



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 25, 2026 – 08:45 AM UTC

PDB ID : 4H5P / pdb_00004h5p
Title : Crystal Structure of Rift Valley Fever Virus Nucleocapsid Protein Tetramer
Bound to Single-stranded RNA
Authors : Raymond, D.D.; Smith, J.L.
Deposited on : 2012-09-18
Resolution : 2.15 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 ⓘ 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

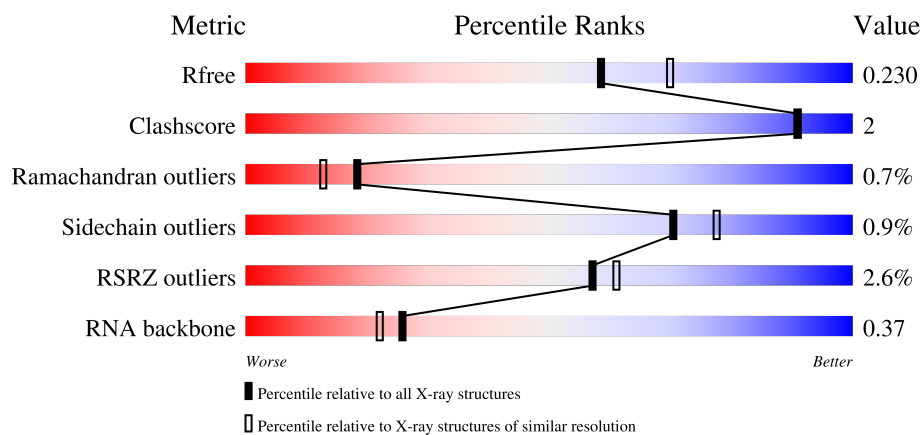
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)
RNA backbone	3983	1112 (2.50-1.82)

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	245	3% 94% 5%
1	B	245	3% 92% 7%
1	C	245	2% 94% 5%
1	D	245	2% 92% 7%

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Mol	Chain	Length	Quality of chain
2	E	14	 86%7%7%
2	F	14	 86%7%7%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8744 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 Nucleocapsid protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	244	Total	C	N	O	S	0	0	0
			1910	1205	343	350	12			
1	B	244	Total	C	N	O	S	0	0	0
			1910	1205	343	350	12			
1	C	244	Total	C	N	O	S	0	0	0
			1910	1205	343	350	12			
1	D	244	Total	C	N	O	S	0	0	0
			1910	1205	343	350	12			

- Molecule 2 is a RNA chain called 28-mer poly(U) RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	14	Total	C	N	O	P	0	0	0
			279	126	28	111	14			
2	F	14	Total	C	N	O	P	0	0	0
			280	126	28	112	14			

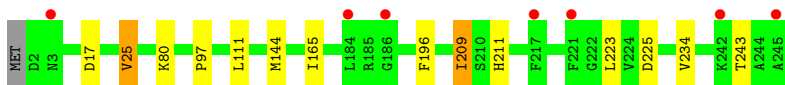
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	97	Total	O	0	0
			97	97		
3	B	122	Total	O	0	0
			122	122		
3	C	141	Total	O	0	0
			141	141		
3	D	112	Total	O	0	0
			112	112		
3	E	37	Total	O	0	0
			37	37		
3	F	36	Total	O	0	0
			36	36		

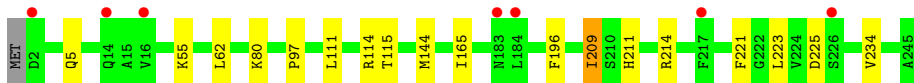
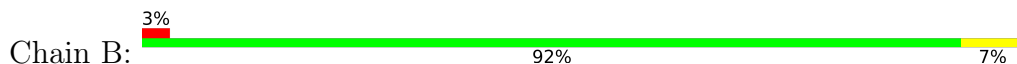
3 Residue-property plots [i](#)

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.

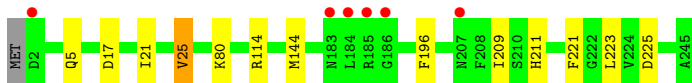
- Molecule 1: Nucleocapsid protein



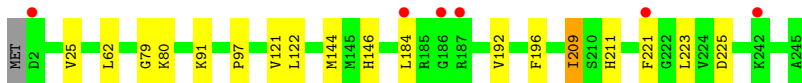
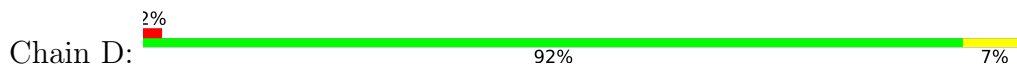
- Molecule 1: Nucleocapsid protein



