

Full wwPDB X-ray Structure Validation Report (i)

Oct 26, 2023 – 04:49 AM EDT

PDB ID : 3HIA

Title : Crystal structure of the choline binding domain of Spr1274 in Streptococcus

pneumoniae

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Deposited on : 2009-05-19

Resolution : 2.38 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
A user guide is available at

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

The types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

 $Mol Probity \quad : \quad 4.02b\text{--}467$

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

Xtriage (Phenix) : 1.13 EDS : 2.36

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

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

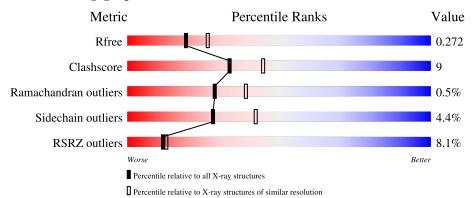
Validation Pipeline (wwPDB-VP) : 2.36

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 2.38 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\AA)}) \end{array}$
R_{free}	130704	5509 (2.40-2.36)
Clashscore	141614	6082 (2.40-2.36)
Ramachandran outliers	138981	5973 (2.40-2.36)
Sidechain outliers	138945	5975 (2.40-2.36)
RSRZ outliers	127900	5397 (2.40-2.36)

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 >=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	94	59%	12%	30%				
1	В	94	74%		11% • 12%				
1	С	94	65%	11%	• 21%				

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
2	PC	A	130	-	X	-	-
3	SO4	С	3	-	-	X	-



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 1973 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 Choline binding protein.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	Λ	66	Total	С	N	О	S	0	0	0
1	Α	00	536	345	87	101	3	0	U	U
1	D	83	Total	С	N	О	S	0	0	0
1	Ъ	0.0	669	428	110	128	3	0	0	
1	C	7.4	Total	С	N	О	S	1	0	0
1		C 74	602	382	100	117	3	1		U

There are 24 discrepancies between the modelled and reference sequences:

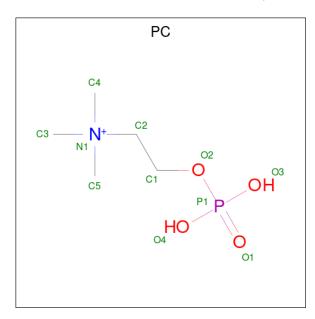
Chain	Residue	Modelled	Actual	Comment	Reference
A	36	MET	-	expression tag	UNP Q8DP99
A	37	GLY	-	expression tag	UNP Q8DP99
A	38	HIS	-	expression tag	UNP Q8DP99
A	39	HIS	-	expression tag	UNP Q8DP99
A	40	HIS	-	expression tag	UNP Q8DP99
A	41	HIS	-	expression tag	UNP Q8DP99
A	42	HIS	-	expression tag	UNP Q8DP99
A	43	HIS	-	expression tag	UNP Q8DP99
В	36	MET	-	expression tag	UNP Q8DP99
В	37	GLY	-	expression tag	UNP Q8DP99
В	38	HIS	-	expression tag	UNP Q8DP99
В	39	HIS	-	expression tag	UNP Q8DP99
В	40	HIS	-	expression tag	UNP Q8DP99
В	41	HIS	-	expression tag	UNP Q8DP99
В	42	HIS	-	expression tag	UNP Q8DP99
В	43	HIS	-	expression tag	UNP Q8DP99
С	36	MET	-	expression tag	UNP Q8DP99
С	37	GLY	-	expression tag	UNP Q8DP99
С	38	HIS	-	expression tag	UNP Q8DP99
С	39	HIS	-	expression tag	UNP Q8DP99
С	40	HIS	-	expression tag	UNP Q8DP99
С	41	HIS	-	expression tag	UNP Q8DP99
С	42	HIS	-	expression tag	UNP Q8DP99



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Chain	Residue	Modelled	Actual	Comment	Reference
С	43	HIS	-	expression tag	UNP Q8DP99

