



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 03:28 PM UTC

PDB ID : 4IJS / pdb_00004ijs
Title : Crystal structure of nucleocapsid protein encoded by the prototypic member of orthobunyavirus
Authors : Li, B.B.; Wang, Q.; Lou, Z.Y.
Deposited on : 2012-12-23
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 ⓘ 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 ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

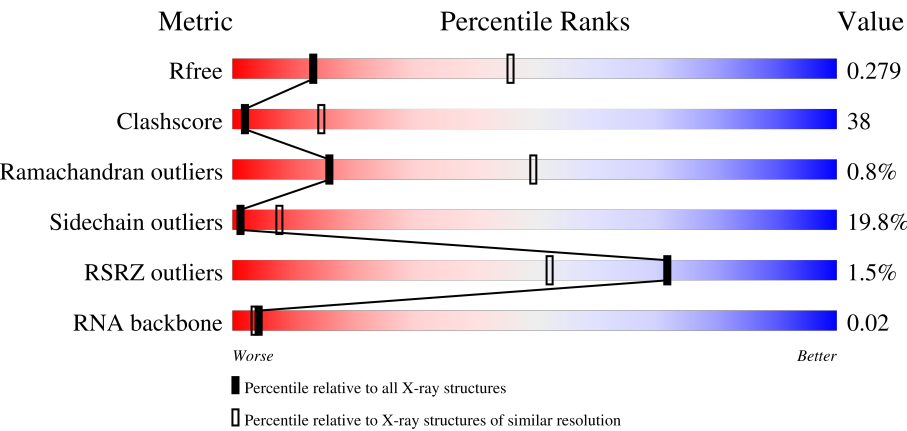
1 Overall quality at a glance i

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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
R _{free}	180053	1466 (3.20-3.20)
Clashscore	190562	1573 (3.20-3.20)
Ramachandran outliers	187476	1548 (3.20-3.20)
Sidechain outliers	187428	1547 (3.20-3.20)
RSRZ outliers	180081	1466 (3.20-3.20)
RNA backbone	3983	1222 (3.50-2.90)

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 $\leq 5\%$. 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	248	44% 35% 12% 6%
1	B	248	2% 43% 37% 13% 6%
1	C	248	2% 39% 41% 14% 6%
1	D	248	33% 44% 15% 6%

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Mol	Chain	Length	Quality of chain
2	E	10	10%70%20%
2	F	10	20%70%10%
2	G	10	10%60%20%10%
2	H	10	10%20%70%10%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8298 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 Nucleoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	232	Total	C	N	O	S	0	0	0
			1865	1205	315	339	6			
1	B	232	Total	C	N	O	S	0	0	0
			1865	1205	315	339	6			
1	C	232	Total	C	N	O	S	0	0	0
			1865	1205	315	339	6			
1	D	232	Total	C	N	O	S	0	0	0
			1865	1205	315	339	6			

There are 68 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-14	MET	-	expression tag	UNP P16495
A	-13	ARG	-	expression tag	UNP P16495
A	-12	GLY	-	expression tag	UNP P16495
A	-11	SER	-	expression tag	UNP P16495
A	-10	HIS	-	expression tag	UNP P16495
A	-9	HIS	-	expression tag	UNP P16495
A	-8	HIS	-	expression tag	UNP P16495
A	-7	HIS	-	expression tag	UNP P16495
A	-6	HIS	-	expression tag	UNP P16495
A	-5	HIS	-	expression tag	UNP P16495
A	-4	GLY	-	expression tag	UNP P16495
A	-3	SER	-	expression tag	UNP P16495
A	-2	ILE	-	expression tag	UNP P16495
A	-1	GLU	-	expression tag	UNP P16495
A	0	GLY	-	expression tag	UNP P16495
A	1	ARG	-	expression tag	UNP P16495
A	83	SER	ASN	engineered mutation	UNP P16495
B	-14	MET	-	expression tag	UNP P16495
B	-13	ARG	-	expression tag	UNP P16495
B	-12	GLY	-	expression tag	UNP P16495
B	-11	SER	-	expression tag	UNP P16495

