

Full wwPDB X-ray Structure Validation Report (i)

May 16, 2020 – 07:51 am BST

PDB ID 3KK4

> Title uncharacterized protein BP1543 from Bordetella pertussis Tohama I

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tural Genomics (MCSG)

Deposited on 2009-11-04

1.95 Å(reported) Resolution

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org A user guide is available at

https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity 4.02b-467

> 1.8.5 (274361), CSD as541be (2020) Mogul

Xtriage (Phenix) 1.13 EDS 2.11

Percentile statistics 20191225.v01 (using entries in the PDB archive December 25th 2019)

> Refmac 5.8.0158

7.0.044 (Gargrove) CCP4 Engh & Huber (2001)

Ideal geometry (proteins) Ideal geometry (DNA, RNA) Parkinson et al. (1996)

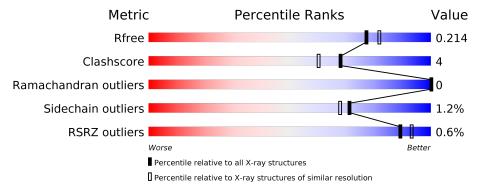
Validation Pipeline (wwPDB-VP) 2.11

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\AA)}) \end{array}$
R_{free}	130704	2580 (1.96-1.96)
Clashscore	141614	2705 (1.96-1.96)
Ramachandran outliers	138981	2678 (1.96-1.96)
Sidechain outliers	138945	2678 (1.96-1.96)
RSRZ outliers	127900	2539 (1.96-1.96)

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 >=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 <=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	125	92%	7% •
1	В	125	95%	
1	С	125	92%	8%
1	D	125	94%	6%

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 crite-



ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	GOL	С	201	_	-	X	-



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4590 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 uncharacterized protein BP1543.

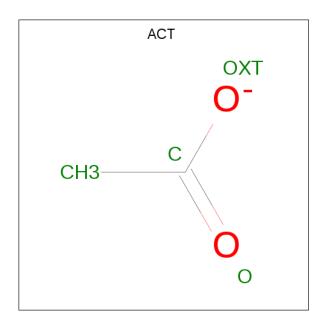
Mol	Chain	Residues		Atoms				ZeroOcc	AltConf	Trace	
1	Λ	125	Total	С	N	О	S	Se	0	5	0
1	A	120	1046	650	197	193	4	2	0	5	0
1	В	125	Total	С	N	О	S	Se	0	3	0
1	Б	120	1027	640	190	191	4	2	0	, J	0
1	С	125	Total	С	N	О	S	Se	0	5	0
1		120	1043	650	194	193	4	2	0	5	0
1	D	125	Total	С	N	О	S	Se	0	3	0
1	ש	120	1024	638	189	191	4	2	U	ა	U

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	_	expression tag	UNP Q7VY20
A	-1	ASN	-	expression tag	UNP Q7VY20
A	0	ALA	_	expression tag	UNP Q7VY20
В	-2	SER	_	expression tag	UNP Q7VY20
В	-1	ASN	_	expression tag	UNP Q7VY20
В	0	ALA	_	expression tag	UNP Q7VY20
С	-2	SER	_	expression tag	UNP Q7VY20
С	-1	ASN	_	expression tag	UNP Q7VY20
С	0	ALA	_	expression tag	UNP Q7VY20
D	-2	SER	-	expression tag	UNP Q7VY20
D	-1	ASN	-	expression tag	UNP Q7VY20
D	0	ALA	_	expression tag	UNP Q7VY20

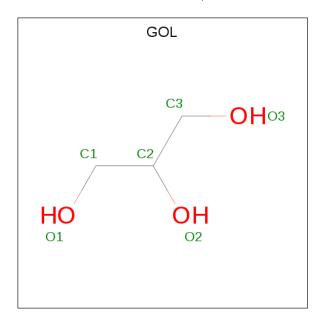
• Molecule 2 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).





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

 \bullet Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $\mathrm{C_3H_8O_3}).$



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	С	1	Total C O 6 3 3	0	0

• Molecule 4 is water.



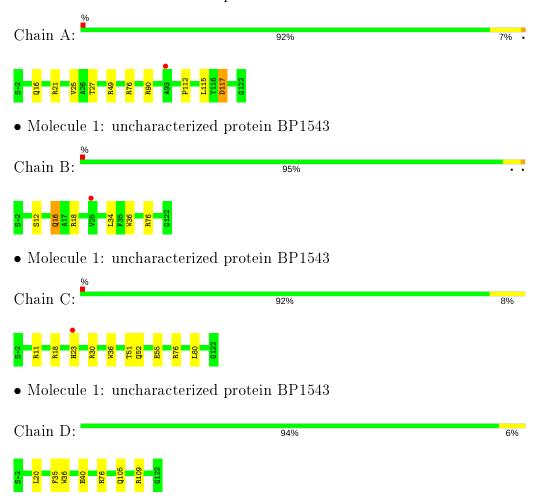
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	97	Total O 97 97	0	0
4	В	113	Total O 113 113	0	0
4	С	116	Total O 116 116	0	0
4	D	114	Total O 114 114	0	0