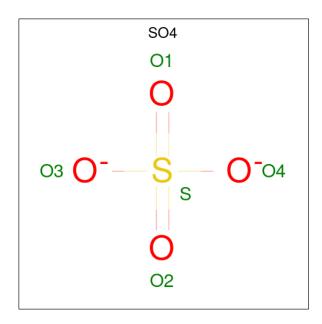
 \bullet Molecule 2 is PHOSPHOCHOLINE (three-letter code: PC) (formula: $\mathrm{C_5H_{15}NO_4P}).$



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C N O 7 5 1 1	0	0
2	В	1	Total C N 5 4 1	0	0
2	В	1	Total C N 5 4 1	0	0
2	В	1	Total C N 5 4 1	0	0
2	В	1	Total C N 5 4 1	0	0
2	С	1	Total C N 5 4 1	0	0
2	С	1	Total C N 5 4 1	0	0

 \bullet Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: $\mathrm{O_4S}).$





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

• Molecule 4 is water.

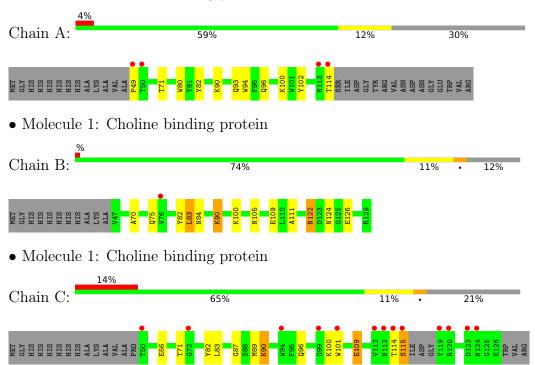
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	38	Total O 38 38	0	0
4	В	42	Total O 42 42	0	0
4	С	34	Total O 34 34	0	0



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: Choline binding protein





4 Data and refinement statistics (i)

Property	Value	Source
Space group	Н 3	Depositor
Cell constants	140.61Å 140.61Å 46.05Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 - 2.38	Depositor
resolution (A)	36.73 - 2.37	EDS
% Data completeness	94.8 (20.00-2.38)	Depositor
(in resolution range)	94.1 (36.73-2.37)	EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	4.62 (at 2.37Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.223 , 0.265	Depositor
it, it free	0.236 , 0.272	DCC
R_{free} test set	1639 reflections (12.62%)	wwPDB-VP
Wilson B-factor (Å ²)	31.9	Xtriage
Anisotropy	1.216	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.31, 35.1	EDS
L-test for twinning ²	$< L >=0.51, < L^2>=0.34$	Xtriage
Estimated twinning fraction	0.026 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	1973	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.80% of the height of the origin peak. No significant pseudotranslation is detected.

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: SO4, PC

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).

Mal	Chain	Boı	nd lengths	Bond angles		
Mol Chain		RMSZ	77 1		# Z > 5	
1	A	0.62	0/555	0.63	1/757 (0.1%)	
1	В	0.54	0/692	0.61	0/946	
1	С	0.74	1/621 (0.2%)	0.65	0/844	
All	All	0.64	1/1868 (0.1%)	0.63	1/2547 (0.0%)	

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(ext{\AA})$
1	С	115	SER	C-O	-7.33	1.09	1.23

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	49	PRO	N-CA-CB	5.81	110.27	103.30

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	536	0	475	5	0
1	В	669	0	594	10	0
1	С	602	0	526	11	0



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Mol	Chain	Non-H	H(model)	$\mathbf{H}(\mathbf{added})$	Clashes	Symm-Clashes
2	A	7	0	13	5	0
2	В	20	0	36	2	0
2	С	10	0	18	0	0
3	A	5	0	0	0	0
3	В	5	0	0	0	0
3	С	5	0	0	2	0
4	A	38	0	0	0	0
4	В	42	0	0	1	0
4	C	34	0	0	3	0
All	All	1973	0	1662	30	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 9.

