wwPDB X-ray Structure Validation Summary Report (i)

Jul 22, 2024 – 09:10 AM EDT

PDB ID	:	8TMY
Title	:	Crystal structure of SARS-CoV-2 spike stem helix peptide in complex with neutralizing antibody CHM-16
Authors	:	Feng, Z.; Wilson, I.A.
Deposited on	:	2023-07-31
Resolution	:	3.07 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 (1)) were used in the production of this report:

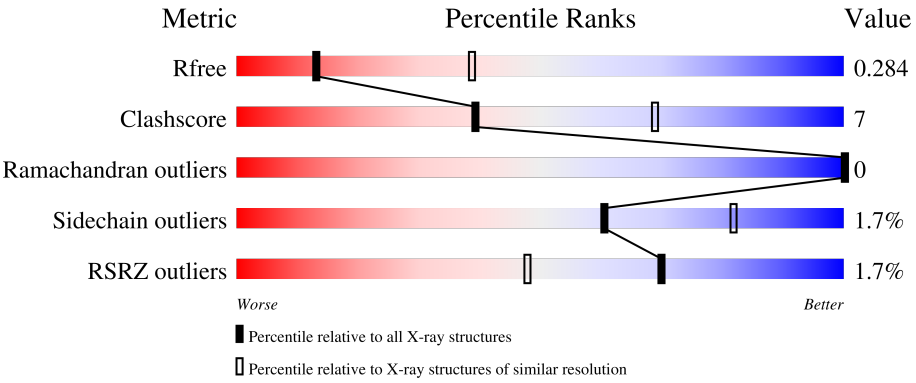
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.37.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

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 3.07 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	1447 (3.10-3.06)
Clashscore	141614	1546 (3.10-3.06)
Ramachandran outliers	138981	1487 (3.10-3.06)
Sidechain outliers	138945	1486 (3.10-3.06)
RSRZ outliers	127900	1416 (3.10-3.06)

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	M	25	44% · 52%
1	N	25	56% 8% 36%
1	S	25	44% · 52%
2	A	221	2% 85% 14%
2	C	221	4% 77% 20% ·

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Mol	Chain	Length	Quality of chain
2	H	221	80% 17%
3	B	212	% 81% 18%
3	D	212	3% 75% 25%
3	L	212	80% 19%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 10123 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 Stem helix peptide of Spike protein S2'.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	M	12	Total	C	N	O	2	1	0
			104	71	15	18			
1	N	16	Total	C	N	O	2	1	0
			137	91	21	25			
1	S	12	Total	C	N	O	0	0	0
			106	71	15	20			

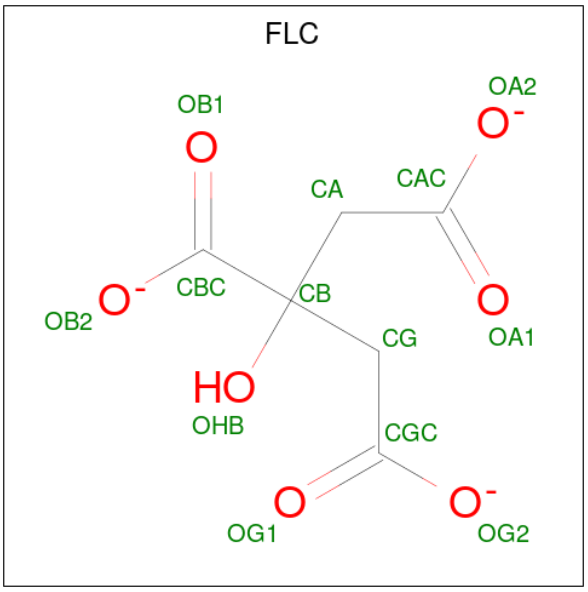
- Molecule 2 is a protein called Neutralizing antibody CHM-16 Heavy Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	213	Total	C	N	O	S	0	0	0
			1601	1011	274	310	6			
2	A	220	Total	C	N	O	S	0	0	0
			1647	1036	282	323	6			
2	C	214	Total	C	N	O	S	0	0	0
			1607	1014	275	312	6			

- Molecule 3 is a protein called Neutralizing antibody CHM-16 Light Chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	212	Total	C	N	O	S	0	0	0
			1636	1022	279	329	6			
3	B	212	Total	C	N	O	S	0	0	0
			1636	1022	279	329	6			
3	D	212	Total	C	N	O	S	0	0	0
			1636	1022	279	329	6			

- Molecule 4 is CITRATE ANION (three-letter code: FLC) (formula: $C_6H_5O_7$).



