



# Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 10:21 pm BST

PDB ID : 5HKE  
Title : bile salt hydrolase from *Lactobacillus salivarius*  
Authors : Hu, X.-J.  
Deposited on : 2016-01-14  
Resolution : 1.90 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 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 : 2.11  
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) : 2.11

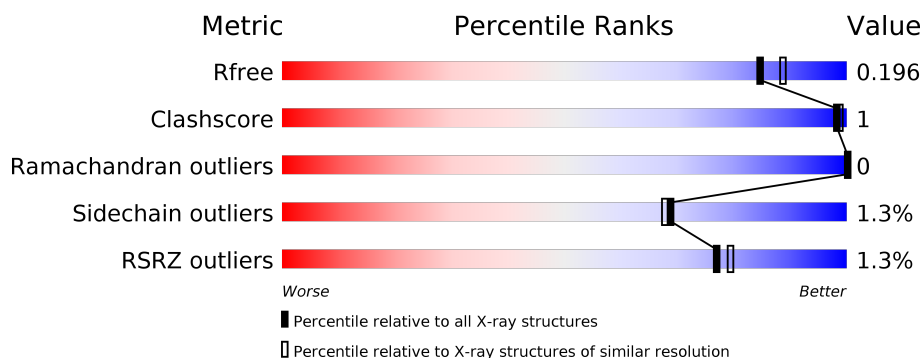
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 1.90 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	6207 (1.90-1.90)
Clashscore	141614	6847 (1.90-1.90)
Ramachandran outliers	138981	6760 (1.90-1.90)
Sidechain outliers	138945	6760 (1.90-1.90)
RSRZ outliers	127900	6082 (1.90-1.90)

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 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	333	<div> <div>2%</div> <div> <div></div> <div>90%</div> <div>5%</div> <div>5%</div> </div> </div>
1	B	333	<div> <div>%</div> <div> <div></div> <div>89%</div> <div>5%</div> <div>5%</div> </div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5552 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 Bile salt hydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	317	Total	C	N	O	S	0	3	0
			2557	1628	419	504	6			
1	B	317	Total	C	N	O	S	0	5	0
			2575	1640	421	508	6			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	325	LEU	-	expression tag	UNP J7H3P9
A	326	GLU	-	expression tag	UNP J7H3P9
A	327	ARG	-	expression tag	UNP J7H3P9
A	328	HIS	-	expression tag	UNP J7H3P9
A	329	HIS	-	expression tag	UNP J7H3P9
A	330	HIS	-	expression tag	UNP J7H3P9
A	331	HIS	-	expression tag	UNP J7H3P9
A	332	HIS	-	expression tag	UNP J7H3P9
A	333	HIS	-	expression tag	UNP J7H3P9
B	325	LEU	-	expression tag	UNP J7H3P9
B	326	GLU	-	expression tag	UNP J7H3P9
B	327	ARG	-	expression tag	UNP J7H3P9
B	328	HIS	-	expression tag	UNP J7H3P9
B	329	HIS	-	expression tag	UNP J7H3P9
B	330	HIS	-	expression tag	UNP J7H3P9
B	331	HIS	-	expression tag	UNP J7H3P9
B	332	HIS	-	expression tag	UNP J7H3P9
B	333	HIS	-	expression tag	UNP J7H3P9

- 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		

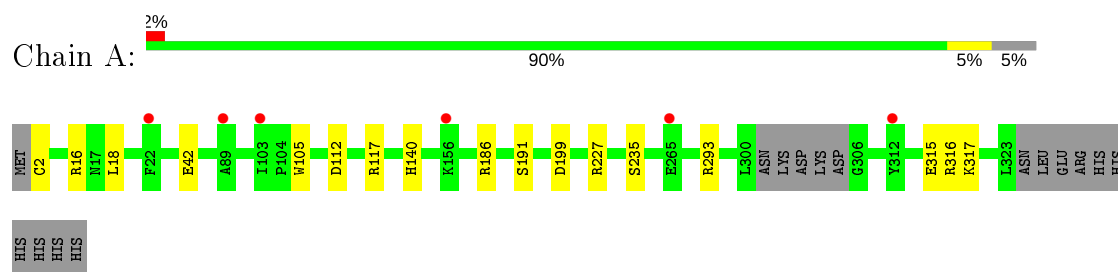
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	195	Total	O	0	0
			195	195		
3	B	205	Total	O	0	0
			205	205		

