



# Full wwPDB X-ray Structure Validation Report ⓘ

Dec 3, 2023 – 02:16 am GMT

PDB ID : 2C86  
Title : x-ray structure of the N and C-terminal domain of coronavirus nucleocapsid protein.  
Authors : Jayaram, H.; Fan, H.; Bowman, B.R.; Ooi, A.; Jayaram, J.; Collinson, E.W.; Lescar, J.; Prasad, B.V.V.  
Deposited on : 2005-12-02  
Resolution : 3.00 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](mailto: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>.

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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 : 2.36  
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) : 2.36

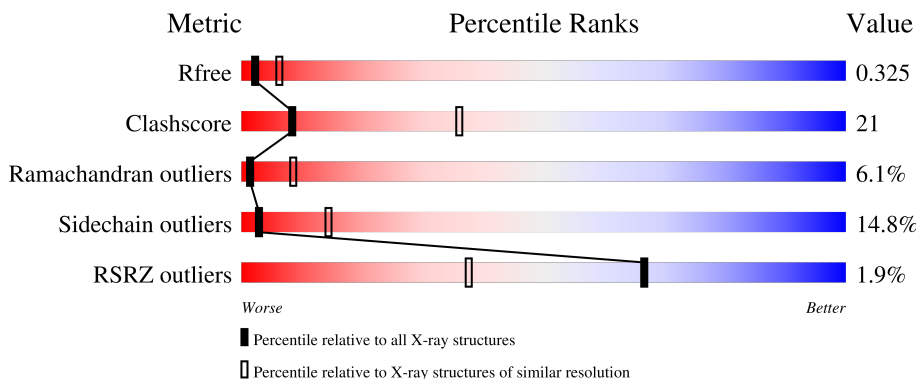
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*


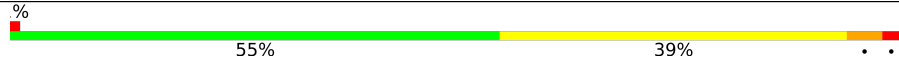
The reported resolution of this entry is 3.00 Å.

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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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  $\geq 3$ , 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	134	
1	B	134	

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2164 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
			Total	C	N	O	S			
1	A	134	1065	675	192	196	2	0	0	0
1	B	134	1065	675	192	196	2	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	85	CYS	LYS	engineered mutation	UNP P69598
B	85	CYS	LYS	engineered mutation	UNP P69598

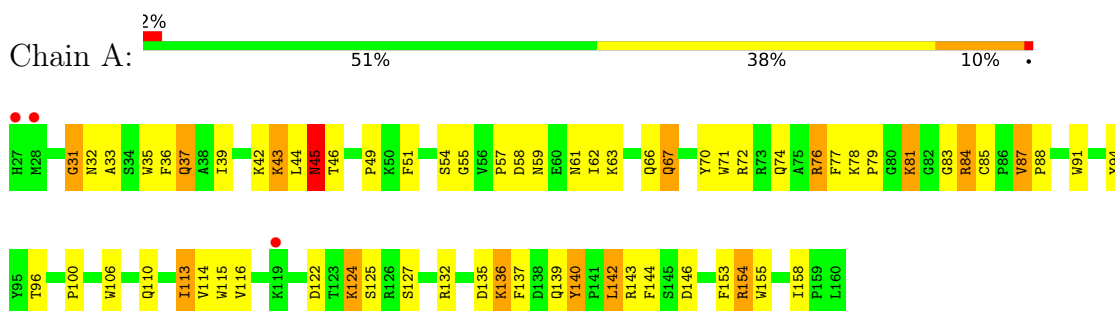
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	20	20	20	0	0
2	B	14	14	14	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: NUCLEOCAPSID PROTEIN



- Molecule 1: NUCLEOCAPSID PROTEIN



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	71.40Å 96.66Å 66.59Å 90.00° 98.53° 90.00°	Depositor
Resolution (Å)	20.00 – 3.00 19.99 – 3.00	Depositor EDS
% Data completeness (in resolution range)	96.6 (20.00-3.00) 96.6 (19.99-3.00)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.75 (at 2.98Å)	Xtrriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.266 , 0.328 0.269 , 0.325	Depositor DCC
$R_{free}$ test set	413 reflections (4.76%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	63.3	Xtrriage
Anisotropy	0.637	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 83.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.46$ , $\langle L^2 \rangle = 0.29$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.88	EDS
Total number of atoms	2164	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	57.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.56% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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	0.53	0/1104	0.64	0/1498
1	B	0.55	0/1104	0.63	0/1498
All	All	0.54	0/2208	0.64	0/2996

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	1065	0	991	54	0
1	B	1065	0	991	32	0
2	A	20	0	0	0	0
2	B	14	0	0	0	0
All	All	2164	0	1982	86	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 21.

