



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 10:12 AM UTC

PDB ID : 5TE1 / pdb_00005te1
Title : C20S, C293G Mutant N-terminal Human ATP Citrate Lyase Bound to 4R-Hydroxycitrate
Authors : Hu, J.; Fraser, M.E.
Deposited on : 2016-09-20
Resolution : 2.25 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

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

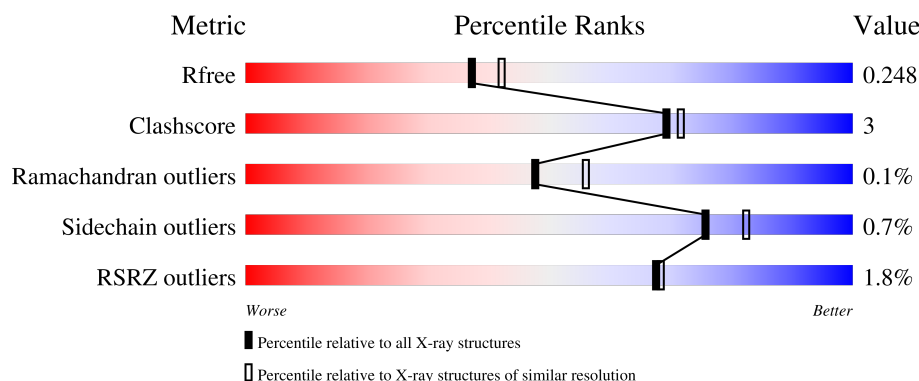
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

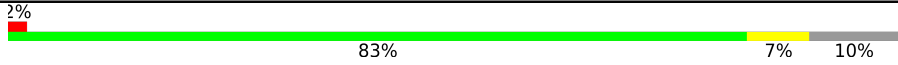
The reported resolution of this entry is 2.25 Å.

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	1898 (2.26-2.26)
Clashscore	190562	2005 (2.26-2.26)
Ramachandran outliers	187476	1965 (2.26-2.26)
Sidechain outliers	187428	1966 (2.26-2.26)
RSRZ outliers	180081	1898 (2.26-2.26)

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	828	
1	B	828	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 23844 atoms, of which 11566 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 ATP-citrate synthase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	742	Total	C	H	N	O	S	0	2	0
			11515	3673	5775	974	1067	26			
1	B	743	Total	C	H	N	O	S	0	2	0
			11529	3677	5781	976	1069	26			

There are 26 discrepancies between the modelled and reference sequences:

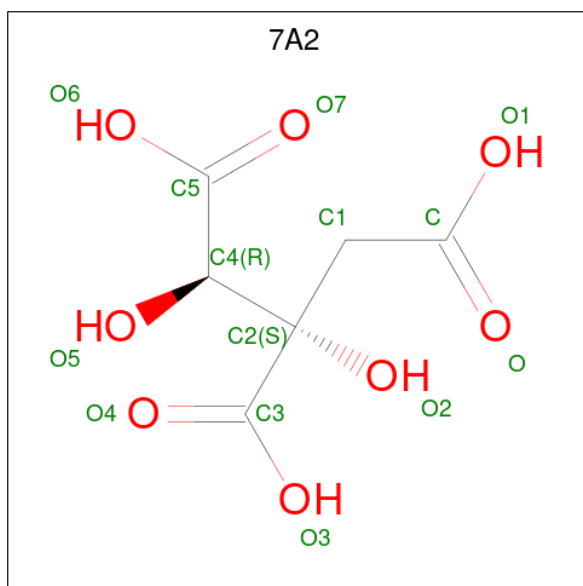
Chain	Residue	Modelled	Actual	Comment	Reference
A	20	SER	CYS	engineered mutation	UNP P53396
A	293	GLY	CYS	engineered mutation	UNP P53396
A	818	ALA	-	expression tag	UNP P53396
A	819	ALA	-	expression tag	UNP P53396
A	820	LEU	-	expression tag	UNP P53396
A	821	GLU	-	expression tag	UNP P53396
A	822	HIS	-	expression tag	UNP P53396
A	823	HIS	-	expression tag	UNP P53396
A	824	HIS	-	expression tag	UNP P53396
A	825	HIS	-	expression tag	UNP P53396
A	826	HIS	-	expression tag	UNP P53396
A	827	HIS	-	expression tag	UNP P53396
A	828	HIS	-	expression tag	UNP P53396
B	20	SER	CYS	engineered mutation	UNP P53396
B	293	GLY	CYS	engineered mutation	UNP P53396
B	818	ALA	-	expression tag	UNP P53396
B	819	ALA	-	expression tag	UNP P53396
B	820	LEU	-	expression tag	UNP P53396
B	821	GLU	-	expression tag	UNP P53396
B	822	HIS	-	expression tag	UNP P53396
B	823	HIS	-	expression tag	UNP P53396
B	824	HIS	-	expression tag	UNP P53396
B	825	HIS	-	expression tag	UNP P53396
B	826	HIS	-	expression tag	UNP P53396
B	827	HIS	-	expression tag	UNP P53396

