wwPDB X-ray Structure Validation Summary Report (i)

Apr 3, 2024 – 03:17 am BST

PDB ID	:	8ONI
Title	:	Human insulin in complex with the analytical antibody S1 Fab
Authors	:	Johansson, E.
Deposited on	:	2023-04-03
Resolution	:	2.30 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 (i)) were used in the production of this report:

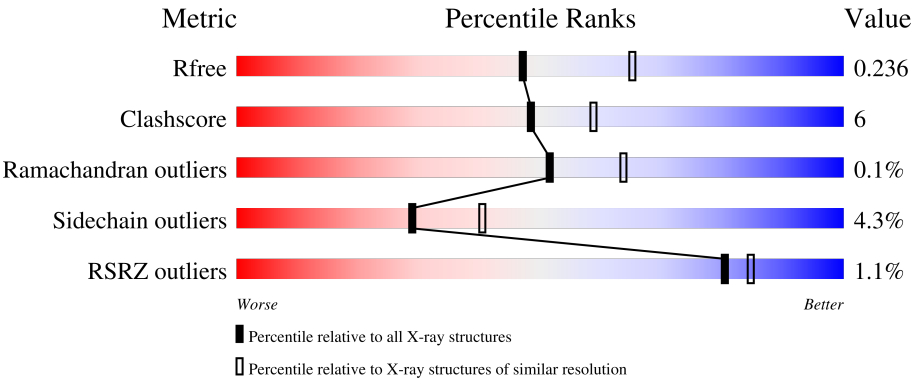
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	C	223	81% 14% 5%
1	H	223	80% 15%
2	D	213	84% 14%
2	L	213	90% 8%
3	A	21	86% 14%

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Mol	Chain	Length	Quality of chain
3	I	21	
4	B	30	
4	F	30	

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 15069 atoms, of which 7079 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 Heavy chain of analytical antibody S1 Fab.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	H	215	Total	C	H	N	O	S	0	2	0
			3277	1048	1616	280	327	6			
1	C	212	Total	C	H	N	O	S	0	0	0
			3213	1031	1585	272	319	6			

- Molecule 2 is a protein called Light chain of analytical antibody S1 Fab.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	L	211	Total	C	H	N	O	S	0	0	0
			3173	1011	1551	270	332	9			
2	D	211	Total	C	H	N	O	S	0	0	0
			3173	1011	1551	270	332	9			

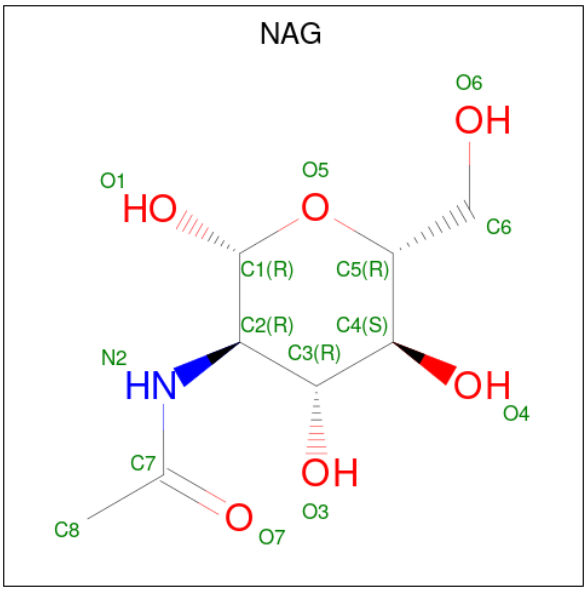
- Molecule 3 is a protein called Insulin A chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	I	21	Total	C	H	N	O	S	0	0	0
			312	99	149	25	35	4			
3	A	21	Total	C	H	N	O	S	0	0	0
			312	99	149	25	35	4			

- Molecule 4 is a protein called Insulin B chain.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
4	B	28	Total	C	H	N	O	S	0	0	0
			437	148	212	37	38	2			
4	F	28	Total	C	H	N	O	S	0	0	0
			438	148	213	37	38	2			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	H	1	Total C H N O 27 8 13 1 5	0	0
5	H	1	Total C H N O 27 8 13 1 5	0	0
5	C	1	Total C H N O 28 8 14 1 5	0	0
5	C	1	Total C H N O 27 8 13 1 5	0	0