All (86) 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:67:GLN:HE21	1:B:67:GLN:HA	1.45	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:58:ASP:HB2	1:B:143:ARG:HB2	1.66	0.77
1:A:135:ASP:N	1:A:136:LYS:HA	2.03	0.73
1:B:150:ASP:OD2	1:B:152:ASN:HB2	1.88	0.73
1:A:35:TRP:HA	1:A:132:ARG:HB2	1.70	0.73
1:A:67:GLN:HE21	1:A:67:GLN:HA	1.54	0.71
1:B:101:ALA:HB1	1:B:104:LEU:HD12	1.72	0.71
1:A:37:GLN:OE1	1:A:155:TRP:HD1	1.74	0.70
1:B:36:PHE:HA	1:B:140:TYR:H	1.60	0.67
1:A:45:ASN:HD22	1:A:45:ASN:H	1.42	0.67
1:A:37:GLN:HE21	1:A:158:ILE:HD12	1.63	0.64
1:A:37:GLN:OE1	1:A:155:TRP:CD1	2.52	0.63
1:A:71:TRP:O	1:A:113:ILE:HA	1.99	0.63
1:A:59:ASN:O	1:A:62:ILE:HG22	1.99	0.62
1:A:66:GLN:HE22	1:A:127:SER:HA	1.65	0.61
1:B:70:TYR:HB3	1:B:115:TRP:CZ3	2.36	0.61
1:A:72:ARG:HD2	1:A:100:PRO:HG2	1.83	0.60
1:A:70:TYR:HB2	1:A:113:ILE:HG22	1.83	0.59
1:A:31:GLY:CA	1:A:32:ASN:HB2	2.34	0.56
1:A:72:ARG:O	1:A:91:TRP:HA	2.05	0.56
1:A:43:LYS:O	1:A:88:PRO:HB3	2.06	0.55
1:A:71:TRP:HB2	1:A:114:VAL:HB	1.89	0.54
1:A:67:GLN:HA	1:A:67:GLN:NE2	2.22	0.54
1:B:139:GLN:H	1:B:140:TYR:HA	1.72	0.54
1:A:87:VAL:HB	1:A:88:PRO:HD2	1.89	0.54
1:A:51:PHE:CD2	1:A:55:GLY:HA2	2.43	0.53
1:A:70:TYR:HB3	1:A:115:TRP:CZ3	2.44	0.53
1:B:29:SER:HB3	1:B:32:ASN:OD1	2.08	0.53
1:B:76:ARG:HH11	1:B:90:ALA:HB2	1.72	0.53
1:B:38:ALA:HB2	1:B:92:TYR:CE2	2.43	0.53
1:B:67:GLN:HA	1:B:67:GLN:NE2	2.21	0.52
1:A:70:TYR:HB2	1:A:113:ILE:CG2	2.39	0.51
1:A:106:TRP:NE1	1:A:116:VAL:O	2.34	0.51
1:A:33:ALA:HB3	1:A:132:ARG:O	2.11	0.51
1:A:63:LYS:HB2	1:A:66:GLN:HG3	1.93	0.51
1:A:35:TRP:O	1:A:140:TYR:HB2	2.11	0.50
1:B:93:PHE:HE2	1:B:95:TYR:CE2	2.29	0.50
1:B:37:GLN:HB3	1:B:139:GLN:HG3	1.94	0.50
1:B:132:ARG:HG3	1:B:137:PHE:HB3	1.93	0.50
1:B:72:ARG:HD2	1:B:100:PRO:HG2	1.94	0.50
1:A:54:SER:N	1:A:146:ASP:OD2	2.44	0.49
1:A:76:ARG:NE	1:A:88:PRO:O	2.38	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:156:ASP:OD1	1:B:156:ASP:N	2.44	0.49
1:A:37:GLN:CB	1:A:139:GLN:HE21	2.27	0.48
1:B:37:GLN:NE2	1:B:155:TRP:HD1	2.11	0.48
1:B:70:TYR:HB3	1:B:115:TRP:CE3	2.49	0.48
1:A:132:ARG:CD	1:A:137:PHE:O	2.61	0.48
1:B:41:ALA:HA	1:B:153:PHE:CD2	2.50	0.47
1:B:51:PHE:CD2	1:B:55:GLY:HA2	2.50	0.47
1:A:42:LYS:HG3	1:A:154:ARG:HG2	1.96	0.47
1:A:37:GLN:CA	1:A:139:GLN:HG2	2.45	0.47
1:B:71:TRP:HA	1:B:92:TYR:O	2.16	0.46
1:B:49:PRO:HB2	1:B:51:PHE:CE1	2.51	0.46
1:A:31:GLY:HA2	1:A:32:ASN:HB2	1.98	0.46
1:A:77:PHE:CD1	1:A:84:ARG:NH2	2.83	0.45
1:A:58:ASP:HB2	1:A:143:ARG:HG3	1.98	0.45
1:A:37:GLN:HB3	1:A:139:GLN:HG2	1.99	0.45
1:A:66:GLN:NE2	1:A:127:SER:HA	2.30	0.45
1:A:45:ASN:HD22	1:A:45:ASN:N	2.05	0.45
1:A:72:ARG:HD2	1:A:100:PRO:CG	2.46	0.45
1:A:122:ASP:HB3	1:A:125:SER:HB3	1.98	0.45
1:A:78:LYS:HD3	1:A:79:PRO:O	2.16	0.45
1:A:132:ARG:HD2	1:A:137:PHE:O	2.18	0.44
1:B:73:ARG:HB2	1:B:91:TRP:CZ2	2.53	0.44
1:A:36:PHE:CD2	1:A:140:TYR:HB3	2.52	0.44
1:A:124:LYS:HB2	1:A:124:LYS:HE2	1.89	0.43
1:A:44:LEU:O	1:A:46:THR:N	2.52	0.43
1:B:37:GLN:HE21	1:B:142:LEU:HB2	1.84	0.43
1:A:39:ILE:HG13	1:A:39:ILE:O	2.19	0.42
1:B:101:ALA:HB1	1:B:104:LEU:CD1	2.47	0.42
1:B:37:GLN:NE2	1:B:155:TRP:CD1	2.86	0.42
1:B:63:LYS:HA	1:B:64:PRO:HD2	1.60	0.42
1:A:83:GLY:O	1:A:84:ARG:HG3	2.19	0.42
1:A:31:GLY:N	1:A:32:ASN:HB2	2.34	0.42
1:A:42:LYS:HE3	1:A:154:ARG:HB3	2.01	0.42
1:A:70:TYR:CE2	1:A:94:TYR:HB2	2.55	0.42
1:B:37:GLN:HB3	1:B:139:GLN:HE21	1.85	0.41
1:A:37:GLN:HA	1:A:139:GLN:HG2	2.02	0.41
1:A:57:PRO:HB3	1:A:142:LEU:CD2	2.51	0.41
1:B:143:ARG:O	1:B:144:PHE:CD2	2.74	0.41
1:A:31:GLY:HA2	1:A:32:ASN:CB	2.50	0.41
1:B:87:VAL:HB	1:B:88:PRO:CD	2.51	0.41
1:B:56:VAL:HA	1:B:57:PRO:HD3	1.94	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:77:PHE:HA	1:A:85:CYS:O	2.22	0.41
1:B:77:PHE:CD1	1:B:84:ARG:NH2	2.88	0.40
1:A:49:PRO:HA	1:A:153:PHE:CE1	2.56	0.40

