Full wwPDB X-ray Structure Validation Report (i)

May 22, 2020 – 01:22 am BST

PDB ID	:	2BEQ
Title	:	Structure of a Proteolytically Resistant Core from the Severe Acute Respiratory Syndrome Coronavirus S2 Fusion Protein
Authors	:	Supekar, V.M.; Bruckmann, C.; Ingallinella, P.; Bianchi, E.; Pessi, A.; Carfi, A.
Deposited on	:	2004-11-29
Resolution	:	1.60 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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:

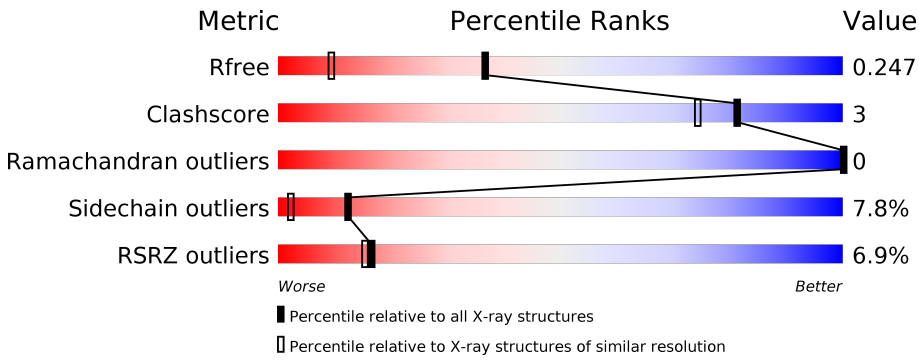
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 1.60 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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	38	82% 13% • •
1	B	38	87% 13%
1	C	38	8% 97% •
2	D	48	4% 92% 8%
2	E	48	8% 77% 21% •
2	F	48	17% 83% 17%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 2110 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 glycoprotein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
1	A	37	270	163	48	59	0	1	1
1	B	38	272	165	48	59	0	0	1
1	C	38	273	165	48	60	0	1	1

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	913	ACE	-	expression tag	UNP P59594
A	950	NH2	-	expression tag	UNP P59594
B	913	ACE	-	expression tag	UNP P59594
B	950	NH2	-	expression tag	UNP P59594
C	913	ACE	-	expression tag	UNP P59594
C	950	NH2	-	expression tag	UNP P59594

- Molecule 2 is a protein called Spike glycoprotein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	D	48	370	230	62	78	0	1	1
2	E	47	359	223	61	75	0	0	2
2	F	48	364	227	61	76	0	0	1

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	1147	ACE	-	expression tag	UNP P59594
D	1194	NH2	-	expression tag	UNP P59594

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Chain	Residue	Modelled	Actual	Comment	Reference
E	1147	ACE	-	expression tag	UNP P59594
E	1194	NH2	-	expression tag	UNP P59594
F	1147	ACE	-	expression tag	UNP P59594
F	1194	NH2	-	expression tag	UNP P59594

- Molecule 3 is water.

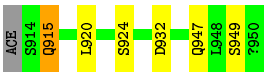
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	24	24	24	0	0
			Total	O		
3	B	28	28	28	0	0
			Total	O		
3	C	23	23	23	0	0
			Total	O		
3	D	46	46	46	0	0
			Total	O		
3	E	47	47	47	0	0
			Total	O		
3	F	34	34	34	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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.

