



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:04 PM GMT

PDB ID : 4H1T  
Title : X-RAY Structure of the Complex VchUPh with Phosphate ion at 1.92Å Resolution.  
Authors : Prokofev, I.I.; Lashkov, A.A.; Gabdoulkhakov, A.G.; Sotnichenko, S.E.; Betzel, C.; Mikhailov, A.M.  
Deposited on : 2012-09-11  
Resolution : 1.92 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  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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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 : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
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) : trunk26865

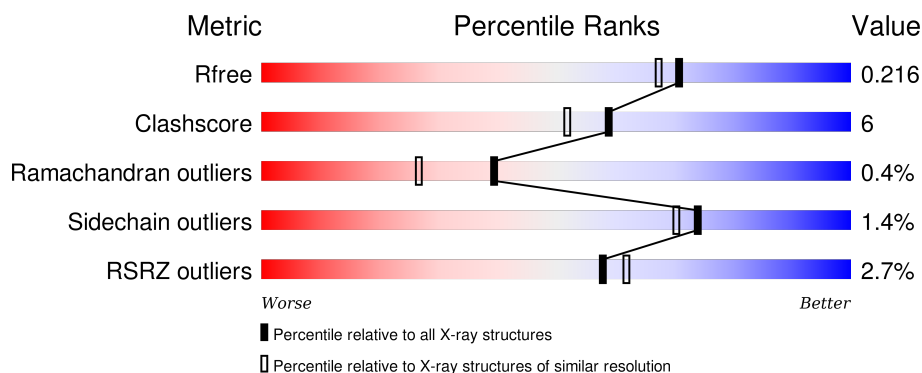
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.92 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))
$R_{free}$	91344	5832 (1.94-1.90)
Clashscore	102246	6540 (1.94-1.90)
Ramachandran outliers	100387	6464 (1.94-1.90)
Sidechain outliers	100360	6465 (1.94-1.90)
RSRZ outliers	91569	5846 (1.94-1.90)

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  $\geq 3$ , 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	253	<div> <div>3%</div> <div>85%</div> <div>15%</div> </div>
1	B	253	<div> <div>8%</div> <div>84%</div> <div>15%</div> </div>
1	C	253	<div> <div>%</div> <div>84%</div> <div>15%</div> </div>
1	D	253	<div> <div>4%</div> <div>83%</div> <div>16%</div> </div>
1	E	253	<div> <div>%</div> <div>86%</div> <div>13%</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	253	

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	EDO	A	302	-	-	-	X
3	EDO	A	304	-	-	-	X
3	EDO	A	305	-	-	-	X
3	EDO	A	306	-	-	-	X
3	EDO	A	307	-	-	-	X
3	EDO	A	308	-	-	-	X
3	EDO	A	309	-	-	-	X
3	EDO	A	310	-	-	-	X
3	EDO	A	311	-	-	-	X
3	EDO	A	314	-	-	-	X
3	EDO	A	315	-	-	-	X
3	EDO	A	316	-	-	-	X
3	EDO	B	306	-	-	-	X
3	EDO	B	309	-	-	-	X
3	EDO	C	305	-	-	-	X
3	EDO	C	306	-	-	-	X
3	EDO	C	307	-	-	X	X
3	EDO	C	310	-	-	-	X
3	EDO	D	303	-	-	-	X
3	EDO	D	304	-	-	-	X
3	EDO	E	304	-	-	-	X
3	EDO	E	306	-	-	-	X
3	EDO	E	307	-	-	-	X
3	EDO	E	308	-	-	-	X
3	EDO	F	304	-	-	-	X
3	EDO	F	306	-	-	-	X
3	EDO	F	308	-	-	-	X
3	EDO	F	310	-	-	-	X
4	EOH	A	312	-	-	-	X
4	EOH	B	308	-	-	-	X
5	PEG	A	320	-	-	-	X
5	PEG	A	322	-	-	-	X
5	PEG	A	323	-	-	-	X
5	PEG	A	324	-	-	-	X
5	PEG	A	326	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	PEG	B	311	-	-	-	X
5	PEG	B	313	-	-	-	X
5	PEG	C	312	-	-	-	X
5	PEG	C	313	-	-	-	X
5	PEG	C	314	-	-	-	X
5	PEG	C	315	-	-	-	X
5	PEG	C	316	-	-	-	X
5	PEG	C	317	-	-	-	X
5	PEG	D	307	-	-	-	X
5	PEG	D	308	-	-	-	X
5	PEG	E	309	-	-	-	X
5	PEG	F	312	-	-	-	X
5	PEG	F	314	-	-	-	X
5	PEG	F	316	-	-	-	X
5	PEG	F	318	-	-	-	X
7	SO4	D	301	-	-	-	X
7	SO4	E	302	-	-	-	X

## 2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 13160 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 Uridine phosphorylase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	251	Total	C	N	O	S	0	10	0
			1934	1218	334	368	14			
1	B	251	Total	C	N	O	S	0	6	0
			1914	1202	331	366	15			
1	C	251	Total	C	N	O	S	0	7	0
			1924	1207	336	368	13			
1	D	250	Total	C	N	O	S	0	5	0
			1899	1191	329	364	15			
1	E	251	Total	C	N	O	S	0	6	0
			1915	1201	334	366	14			
1	F	250	Total	C	N	O	S	0	5	0
			1899	1194	331	361	13			

- 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	E	1	Total	Na	0	0
			1	1		

- Molecule 3 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
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		

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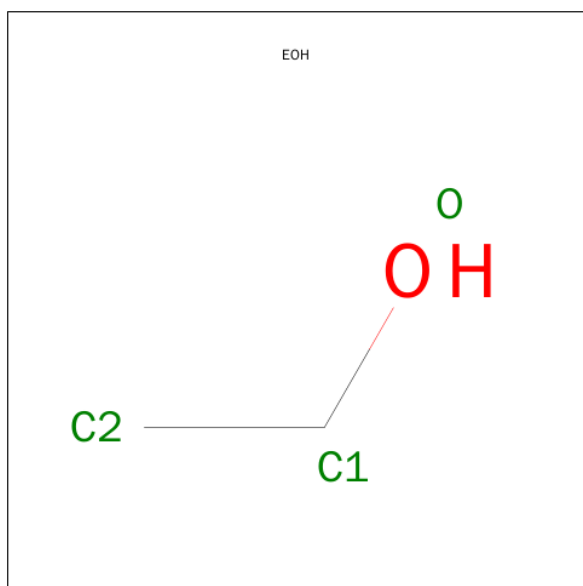
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 4	C 2	O 2	0	0
3	A	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	B	1	Total 4	C 2	O 2	0	0
3	C	1	Total 4	C 2	O 2	0	0
3	C	1	Total 4	C 2	O 2	0	0
3	C	1	Total 4	C 2	O 2	0	0
3	C	1	Total 4	C 2	O 2	0	0
3	C	1	Total 4	C 2	O 2	0	0
3	C	1	Total 4	C 2	O 2	0	0
3	C	1	Total 4	C 2	O 2	0	0
3	D	1	Total 4	C 2	O 2	0	0
3	D	1	Total 4	C 2	O 2	0	0
3	D	1	Total 4	C 2	O 2	0	0
3	D	1	Total 4	C 2	O 2	0	0
3	E	1	Total 4	C 2	O 2	0	0
3	E	1	Total 4	C 2	O 2	0	0
3	E	1	Total 4	C 2	O 2	0	0
3	E	1	Total 4	C 2	O 2	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	E	1	Total C O 4 2 2	0	0
3	F	1	Total C O 4 2 2	0	0
3	F	1	Total C O 4 2 2	0	0
3	F	1	Total C O 4 2 2	0	0
3	F	1	Total C O 4 2 2	0	0
3	F	1	Total C O 4 2 2	0	0
3	F	1	Total C O 4 2 2	0	0
3	F	1	Total C O 4 2 2	0	0

