



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 7, 2024 – 12:20 PM JST

PDB ID : 8Z62  
Title : Crystal structure of rRNA (uracil-C5)-methyltransferase from *Pyrococcus horikoshii* OT3  
Authors : Saha, S.; Kanaujia, S.P.  
Deposited on : 2024-04-18  
Resolution : 3.20 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](mailto: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>.

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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 : 3.0  
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)  
CCP4 : 9.0.003 (Gargrove)  
Density-Fitness : 1.0.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.39

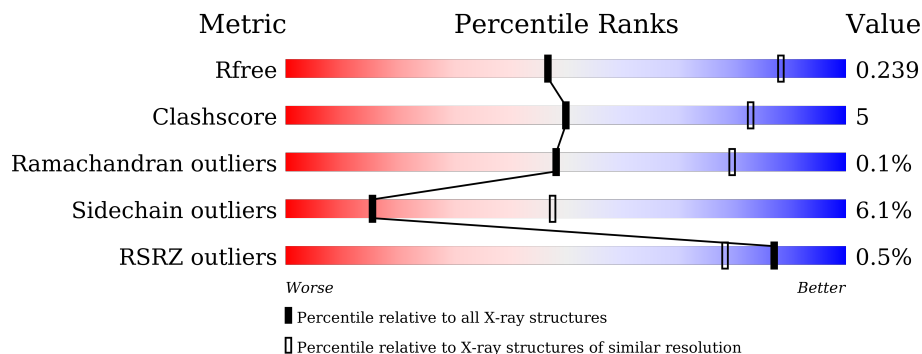
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.20 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))
$R_{free}$	164625	1370 (3.20-3.20)
Clashscore	180529	1497 (3.20-3.20)
Ramachandran outliers	177936	1479 (3.20-3.20)
Sidechain outliers	177891	1478 (3.20-3.20)
RSRZ outliers	164620	1371 (3.20-3.20)

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  $\geq 3$ , 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	412	 84% 13% .
1	B	412	 82% 16% .

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
3	SO4	A	502	-	-	X	-

## 2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 6803 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.

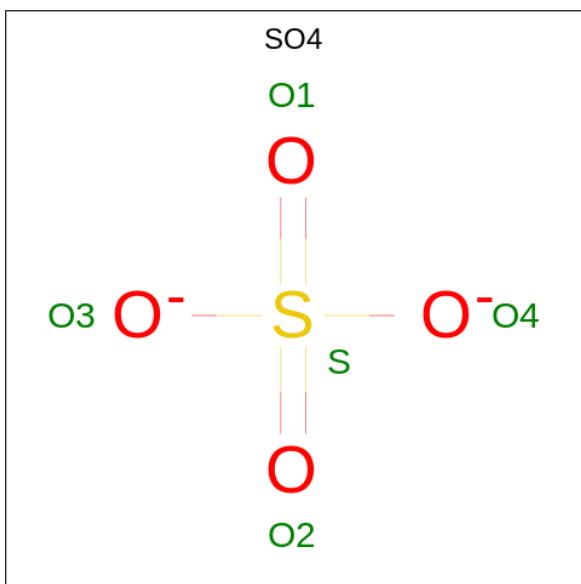
- Molecule 1 is a protein called 23S rRNA (uracil(747)-C(5))-methyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	410	3321	2148	569	591	13	0	2	0
1	B	410	3313	2143	566	591	13	0	1	0

- Molecule 2 is SODIUM ION (three-letter code: NA) (formula: Na).

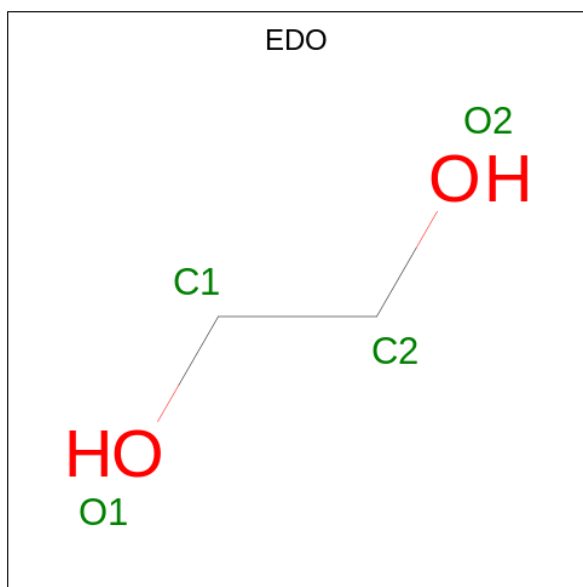
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Na	0	0
			1	1		
2	B	1	Total	Na	0	0
			1	1		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

