



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 10, 2023 – 12:50 AM EDT

PDB ID : 7SXL
Title : Plasmodium falciparum apicoplast DNA polymerase (exo-minus) without affinity tag
Authors : Nieto, N.; Chheda, P.; Kerns, R.; Nelson, S.; Honzatko, R.
Deposited on : 2021-11-23
Resolution : 2.70 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35.1
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35.1

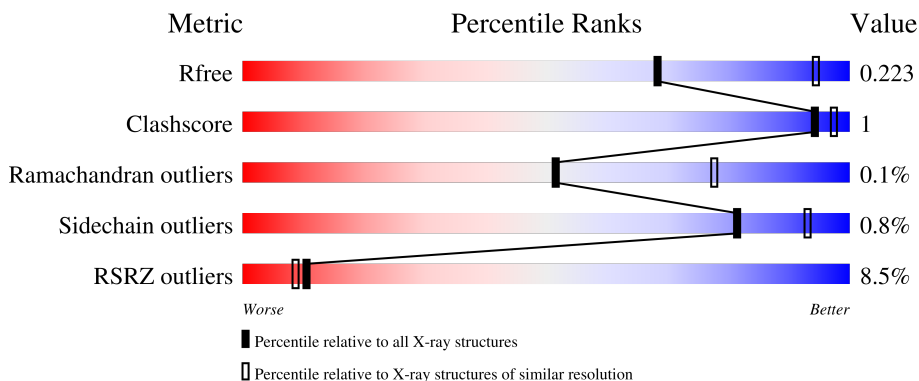
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	130704	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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	628	 7% 87% 9%
1	B	628	 8% 87% 9%

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 19897 atoms, of which 9854 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.

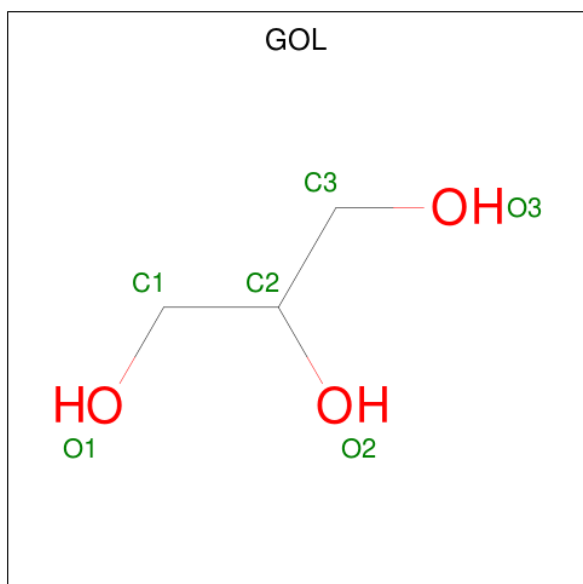
- Molecule 1 is a protein called Plastid replication-repair enzyme.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	H	N	O				S
1	A	574	9663	3086	4872	799	890	16	0	3	0
1	B	574	9705	3098	4896	802	893	16	0	5	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	82	ASN	ASP	conflict	UNP Q8ILY1
A	84	GLN	GLU	conflict	UNP Q8ILY1
B	82	ASN	ASP	conflict	UNP Q8ILY1
B	84	GLN	GLU	conflict	UNP Q8ILY1

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			13	3	7	3		
2	B	1	Total	C	H	O	0	0
			13	3	7	3		

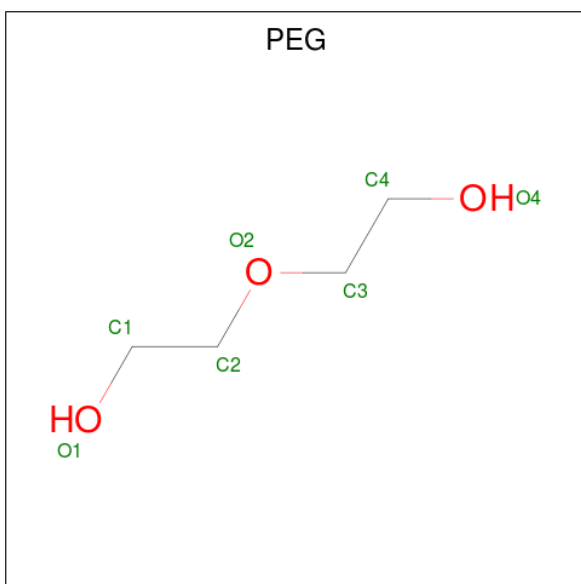
- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