- Molecule 4 is ETHANOL (three-letter code: EOH) (formula: C<sub>2</sub>H<sub>6</sub>O).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 3 2 1	0	0
4	A	1	Total C O 3 2 1	0	0
4	B	1	Total C O 3 2 1	0	0

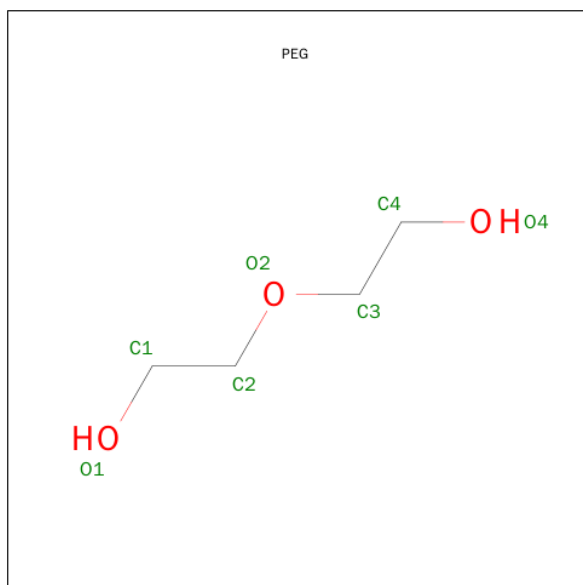
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			3	2	1		
4	D	1	Total	C	O	0	0
			3	2	1		
4	F	1	Total	C	O	0	0
			3	2	1		

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



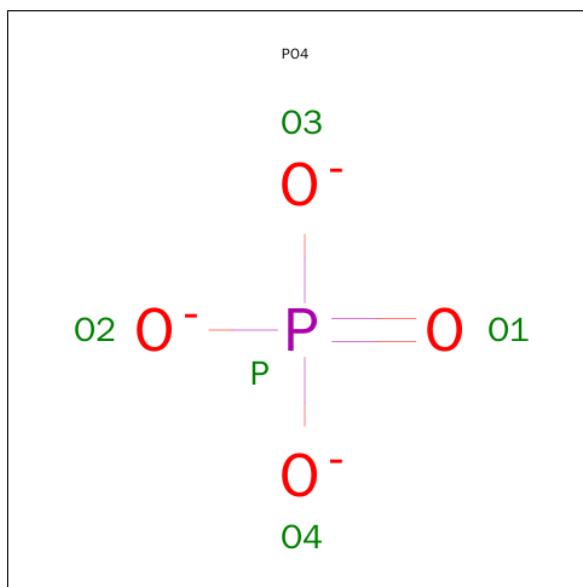
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	A	1	Total	C	O	0	0
			7	4	3		
5	B	1	Total	C	O	0	0
			7	4	3		

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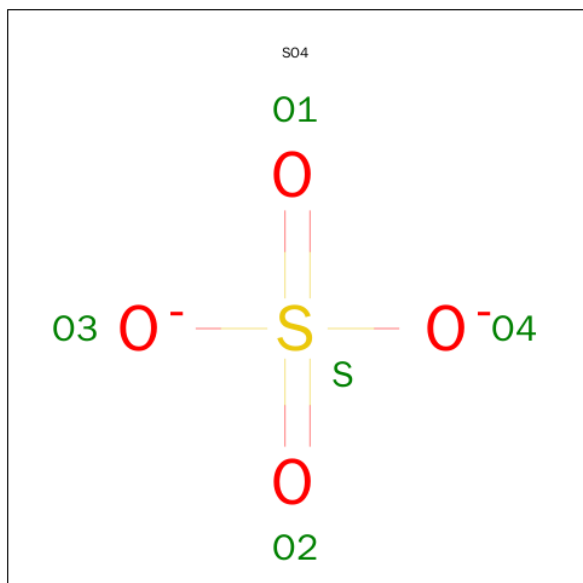
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			7	4	3		
5	B	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	C	1	Total	C	O	0	0
			7	4	3		
5	D	1	Total	C	O	0	0
			7	4	3		
5	D	1	Total	C	O	0	0
			7	4	3		
5	E	1	Total	C	O	0	0
			7	4	3		
5	E	1	Total	C	O	0	0
			6	4	2		
5	E	1	Total	C	O	0	0
			7	4	3		
5	F	1	Total	C	O	0	0
			7	4	3		
5	F	1	Total	C	O	0	0
			7	4	3		
5	F	1	Total	C	O	0	0
			7	4	3		
5	F	1	Total	C	O	0	0
			7	4	3		
5	F	1	Total	C	O	0	0
			7	4	3		
5	F	1	Total	C	O	0	0
			7	4	3		

- Molecule 6 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	O	P	0	0
			5	4	1		
6	B	1	Total	O	P	0	0
			5	4	1		
6	C	1	Total	O	P	0	0
			5	4	1		
6	F	1	Total	O	P	0	0
			5	4	1		

- Molecule 7 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	1	Total O S 5 4 1	0	0
7	B	1	Total O S 5 4 1	0	0
7	C	1	Total O S 5 4 1	0	0
7	D	1	Total O S 5 4 1	0	0
7	E	1	Total O S 5 4 1	0	0
7	E	1	Total O S 5 4 1	0	0
7	F	1	Total O S 5 4 1	0	0

- Molecule 8 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	C	1	Total K 1 1	0	0

- Molecule 9 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	C	1	Total Cl 1 1	0	0
9	F	1	Total Cl 1 1	0	0

- Molecule 10 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	196	Total O 196 196	0	0
10	B	165	Total O 165 165	0	0
10	C	233	Total O 233 233	0	0
10	D	202	Total O 202 202	0	0
10	E	206	Total O 206 206	0	0

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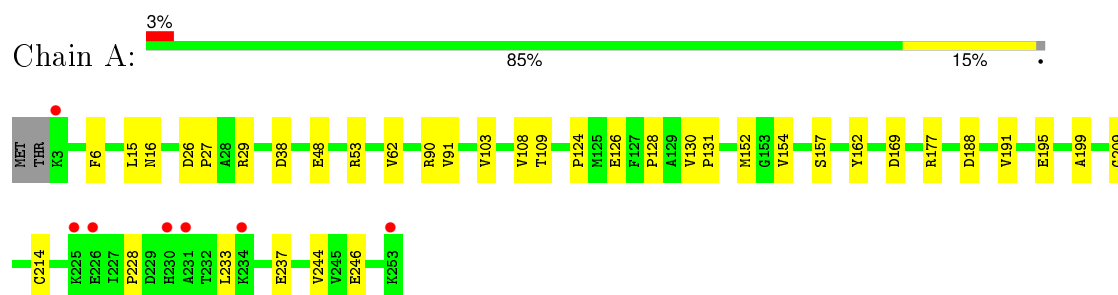
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	F	228	Total 228	O 228	0	0

