

wwPDB X-ray Structure Validation Summary Report (i)

Nov 23, 2023 – 02:18 AM JST

PDB ID : 7Y8J

Title: 3D1 in complex with 6-mer HR1 peptide from SARS-CoV-2

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Resolution : 1.03 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 : 2.36

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)

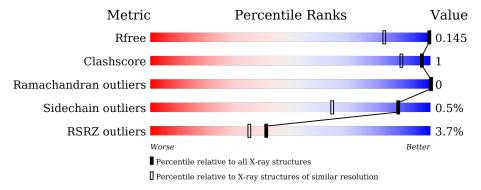
Validation Pipeline (wwPDB-VP) : 2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY\ DIFFRACTION$

The reported resolution of this entry is 1.03 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},\ {\rm resolution\ range}({\rm \AA})) \end{array}$
R_{free}	130704	1596 (1.10-0.98)
Clashscore	141614	1677 (1.10-0.98)
Ramachandran outliers	138981	1591 (1.10-0.98)
Sidechain outliers	138945	1589 (1.10-0.98)
RSRZ outliers	127900	1557 (1.10-0.98)

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	Н	122	95% 5%	
2	A	7	14%	•
3	L	114	99%	•



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4342 atoms, of which 1723 are hydrogens and 385 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 3D1.

Mol	Chain	Residues		Atoms						ZeroOcc	AltConf	Trace
1	Н	122	Total	C	D	Н	N	0	S	0	116	0
			2011	592	192	889	154	180	4			

• Molecule 2 is a protein called Spike protein S2'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace		
2	Λ	7	Total	С	D	Н	N	О	0	5	1	Ī
	A	1	100	27	11	41	10	11	0	5	1	

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	956	GLY	ALA	variant	UNP P0DTC2

• Molecule 3 is a protein called light chain of 3D1.

\mathbf{Mol}	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace	
3	L	114	Total 1801	C 511	D 182	H 793	N 135	O 178	S 2	0	107	0

• Molecule 4 is water.

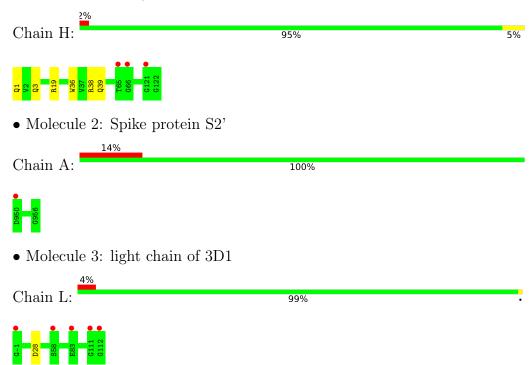
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	Н	204	Total O 204 204	0	0
4	A	14	Total O 14 14	0	0
4	L	212	Total O 212 212	0	0



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 3D1





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	36.97Å 69.81Å 51.06Å	Domositon
a, b, c, α , β , γ	90.00° 110.46° 90.00°	Depositor
Resolution (Å)	24.59 - 1.03	Depositor
Resolution (A)	24.58 - 1.03	EDS
% Data completeness	71.9 (24.59-1.03)	Depositor
(in resolution range)	71.9 (24.58-1.03)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.05 \; (at \; 1.03 \text{Å})$	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.134 , 0.145	Depositor
10, 10 free	0.134 , 0.145	DCC
R_{free} test set	1989 reflections (2.33%)	wwPDB-VP
Wilson B-factor (Å ²)	11.0	Xtriage
Anisotropy	0.170	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.39, 42.4	EDS
L-test for twinning ²	$< L > = 0.49, < L^2> = 0.32$	Xtriage
Estimated twinning fraction	0.032 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	4342	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 9.01% 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: PCA

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	Bo	nd lengths	Bond angles		
IVIOI	ol Chain $ \frac{1}{RMSZ} $		# Z > 5	RMSZ	# Z >5	
1	Н	1.46	22/1879~(1.2%)	0.94	$12/2555 \ (0.5\%)$	
2	A	0.51	0/86	0.64	0/117	
3	L	0.49	0/1612	0.72	0/2192	
All	All	1.11	22/3577~(0.6%)	0.84	12/4864 (0.2%)	