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-10	HIS	-	expression tag	UNP P16495
B	-9	HIS	-	expression tag	UNP P16495
B	-8	HIS	-	expression tag	UNP P16495
B	-7	HIS	-	expression tag	UNP P16495
B	-6	HIS	-	expression tag	UNP P16495
B	-5	HIS	-	expression tag	UNP P16495
B	-4	GLY	-	expression tag	UNP P16495
B	-3	SER	-	expression tag	UNP P16495
B	-2	ILE	-	expression tag	UNP P16495
B	-1	GLU	-	expression tag	UNP P16495
B	0	GLY	-	expression tag	UNP P16495
B	1	ARG	-	expression tag	UNP P16495
B	83	SER	ASN	engineered mutation	UNP P16495
C	-14	MET	-	expression tag	UNP P16495
C	-13	ARG	-	expression tag	UNP P16495
C	-12	GLY	-	expression tag	UNP P16495
C	-11	SER	-	expression tag	UNP P16495
C	-10	HIS	-	expression tag	UNP P16495
C	-9	HIS	-	expression tag	UNP P16495
C	-8	HIS	-	expression tag	UNP P16495
C	-7	HIS	-	expression tag	UNP P16495
C	-6	HIS	-	expression tag	UNP P16495
C	-5	HIS	-	expression tag	UNP P16495
C	-4	GLY	-	expression tag	UNP P16495
C	-3	SER	-	expression tag	UNP P16495
C	-2	ILE	-	expression tag	UNP P16495
C	-1	GLU	-	expression tag	UNP P16495
C	0	GLY	-	expression tag	UNP P16495
C	1	ARG	-	expression tag	UNP P16495
C	83	SER	ASN	engineered mutation	UNP P16495
D	-14	MET	-	expression tag	UNP P16495
D	-13	ARG	-	expression tag	UNP P16495
D	-12	GLY	-	expression tag	UNP P16495
D	-11	SER	-	expression tag	UNP P16495
D	-10	HIS	-	expression tag	UNP P16495
D	-9	HIS	-	expression tag	UNP P16495
D	-8	HIS	-	expression tag	UNP P16495
D	-7	HIS	-	expression tag	UNP P16495
D	-6	HIS	-	expression tag	UNP P16495
D	-5	HIS	-	expression tag	UNP P16495
D	-4	GLY	-	expression tag	UNP P16495
D	-3	SER	-	expression tag	UNP P16495

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-2	ILE	-	expression tag	UNP P16495
D	-1	GLU	-	expression tag	UNP P16495
D	0	GLY	-	expression tag	UNP P16495
D	1	ARG	-	expression tag	UNP P16495
D	83	SER	ASN	engineered mutation	UNP P16495

- Molecule 2 is a RNA chain called RNA (5'-R(P*AP*AP*AP*AP*AP*AP*AP*AP*A)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	10	Total	C	N	O	P	0	0	0
			220	100	50	60	10			
2	F	9	Total	C	N	O	P	0	0	0
			198	90	45	54	9			
2	G	9	Total	C	N	O	P	0	0	0
			198	90	45	54	9			
2	H	9	Total	C	N	O	P	0	0	0
			198	90	45	54	9			

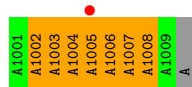
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	10	Total	O	0	0
			10	10		
3	B	6	Total	O	0	0
			6	6		
3	C	3	Total	O	0	0
			3	3		
3	D	2	Total	O	0	0
			2	2		
3	E	1	Total	O	0	0
			1	1		
3	H	2	Total	O	0	0
			2	2		





- Molecule 2: RNA (5'-R(P*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, α , β , γ	106.14Å 106.14Å 485.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.75 – 3.20 40.75 – 3.20	Depositor EDS
% Data completeness (in resolution range)	90.4 (40.75-3.20) 97.5 (40.75-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.49 (at 3.19Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.220 , 0.276 0.250 , 0.279	Depositor DCC
R_{free} test set	1203 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	93.1	Xtriage
Anisotropy	0.507	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 65.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	8298	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.34% 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

5.1 Standard geometry

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	1.09	9/1909 (0.5%)	1.27	18/2581 (0.7%)
1	B	1.02	5/1909 (0.3%)	1.20	16/2581 (0.6%)
1	C	0.79	0/1909	1.16	13/2581 (0.5%)
1	D	1.00	4/1909 (0.2%)	1.28	19/2581 (0.7%)
2	E	0.66	0/249	0.81	0/386
2	F	0.58	0/224	0.89	0/347
2	G	0.55	0/224	0.66	0/347
2	H	0.45	0/224	0.60	0/347
All	All	0.95	18/8557 (0.2%)	1.18	66/11751 (0.6%)

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 mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	2
1	B	0	1
1	C	0	1
All	All	0	4

The worst 5 of 18 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	68	TRP	CA-C	-6.54	1.44	1.52
1	B	83	SER	C-N	5.74	1.41	1.33
1	D	78	PRO	N-CD	5.66	1.55	1.47
1	B	86	PRO	N-CD	5.51	1.55	1.47
1	A	60	GLU	CA-C	-5.48	1.45	1.52