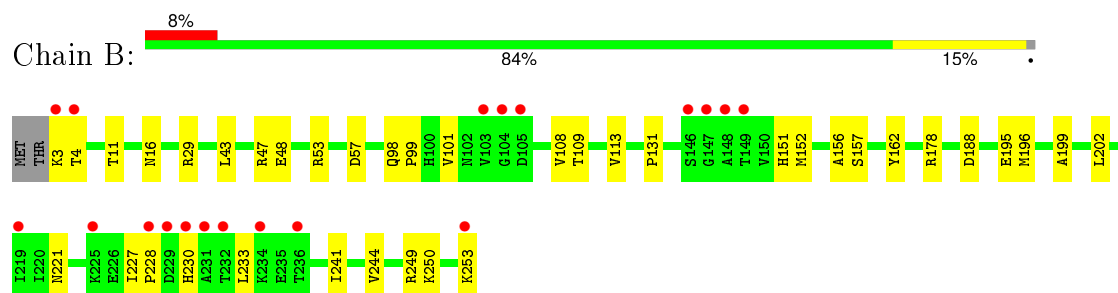
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

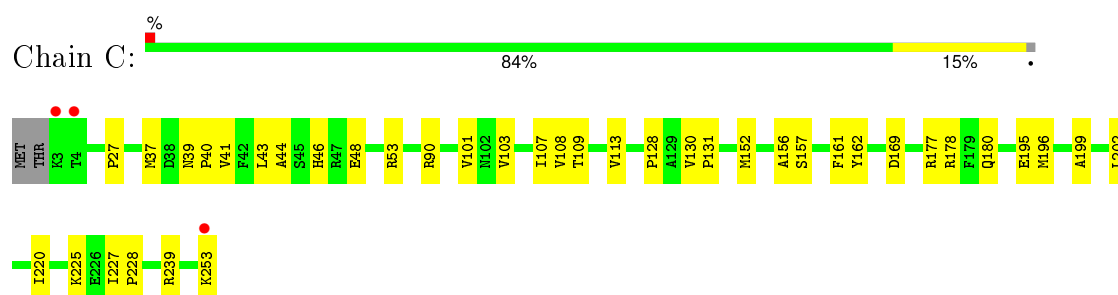
#### • Molecule 1: Uridine phosphorylase



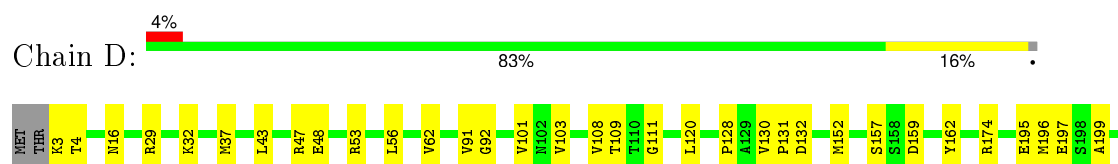
#### • Molecule 1: Uridine phosphorylase

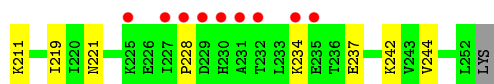


#### • Molecule 1: Uridine phosphorylase

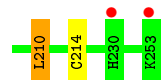
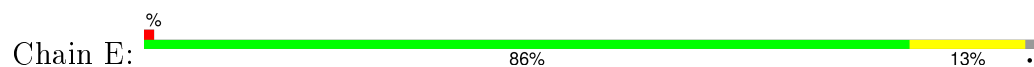


#### • Molecule 1: Uridine phosphorylase

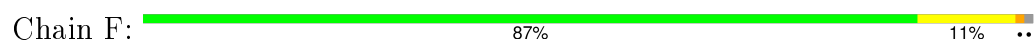




- Molecule 1: Uridine phosphorylase



- Molecule 1: Uridine phosphorylase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	63.69Å 71.08Å 87.94Å 69.62° 72.56° 85.74°	Depositor
Resolution (Å)	26.27 – 1.92 29.36 – 1.92	Depositor EDS
% Data completeness (in resolution range)	98.2 (26.27-1.92) 87.4 (29.36-1.92)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.04	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.80 (at 1.92Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.3_928)	Depositor
R, $R_{free}$	0.177 , 0.217 0.178 , 0.216	Depositor DCC
$R_{free}$ test set	5130 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	10.7	Xtriage
Anisotropy	0.184	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.38 , 41.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 102746 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	13160	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	13.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.43% 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, 0.375 respectively for untwinned datasets, and 0.333, 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, NA, K, EOH, EDO, SO4, PEG, 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	0.24	0/1992	0.44	0/2701
1	B	0.23	0/1960	0.45	0/2655
1	C	0.24	0/1970	0.46	0/2671
1	D	0.24	0/1942	0.44	0/2633
1	E	0.24	0/1961	0.45	0/2658
1	F	0.25	0/1945	0.47	1/2638 (0.0%)
All	All	0.24	0/11770	0.45	1/15956 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	229	ASP	CB-CG-OD2	5.16	122.94	118.30

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	1934	0	1970	25	0
1	B	1914	0	1935	24	0
1	C	1924	0	1943	28	0
1	D	1899	0	1910	27	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	1915	0	1935	22	0
1	F	1899	0	1925	24	0
2	A	1	0	0	0	0
2	E	1	0	0	0	0
3	A	64	0	96	4	0
3	B	20	0	30	1	0
3	C	24	0	36	7	0
3	D	16	0	24	4	0
3	E	20	0	30	0	0
3	F	28	0	42	7	0
4	A	6	0	12	0	0
4	B	3	0	6	0	0
4	C	3	0	6	1	0
4	D	3	0	6	0	0
4	F	3	0	6	0	0
5	A	49	0	70	2	0
5	B	21	0	30	3	0
5	C	42	0	60	5	0
5	D	14	0	20	0	0
5	E	20	0	27	0	0
5	F	49	0	70	3	0
6	B	10	0	0	1	0
6	C	5	0	0	0	0
6	F	5	0	0	0	0
7	B	10	0	0	0	0
7	C	5	0	0	1	0
7	D	5	0	0	0	0
7	E	10	0	0	1	0
7	F	5	0	0	0	0
8	C	1	0	0	0	0
9	C	1	0	0	0	0
9	F	1	0	0	0	0
10	A	196	0	0	0	0
10	B	165	0	0	0	0
10	C	233	0	0	2	0
10	D	202	0	0	0	0
10	E	206	0	0	0	0
10	F	228	0	0	2	0
All	All	13160	0	12189	139	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 6.

