



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:10 PM UTC

PDB ID : 8XK7 / pdb_00008xk7
Title : binary complex of DNA polymerase SFM4-3 recognizing C2 methoxy nucleotide
Authors : Wen, C.; Liu, H.; Yang, L.; Gong, W.
Deposited on : 2023-12-22
Resolution : 2.00 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

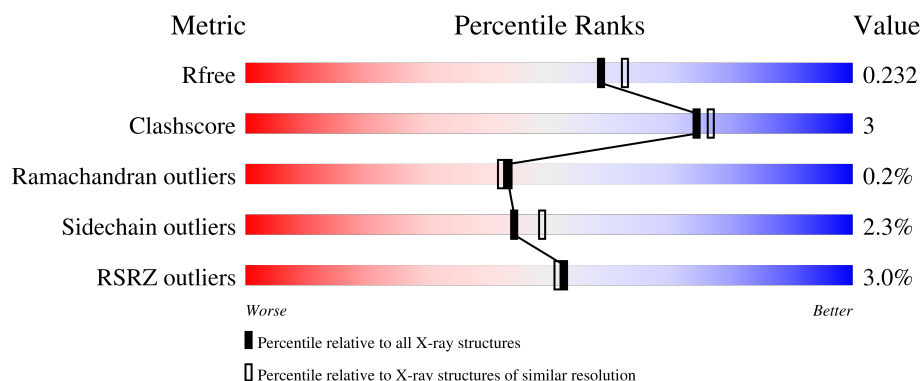
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	554	3% 87% 11%
2	B	17	71% 29%
3	C	13	69% 23% 8%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 5330 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 DNA polymerase I, thermostable.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	546	Total	C	N	O	S	0	2	0
			4333	2751	789	781	12			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	294	MET	LEU	conflict	UNP P19821
A	518	ALA	VAL	conflict	UNP P19821
A	583	SER	ASN	conflict	UNP P19821
A	614	GLU	ILE	conflict	UNP P19821
A	615	GLY	GLU	conflict	UNP P19821
A	655	ASN	ASP	conflict	UNP P19821
A	681	LYS	GLU	conflict	UNP P19821
A	742	GLN	GLU	conflict	UNP P19821
A	747	ARG	MET	conflict	UNP P19821
A	833	ALA	-	expression tag	UNP P19821
A	834	ALA	-	expression tag	UNP P19821
A	835	LYS	-	expression tag	UNP P19821
A	836	LEU	-	expression tag	UNP P19821
A	837	ALA	-	expression tag	UNP P19821
A	838	ALA	-	expression tag	UNP P19821
A	839	ALA	-	expression tag	UNP P19821
A	840	LEU	-	expression tag	UNP P19821
A	841	GLU	-	expression tag	UNP P19821
A	842	HIS	-	expression tag	UNP P19821
A	843	HIS	-	expression tag	UNP P19821
A	844	HIS	-	expression tag	UNP P19821
A	845	HIS	-	expression tag	UNP P19821
A	846	HIS	-	expression tag	UNP P19821
A	847	HIS	-	expression tag	UNP P19821

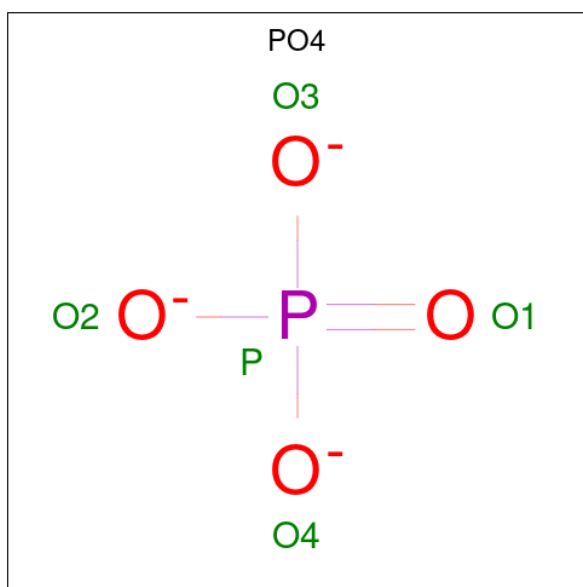
- Molecule 2 is a DNA chain called DNA(5'-D(*AP*AP*AP*CP*GP*GP*CP*GP*CP*CP*GP*TP*GP*GP*TP*CP*OMG)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	17	Total	C	N	O	P	0	0	0
			354	166	69	102	17			