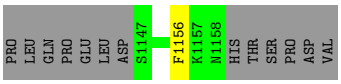
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C O 13 6 7	0	0

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.

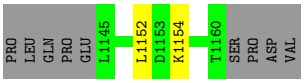
• Molecule 1: Stem helix peptide of Spike protein S2'

Chain M:



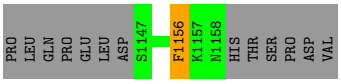
• Molecule 1: Stem helix peptide of Spike protein S2'

Chain N:



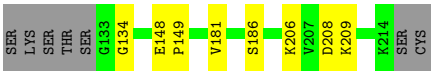
• Molecule 1: Stem helix peptide of Spike protein S2'

Chain S:



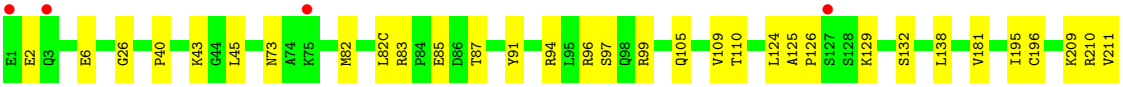
• Molecule 2: Neutralizing antibody CHM-16 Heavy Chain

Chain H:

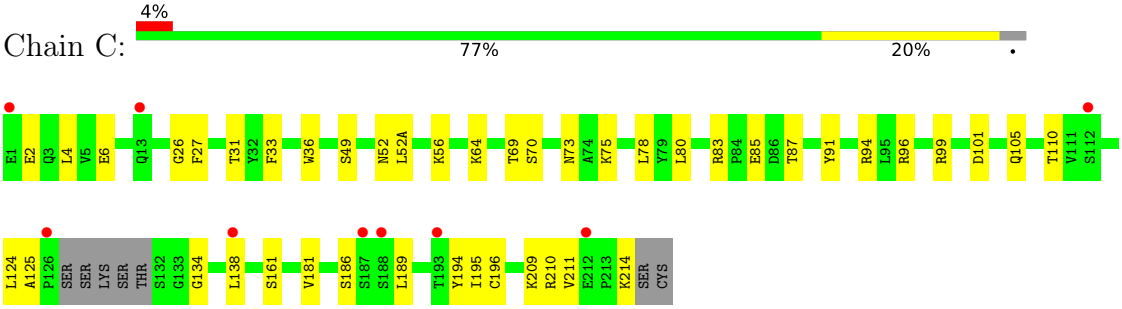


• Molecule 2: Neutralizing antibody CHM-16 Heavy Chain

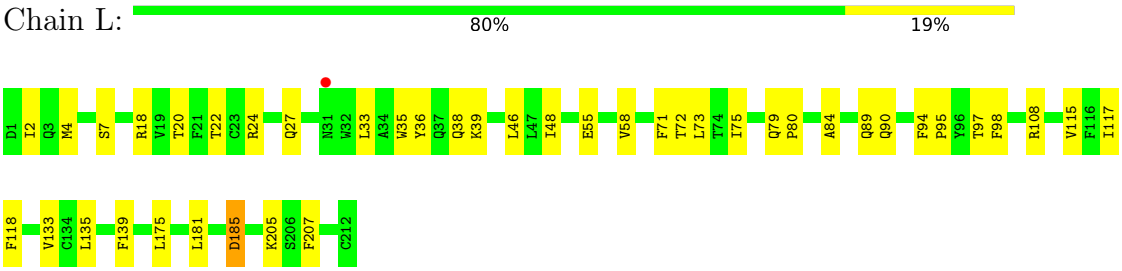
Chain A:



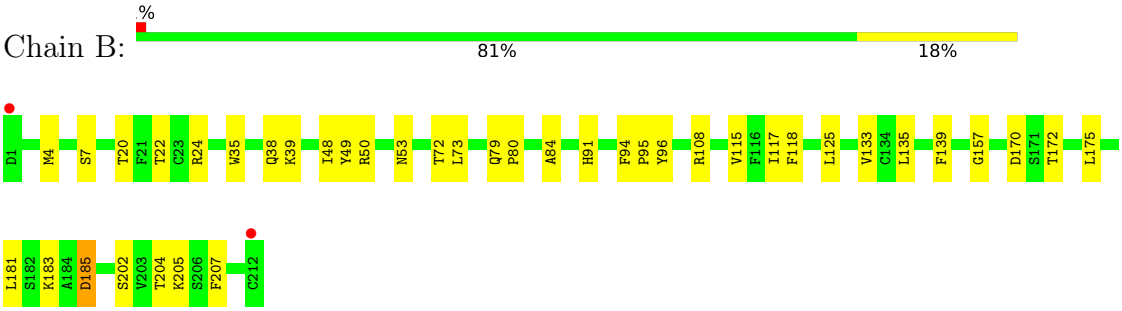
• Molecule 2: Neutralizing antibody CHM-16 Heavy Chain



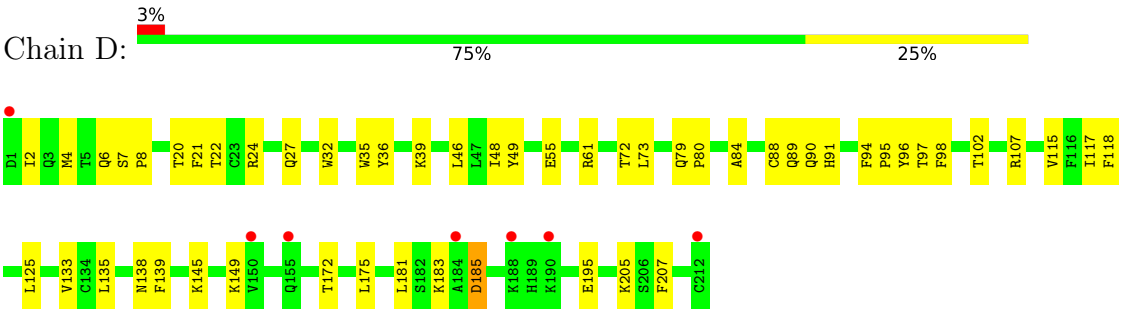
• Molecule 3: Neutralizing antibody CHM-16 Light Chain



• Molecule 3: Neutralizing antibody CHM-16 Light Chain



• Molecule 3: Neutralizing antibody CHM-16 Light Chain



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, α, β, γ	73.46Å 73.68Å 330.62Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	33.06 – 3.07 33.06 – 3.07	Depositor EDS
% Data completeness (in resolution range)	93.0 (33.06-3.07) 93.0 (33.06-3.07)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.59 (at 3.06Å)	Xtriage
Refinement program	PHENIX (1.19.2_4158: ???)	Depositor
R, R_{free}	0.243 , 0.286 0.243 , 0.284	Depositor DCC
R_{free} test set	2017 reflections (6.26%)	wwPDB-VP
Wilson B-factor (Å^2)	59.2	Xtriage
Anisotropy	0.703	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 49.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.42$, $< L^2 > = 0.25$	Xtriage
Estimated twinning fraction	0.055 for k,h,-l	Xtriage
F_o,F_c correlation	0.88	EDS
Total number of atoms	10123	wwPDB-VP
Average B, all atoms (Å^2)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.87% of the height of the origin peak. No significant pseudotranslation is detected.*

[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: FLC

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	M	0.25	0/109	0.27	0/143
1	N	0.24	0/143	0.36	0/190
1	S	0.25	0/108	0.29	0/141
2	A	0.25	0/1687	0.52	0/2295
2	C	0.25	0/1646	0.52	0/2239
2	H	0.25	0/1640	0.51	0/2231
3	B	0.25	0/1671	0.50	0/2270
3	D	0.25	0/1671	0.50	0/2270
3	L	0.25	0/1671	0.50	0/2270
All	All	0.25	0/10346	0.50	0/14049

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	M	104	0	97	0	0
1	N	137	0	126	2	0
1	S	106	0	99	1	0
2	A	1647	0	1611	25	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	1607	0	1570	32	0
2	H	1601	0	1565	23	0
3	B	1636	0	1578	27	0
3	D	1636	0	1578	34	0
3	L	1636	0	1578	26	0
4	B	13	0	5	0	0
All	All	10123	0	9807	148	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 7.