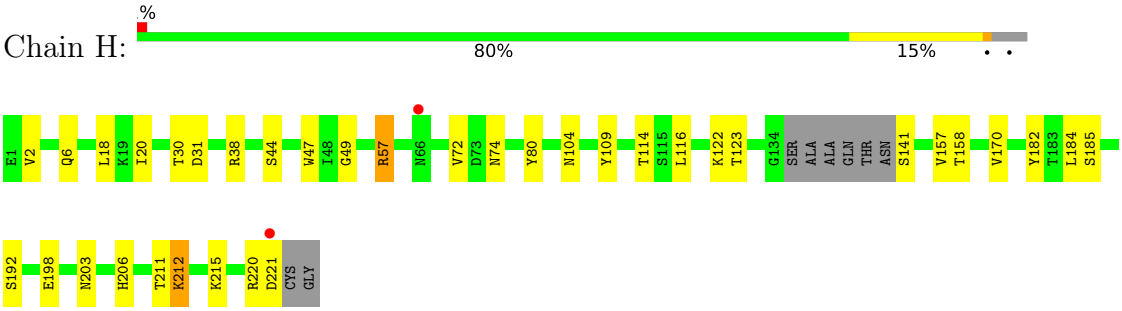
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	H	145	Total O 145 145	0	0
6	L	149	Total O 149 149	0	0
6	C	126	Total O 126 126	0	0
6	D	141	Total O 141 141	0	0
6	I	12	Total O 12 12	0	0
6	B	19	Total O 19 19	0	0
6	A	17	Total O 17 17	0	0
6	F	16	Total O 16 16	0	0

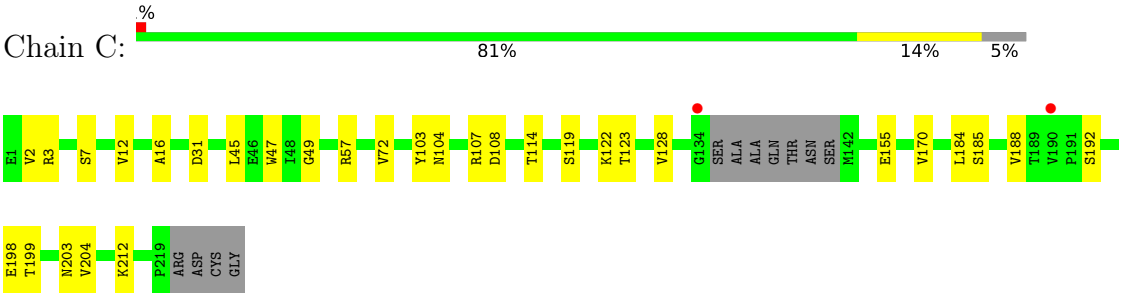
3 Residue-property plots (i)

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.

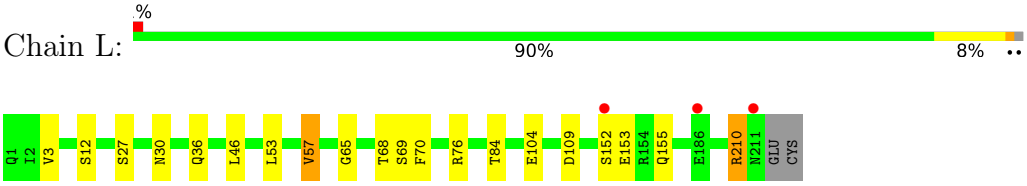
• Molecule 1: Heavy chain of analytical antibody S1 Fab



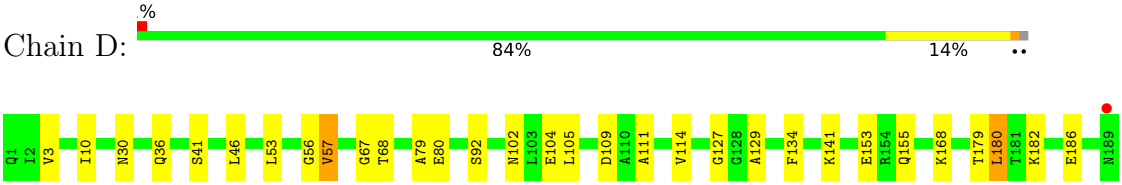
• Molecule 1: Heavy chain of analytical antibody S1 Fab

