



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 6, 2020 – 10:28 AM BST

PDB ID : 7BQA
Title : Crystal structure of ASFV p35
Authors : Li, G.B.; Fu, D.; Chen, C.; Guo, Y.
Deposited on : 2020-03-24
Resolution : 2.10 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
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

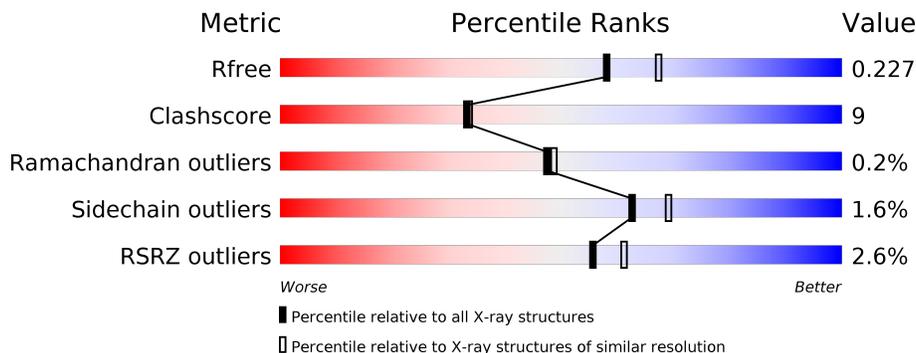
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 $\leq 5\%$. 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	339	
1	B	339	

2 Entry composition i

There are 2 unique types of molecules in this entry. The entry contains 4663 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 60 kDa polyprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	B	268	2200	1423	365	403	9	0	0	0
1	A	268	2205	1426	366	404	9	0	0	0

There are 70 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	ARG	-	expression tag	UNP A0A0A1E146
B	-2	SER	-	expression tag	UNP A0A0A1E146
B	-1	PRO	-	expression tag	UNP A0A0A1E146
B	0	TRP	-	expression tag	UNP A0A0A1E146
B	305	LEU	-	expression tag	UNP A0A0A1E146
B	306	GLU	-	expression tag	UNP A0A0A1E146
B	307	SER	-	expression tag	UNP A0A0A1E146
B	308	ARG	-	expression tag	UNP A0A0A1E146
B	309	GLY	-	expression tag	UNP A0A0A1E146
B	310	PRO	-	expression tag	UNP A0A0A1E146
B	311	PHE	-	expression tag	UNP A0A0A1E146
B	312	GLU	-	expression tag	UNP A0A0A1E146
B	313	GLY	-	expression tag	UNP A0A0A1E146
B	314	LYS	-	expression tag	UNP A0A0A1E146
B	315	PRO	-	expression tag	UNP A0A0A1E146
B	316	ILE	-	expression tag	UNP A0A0A1E146
B	317	PRO	-	expression tag	UNP A0A0A1E146
B	318	ASN	-	expression tag	UNP A0A0A1E146
B	319	PRO	-	expression tag	UNP A0A0A1E146
B	320	LEU	-	expression tag	UNP A0A0A1E146
B	321	LEU	-	expression tag	UNP A0A0A1E146
B	322	GLY	-	expression tag	UNP A0A0A1E146
B	323	LEU	-	expression tag	UNP A0A0A1E146
B	324	ASP	-	expression tag	UNP A0A0A1E146
B	325	SER	-	expression tag	UNP A0A0A1E146

