



Full wwPDB X-ray Structure Validation Report

Sep 20, 2023 – 01:35 AM EDT

PDB ID : 5EG8
Title : The cap binding site of influenza virus protein PB2 as a drug target
Authors : Liu, Y.; Zheng, X.; Severin, C.; Rocha de Moura, T.; Li, K.; Luo, M.
Deposited on : 2015-10-26
Resolution : 1.54 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  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](#) ) 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 : 2.35.1
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) : 2.35.1

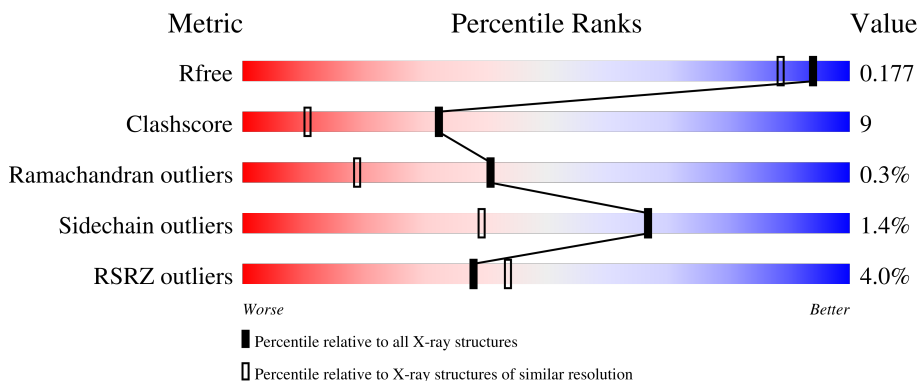
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.54 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	2556 (1.56-1.52)
Clashscore	141614	2634 (1.56-1.52)
Ramachandran outliers	138981	2580 (1.56-1.52)
Sidechain outliers	138945	2577 (1.56-1.52)
RSRZ outliers	127900	2524 (1.56-1.52)

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 $\leq 5\%$. 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	163	
1	B	163	

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	SCN	A	504	-	-	X	-

2 Entry composition [i](#)

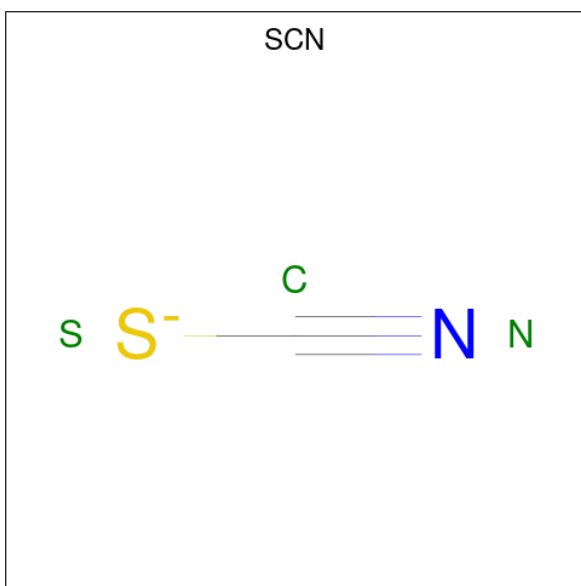
There are 3 unique types of molecules in this entry. The entry contains 3088 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Polymerase basic protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	163	1374	859	254	250	11	0	11	0
1	B	163	1353	847	251	244	11	0	8	0

- Molecule 2 is THIOCYANATE ION (three-letter code: SCN) (formula: CNS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	S		
2	A	1	3	1	1	1	0	0
2	A	1	3	1	1	1	0	0
2	A	1	3	1	1	1	0	0
2	A	1	3	1	1	1	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total 3	C 1	N 1	S 1	0	0
2	B	1	Total 3	C 1	N 1	S 1	0	0
2	B	1	Total 3	C 1	N 1	S 1	0	0
2	B	1	Total 3	C 1	N 1	S 1	0	0