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	$\operatorname{Ideal}(ext{\AA})$
1	Н	38[B]	ARG	CZ-NH1	16.45	1.54	1.33
1	Н	38[C]	ARG	CZ-NH1	16.45	1.54	1.33
1	Н	38[A]	ARG	CZ-NH1	16.45	1.54	1.33
1	Н	38[B]	ARG	CZ-NH2	13.41	1.50	1.33
1	Н	38[C]	ARG	CZ-NH2	13.41	1.50	1.33

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$Ideal(^{o})$
1	Н	38[B]	ARG	CD-NE-CZ	-7.45	113.17	123.60
1	Н	38[C]	ARG	CD-NE-CZ	-7.45	113.17	123.60
1	Н	38[A]	ARG	CD-NE-CZ	-7.45	113.17	123.60
1	Н	19[B]	ARG	NE-CZ-NH2	6.03	123.32	120.30
1	Н	19[C]	ARG	NE-CZ-NH2	6.03	123.32	120.30

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	Н	1122	889	55	0	0
2	A	59	41	3	0	0
3	L	1008	793	87	0	0
4	A	14	0	0	0	0
4	Н	204	0	0	1	0
4	L	212	0	0	1	0
All	All	2619	1723	145	2	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 1.

All (2) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

A + a ma 1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	${ m distance} ({ m \AA})$	$overlap(\AA)$

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	ntiles
1	Н	$238/122 \ (195\%)$	236 (99%)	2 (1%)	0	100	100
2	A	10/7 (143%)	10 (100%)	0	0	100	100
3	L	217/114 (190%)	205 (94%)	12 (6%)	0	100	100
All	All	465/243 (191%)	451 (97%)	14 (3%)	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	Н	193/97~(199%)	193 (100%)	0	100	100	
2	A	11/6 (183%)	11 (100%)	0	100	100	
3	L	177/92 (192%)	175 (99%)	2 (1%)	73	41	
All	All	381/195 (195%)	379 (100%)	2 (0%)	88	65	

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	L	28[A]	ASP
3	L	28[B]	ASP

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

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

1 non-standard protein/DNA/RNA residue 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	pe Chain	Res	Pos	Ros Ii	Link	Bond lengths			Bond angles		
					Link	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2		
	1	PCA	Н	1	1	7,8,9	1.22	1 (14%)	9,10,12	1.57	3 (33%)		

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	Н	1	1	-	0/0/11/13	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(A)	$Ideal(\AA)$
1	Н	1	PCA	CA-N	-2.57	1.43	1.46

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$Ideal(^{o})$
1	Н	1	PCA	O-C-CA	-2.73	117.63	124.78
1	Н	1	PCA	CB-CA-C	-2.50	109.27	112.70
1	Н	1	PCA	OE-CD-CG	-2.07	123.15	126.76

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)

There are no ligands in this entry.

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>	# RSRZ > 2	$OWAB(Å^2)$	Q<0.9
1	Н	121/122~(99%)	0.04	3 (2%) 57 50	9, 11, 20, 49	0
2	A	7/7 (100%)	0.67	1 (14%) 2 6	10, 14, 18, 34	0
3	L	114/114 (100%)	0.09	5 (4%) 34 29	9, 12, 23, 60	0
All	All	242/243 (99%)	0.08	9 (3%) 41 35	9, 12, 23, 60	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	950	ASP	5.1
1	Н	121[A]	GLY	4.5
3	L	112[A]	GLY	3.4
1	Н	65[A]	THR	3.3
3	L	58[A]	SER	3.0

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^{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
1	PCA	Η	1	8/9	0.93	0.13	14,22,34,34	0

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.



6.4 Ligands (i)

There are no ligands in this entry.

6.5 Other polymers (i)

There are no such residues in this entry.