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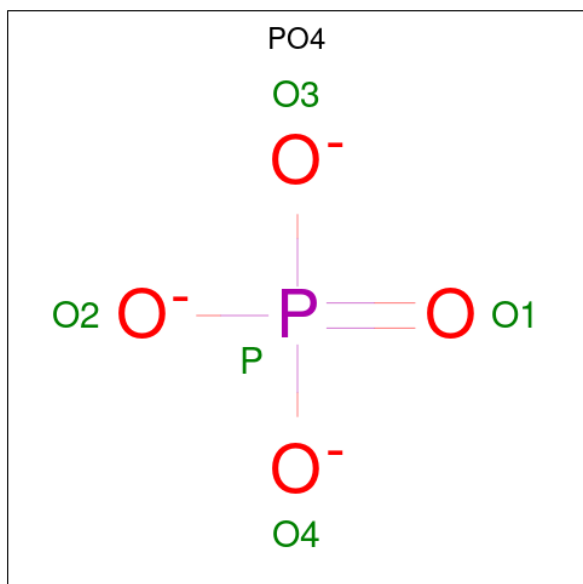
Chain	Residue	Modelled	Actual	Comment	Reference
B	828	HIS	-	expression tag	UNP P53396

- Molecule 2 is 3-C-carboxy-2-deoxy-L-threo-pentonic acid (CCD ID: 7A2) (formula: $C_6H_8O_8$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			19	6	5	8		
2	B	1	Total	C	H	O	0	0
			19	6	5	8		

- Molecule 3 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O P 5 4 1	0	0
3	B	1	Total O P 5 4 1	0	0

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Na 1 1	0	0
4	B	1	Total Na 1 1	0	0

- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	383	Total O 383 383	0	0
5	B	367	Total O 367 367	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	98.77Å 73.32Å 131.37Å 90.00° 97.06° 90.00°	Depositor
Resolution (Å)	49.01 – 2.25 49.01 – 2.25	Depositor EDS
% Data completeness (in resolution range)	92.9 (49.01-2.25) 89.2 (49.01-2.25)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.07 (at 2.24Å)	Xtriage
Refinement program	PHENIX (1.10_2152: ???)	Depositor
R, R_{free}	0.188 , 0.247 0.190 , 0.248	Depositor DCC
R_{free} test set	4132 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	19.1	Xtriage
Anisotropy	0.595	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 50.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	23844	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 19.36% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: NA, 7A2, PO4

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	0.58	0/5874	0.67	0/7954
1	B	0.59	0/5882	0.68	0/7965
All	All	0.59	0/11756	0.68	0/15919

There are no bond length outliers.

There are no bond angle outliers.

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	5740	5775	5769	40	0
1	B	5748	5781	5775	40	0
2	A	14	5	0	0	0
2	B	14	5	0	0	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	383	0	0	14	1
5	B	367	0	0	6	0
All	All	12278	11566	11544	80	1

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 3.