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

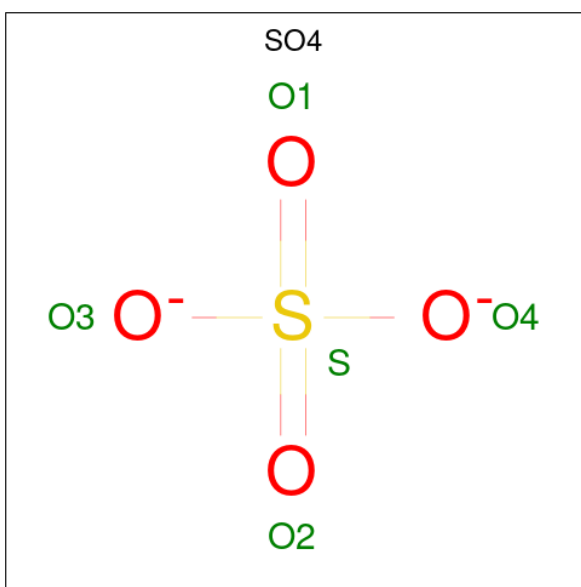
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	13	Total	C	N	O	P	0	0	0
			265	125	53	75	12			

- Molecule 4 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



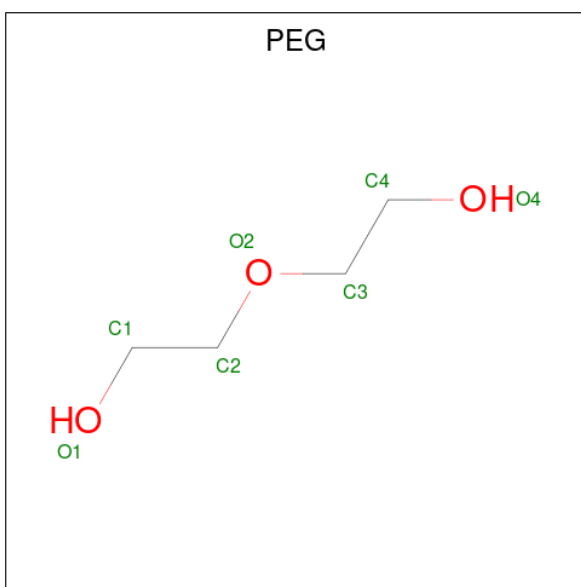
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	P	0	0
			5	4	1		
4	A	1	Total	O	P	0	0
			5	4	1		

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 6 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			7	4	3		

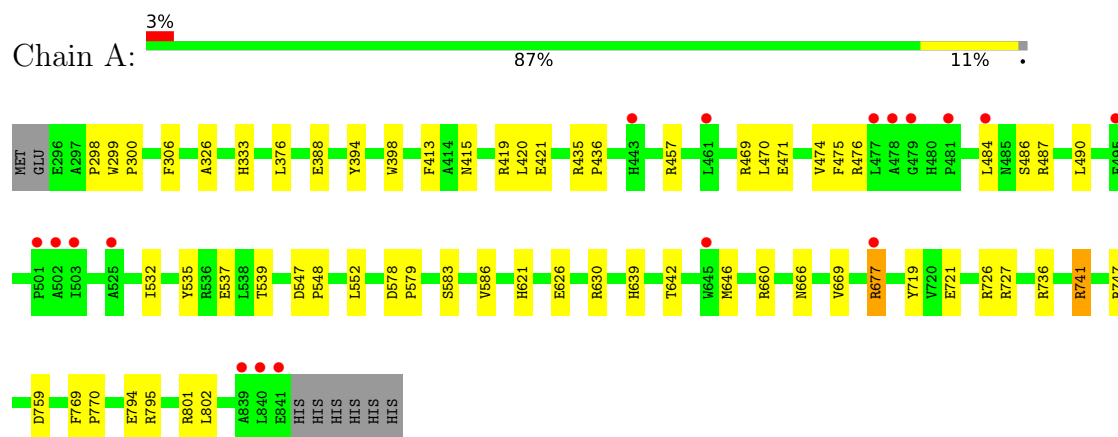
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	272	Total 272	O 272	0	0
7	B	42	Total 42	O 42	0	0
7	C	32	Total 32	O 32	0	0

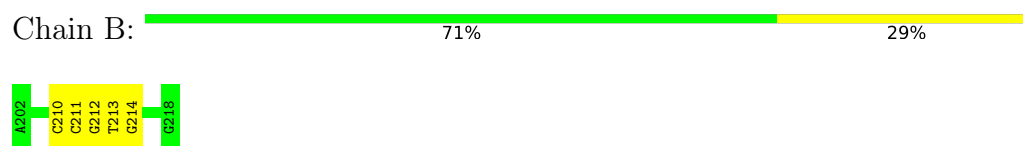
3 Residue-property plots [i](#)

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.