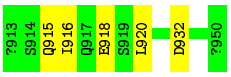
- Molecule 1: Spike glycoprotein

Chain A:



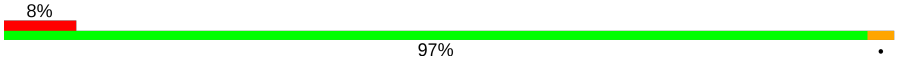
- Molecule 1: Spike glycoprotein

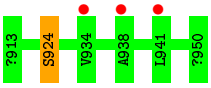
Chain B:



- Molecule 1: Spike glycoprotein

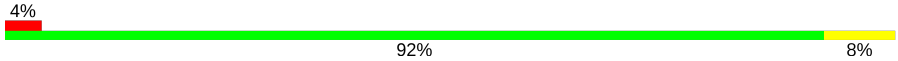
Chain C:

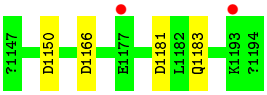




- Molecule 2: Spike glycoprotein

Chain D:





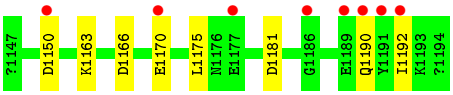
- Molecule 2: Spike glycoprotein

Chain E:

- Molecule 2: Spike glycoprotein

Chain F:

17%
83%
17%


?1147
D1150
K1163
D1166
E1170
L1175
N1176
E1177
D1181
G1186
E1189
Q1190
Y1191
I1192
K1193
?1194

4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	99.91Å 42.90Å 59.83Å 90.00° 116.69° 90.00°	Depositor
Resolution (Å)	30.00 – 1.60 20.22 – 1.60	Depositor EDS
% Data completeness (in resolution range)	99.7 (30.00-1.60) 99.7 (20.22-1.60)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	4.26 (at 1.60Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.199 , 0.241 0.207 , 0.247	Depositor DCC
R_{free} test set	1521 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å^2)	26.2	Xtriage
Anisotropy	0.583	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 48.9	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	2110	wwPDB-VP
Average B, all atoms (Å^2)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.86% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] 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.

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: ACE, NH2

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	A	0.77	0/273	0.85	1/370 (0.3%)
1	B	0.79	0/268	0.85	1/364 (0.3%)
1	C	0.72	0/274	0.82	0/372
2	D	0.72	0/374	0.97	4/503 (0.8%)
2	E	0.89	0/359	1.04	2/481 (0.4%)
2	F	0.86	1/362 (0.3%)	0.99	3/488 (0.6%)
All	All	0.80	1/1910 (0.1%)	0.93	11/2578 (0.4%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	1170	GLU	CD-OE2	5.52	1.31	1.25

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	F	1150	ASP	CB-CG-OD2	7.42	124.98	118.30
2	D	1150	ASP	CB-CG-OD2	7.26	124.84	118.30
2	F	1166	ASP	CB-CG-OD2	6.83	124.45	118.30
1	B	932	ASP	CB-CG-OD2	6.70	124.33	118.30
2	E	1150	ASP	CB-CG-OD2	6.53	124.18	118.30
2	E	1166	ASP	CB-CG-OD2	6.20	123.88	118.30
1	A	932	ASP	CB-CG-OD2	6.10	123.79	118.30
2	D	1181	ASP	CB-CG-OD2	6.06	123.75	118.30
2	D	1166[A]	ASP	CB-CG-OD2	5.75	123.48	118.30
2	D	1166[B]	ASP	CB-CG-OD2	5.75	123.48	118.30
2	F	1181	ASP	CB-CG-OD2	5.38	123.14	118.30

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	A	270	0	279	1	0
1	B	272	0	282	3	0
1	C	273	0	283	2	0
2	D	370	0	371	0	0
2	E	359	0	361	9	0
2	F	364	0	364	0	0
3	A	24	0	0	0	0
3	B	28	0	0	0	0
3	C	23	0	0	0	0
3	D	46	0	0	0	0
3	E	47	0	0	0	0
3	F	34	0	0	0	0
All	All	2110	0	1940	10	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.