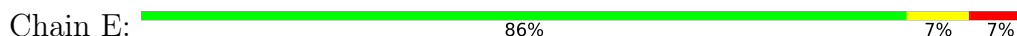
- Molecule 1: Nucleocapsid protein



- Molecule 1: Nucleocapsid protein



- Molecule 2: 28-mer poly(U) RNA



- Molecule 2: 28-mer poly(U) RNA

Chain F:  86% 7% 7%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	77.64Å 193.18Å 77.42Å 90.00° 108.89° 90.00°	Depositor
Resolution (Å)	31.48 – 2.15 31.48 – 2.15	Depositor EDS
% Data completeness (in resolution range)	95.5 (31.48-2.15) 95.4 (31.48-2.15)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.11	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 2.16Å)	Xtriage
Refinement program	BUSTER-TNT BUSTER 2.10.0, BUSTER 2.10	Depositor
R, R_{free}	0.180 , 0.219 0.194 , 0.230	Depositor DCC
R_{free} test set	2828 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	26.5	Xtriage
Anisotropy	0.293	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 49.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	8744	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.18% 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	0.76	0/1947	1.30	10/2626 (0.4%)
1	B	0.77	0/1947	1.27	7/2626 (0.3%)
1	C	0.79	0/1947	1.27	6/2626 (0.2%)
1	D	0.76	0/1947	1.27	7/2626 (0.3%)
2	E	0.92	1/306 (0.3%)	0.83	0/470
2	F	0.95	1/307 (0.3%)	0.87	0/472
All	All	0.78	2/8401 (0.0%)	1.25	30/11446 (0.3%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	8	U	C1'-N1	5.14	1.56	1.48
2	F	8	U	C1'-N1	5.05	1.56	1.48

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	221	PHE	CA-CB-CG	9.74	123.54	113.80
1	D	221	PHE	CA-CB-CG	8.10	121.90	113.80
1	D	196	PHE	CA-CB-CG	6.79	120.59	113.80
1	C	221	PHE	CA-CB-CG	-6.37	107.43	113.80
1	C	17	ASP	CA-CB-CG	5.77	118.37	112.60
1	C	196	PHE	CA-CB-CG	5.77	119.57	113.80
1	B	111	LEU	CA-C-N	5.74	128.76	120.38
1	B	111	LEU	C-N-CA	5.74	128.76	120.38
1	A	196	PHE	CA-CB-CG	5.54	119.34	113.80
1	B	196	PHE	CA-CB-CG	5.51	119.31	113.80
1	A	211	HIS	CA-C-N	5.45	127.52	120.44
1	A	211	HIS	C-N-CA	5.45	127.52	120.44
1	A	225	ASP	CA-CB-CG	5.42	118.02	112.60
1	A	111	LEU	CA-C-N	5.42	127.54	120.28
1	A	111	LEU	C-N-CA	5.42	127.54	120.28
1	A	17	ASP	CA-CB-CG	5.34	117.94	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	211	HIS	CA-C-N	5.31	127.34	120.44
1	B	211	HIS	C-N-CA	5.31	127.34	120.44
1	A	243	THR	CA-C-N	5.23	128.27	120.90
1	A	243	THR	C-N-CA	5.23	128.27	120.90
1	D	211	HIS	CA-C-N	5.22	127.22	120.44
1	D	211	HIS	C-N-CA	5.22	127.22	120.44
1	C	211	HIS	CA-C-N	5.21	127.21	120.44
1	C	211	HIS	C-N-CA	5.21	127.21	120.44
1	B	225	ASP	CA-CB-CG	5.16	117.76	112.60
1	A	25	VAL	N-CA-CB	5.11	117.48	110.54
1	D	79	GLY	CA-C-N	5.08	127.40	120.54
1	D	79	GLY	C-N-CA	5.08	127.40	120.54
1	C	225	ASP	CA-CB-CG	5.08	117.68	112.60
1	D	225	ASP	CA-CB-CG	5.05	117.65	112.60

There are no chirality outliers.

There are no planarity outliers.

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	1910	0	1925	4	0
1	B	1910	0	1925	7	0
1	C	1910	0	1925	6	0
1	D	1910	0	1925	9	0
2	E	279	0	141	3	0
2	F	280	0	141	4	0
3	A	97	0	0	0	0
3	B	122	0	0	0	0
3	C	141	0	0	1	1
3	D	112	0	0	1	1
3	E	37	0	0	0	0
3	F	36	0	0	0	0
All	All	8744	0	7982	27	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 2.