All (30) 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:124:ASN:HB2	2:B:132:PC:H42	1.35	1.07
1:C:114:THR:HG22	1:C:115:SER:H	1.11	1.06
1:C:101:TRP:HA	4:C:144:HOH:O	1.58	1.04
1:C:96:GLN:HA	4:C:144:HOH:O	1.57	1.03
1:C:114:THR:HG22	1:C:115:SER:N	1.94	0.83
1:C:100:LYS:O	4:C:144:HOH:O	1.98	0.81
1:C:114:THR:CG2	1:C:115:SER:H	1.94	0.73
2:A:130:PC:H11	3:C:3:SO4:O2	1.94	0.68
2:A:130:PC:C1	3:C:3:SO4:O2	2.51	0.58
1:B:82:TYR:CD2	1:B:90:LYS:HD2	2.40	0.56
1:C:82:TYR:HD2	1:C:90:LYS:HD2	1.71	0.55
1:B:82:TYR:HD2	1:B:90:LYS:HD2	1.74	0.53
1:B:122:ASN:HB3	1:B:124:ASN:H	1.74	0.52
2:A:130:PC:O2	2:A:130:PC:C4	2.56	0.52
1:B:70:ALA:O	1:B:83:LEU:HD23	2.10	0.52
1:C:82:TYR:CD2	1:C:90:LYS:HD2	2.45	0.51
1:A:90:LYS:HE3	1:A:93:GLN:OE1	2.13	0.49
1:B:124:ASN:HB2	2:B:132:PC:C4	2.26	0.48
1:A:94:TRP:HA	1:A:102:TYR:O	2.14	0.48
2:A:130:PC:O2	2:A:130:PC:H42	2.15	0.45
1:A:80:TRP:CD2	2:A:130:PC:H53	2.52	0.44
1:C:83:LEU:HD23	1:C:89:MET:HA	1.99	0.44
1:B:100:LYS:HB3	1:B:126:GLU:HG3	2.01	0.43
1:A:96:GLN:HA	1:A:100:LYS:O	2.19	0.43



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Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	$\operatorname{distance}\ (ext{\AA})$	overlap (Å)
1:B:105:ASN:OD1	1:B:109:GLU:HG2	2.18	0.43
1:C:71:THR:HG22	1:C:87:GLY:HA2	2.00	0.43
1:B:111:ALA:HA	4:B:134:HOH:O	2.20	0.41
1:A:82:TYR:CD2	1:A:90:LYS:HD2	2.55	0.41
1:C:109:GLU:H	1:C:109:GLU:HG2	1.56	0.41
1:B:84:ASN:HD21	1:B:90:LYS:HG3	1.86	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	Perce	entiles	
1	A	64/94 (68%)	62 (97%)	2 (3%)	0	100	100
1	В	81/94 (86%)	79 (98%)	1 (1%)	1 (1%)	13	17
1	С	70/94 (74%)	67 (96%)	3 (4%)	0	100	100
All	All	215/282 (76%)	208 (97%)	6 (3%)	1 (0%)	29	39

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	В	122	ASN

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	54/77 (70%)	52 (96%)	2 (4%)	34 50
1	В	68/77 (88%)	65 (96%)	3 (4%)	28 42
1	С	61/77 (79%)	58 (95%)	3 (5%)	25 38
All	All	183/231 (79%)	175 (96%)	8 (4%)	28 42

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

Mol	Chain	Res	Type
1	A	71	THR
1	A	114	THR
1	В	75	GLN
1	В	83	LEU
1	В	90	LYS
1	С	56	GLU
1	С	90	LYS
1	С	109	GLU

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

Mol	Chain	Res	Type
1	В	84	ASN
1	С	93	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

10 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).