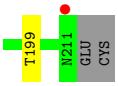


• Molecule 2: Light chain of analytical antibody S1 Fab



• Molecule 2: Light chain of analytical antibody S1 Fab



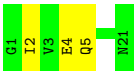


• Molecule 3: Insulin A chain

Chain I:

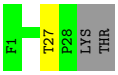
• Molecule 3: Insulin A chain

Chain A:



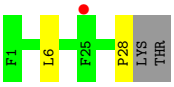
• Molecule 4: Insulin B chain

Chain B:



• Molecule 4: Insulin B chain

Chain F:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	83.31Å 71.90Å 99.64Å 90.00° 112.39° 90.00°	Depositor
Resolution (Å)	41.62 – 2.30 41.62 – 2.30	Depositor EDS
% Data completeness (in resolution range)	97.6 (41.62-2.30) 94.7 (41.62-2.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	6.72 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.197 , 0.237 0.197 , 0.236	Depositor DCC
R_{free} test set	2355 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å^2)	24.3	Xtriage
Anisotropy	0.413	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.37 , 43.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.47$, $< L^2 > = 0.30$	Xtriage
Estimated twinning fraction	0.048 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.93	EDS
Total number of atoms	15069	wwPDB-VP
Average B, all atoms (Å^2)	33.0	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 40.88 % 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 2.5646e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

[1] Intensities estimated from amplitudes.

[2] Theoretical 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.

5 Model quality

5.1 Standard geometry

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

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	C	0.55	0/1673	0.58	0/2284
1	H	0.59	0/1715	0.58	0/2339
2	D	0.58	0/1660	0.57	0/2257
2	L	0.56	0/1660	0.56	0/2257
3	A	0.60	0/164	0.48	0/220
3	I	0.62	0/164	0.44	0/220
4	B	0.62	0/232	0.55	0/314
4	F	0.59	0/232	0.54	0/314
All	All	0.58	0/7500	0.57	0/10205

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

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	C	1628	1585	1585	18	1
1	H	1661	1616	1602	24	0
2	D	1622	1551	1551	22	0
2	L	1622	1551	1551	12	0
3	A	163	149	149	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	I	163	149	149	2	0
4	B	225	212	212	0	1
4	F	225	213	212	1	0
5	C	28	27	26	2	0
5	H	28	26	26	2	0
6	A	17	0	0	5	0
6	B	19	0	0	0	1
6	C	126	0	0	10	1
6	D	141	0	0	10	0
6	F	16	0	0	1	0
6	H	145	0	0	9	0
6	I	12	0	0	1	2
6	L	149	0	0	9	2
All	All	7990	7079	7063	86	4

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 6.

The worst 5 of 86 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:C:31:ASP:OD1	6:C:401:HOH:O	1.82	0.95
2:L:210:ARG:NH2	6:L:302:HOH:O	2.04	0.90
1:C:119:SER:O	6:C:402:HOH:O	1.92	0.87
2:D:141:LYS:NZ	6:D:303:HOH:O	2.06	0.87
1:H:57:ARG:NH2	6:H:404:HOH:O	2.09	0.86

All (4) 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)
6:L:422:HOH:O	6:I:107:HOH:O[2_545]	2.05	0.15
1:C:3:ARG:NH2	4:B:27:THR:O[1_655]	2.13	0.07
6:C:463:HOH:O	6:I:112:HOH:O[1_655]	2.15	0.05
6:L:361:HOH:O	6:B:110:HOH:O[2_545]	2.19	0.01