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	326	THR	-	expression tag	UNP A0A0A1E146
B	327	ARG	-	expression tag	UNP A0A0A1E146
B	328	THR	-	expression tag	UNP A0A0A1E146
B	329	GLY	-	expression tag	UNP A0A0A1E146
B	330	HIS	-	expression tag	UNP A0A0A1E146
B	331	HIS	-	expression tag	UNP A0A0A1E146
B	332	HIS	-	expression tag	UNP A0A0A1E146
B	333	HIS	-	expression tag	UNP A0A0A1E146
B	334	HIS	-	expression tag	UNP A0A0A1E146
B	335	HIS	-	expression tag	UNP A0A0A1E146
A	-3	ARG	-	expression tag	UNP A0A0A1E146
A	-2	SER	-	expression tag	UNP A0A0A1E146
A	-1	PRO	-	expression tag	UNP A0A0A1E146
A	0	TRP	-	expression tag	UNP A0A0A1E146
A	305	LEU	-	expression tag	UNP A0A0A1E146
A	306	GLU	-	expression tag	UNP A0A0A1E146
A	307	SER	-	expression tag	UNP A0A0A1E146
A	308	ARG	-	expression tag	UNP A0A0A1E146
A	309	GLY	-	expression tag	UNP A0A0A1E146
A	310	PRO	-	expression tag	UNP A0A0A1E146
A	311	PHE	-	expression tag	UNP A0A0A1E146
A	312	GLU	-	expression tag	UNP A0A0A1E146
A	313	GLY	-	expression tag	UNP A0A0A1E146
A	314	LYS	-	expression tag	UNP A0A0A1E146
A	315	PRO	-	expression tag	UNP A0A0A1E146
A	316	ILE	-	expression tag	UNP A0A0A1E146
A	317	PRO	-	expression tag	UNP A0A0A1E146
A	318	ASN	-	expression tag	UNP A0A0A1E146
A	319	PRO	-	expression tag	UNP A0A0A1E146
A	320	LEU	-	expression tag	UNP A0A0A1E146
A	321	LEU	-	expression tag	UNP A0A0A1E146
A	322	GLY	-	expression tag	UNP A0A0A1E146
A	323	LEU	-	expression tag	UNP A0A0A1E146
A	324	ASP	-	expression tag	UNP A0A0A1E146
A	325	SER	-	expression tag	UNP A0A0A1E146
A	326	THR	-	expression tag	UNP A0A0A1E146
A	327	ARG	-	expression tag	UNP A0A0A1E146
A	328	THR	-	expression tag	UNP A0A0A1E146
A	329	GLY	-	expression tag	UNP A0A0A1E146
A	330	HIS	-	expression tag	UNP A0A0A1E146
A	331	HIS	-	expression tag	UNP A0A0A1E146
A	332	HIS	-	expression tag	UNP A0A0A1E146

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
A	333	HIS	-	expression tag	UNP A0A0A1E146
A	334	HIS	-	expression tag	UNP A0A0A1E146
A	335	HIS	-	expression tag	UNP A0A0A1E146

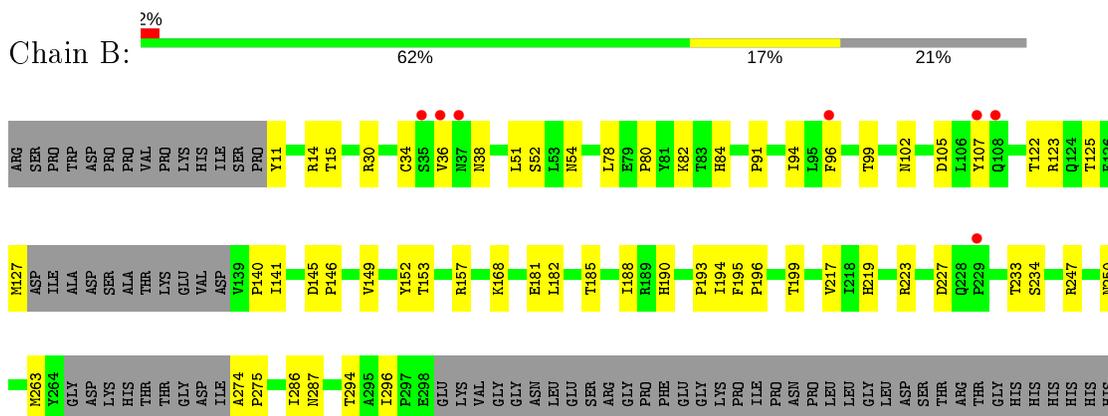
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	123	Total 123	O 123	0	0
2	A	135	Total 135	O 135	0	0

