

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

#### Aug 8, 2020 – 11:48 PM BST

PDB ID : 4ZPV

Title: Structure of MERS-Coronavirus Spike Receptor-binding Domain (England1

Strain) in Complex with Vaccine-Elicited Murine Neutralizing Antibody D12

(Crystal Form 2)

Authors: Joyce, M.G.; Mascola, J.R.; Graham, B.S.; Kwong, P.D.

Deposited on : 2015-05-08

Resolution : 3.20 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 : 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.13.1

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)

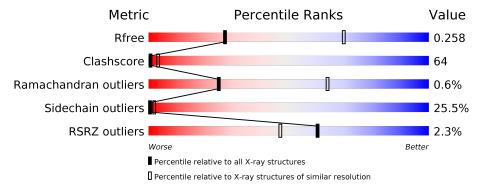
Validation Pipeline (wwPDB-VP) : 2.13.1

## 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 3.20 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar \; resolution} \\ (\#{\rm Entries, \; resolution \; range(\AA)}) \end{array}$
$R_{free}$	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 on 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	A	216	38%	45%	15%	<del>.</del> .		
1	Н	216	40%	42%	16%	<del>-</del> .		
2	В	214	43%	39%	16%	<del>.</del>		
2	L	214	36%	46%	18%	•		
3	R	208	% 45%	42%	13%			
3	S	208	36%	43%	19%			



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
4	NAG	R	601	X	-	-	-
4	NAG	R	602	-	-	-	X



# 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 9733 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 D12 Fab Heavy chain.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
1	Н	213	Total 1595	C 1005	N 259	() 322	S	0	0	0
						022	9			
1	Δ	213	l Total	С	Ν	O	S	0	0	0
1		210	1594	1004	260	321	9			

• Molecule 2 is a protein called D12 Fab light chain.

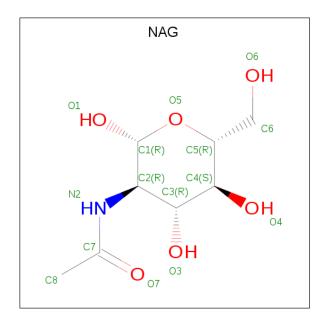
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace	
2	T.	212	Total	С	N	О	S	0	0	0
	L	212	1651	1023	282	340	6	U	0	
9	D	212	Total	С	N	О	S	0	0	0
	Б	212	1651	1023	282	340	6	0	U	

• Molecule 3 is a protein called Spike glycoprotein.

Mol	Chain	Residues	${f Atoms}$				ZeroOcc	AltConf	Trace	
3	S	207		C 1023	= -	O 314	S 11	0	0	0
3	R	208	Total 1611	C 1029		O 315	S 11	0	0	0

• Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).





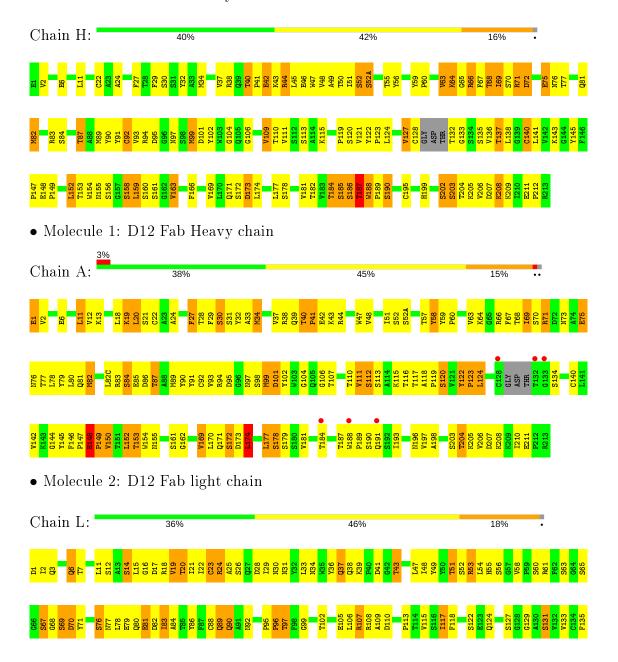
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	R	1	Total C N O 14 8 1 5	0	0
4	R	1	Total C N O 14 8 1 5	0	0