Mal	Trino	Chain	Dag	T inle	В	ond leng	$_{ m gths}$	Е	ond ang	gles
Mol	Type	Chain	Res	Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z >2
2	PC	В	133	-	4,4,10	0.43	0	6,6,15	1.41	1 (16%)
2	PC	С	131	-	4,4,10	0.45	0	6,6,15	1.64	1 (16%)
2	PC	В	131	-	4,4,10	0.60	0	6,6,15	1.54	1 (16%)
2	PC	В	130	-	4,4,10	0.46	0	6,6,15	1.66	1 (16%)
2	PC	A	130	-	6,6,10	2.25	2 (33%)	8,8,15	2.26	4 (50%)
3	SO4	С	3	-	4,4,4	0.06	0	6,6,6	0.42	0
3	SO4	A	1	-	4,4,4	0.19	0	6,6,6	0.49	0
3	SO4	В	2	-	4,4,4	0.27	0	6,6,6	0.34	0
2	PC	В	132	-	4,4,10	0.55	0	6,6,15	1.42	1 (16%)
2	PC	С	130	-	4,4,10	0.52	0	6,6,15	1.59	1 (16%)

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
2	PC	A	130	-	-	4/4/4/8	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(\text{\AA})$
2	A	130	PC	O2-C1	-4.55	1.18	1.42
2	A	130	PC	C5-N1	-2.07	1.44	1.50

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$Ideal(^{o})$
2	A	130	PC	C3-N1-C2	3.87	125.74	109.92
2	В	130	PC	C5-N1-C2	3.41	127.20	109.41
2	С	131	PC	C5-N1-C2	3.38	127.03	109.41
2	В	131	PC	C5-N1-C2	3.36	126.95	109.41



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Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
2	С	130	PC	C5-N1-C2	3.24	126.30	109.41
2	В	132	PC	C3-N1-C2	3.05	125.31	109.41
2	В	133	PC	C3-N1-C2	2.98	124.96	109.41
2	A	130	PC	C5-N1-C2	-2.92	97.97	109.92
2	A	130	PC	O2-C1-C2	2.68	123.65	111.24
2	A	130	PC	C5-N1-C3	-2.45	102.68	108.97

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	130	PC	C1-C2-N1-C4
2	A	130	PC	C1-C2-N1-C5
2	A	130	PC	C1-C2-N1-C3
2	A	130	PC	O2-C1-C2-N1

There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	130	PC	5	0
3	С	3	SO4	2	0
2	В	132	PC	2	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 $>$	# RSRZ > 2	$OWAB(A^2)$	Q<0.9
1	A	66/94 (70%)	0.40	4 (6%) 21 23	21, 29, 43, 50	2 (3%)
1	В	83/94 (88%)	0.23	1 (1%) 79 80	28, 35, 43, 46	1 (1%)
1	С	74/94 (78%)	0.87	13 (17%) 1 1	17, 33, 58, 60	6 (8%)
All	All	223/282 (79%)	0.49	18 (8%) 12 13	17, 33, 50, 60	9 (4%)

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	114	THR	6.1
1	С	113	ASN	4.1
1	С	50	THR	3.8
1	С	112	VAL	3.7
1	С	120	ARG	3.4
1	С	124	ASN	3.4
1	С	94	TRP	3.3
1	С	114	THR	3.2
1	С	115	SER	3.2
1	A	113	ASN	3.0
1	A	50	THR	2.9
1	С	119	TYR	2.7
1	A	49	PRO	2.6
1	В	76	VAL	2.6
1	С	123	ASP	2.5
1	С	99	GLY	2.2
1	С	72	GLY	2.1
1	С	101	TRP	2.1

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^{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
2	PC	С	131	5/11	0.77	0.28	50,51,51,51	5
2	PC	В	131	5/11	0.88	0.24	32,33,35,36	0
2	PC	В	130	5/11	0.91	0.27	27,28,31,31	0
2	PC	В	133	5/11	0.93	0.17	36,36,37,37	0
2	PC	С	130	5/11	0.94	0.18	45,45,46,47	0
2	PC	A	130	7/11	0.94	0.29	48,49,49,50	0
2	PC	В	132	5/11	0.95	0.26	36,36,36,37	0
3	SO4	В	2	5/5	0.96	0.13	25,25,26,27	1
3	SO4	С	3	5/5	0.97	0.13	46,47,47,48	0
3	SO4	A	1	5/5	0.98	0.13	29,32,33,33	0

6.5 Other polymers (i)

There are no such residues in this entry.