All (139) 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:D:92:GLY:HA2	3:D:304:EDO:H12	1.69	0.75
1:F:196:MET:HG3	3:F:304:EDO:H12	1.69	0.75
1:F:188:ASP:HA	5:F:318:PEG:H42	1.70	0.74
1:C:227:ILE:HG12	3:C:310:EDO:H22	1.70	0.74
1:F:230:HIS:HB2	3:F:307:EDO:H21	1.68	0.73
1:B:250:LYS:HA	1:B:253:LYS:HD3	1.69	0.73
1:A:126[A]:GLU:OE2	1:F:178[A]:ARG:NH2	2.25	0.69
1:F:178[A]:ARG:NH1	10:F:525:HOH:O	2.21	0.68
1:C:177[A]:ARG:NH2	1:E:177:ARG:O	2.28	0.68
1:E:128:PRO:HB2	1:E:130[B]:VAL:HG13	1.75	0.67
1:C:196:MET:HG3	3:C:307:EDO:H11	1.76	0.66
1:A:177:ARG:O	1:E:177:ARG:NH2	2.28	0.66
1:F:165:GLN:HE22	3:F:304:EDO:H21	1.62	0.64
1:F:230:HIS:HB2	3:F:307:EDO:C2	2.27	0.64
1:C:169:ASP:HB2	3:C:310:EDO:H21	1.80	0.64
1:A:6:PHE:HA	5:A:323:PEG:H32	1.80	0.63
1:E:16:ASN:HB2	1:E:53:ARG:HD2	1.79	0.63
1:C:48:GLU:HB3	1:D:48:GLU:HB3	1.81	0.62
1:B:230:HIS:HA	1:B:233:LEU:HD12	1.81	0.62
1:F:37:MET:HG2	1:F:56:LEU:HD13	1.81	0.62
1:D:16:ASN:HB2	1:D:53:ARG:HD2	1.83	0.61
1:B:29:ARG:NH2	6:B:301:PO4:O2	2.36	0.58
1:E:48:GLU:HB3	1:F:48:GLU:HB3	1.85	0.58
1:F:185:GLU:HB2	3:F:310:EDO:H21	1.85	0.58
1:D:196:MET:HG3	3:D:305:EDO:H12	1.85	0.58
1:A:29[B]:ARG:NH1	1:A:237:GLU:OE1	2.37	0.57
1:F:230:HIS:HB2	3:F:307:EDO:C1	2.33	0.57
1:D:128:PRO:HB2	1:D:130[B]:VAL:HG13	1.85	0.57
1:A:48:GLU:HB3	1:B:48:GLU:HB3	1.88	0.56
3:A:308:EDO:H11	1:B:47:ARG:HH22	1.71	0.56
1:C:178:ARG:NH2	10:C:625:HOH:O	2.36	0.56
1:B:16:ASN:HB2	1:B:53:ARG:HD2	1.88	0.56
1:F:157:SER:HB3	1:F:199:ALA:HB2	1.88	0.55
1:A:154[A]:VAL:HG23	1:A:191:VAL:HA	1.88	0.55
1:C:195:GLU:HA	3:C:307:EDO:H22	1.89	0.54
1:A:103:VAL:HG21	1:A:228:PRO:HG3	1.90	0.54
5:C:316:PEG:H31	1:D:120:LEU:HD13	1.90	0.54
1:E:37:MET:HG2	1:E:56:LEU:HD13	1.89	0.54
1:A:16:ASN:HB2	1:A:53:ARG:HD2	1.90	0.54
1:C:157:SER:HB3	1:C:199:ALA:HB2	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:57:ASP:OD1	1:B:249:ARG:NH1	2.42	0.52
1:F:113:VAL:HB	1:F:156:ALA:HA	1.92	0.52
1:C:239:ARG:NH1	7:C:304:SO4:O2	2.42	0.52
1:F:128:PRO:HB2	1:F:130[B]:VAL:HG13	1.92	0.52
1:F:124:PRO:HB2	1:F:126:GLU:OE1	2.10	0.52
1:A:157:SER:HB3	1:A:199:ALA:HB2	1.93	0.51
5:C:316:PEG:H12	1:D:120:LEU:HD22	1.93	0.51
1:B:157:SER:HB3	1:B:199:ALA:HB2	1.92	0.51
1:D:29:ARG:HG3	3:D:304:EDO:H21	1.92	0.50
1:D:157:SER:HB3	1:D:199:ALA:HB2	1.94	0.50
1:D:130[B]:VAL:HG11	1:E:111:GLY:HA3	1.93	0.50
3:D:303:EDO:H21	1:E:206:ALA:HB1	1.94	0.50
1:C:161:PHE:HD1	3:C:307:EDO:H12	1.76	0.49
1:F:249:ARG:NH1	10:F:559:HOH:O	2.44	0.49
1:E:26:ASP:HB3	1:E:29[B]:ARG:HD2	1.93	0.49
1:A:177:ARG:HE	3:A:303:EDO:H12	1.77	0.49
1:E:90:ARG:HG2	1:E:214[B]:CYS:SG	2.53	0.49
1:C:37:MET:HA	5:C:317:PEG:H42	1.95	0.49
1:B:196:MET:HG3	3:B:306:EDO:H22	1.94	0.48
1:A:188:ASP:O	1:E:174[B]:ARG:NH2	2.46	0.48
1:D:43:LEU:HD11	1:D:53:ARG:HB2	1.94	0.48
1:D:111:GLY:HA3	1:E:130[B]:VAL:HG11	1.95	0.48
1:E:157:SER:HB3	1:E:199:ALA:HB2	1.96	0.48
1:D:29:ARG:HD2	1:D:32:LYS:HD2	1.96	0.47
1:B:43:LEU:HD11	1:B:53:ARG:HB2	1.96	0.47
5:F:314:PEG:H21	5:F:314:PEG:H41	1.71	0.47
1:D:37:MET:HG2	1:D:56:LEU:HD13	1.97	0.47
1:F:90:ARG:NE	1:F:195:GLU:OE2	2.44	0.46
1:A:124:PRO:HB2	1:A:126[B]:GLU:OE2	2.16	0.46
1:A:91:VAL:HB	1:A:244:VAL:HG21	1.97	0.46
1:E:88:PHE:HE2	1:E:210:LEU:HG	1.81	0.46
1:A:209:GLY:HA3	5:F:314:PEG:H32	1.98	0.46
1:A:128:PRO:HB2	1:A:130[A]:VAL:HG13	1.98	0.46
1:B:178:ARG:NE	5:B:313:PEG:O1	2.32	0.45
1:B:4:THR:HG22	1:B:11:THR:HG22	1.98	0.45
1:E:108:VAL:HB	1:E:152:MET:SD	2.57	0.45
1:B:3:LYS:HE2	1:B:3:LYS:HB2	1.86	0.45
1:B:151:HIS:HA	5:B:311:PEG:H22	1.98	0.45
1:F:43:LEU:HD11	1:F:53:ARG:HB2	1.98	0.45
1:B:131:PRO:HD3	1:B:202:LEU:HD13	1.98	0.45
1:D:103:VAL:HG21	1:D:228:PRO:HG3	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:188:ASP:HB3	1:D:174:ARG:HD2	1.98	0.45
1:F:230:HIS:CG	1:F:230:HIS:O	2.69	0.45
1:C:227:ILE:CG1	3:C:310:EDO:H22	2.43	0.44
1:C:40:PRO:HD2	5:C:313:PEG:H22	1.99	0.44
1:E:109:THR:O	1:E:131:PRO:HG3	2.18	0.44
1:D:109:THR:O	1:D:131:PRO:HG3	2.17	0.44
1:E:166:GLU:HG2	1:E:168:TYR:CE2	2.52	0.44
1:B:109:THR:O	1:B:131:PRO:HG3	2.18	0.44
1:B:113:VAL:HB	1:B:156:ALA:HA	2.00	0.43
1:C:108:VAL:HB	1:C:152:MET:SD	2.58	0.43
1:C:44:ALA:HB1	1:C:46:HIS:CE1	2.53	0.43
1:E:15:LEU:HG	1:E:62:VAL:HG21	2.00	0.43
1:E:26:ASP:HA	1:E:27:PRO:HD2	1.85	0.43
1:C:220:ILE:HD11	1:C:225:LYS:HG3	2.01	0.43
1:F:211:LYS:HG2	3:F:306:EDO:H22	2.00	0.43
1:F:23:ILE:HG13	1:F:90:ARG:HA	2.01	0.43
1:A:109:THR:O	1:A:131:PRO:HG3	2.19	0.43
1:D:101:VAL:O	1:D:221:ASN:ND2	2.51	0.43
1:D:130[B]:VAL:HG12	1:E:130[B]:VAL:HG12	2.00	0.43
1:A:90:ARG:HB3	1:A:214[A]:CYS:HA	2.01	0.42
1:B:178:ARG:HG2	5:B:313:PEG:H21	2.00	0.42
1:A:233:LEU:HB3	3:A:318:EDO:H21	2.01	0.42
1:D:108:VAL:HB	1:D:152:MET:SD	2.60	0.42
1:C:161:PHE:CD1	3:C:307:EDO:H12	2.54	0.42
1:A:90:ARG:HB3	1:A:214[B]:CYS:HA	2.01	0.42
1:C:101:VAL:HG11	1:C:107:ILE:HD11	2.02	0.42
1:A:26:ASP:HA	1:A:27:PRO:HD2	1.90	0.42
1:C:180:GLN:NE2	10:C:558:HOH:O	2.44	0.42
1:C:103:VAL:HG21	4:C:311:EOH:H12	2.01	0.42
1:C:113:VAL:HB	1:C:156:ALA:HA	2.01	0.42
1:A:108:VAL:HB	1:A:152:MET:SD	2.60	0.42
1:E:43:LEU:HD11	1:E:53:ARG:HB2	2.00	0.41
1:B:241:ILE:HA	1:B:244:VAL:HG12	2.02	0.41
1:D:91:VAL:HB	1:D:244:VAL:HG21	2.01	0.41
1:D:234:LYS:HE2	1:D:234:LYS:HB3	1.90	0.41
1:D:103:VAL:HG13	1:D:219:ILE:HA	2.02	0.41
1:B:101:VAL:O	1:B:221:ASN:ND2	2.52	0.41
1:C:227:ILE:HA	1:C:228:PRO:HD3	1.92	0.41
1:C:90:ARG:HH21	1:C:195:GLU:CG	2.34	0.41
1:E:78:GLU:HG2	1:F:162:TYR:CD2	2.55	0.41
1:D:195:GLU:CD	1:D:197:GLU:H	2.22	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:98:GLN:HA	1:B:99:PRO:HD3	1.89	0.41
1:A:169:ASP:N	1:A:169:ASP:OD1	2.44	0.41
1:B:108:VAL:HB	1:B:152:MET:SD	2.61	0.41
1:D:132:ASP:OD1	1:D:211:LYS:HG3	2.21	0.41
1:F:48:GLU:HG3	1:F:67:GLY:HA3	2.03	0.41
1:C:39[A]:ASN:HA	5:C:313:PEG:H32	2.04	0.41
1:B:227:ILE:HA	1:B:228:PRO:HD3	1.91	0.40
1:A:38:ASP:OD2	5:A:320:PEG:H11	2.22	0.40
1:C:27:PRO:HD2	1:D:47:ARG:HA	2.03	0.40
3:A:303:EDO:H22	7:E:303:SO4:O1	2.20	0.40
1:C:128:PRO:HB2	1:C:130[A]:VAL:HG13	2.02	0.40
1:A:15:LEU:HG	1:A:62:VAL:CG2	2.52	0.40
1:D:132:ASP:CG	1:D:211:LYS:HG3	2.42	0.40
1:C:41:VAL:HG11	1:C:53:ARG:NH2	2.37	0.40
1:C:109:THR:O	1:C:131:PRO:HG3	2.22	0.40
1:F:66:THR:HB	1:F:73:THR:HA	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	259/253 (102%)	251 (97%)	7 (3%)	1 (0%)	39	27
1	B	255/253 (101%)	249 (98%)	5 (2%)	1 (0%)	39	27
1	C	256/253 (101%)	249 (97%)	6 (2%)	1 (0%)	39	27
1	D	253/253 (100%)	249 (98%)	3 (1%)	1 (0%)	39	27
1	E	255/253 (101%)	247 (97%)	7 (3%)	1 (0%)	39	27
1	F	253/253 (100%)	250 (99%)	2 (1%)	1 (0%)	39	27
All	All	1531/1518 (101%)	1495 (98%)	30 (2%)	6 (0%)	39	27

