



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 20, 2022 – 04:05 PM EST

PDB ID : 7RQR  
Title : Structure of chimeric antibody L9heavy\_F10light with PfCSP peptide NANPNVDP  
Authors : Hurlburt, N.K.; Pancera, M.  
Deposited on : 2021-08-06  
Resolution : 2.23 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	:	2.26
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)	:	2.26

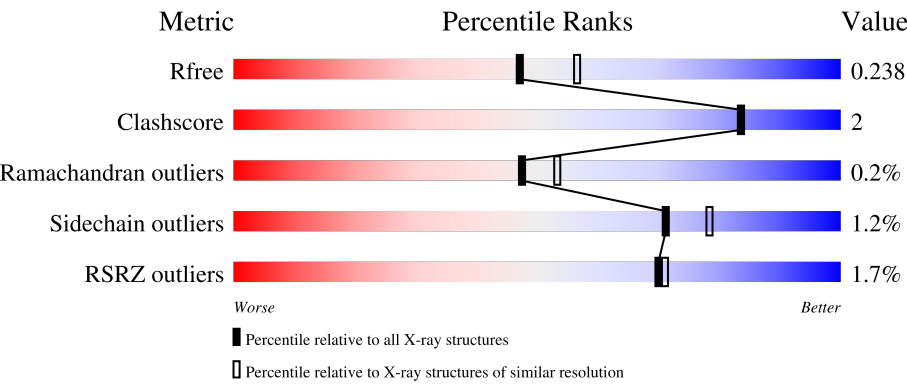
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.23 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 <sub>free</sub>	130704	2391 (2.26-2.22)
Clashscore	141614	2539 (2.26-2.22)
Ramachandran outliers	138981	2489 (2.26-2.22)
Sidechain outliers	138945	2490 (2.26-2.22)
RSRZ outliers	127900	2353 (2.26-2.22)

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	227	<div><div>2%</div><div>89%</div><div>5%</div><div>5%</div></div>
1	H	227	<div><div>2%</div><div>88%</div><div>8%</div><div>..</div></div>
2	B	214	<div><div>%</div><div>92%</div><div>7%</div></div>
2	L	214	<div><div>%</div><div>92%</div><div>7%</div></div>
3	C	8	<div><div>75%</div><div>25%</div></div>

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
3	P	8	<div><div></div><div>75%</div><div>25%</div></div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7096 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 L9 Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	215	Total	C	N	O	S	0	0	0
			1634	1040	273	314	7			
1	H	220	Total	C	N	O	S	0	0	0
			1666	1058	279	322	7			

- Molecule 2 is a protein called F10 Kappa Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	213	Total	C	N	O	S	0	0	0
			1634	1018	276	335	5			
2	L	213	Total	C	N	O	S	0	0	0
			1638	1021	277	335	5			

- Molecule 3 is a protein called PfCSP peptide NANPNVDP.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	6	Total	C	N	O	0	0	0
			43	25	8	10			
3	P	6	Total	C	N	O	0	0	0
			43	25	8	10			

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

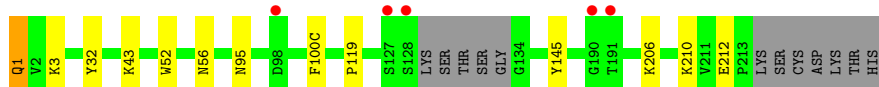
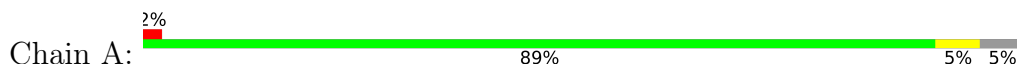
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	123	Total	O	0	0
			123	123		
5	B	89	Total	O	0	0
			89	89		
5	C	2	Total	O	0	0
			2	2		
5	H	108	Total	O	0	0
			108	108		
5	L	111	Total	O	0	0
			111	111		
5	P	1	Total	O	0	0
			1	1		

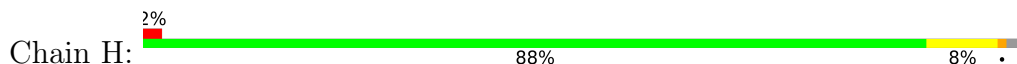
### 3 Residue-property plots [i](#)

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.

