



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2018 – 08:23 pm GMT

PDB ID : 1WP7
Title : crystal structure of Nipah Virus fusion core
Authors : Xu, Y.; Liu, Y.; Lou, Z.; Su, N.; Bai, Z.; Gao, G.F.; Rao, Z.
Deposited on : 2004-08-31
Resolution : 2.20 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 ⓘ 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	:	trunk30967
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac	:	5.8.0158
CCP4	:	7.0 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk30967

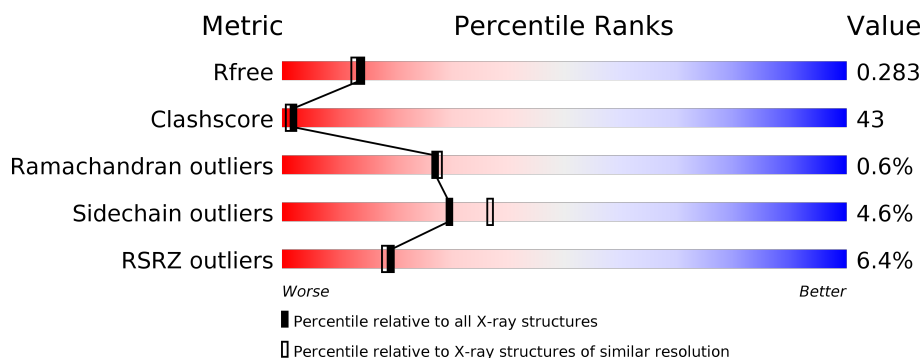
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	111664	4343 (2.20-2.20)
Clashscore	122126	5027 (2.20-2.20)
Ramachandran outliers	120053	4952 (2.20-2.20)
Sidechain outliers	120020	4953 (2.20-2.20)
RSRZ outliers	108989	4245 (2.20-2.20)

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. 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	89	<div> <div>8%</div> <div> <div></div> <div>38%</div> <div>34%</div> <div>28%</div> </div> </div>
1	B	89	<div> <div>3%</div> <div> <div></div> <div>31%</div> <div>37%</div> <div>29%</div> </div> </div>
1	C	89	<div> <div>2%</div> <div> <div></div> <div>30%</div> <div>33%</div> <div>6%</div> <div>31%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1569 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 fusion protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	64	Total	C	N	O	S	0	0	0
			501	309	84	107	1			
1	B	63	Total	C	N	O	S	0	0	0
			492	304	82	105	1			
1	C	61	Total	C	N	O	S	0	0	0
			473	293	79	100	1			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	445	GLY	-	LINKER	UNP Q8QU00
A	446	GLY	-	LINKER	UNP Q8QU00
A	447	SER	-	LINKER	UNP Q8QU00
A	448	GLY	-	LINKER	UNP Q8QU00
A	449	GLY	-	LINKER	UNP Q8QU00
A	450	SER	-	LINKER	UNP Q8QU00
A	451	GLY	-	LINKER	UNP Q8QU00
A	452	GLY	-	LINKER	UNP Q8QU00
A	486	HIS	-	EXPRESSION TAG	UNP Q8QU00
A	487	HIS	-	EXPRESSION TAG	UNP Q8QU00
A	488	HIS	-	EXPRESSION TAG	UNP Q8QU00
A	489	HIS	-	EXPRESSION TAG	UNP Q8QU00
A	490	HIS	-	EXPRESSION TAG	UNP Q8QU00
A	491	HIS	-	EXPRESSION TAG	UNP Q8QU00
B	445	GLY	-	LINKER	UNP Q8QU00
B	446	GLY	-	LINKER	UNP Q8QU00
B	447	SER	-	LINKER	UNP Q8QU00
B	448	GLY	-	LINKER	UNP Q8QU00
B	449	GLY	-	LINKER	UNP Q8QU00
B	450	SER	-	LINKER	UNP Q8QU00
B	451	GLY	-	LINKER	UNP Q8QU00
B	452	GLY	-	LINKER	UNP Q8QU00
B	486	HIS	-	EXPRESSION TAG	UNP Q8QU00