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	162	TYR
1	F	162	TYR
1	B	162	TYR
1	C	162	TYR
1	D	162	TYR
1	E	162	TYR

### 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	211/203 (104%)	208 (99%)	3 (1%)	74	70
1	B	207/203 (102%)	206 (100%)	1 (0%)	92	92
1	C	208/203 (102%)	205 (99%)	3 (1%)	74	70
1	D	205/203 (101%)	199 (97%)	6 (3%)	50	39
1	E	207/203 (102%)	204 (99%)	3 (1%)	74	70
1	F	205/203 (101%)	201 (98%)	4 (2%)	63	56
All	All	1243/1218 (102%)	1223 (98%)	20 (2%)	74	65

All (20) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	195	GLU
1	A	246[A]	GLU
1	A	246[B]	GLU
1	B	195	GLU
1	C	43	LEU
1	C	202	LEU
1	C	253	LYS
1	D	3	LYS
1	D	4	THR
1	D	62	VAL
1	D	159	ASP

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Mol	Chain	Res	Type
1	D	237	GLU
1	D	242	LYS
1	E	176	VAL
1	E	195	GLU
1	E	210	LEU
1	F	77[A]	VAL
1	F	77[B]	VAL
1	F	178[A]	ARG
1	F	178[B]	ARG

