

# wwPDB X-ray Structure Validation Summary Report (i)

#### Nov 22, 2023 – 11:50 AM JST

PDB ID	:	7VMU
Title	:	Crystal Structure of SARS-CoV Spike Receptor-Binding Domain Complexed
		with Neutralizing Antibody
Authors	:	Guo, Y.; Wang, W.; Jiao, P.; Yang, H.; Rao, Z.; Cheng, G.
Deposited on	:	2021-10-09
Resolution	:	2.89  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:

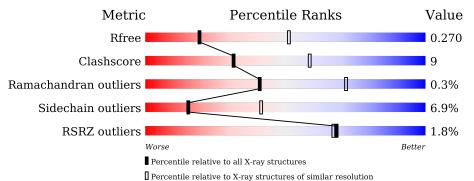
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
$\mathrm{EDS}$	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)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

# 1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.89 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	$\begin{array}{c} \textbf{Whole archive} \\ \textbf{(\#Entries)} \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R <sub>free</sub>	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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	А	245	65%	25%	10%			
2	В	181	73%	23%	••			



## 2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 3064 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 scFv E4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	А	220	Total 1659	C 1039	N 285	0 327	S 8	0	0	0

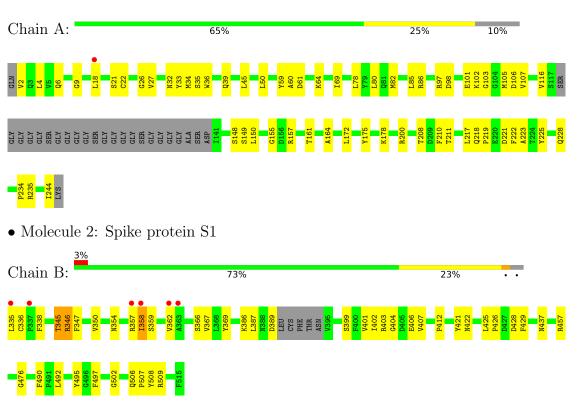
• Molecule 2 is a protein called Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	В	176	Total 1405	C 902	N 234	O 263	S 6	0	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: scFv E4



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 2 2	Depositor
Cell constants	97.02Å 97.02Å 93.24Å	Deperitor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	43.39 - 2.89	Depositor
Resolution (A)	43.39 - 2.89	EDS
% Data completeness	90.7 (43.39-2.89)	Depositor
(in resolution range)	90.7(43.39-2.89)	EDS
R <sub>merge</sub>	0.15	Depositor
$\frac{\mathrm{R}_{sym}}{< I/\sigma(I) > 1}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	$1.70 (at 2.90 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
D D	0.241 , $0.273$	Depositor
$R, R_{free}$	0.244 , $0.270$	DCC
R <sub>free</sub> test set	497 reflections $(5.24\%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	56.3	Xtriage
Anisotropy	0.143	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.36, 31.1	EDS
L-test for twinning <sup>2</sup>	$<  L  > = 0.49, < L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.019 for -h,-l,-k	Xtriage
Estimated twinning fraction	0.013 for l,-k,h	Attrage
$\mathbf{F}_o, \mathbf{F}_c$ correlation	0.89	EDS
Total number of atoms	3064	wwPDB-VP
Average B, all atoms $(Å^2)$	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.49% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;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.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 5 Model quality (i)

### 5.1 Standard geometry (i)

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		lengths	Bond angles		
		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	А	0.47	0/1693	0.70	0/2298	
2	В	0.66	0/1444	0.73	0/1961	
All	All	0.57	0/3137	0.71	0/4259	

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 (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	А	1659	0	1622	36	0
2	В	1405	0	1327	19	0
All	All	3064	0	2949	54	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 9.

The worst 5 of 54 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:35:SER:HB3	1:A:50:LEU:HD23	1.56	0.88	
1:A:82:MET:HB3	1:A:85:LEU:HD11	1.58	0.85	

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)	
1:A:59:TYR:HB2	1:A:64:LYS:HG2	1.71	0.72	
1:A:178:LYS:HG2	1:A:223:ALA:HB2	1.79	0.64	
1:A:161:THR:HG22	1:A:211:THR:HG22	1.81	0.63	

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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	А	216/245~(88%)	197 (91%)	18 (8%)	1 (0%)	29	61	
2	В	172/181~(95%)	156 (91%)	16~(9%)	0	100	100	
All	All	388/426~(91%)	353~(91%)	34~(9%)	1 (0%)	41	71	

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	А	103	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	А	182/190~(96%)	176~(97%)	6 (3%)	38 72
2	В	152/157~(97%)	135~(89%)	17 (11%)	6 18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	334/347~(96%)	311~(93%)	23~(7%)	15 41

5 of 23 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	В	362	VAL
2	В	369	TYR
2	В	367	VAL
2	В	386	LYS
2	В	335	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	А	229	GLN
2	В	388	ASN
2	В	498	GLN
1	А	166	GLN
1	А	32	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)

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	$\langle RSRZ \rangle$	#RSRZ>2	$OWAB(Å^2)$	Q < 0.9
1	А	220/245~(89%)	0.07	1 (0%) 91 91	31, 45, 64, 75	0
2	В	176/181~(97%)	0.03	6 (3%) 45 40	30, 47, 82, 92	0
All	All	396/426~(92%)	0.05	7 (1%) 68 67	30, 46, 75, 92	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	В	362	VAL	5.0
2	В	335	LEU	2.9
2	В	357	ARG	2.7
2	В	363	ALA	2.7
2	В	358	ILE	2.4

#### 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)

There are no ligands in this entry.

#### 6.5 Other polymers (i)

There are no such residues in this entry.