- Molecule 5 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C<sub>4</sub>H<sub>10</sub>O<sub>3</sub>).



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

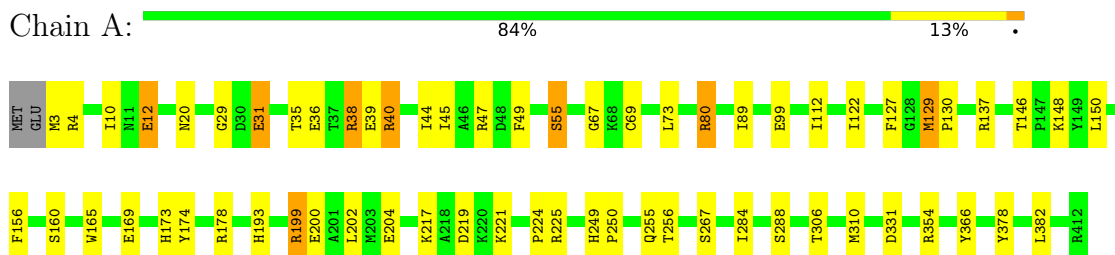
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	64	Total O 64 64	0	0
6	B	46	Total O 46 46	0	0

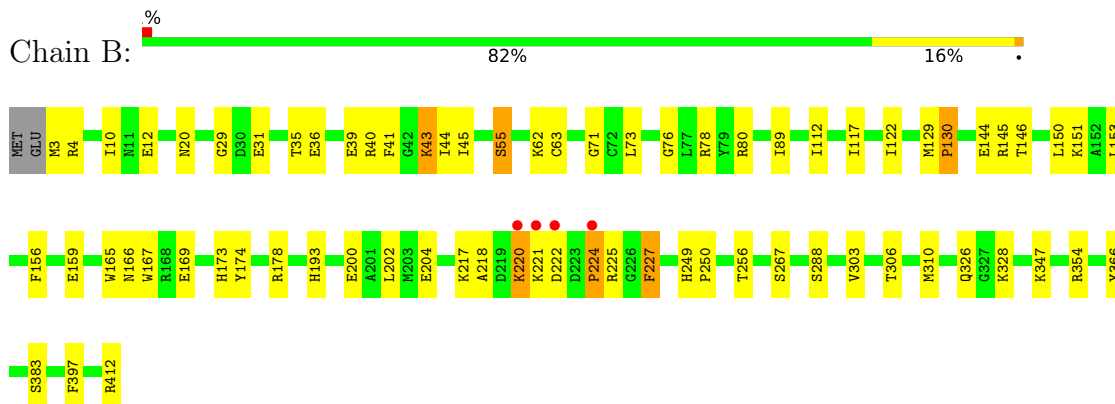
### 3 Residue-property plots

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: 23S rRNA (uracil(747)-C(5))-methyltransferase



- Molecule 1: 23S rRNA (uracil(747)-C(5))-methyltransferase



## 4 Data and refinement statistics i

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	91.89Å 96.61Å 122.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	75.83 – 3.20 75.83 – 3.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (75.83-3.20) 100.0 (75.83-3.20)	Depositor EDS
$R_{merge}$	0.22	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.02 (at 3.19Å)	Xtrriage
Refinement program	REFMAC 5.8.0352	Depositor
R, $R_{free}$	0.169 , 0.237 0.178 , 0.239	Depositor DCC
$R_{free}$ test set	928 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	46.8	Xtrriage
Anisotropy	0.541	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 60.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	0.026 for k,h,-l	Xtrriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	6803	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	48.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.66% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: PEG, EDO, SO4, NA