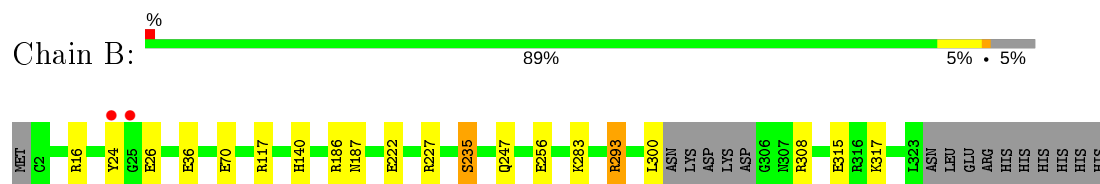
### 3 Residue-property plots [i](#)

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



- Molecule 1: Bile salt hydrolase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.79Å 87.36Å 86.77Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.50 – 1.90 27.73 – 1.90	Depositor EDS
% Data completeness (in resolution range)	99.2 (45.50-1.90) 99.2 (27.73-1.90)	Depositor EDS
$R_{merge}$	0.05	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	4.08 (at 1.89Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, $R_{free}$	0.152 , 0.185 0.165 , 0.196	Depositor DCC
$R_{free}$ test set	2619 reflections (4.79%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	18.5	Xtriage
Anisotropy	0.017	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 45.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.009 for k,h,-l 0.006 for -l,-k,-h 0.006 for -h,l,k 0.000 for l,h,k 0.000 for k,l,h	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	5552	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.98% 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, OCS

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	1.05	6/2602 (0.2%)	0.95	7/3530 (0.2%)
1	B	1.02	4/2621 (0.2%)	0.97	8/3556 (0.2%)
All	All	1.04	10/5223 (0.2%)	0.96	15/7086 (0.2%)

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	222	GLU	CD-OE1	-7.15	1.17	1.25
1	B	235	SER	CB-OG	-6.56	1.33	1.42
1	B	315	GLU	C-O	6.51	1.35	1.23
1	A	191	SER	CB-OG	-6.18	1.34	1.42
1	B	36	GLU	CD-OE2	-5.87	1.19	1.25
1	A	315	GLU	C-O	5.79	1.34	1.23
1	A	235	SER	CB-OG	-5.47	1.35	1.42
1	A	42	GLU	CD-OE1	5.43	1.31	1.25
1	A	105	TRP	CE3-CZ3	5.24	1.47	1.38
1	A	199	ASP	CB-CG	-5.12	1.41	1.51

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	293	ARG	NE-CZ-NH2	-7.98	116.31	120.30
1	B	308	ARG	NE-CZ-NH2	7.67	124.13	120.30
1	B	186	ARG	NE-CZ-NH1	7.41	124.01	120.30
1	A	227	ARG	NE-CZ-NH2	7.04	123.82	120.30
1	B	117	ARG	NE-CZ-NH2	-6.78	116.91	120.30
1	B	227	ARG	NE-CZ-NH2	6.36	123.48	120.30
1	B	256	GLU	OE1-CD-OE2	5.85	130.32	123.30
1	B	293	ARG	NE-CZ-NH2	-5.78	117.41	120.30
1	A	112	ASP	CB-CG-OD1	5.72	123.45	118.30

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	199	ASP	CB-CG-OD2	-5.63	113.23	118.30
1	A	117	ARG	NE-CZ-NH1	5.40	123.00	120.30
1	B	300	LEU	CA-C-O	-5.17	109.25	120.10
1	B	117	ARG	NE-CZ-NH1	5.10	122.85	120.30
1	A	316	ARG	NE-CZ-NH1	5.08	122.84	120.30
1	A	186	ARG	NE-CZ-NH1	5.04	122.82	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	2557	0	2479	1	0
1	B	2575	0	2490	5	0
2	A	10	0	0	0	0
2	B	10	0	0	0	0
3	A	195	0	0	0	0
3	B	205	0	0	2	1
All	All	5552	0	4969	6	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