The worst 5 of 148 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:A:96:ARG:HG2	2:A:99:ARG:HG3	1.32	1.10
2:C:96:ARG:HD3	2:C:99:ARG:HG3	1.55	0.89
2:A:6:GLU:H	2:A:105:GLN:HE22	1.29	0.80
2:A:2:GLU:HA	2:A:26:GLY:HA3	1.68	0.76
3:L:139:PHE:HZ	3:L:175:LEU:HD13	1.53	0.74

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	Percentiles	
1	M	11/25 (44%)	11 (100%)	0	0	100	100
1	N	15/25 (60%)	15 (100%)	0	0	100	100
1	S	10/25 (40%)	10 (100%)	0	0	100	100
2	A	218/221 (99%)	205 (94%)	13 (6%)	0	100	100
2	C	210/221 (95%)	200 (95%)	10 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	H	209/221 (95%)	199 (95%)	10 (5%)	0	100	100
3	B	210/212 (99%)	202 (96%)	8 (4%)	0	100	100
3	D	210/212 (99%)	202 (96%)	8 (4%)	0	100	100
3	L	210/212 (99%)	202 (96%)	8 (4%)	0	100	100
All	All	1303/1374 (95%)	1246 (96%)	57 (4%)	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	M	10/25 (40%)	9 (90%)	1 (10%)	7	27
1	N	14/25 (56%)	14 (100%)	0	100	100
1	S	11/25 (44%)	10 (91%)	1 (9%)	9	31
2	A	184/187 (98%)	183 (100%)	1 (0%)	88	94
2	C	178/187 (95%)	176 (99%)	2 (1%)	73	88
2	H	177/187 (95%)	175 (99%)	2 (1%)	73	88
3	B	184/186 (99%)	180 (98%)	4 (2%)	52	76
3	D	184/186 (99%)	180 (98%)	4 (2%)	52	76
3	L	184/186 (99%)	180 (98%)	4 (2%)	52	76
All	All	1126/1194 (94%)	1107 (98%)	19 (2%)	60	82

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	C	161	SER
3	D	107	ARG
3	D	185	ASP
3	D	24	ARG
2	A	73	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates

There are no monosaccharides in this entry.

5.6 Ligand geometry

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	FLC	B	301	-	12,12,12	0.15	0	17,17,17	0.20	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	FLC	B	301	-	-	6/16/16/16	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	301	FLC	CA-CB-CBC-OB1
4	B	301	FLC	CA-CB-CBC-OB2
4	B	301	FLC	OHB-CB-CBC-OB1
4	B	301	FLC	OHB-CB-CBC-OB2
4	B	301	FLC	CB-CG-CGC-OG1

There are no ring outliers.

No monomer is involved in short contacts.

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	M	12/25 (48%)	0.22	0 100 100	68, 83, 97, 98	0
1	N	16/25 (64%)	0.12	0 100 100	56, 63, 77, 85	0
1	S	12/25 (48%)	0.01	0 100 100	63, 77, 88, 92	0
2	A	220/221 (99%)	0.03	4 (1%) 68 46	22, 59, 98, 127	0
2	C	214/221 (96%)	0.25	9 (4%) 36 18	33, 66, 96, 115	0
2	H	213/221 (96%)	-0.24	0 100 100	21, 49, 79, 97	0
3	B	212/212 (100%)	-0.12	2 (0%) 84 68	27, 49, 83, 120	0
3	D	212/212 (100%)	0.27	7 (3%) 46 24	35, 65, 111, 121	0
3	L	212/212 (100%)	-0.23	1 (0%) 91 80	25, 46, 88, 109	0
All	All	1323/1374 (96%)	-0.00	23 (1%) 70 48	21, 56, 95, 127	0

The worst 5 of 23 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	112	SER	5.0
3	B	1	ASP	4.6
3	D	190	LYS	4.1
2	A	1	GLU	3.7
3	D	150	VAL	3.1

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
4	FLC	B	301	13/13	0.83	0.26	68,78,96,104	0

6.5 Other polymers

There are no such residues in this entry.