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Chain	Residue	Modelled	Actual	Comment	Reference
B	487	HIS	-	EXPRESSION TAG	UNP Q8QU00
B	488	HIS	-	EXPRESSION TAG	UNP Q8QU00
B	489	HIS	-	EXPRESSION TAG	UNP Q8QU00
B	490	HIS	-	EXPRESSION TAG	UNP Q8QU00
B	491	HIS	-	EXPRESSION TAG	UNP Q8QU00
C	445	GLY	-	LINKER	UNP Q8QU00
C	446	GLY	-	LINKER	UNP Q8QU00
C	447	SER	-	LINKER	UNP Q8QU00
C	448	GLY	-	LINKER	UNP Q8QU00
C	449	GLY	-	LINKER	UNP Q8QU00
C	450	SER	-	LINKER	UNP Q8QU00
C	451	GLY	-	LINKER	UNP Q8QU00
C	452	GLY	-	LINKER	UNP Q8QU00
C	486	HIS	-	EXPRESSION TAG	UNP Q8QU00
C	487	HIS	-	EXPRESSION TAG	UNP Q8QU00
C	488	HIS	-	EXPRESSION TAG	UNP Q8QU00
C	489	HIS	-	EXPRESSION TAG	UNP Q8QU00
C	490	HIS	-	EXPRESSION TAG	UNP Q8QU00
C	491	HIS	-	EXPRESSION TAG	UNP Q8QU00

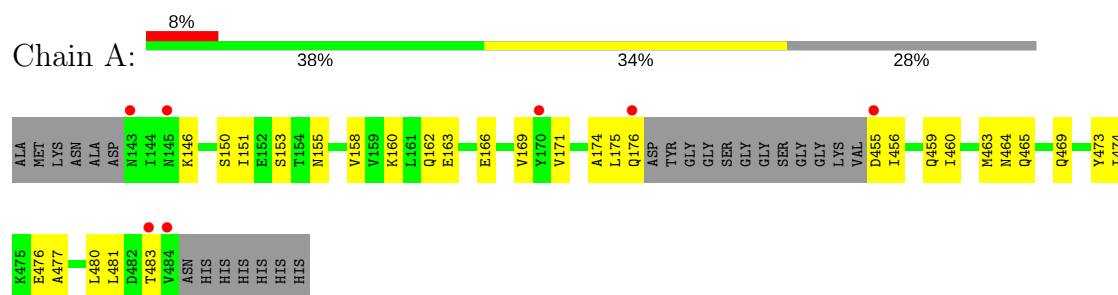
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	32	Total O 32 32	0	0
2	B	33	Total O 33 33	0	0
2	C	38	Total O 38 38	0	0

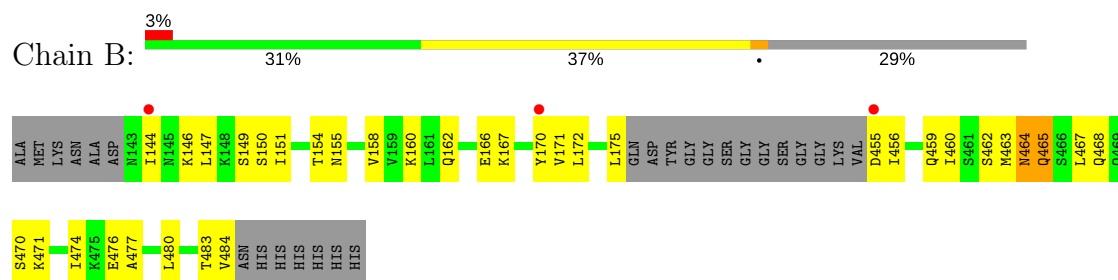
3 Residue-property plots [i](#)

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.

