



# wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 20, 2021 – 08:41 AM JST

PDB ID : 7BXB  
Title : Crystal structure of Ca\_00311  
Authors : Fan, C.P.  
Deposited on : 2020-04-18  
Resolution : 1.72 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 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	:	2.18
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)	:	2.18

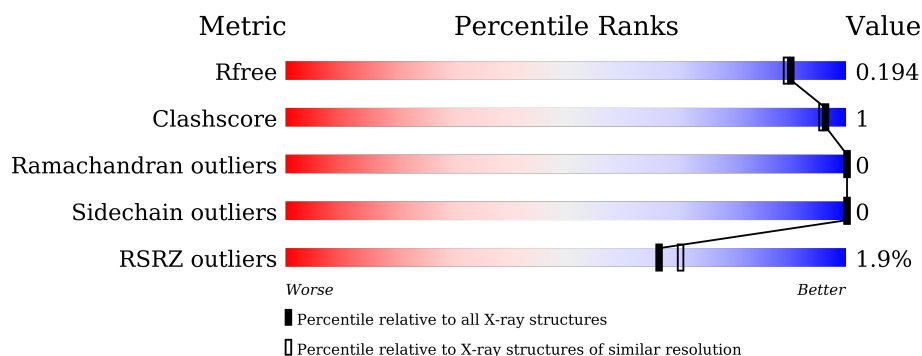
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.72 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	5722 (1.74-1.70)
Clashscore	141614	6152 (1.74-1.70)
Ramachandran outliers	138981	6051 (1.74-1.70)
Sidechain outliers	138945	6051 (1.74-1.70)
RSRZ outliers	127900	5629 (1.74-1.70)

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  $\geq 3$ , 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	220	<div> <div>%</div> <div>98%</div> <div>.</div> </div>
1	B	220	<div> <div>%</div> <div>98%</div> <div>.</div> </div>
1	C	220	<div> <div>3%</div> <div>96%</div> <div>.</div> </div>
1	D	220	<div> <div>2%</div> <div>97%</div> <div>.</div> </div>
1	E	220	<div> <div>97%</div> <div>.</div> </div>
1	F	220	<div> <div>3%</div> <div>96%</div> <div>.</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 11650 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.

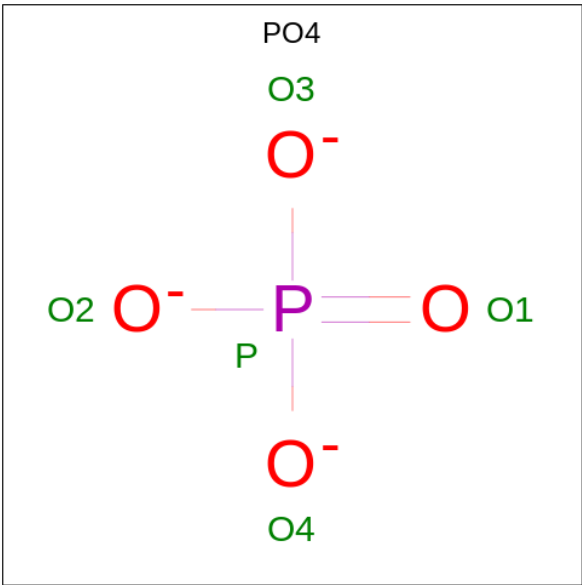
- Molecule 1 is a protein called GDSL-like Lipase/Acylhydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	220	Total	C	N	O	S	0	0	0
			1699	1066	293	323	17			
1	B	220	Total	C	N	O	S	0	0	0
			1687	1060	293	317	17			
1	C	220	Total	C	N	O	S	0	0	0
			1695	1064	293	321	17			
1	D	220	Total	C	N	O	S	0	0	0
			1686	1060	293	316	17			
1	E	220	Total	C	N	O	S	0	0	0
			1699	1066	293	323	17			
1	F	220	Total	C	N	O	S	0	0	0
			1687	1060	292	318	17			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ALA	-	expression tag	UNP A0A381K2L8
B	0	ALA	-	expression tag	UNP A0A381K2L8
C	0	ALA	-	expression tag	UNP A0A381K2L8
D	0	ALA	-	expression tag	UNP A0A381K2L8
E	0	ALA	-	expression tag	UNP A0A381K2L8
F	0	ALA	-	expression tag	UNP A0A381K2L8

- Molecule 2 is PHOSPHATE ION (three-letter code: PO4) (formula: O<sub>4</sub>P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	B	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	C	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	D	1	Total	O	P	0	0
			5	4	1		
2	E	1	Total	O	P	0	0
			5	4	1		
2	E	1	Total	O	P	0	0
			5	4	1		
2	E	1	Total	O	P	0	0
			5	4	1		
2	F	1	Total	O	P	0	0
			5	4	1		

Continued on next page...

