

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

May 9, 2022 – 11:28 am BST

PDB ID	:	$7 \mathrm{QEZ}$
Title	:	Crystal structure of the SARS-CoV-2 RBD in complex with the ultrapotent
		antibody CV2.1169 and CR3022
Authors	:	Fernandez, I.; Rey, F.A.
Deposited on	:	2021-12-03
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 following versions of software and data (see references (1)) were used in the production of this report:

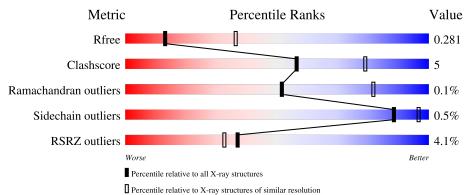
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.28.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0267
CCP4	:	7.1.010 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber $(2001)$
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.28.1

# 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
$R_{free}$	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 cha	in	
1	А	206	3%		89%		6% 5%
2	Е	229	3%		80%		13% 7%
3	F	221			85%		14% •
4	Н	225	3%	45%	10%	45%	
5	L	215	7%	43%	7%	50%	



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
7	SO4	L	301	-	-	Х	-



# 2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 6633 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 Spike protein S1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	А	196	Total 1552	C 997	N 259	0 288	S 8	0	0	0

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
А	367	PHE	VAL	variant	UNP P0DTC2
А	529	GLY	-	expression tag	UNP P0DTC2
А	530	SER	-	expression tag	UNP P0DTC2
А	531	GLY	-	expression tag	UNP P0DTC2
А	532	ASP	-	expression tag	UNP P0DTC2
А	533	ASP	-	expression tag	UNP P0DTC2
А	534	ASP	-	expression tag	UNP P0DTC2
А	535	ASP	-	expression tag	UNP P0DTC2
А	536	LYS	-	expression tag	UNP P0DTC2

• Molecule 2 is a protein called CR3022 heavy chain.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
2	Е	214	Total 1596	C 1016	N 259	0 313	S 8	46	0	0

• Molecule 3 is a protein called CR3022 light chain.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
3	F	218	Total	С	Ν	0	$\mathbf{S}$	24	0	0
	1	210	1694	1065	281	344	4	21	0	V

• Molecule 4 is a protein called CV2.1169 IgA heavy chain.

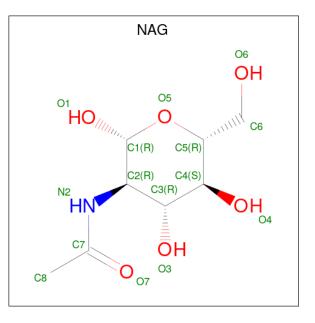


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
4	Н	123	Total 941	C 589	N 161	O 184	S 7	0	0	0

• Molecule 5 is a protein called CV2.1169 light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	L	108	Total 830	C 522	N 142	0 164	${ m S} { m 2}$	0	0	0

• Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	А	1	Total         C         N         O           14         8         1         5	0	0

• Molecule 7 is SULFATE ION (three-letter code: SO4) (formula:  $O_4S$ ).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	L	1	Total 5	0 4	S 1	0	0

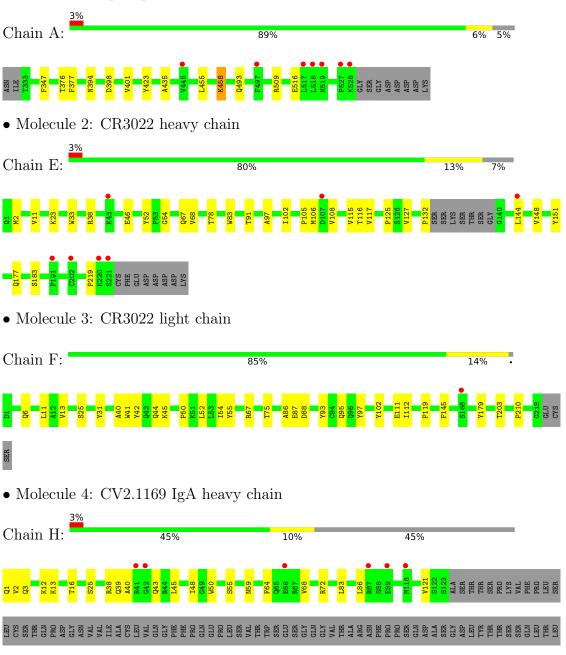
• Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	А	1	Total O 1 1	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.

