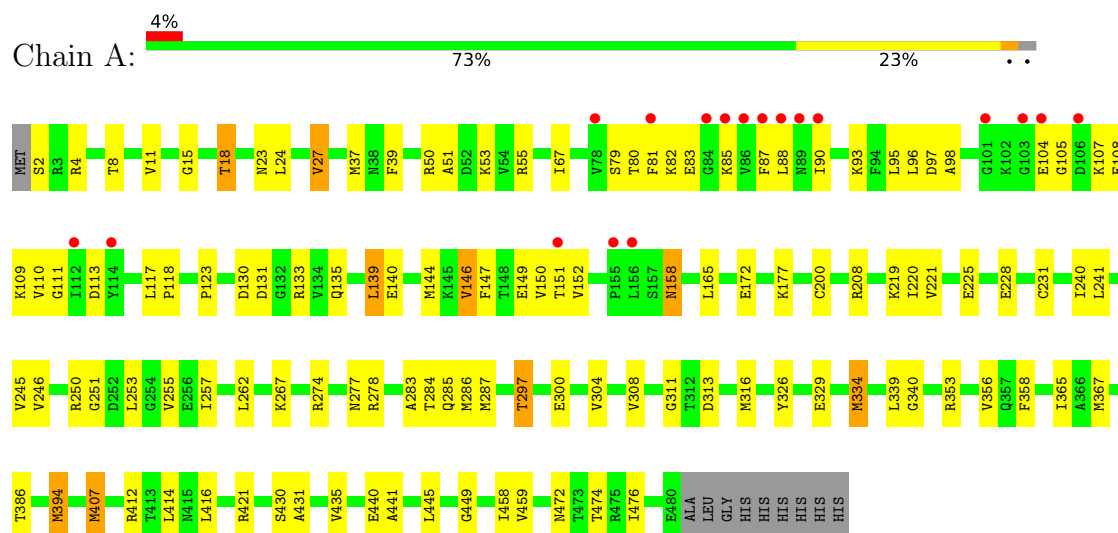
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	77	Total	O	0	0
			77	77		
4	B	105	Total	O	0	0
			105	105		
4	C	47	Total	O	0	0
			47	47		
4	D	15	Total	O	0	0
			15	15		

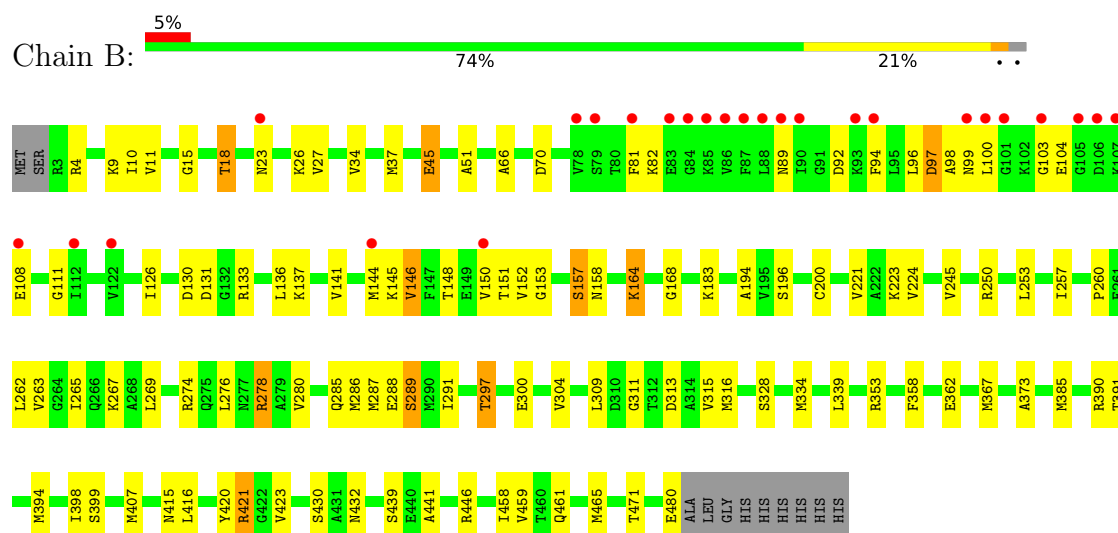
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