All (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:A:486:GLN:OE1	5:A:1001:HOH:O	1.93	0.85
1:A:334:ASP:O	5:A:1002:HOH:O	2.03	0.77
1:A:66:ARG:NH2	1:A:216:ASP:OD1	2.18	0.75
1:A:37:ASP:OD2	1:A:37:ASP:N	2.22	0.73
1:B:30:LYS:NZ	1:B:53:GLN:OE1	2.25	0.70
1:B:240:PRO:O	5:B:1001:HOH:O	2.09	0.69
1:B:486:GLN:OE1	5:B:1002:HOH:O	2.14	0.64
1:A:788:ARG:NH2	1:A:792:GLU:OE2	2.30	0.63
1:A:408:GLU:H	1:A:408:GLU:CD	2.07	0.63
1:A:193:GLU:OE2	5:A:1003:HOH:O	2.16	0.62
1:B:389:ARG:NH1	1:B:393:GLU:OE1	2.35	0.59
1:B:766:ASN:ND2	5:B:1011:HOH:O	2.34	0.59
1:A:240:PRO:O	5:A:1004:HOH:O	2.16	0.59
1:B:656:SER:OG	1:B:679:ASP:OD2	2.16	0.56
1:B:661:SER:OG	1:B:667[A]:SER:OG	2.25	0.55
1:A:422:ARG:HB3	5:A:1055:HOH:O	2.06	0.55
1:B:257:ASP:OD2	5:B:1003:HOH:O	2.18	0.54
1:A:389:ARG:NH1	1:A:393:GLU:OE1	2.40	0.54
1:A:89:LEU:O	5:A:1005:HOH:O	2.18	0.54
1:B:362:ARG:NH1	1:B:397:THR:OG1	2.31	0.53
1:A:495:ARG:NH2	5:A:1032:HOH:O	2.41	0.53
1:A:656:SER:OG	1:A:679:ASP:OD2	2.23	0.52
1:B:66:ARG:NH2	1:B:216:ASP:OD1	2.43	0.50
1:A:422:ARG:CB	5:A:1055:HOH:O	2.60	0.49
1:A:230:LYS:NZ	5:A:1024:HOH:O	2.36	0.48
1:B:337:ILE:HD12	1:B:418:ALA:HB1	1.96	0.48
1:A:513:LEU:HD22	1:A:524:PRO:HB3	1.96	0.47
1:A:669:GLU:OE2	5:A:1008:HOH:O	2.20	0.47
1:A:423:PRO:O	5:A:1007:HOH:O	2.20	0.47
1:B:205:LEU:HD11	1:B:212:VAL:CG1	2.45	0.47
1:A:21:THR:N	5:A:1028:HOH:O	2.39	0.47
1:A:507:ARG:N	1:A:507:ARG:HD3	2.30	0.46
1:B:378:ARG:HA	1:B:405:PHE:O	2.15	0.46
1:A:507:ARG:HD3	1:A:507:ARG:H	1.80	0.46
1:B:507:ARG:HD3	1:B:507:ARG:N	2.30	0.46
1:A:200:LEU:CD1	1:A:217:LEU:HD11	2.46	0.46
1:A:40:TRP:CE3	1:A:82:LYS:HE2	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:200:LEU:CD1	1:B:217:LEU:HD11	2.47	0.45
1:B:334:ASP:CG	1:B:422:ARG:HD3	2.42	0.45
1:B:89:LEU:HD13	1:B:105:PHE:CE1	2.52	0.44
1:B:162:PRO:O	1:B:166:LYS:HD3	2.17	0.44
1:A:659:TYR:CZ	1:A:684:GLY:HA3	2.52	0.44
1:B:87:PRO:O	1:B:91:GLN:HG3	2.17	0.44
1:B:161:ASN:O	1:B:164:ASP:N	2.50	0.44
1:B:232:LYS:HG3	5:B:1229:HOH:O	2.16	0.44
1:B:513:LEU:HD22	1:B:524:PRO:HB3	1.99	0.44
1:A:17:LYS:HG3	1:A:29:PHE:HZ	1.83	0.44
1:B:123:ILE:HA	1:B:131:TYR:O	2.18	0.44
1:A:337:ILE:HD12	1:A:418:ALA:HB1	2.00	0.43
1:A:697:PHE:HB2	1:A:723:GLU:HG2	2.00	0.43
1:B:200:LEU:HD11	1:B:217:LEU:HD11	1.99	0.43
1:B:37:ASP:OD2	1:B:37:ASP:N	2.51	0.43
1:B:268:LEU:HD21	1:B:326:LEU:HD13	2.00	0.43
1:A:229:CYS:O	1:A:230:LYS:C	2.60	0.43
1:B:131:TYR:CE2	1:B:151:LYS:HE2	2.54	0.43
1:A:40:TRP:O	1:A:44:LEU:HG	2.19	0.43
1:B:133:LEU:CD2	1:B:151:LYS:HG3	2.49	0.43
1:B:152:LEU:HD11	1:B:164:ASP:HB3	2.02	0.42
1:A:362:ARG:NH1	1:A:397:THR:OG1	2.33	0.42
1:A:337:ILE:CD1	1:A:418:ALA:HB1	2.50	0.42
1:A:410:HIS:O	1:A:411:MET:C	2.63	0.42
1:B:659:TYR:CZ	1:B:684:GLY:HA3	2.55	0.42
1:A:66:ARG:HD3	5:A:1075:HOH:O	2.19	0.42
1:B:40:TRP:O	1:B:44:LEU:HG	2.20	0.41
1:B:611:LYS:O	1:B:615:GLN:HG3	2.20	0.41
1:B:257:ASP:OD2	5:B:1004:HOH:O	2.22	0.41
1:A:679:ASP:OD1	1:A:679:ASP:N	2.52	0.41
1:A:157:ASP:N	5:A:1023:HOH:O	2.36	0.41
1:B:39:ASP:OD1	1:B:39:ASP:C	2.64	0.41
1:B:408:GLU:H	1:B:408:GLU:CD	2.28	0.40
1:A:54:ASN:ND2	1:A:75:ASN:OD1	2.37	0.40
1:A:205:LEU:HD11	1:A:212:VAL:CG1	2.51	0.40
1:A:350:VAL:O	1:A:354:PHE:HB2	2.21	0.40
1:B:507:ARG:HD3	1:B:507:ARG:H	1.87	0.40
1:A:268:LEU:HD23	1:A:268:LEU:HA	1.97	0.40
1:B:708:PRO:O	1:B:711:LYS:HE3	2.21	0.40
1:B:203:ASN:HA	1:B:204:PRO:HA	1.89	0.40
1:B:357:ILE:HG21	1:B:391:MET:HE1	2.04	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:659:TYR:HA	1:B:714:VAL:O	2.21	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:A:1368:HOH:O	5:A:1377:HOH:O[2_645]	1.98	0.22