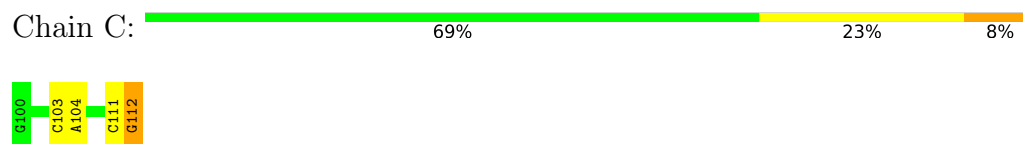
- Molecule 1: DNA polymerase I, thermostable



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



- Molecule 3: DNA(5'-D(*GP*AP*CP*CP*AP*CP*GP*GP*CP*GP*CP*CP*OMG)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	61.61Å 65.63Å 107.38Å 90.00° 103.51° 90.00°	Depositor
Resolution (Å)	24.41 – 2.00 24.41 – 2.00	Depositor EDS
% Data completeness (in resolution range)	98.8 (24.41-2.00) 98.8 (24.41-2.00)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.19 (at 1.99Å)	Xtriage
Refinement program	REFMAC 5.8.0352	Depositor
R, R_{free}	0.192 , 0.231 0.201 , 0.232	Depositor DCC
R_{free} test set	2832 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	32.3	Xtriage
Anisotropy	0.083	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 30.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5330	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.82% 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: SO4, PEG, OMG, 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	0.55	2/4424 (0.0%)	0.89	1/5991 (0.0%)
2	B	0.49	0/370	1.09	0/569
3	C	0.48	0/270	0.94	0/414
All	All	0.54	2/5064 (0.0%)	0.91	1/6974 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	9

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	621	HIS	CE1-NE2	6.59	1.39	1.32
1	A	639	HIS	CE1-NE2	5.52	1.38	1.32

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	759	ASP	CA-CB-CG	6.11	118.71	112.60

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	457	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	A	469	ARG	Sidechain
1	A	476	ARG	Sidechain
1	A	630	ARG	Sidechain
1	A	677	ARG	Sidechain
1	A	741	ARG	Sidechain
1	A	747	ARG	Sidechain
1	A	795	ARG	Sidechain
1	A	801	ARG	Sidechain

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	4333	0	4390	26	0
2	B	354	0	192	3	0
3	C	265	0	147	3	0
4	A	10	0	0	0	0
5	A	15	0	0	0	0
6	A	7	0	10	1	0
7	A	272	0	0	1	0
7	B	42	0	0	0	0
7	C	32	0	0	0	0
All	All	5330	0	4739	30	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 3.

All (30) 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:415[A]:ASN:HD21	1:A:419:ARG:HH21	1.46	0.62
1:A:376:LEU:HD22	1:A:420:LEU:CD1	2.30	0.61
1:A:388:GLU:HG3	1:A:398:TRP:CD1	2.42	0.54
1:A:719:TYR:CD1	1:A:727:ARG:HG3	2.43	0.54
1:A:470:LEU:O	1:A:474:VAL:HG23	2.10	0.52
3:C:103:DC:H2"	3:C:104:DA:C8	2.44	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:376:LEU:HD11	1:A:413:PHE:CE1	2.46	0.51
1:A:471:GLU:HG2	1:A:475:PHE:CZ	2.46	0.51
1:A:578:ASP:OD1	7:A:1001:HOH:O	2.19	0.51
1:A:298:PRO:O	1:A:333:HIS:HD2	1.95	0.50
2:B:213:DT:H2''	2:B:214:DG:C8	2.48	0.49
1:A:486:SER:HA	2:B:212:DG:H4'	1.95	0.48
1:A:552:LEU:HD22	6:A:906:PEG:H11	1.96	0.47
1:A:721:GLU:HA	1:A:726:ARG:O	2.14	0.47
1:A:490:LEU:HD11	1:A:532:ILE:HD13	1.97	0.47
1:A:547:ASP:HB2	1:A:548:PRO:HD3	1.97	0.46
1:A:306:PHE:O	1:A:326:ALA:HA	2.17	0.45
1:A:394:TYR:O	1:A:415[B]:ASN:ND2	2.50	0.45
1:A:583:SER:HA	3:C:111:DC:O4'	2.18	0.44
1:A:666:ASN:O	1:A:669:VAL:HG12	2.18	0.44
3:C:111:DC:H2'	3:C:112:OMG:C8	2.53	0.44
1:A:484:LEU:HB3	1:A:535:TYR:CE1	2.53	0.43
1:A:736:ARG:HH11	1:A:736:ARG:HG2	1.83	0.43
1:A:769:PHE:N	1:A:770:PRO:HD2	2.33	0.43
1:A:535:TYR:CZ	1:A:539:THR:HG21	2.55	0.42
1:A:299:TRP:CG	1:A:300:PRO:HA	2.54	0.42
1:A:415[A]:ASN:HD21	1:A:419:ARG:NH2	2.15	0.42
1:A:435:ARG:N	1:A:436:PRO:HD2	2.35	0.42
2:B:210:DC:H2''	2:B:211:DC:O5'	2.20	0.41
1:A:642:THR:O	1:A:646:MET:HG2	2.20	0.41