• Molecule 1: Pyruvate kinase

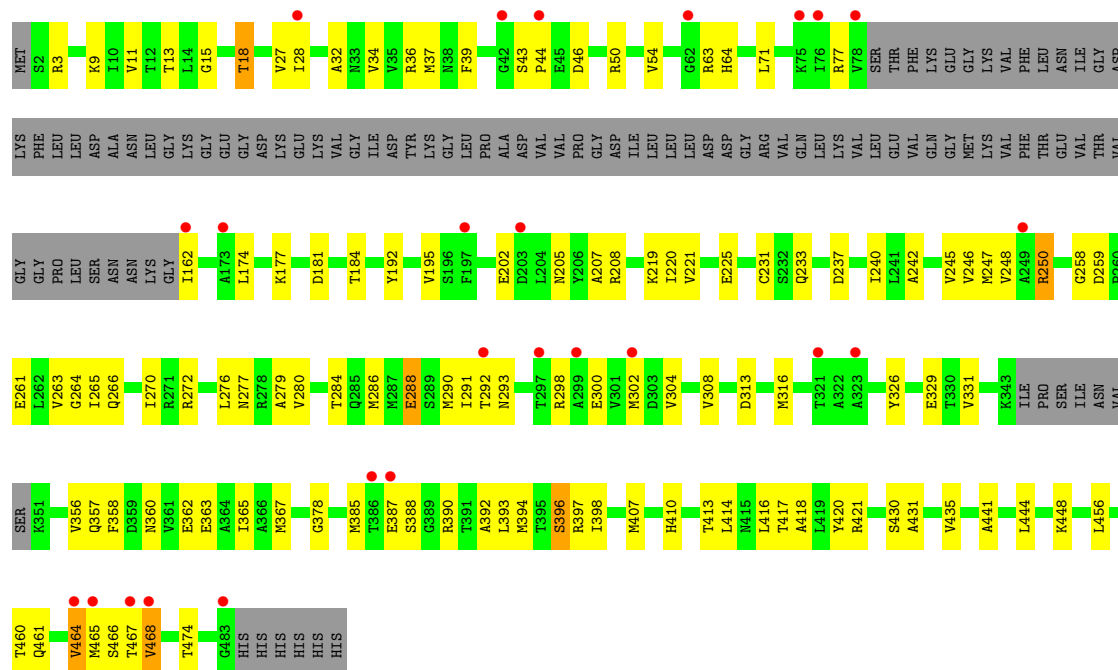


• Molecule 1: Pyruvate kinase



• Molecule 1: Pyruvate kinase





4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	117.69Å 137.30Å 139.22Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.95 – 2.68 32.95 – 2.68	Depositor EDS
% Data completeness (in resolution range)	98.5 (32.95-2.68) 98.6 (32.95-2.68)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.51 (at 2.68Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.210 , 0.259 (Not available) , 0.250	Depositor DCC
R_{free} test set	3101 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å ²)	51.5	Xtriage
Anisotropy	0.032	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 42.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.017 for -h,l,k	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	13318	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.98% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, CIT

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	0.41	0/3615	0.67	2/4882 (0.0%)
1	B	0.42	0/3609	0.65	0/4874
1	C	0.39	0/2981	0.63	0/4025
1	D	0.35	0/2949	0.59	0/3981
All	All	0.40	0/13154	0.64	2/17762 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	283	ALA	CA-C-N	5.41	131.87	121.54
1	A	283	ALA	C-N-CA	5.41	131.87	121.54

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	3579	0	3678	90	0
1	B	3573	0	3674	80	0
1	C	2955	0	3029	58	0
1	D	2924	0	2998	77	0
2	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	2	0	0	0	0
2	D	1	0	0	0	0
3	A	13	0	5	0	0
3	C	13	0	5	0	0
3	D	13	0	5	1	0
4	A	77	0	0	3	0
4	B	105	0	0	4	0
4	C	47	0	0	1	0
4	D	15	0	0	1	0
All	All	13318	0	13394	299	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 11.