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	738/828 (89%)	723 (98%)	14 (2%)	1 (0%)	48	56
1	B	739/828 (89%)	721 (98%)	18 (2%)	0	100	100
All	All	1477/1656 (89%)	1444 (98%)	32 (2%)	1 (0%)	48	56

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	489	SER

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	611/678 (90%)	607 (99%)	4 (1%)	76	82
1	B	612/678 (90%)	607 (99%)	5 (1%)	73	80
All	All	1223/1356 (90%)	1214 (99%)	9 (1%)	76	82

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	SER
1	A	37	ASP
1	A	94	THR
1	A	186	SER
1	B	37	ASP
1	B	186	SER
1	B	298	VAL
1	B	358	VAL
1	B	485	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	777	GLN
1	B	150	GLN
1	B	671	ASN
1	B	777	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 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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
2	7A2	A	901	-	12,13,13	0.89	0	13,19,19	1.32	3 (23%)
3	PO4	B	902	-	4,4,4	0.69	0	6,6,6	1.36	1 (16%)
3	PO4	A	902	-	4,4,4	1.07	0	6,6,6	0.76	0
2	7A2	B	901	-	12,13,13	1.08	0	13,19,19	1.65	3 (23%)

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	7A2	A	901	-	-	2/21/21/21	-
2	7A2	B	901	-	-	2/21/21/21	-

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	901	7A2	C1-C2-C3	-3.09	106.22	110.56
2	B	901	7A2	O-C-C1	-3.03	114.38	122.95
2	B	901	7A2	C1-C2-C3	-2.76	106.69	110.56
2	B	901	7A2	O1-C-C1	2.72	122.95	114.35
2	A	901	7A2	O6-C5-C4	2.62	123.18	112.80
3	B	902	PO4	O2-P-O1	-2.31	102.77	110.95
2	A	901	7A2	O7-C5-C4	-2.30	113.09	122.45

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	901	7A2	C2-C4-C5-O6
2	A	901	7A2	C2-C4-C5-O7
2	B	901	7A2	O5-C4-C5-O6
2	B	901	7A2	C4-C2-C3-O4

There are no ring outliers.

No monomer is involved in short contacts.

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	742/828 (89%)	-0.04	15 (2%)	65 65	13, 26, 50, 87	2 (0%)
1	B	743/828 (89%)	-0.01	12 (1%)	70 71	12, 27, 52, 92	2 (0%)
All	All	1485/1656 (89%)	-0.02	27 (1%)	67 68	12, 27, 51, 92	4 (0%)

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	137	GLU	3.9
1	B	485	LEU	3.9
1	A	235	ASP	3.8
1	A	813	ALA	3.5
1	A	485	LEU	3.1
1	B	68	LYS	3.1
1	B	813	ALA	3.0
1	A	137	GLU	3.0
1	B	235	ASP	2.9
1	B	545	HIS	2.8
1	A	67	GLY	2.6
1	A	68	LYS	2.5
1	B	65	ARG	2.5
1	A	812	PRO	2.5
1	A	765	ALA	2.4
1	A	764	CYS	2.3
1	B	101	PHE	2.3
1	A	766	ASN	2.2
1	B	69	LEU	2.2
1	A	136	HIS	2.2
1	B	149	ALA	2.2
1	A	507	ARG	2.2
1	B	426	ASN	2.2
1	A	755	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	101	PHE	2.1
1	B	650	LYS	2.0
1	A	86	LYS	2.0

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 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(Å ²)	Q<0.9
4	NA	B	903	1/1	0.89	0.20	43,43,43,43	0
4	NA	A	903	1/1	0.95	0.07	34,34,34,34	0
2	7A2	A	901	14/14	0.95	0.08	21,27,40,41	0
2	7A2	B	901	14/14	0.96	0.08	18,27,37,38	0
3	PO4	A	902	5/5	0.96	0.09	27,29,32,34	0
3	PO4	B	902	5/5	0.97	0.07	28,28,29,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.