

wwPDB X-ray Structure Validation Summary Report (i)

May 18, 2023 – 04:04 PM EDT

PDB ID : 8GB8

Title: Crystal structure of SARS-CoV-2 BA.2 receptor binding domain in complex

with neutralizing antibody 20A7

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Deposited on : 2023-02-24

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 (1)) were used in the production of this report:

 $Mol Probity \quad : \quad 4.02b\text{--}467$

Mogul: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.32.2

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)

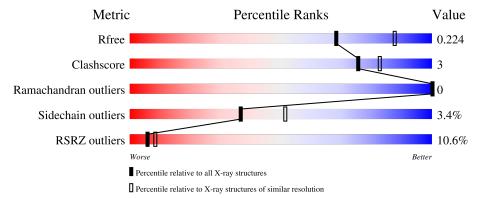
Validation Pipeline (wwPDB-VP) : 2.32.2

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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries},{\rm resolution\ range}(\mathring{\rm A})) \end{array}$
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	Е	231	74%	6 16%
2	Н	224	88%	8% •
3	L	214	88%	10% •



2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 5044 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.

\mathbf{Mol}	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace	
1	E	195	Total 1555	C 1004	N 262	O 281	S 8	0	0	0	

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Е	339	ASP	GLY	variant	UNP P0DTC2
E	371	PHE	SER	variant	UNP P0DTC2
Е	373	PRO	SER	variant	UNP P0DTC2
Е	375	PHE	SER	variant	UNP P0DTC2
Е	376	ALA	THR	variant	UNP P0DTC2
Е	405	ASN	ASP	variant	UNP P0DTC2
Е	408	SER	ARG	variant	UNP P0DTC2
Е	417	ASN	LYS	variant	UNP P0DTC2
Е	440	LYS	ASN	variant	UNP P0DTC2
Е	477	ASN	SER	variant	UNP P0DTC2
Е	478	LYS	THR	variant	UNP P0DTC2
E	484	ALA	GLU	variant	UNP P0DTC2
Е	493	ARG	GLN	variant	UNP P0DTC2
Е	498	ARG	GLN	variant	UNP P0DTC2
Е	501	TYR	ASN	variant	UNP P0DTC2
Е	505	HIS	TYR	variant	UNP P0DTC2
Е	542	SER	-	expression tag	UNP P0DTC2
Е	543	GLY	-	expression tag	UNP P0DTC2
Е	544	HIS	-	expression tag	UNP P0DTC2
Е	545	HIS	-	expression tag	UNP P0DTC2
Е	546	HIS	-	expression tag	UNP P0DTC2
Е	547	HIS	-	expression tag	UNP P0DTC2
Е	548	HIS	-	expression tag	UNP P0DTC2
Е	549	HIS	-	expression tag	UNP P0DTC2

• Molecule 2 is a protein called 20A7 Heavy chain.

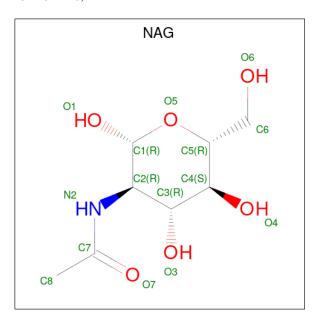


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
2	Н	217	Total 1628	C 1024	N 279	O 319	S	0	0	0

• Molecule 3 is a protein called 20A7 Light chain.

Mol	Chain	Residues		\mathbf{At}	oms			ZeroOcc	AltConf	Trace
3	L	211	Total 1624	C 1018	N 277	O 325	S 4	0	1	0

 \bullet Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $\rm C_8H_{15}NO_6).$



Mol	Chain	Residues	A	tor	ns		ZeroOcc	AltConf
4	Е	1	Total 14	C 8	N 1	O 5	0	0

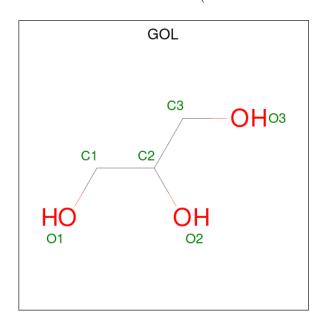
 \bullet Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $\mathrm{C_2H_6O_2}).$