The worst 5 of 299 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:A:81:PHE:HB3	1:A:104:GLU:HA	1.49	0.94
1:B:367:MET:HE1	1:B:398:ILE:HD11	1.57	0.84
1:B:82:LYS:HE2	1:B:104:GLU:HB2	1.60	0.84
1:B:100:LEU:HD21	1:B:103:GLY:H	1.44	0.81
1:D:231:CYS:SG	4:D:612:HOH:O	2.39	0.80

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

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	382/391 (98%)	364 (95%)	18 (5%)	23	47
1	B	382/391 (98%)	368 (96%)	14 (4%)	30	56
1	C	313/391 (80%)	294 (94%)	19 (6%)	17	37
1	D	309/391 (79%)	297 (96%)	12 (4%)	28	54
All	All	1386/1564 (89%)	1323 (96%)	63 (4%)	24	49

5 of 63 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	297	THR
1	D	250	ARG
1	C	77	ARG
1	D	233	GLN
1	D	396	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	205	ASN
1	D	266	GLN
1	D	415	ASN
1	D	277	ASN
1	D	325	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 oligosaccharides in this entry.

5.6 Ligand geometry

Of 7 ligands modelled in this entry, 4 are monoatomic - leaving 3 for Mogul analysis.

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
3	CIT	A	502	-	12,12,12	1.59	2 (16%)	17,17,17	2.28	10 (58%)
3	CIT	D	502	-	12,12,12	1.06	0	17,17,17	1.11	0
3	CIT	C	503	-	12,12,12	1.47	1 (8%)	17,17,17	2.16	6 (35%)

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
3	CIT	A	502	-	-	5/16/16/16	-
3	CIT	D	502	-	-	12/16/16/16	-
3	CIT	C	503	-	-	5/16/16/16	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	502	CIT	C3-C6	3.51	1.57	1.53
3	C	503	CIT	C3-C6	3.18	1.56	1.53
3	A	502	CIT	O7-C3	2.20	1.47	1.43

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	503	CIT	O6-C6-C3	4.64	122.05	113.14
3	A	502	CIT	O7-C3-C6	-3.66	103.77	108.96
3	A	502	CIT	O2-C1-O1	-3.29	114.86	123.33
3	C	503	CIT	O7-C3-C4	-3.29	101.88	109.38
3	A	502	CIT	O2-C1-C2	3.22	124.54	114.35

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	502	CIT	C1-C2-C3-O7
3	A	502	CIT	C1-C2-C3-C4
3	A	502	CIT	C1-C2-C3-C6
3	C	503	CIT	C1-C2-C3-O7
3	C	503	CIT	C1-C2-C3-C4

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	502	CIT	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

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, 95th 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 ²)	Q<0.9
1	A	479/489 (97%)	0.03	18 (3%) 44 39	29, 45, 97, 148	0
1	B	478/489 (97%)	0.04	26 (5%) 31 27	30, 44, 106, 152	0
1	C	397/489 (81%)	0.26	17 (4%) 40 35	36, 57, 89, 123	0
1	D	392/489 (80%)	0.51	25 (6%) 25 22	38, 67, 93, 131	0
All	All	1746/1956 (89%)	0.19	86 (4%) 35 30	29, 53, 97, 152	0

The worst 5 of 86 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	84	GLY	5.9
1	A	84	GLY	5.2
1	B	108	GLU	5.2
1	B	90	ILE	4.8
1	A	90	ILE	4.5

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 oligosaccharides 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. The B-factors column lists the minimum, median, 95th 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	B-factors($\text{\AA}^2$)	Q<0.9
3	CIT	D	502	13/13	0.85	0.11	57,66,71,74	0
3	CIT	C	503	13/13	0.89	0.09	44,54,59,66	0
3	CIT	A	502	13/13	0.89	0.09	43,50,60,60	0
2	MG	A	501	1/1	0.92	0.07	43,43,43,43	0
2	MG	D	501	1/1	0.93	0.21	51,51,51,51	0
2	MG	C	501	1/1	0.95	0.11	58,58,58,58	0
2	MG	C	502	1/1	0.97	0.23	31,31,31,31	0

6.5 Other polymers [i](#)

There are no such residues in this entry.