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 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: uncharacterized protein BP1543





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	48.21Å 72.46Å 61.74Å	Domositon
a, b, c, α , β , γ	90.00° 112.05° 90.00°	Depositor
Resolution (Å)	50.00 - 1.95	Depositor
Resolution (A)	30.15 - 1.95	EDS
% Data completeness	99.6 (50.00-1.95)	Depositor
(in resolution range)	99.6 (30.15-1.95)	EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	12.44 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
D D	0.145 , 0.199	Depositor
R, R_{free}	0.168 , 0.214	DCC
R_{free} test set	1457 reflections $(5.07%)$	wwPDB-VP
Wilson B-factor (Å ²)	17.3	Xtriage
Anisotropy	0.447	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.36 , 35.8	EDS
L-test for twinning ²	$< L >=0.50, < L^2>=0.33$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4590	wwPDB-VP
Average B, all atoms (Å ²)	10.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The analyses of the Patterson function reveals a significant off-origin peak that is 63.23 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 9.9869e-06. The detected translational NCS is most likely also responsible for the elevated intensity ratio.

²Theoretical values of <|L|>, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

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: GOL, CME, ACT

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		
IVIOI	Chain	$\mid \text{RMSZ} \mid \# Z > 5$		RMSZ	# Z > 5	
1	A	0.56	0/1048	0.64	0/1411	
1	В	0.57	0/1029	0.64	0/1386	
1	С	0.58	0/1045	0.65	0/1407	
1	D	0.57	0/1026	0.62	0/1382	
All	All	0.57	0/4148	0.64	0/5586	

There are no bond length outliers.

There are no bond angle outliers.

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	$\mathbf{H}(\mathbf{model})$	$\mathbf{H}(\mathbf{added})$	Clashes	Symm-Clashes
1	A	1046	0	1048	11	1
1	В	1027	0	1027	6	0
1	С	1043	0	1046	11	0
1	D	1024	0	1024	7	0
2	A	4	0	3	0	0
3	С	6	0	8	4	0
4	A	97	0	0	2	0
4	В	113	0	0	0	0
4	С	116	0	0	3	0

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Mol	Chain	Non-H	H(model)	$\mathbf{H}(\mathbf{added})$	Clashes	Symm-Clashes
4	D	114	0	0	2	1
All	All	4590	0	4156	32	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 4.

All (32) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
		${f distance}({f \AA})$	$oxed{ ext{overlap } (ext{Å}) }$
1:A:49[B]:ARG:HH11	1:A:49[B]:ARG:HG3	1.07	1.12
1:A:49[B]:ARG:CG	1:A:49[B]:ARG:HH11	1.81	0.93
1:A:117[A]:ASP:OD1	4:A:283:HOH:O	2.03	0.76
1:C:30[B]:ARG:CG	1:C:30[B]:ARG:HH21	2.00	0.75
1:A:49[B]:ARG:NH1	1:A:49[B]:ARG:HG3	1.89	0.75
1:A:117[A]:ASP:OD1	4:A:128:HOH:O	2.07	0.72
1:C:30[B]:ARG:HG3	1:C:30[B]:ARG:HH21	1.59	0.67
1:A:76:ARG:HD3	1:B:76:ARG:HD3	1.78	0.65
1:B:16[A]:GLN:NE2	1:B:18:ARG:HH21	1.96	0.62
1:A:25:VAL:O	1:A:27[A]:THR:HG23	2.02	0.59
1:C:30[B]:ARG:NH2	1:C:30[B]:ARG:CG	2.64	0.56
1:A:49[B]:ARG:CG	1:A:49[B]:ARG:NH1	2.50	0.56
1:D:105[B]:GLN:HE22	1:D:109:ARG:HH21	1.51	0.55
1:A:90:ARG:HH21	3:C:201:GOL:H32	1.72	0.55
1:B:16[A]:GLN:HG2	1:B:36:TRP:CD1	2.42	0.54
1:C:18:ARG:HG3	1:C:36:TRP:CZ2	2.42	0.54
1:D:36:TRP:O	1:D:40:GLU:HG3	2.09	0.53
1:B:16[A]:GLN:HG2	1:B:36:TRP:NE1	2.24	0.53
1:C:76:ARG:HD3	1:D:76:ARG:HD3	1.92	0.52
1:B:16[A]:GLN:HE22	1:B:18:ARG:HH21	1.62	0.48
1:D:105[A]:GLN:HG3	4:D:133:HOH:O	2.14	0.48
1:D:105[A]:GLN:HG2	4:D:140:HOH:O	2.14	0.46
1:C:51:THR:HG23	3:C:201:GOL:H2	1.97	0.45
1:A:112:PRO:HD2	1:A:115:LEU:HD12	1.99	0.44
1:C:51:THR:CG2	3:C:201:GOL:H2	2.48	0.44
1:C:80:LEU:HD22	1:D:35:PHE:CE2	2.52	0.44
1:C:30[B]:ARG:NH2	4:C:383:HOH:O	2.50	0.44
1:A:90:ARG:NH2	3:C:201:GOL:H32	2.33	0.43
4:C:141:HOH:O	1:D:105[A]:GLN:HB3	2.19	0.42
1:B:12:SER:HB2	1:B:34:LEU:HB2	2.01	0.41
1:C:52:GLN:HA	1:C:55[B]:GLU:HG2	2.04	0.40
1:C:11:ARG:HD2	4:C:429:HOH:O	2.21	0.40