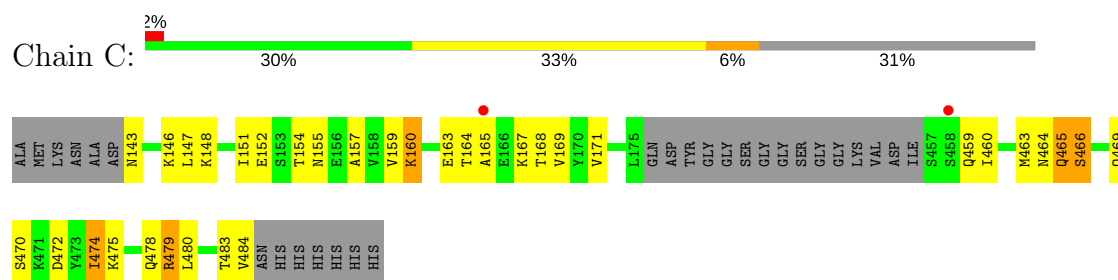
• Molecule 1: fusion protein



• Molecule 1: fusion protein



• Molecule 1: fusion protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	31.66Å 31.73Å 51.26Å 80.71° 86.34° 65.81°	Depositor
Resolution (Å)	50.00 – 2.20 24.79 – 2.10	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-2.20) 88.7 (24.79-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.90 (at 2.10Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.225 , 0.280 0.225 , 0.283	Depositor DCC
R_{free} test set	525 reflections (5.33%)	wwPDB-VP
Wilson B-factor (Å ²)	28.1	Xtriage
Anisotropy	0.362	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 72.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	1569	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.40% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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	0.32	0/501	0.53	0/673
1	B	0.33	0/492	0.54	0/661
1	C	0.34	0/473	0.52	0/635
All	All	0.33	0/1466	0.53	0/1969

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	501	0	515	41	0
1	B	492	0	507	50	0
1	C	473	0	488	47	0
2	A	32	0	0	13	0
2	B	33	0	0	23	0
2	C	38	0	0	25	0
All	All	1569	0	1510	129	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 43.

The worst 5 of 129 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:C:168:THR:HA	2:C:5:HOH:O	1.60	1.01
1:C:146:LYS:HD3	1:C:483:THR:HG23	1.52	0.91
1:B:477:ALA:HA	2:B:33:HOH:O	1.74	0.87
1:A:146:LYS:HB3	2:A:65:HOH:O	1.77	0.85
1:B:480:LEU:HB2	2:B:33:HOH:O	1.76	0.84

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	60/89 (67%)	59 (98%)	0	1 (2%)	10	7
1	B	59/89 (66%)	58 (98%)	1 (2%)	0	100	100
1	C	57/89 (64%)	56 (98%)	1 (2%)	0	100	100
All	All	176/267 (66%)	173 (98%)	2 (1%)	1 (1%)	27	28

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	175	LEU

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	60/77 (78%)	60 (100%)	0	100	100
1	B	59/77 (77%)	57 (97%)	2 (3%)	40	50
1	C	56/77 (73%)	50 (89%)	6 (11%)	7	6
All	All	175/231 (76%)	167 (95%)	8 (5%)	29	37

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

Mol	Chain	Res	Type
1	C	464	ASN
1	C	479	ARG
1	C	466	SER
1	C	160	LYS
1	C	465	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	143	ASN
1	A	145	ASN
1	A	469	GLN
1	C	464	ASN
1	C	468	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

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	64/89 (71%)	0.32	7 (10%) 5 4	23, 38, 63, 75	0
1	B	63/89 (70%)	0.18	3 (4%) 30 29	22, 40, 56, 67	0
1	C	61/89 (68%)	0.16	2 (3%) 46 44	22, 38, 53, 60	0
All	All	188/267 (70%)	0.22	12 (6%) 19 18	22, 39, 59, 75	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	455	ASP	4.6
1	A	176	GLN	3.2
1	B	144	ILE	3.0
1	B	170	TYR	2.9
1	B	455	ASP	2.8

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.