All (6) 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:B:187[B]:ASN:ND2	3:B:501:HOH:O	2.09	0.78
1:B:235:SER:HB2	1:B:247:GLN:HE21	1.56	0.71
1:B:26:GLU:OE1	3:B:502:HOH:O	2.18	0.56
1:B:24[B]:TYR:CD1	1:B:24[B]:TYR:N	2.77	0.52
1:B:70:GLU:O	1:B:283:LYS:HE3	2.09	0.51
1:A:2:OCS:OD3	1:A:18:LEU:HD12	2.20	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the sym-



metry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:692:HOH:O	3:B:692:HOH:O[2_775]	2.03	0.17

## 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	316/333 (95%)	310 (98%)	6 (2%)	0	100	100
1	B	318/333 (96%)	312 (98%)	6 (2%)	0	100	100
All	All	634/666 (95%)	622 (98%)	12 (2%)	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	282/295 (96%)	279 (99%)	3 (1%)	73	73
1	B	284/295 (96%)	280 (99%)	4 (1%)	67	65
All	All	566/590 (96%)	559 (99%)	7 (1%)	69	70

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	16	ARG

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	A	140	HIS
1	A	317	LYS
1	B	16	ARG
1	B	140	HIS
1	B	293	ARG
1	B	317	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	247	GLN

### 5.3.3 RNA ⓘ

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	$\# Z  > 2$
1	OCS	A	2	1	7,8,9	2.70	2 (28%)	6,11,13	1.72	2 (33%)
1	OCS	B	2	1	7,8,9	3.07	3 (42%)	6,11,13	7.41	4 (66%)

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
1	OCS	A	2	1	-	0/4/7/9	-

*Continued on next page...*

*Continued from previous page...*

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	OCS	B	2	1	-	0/4/7/9	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	2	OCS	OD1-SG	6.88	1.65	1.45
1	A	2	OCS	OD1-SG	6.49	1.64	1.45
1	B	2	OCS	OD2-SG	-2.89	1.37	1.47
1	B	2	OCS	CB-CA	2.50	1.56	1.53
1	A	2	OCS	O-C	2.22	1.28	1.19

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	2	OCS	OD3-SG-CB	-14.32	89.92	106.94
1	B	2	OCS	OD2-SG-OD3	7.86	130.49	111.27
1	B	2	OCS	OD1-SG-CB	6.67	114.87	106.94
1	B	2	OCS	OD3-SG-OD1	-4.10	99.76	113.95
1	A	2	OCS	OD2-SG-CB	3.32	111.03	105.74
1	A	2	OCS	OD3-SG-OD1	-2.24	106.18	113.95

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	2	OCS	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

4 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	A	401	-	4,4,4	1.46	1 (25%)	6,6,6	0.66	0
2	PO4	B	401	-	4,4,4	1.01	0	6,6,6	1.09	0
2	PO4	A	402	-	4,4,4	1.18	1 (25%)	6,6,6	1.01	0
2	PO4	B	402	-	4,4,4	1.22	0	6,6,6	1.18	0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	PO4	P-O1	2.77	1.57	1.50
2	A	402	PO4	P-O1	2.08	1.55	1.50

There are no bond angle outliers.

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 [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	316/333 (94%)	-0.10	6 (1%) 66 69	12, 17, 33, 52	0
1	B	316/333 (94%)	-0.14	2 (0%) 89 90	12, 17, 32, 46	0
All	All	632/666 (94%)	-0.12	8 (1%) 77 79	12, 17, 33, 52	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	24[A]	TYR	6.5
1	A	265	GLU	3.6
1	A	22	PHE	2.6
1	A	156	LYS	2.5
1	B	25	GLY	2.4
1	A	103	ILE	2.3
1	A	89	ALA	2.2
1	A	312[A]	TYR	2.0

### 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, 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
1	OCS	A	2	9/10	0.95	0.12	14,17,30,48	0
1	OCS	B	2	9/10	0.95	0.12	14,19,34,45	0

### 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. 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( $\text{\AA}^2$ )	Q<0.9
2	PO4	B	402	5/5	0.86	0.34	46,48,51,61	0
2	PO4	A	402	5/5	0.86	0.33	46,48,51,52	0
2	PO4	B	401	5/5	0.95	0.23	33,34,39,42	0
2	PO4	A	401	5/5	0.98	0.28	27,28,34,34	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.