All (1) 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			$egin{array}{c} ext{Clash} \ ext{overlap } (ext{Å}) \end{array}$
1:A:21[B]:ARG:NH2	4:D:158:HOH:O[2_645]	1.79	0.41

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	Perce	entiles
1	A	$127/125 \; (102\%)$	125 (98%)	2 (2%)	0	100	100
1	В	$125/125 \; (100\%)$	123 (98%)	2 (2%)	0	100	100
1	С	$127/125 \; (102\%)$	124 (98%)	3 (2%)	0	100	100
1	D	$125/125 \; (100\%)$	122 (98%)	3 (2%)	0	100	100
All	All	504/500 (101%)	494 (98%)	10 (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	$109/102 \; (107\%)$	105 (96%)	4 (4%)	34	22	
1	В	107/102 (105%)	105 (98%)	2 (2%)	57	50	
1	С	109/102 (107%)	108 (99%)	1 (1%)	78	77	
1	D	107/102 (105%)	106 (99%)	1 (1%)	78	77	

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	432/408 (106%)	424 (98%)	8 (2%)	71 50	

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type		
1	A	16[A]	GLN		
1	A	16[B]	GLN		
1	A	117[A]	ASP		
1	A	117[B]	ASP		
1	В	16[A]	GLN		
1	В	16[B]	GLN		
1	С	23	HIS		
1	D	20	LEU		

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

Mol	Chain	Res	Type
1	A	105	GLN
1	В	33	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

4 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	Туре	Chain	Res	$\operatorname{Res} \left \operatorname{Link} \right $	Bond lengths			Bond angles		
	Type				Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	CME	С	2	1	8,9,10	0.63	0	5,9,11	0.93	0
1	CME	D	2	1	8,9,10	0.76	0	5,9,11	1.12	1 (20%)



Mol	Type	Chain	Dog	tes Link	Bond lengths			Bond angles		
			nes		Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	CME	A	2	1	8,9,10	0.77	0	5,9,11	1.20	1 (20%)
1	CME	В	2	1	8,9,10	0.74	0	5,9,11	1.54	1 (20%)

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	CME	С	2	1	-	0/5/8/10	_
1	CME	D	2	1	-	0/5/8/10	_
1	CME	A	2	1	-	0/5/8/10	-
1	CME	В	2	1	-	0/5/8/10	_

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$Ideal(^{o})$
1	В	2	CME	CB-SG-SD	3.26	112.27	103.82
1	D	2	CME	CB-SG-SD	2.37	109.96	103.82
1	A	2	CME	CB-SG-SD	2.16	109.42	103.82

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

2 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	Dog	Link	В	Bond lengths			Bond angles		
MIOI	Type	Chain	nes	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
2	ACT	A	201	-	1,3,3	1.16	0	0,3,3	0.00	=	
3	GOL	С	201	-	5,5,5	0.30	0	5,5,5	0.40	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	GOL	С	201	_	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	С	201	GOL	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^{th} 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 $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q < 0.9
1	A	122/125 (97%)	-0.36	1 (0%) 86 90	3, 10, 15, 27	0
1	В	122/125 (97%)	-0.35	1 (0%) 86 90	2, 8, 14, 27	0
1	С	122/125 (97%)	-0.36	1 (0%) 86 90	2, 8, 15, 23	0
1	D	$122/125 \ (97\%)$	-0.45	0 100 100	3, 9, 15, 26	0
All	All	488/500 (97%)	-0.38	3 (0%) 89 93	2, 9, 15, 27	0

All (3) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	В	25	VAL	2.7
1	С	23	HIS	2.4
1	A	93	ALA	2.3

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^{th} 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	${f B-factors}({f \AA}^2)$	Q<0.9
1	CME	С	2	10/11	0.93	0.13	9,9,12,17	4
1	CME	D	2	10/11	0.95	0.11	11,12,12,12	4
1	CME	A	2	10/11	0.95	0.11	12,13,14,15	4
1	CME	В	2	10/11	0.96	0.10	9,11,12,13	4

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^{th} 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
3	GOL	С	201	6/6	0.76	0.30	60,60,61,61	0
2	ACT	A	201	4/4	0.88	0.15	47,48,48,48	0

6.5 Other polymers (i)

There are no such residues in this entry.