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	0.43	0/3403	0.80	2/4591 (0.0%)
1	B	0.39	0/3392	0.74	2/4577 (0.0%)
All	All	0.41	0/6795	0.77	4/9168 (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	6
1	B	0	2
All	All	0	8

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	B	130	PRO	N-CA-C	-6.38	95.50	112.10
1	B	71	GLY	N-CA-C	5.48	126.80	113.10
1	A	69	CYS	CB-CA-C	-5.04	100.31	110.40
1	A	69	CYS	N-CA-CB	5.01	119.61	110.60

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	137[A]	ARG	Sidechain
1	A	137[B]	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	A	199	ARG	Sidechain
1	A	354	ARG	Sidechain
1	A	47	ARG	Sidechain
1	A	80	ARG	Sidechain
1	B	354	ARG	Sidechain
1	B	78	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	3321	0	3389	37	0
1	B	3313	0	3376	39	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	10	0	0	4	0
4	A	12	0	18	0	0
5	A	21	0	30	0	0
5	B	14	0	20	1	0
6	A	64	0	0	2	0
6	B	46	0	0	3	0
All	All	6803	0	6833	70	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 5.

All (70) 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:284:ILE:O	1:A:284:ILE:HG13	1.42	1.12
1:A:38:ARG:HD3	3:A:502:SO4:O4	1.85	0.76
1:A:284:ILE:O	1:A:284:ILE:CG1	2.24	0.76
1:B:224:PRO:HG3	6:B:630:HOH:O	1.86	0.74
1:A:255:GLN:HG2	6:A:604:HOH:O	1.87	0.73
1:A:129:MET:O	6:A:601:HOH:O	2.14	0.66
1:A:40:ARG:NH1	3:A:502:SO4:O3	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:29:GLY:HA3	1:A:55:SER:HB2	1.80	0.63
1:B:218:ALA:HB2	1:B:227:PHE:CZ	2.41	0.56
1:A:112:ILE:HD12	1:A:178:ARG:HG2	1.88	0.56
1:B:193:HIS:CE1	1:B:217:LYS:HE3	2.41	0.55
1:B:3:MET:HA	6:B:628:HOH:O	2.07	0.55
1:A:44:ILE:C	1:A:45:ILE:HD12	2.28	0.54
1:B:122:ILE:HD13	1:B:153:LEU:HD23	1.90	0.54
1:B:44:ILE:C	1:B:45:ILE:HD12	2.30	0.53
1:B:63:CYS:SG	1:B:76:GLY:HA2	2.48	0.52
1:A:173:HIS:ND1	1:A:217:LYS:NZ	2.50	0.52
1:A:40:ARG:NH1	3:A:502:SO4:O2	2.43	0.52
1:B:29:GLY:HA3	1:B:55:SER:HB2	1.90	0.52
1:A:221:LYS:HE3	1:B:36:GLU:HG3	1.91	0.51
1:B:145:ARG:HD3	6:B:625:HOH:O	2.11	0.51
1:B:122:ILE:CD1	1:B:153:LEU:HD23	2.41	0.50
1:B:303:VAL:O	1:B:326:GLN:NE2	2.43	0.50
1:B:383:SER:O	1:B:412:ARG:NH1	2.45	0.50
1:B:165:TRP:CZ3	1:B:169:GLU:HA	2.48	0.49
1:A:173:HIS:CD2	1:A:174:TYR:CE1	3.01	0.48
1:B:173:HIS:CD2	1:B:174:TYR:CE1	3.01	0.48
1:A:130:PRO:HD3	1:B:41:PHE:H	1.78	0.48
1:B:10:ILE:HD12	1:B:89:ILE:HD11	1.95	0.48
1:A:40:ARG:NH1	3:A:502:SO4:S	2.87	0.47
1:A:200:GLU:OE2	1:A:204:GLU:OE2	2.32	0.47