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	C	208/223 (93%)	205 (99%)	3 (1%)	0	100 100
1	H	213/223 (96%)	205 (96%)	8 (4%)	0	100 100
2	D	209/213 (98%)	203 (97%)	5 (2%)	1 (0%)	29 35
2	L	209/213 (98%)	200 (96%)	9 (4%)	0	100 100
3	A	19/21 (90%)	18 (95%)	1 (5%)	0	100 100
3	I	19/21 (90%)	19 (100%)	0	0	100 100
4	B	26/30 (87%)	25 (96%)	1 (4%)	0	100 100
4	F	26/30 (87%)	26 (100%)	0	0	100 100
All	All	929/974 (95%)	901 (97%)	27 (3%)	1 (0%)	51 64

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	67	GLY

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	C	187/195 (96%)	178 (95%)	9 (5%)	25 36
1	H	192/195 (98%)	180 (94%)	12 (6%)	18 24
2	D	186/188 (99%)	181 (97%)	5 (3%)	44 61
2	L	186/188 (99%)	177 (95%)	9 (5%)	25 36

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
3	A	20/20 (100%)	20 (100%)	0	100 100
3	I	20/20 (100%)	20 (100%)	0	100 100
4	B	24/26 (92%)	24 (100%)	0	100 100
4	F	24/26 (92%)	23 (96%)	1 (4%)	30 42
All	All	839/858 (98%)	803 (96%)	36 (4%)	29 40

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	203	ASN
4	F	6	LEU
1	C	212	LYS
2	D	104	GLU
2	L	12	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	H	5	GLN
2	L	156	ASN
2	D	155	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)

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	$\#\|Z\| > 2$
5	NAG	H	301	-	14,14,15	0.29	0	17,19,21	0.47	0
5	NAG	C	302	1	14,14,15	0.67	1 (7%)	17,19,21	0.49	0
5	NAG	H	302	-	14,14,15	0.26	0	17,19,21	0.61	0
5	NAG	C	301	1	14,14,15	0.49	0	17,19,21	1.24	1 (5%)

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
5	NAG	H	301	-	-	1/6/23/26	0/1/1/1
5	NAG	C	302	1	-	4/6/23/26	0/1/1/1
5	NAG	H	302	-	-	4/6/23/26	0/1/1/1
5	NAG	C	301	1	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	302	NAG	O5-C1	2.03	1.47	1.43

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	C	301	NAG	C1-O5-C5	4.62	118.46	112.19

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	C	301	NAG	O5-C5-C6-O6
5	H	302	NAG	O5-C5-C6-O6
5	C	301	NAG	C4-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
5	C	302	NAG	O5-C5-C6-O6
5	C	302	NAG	C8-C7-N2-C2

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	H	301	NAG	2	0
5	C	302	NAG	1	0
5	C	301	NAG	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

6.1 Protein, DNA and RNA chains

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(Å^2)	Q<0.9
1	C	212/223 (95%)	0.23	2 (0%) 84 88	20, 32, 50, 64	0
1	H	215/223 (96%)	0.07	2 (0%) 84 88	20, 28, 39, 62	0
2	D	211/213 (99%)	0.02	2 (0%) 84 88	19, 28, 48, 61	0
2	L	211/213 (99%)	0.01	3 (1%) 75 80	20, 27, 49, 57	0
3	A	21/21 (100%)	0.20	0 100 100	22, 33, 42, 47	0
3	I	21/21 (100%)	-0.05	0 100 100	23, 30, 36, 38	0
4	B	28/30 (93%)	0.09	0 100 100	20, 22, 36, 46	0
4	F	28/30 (93%)	0.14	1 (3%) 42 49	19, 23, 44, 49	0
All	All	947/974 (97%)	0.09	10 (1%) 80 85	19, 29, 48, 64	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	134	GLY	3.4
1	H	221	ASP	2.9
4	F	25	PHE	2.6
2	L	152	SER	2.5
2	L	211	ASN	2.4

6.2 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

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	B-factors(Å^2)	Q<0.9
5	NAG	H	302	14/15	0.64	0.27	56,68,82,87	0
5	NAG	H	301	14/15	0.80	0.20	36,46,59,62	0
5	NAG	C	301	14/15	0.83	0.14	33,43,52,58	0
5	NAG	C	302	14/15	0.83	0.39	48,60,68,74	0

6.5 Other polymers

There are no such residues in this entry.