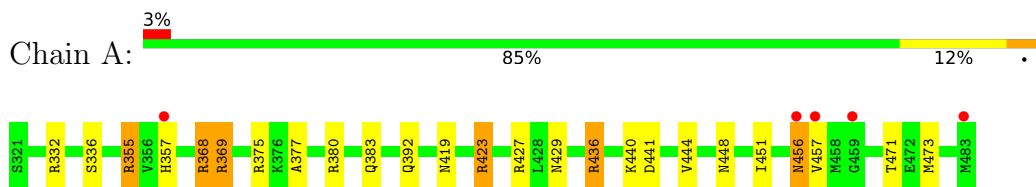
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	165	Total 165	O 165	0	0
3	B	172	Total 172	O 172	0	0

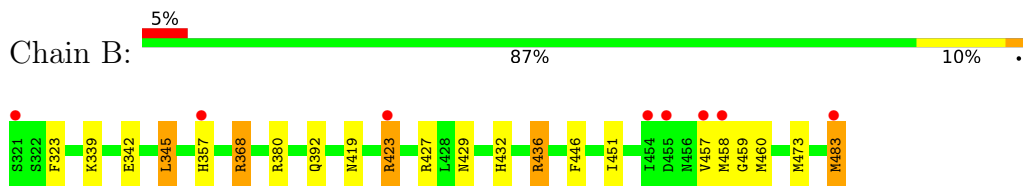
3 Residue-property plots [i](#)

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: Polymerase basic protein 2



- Molecule 1: Polymerase basic protein 2



4 Data and refinement statistics i

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α , β , γ	54.61Å 54.61Å 196.49Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	14.63 – 1.54 14.63 – 1.54	Depositor EDS
% Data completeness (in resolution range)	97.2 (14.63-1.54) 97.3 (14.63-1.54)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	12.12 (at 1.54Å)	Xtrriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.122 , 0.177 0.122 , 0.177	Depositor DCC
R_{free} test set	2546 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	16.5	Xtrriage
Anisotropy	0.464	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 39.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.480 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	3088	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.59% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: SCN

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	0.98	1/1403 (0.1%)	1.29	15/1875 (0.8%)
1	B	0.93	1/1379 (0.1%)	1.22	11/1843 (0.6%)
All	All	0.95	2/2782 (0.1%)	1.26	26/3718 (0.7%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	380	ARG	CZ-NH2	-7.30	1.23	1.33
1	B	380	ARG	CZ-NH2	-7.24	1.23	1.33

All (26) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	436	ARG	NE-CZ-NH2	-14.79	112.91	120.30
1	A	423[A]	ARG	NE-CZ-NH2	-14.42	113.09	120.30
1	A	423[B]	ARG	NE-CZ-NH2	-14.42	113.09	120.30
1	A	423[A]	ARG	NE-CZ-NH1	14.08	127.34	120.30
1	A	423[B]	ARG	NE-CZ-NH1	14.08	127.34	120.30
1	A	436	ARG	NE-CZ-NH2	-14.00	113.30	120.30
1	B	436	ARG	NE-CZ-NH1	12.39	126.50	120.30
1	B	423[A]	ARG	NE-CZ-NH2	11.37	125.98	120.30
1	B	423[B]	ARG	NE-CZ-NH2	11.37	125.98	120.30
1	B	423[A]	ARG	NE-CZ-NH1	-10.22	115.19	120.30
1	B	423[B]	ARG	NE-CZ-NH1	-10.22	115.19	120.30
1	A	436	ARG	NE-CZ-NH1	9.98	125.29	120.30
1	B	380	ARG	NE-CZ-NH1	8.00	124.30	120.30
1	A	380	ARG	NE-CZ-NH1	7.86	124.23	120.30
1	B	380	ARG	NE-CZ-NH2	-6.86	116.87	120.30
1	A	369	ARG	NE-CZ-NH2	-6.34	117.13	120.30
1	A	380	ARG	NE-CZ-NH2	-6.23	117.19	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	345	LEU	CB-CG-CD1	6.01	121.22	111.00
1	B	368	ARG	NE-CZ-NH2	-5.95	117.33	120.30
1	A	368	ARG	NE-CZ-NH2	-5.50	117.55	120.30
1	A	423[A]	ARG	CD-NE-CZ	5.37	131.12	123.60
1	A	423[B]	ARG	CD-NE-CZ	5.37	131.12	123.60
1	A	436	ARG	CG-CD-NE	-5.24	100.79	111.80
1	B	446	PHE	CB-CG-CD1	5.19	124.43	120.80
1	A	441	ASP	CB-CG-OD1	5.07	122.86	118.30
1	A	436	ARG	CD-NE-CZ	5.06	130.69	123.60

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	1374	0	1412	28	0
1	B	1353	0	1395	26	0
2	A	12	0	0	3	0
2	B	12	0	0	1	0
3	A	165	0	0	6	1
3	B	172	0	0	8	1
All	All	3088	0	2807	49	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 9.