1:A:127:PHE:CZ	1:A:224:PRO:HD3	2.49	0.47
1:A:193:HIS:CE1	1:A:217:LYS:HE2	2.49	0.47
1:B:200:GLU:OE2	1:B:204:GLU:OE2	2.32	0.47
1:A:129:MET:HG3	1:B:41:PHE:CE2	2.50	0.47
1:B:146:THR:O	1:B:150:LEU:HG	2.15	0.47
1:B:112:ILE:HD12	1:B:178:ARG:HG2	1.98	0.46
1:A:146:THR:O	1:A:150:LEU:HG	2.17	0.45
1:B:306:THR:O	1:B:310:MET:HG2	2.16	0.45
1:A:12:GLU:H	1:A:12:GLU:CD	2.19	0.45
1:A:306:THR:O	1:A:310:MET:HG2	2.16	0.45
1:A:156:PHE:CE1	1:A:202:LEU:HB2	2.52	0.45
1:A:129:MET:HB2	1:B:40:ARG:HE	1.82	0.44
1:B:200:GLU:O	1:B:204:GLU:HB2	2.18	0.44
1:B:156:PHE:CE1	1:B:202:LEU:HB2	2.53	0.44
1:B:166:ASN:O	1:B:167:TRP:HB2	2.18	0.44
1:B:130:PRO:HG2	5:B:503:PEG:H32	1.99	0.43
1:B:173:HIS:ND1	1:B:217:LYS:NZ	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:160:SER:OG	1:A:160:SER:O	2.37	0.43
1:A:165:TRP:CZ3	1:A:169:GLU:HA	2.53	0.43
1:A:4:ARG:NH1	1:A:31:GLU:OE1	2.52	0.42
1:B:193:HIS:HE2	1:B:217:LYS:HZ1	1.67	0.42
1:A:193:HIS:CE1	1:A:217:LYS:CE	3.01	0.42
1:A:249:HIS:CG	1:A:250:PRO:HD2	2.54	0.42
1:A:10:ILE:HD12	1:A:89:ILE:HD11	2.02	0.42
1:A:378:TYR:HA	1:A:382:LEU:HB2	2.02	0.42
1:B:4:ARG:NH1	1:B:31:GLU:OE1	2.54	0.41
1:B:43:LYS:HB3	1:B:45:ILE:HD11	2.01	0.41
1:B:62:LYS:HD3	1:B:62:LYS:HA	1.63	0.41
1:B:193:HIS:NE2	1:B:217:LYS:CE	2.83	0.41
1:A:45:ILE:HD12	1:A:45:ILE:N	2.35	0.41
1:A:49:PHE:CZ	1:A:67:GLY:HA3	2.55	0.41
1:A:122:ILE:HG21	1:A:150:LEU:HD22	2.02	0.41
1:B:45:ILE:HD12	1:B:45:ILE:N	2.35	0.41
1:A:36:GLU:HB2	1:B:221:LYS:NZ	2.36	0.41
1:A:221:LYS:HE3	1:B:36:GLU:CB	2.51	0.40
1:B:249:HIS:CG	1:B:250:PRO:HD2	2.56	0.40
1:A:219:ASP:OD2	1:A:221:LYS:HB3	2.22	0.40
1:B:117:ILE:HG12	1:B:153:LEU:HD21	2.02	0.40
1:B:193:HIS:ND1	1:B:220:LYS:HG3	2.36	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	410/412 (100%)	393 (96%)	17 (4%)	0	100	100
1	B	409/412 (99%)	391 (96%)	17 (4%)	1 (0%)	44	75
All	All	819/824 (99%)	784 (96%)	34 (4%)	1 (0%)	48	80

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	224	PRO

### 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	361/361 (100%)	340 (94%)	21 (6%)	17	49
1	B	360/361 (100%)	336 (93%)	24 (7%)	13	44
All	All	721/722 (100%)	676 (94%)	45 (6%)	15	47

All (45) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	MET
1	A	12	GLU
1	A	20	ASN
1	A	31	GLU
1	A	35	THR
1	A	38	ARG
1	A	39	GLU
1	A	40	ARG
1	A	55	SER
1	A	73	LEU
1	A	80	ARG
1	A	99	GLU
1	A	129	MET
1	A	148	LYS
1	A	199	ARG
1	A	225	ARG
1	A	256	THR
1	A	267	SER
1	A	288	SER
1	A	331	ASP
1	A	366	TYR
1	B	12	GLU