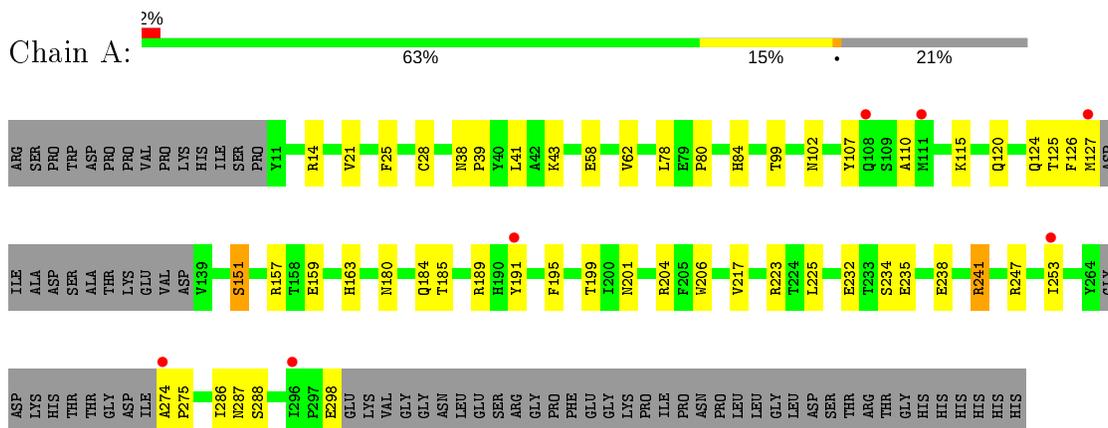
3 Residue-property plots [i](#)

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: 60 kDa polyprotein



- Molecule 1: 60 kDa polyprotein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	58.07Å 89.56Å 65.08Å 90.00° 89.95° 90.00°	Depositor
Resolution (Å)	48.72 – 2.10 48.72 – 2.10	Depositor EDS
% Data completeness (in resolution range)	95.3 (48.72-2.10) 95.3 (48.72-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.59 (at 2.10Å)	Xtriage
Refinement program	PHENIX 1.15.2_3472	Depositor
R, R_{free}	0.200 , 0.228 0.200 , 0.227	Depositor DCC
R_{free} test set	1772 reflections (4.78%)	wwPDB-VP
Wilson B-factor (Å ²)	21.2	Xtriage
Anisotropy	0.061	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 31.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	0.327 for h,-k,-l	Xtriage
Reported twinning fraction	0.340 for h,-k,-l	Depositor
Outliers	0 of 37034 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	4663	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.62% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² 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.

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	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.26	0/2268	0.42	0/3093
1	B	0.25	0/2263	0.42	0/3086
All	All	0.26	0/4531	0.42	0/6179

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	A	2205	0	2141	38	2
1	B	2200	0	2130	39	1
2	A	135	0	0	12	1
2	B	123	0	0	12	1
All	All	4663	0	4271	75	3

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 75 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:191:TYR:OH	2:A:401:HOH:O	1.82	0.96

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:184:GLN:HG3	1:A:185:THR:HG23	1.63	0.81
1:A:287:ASN:ND2	2:A:402:HOH:O	2.05	0.78
1:B:34:CYS:O	2:B:403:HOH:O	2.04	0.76
1:A:127:MET:O	2:A:403:HOH:O	2.06	0.72

All (3) 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	Interatomic distance (Å)	Clash overlap (Å)
1:A:151:SER:OG	1:A:232:GLU:OE2[2_355]	2.01	0.19
2:B:476:HOH:O	2:A:521:HOH:O[1_554]	2.10	0.10
1:B:145:ASP:OD1	1:A:124:GLN:NE2[2_445]	2.17	0.03

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	262/339 (77%)	252 (96%)	10 (4%)	0	100	100
1	B	262/339 (77%)	248 (95%)	13 (5%)	1 (0%)	34	32
All	All	524/678 (77%)	500 (95%)	23 (4%)	1 (0%)	47	49

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	36	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	Percentiles	
1	A	247/309 (80%)	242 (98%)	5 (2%)	55	60
1	B	245/309 (79%)	242 (99%)	3 (1%)	71	77
All	All	492/618 (80%)	484 (98%)	8 (2%)	62	69

5 of 8 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	115	LYS
1	A	241	ARG
1	A	151	SER
1	B	234	SER
1	A	126	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	84	HIS
1	A	120	GLN
1	A	184	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](#)

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	268/339 (79%)	0.03	7 (2%) 56 61	11, 22, 44, 83	0
1	B	268/339 (79%)	0.13	7 (2%) 56 61	14, 25, 46, 104	0
All	All	536/678 (79%)	0.08	14 (2%) 56 61	11, 24, 46, 104	0

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	36	VAL	12.9
1	B	37	ASN	5.7
1	A	127	MET	3.0
1	B	107	TYR	3.0
1	A	253	ILE	2.7

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.