## 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: D12 Fab Heavy chain

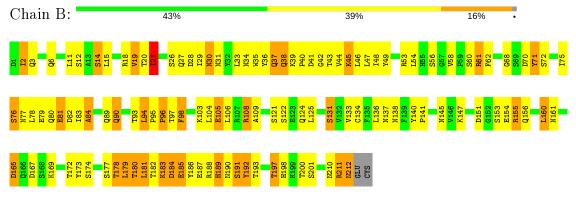




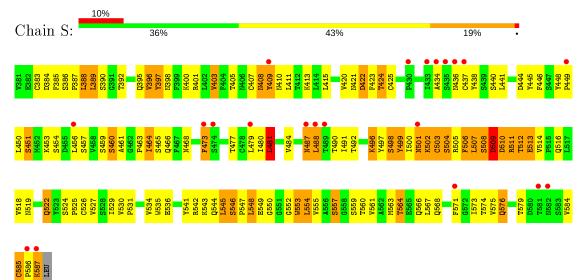
 $4\mathrm{ZPV}$ 



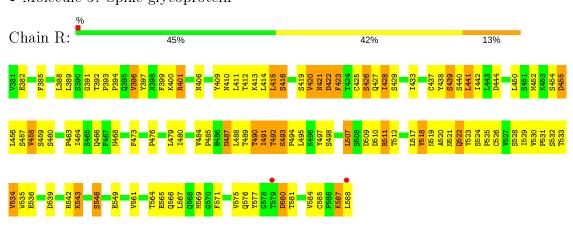
• Molecule 2: D12 Fab light chain



• Molecule 3: Spike glycoprotein



• Molecule 3: Spike glycoprotein





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	76.18Å 106.14Å 171.07Å	Depositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.55 - 3.20	Depositor
resolution (A)	43.55 - 3.20	EDS
% Data completeness	82.3 (43.55-3.20)	Depositor
(in resolution range)	75.7 (43.55-3.20)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.03 (at 3.19Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
D D.	0.223 , 0.281	Depositor
$R, R_{free}$	0.233 , $0.258$	DCC
$R_{free}$ test set	942 reflections $(4.85\%)$	wwPDB-VP
Wilson B-factor $(\mathring{A}^2)$	55.0	Xtriage
Anisotropy	0.477	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.29, 54.3	EDS
L-test for twinning <sup>2</sup>	$ < L > = 0.47, < L^2> = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	9733	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 3.57% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>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.



<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

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		
MIOI	Chain	RMSZ	# Z >5	RMSZ	# Z  > 5	
1	A	0.97	0/1632	0.85	$2/2226 \ (0.1\%)$	
1	Н	0.81	0/1633	0.76	$1/2227 \; (0.0\%)$	
2	В	0.98	0/1685	0.84	$2/2290 \ (0.1\%)$	
2	L	0.92	0/1685	0.77	$1/2290 \ (0.0\%)$	
3	R	0.85	0/1651	0.68	0/2254	
3	S	0.66	0/1643	0.76	$2/2243 \ (0.1\%)$	
All	All	0.87	0/9929	0.78	8/13530 (0.1%)	

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a maintain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	Н	0	2
3	S	0	2
All	All	0	4

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$Ideal(^{o})$
1	Н	148	GLU	C-N-CD	-11.92	94.38	120.60
2	В	96	PRO	CA-N-CD	-6.80	101.98	111.50
2	L	11	LEU	CB-CG-CD2	-6.53	99.91	111.00
3	S	509	ASP	N-CA-C	-6.43	93.64	111.00
2	В	21	ILE	CB-CA-C	-6.23	99.15	111.60

There are no chirality outliers.

All (4) planarity outliers are listed below:



Mol	Chain	Res	Type	Group
1	Н	187	THR	Mainchain,Peptide
3	S	509	ASP	Peptide
3	S	510	ASP	Peptide

## 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	A	1594	0	1547	230	4
1	Н	1595	0	1552	192	0
2	В	1651	0	1582	191	1
2	L	1651	0	1584	174	1
3	R	1611	0	1568	162	4
3	S	1603	0	1561	323	0
4	R	28	0	26	2	0
All	All	9733	0	9420	1230	5

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 64.

The worst 5 of 1230 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{aligned} &  ext{Interatomic} \ &  ext{distance} \ &  ext{(Å)} \end{aligned}$	$egin{aligned}  ext{Clash} \  ext{overlap } ( ext{Å}) \end{aligned}$
2:B:180:THR:C	2:B:181:LEU:HD23	1.18	1.54
3:S:385:PHE:CZ	3:S:409:TYR:HD2	1.22	1.52
3:S:396:VAL:HG23	3:S:446:PHE:CD1	1.46	1.49
3:S:437:CYS:SG	3:S:585:CYS:CB	2.04	1.45
1:A:173:ASP:C	1:A:174:LEU:HD23	1.34	1.43

All (5) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	$\begin{array}{c} \text{Interatomic} \\ \text{distance (Å)} \end{array}$	Clash overlap (Å)
3:R:511:ARG:NH2	1:A:115:LYS:CE[4_455]	0.40	1.80
3:R:511:ARG:NH2	1:A:115:LYS:CD[4_455]	1.61	0.59
3:R:511:ARG:CZ	1:A:115:LYS:NZ[4_455]	1.78	0.42

Continued on next page...