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	546/554 (99%)	532 (97%)	13 (2%)	1 (0%)	43 42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	586	VAL

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	441/449 (98%)	431 (98%)	10 (2%)	44	49

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	421	GLU
1	A	487	ARG
1	A	537	GLU
1	A	579	PRO
1	A	626	GLU
1	A	660	ARG
1	A	677	ARG
1	A	741	ARG
1	A	794	GLU
1	A	802	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	333	HIS
1	A	485	ASN
1	A	666	ASN
1	A	754	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	OMG	B	218	2	23,26,27	0.37	0	32,38,41	0.52	0
3	OMG	C	112	3,2	23,26,27	0.35	0	32,38,41	0.59	1 (3%)

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	OMG	B	218	2	-	0/9/27/28	0/3/3/3
3	OMG	C	112	3,2	-	1/9/27/28	0/3/3/3

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	112	OMG	O2'-C2'-C1'	2.23	113.22	108.99

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	112	OMG	C3'-C2'-O2'-CM2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	112	OMG	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

6 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	$\# Z > 2$
4	PO4	A	901	-	4,4,4	1.03	1 (25%)	6,6,6	0.49	0
4	PO4	A	902	-	4,4,4	0.81	0	6,6,6	0.53	0
6	PEG	A	906	-	6,6,6	0.18	0	5,5,5	0.11	0
5	SO4	A	904	-	4,4,4	0.31	0	6,6,6	0.07	0
5	SO4	A	903	-	4,4,4	0.33	0	6,6,6	0.23	0
5	SO4	A	905	-	4,4,4	0.28	0	6,6,6	0.10	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	PEG	A	906	-	-	1/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	901	PO4	P-O1	2.00	1.55	1.50

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	906	PEG	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	906	PEG	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	546/554 (98%)	0.18	17 (3%)	51	50	14, 36, 60, 82	2 (0%)
2	B	16/17 (94%)	-0.27	0	100	100	26, 37, 56, 59	0
3	C	12/13 (92%)	-0.01	0	100	100	27, 39, 59, 60	0
All	All	574/584 (98%)	0.17	17 (2%)	52	51	14, 36, 60, 82	2 (0%)

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	645	TRP	3.2
1	A	461	LEU	3.0
1	A	501	PRO	2.9
1	A	479	GLY	2.7
1	A	503	ILE	2.6
1	A	495	PHE	2.5
1	A	502	ALA	2.5
1	A	839	ALA	2.5
1	A	481	PRO	2.4
1	A	840	LEU	2.3
1	A	677	ARG	2.3
1	A	478	ALA	2.3
1	A	477	LEU	2.3
1	A	525	ALA	2.2
1	A	484	LEU	2.2
1	A	443[A]	HIS	2.1
1	A	841	GLU	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [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
2	OMG	B	218	24/25	0.89	0.10	45,55,67,70	0
3	OMG	C	112	24/25	0.96	0.06	26,28,33,36	0

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
5	SO4	A	904	5/5	0.63	0.13	83,90,94,94	0
5	SO4	A	905	5/5	0.72	0.11	66,74,76,83	0
6	PEG	A	906	7/7	0.85	0.15	52,60,65,69	0
5	SO4	A	903	5/5	0.87	0.17	51,58,60,60	0
4	PO4	A	901	5/5	0.89	0.17	52,53,59,59	0
4	PO4	A	902	5/5	0.95	0.07	47,49,52,53	0

6.5 Other polymers [i](#)

There are no such residues in this entry.