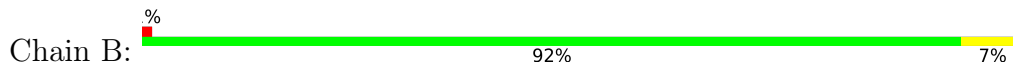
- Molecule 1: L9 Heavy Chain



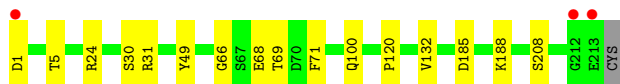
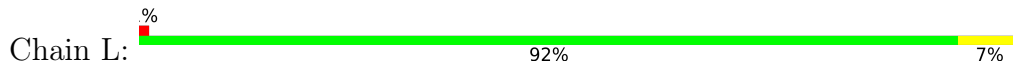
- Molecule 1: L9 Heavy Chain



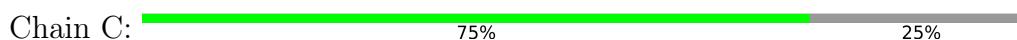
- Molecule 2: F10 Kappa Chain



- Molecule 2: F10 Kappa Chain



- Molecule 3: PfCSP peptide NANPNVDP



- Molecule 3: PfCSP peptide NANPNVDP

Chain P:



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	71.50Å 85.82Å 145.46Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.83 – 2.23 43.83 – 2.23	Depositor EDS
% Data completeness (in resolution range)	99.5 (43.83-2.23) 99.5 (43.83-2.23)	Depositor EDS
$R_{merge}$	0.19	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.79 (at 2.22Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, $R_{free}$	0.189 , 0.238 0.189 , 0.238	Depositor DCC
$R_{free}$ test set	2131 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	35.7	Xtriage
Anisotropy	0.223	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 54.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	7096	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	40.0	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 31.58 % 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 1.0816e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: PCA, EDO

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	0.26	0/1671	0.50	1/2277 (0.0%)
1	H	0.27	0/1704	0.48	0/2322
2	B	0.26	0/1667	0.47	0/2264
2	L	0.26	0/1671	0.46	0/2268
3	C	0.23	0/43	0.38	0/59
3	P	0.23	0/43	0.39	0/59
All	All	0.26	0/6799	0.48	1/9249 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	H	0	1
All	All	0	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	1	PCA	O-C-N	-8.04	109.84	122.70

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1	PCA	Mainchain

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Group
1	H	1	PCA	Mainchain

## 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	1634	0	1577	5	1
1	H	1666	0	1611	12	0
2	B	1634	0	1580	8	1
2	L	1638	0	1591	9	0
3	C	43	0	36	0	0
3	P	43	0	36	0	0
4	A	4	0	6	1	0
5	A	123	0	0	1	0
5	B	89	0	0	1	0
5	C	2	0	0	0	0
5	H	108	0	0	2	0
5	L	111	0	0	0	0
5	P	1	0	0	0	0
All	All	7096	0	6437	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 2.

All (32) 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)
2:L:5:THR:HA	2:L:100:GLN:HE22	1.51	0.74
1:H:59:TYR:HB2	1:H:64:LYS:HG2	1.72	0.70
1:H:43:LYS:NZ	5:H:301:HOH:O	2.22	0.68
2:B:210:ASN:HB2	2:B:213:GLU:HG3	1.78	0.64
1:A:119:PRO:HB3	1:A:145:TYR:HB3	1.79	0.64
2:B:103:LYS:NZ	5:B:302:HOH:O	2.32	0.63
1:H:129:LYS:HE2	2:L:208:SER:O	2.01	0.60
1:H:119:PRO:HB3	1:H:145:TYR:HB3	1.86	0.57
1:H:159:LEU:HD21	1:H:182:VAL:HG21	1.88	0.55

*Continued on next page...*

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:191:VAL:HG22	2:B:210:ASN:HD22	1.72	0.54
2:B:151:ASP:OD2	2:B:189:HIS:HB3	2.08	0.54
1:A:32:TYR:H	4:A:301:EDO:H12	1.73	0.52
2:L:30:SER:OG	2:L:31:ARG:N	2.44	0.51
1:A:210:LYS:HE2	1:A:212:GLU:OE2	2.11	0.50
2:B:183:LYS:O	2:B:187:GLU:HG3	2.11	0.49
1:H:100(B):PRO:HG3	2:L:49:TYR:CE1	2.47	0.49
2:L:185:ASP:HA	2:L:188:LYS:HE2	1.94	0.49
1:H:18:LEU:HB3	1:H:82:MET:HE2	1.95	0.48
1:A:56:ASN:ND2	5:A:402:HOH:O	2.31	0.48
2:L:66:GLY:HA3	2:L:71:PHE:HA	1.95	0.48
1:A:95:ASN:HA	1:A:100(C):PHE:O	2.15	0.47
1:H:127:SER:H	1:H:130:SER:HB2	1.83	0.44
1:H:82:MET:HB3	1:H:82(C):LEU:HD21	2.00	0.43
1:H:127:SER:OG	1:H:128:SER:N	2.52	0.42
1:H:16:ARG:NH2	5:H:302:HOH:O	2.36	0.42
2:L:24:ARG:HA	2:L:69:THR:O	2.19	0.42
2:L:120:PRO:HD3	2:L:132:VAL:HG22	2.00	0.42
2:B:103:LYS:HE3	2:B:105:GLU:OE2	2.20	0.41
1:H:43:LYS:HD2	1:H:44:GLY:H	1.85	0.41
2:B:186:TYR:C	2:B:188:LYS:H	2.24	0.41
2:L:5:THR:HA	2:L:100:GLN:NE2	2.29	0.41
2:B:93:SER:OG	2:B:94:TYR:N	2.51	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	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3:LYS:NZ	2:B:3:GLN:OE1[4_555]	2.16	0.04

