



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 12, 2017 – 08:19 AM EST

PDB ID : 4O3M
Title : Ternary complex of Bloom's syndrome helicase
Authors : Swan, M.K.; Bertrand, J.
Deposited on : unknown
Resolution : 2.30 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

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

with specific help available everywhere you see the ⓘ symbol.

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 : rb-20030345
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) : rb-20030345

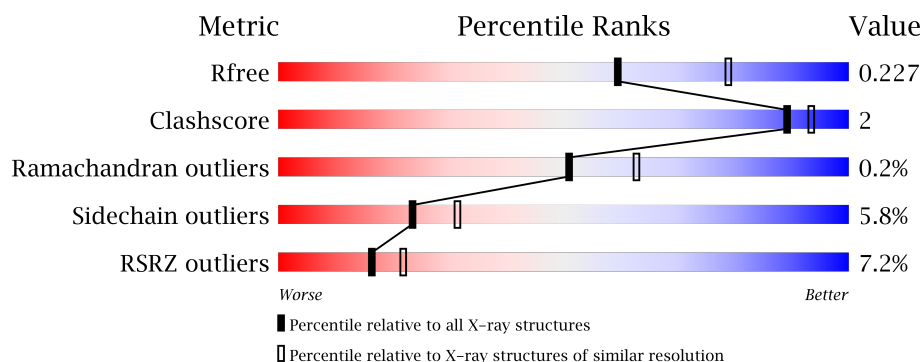
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	4130 (2.30-2.30)
Clashscore	112137	4751 (2.30-2.30)
Ramachandran outliers	110173	4705 (2.30-2.30)
Sidechain outliers	110143	4704 (2.30-2.30)
RSRZ outliers	101464	4156 (2.30-2.30)

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 ≥ 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	659	<div> <div>6%</div> <div>83%</div> <div>9%</div> <div>7%</div> </div>
2	P	16	<div> <div>6%</div> <div>69%</div> <div>6%</div> <div>25%</div> </div>
3	T	24	<div> <div>13%</div> <div>54%</div> <div>13%</div> <div>33%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
7	EDO	A	1305	-	-	-	X
7	EDO	A	1306	-	-	-	X
7	EDO	A	1307	-	-	-	X
7	EDO	A	1309	-	-	-	X
7	EDO	A	1310	-	-	-	X

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 5427 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 Bloom syndrome protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	613	Total	C	N	O	S	0	2	0
			4736	3010	815	877	34			

- Molecule 2 is a DNA chain called 5'-D(*AP*GP*CP*GP*TP*CP*GP*AP*GP*AP*TP*CP*CP*AP*AP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	12	Total	C	N	O	P	0	0	0
			246	116	46	72	12			

- Molecule 3 is a DNA chain called 5'-D(*CP*TP*TP*GP*GP*AP*TP*CP*TP*CP*GP*A*P*CP*GP*CP*TP*CP*TP*CP*CP*TP*TP*A)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	T	16	Total	C	N	O	P	0	0	0
			324	154	56	98	16			

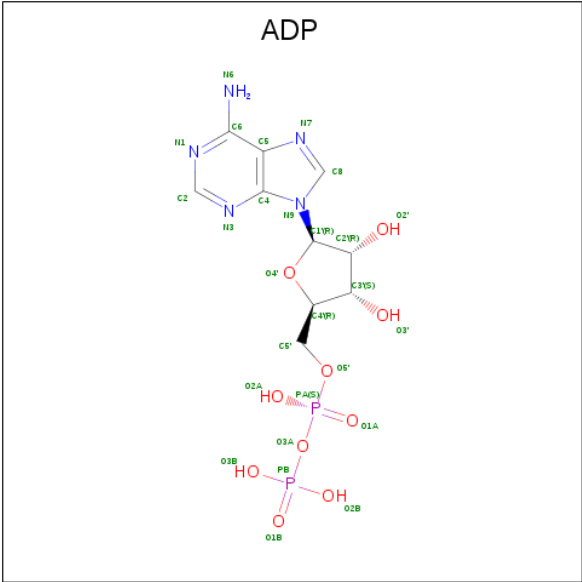
- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Ca	0	0
			1	1		