*Continued from previous page...*

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

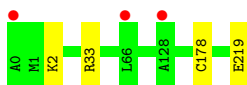
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	245	Total	O	0	0
			245	245		
3	B	242	Total	O	0	0
			242	242		
3	C	226	Total	O	0	0
			226	226		
3	D	228	Total	O	0	0
			228	228		
3	E	255	Total	O	0	0
			255	255		
3	F	226	Total	O	0	0
			226	226		

### 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.

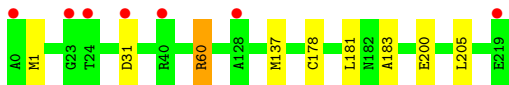
- Molecule 1: GDSL-like Lipase/Acylhydrolase



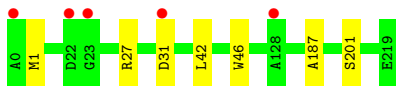
- Molecule 1: GDSL-like Lipase/Acylhydrolase



- Molecule 1: GDSL-like Lipase/Acylhydrolase



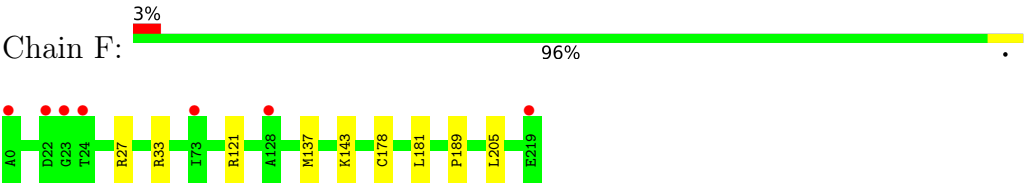
- Molecule 1: GDSL-like Lipase/Acylhydrolase



- Molecule 1: GDSL-like Lipase/Acylhydrolase



- Molecule 1: GDSL-like Lipase/Acylhydrolase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	112.93Å 112.93Å 305.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.57 – 1.72 48.57 – 1.71	Depositor EDS
% Data completeness (in resolution range)	99.8 (48.57-1.72) 99.8 (48.57-1.71)	Depositor EDS
$R_{merge}$	0.14	Depositor
$R_{sym}$	0.14	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.46 (at 1.72Å)	Xtriage
Refinement program	PHENIX 1.15.2_3472	Depositor
R, $R_{free}$	0.161 , 0.194 0.160 , 0.194	Depositor DCC
$R_{free}$ test set	1999 reflections (0.95%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	19.2	Xtriage
Anisotropy	0.021	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 44.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	11650	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.25% 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: 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	0.71	1/1738 (0.1%)	0.77	1/2357 (0.0%)
1	B	0.71	1/1726 (0.1%)	0.80	5/2342 (0.2%)
1	C	0.66	1/1734 (0.1%)	0.80	3/2352 (0.1%)
1	D	0.61	0/1725	0.79	3/2342 (0.1%)
1	E	0.70	1/1738 (0.1%)	0.81	4/2357 (0.2%)
1	F	0.76	1/1726 (0.1%)	0.79	4/2342 (0.2%)
All	All	0.69	5/10387 (0.0%)	0.79	20/14092 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	178	CYS	CB-SG	-15.95	1.55	1.82
1	A	178	CYS	CB-SG	-11.76	1.62	1.82
1	E	178	CYS	CB-SG	-7.04	1.70	1.82
1	B	178	CYS	CB-SG	-5.88	1.72	1.81
1	C	178	CYS	CB-SG	-5.35	1.73	1.81

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	1	MET	CG-SD-CE	-8.80	86.12	100.20
1	D	1	MET	CG-SD-CE	-8.13	87.19	100.20
1	F	33	ARG	NE-CZ-NH2	-7.51	116.54	120.30
1	F	27	ARG	NE-CZ-NH1	7.30	123.95	120.30
1	F	27	ARG	NE-CZ-NH2	-7.27	116.67	120.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1699	0	1624	1	0
1	B	1687	0	1612	0	0
1	C	1695	0	1620	7	0
1	D	1686	0	1612	2	0
1	E	1699	0	1624	3	0
1	F	1687	0	1610	6	0
2	A	10	0	0	0	0
2	B	15	0	0	0	0
2	C	10	0	0	0	0
2	D	15	0	0	0	0
2	E	15	0	0	0	0
2	F	10	0	0	0	0
3	A	245	0	0	0	1
3	B	242	0	0	0	1
3	C	226	0	0	1	1
3	D	228	0	0	0	1
3	E	255	0	0	2	1
3	F	226	0	0	0	1
All	All	11650	0	9702	19	3

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.

The worst 5 of 19 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:E:137:MET:HE1	1:E:183:ALA:HB2	1.59	0.85
1:E:40:ARG:NH1	3:E:402:HOH:O	2.05	0.82
1:C:137:MET:HE2	1:C:183:ALA:HB2	1.63	0.80
1:E:60:ARG:NH1	3:E:401:HOH:O	1.92	0.64
1:F:137:MET:HE1	1:F:205:LEU:HD11	1.84	0.59

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:E:577:HOH:O	3:F:424:HOH:O[6_444]	2.04	0.16
3:A:402:HOH:O	3:C:565:HOH:O[3_455]	2.08	0.12
3:B:403:HOH:O	3:D:514:HOH:O[6_454]	2.11	0.09

## 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	218/220 (99%)	209 (96%)	9 (4%)	0	100	100
1	B	218/220 (99%)	210 (96%)	8 (4%)	0	100	100
1	C	218/220 (99%)	210 (96%)	8 (4%)	0	100	100
1	D	218/220 (99%)	209 (96%)	9 (4%)	0	100	100
1	E	218/220 (99%)	208 (95%)	10 (5%)	0	100	100
1	F	218/220 (99%)	210 (96%)	8 (4%)	0	100	100
All	All	1308/1320 (99%)	1256 (96%)	52 (4%)	0	100	100

There are no Ramachandran outliers to report.