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

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	4	Total	Cl	0	0
			4	4		
4	B	4	Total	Cl	0	0
			4	4		

- Molecule 5 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



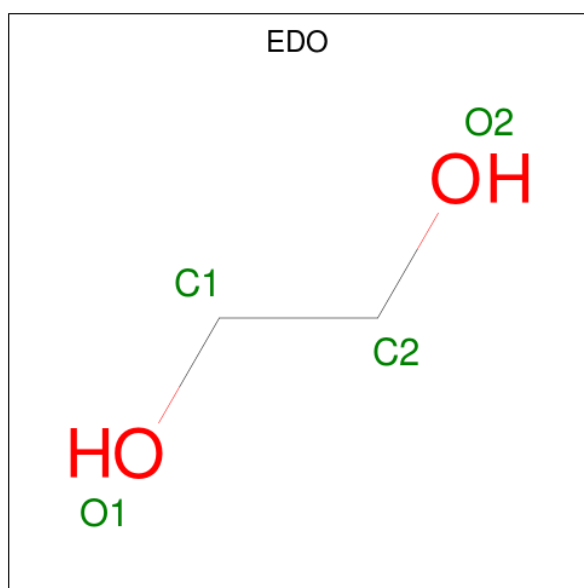
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	H	O	0	0
			17	4	10	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	H	O	0	0
			17	4	10	3		
5	A	1	Total	C	H	O	0	0
			17	4	10	3		
5	A	1	Total	C	H	O	0	0
			17	4	10	3		
5	B	1	Total	C	H	O	0	0
			17	4	10	3		
5	B	1	Total	C	H	O	0	0
			17	4	10	3		

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	H	O	0	0
			10	2	6	2		
6	B	1	Total	C	H	O	0	0
			10	2	6	2		

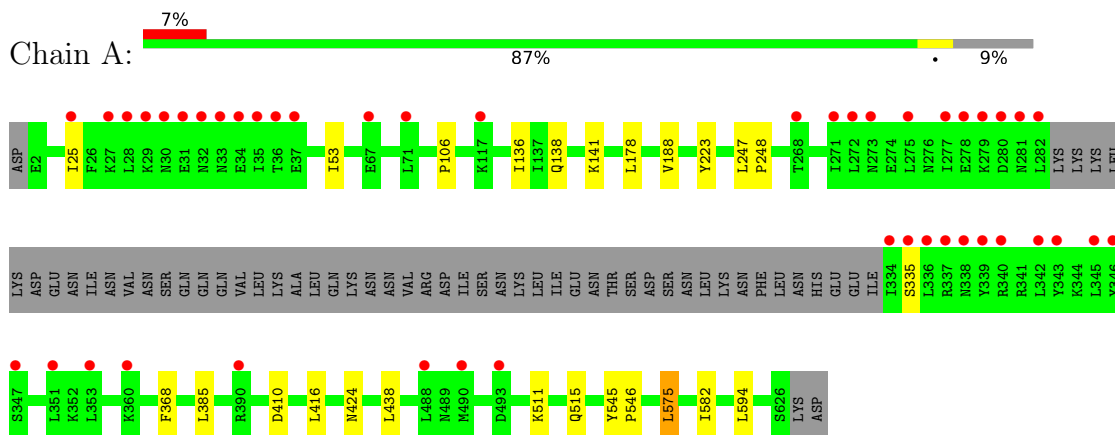
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	195	Total	O	0	0
			195	195		
7	B	176	Total	O	0	0
			176	176		