All (10) 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:B:916:ILE:HD11	2:E:1179:LEU:HD11	1.45	0.99
2:E:1149:GLY:C	2:E:1151:ILE:H	1.92	0.73
1:B:916:ILE:CD1	2:E:1179:LEU:HD11	2.26	0.57
2:E:1149:GLY:HA2	2:E:1151:ILE:HG12	1.87	0.56
1:B:916:ILE:HD11	2:E:1179:LEU:CD1	2.28	0.56
2:E:1149:GLY:C	2:E:1151:ILE:N	2.61	0.49
1:C:924[B]:SER:OG	2:E:1165:ILE:HG23	2.16	0.46
1:C:924[A]:SER:OG	2:E:1169:ASN:ND2	2.48	0.45
2:E:1149:GLY:CA	2:E:1151:ILE:HG12	2.47	0.43
1:A:915:GLN:HB2	1:A:915:GLN:HE21	1.67	0.42

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	A	36/38 (95%)	36 (100%)	0	0	100	100
1	B	36/38 (95%)	36 (100%)	0	0	100	100
1	C	37/38 (97%)	37 (100%)	0	0	100	100
2	D	47/48 (98%)	45 (96%)	2 (4%)	0	100	100
2	E	45/48 (94%)	43 (96%)	2 (4%)	0	100	100
2	F	46/48 (96%)	46 (100%)	0	0	100	100
All	All	247/258 (96%)	243 (98%)	4 (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	A	33/32 (103%)	27 (82%)	6 (18%)	1	0
1	B	32/32 (100%)	29 (91%)	3 (9%)	8	1
1	C	33/32 (103%)	31 (94%)	2 (6%)	18	4
2	D	42/41 (102%)	41 (98%)	1 (2%)	49	24
2	E	40/41 (98%)	37 (92%)	3 (8%)	13	2
2	F	40/41 (98%)	36 (90%)	4 (10%)	7	1
All	All	220/219 (100%)	201 (91%)	19 (9%)	12	1

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	915	GLN
1	A	920	LEU
1	A	924[A]	SER
1	A	924[B]	SER
1	A	947	GLN
1	A	949	SER
1	B	915	GLN
1	B	918	GLU
1	B	920	LEU
1	C	924[A]	SER
1	C	924[B]	SER
2	D	1183	GLN
2	E	1170	GLU
2	E	1182	LEU
2	E	1193	LYS
2	F	1163	LYS
2	F	1175	LEU
2	F	1190	GLN
2	F	1192	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	915	GLN
1	B	917	GLN
1	B	936	GLN
1	B	939	GLN
1	C	936	GLN
1	C	939	GLN
2	D	1169	ASN
2	D	1176	ASN
2	E	1169	ASN
2	F	1169	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 carbohydrates 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, 95th 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			OWAB(Å^2)	Q<0.9
1	A	36/38 (94%)	0.36	0	100	100	23, 29, 43, 44	0
1	B	36/38 (94%)	0.25	0	100	100	21, 27, 37, 42	0
1	C	36/38 (94%)	0.65	3 (8%)	11	10	20, 26, 37, 39	0
2	D	46/48 (95%)	0.29	2 (4%)	35	32	26, 36, 46, 48	0
2	E	46/48 (95%)	0.24	4 (8%)	10	9	23, 31, 42, 50	0
2	F	46/48 (95%)	0.88	8 (17%)	1	1	26, 39, 50, 53	0
All	All	246/258 (95%)	0.45	17 (6%)	16	15	20, 33, 46, 53	0

All (17) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	1191	TYR	5.3
2	F	1177	GLU	3.6
2	F	1190	GLN	2.9
2	D	1177	GLU	2.8
1	C	938	ALA	2.8
2	E	1149	GLY	2.7
1	C	934	VAL	2.6
2	F	1192	ILE	2.6
2	E	1148	LEU	2.5
2	D	1193	LYS	2.5
2	F	1189	GLU	2.4
2	F	1186	GLY	2.4
1	C	941	LEU	2.4
2	F	1170	GLU	2.3
2	F	1150	ASP	2.3
2	E	1180	ILE	2.1
2	E	1150	ASP	2.0

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 carbohydrates 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.