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

Mol	Chain	Res	Type
1	B	144	GLN
1	D	144	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 93 ligands modelled in this entry, 5 are monoatomic - leaving 88 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
3	EDO	A	302	-	3,3,3	0.45	0	2,2,2	0.46	0
3	EDO	A	303	-	3,3,3	0.45	0	2,2,2	0.43	0
3	EDO	A	304	-	3,3,3	0.49	0	2,2,2	0.33	0
3	EDO	A	305	-	3,3,3	0.46	0	2,2,2	0.44	0
3	EDO	A	306	-	3,3,3	0.45	0	2,2,2	0.45	0
3	EDO	A	307	-	3,3,3	0.46	0	2,2,2	0.43	0
3	EDO	A	308	-	3,3,3	0.47	0	2,2,2	0.44	0
3	EDO	A	309	-	3,3,3	0.48	0	2,2,2	0.40	0
3	EDO	A	310	-	3,3,3	0.48	0	2,2,2	0.33	0
3	EDO	A	311	-	3,3,3	0.49	0	2,2,2	0.37	0
4	EOH	A	312	-	2,2,2	0.45	0	1,1,1	0.16	0
3	EDO	A	313	-	3,3,3	0.47	0	2,2,2	0.42	0
3	EDO	A	314	-	3,3,3	0.47	0	2,2,2	0.43	0
3	EDO	A	315	-	3,3,3	0.47	0	2,2,2	0.41	0
3	EDO	A	316	-	3,3,3	0.47	0	2,2,2	0.42	0
3	EDO	A	317	-	3,3,3	0.48	0	2,2,2	0.43	0
3	EDO	A	318	-	3,3,3	0.46	0	2,2,2	0.42	0
4	EOH	A	319	-	2,2,2	0.45	0	1,1,1	0.18	0
5	PEG	A	320	-	6,6,6	0.63	0	5,5,5	0.66	0
5	PEG	A	321	-	6,6,6	0.63	0	5,5,5	0.71	0
5	PEG	A	322	-	6,6,6	0.60	0	5,5,5	0.69	0
5	PEG	A	323	-	6,6,6	0.62	0	5,5,5	0.66	0
5	PEG	A	324	-	6,6,6	0.63	0	5,5,5	0.72	0
5	PEG	A	325	-	6,6,6	0.64	0	5,5,5	0.72	0
5	PEG	A	326	-	6,6,6	0.63	0	5,5,5	0.74	0
6	PO4	B	301	-	4,4,4	0.45	0	6,6,6	0.27	0
6	PO4	B	302	-	4,4,4	0.48	0	6,6,6	0.27	0
7	SO4	B	303	-	4,4,4	0.22	0	6,6,6	0.08	0
7	SO4	B	304	-	4,4,4	0.22	0	6,6,6	0.09	0
3	EDO	B	305	-	3,3,3	0.47	0	2,2,2	0.45	0
3	EDO	B	306	-	3,3,3	0.46	0	2,2,2	0.43	0
3	EDO	B	307	-	3,3,3	0.47	0	2,2,2	0.43	0
4	EOH	B	308	-	2,2,2	0.45	0	1,1,1	0.17	0
3	EDO	B	309	-	3,3,3	0.48	0	2,2,2	0.40	0
3	EDO	B	310	-	3,3,3	0.46	0	2,2,2	0.42	0
5	PEG	B	311	-	6,6,6	0.64	0	5,5,5	0.69	0
5	PEG	B	312	-	6,6,6	0.63	0	5,5,5	0.68	0
5	PEG	B	313	-	6,6,6	0.62	0	5,5,5	0.72	0
6	PO4	C	301	-	4,4,4	0.48	0	6,6,6	0.28	0
7	SO4	C	304	-	4,4,4	0.23	0	6,6,6	0.08	0
3	EDO	C	305	-	3,3,3	0.38	0	2,2,2	0.44	0
3	EDO	C	306	-	3,3,3	0.46	0	2,2,2	0.42	0
3	EDO	C	307	-	3,3,3	0.45	0	2,2,2	0.41	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	EDO	C	308	-	3,3,3	0.44	0	2,2,2	0.43	0
3	EDO	C	309	-	3,3,3	0.47	0	2,2,2	0.41	0
3	EDO	C	310	-	3,3,3	0.51	0	2,2,2	0.27	0
4	EOH	C	311	-	2,2,2	0.45	0	1,1,1	0.14	0
5	PEG	C	312	-	6,6,6	0.63	0	5,5,5	0.68	0
5	PEG	C	313	-	6,6,6	0.64	0	5,5,5	0.65	0
5	PEG	C	314	-	6,6,6	0.62	0	5,5,5	0.77	0
5	PEG	C	315	-	6,6,6	0.70	0	5,5,5	0.75	0
5	PEG	C	316	-	6,6,6	0.64	0	5,5,5	0.72	0
5	PEG	C	317	-	6,6,6	0.63	0	5,5,5	0.69	0
7	SO4	D	301	-	4,4,4	0.20	0	6,6,6	0.09	0
3	EDO	D	302	-	3,3,3	0.46	0	2,2,2	0.43	0
3	EDO	D	303	-	3,3,3	0.45	0	2,2,2	0.40	0
3	EDO	D	304	-	3,3,3	0.48	0	2,2,2	0.37	0
3	EDO	D	305	-	3,3,3	0.48	0	2,2,2	0.41	0
4	EOH	D	306	-	2,2,2	0.45	0	1,1,1	0.20	0
5	PEG	D	307	-	6,6,6	0.62	0	5,5,5	0.77	0
5	PEG	D	308	-	6,6,6	0.63	0	5,5,5	0.70	0
7	SO4	E	302	-	4,4,4	0.22	0	6,6,6	0.08	0
7	SO4	E	303	-	4,4,4	0.38	0	6,6,6	0.18	0
3	EDO	E	304	-	3,3,3	0.46	0	2,2,2	0.45	0
3	EDO	E	305	-	3,3,3	0.46	0	2,2,2	0.41	0
3	EDO	E	306	-	3,3,3	0.47	0	2,2,2	0.50	0
3	EDO	E	307	-	3,3,3	0.47	0	2,2,2	0.35	0
3	EDO	E	308	-	3,3,3	0.48	0	2,2,2	0.38	0
5	PEG	E	309	-	6,6,6	0.64	0	5,5,5	0.72	0
5	PEG	E	310	-	5,5,6	0.57	0	4,4,5	0.87	0
5	PEG	E	311	-	6,6,6	0.64	0	5,5,5	0.70	0
6	PO4	F	301	-	4,4,4	0.49	0	6,6,6	0.28	0
7	SO4	F	303	-	4,4,4	0.20	0	6,6,6	0.07	0
3	EDO	F	304	-	3,3,3	0.44	0	2,2,2	0.41	0
3	EDO	F	305	-	3,3,3	0.46	0	2,2,2	0.43	0
3	EDO	F	306	-	3,3,3	0.44	0	2,2,2	0.42	0
3	EDO	F	307	-	3,3,3	0.46	0	2,2,2	0.38	0
3	EDO	F	308	-	3,3,3	0.53	0	2,2,2	0.24	0