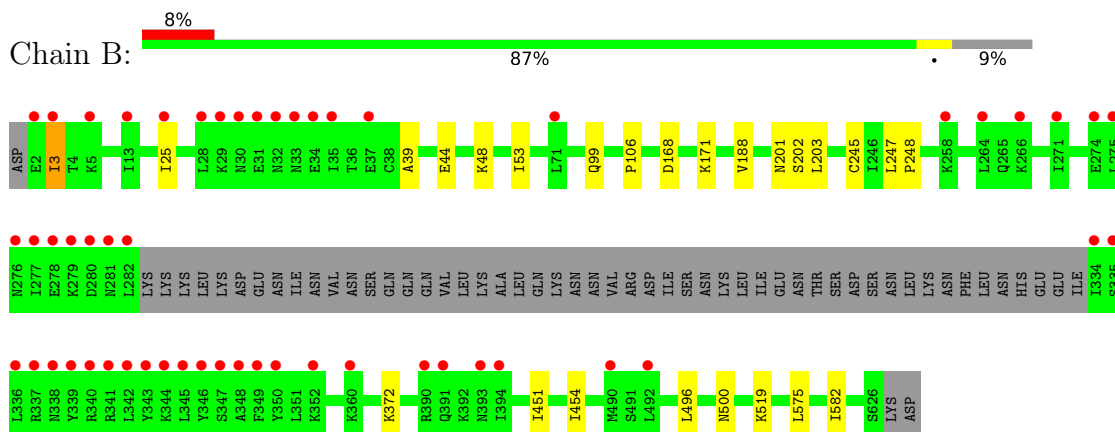
3 Residue-property plots [i](#)

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: Plastid replication-repair enzyme



- Molecule 1: Plastid replication-repair enzyme



4 Data and refinement statistics

Property	Value	Source
Space group	P 65	Depositor
Cell constants a, b, c, α , β , γ	145.37Å 145.37Å 164.94Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	19.91 – 2.70 47.58 – 2.70	Depositor EDS
% Data completeness (in resolution range)	99.9 (19.91-2.70) 94.6 (47.58-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.95 (at 2.69Å)	Xtrriage
Refinement program	PHENIX 1.19_4092	Depositor
R, R_{free}	0.191 , 0.224 0.190 , 0.223	Depositor DCC
R_{free} test set	2005 reflections (3.70%)	wwPDB-VP
Wilson B-factor (Å ²)	54.5	Xtrriage
Anisotropy	0.054	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 50.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.041 for h,-h-k,-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	19897	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.63% 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: CL, PEG, GOL, NA, 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	0.30	0/4874	0.46	0/6564
1	B	0.30	0/4892	0.46	0/6586
All	All	0.30	0/9766	0.46	0/13150

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 [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	4791	4872	4867	12	0
1	B	4809	4896	4889	13	0
2	A	6	7	8	0	0
2	B	6	7	8	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	4	0	0	0	0
4	B	4	0	0	0	0
5	A	28	40	40	0	0
5	B	14	20	20	0	0
6	A	4	6	6	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	4	6	6	0	0
7	A	195	0	0	0	0
7	B	176	0	0	2	0
All	All	10043	9854	9844	25	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 1.

All (25) 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:575:LEU:HD22	1:A:582:ILE:HD12	1.82	0.60
1:A:25:ILE:HD12	1:A:25:ILE:N	2.22	0.55
1:B:202:SER:O	1:B:203:LEU:HD23	2.10	0.52
1:B:496:LEU:O	1:B:500:ASN:ND2	2.44	0.50
1:B:44:GLU:OE2	1:B:48:LYS:NZ	2.46	0.49
1:A:575:LEU:C	1:A:575:LEU:HD23	2.34	0.48
1:A:416:LEU:HD13	1:A:438:LEU:HD23	1.96	0.47
1:B:201:ASN:OD1	1:B:202:SER:N	2.49	0.45
1:B:451:ILE:HA	1:B:454:ILE:HD12	1.98	0.45
1:B:575:LEU:HD22	1:B:582:ILE:HD12	2.00	0.44
1:B:247:LEU:HB2	1:B:248:PRO:HD3	2.00	0.43
1:A:247:LEU:HB2	1:A:248:PRO:HD3	2.00	0.43
1:A:385:LEU:HD13	1:A:575:LEU:HD12	2.00	0.43
1:A:545:TYR:HB3	1:A:546:PRO:HD3	2.00	0.43
1:A:53:ILE:HD12	1:A:188:VAL:HG11	2.00	0.43
1:B:53:ILE:HD12	1:B:188:VAL:HG11	2.00	0.43
1:A:141:LYS:NZ	1:A:368:PHE:O	2.48	0.42
1:B:168:ASP:O	1:B:171:LYS:HG2	2.19	0.42
1:B:25:ILE:HD13	1:B:39:ALA:HB2	2.02	0.42
1:A:136:ILE:HD13	1:A:223:TYR:HB2	2.01	0.42
1:B:3:ILE:H	1:B:3:ILE:HD12	1.85	0.41
1:A:511:LYS:O	1:A:515:GLN:HG2	2.21	0.41
1:B:372:LYS:NZ	7:B:805:HOH:O	2.52	0.40
1:B:519:LYS:NZ	7:B:808:HOH:O	2.55	0.40
1:A:138:GLN:HG2	1:A:178:LEU:HB2	2.03	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	573/628 (91%)	549 (96%)	23 (4%)	1 (0%)	47	73
1	B	575/628 (92%)	558 (97%)	17 (3%)	0	100	100
All	All	1148/1256 (91%)	1107 (96%)	40 (4%)	1 (0%)	51	78