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

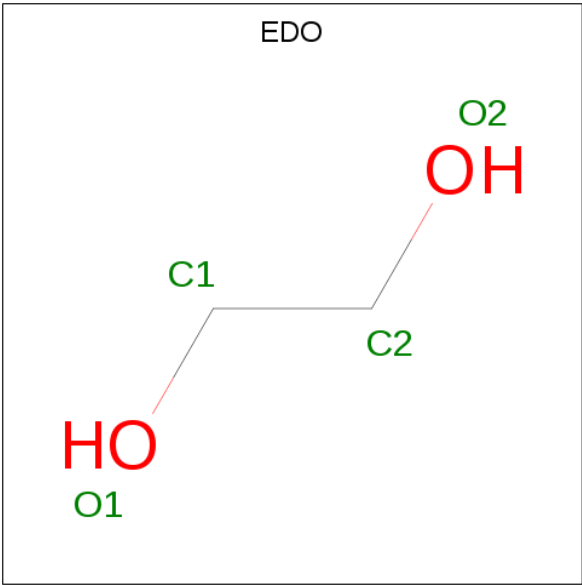
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total	Zn	0	0
			1	1		

- Molecule 6 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: C₁₀H₁₅N₅O₁₀P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 7 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		
7	A	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	1	Total C O 4 2 2	0	0
7	A	1	Total C O 4 2 2	0	0
7	A	1	Total C O 4 2 2	0	0
7	A	1	Total C O 4 2 2	0	0
7	A	1	Total C O 4 2 2	0	0

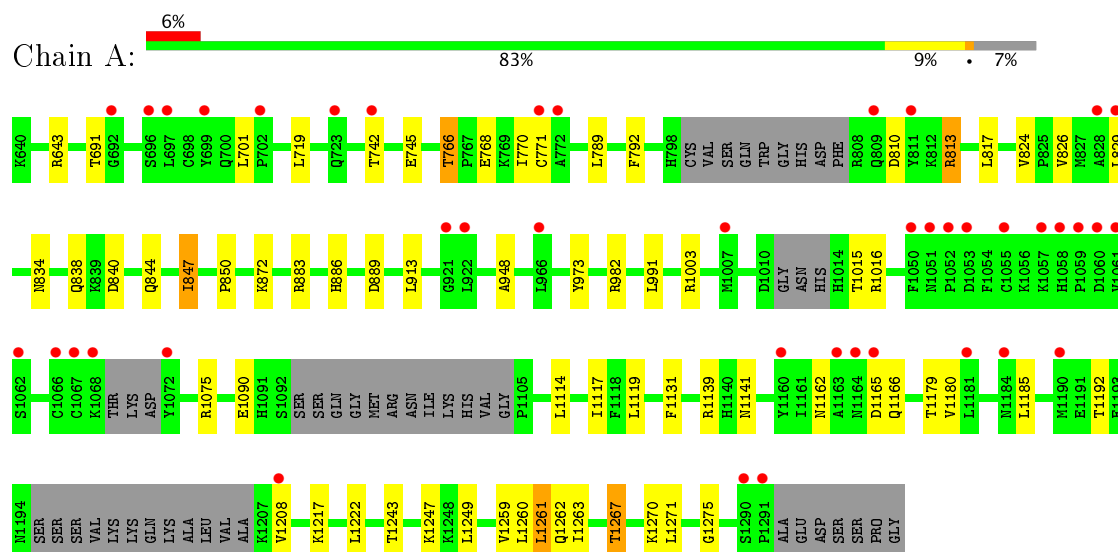
- Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	58	Total O 58 58	0	0
8	P	1	Total O 1 1	0	0
8	T	1	Total O 1 1	0	0

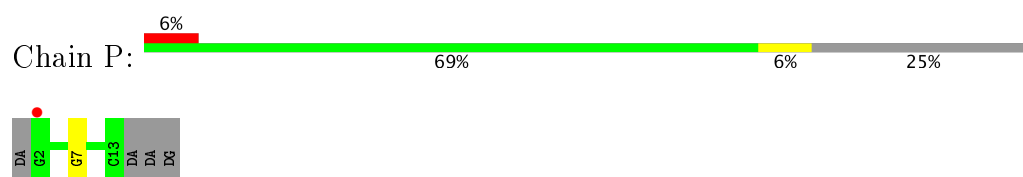
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Bloom syndrome protein



- Molecule 2: 5'-D(*AP*GP*CP*GP*TP*CP*GP*AP*GP*AP*TP*CP*CP*AP*AP*G)-3'



- Molecule 3: 5'-D(*CP*TP*TP*GP*GP*AP*TP*CP*TP*CP*GP*AP*CP*GP*CP*TP*CP*TP*CP*CP*CP*TP*TP*A)-3'