### 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	175/176 (99%)	175 (100%)	0	100	100
1	B	172/176 (98%)	172 (100%)	0	100	100
1	C	174/176 (99%)	174 (100%)	0	100	100

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	172/176 (98%)	172 (100%)	0	100	100
1	E	175/176 (99%)	175 (100%)	0	100	100
1	F	172/176 (98%)	172 (100%)	0	100	100
All	All	1040/1056 (98%)	1040 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	175	GLN
1	C	157	HIS
1	F	103	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry ⓘ

15 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
2	PO4	E	302	-	4,4,4	1.57	1 (25%)	6,6,6	0.99	0
2	PO4	E	303	-	4,4,4	0.77	0	6,6,6	0.46	0
2	PO4	F	302	-	4,4,4	1.52	1 (25%)	6,6,6	1.20	0
2	PO4	A	302	-	4,4,4	1.21	1 (25%)	6,6,6	1.16	1 (16%)
2	PO4	B	303	-	4,4,4	0.84	0	6,6,6	0.68	0
2	PO4	F	301	-	4,4,4	1.54	0	6,6,6	1.22	0
2	PO4	B	302	-	4,4,4	1.35	0	6,6,6	1.48	1 (16%)
2	PO4	A	301	-	4,4,4	0.77	0	6,6,6	0.87	0
2	PO4	C	302	-	4,4,4	1.11	0	6,6,6	0.80	0
2	PO4	D	302	-	4,4,4	1.02	0	6,6,6	1.17	1 (16%)
2	PO4	E	301	-	4,4,4	0.99	0	6,6,6	1.14	0
2	PO4	D	303	-	4,4,4	0.90	0	6,6,6	0.44	0
2	PO4	D	301	-	4,4,4	1.02	0	6,6,6	1.33	0
2	PO4	C	301	-	4,4,4	1.15	0	6,6,6	1.08	0
2	PO4	B	301	-	4,4,4	0.78	0	6,6,6	0.82	0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	302	PO4	P-O2	-2.64	1.46	1.54
2	F	302	PO4	P-O2	-2.52	1.47	1.54
2	A	302	PO4	P-O3	-2.24	1.47	1.54

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	302	PO4	O2-P-O1	-2.49	101.77	110.89
2	A	302	PO4	O4-P-O3	2.47	115.91	107.97
2	D	302	PO4	O4-P-O2	-2.12	101.15	107.97

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues ⓘ

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	220/220 (100%)	-0.06	3 (1%) 75 79	13, 19, 38, 51	0
1	B	220/220 (100%)	-0.14	3 (1%) 75 79	13, 19, 38, 48	0
1	C	220/220 (100%)	0.14	7 (3%) 47 52	13, 20, 40, 64	0
1	D	220/220 (100%)	-0.00	5 (2%) 60 65	14, 20, 41, 64	0
1	E	220/220 (100%)	-0.15	0 100 100	12, 18, 36, 48	0
1	F	220/220 (100%)	0.02	7 (3%) 47 52	13, 20, 38, 55	0
All	All	1320/1320 (100%)	-0.03	25 (1%) 66 70	12, 19, 38, 64	0

The worst 5 of 25 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	23	GLY	5.9
1	C	40	ARG	4.4
1	D	0	ALA	4.2
1	C	128	ALA	3.6
1	F	0	ALA	3.5

### 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
2	PO4	B	303	5/5	0.61	0.25	79,83,85,86	0
2	PO4	E	303	5/5	0.75	0.24	75,78,82,83	0
2	PO4	D	303	5/5	0.82	0.18	63,65,73,79	0
2	PO4	B	302	5/5	0.98	0.09	28,28,35,36	0
2	PO4	A	301	5/5	0.98	0.07	25,27,32,33	0
2	PO4	C	301	5/5	0.98	0.06	17,19,22,23	0
2	PO4	C	302	5/5	0.98	0.07	22,25,31,34	0
2	PO4	D	302	5/5	0.98	0.08	24,29,31,33	0
2	PO4	A	302	5/5	0.98	0.06	15,17,19,21	0
2	PO4	E	301	5/5	0.98	0.07	13,17,19,21	0
2	PO4	E	302	5/5	0.98	0.08	21,23,31,33	0
2	PO4	B	301	5/5	0.98	0.07	16,19,21,21	0
2	PO4	F	302	5/5	0.98	0.08	27,32,38,44	0
2	PO4	F	301	5/5	0.99	0.05	15,17,20,24	0
2	PO4	D	301	5/5	0.99	0.05	16,18,20,22	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.