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	335	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	541/591 (92%)	536 (99%)	5 (1%)	78	92
1	B	543/591 (92%)	539 (99%)	4 (1%)	84	94
All	All	1084/1182 (92%)	1075 (99%)	9 (1%)	81	93

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

Mol	Chain	Res	Type
1	A	106	PRO
1	A	410	ASP
1	A	424	ASN
1	A	575	LEU
1	A	594	LEU

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Mol	Chain	Res	Type
1	B	3	ILE
1	B	99	GLN
1	B	106	PRO
1	B	245	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 20 ligands modelled in this entry, 10 are monoatomic - leaving 10 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	$\# Z > 2$
5	PEG	A	709	-	6,6,6	0.18	0	5,5,5	0.06	0
2	GOL	B	701	-	5,5,5	0.70	0	5,5,5	1.02	0
2	GOL	A	701	-	5,5,5	0.73	0	5,5,5	0.95	0
6	EDO	B	709	-	3,3,3	0.53	0	2,2,2	0.27	0
5	PEG	B	708	-	6,6,6	0.23	0	5,5,5	0.12	0
5	PEG	A	707	-	6,6,6	0.24	0	5,5,5	0.10	0
5	PEG	A	710	-	6,6,6	0.20	0	5,5,5	0.06	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
6	EDO	A	711	-	3,3,3	0.56	0	2,2,2	0.18	0
5	PEG	B	707	-	6,6,6	0.20	0	5,5,5	0.07	0
5	PEG	A	708	-	6,6,6	0.27	0	5,5,5	0.15	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
5	PEG	A	709	-	-	1/4/4/4	-
2	GOL	B	701	-	-	0/4/4/4	-
2	GOL	A	701	-	-	0/4/4/4	-
6	EDO	B	709	-	-	0/1/1/1	-
5	PEG	B	708	-	-	1/4/4/4	-
5	PEG	A	707	-	-	1/4/4/4	-
5	PEG	A	710	-	-	3/4/4/4	-
6	EDO	A	711	-	-	0/1/1/1	-
5	PEG	B	707	-	-	1/4/4/4	-
5	PEG	A	708	-	-	1/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	709	PEG	O2-C3-C4-O4
5	A	710	PEG	O2-C3-C4-O4
5	B	708	PEG	O1-C1-C2-O2
5	A	710	PEG	C4-C3-O2-C2
5	A	708	PEG	O1-C1-C2-O2
5	A	710	PEG	C1-C2-O2-C3
5	A	707	PEG	O2-C3-C4-O4
5	B	707	PEG	O2-C3-C4-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	574/628 (91%)	0.56	45 (7%) 13 11	41, 63, 148, 204	0
1	B	574/628 (91%)	0.64	53 (9%) 9 7	40, 64, 154, 215	0
All	All	1148/1256 (91%)	0.60	98 (8%) 10 9	40, 63, 153, 215	0

All (98) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	336	LEU	12.2
1	B	282	LEU	11.5
1	A	336	LEU	9.6
1	A	282	LEU	8.2
1	A	339	TYR	7.7
1	B	275	LEU	7.2
1	B	29	LYS	6.4
1	A	281	ASN	6.1
1	B	337	ARG	6.1
1	A	279	LYS	5.9
1	A	334	ILE	5.6
1	B	279	LYS	5.6
1	B	281	ASN	5.6
1	B	280	ASP	5.6
1	A	275	LEU	5.5
1	A	337	ARG	5.4
1	B	339	TYR	5.3
1	A	28	LEU	5.2
1	B	345	LEU	5.2
1	B	334	ILE	5.1
1	B	271	ILE	4.9
1	B	340	ARG	4.8
1	A	345	LEU	4.8
1	B	31	GLU	4.7