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	E	1	Total C O 4 2 2	0	0
5	L	1	Total C O 4 2 2	0	0
5	L	1	Total C O 4 2 2	0	0

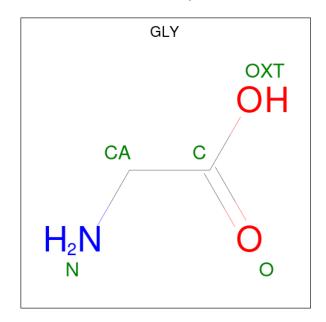
 \bullet Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $\mathrm{C_3H_8O_3}).$



Mol	Chain	Residues	Aton	ns	ZeroOcc	AltConf
6	L	1	Total (C O 3	0	0

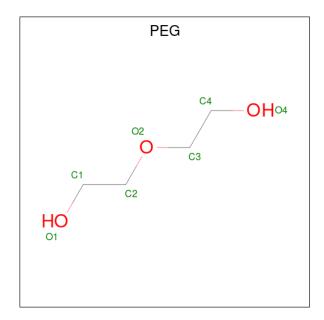


 \bullet Molecule 7 is GLYCINE (three-letter code: GLY) (formula: $\mathrm{C_2H_5NO_2}).$



Mol	Chain	Residues	A	tor	ns		ZeroOcc	AltConf
7	L	1	Total 4	C 2	N 1	O 1	0	0

• Molecule 8 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	L	1	Total C O 7 4 3	0	0

• Molecule 9 is water.



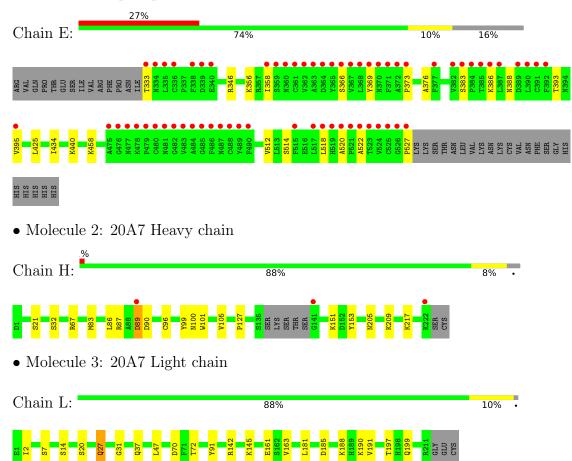
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	Е	27	Total O 27 27	0	0
9	Н	88	Total O 88 88	0	0
9	L	79	Total O 79 79	0	0



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





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	44.54Å 132.18Å 170.47Å	Donositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.10 - 2.30	Depositor
Resolution (A)	43.10 - 2.30	EDS
% Data completeness	99.3 (43.10-2.30)	Depositor
(in resolution range)	99.3 (43.10-2.30)	EDS
R_{merge}	0.99	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.29 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.19.2	Depositor
D D.	0.200 , 0.228	Depositor
R, R_{free}	0.195 , 0.224	DCC
R_{free} test set	2321 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	44.8	Xtriage
Anisotropy	0.449	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.33, 46.0	EDS
L-test for twinning ²	$ < L >=0.48, < L^2>=0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5044	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.85% 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: GOL, NAG, EDO, PEG

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	Bo	nd angles
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	Е	0.26	0/1602	0.49	1/2180 (0.0%)
2	Н	0.25	0/1665	0.50	0/2270
3	L	0.26	0/1661	0.52	0/2260
All	All	0.25	0/4928	0.50	1/6710 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$Ideal(^{o})$
1	Ε	527	PRO	N-CA-CB	6.07	110.58	103.30

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	Е	1555	0	1473	10	0
2	Н	1628	0	1594	8	0
3	L	1624	0	1580	12	0
4	Е	14	0	13	0	0
5	Е	4	0	6	0	0
5	L	8	0	12	0	0
6	L	6	0	8	0	0

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	.,	10	1

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	L	4	0	2	0	0
8	L	7	0	10	0	0
9	Ε	27	0	0	2	0
9	Н	88	0	0	2	0
9	L	79	0	0	5	0
All	All	5044	0	4698	30	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 3.