The worst 5 of 66 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	68	TRP	N-CA-C	-13.25	87.81	109.40
1	A	34	LEU	N-CA-C	-10.70	92.95	110.17
1	D	170	LYS	N-CA-C	10.51	125.48	112.87
1	C	215	LYS	N-CA-C	9.82	125.93	113.55
1	D	129	LYS	N-CA-C	-9.54	96.39	110.23

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	33	GLY	Peptide
1	A	65	LEU	Peptide
1	B	82	ASN	Peptide
1	C	12	ASN	Peptide

5.2 Too-close contacts ⓘ

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	1865	0	1878	145	0
1	B	1865	0	1878	154	1
1	C	1865	0	1878	144	0
1	D	1865	0	1878	154	0
2	E	220	0	111	2	0
2	F	198	0	100	16	0
2	G	198	0	100	14	0
2	H	198	0	100	8	0
3	A	10	0	0	0	0
3	B	6	0	0	1	0
3	C	3	0	0	0	0
3	D	2	0	0	0	0
3	E	1	0	0	0	0
3	H	2	0	0	0	0
All	All	8298	0	7923	610	1

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 38.

The worst 5 of 610 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:157:PHE:CE2	1:C:185:TYR:CE1	1.94	1.55
1:C:157:PHE:CZ	1:C:185:TYR:CD1	2.01	1.47
1:D:169:ARG:NH2	1:D:215:LYS:HG2	1.08	1.39
1:D:169:ARG:NH2	1:D:215:LYS:CG	1.82	1.38
1:C:157:PHE:CE2	1:C:185:TYR:HE1	1.35	1.35

All (1) 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:B:174:PRO:O	1:B:233:MET:CE[3_545]	1.93	0.27

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	230/248 (93%)	203 (88%)	24 (10%)	3 (1%)	9	40
1	B	230/248 (93%)	203 (88%)	26 (11%)	1 (0%)	30	62
1	C	230/248 (93%)	205 (89%)	23 (10%)	2 (1%)	14	47
1	D	230/248 (93%)	194 (84%)	35 (15%)	1 (0%)	30	62
All	All	920/992 (93%)	805 (88%)	108 (12%)	7 (1%)	16	50

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	82	ASN
1	B	169	ARG
1	C	78	PRO
1	A	228	LYS
1	C	220	ALA

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	200/215 (93%)	169 (84%)	31 (16%)	2	14
1	B	200/215 (93%)	161 (80%)	39 (20%)	1	8
1	C	200/215 (93%)	155 (78%)	45 (22%)	1	5
1	D	200/215 (93%)	157 (78%)	43 (22%)	1	6
All	All	800/860 (93%)	642 (80%)	158 (20%)	1	8

5 of 158 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	4	LEU
1	D	168	GLN
1	D	30	HIS
1	D	72	VAL
1	D	205	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	232	ASN
1	C	168	GLN
1	B	64	ASN
1	B	12	ASN
1	C	76	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	E	9/10 (90%)	9 (100%)	1 (11%)
2	F	8/10 (80%)	7 (87%)	2 (25%)
2	G	8/10 (80%)	5 (62%)	0
2	H	8/10 (80%)	6 (75%)	1 (12%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
All	All	33/40 (82%)	27 (81%)	4 (12%)

5 of 27 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	E	1002	A
2	E	1003	A
2	E	1004	A
2	E	1005	A
2	E	1006	A

All (4) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	E	1002	A
2	F	1005	A
2	F	1006	A
2	H	1002	A

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 oligosaccharides 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	232/248 (93%)	-0.18	2 (0%) 81 64	26, 50, 78, 101	0
1	B	232/248 (93%)	-0.03	4 (1%) 69 49	25, 62, 90, 122	0
1	C	232/248 (93%)	0.02	5 (2%) 62 42	23, 76, 104, 127	0
1	D	232/248 (93%)	0.03	2 (0%) 81 64	27, 69, 102, 125	0
2	E	10/10 (100%)	0.45	0 100 100	52, 75, 84, 95	0
2	F	9/10 (90%)	0.38	0 100 100	75, 86, 96, 106	0
2	G	9/10 (90%)	0.33	0 100 100	86, 96, 108, 111	0
2	H	9/10 (90%)	0.63	1 (11%) 10 7	83, 100, 114, 120	0
All	All	965/1032 (93%)	-0.02	14 (1%) 72 52	23, 66, 101, 127	0

The worst 5 of 14 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	84	PRO	4.2
1	A	13	THR	3.1
1	B	60	GLU	2.9
1	C	6	PHE	2.7
1	B	76	ASN	2.6

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 oligosaccharides 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.