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	211/227 (93%)	208 (99%)	3 (1%)	0	100	100
1	H	218/227 (96%)	214 (98%)	4 (2%)	0	100	100
2	B	211/214 (99%)	199 (94%)	11 (5%)	1 (0%)	29	28
2	L	211/214 (99%)	204 (97%)	6 (3%)	1 (0%)	29	28
3	C	4/8 (50%)	4 (100%)	0	0	100	100
3	P	4/8 (50%)	4 (100%)	0	0	100	100
All	All	859/898 (96%)	833 (97%)	24 (3%)	2 (0%)	47	53

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	L	68	GLU
2	B	68	GLU

### 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	181/192 (94%)	178 (98%)	3 (2%)	60	68
1	H	185/192 (96%)	181 (98%)	4 (2%)	52	59
2	B	185/188 (98%)	184 (100%)	1 (0%)	88	92
2	L	186/188 (99%)	185 (100%)	1 (0%)	88	92
3	C	5/7 (71%)	5 (100%)	0	100	100
3	P	5/7 (71%)	5 (100%)	0	100	100
All	All	747/774 (96%)	738 (99%)	9 (1%)	71	78

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	43	LYS
1	A	52	TRP
1	A	206	LYS

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
2	B	145	LYS
1	H	52	TRP
1	H	71	ARG
1	H	127	SER
1	H	132	SER
2	L	1	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	147	GLN
2	B	210	ASN
1	H	73	ASN
2	L	100	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	PCA	A	1	1	7,8,9	1.82	1 (14%)	9,10,12	2.16	5 (55%)
1	PCA	H	1	1	7,8,9	1.81	1 (14%)	9,10,12	2.12	5 (55%)

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	PCA	A	1	1	-	0/0/11/13	0/1/1/1
1	PCA	H	1	1	-	0/0/11/13	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1	PCA	CD-N	4.69	1.46	1.34
1	H	1	PCA	CD-N	4.67	1.46	1.34

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	1	PCA	OE-CD-CG	-3.03	121.47	126.76
1	A	1	PCA	CA-N-CD	-3.00	103.31	113.58
1	A	1	PCA	OE-CD-CG	-2.97	121.58	126.76
1	H	1	PCA	CA-N-CD	-2.88	103.72	113.58
1	A	1	PCA	CB-CA-N	2.66	110.95	103.30
1	H	1	PCA	CB-CA-N	2.64	110.88	103.30
1	H	1	PCA	CG-CD-N	2.46	114.75	108.39
1	A	1	PCA	CB-CA-C	-2.45	109.33	112.70
1	A	1	PCA	CG-CD-N	2.42	114.65	108.39
1	H	1	PCA	CB-CA-C	-2.37	109.45	112.70

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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

1 ligand is 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	$\# Z  > 2$
4	EDO	A	301	-	3,3,3	0.45	0	2,2,2	0.36	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
4	EDO	A	301	-	-	0/1/1/1	-

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 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	301	EDO	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 [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	214/227 (94%)	-0.07	5 (2%) 60 61	21, 36, 65, 91	0
1	H	219/227 (96%)	-0.01	4 (1%) 68 69	23, 36, 67, 89	0
2	B	213/214 (99%)	0.02	3 (1%) 75 76	22, 38, 80, 102	0
2	L	213/214 (99%)	-0.13	3 (1%) 75 76	23, 37, 65, 100	0
3	C	6/8 (75%)	0.21	0 100 100	36, 44, 62, 65	0
3	P	6/8 (75%)	0.13	0 100 100	39, 47, 57, 65	0
All	All	871/898 (96%)	-0.04	15 (1%) 70 71	21, 37, 69, 102	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	128	SER	5.2
1	H	132	SER	4.2
2	B	212	GLY	4.1
2	L	213	GLU	3.5
2	L	212	GLY	3.4
1	H	133	GLY	3.3
1	A	191	THR	2.6
1	A	190	GLY	2.6
2	B	209	PHE	2.5
1	A	127	SER	2.4
2	L	1	ASP	2.3
1	H	129	LYS	2.3
2	B	202	SER	2.3
1	H	99	GLY	2.3
1	A	98	ASP	2.1



## 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( $\text{\AA}^2$ )	Q<0.9
1	PCA	H	1	8/9	0.70	0.35	69,80,84,87	0
1	PCA	A	1	8/9	0.86	0.30	42,64,69,73	0

## 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( $\text{\AA}^2$ )	Q<0.9
4	EDO	A	301	4/4	0.60	0.32	52,56,56,57	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.