The worst 5 of 30 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
1:E:373:PRO:O	9:E:701:HOH:O	1.95	0.83
3:L:72:THR:OG1	9:L:401:HOH:O	2.07	0.73
1:E:514:SER:OG	9:E:702:HOH:O	2.06	0.72
3:L:199:GLN:OE1	9:L:403:HOH:O	2.15	0.63
3:L:2:ILE:HG12	3:L:27:GLN:HG2	1.82	0.61

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	E	193/231 (84%)	185 (96%)	8 (4%)	0	100	100
2	Н	213/224 (95%)	211 (99%)	2 (1%)	0	100	100
3	L	210/214 (98%)	205 (98%)	5 (2%)	0	100	100
All	All	616/669 (92%)	601 (98%)	15 (2%)	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	${f E}$	166/202~(82%)	160 (96%)	6 (4%)	35	49	
2	Н	184/191 (96%)	177 (96%)	7 (4%)	33	47	
3	L	182/183 (100%)	177 (97%)	5 (3%)	44	61	
All	All	532/576 (92%)	514 (97%)	18 (3%)	37	51	

5 of 18 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	L	14	SER
3	L	181	LEU
3	L	27	GLN
2	Н	89	ASP
3	L	7	SER

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)

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)

7 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	Mol Type Chain R		hain Res Link		Вс	Bond lengths			Bond angles		
MIOI	Type	Chain	res	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
5	EDO	Е	602	-	3,3,3	0.47	0	2,2,2	0.34	0	
6	GOL	L	301	-	5,5,5	0.89	0	5,5,5	1.01	0	
7	GLY	L	302	-	3,3,4	0.63	0	0,2,4	-	-	
5	EDO	L	305	-	3,3,3	0.45	0	2,2,2	0.33	0	
5	EDO	L	304	-	3,3,3	0.45	0	2,2,2	0.37	0	
8	PEG	L	303	-	6,6,6	0.10	0	5,5,5	0.09	0	
4	NAG	Е	601	1	14,14,15	0.26	0	17,19,21	0.39	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
5	EDO	E	602	-	-	0/1/1/1	-
6	GOL	L	301	-	-	2/4/4/4	-
7	GLY	L	302	-	-	0/0/1/2	-
5	EDO	L	305	-	-	0/1/1/1	-
5	EDO	L	304	-	-	0/1/1/1	-
8	PEG	L	303	-	-	1/4/4/4	-
4	NAG	Е	601	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

N.	Iol	Chain	Res	Type	Atoms	
	6	L	301	GOL	O1-C1-C2-O2	

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Mol	Chain	Res	Type	Atoms
4	Е	601	NAG	O5-C5-C6-O6
6	L	301	GOL	O1-C1-C2-C3
8	L	303	PEG	O2-C3-C4-O4
4	Е	601	NAG	C4-C5-C6-O6

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 (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 > 2	$\mathbf{OWAB}(\mathbf{\mathring{A}}^2)$	Q < 0.9
1	E	195/231~(84%)	1.55	63 (32%) 0 0	35, 67, 132, 146	0
2	Н	217/224 (96%)	0.02	3 (1%) 75 80	29, 43, 66, 95	0
3	L	211/214 (98%)	-0.09	0 100 100	28, 43, 67, 74	0
All	All	623/669 (93%)	0.46	66 (10%) 6 8	28, 47, 121, 146	0

The worst 5 of 66 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	Е	368	LEU	13.3
1	Е	387	LEU	8.0
1	Е	517	LEU	8.0
1	Е	363	ALA	7.8
1	Е	362	VAL	7.6

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, 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
4	NAG	Е	601	14/15	0.45	0.38	64,130,136,140	0
7	GLY	L	302	4/5	0.72	0.21	75,79,86,91	0
5	EDO	L	304	4/4	0.89	0.17	45,63,64,65	0
5	EDO	L	305	4/4	0.90	0.19	53,68,73,75	0
6	GOL	L	301	6/6	0.92	0.18	46,50,61,68	0
5	EDO	Е	602	4/4	0.95	0.14	52,54,55,63	0
8	PEG	L	303	7/7	0.95	0.15	37,46,50,66	0

6.5 Other polymers (i)

There are no such residues in this entry.