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Mol	Chain	Res	Type	RSRZ
1	B	335	SER	4.7
1	A	338	ASN	4.6
1	B	346	TYR	4.5
1	B	347	SER	4.5
1	B	348	ALA	4.4
1	B	344	LYS	4.3
1	A	35	ILE	4.3
1	A	36	THR	4.3
1	A	278	GLU	4.3
1	B	343	TYR	4.1
1	A	271	ILE	4.1
1	A	335	SER	4.0
1	A	34	GLU	4.0
1	A	280	ASP	3.9
1	B	37	GLU	3.8
1	B	342	LEU	3.7
1	A	37	GLU	3.7
1	B	2	GLU	3.6
1	A	340	ARG	3.5
1	B	338	ASN	3.3
1	A	272	LEU	3.3
1	B	5	LYS	3.3
1	A	268	THR	3.2
1	A	277	ILE	3.2
1	B	277	ILE	3.2
1	A	360	LYS	3.2
1	A	117	LYS	3.2
1	B	33	ASN	3.1
1	B	34	GLU	3.0
1	B	35	ILE	3.0
1	A	343	TYR	3.0
1	B	393	ASN	3.0
1	A	346	TYR	2.9
1	B	391	GLN	2.9
1	A	32	ASN	2.9
1	B	274	GLU	2.8
1	B	28	LEU	2.8
1	A	342	LEU	2.7
1	B	350	TYR	2.7
1	B	341	ARG	2.7
1	B	390	ARG	2.7
1	B	278	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
1	B	25	ILE	2.6
1	A	390	ARG	2.6
1	B	264	LEU	2.6
1	A	31	GLU	2.6
1	B	32	ASN	2.6
1	A	29	LYS	2.5
1	A	25	ILE	2.5
1	A	71	LEU	2.5
1	A	490	MET	2.4
1	A	33	ASN	2.4
1	B	276	ASN	2.4
1	A	347	SER	2.4
1	B	71	LEU	2.4
1	B	394	ILE	2.4
1	B	352	LYS	2.3
1	A	67	GLU	2.3
1	A	351	LEU	2.3
1	A	273	ASN	2.3
1	A	488	LEU	2.3
1	A	493	ASP	2.3
1	B	360	LYS	2.3
1	B	3	ILE	2.3
1	B	30	ASN	2.2
1	B	492	LEU	2.1
1	A	353	LEU	2.1
1	B	490	MET	2.1
1	B	349	PHE	2.1
1	B	266	LYS	2.0
1	B	13	ILE	2.0
1	A	30	ASN	2.0
1	B	258	LYS	2.0
1	A	27	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 monosaccharides 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
3	NA	B	702	1/1	0.79	0.20	56,56,56,56	0
5	PEG	A	708	7/7	0.83	0.24	60,72,79,81	0
2	GOL	A	701	6/6	0.86	0.39	79,85,101,103	0
3	NA	A	702	1/1	0.87	0.10	53,53,53,53	0
5	PEG	A	707	7/7	0.88	0.24	64,77,85,88	0
5	PEG	A	710	7/7	0.88	0.21	62,74,80,80	0
5	PEG	B	707	7/7	0.88	0.23	64,77,84,89	0
5	PEG	A	709	7/7	0.90	0.22	54,64,72,72	0
5	PEG	B	708	7/7	0.91	0.17	55,66,75,75	0
2	GOL	B	701	6/6	0.92	0.41	80,93,105,111	0
4	CL	B	706	1/1	0.92	0.15	74,74,74,74	0
6	EDO	A	711	4/4	0.92	0.21	60,72,77,78	0
6	EDO	B	709	4/4	0.92	0.21	59,71,77,78	0
4	CL	B	705	1/1	0.94	0.12	64,64,64,64	0
4	CL	A	703	1/1	0.94	0.24	58,58,58,58	0
4	CL	A	706	1/1	0.95	0.14	73,73,73,73	0
4	CL	A	705	1/1	0.96	0.12	65,65,65,65	0
4	CL	B	703	1/1	0.97	0.15	62,62,62,62	0
4	CL	A	704	1/1	0.99	0.14	55,55,55,55	0
4	CL	B	704	1/1	0.99	0.10	49,49,49,49	0

6.5 Other polymers [i](#)

There are no such residues in this entry.