All (49) 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:A:451:ILE:HD12	1:A:473:MET:CE	1.58	1.33
1:B:460:MET:HE2	3:B:754:HOH:O	1.45	1.15
1:A:451:ILE:HD12	1:A:473:MET:HE1	1.37	1.05
1:B:460:MET:CE	3:B:754:HOH:O	2.01	1.04
1:A:451:ILE:HD12	1:A:473:MET:HE3	1.41	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:383[A]:GLN:HG2	3:A:631:HOH:O	1.68	0.94
1:B:432[B]:HIS:CD2	3:B:636:HOH:O	2.23	0.90
1:B:432[B]:HIS:HD2	3:B:636:HOH:O	1.56	0.89
1:B:451:ILE:HD12	1:B:473:MET:CE	2.04	0.88
1:B:451:ILE:HD12	1:B:473:MET:HE2	1.61	0.83
1:A:375[B]:ARG:HE	1:A:383[B]:GLN:HE21	1.27	0.80
1:A:419:ASN:HD22	1:A:427:ARG:HH12	1.31	0.78
1:A:451:ILE:CD1	1:A:473:MET:CE	2.54	0.73
1:A:451:ILE:CD1	1:A:473:MET:HE3	2.20	0.72
1:B:483[A]:MET:HG3	3:B:719:HOH:O	1.87	0.72
1:B:419:ASN:HD22	1:B:427:ARG:HH12	1.34	0.72
1:B:342:GLU:OE1	3:B:601:HOH:O	2.07	0.72
1:A:357:HIS:CE1	1:B:423[A]:ARG:HD2	2.26	0.71
1:B:451:ILE:HD12	1:B:473:MET:HE1	1.76	0.68
1:A:375[B]:ARG:HE	1:A:383[B]:GLN:NE2	1.93	0.67
1:A:357:HIS:HE1	1:B:423[A]:ARG:HH21	1.44	0.65
1:A:456:ASN:HD21	1:A:471:THR:HB	1.61	0.65
1:B:339:LYS:HE2	1:B:357:HIS:NE2	2.15	0.60
1:A:357:HIS:CE1	1:B:423[A]:ARG:HH21	2.21	0.58
1:B:429[B]:ASN:OD1	1:B:429[B]:ASN:C	2.42	0.57
1:B:458:MET:HG2	1:B:459:GLY:H	1.71	0.56
1:A:451:ILE:CD1	1:A:473:MET:HE1	2.26	0.54
1:A:355:ARG:HD2	3:A:601:HOH:O	2.09	0.53
1:A:429[B]:ASN:OD1	1:A:429[B]:ASN:C	2.50	0.50
1:B:451:ILE:CD1	1:B:473:MET:HE1	2.41	0.49
1:A:332:ARG:NH1	1:A:336:SER:HA	2.28	0.48
1:A:383[A]:GLN:CG	3:A:631:HOH:O	2.44	0.48
1:A:423[B]:ARG:HG3	3:A:669:HOH:O	2.14	0.48
1:B:423[A]:ARG:NE	3:B:604:HOH:O	2.47	0.47
1:A:357:HIS:HE1	1:B:423[A]:ARG:NH2	2.11	0.47
1:A:368:ARG:HH22	1:B:392:GLN:HE21	1.63	0.47
1:B:457:VAL:HG13	1:B:458:MET:HB2	1.97	0.46
1:B:457:VAL:CG1	1:B:458:MET:HB2	2.47	0.45
1:A:423[B]:ARG:HG2	1:B:323:PHE:CE2	2.53	0.44
1:A:444:VAL:HG13	1:A:448:ASN:ND2	2.33	0.44
1:A:377:ALA:HB1	2:A:502:SCN:C	2.49	0.43
2:B:504:SCN:C	3:B:611:HOH:O	2.66	0.43
1:A:392:GLN:HE21	1:B:368:ARG:HH22	1.66	0.43
2:A:504:SCN:S	1:B:436:ARG:HD3	2.60	0.42
1:A:369:ARG:HA	1:A:369:ARG:HD2	1.87	0.42
2:A:504:SCN:C	3:A:637:HOH:O	2.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:440:LYS:HE3	3:A:748:HOH:O	2.21	0.41
1:A:436:ARG:HA	1:A:436:ARG:HD2	1.90	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)
3:A:657:HOH:O	3:B:649:HOH:O[6_665]	0.16	2.04