All (27) 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:209:ILE:H	1:B:5:GLN:HE21	1.28	0.81
2:E:8:U:H6	2:E:8:U:H5''	1.48	0.78
2:F:8:U:H6	2:F:8:U:H5''	1.50	0.76
1:C:5:GLN:HE21	1:D:209:ILE:H	1.53	0.55
1:B:55:LYS:HE2	1:B:114:ARG:NH1	2.21	0.55
2:E:8:U:H5''	2:E:8:U:C6	2.37	0.52
1:A:209:ILE:N	1:B:5:GLN:HE21	2.02	0.51
1:C:25:VAL:HG11	1:D:122:LEU:HD22	1.93	0.49
1:D:62:LEU:CD2	1:D:146:HIS:CD2	2.95	0.49
1:D:91:LYS:HG2	3:D:412:HOH:O	2.13	0.47
1:D:62:LEU:HD23	1:D:146:HIS:CD2	2.50	0.47
2:F:8:U:H5''	2:F:8:U:C6	2.39	0.47
1:B:209:ILE:HG22	1:B:214:ARG:HG3	1.98	0.46
2:F:8:U:H6	2:F:8:U:C5'	2.25	0.45
1:B:62:LEU:HD11	1:B:115:THR:HG23	1.99	0.44
1:D:144:MET:HE3	1:D:223:LEU:HD22	1.99	0.44
2:E:8:U:C6	2:E:8:U:C5'	3.01	0.43
1:B:144:MET:HE3	1:B:223:LEU:HD22	2.00	0.42
1:A:165:ILE:HD13	1:A:234:VAL:HG11	2.00	0.42
1:C:25:VAL:HG11	1:D:122:LEU:CD2	2.50	0.42
1:C:144:MET:HE3	1:C:223:LEU:HD22	2.02	0.41
1:C:21:ILE:CG2	1:D:121:VAL:HG11	2.50	0.41
1:A:144:MET:HE3	1:A:223:LEU:HD22	2.01	0.41
1:C:114:ARG:NH2	3:C:429:HOH:O	2.53	0.41
1:D:184:LEU:HB3	1:D:192:VAL:HG22	2.02	0.41
1:B:165:ILE:HD13	1:B:234:VAL:HG11	2.03	0.41
2:F:8:U:C6	2:F:8:U:C5'	3.02	0.40

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)
3:C:316:HOH:O	3:D:313:HOH:O[2_554]	2.11	0.09

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	242/245 (99%)	234 (97%)	6 (2%)	2 (1%)	16	10
1	B	242/245 (99%)	234 (97%)	6 (2%)	2 (1%)	16	10
1	C	242/245 (99%)	234 (97%)	7 (3%)	1 (0%)	30	26
1	D	242/245 (99%)	234 (97%)	6 (2%)	2 (1%)	16	10
All	All	968/980 (99%)	936 (97%)	25 (3%)	7 (1%)	18	13

All (7) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	209	ILE
1	B	209	ILE
1	C	209	ILE
1	D	209	ILE
1	A	97	PRO
1	B	97	PRO
1	D	97	PRO

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	197/198 (100%)	195 (99%)	2 (1%)	68	75
1	B	197/198 (100%)	196 (100%)	1 (0%)	81	87
1	C	197/198 (100%)	195 (99%)	2 (1%)	68	75

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	197/198 (100%)	195 (99%)	2 (1%)	68	75
All	All	788/792 (100%)	781 (99%)	7 (1%)	70	77

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	VAL
1	A	80	LYS
1	B	80	LYS
1	C	25	VAL
1	C	80	LYS
1	D	25	VAL
1	D	80	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	GLN
1	A	88	ASN
1	A	181	ASN
1	A	183	ASN
1	B	5	GLN
1	B	10	GLN
1	B	19	ASN
1	B	88	ASN
1	B	198	GLN
1	B	239	GLN
1	C	5	GLN
1	C	31	GLN
1	C	88	ASN
1	C	181	ASN
1	C	183	ASN
1	C	239	GLN
1	D	88	ASN
1	D	239	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	E	13/14 (92%)	2 (15%)	1 (7%)
2	F	13/14 (92%)	2 (15%)	1 (7%)
All	All	26/28 (92%)	4 (15%)	2 (7%)

All (4) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	E	8	U
2	E	9	U
2	F	8	U
2	F	9	U

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	E	8	U
2	F	8	U

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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	244/245 (99%)	0.16	7 (2%) 53 57	16, 42, 84, 102	0
1	B	244/245 (99%)	-0.01	7 (2%) 53 57	18, 34, 61, 73	0
1	C	244/245 (99%)	-0.18	6 (2%) 58 62	15, 31, 62, 89	0
1	D	244/245 (99%)	0.10	6 (2%) 58 62	16, 37, 72, 98	0
2	E	14/14 (100%)	-0.73	0 100 100	28, 36, 43, 47	0
2	F	14/14 (100%)	-0.81	0 100 100	30, 34, 40, 40	0
All	All	1004/1008 (99%)	-0.01	26 (2%) 57 61	15, 35, 71, 102	0

All (26) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	217	PHE	4.2
1	A	221	PHE	3.8
1	B	2	ASP	3.6
1	A	184	LEU	3.5
1	B	184	LEU	2.9
1	D	2	ASP	2.9
1	C	184	LEU	2.9
1	D	221	PHE	2.9
1	C	185	ARG	2.4
1	A	186	GLY	2.4
1	C	2	ASP	2.4
1	B	226	SER	2.4
1	D	184	LEU	2.4
1	B	183	ASN	2.4
1	A	3	ASN	2.3
1	B	14	GLN	2.3
1	A	242	LYS	2.3
1	D	186	GLY	2.3
1	A	245	ALA	2.1

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Mol	Chain	Res	Type	RSRZ
1	D	187	ARG	2.1
1	C	186	GLY	2.1
1	C	183	ASN	2.1
1	B	16	VAL	2.1
1	D	242	LYS	2.1
1	B	217	PHE	2.1
1	C	207	ASN	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 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.