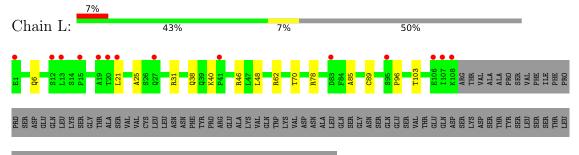


• Molecule 1: Spike protein S1



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 $\bullet$  Molecule 5: CV2.1169 light chain





## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41	Depositor
Cell constants	97.75Å 97.75Å 164.47Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	$90.00^{\circ}$ $90.00^{\circ}$ $90.00^{\circ}$	Depositor
Resolution (Å)	48.88 - 2.89	Depositor
Resolution (A)	48.88 - 2.88	EDS
% Data completeness	$99.8 \ (48.88 - 2.89)$	Depositor
(in resolution range)	93.1 (48.88-2.88)	EDS
R <sub>merge</sub>	0.26	Depositor
R <sub>sym</sub>	(Not available)	Depositor
$< I/\sigma(I) > 1$	$0.57 (at 2.91 \text{\AA})$	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
D D.	0.239 , $0.281$	Depositor
$R, R_{free}$	0.239 , $0.281$	DCC
$R_{free}$ test set	1794 reflections $(5.19%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	72.1	Xtriage
Anisotropy	0.049	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	(Not available), (Not available)	EDS
L-test for $twinning^2$	$< L >=0.42, < L^2>=0.25$	Xtriage
Estimated twinning fraction	0.188 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	6633	wwPDB-VP
Average B, all atoms $(Å^2)$	91.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 2.89% 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)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG, SO4

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	А	0.26	0/1597	0.43	0/2173	
2	Е	0.26	0/1637	0.48	0/2230	
3	F	0.25	0/1732	0.44	0/2355	
4	Н	0.24	0/960	0.46	0/1303	
5	L	0.27	0/850	0.46	0/1154	
All	All	0.26	0/6776	0.45	0/9215	

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	1552	0	1468	8	0
2	Ε	1596	0	1574	19	0
3	F	1694	0	1643	18	0
4	Н	941	0	915	14	0
5	L	830	0	808	10	0
6	А	14	0	13	0	0
7	L	5	0	0	3	0
8	А	1	0	0	0	0
All	All	6633	0	6421	65	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 5.

The worst 5 of 65 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)
4:H:2:VAL:HA	4:H:25:SER:O	1.85	0.77
2:E:2:MET:HB3	2:E:108:VAL:HG21	1.67	0.76
2:E:102:ILE:O	3:F:102:TYR:OH	2.11	0.69
2:E:91:THR:HG22	2:E:117:VAL:H	1.58	0.66
4:H:1:GLN:OE1	4:H:3:GLN:NE2	2.26	0.64

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	А	194/206~(94%)	182 (94%)	12~(6%)	0	100	100
2	Ε	210/229~(92%)	202 (96%)	8 (4%)	0	100	100
3	F	216/221~(98%)	207~(96%)	9~(4%)	0	100	100
4	Н	121/225~(54%)	117 (97%)	4(3%)	0	100	100
5	L	106/215~(49%)	97~(92%)	8 (8%)	1 (1%)	17	48
All	All	847/1096~(77%)	805~(95%)	41 (5%)	1 (0%)	51	82

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	L	96	PRO



#### 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 side chain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Analysed Rotameric Outliers		Percentiles		
1	А	168/177~(95%)	166 (99%)	2(1%)	71 91		
2	Е	180/194~(93%)	180 (100%)	0	100 100		
3	F	193/196~(98%)	192 (100%)	1 (0%)	88 96		
4	Н	103/193~(53%)	102 (99%)	1 (1%)	76 92		
5	L	91/187~(49%)	91 (100%)	0	100 100		
All	All	735/947~(78%)	731 (100%)	4 (0%)	88 96		

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	377	PHE
1	А	458	LYS
3	F	31	TYR
4	Н	72	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	А	394	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)

2 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).

Mal	Mol Type Chain H		Chain Res Link		Bo	Bond lengths			ond ang	les
Mol Type Chain	Unam	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z  > 2	
7	SO4	L	301	-	4,4,4	0.13	0	6,6,6	0.07	0
6	NAG	А	601	1	14,14,15	0.23	0	17,19,21	0.40	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
6	NAG	А	601	1	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	L	301	SO4	3	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 (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	$\mathbf{OWAB}(\mathbf{\AA}^2)$	$\mathbf{Q}{<}0.9$
1	А	196/206~(95%)	0.34	7 (3%) 42 37	49, 84, 143, 181	0
2	Е	207/229~(90%)	0.35	7 (3%) 45 40	54, 79, 119, 177	0
3	F	214/221~(96%)	0.20	1 (0%) 91 91	53, 80, 114, 141	0
4	Н	123/225~(54%)	0.25	6 (4%) 29 26	56, 96, 139, 173	0
5	L	108/215~(50%)	0.73	14 (12%) 3 2	77, 116, 174, 208	0
All	All	848/1096~(77%)	0.34	35 (4%) 37 32	49, 86, 145, 208	0

The worst 5 of 35 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	А	518	LEU	5.8
5	L	107	ILE	5.7
5	L	13	LEU	5.6
5	L	12	SER	4.7
2	Ε	43	LYS	4.6

### 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,



Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
6	NAG	А	601	14/15	0.76	0.32	108,119,130,130	0
7	SO4	L	301	5/5	0.97	0.12	94,96,103,109	0

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.

### 6.5 Other polymers (i)

There are no such residues in this entry.