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	100.93Å 164.68Å 50.98Å 90.00° 90.14° 90.00°	Depositor
Resolution (Å)	35.91 – 2.30 35.91 – 2.30	Depositor EDS
% Data completeness (in resolution range)	94.0 (35.91-2.30) 94.0 (35.91-2.30)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	0.03	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.63 (at 2.29Å)	Xtriage
Refinement program	BUSTER 2.11.5	Depositor
R, R_{free}	0.181 , 0.215 0.190 , 0.227	Depositor DCC
R_{free} test set	1735 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	53.8	Xtriage
Anisotropy	0.914	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 60.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.012 for -1/2*h+1/2*k,3/2*h+1/2*k,-l 0.015 for -1/2*h-1/2*k,-3/2*h+1/2*k,-l 0.013 for 1/2*h+1/2*k,3/2*h-1/2*k,-l 0.009 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.031 for -h,-k,l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5427	wwPDB-VP
Average B, all atoms (Å ²)	85.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.90% 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: ZN, CA, ADP, EDO

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	0.50	0/4833	0.68	0/6545
2	P	1.07	0/275	0.94	0/422
3	T	1.10	0/361	0.95	0/554
All	All	0.60	0/5469	0.72	0/7521

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	4736	0	4591	22	0
2	P	246	0	135	1	0
3	T	324	0	181	2	0
4	A	1	0	0	0	0
5	A	1	0	0	0	0
6	A	27	0	12	0	0
7	A	32	0	48	1	0
8	A	58	0	0	0	0
8	P	1	0	0	0	0
8	T	1	0	0	0	0
All	All	5427	0	4967	23	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 2.

All (23) 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:771:CYS:HB3	1:A:813:ARG:HD3	1.64	0.79
1:A:948:ALA:HB2	3:T:18:DT:H5'	1.78	0.64
1:A:1141:ASN:HD21	1:A:1192:THR:H	1.48	0.61
1:A:840:ASP:O	1:A:844:GLN:HB2	2.04	0.58
1:A:766:THR:HG23	1:A:768:GLU:HG3	1.86	0.57
1:A:1162:ASN:HD21	1:A:1166:GLN:HE21	1.53	0.56
1:A:1259:VAL:O	1:A:1262:GLN:HG3	2.07	0.55
1:A:1260:LEU:HA	1:A:1263:ILE:HD12	1.89	0.55
1:A:883:ARG:HE	1:A:913:LEU:HD13	1.73	0.53
1:A:1271:LEU:O	1:A:1275:GLY:HA3	2.11	0.51
3:T:13:DC:H2''	3:T:14:DG:C8	2.45	0.51
1:A:872:LYS:HD2	2:P:7:DG:H5'	1.93	0.50
1:A:847:ILE:HG13	1:A:850:PRO:HB3	1.94	0.49
1:A:886:HIS:HB3	1:A:889:ASP:HB2	1.95	0.48
1:A:1261:LEU:HD12	7:A:1305:EDO:H11	1.97	0.46
1:A:792:PHE:HB2	1:A:826:VAL:HG22	1.98	0.46
1:A:770:ILE:HD12	1:A:817:LEU:HD11	1.99	0.44
1:A:1267:THR:HG22	1:A:1270:LYS:H	1.82	0.43
1:A:834:ASN:O	1:A:838:GLN:HG3	2.19	0.42
1:A:1117:ILE:O	1:A:1131:PHE:HA	2.21	0.41
1:A:973:TYR:CE1	1:A:991:LEU:HD12	2.55	0.41
1:A:1119:LEU:HD11	1:A:1139:ARG:HA	2.03	0.40
1:A:691:THR:HG21	1:A:982:ARG:CZ	2.51	0.40

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	603/659 (92%)	586 (97%)	16 (3%)	1 (0%)	51 63

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1208	VAL

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	504/587 (86%)	475 (94%)	29 (6%)	23 31

All (29) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	643	ARG
1	A	701	LEU
1	A	719	LEU
1	A	742	THR
1	A	745	GLU
1	A	766	THR
1	A	789	LEU
1	A	810	ASP
1	A	813	ARG
1	A	824	VAL
1	A	829	LEU
1	A	847	ILE
1	A	1003	ARG
1	A	1015	THR
1	A	1016	ARG
1	A	1075	ARG
1	A	1090	GLU
1	A	1114	LEU
1	A	1165	ASP
1	A	1179	THR