3	EDO	F	309	-	3,3,3	0.49	0	2,2,2	0.40	0
3	EDO	F	310	-	3,3,3	0.47	0	2,2,2	0.40	0
4	EOH	F	311	-	2,2,2	0.45	0	1,1,1	0.20	0
5	PEG	F	312	-	6,6,6	0.64	0	5,5,5	0.65	0
5	PEG	F	313	-	6,6,6	0.63	0	5,5,5	0.69	0
5	PEG	F	314	-	6,6,6	0.61	0	5,5,5	1.27	1 (20%)
5	PEG	F	315	-	6,6,6	0.62	0	5,5,5	0.70	0
5	PEG	F	316	-	6,6,6	0.63	0	5,5,5	0.70	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	PEG	F	317	-	6,6,6	0.64	0	5,5,5	0.70	0
5	PEG	F	318	-	6,6,6	0.57	0	5,5,5	0.81	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
3	EDO	A	302	-	-	0/1/1/1	0/0/0/0
3	EDO	A	303	-	-	0/1/1/1	0/0/0/0
3	EDO	A	304	-	-	0/1/1/1	0/0/0/0
3	EDO	A	305	-	-	0/1/1/1	0/0/0/0
3	EDO	A	306	-	-	0/1/1/1	0/0/0/0
3	EDO	A	307	-	-	0/1/1/1	0/0/0/0
3	EDO	A	308	-	-	0/1/1/1	0/0/0/0
3	EDO	A	309	-	-	0/1/1/1	0/0/0/0
3	EDO	A	310	-	-	0/1/1/1	0/0/0/0
3	EDO	A	311	-	-	0/1/1/1	0/0/0/0
4	EOH	A	312	-	-	0/0/0/0	0/0/0/0
3	EDO	A	313	-	-	0/1/1/1	0/0/0/0
3	EDO	A	314	-	-	0/1/1/1	0/0/0/0
3	EDO	A	315	-	-	0/1/1/1	0/0/0/0
3	EDO	A	316	-	-	0/1/1/1	0/0/0/0
3	EDO	A	317	-	-	0/1/1/1	0/0/0/0
3	EDO	A	318	-	-	0/1/1/1	0/0/0/0
4	EOH	A	319	-	-	0/0/0/0	0/0/0/0
5	PEG	A	320	-	-	0/4/4/4	0/0/0/0
5	PEG	A	321	-	-	0/4/4/4	0/0/0/0
5	PEG	A	322	-	-	0/4/4/4	0/0/0/0
5	PEG	A	323	-	-	0/4/4/4	0/0/0/0
5	PEG	A	324	-	-	0/4/4/4	0/0/0/0
5	PEG	A	325	-	-	0/4/4/4	0/0/0/0
5	PEG	A	326	-	-	0/4/4/4	0/0/0/0
6	PO4	B	301	-	-	0/0/0/0	0/0/0/0
6	PO4	B	302	-	-	0/0/0/0	0/0/0/0
7	SO4	B	303	-	-	0/0/0/0	0/0/0/0
7	SO4	B	304	-	-	0/0/0/0	0/0/0/0
3	EDO	B	305	-	-	0/1/1/1	0/0/0/0
3	EDO	B	306	-	-	0/1/1/1	0/0/0/0
3	EDO	B	307	-	-	0/1/1/1	0/0/0/0
4	EOH	B	308	-	-	0/0/0/0	0/0/0/0
3	EDO	B	309	-	-	0/1/1/1	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	B	310	-	-	0/1/1/1	0/0/0/0
5	PEG	B	311	-	-	0/4/4/4	0/0/0/0
5	PEG	B	312	-	-	0/4/4/4	0/0/0/0
5	PEG	B	313	-	-	0/4/4/4	0/0/0/0
6	PO4	C	301	-	-	0/0/0/0	0/0/0/0
7	SO4	C	304	-	-	0/0/0/0	0/0/0/0
3	EDO	C	305	-	-	0/1/1/1	0/0/0/0
3	EDO	C	306	-	-	0/1/1/1	0/0/0/0
3	EDO	C	307	-	-	0/1/1/1	0/0/0/0
3	EDO	C	308	-	-	0/1/1/1	0/0/0/0
3	EDO	C	309	-	-	0/1/1/1	0/0/0/0
3	EDO	C	310	-	-	0/1/1/1	0/0/0/0
4	EOH	C	311	-	-	0/0/0/0	0/0/0/0
5	PEG	C	312	-	-	0/4/4/4	0/0/0/0
5	PEG	C	313	-	-	0/4/4/4	0/0/0/0
5	PEG	C	314	-	-	0/4/4/4	0/0/0/0
5	PEG	C	315	-	-	0/4/4/4	0/0/0/0
5	PEG	C	316	-	-	0/4/4/4	0/0/0/0
5	PEG	C	317	-	-	0/4/4/4	0/0/0/0
7	SO4	D	301	-	-	0/0/0/0	0/0/0/0
3	EDO	D	302	-	-	0/1/1/1	0/0/0/0
3	EDO	D	303	-	-	0/1/1/1	0/0/0/0
3	EDO	D	304	-	-	0/1/1/1	0/0/0/0
3	EDO	D	305	-	-	0/1/1/1	0/0/0/0
4	EOH	D	306	-	-	0/0/0/0	0/0/0/0
5	PEG	D	307	-	-	0/4/4/4	0/0/0/0
5	PEG	D	308	-	-	0/4/4/4	0/0/0/0
7	SO4	E	302	-	-	0/0/0/0	0/0/0/0
7	SO4	E	303	-	-	0/0/0/0	0/0/0/0
3	EDO	E	304	-	-	0/1/1/1	0/0/0/0
3	EDO	E	305	-	-	0/1/1/1	0/0/0/0
3	EDO	E	306	-	-	0/1/1/1	0/0/0/0
3	EDO	E	307	-	-	0/1/1/1	0/0/0/0
3	EDO	E	308	-	-	0/1/1/1	0/0/0/0
5	PEG	E	309	-	-	0/4/4/4	0/0/0/0
5	PEG	E	310	-	-	0/3/3/4	0/0/0/0
5	PEG	E	311	-	-	0/4/4/4	0/0/0/0
6	PO4	F	301	-	-	0/0/0/0	0/0/0/0
7	SO4	F	303	-	-	0/0/0/0	0/0/0/0
3	EDO	F	304	-	-	0/1/1/1	0/0/0/0
3	EDO	F	305	-	-	0/1/1/1	0/0/0/0
3	EDO	F	306	-	-	0/1/1/1	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	F	307	-	-	0/1/1/1	0/0/0/0
3	EDO	F	308	-	-	0/1/1/1	0/0/0/0
3	EDO	F	309	-	-	0/1/1/1	0/0/0/0
3	EDO	F	310	-	-	0/1/1/1	0/0/0/0
4	EOH	F	311	-	-	0/0/0/0	0/0/0/0
5	PEG	F	312	-	-	0/4/4/4	0/0/0/0
5	PEG	F	313	-	-	0/4/4/4	0/0/0/0
5	PEG	F	314	-	-	0/4/4/4	0/0/0/0
5	PEG	F	315	-	-	0/4/4/4	0/0/0/0
5	PEG	F	316	-	-	0/4/4/4	0/0/0/0
5	PEG	F	317	-	-	0/4/4/4	0/0/0/0
5	PEG	F	318	-	-	0/4/4/4	0/0/0/0