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Mol	Chain	Res	Type
1	B	20	ASN
1	B	35	THR
1	B	39	GLU
1	B	43	LYS
1	B	55	SER
1	B	73	LEU
1	B	80	ARG
1	B	129	MET
1	B	144	GLU
1	B	151	LYS
1	B	159	GLU
1	B	220	LYS
1	B	222	ASP
1	B	225	ARG
1	B	227	PHE
1	B	256	THR
1	B	267	SER
1	B	288	SER
1	B	328	LYS
1	B	347	LYS
1	B	366	TYR
1	B	397[A]	PHE
1	B	397[B]	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	65	HIS
1	B	75	GLN

### 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 oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 2 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	507	-	6,6,6	0.20	0	5,5,5	0.19	0
4	EDO	A	504	-	3,3,3	0.40	0	2,2,2	0.48	0
5	PEG	B	503	-	6,6,6	0.52	0	5,5,5	0.30	0
3	SO4	A	503	-	4,4,4	0.36	0	6,6,6	0.19	0
4	EDO	A	506	-	3,3,3	0.39	0	2,2,2	0.41	0
4	EDO	A	505	-	3,3,3	0.08	0	2,2,2	0.06	0
5	PEG	A	508	-	6,6,6	0.46	0	5,5,5	0.36	0
5	PEG	B	502	-	6,6,6	0.34	0	5,5,5	0.33	0
3	SO4	A	502	-	4,4,4	0.28	0	6,6,6	0.22	0
5	PEG	A	509	-	6,6,6	0.31	0	5,5,5	0.21	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	507	-	-	1/4/4/4	-
4	EDO	A	504	-	-	0/1/1/1	-
5	PEG	B	503	-	-	1/4/4/4	-
4	EDO	A	506	-	-	1/1/1/1	-
4	EDO	A	505	-	-	0/1/1/1	-
5	PEG	A	508	-	-	2/4/4/4	-
5	PEG	B	502	-	-	3/4/4/4	-
5	PEG	A	509	-	-	0/4/4/4	-

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	508	PEG	C1-C2-O2-C3
5	A	507	PEG	O2-C3-C4-O4
4	A	506	EDO	O1-C1-C2-O2
5	A	508	PEG	O1-C1-C2-O2
5	B	502	PEG	O1-C1-C2-O2
5	B	502	PEG	O2-C3-C4-O4
5	B	503	PEG	O1-C1-C2-O2
5	B	502	PEG	C4-C3-O2-C2

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	503	PEG	1	0
3	A	502	SO4	4	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	410/412 (99%)	-0.63	0 <a href="#">100</a> <a href="#">100</a>	12, 34, 62, 103	2 (0%)
1	B	410/412 (99%)	-0.29	4 (0%) <a href="#">79</a> <a href="#">66</a>	18, 57, 92, 155	1 (0%)
All	All	820/824 (99%)	-0.46	4 (0%) <a href="#">87</a> <a href="#">78</a>	12, 43, 85, 155	3 (0%)

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	224	PRO	4.0
1	B	222	ASP	3.2
1	B	221	LYS	2.8
1	B	220	LYS	2.5

### 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 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
5	PEG	B	502	7/7	0.87	0.18	45,51,52,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	PEG	A	509	7/7	0.88	0.15	55,56,60,65	0
5	PEG	A	507	7/7	0.92	0.13	49,53,60,60	0
5	PEG	B	503	7/7	0.92	0.11	41,43,47,47	0
4	EDO	A	505	4/4	0.93	0.13	53,53,53,55	0
2	NA	A	501	1/1	0.94	0.12	11,11,11,11	0
4	EDO	A	504	4/4	0.94	0.07	29,35,38,39	0
5	PEG	A	508	7/7	0.94	0.13	28,30,38,41	0
4	EDO	A	506	4/4	0.95	0.06	26,31,34,36	0
2	NA	B	501	1/1	0.95	0.10	17,17,17,17	0
3	SO4	A	502	5/5	0.97	0.05	44,49,51,58	0
3	SO4	A	503	5/5	0.99	0.04	51,52,56,56	0

## 6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.