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Mol	Chain	Res	Type
1	A	1180	VAL
1	A	1185	LEU
1	A	1217	LYS
1	A	1222	LEU
1	A	1243	THR
1	A	1247	LYS
1	A	1249	LEU
1	A	1261	LEU
1	A	1267	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	666	HIS
1	A	752	GLN
1	A	932	GLN
1	A	988	HIS
1	A	1019	HIS
1	A	1112	ASN
1	A	1141	ASN
1	A	1166	GLN
1	A	1175	ASN
1	A	1236	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 2 are monoatomic - leaving 9 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	$\# Z > 2$
6	ADP	A	1303	4	25,29,29	0.60	0	24,45,45	0.71	0
7	EDO	A	1304	-	3,3,3	0.79	0	2,2,2	0.20	0
7	EDO	A	1305	-	3,3,3	0.43	0	2,2,2	0.41	0
7	EDO	A	1306	-	3,3,3	0.75	0	2,2,2	0.24	0
7	EDO	A	1307	-	3,3,3	0.63	0	2,2,2	0.19	0
7	EDO	A	1308	-	3,3,3	0.68	0	2,2,2	0.17	0
7	EDO	A	1309	-	3,3,3	0.61	0	2,2,2	0.20	0
7	EDO	A	1310	-	3,3,3	0.80	0	2,2,2	0.07	0
7	EDO	A	1311	-	3,3,3	0.51	0	2,2,2	0.34	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
6	ADP	A	1303	4	-	0/12/32/32	0/3/3/3
7	EDO	A	1304	-	-	0/1/1/1	0/0/0/0
7	EDO	A	1305	-	-	0/1/1/1	0/0/0/0
7	EDO	A	1306	-	-	0/1/1/1	0/0/0/0
7	EDO	A	1307	-	-	0/1/1/1	0/0/0/0
7	EDO	A	1308	-	-	0/1/1/1	0/0/0/0
7	EDO	A	1309	-	-	0/1/1/1	0/0/0/0
7	EDO	A	1310	-	-	0/1/1/1	0/0/0/0
7	EDO	A	1311	-	-	0/1/1/1	0/0/0/0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	A	1305	EDO	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 ⓘ

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	613/659 (93%)	0.37	42 (6%) 18 23	50, 75, 127, 156	0
2	P	12/16 (75%)	1.18	1 (8%) 12 16	93, 124, 179, 181	0
3	T	16/24 (66%)	1.11	3 (18%) 1 2	99, 131, 159, 170	0
All	All	641/699 (91%)	0.40	46 (7%) 16 22	50, 75, 131, 181	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	P	2	DG	7.3
1	A	1059	PRO	7.1
1	A	1067	CYS	6.7
1	A	1050	PHE	5.9
1	A	1066	CYS	5.5
1	A	1208	VAL	4.9
3	T	4	DG	4.7
1	A	1055	CYS	4.6
1	A	1060	ASP	4.4
3	T	19	DC	4.3
1	A	1291	PRO	3.9
1	A	772	ALA	3.9
1	A	1062	SER	3.9
1	A	1052	PRO	3.8
1	A	1160	TYR	3.6
1	A	1163	ALA	3.5
1	A	809	GLN	3.3
1	A	811	TYR	3.3
1	A	1072	TYR	3.3
1	A	1290	SER	2.9
1	A	921	GLY	2.8
1	A	771	CYS	2.8
1	A	1053	ASP	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	1164	ASN	2.8
1	A	697	LEU	2.8
1	A	829	LEU	2.7
1	A	742	THR	2.7
1	A	1181	LEU	2.7
1	A	1051	ASN	2.7
3	T	5	DG	2.6
1	A	1007	MET	2.6
1	A	1068	LYS	2.6
1	A	1057	LYS	2.5
1	A	1184	ASN	2.5
1	A	966	LEU	2.4
1	A	1165	ASP	2.4
1	A	1058	HIS	2.2
1	A	696	SER	2.2
1	A	1061	VAL	2.1
1	A	828	ALA	2.1
1	A	723	GLN	2.0
1	A	1190	MET	2.0
1	A	699	TYR	2.0
1	A	922	LEU	2.0
1	A	692	GLY	2.0
1	A	702	PRO	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 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, 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	LLDF	B-factors(\AA^2)	Q<0.9
7	EDO	A	1309	4/4	0.82	0.36	9.29	94,95,96,98	0
7	EDO	A	1307	4/4	0.82	0.17	4.64	94,94,95,96	0
7	EDO	A	1305	4/4	0.71	0.28	4.35	102,105,108,110	0
7	EDO	A	1306	4/4	0.85	0.27	3.19	72,79,83,83	0
7	EDO	A	1310	4/4	0.77	0.28	3.04	79,80,81,81	0
7	EDO	A	1308	4/4	0.85	0.15	1.19	85,88,93,94	0
6	ADP	A	1303	27/27	0.97	0.18	-0.32	56,62,67,75	0
7	EDO	A	1304	4/4	0.93	0.16	-0.56	63,70,75,76	0
7	EDO	A	1311	4/4	0.89	0.10	-1.06	108,108,109,109	0
5	ZN	A	1302	1/1	0.98	0.04	-1.60	98,98,98,98	0
4	CA	A	1301	1/1	0.93	0.28	-	107,107,107,107	0

6.5 Other polymers [i](#)

There are no such residues in this entry.