Continued from previous page...

Atom-1	Atom-2	$egin{aligned}  ext{Interatomic} \  ext{distance} \ ( ext{Å}) \end{aligned}$	$egin{array}{c}  ext{Clash} \  ext{overlap } ( ext{Å}) \end{array}$
3:R:511:ARG:NE	1:A:115:LYS:CE[4_455]	1.93	0.27
2:L:53:ARG:NH2	2:B:18:ARG:NH1[2_455]	2.13	0.07

## 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	Percentile	S
1	A	$209/216 \ (97\%)$	203 (97%)	3 (1%)	3 (1%)	11 46	
1	Н	209/216 (97%)	205 (98%)	3 (1%)	1 (0%)	29 67	
2	В	210/214 (98%)	202 (96%)	6 (3%)	2 (1%)	15 54	
2	L	210/214 (98%)	202 (96%)	7 (3%)	1 (0%)	29 67	
3	R	206/208~(99%)	196 (95%)	9 (4%)	1 (0%)	29 67	
3	S	205/208~(99%)	196 (96%)	9 (4%)	0	100 100	
All	All	1249/1276~(98%)	1204 (96%)	37 (3%)	8 (1%)	25 64	

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	Н	149	PRO
1	A	149	PRO
2	В	81	GLU
1	A	123	PRO
3	R	458	VAL

#### 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	Percen	tiles
1	A	182/186 (98%)	135 (74%)	47 (26%)	0	2
1	Н	182/186 (98%)	132 (72%)	50 (28%)	0	1
2	В	190/192 (99%)	145 (76%)	45 (24%)	1	3
2	L	190/192 (99%)	135 (71%)	55 (29%)	0	1
3	R	190/190 (100%)	151 (80%)	39 (20%)	1	6
3	S	189/190 (100%)	139 (74%)	50 (26%)	0	2
All	All	1123/1136 (99%)	837 (74%)	286 (26%)	0	2

5 of 286 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	S	498	SER
3	R	416	SER
1	A	107	THR
3	S	503	CYS
3	S	546	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	${f Res}$	Type
3	S	395	GLN
3	S	522	GLN
1	A	171	GLN
3	S	408	ASN
3	S	471	GLN

#### 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).

Mol	Tuno	Chain	Res	Link	Bo	nd leng	${ m ths}$	В	ond ang	les
10101	Type	Chain	nes	Link	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
4	NAG	R	601	3	14,14,15	0.29	0	17,19,21	0.61	0
4	NAG	R	602	3	14,14,15	0.29	0	17,19,21	0.61	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	NAG	R	601	3	1/1/5/7	4/6/23/26	0/1/1/1
4	NAG	R	602	3	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	R	601	NAG	C1

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	R	601	NAG	C8-C7-N2-C2
4	R	601	NAG	O7-C7-N2-C2
4	R	602	NAG	C1-C2-N2-C7

Continued on next page...



Continued from previous page...

N	Mol	Chain	Res	Type	Atoms
	4	R	601	NAG	C4-C5-C6-O6
	4	R	601	NAG	O5-C5-C6-O6

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	R	601	NAG	1	0
4	R	602	NAG	1	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	<rsrz></rsrz>	$\#\mathrm{RSRZ}{>}2$	$\mathrm{OWAB}(\mathrm{\AA}^2)$	Q < 0.9
1	A	213/216 (98%)	0.10	6 (2%) 53 37	39, 73, 119, 169	0
1	Н	213/216 (98%)	-0.34	0 100 100	26, 49, 84, 133	0
2	В	212/214 (99%)	-0.16	0 100 100	25, 57, 96, 135	0
2	L	212/214 (99%)	-0.39	0 100 100	25, 47, 77, 92	0
3	R	208/208 (100%)	-0.10	2 (0%) 82 72	28, 68, 121, 228	0
3	S	207/208 (99%)	0.58	21 (10%) 7 4	53, 102, 183, 294	0
All	All	$1265/1276 \ (99\%)$	-0.06	29 (2%) 60 47	25, 63, 126, 294	0

The worst 5 of 29 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	S	434	ALA	6.4
3	S	582	ASN	4.9
3	S	433	ILE	4.4
3	S	571	PHE	3.7
1	A	128	CYS	3.6

## 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	${f B-factors}({f A}^2)$	Q<0.9
4	NAG	R	602	14/15	0.75	0.52	20,20,20,20	0
4	NAG	R	601	14/15	0.80	0.43	20,20,20,20	0

## 6.5 Other polymers (i)

There are no such residues in this entry.