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	314	PEG	C3-O2-C2	2.43	123.77	113.31

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

26 monomers are involved in 39 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	303	EDO	2	0
3	A	308	EDO	1	0
3	A	318	EDO	1	0
5	A	320	PEG	1	0
5	A	323	PEG	1	0
6	B	301	PO4	1	0
3	B	306	EDO	1	0
5	B	311	PEG	1	0
5	B	313	PEG	2	0
7	C	304	SO4	1	0
3	C	307	EDO	4	0
3	C	310	EDO	3	0
4	C	311	EOH	1	0
5	C	313	PEG	2	0
5	C	316	PEG	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	317	PEG	1	0
3	D	303	EDO	1	0
3	D	304	EDO	2	0
3	D	305	EDO	1	0
7	E	303	SO4	1	0
3	F	304	EDO	2	0
3	F	306	EDO	1	0
3	F	307	EDO	3	0
3	F	310	EDO	1	0
5	F	314	PEG	2	0
5	F	318	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 ⓘ

### 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, 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	251/253 (99%)	-0.07	7 (2%) 56 60	4, 10, 27, 56	0
1	B	251/253 (99%)	0.16	19 (7%) 17 19	4, 11, 34, 59	0
1	C	251/253 (99%)	-0.25	3 (1%) 81 83	4, 8, 20, 54	0
1	D	250/253 (98%)	-0.07	9 (3%) 46 50	4, 9, 27, 53	0
1	E	251/253 (99%)	-0.28	2 (0%) 87 89	4, 9, 22, 57	0
1	F	250/253 (98%)	-0.26	1 (0%) 93 94	4, 7, 21, 40	0
All	All	1504/1518 (99%)	-0.13	41 (2%) 58 62	4, 9, 26, 59	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	232	THR	5.6
1	E	253	LYS	5.6
1	B	147	GLY	5.4
1	B	149	THR	5.3
1	B	231	ALA	4.9
1	C	253	LYS	4.8
1	D	230	HIS	4.6
1	D	231	ALA	4.4
1	A	253	LYS	4.4
1	B	229	ASP	3.9
1	B	230	HIS	3.9
1	D	229	ASP	3.8
1	B	236	THR	3.8
1	B	148	ALA	3.7
1	B	234	LYS	3.7
1	B	104	GLY	3.6
1	A	3	LYS	3.6
1	A	231	ALA	3.5
1	D	225	LYS	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	103	VAL	3.1
1	F	230	HIS	3.1
1	A	230	HIS	2.9
1	C	3	LYS	2.9
1	B	228	PRO	2.7
1	C	4	THR	2.6
1	B	4	THR	2.6
1	B	3	LYS	2.6
1	A	234	LYS	2.6
1	A	226	GLU	2.6
1	D	232	THR	2.6
1	B	225	LYS	2.6
1	A	225	LYS	2.5
1	D	228	PRO	2.5
1	D	234	LYS	2.5
1	E	230	HIS	2.4
1	B	219	ILE	2.3
1	B	253	LYS	2.1
1	D	227	ILE	2.1
1	B	146	SER	2.1
1	B	105	ASP	2.1
1	D	235	GLU	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, 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	EDO	A	316	4/4	0.90	0.25	39.99	23,23,37,44	0
3	EDO	E	307	4/4	0.72	0.37	18.29	13,17,24,26	4
5	PEG	C	317	7/7	0.31	0.46	16.56	46,55,61,72	0
3	EDO	A	310	4/4	0.62	0.34	16.25	16,26,26,38	4
3	EDO	C	305	4/4	0.93	0.26	16.19	4,5,6,8	4
3	EDO	A	315	4/4	0.75	0.38	15.21	10,24,34,38	4
3	EDO	B	309	4/4	0.77	0.34	15.14	27,36,40,44	0
4	EOH	A	312	3/3	0.89	0.30	15.04	21,21,24,35	0
5	PEG	F	316	7/7	0.42	0.45	15.02	42,45,53,63	0
5	PEG	C	316	7/7	0.80	0.33	14.56	15,30,52,58	0
3	EDO	C	310	4/4	0.88	0.36	14.23	23,26,33,38	0
5	PEG	F	312	7/7	0.87	0.26	13.78	21,28,46,48	0
3	EDO	E	304	4/4	0.86	0.23	13.18	8,11,15,17	4
5	PEG	A	326	7/7	0.80	0.29	13.11	18,26,56,61	0
4	EOH	B	308	3/3	0.91	0.26	13.04	19,19,22,30	0
3	EDO	A	314	4/4	0.82	0.32	12.95	33,37,40,47	0
3	EDO	E	306	4/4	0.77	0.30	11.83	15,16,20,22	4
3	EDO	D	303	4/4	0.91	0.21	10.79	8,10,12,33	4
3	EDO	A	304	4/4	0.79	0.27	10.65	13,15,16,28	4
5	PEG	D	308	7/7	0.68	0.30	10.17	28,33,42,49	0
5	PEG	C	315	7/7	0.87	0.23	10.13	15,24,37,37	7
5	PEG	F	318	7/7	0.76	0.36	9.60	13,20,25,26	7
3	EDO	F	306	4/4	0.89	0.21	9.59	13,13,17,18	4
5	PEG	A	320	7/7	0.79	0.35	9.57	17,41,48,48	0
5	PEG	E	309	7/7	0.80	0.39	8.67	21,26,44,48	0
3	EDO	A	308	4/4	0.65	0.23	8.53	30,33,40,45	0
3	EDO	E	308	4/4	0.79	0.25	8.32	21,33,39,60	0
7	SO4	D	301	5/5	0.93	0.19	8.17	22,23,43,47	0
3	EDO	A	309	4/4	0.85	0.33	7.44	22,26,27,37	4
5	PEG	B	313	7/7	0.72	0.27	7.20	21,32,39,43	0
5	PEG	A	324	7/7	0.92	0.25	6.49	25,37,48,50	0
3	EDO	A	302	4/4	0.79	0.23	6.07	11,16,24,28	4
3	EDO	C	307	4/4	0.86	0.23	6.02	9,25,27,31	4
3	EDO	B	306	4/4	0.84	0.26	5.30	9,17,24,25	4
5	PEG	C	313	7/7	0.91	0.23	5.00	22,22,33,44	0
5	PEG	F	314	7/7	0.69	0.25	4.92	13,20,39,44	7
3	EDO	A	311	4/4	0.84	0.23	4.88	26,31,37,44	0
3	EDO	A	306	4/4	0.94	0.20	4.83	13,16,18,19	4
5	PEG	D	307	7/7	0.88	0.19	4.80	25,31,44,45	0
3	EDO	A	305	4/4	0.83	0.24	4.72	18,29,37,44	0
3	EDO	F	308	4/4	0.72	0.25	4.72	24,39,39,40	4
5	PEG	B	311	7/7	0.83	0.24	4.18	21,33,49,52	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	EDO	A	307	4/4	0.81	0.23	4.12	17,17,25,30	4
3	EDO	F	304	4/4	0.88	0.19	3.77	11,24,24,31	0
3	EDO	D	304	4/4	0.90	0.19	3.77	17,18,32,41	0
7	SO4	E	302	5/5	0.94	0.19	3.70	38,46,58,58	0
5	PEG	C	314	7/7	0.87	0.27	3.67	15,31,37,42	0
5	PEG	C	312	7/7	0.83	0.21	3.32	11,18,31,36	7
3	EDO	C	306	4/4	0.90	0.18	3.25	10,15,22,27	4
5	PEG	A	323	7/7	0.69	0.40	3.15	47,53,58,59	0
5	PEG	A	322	7/7	0.74	0.38	2.51	15,32,55,58	0
3	EDO	F	310	4/4	0.94	0.20	2.34	17,25,28,29	0
4	EOH	D	306	3/3	0.87	0.18	1.99	23,23,26,30	0
3	EDO	D	305	4/4	0.89	0.16	1.78	7,23,32,34	0
2	NA	E	301	1/1	1.00	0.11	1.33	3,3,3,3	0
3	EDO	A	318	4/4	0.85	0.24	0.73	34,36,38,48	0
3	EDO	A	303	4/4	0.88	0.13	0.71	20,21,24,24	0
3	EDO	F	307	4/4	0.92	0.18	0.62	21,22,26,43	0
6	PO4	B	301	5/5	0.97	0.10	-1.07	14,17,19,19	0
6	PO4	F	301	5/5	0.99	0.07	-1.36	5,5,8,8	0
6	PO4	C	301	5/5	0.99	0.08	-1.60	4,4,6,7	0
2	NA	A	301	1/1	1.00	0.07	-1.66	3,3,3,3	0
9	CL	F	302	1/1	0.98	0.07	-2.44	15,15,15,15	0
9	CL	C	303	1/1	0.99	0.05	-3.43	13,13,13,13	0
8	K	C	302	1/1	0.99	0.04	-3.69	14,14,14,14	0
4	EOH	F	311	3/3	0.90	0.42	-	34,34,36,42	0
6	PO4	B	302	5/5	0.92	0.33	-	42,43,63,68	0
7	SO4	B	304	5/5	0.90	0.29	-	41,48,77,79	0
7	SO4	E	303	5/5	0.88	0.42	-	42,44,66,85	0
3	EDO	A	317	4/4	0.82	0.30	-	32,36,41,52	0
7	SO4	B	303	5/5	0.97	0.10	-	23,25,36,40	0
4	EOH	A	319	3/3	0.89	0.24	-	26,26,36,44	0
3	EDO	A	313	4/4	0.93	0.23	-	14,19,21,23	4
3	EDO	D	302	4/4	0.90	0.16	-	26,28,35,53	0
3	EDO	E	305	4/4	0.91	0.18	-	3,9,12,38	4
3	EDO	F	305	4/4	0.85	0.19	-	2,10,25,26	0
7	SO4	C	304	5/5	0.82	0.35	-	65,69,85,88	0
3	EDO	B	310	4/4	0.64	0.30	-	42,50,51,55	0
4	EOH	C	311	3/3	0.92	0.15	-	16,16,25,36	0
7	SO4	F	303	5/5	0.94	0.21	-	20,24,32,33	0
3	EDO	C	308	4/4	0.86	0.21	-	10,10,11,16	4
5	PEG	A	325	7/7	0.73	0.31	-	33,48,64,69	0
3	EDO	B	305	4/4	0.85	0.28	-	35,36,41,43	0
5	PEG	E	311	7/7	0.83	0.52	-	17,50,70,73	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
5	PEG	F	315	7/7	0.85	0.27	-	23,40,51,58	0
5	PEG	A	321	7/7	0.77	0.47	-	34,40,65,65	0
5	PEG	F	313	7/7	0.76	0.32	-	28,53,62,63	0
3	EDO	C	309	4/4	0.73	0.19	-	33,43,44,53	0
3	EDO	B	307	4/4	0.83	0.38	-	29,33,37,37	4
5	PEG	B	312	7/7	0.82	0.41	-	18,29,51,55	0
3	EDO	F	309	4/4	0.76	0.35	-	31,33,52,52	0
5	PEG	E	310	6/7	0.85	0.17	-	15,28,34,36	0
5	PEG	F	317	7/7	0.65	0.55	-	28,39,50,67	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.