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	171/163 (105%)	167 (98%)	3 (2%)	1 (1%)	25	7
1	B	168/163 (103%)	164 (98%)	4 (2%)	0	100	100
All	All	339/326 (104%)	331 (98%)	7 (2%)	1 (0%)	41	19

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	457	VAL

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	153/142 (108%)	151 (99%)	2 (1%)	69	42
1	B	150/142 (106%)	147 (98%)	3 (2%)	55	24
All	All	303/284 (107%)	298 (98%)	5 (2%)	67	31

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	355	ARG
1	A	456	ASN
1	B	345	LEU
1	B	483[A]	MET
1	B	483[B]	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	357	HIS
1	A	392	GLN
1	A	419	ASN
1	A	448	ASN
1	A	456	ASN
1	B	392	GLN
1	B	419	ASN

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](#)

8 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	SCN	B	504	-	1,2,2	2.23	1 (100%)	0,1,1	-	-
2	SCN	B	501	-	1,2,2	1.09	0	0,1,1	-	-
2	SCN	A	502	-	1,2,2	0.34	0	0,1,1	-	-
2	SCN	B	503	-	1,2,2	0.14	0	0,1,1	-	-
2	SCN	A	504	-	1,2,2	1.79	0	0,1,1	-	-
2	SCN	B	502	-	1,2,2	1.05	0	0,1,1	-	-
2	SCN	A	501	-	1,2,2	1.45	0	0,1,1	-	-
2	SCN	A	503	-	1,2,2	1.41	0	0,1,1	-	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	504	SCN	C-N	2.23	1.22	1.15

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	504	SCN	1	0
2	A	502	SCN	1	0
2	A	504	SCN	2	0

5.7 Other polymers [i](#)

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, 95th 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 ²)	Q<0.9
1	A	163/163 (100%)	0.07	5 (3%) 49 56	12, 20, 43, 67	0
1	B	163/163 (100%)	0.20	8 (4%) 29 33	12, 20, 46, 69	0
All	All	326/326 (100%)	0.13	13 (3%) 38 44	12, 20, 46, 69	0

All (13) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	458	MET	3.7
1	B	455	ASP	3.3
1	A	456	ASN	3.2
1	A	483[A]	MET	2.8
1	A	357	HIS	2.7
1	B	423[A]	ARG	2.3
1	B	454	ILE	2.3
1	B	321	SER	2.2
1	A	457	VAL	2.2
1	B	457	VAL	2.1
1	B	483[A]	MET	2.1
1	A	459	GLY	2.0
1	B	357	HIS	2.0

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, 95th 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 ²)	Q<0.9
2	SCN	B	504	3/3	0.61	0.21	36,36,43,81	0
2	SCN	A	504	3/3	0.93	0.21	41,41,42,91	0
2	SCN	B	503	3/3	0.95	0.27	37,37,40,43	0
2	SCN	A	502	3/3	0.95	0.10	40,40,43,43	0
2	SCN	A	503	3/3	0.98	0.08	21,21,25,27	0
2	SCN	B	501	3/3	0.98	0.10	35,35,35,38	0
2	SCN	A	501	3/3	0.99	0.08	31,31,34,39	0
2	SCN	B	502	3/3	0.99	0.09	24,24,26,27	0

6.5 Other polymers [i](#)

There are no such residues in this entry.