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	132/134 (98%)	109 (83%)	19 (14%)	4 (3%)	4	24
1	B	132/134 (98%)	108 (82%)	12 (9%)	12 (9%)	1	3
All	All	264/268 (98%)	217 (82%)	31 (12%)	16 (6%)	1	8

All (16) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	45	ASN
1	B	64	PRO
1	B	144	PHE
1	A	31	GLY
1	A	81	LYS
1	B	147	GLY
1	A	37	GLN
1	B	45	ASN
1	B	54	SER
1	B	61	ASN
1	B	96	THR
1	B	108	ASP
1	B	137	PHE
1	B	67	GLN
1	B	119	LYS

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Mol	Chain	Res	Type
1	B	159	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	108/108 (100%)	90 (83%)	18 (17%)	2	11
1	B	108/108 (100%)	94 (87%)	14 (13%)	4	19
All	All	216/216 (100%)	184 (85%)	32 (15%)	3	14

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	43	LYS
1	A	45	ASN
1	A	61	ASN
1	A	67	GLN
1	A	74	GLN
1	A	76	ARG
1	A	81	LYS
1	A	84	ARG
1	A	87	VAL
1	A	96	THR
1	A	110	GLN
1	A	113	ILE
1	A	124	LYS
1	A	136	LYS
1	A	140	TYR
1	A	142	LEU
1	A	144	PHE
1	A	154	ARG
1	B	43	LYS
1	B	63	LYS
1	B	67	GLN
1	B	74	GLN

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Mol	Chain	Res	Type
1	B	96	THR
1	B	114	VAL
1	B	123	THR
1	B	135	ASP
1	B	137	PHE
1	B	140	TYR
1	B	144	PHE
1	B	154	ARG
1	B	156	ASP
1	B	160	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	45	ASN
1	A	66	GLN
1	A	67	GLN
1	A	139	GLN
1	B	37	GLN
1	B	67	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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	134/134 (100%)	-0.07	3 (2%) 62 33	39, 58, 74, 87	0
1	B	134/134 (100%)	0.06	2 (1%) 73 46	39, 58, 74, 87	0
All	All	268/268 (100%)	-0.00	5 (1%) 66 37	39, 58, 74, 87	0

All (5) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	28	MET	3.2
1	B	27	HIS	2.8
1	A	27	HIS	2.4
1	B	135	ASP	2.2
1	A	119	LYS	2.1

### 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.