



wwPDB X-ray Structure Validation Summary Report ⓘ

May 16, 2020 – 03:08 am BST

PDB ID : 1NOV
Title : NODAMURA VIRUS
Authors : Natarajan, P.; Johnson, J.E.
Deposited on : 1997-09-16
Resolution : 3.50 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	:	2.11
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)	:	2.11

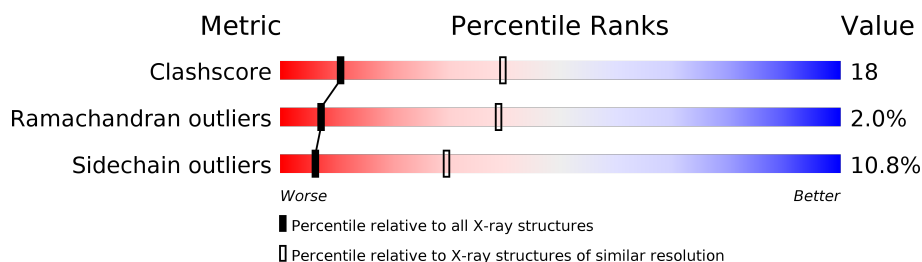
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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))
Clashscore	141614	1036 (3.58-3.42)
Ramachandran outliers	138981	1005 (3.58-3.42)
Sidechain outliers	138945	1006 (3.58-3.42)

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 $\leq 5\%$.

Mol	Chain	Length	Quality of chain
1	A	355	
1	B	355	
1	C	355	
2	D	44	
2	E	44	
2	F	44	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7451 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 NODAMURA VIRUS COAT PROTEINS.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	309	Total	C	N	O	S	0	0	0
			2300	1468	373	445	14			
1	B	309	Total	C	N	O	S	0	0	0
			2297	1465	373	445	14			
1	C	324	Total	C	N	O	S	0	0	0
			2434	1541	412	467	14			

- Molecule 2 is a protein called NODAMURA VIRUS COAT PROTEINS.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	D	20	Total	C	N	O	0	0	0
			149	96	28	25			
2	E	17	Total	C	N	O	0	0	0
			134	87	25	22			
2	F	17	Total	C	N	O	0	0	0
			137	88	26	23			

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	562.09Å 354.13Å 612.77Å 90.00° 110.89° 90.00°	Depositor
Resolution (Å)	8.00 – 3.50 20.00 – 3.30	Depositor EDS
% Data completeness (in resolution range)	48.1 (8.00-3.50) 51.3 (20.00-3.30)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	8.10 (at 3.29Å)	Xtriage
Refinement program	X-PLOR 3.8	Depositor
R, R_{free}	0.296 , (Not available) 0.486 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	27.4	Xtriage
Anisotropy	0.234	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 78.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.38$, $\langle L^2 \rangle = 0.20$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.06	EDS
Total number of atoms	7451	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.65% 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	0.42	0/2356	0.77	2/3221 (0.1%)
1	B	0.42	0/2353	0.78	3/3217 (0.1%)
1	C	0.42	0/2490	0.79	6/3396 (0.2%)
2	D	0.47	0/151	0.71	0/203
2	E	0.48	0/136	0.78	0/182
2	F	0.50	0/139	0.88	1/186 (0.5%)
All	All	0.42	0/7625	0.78	12/10405 (0.1%)

There are no bond length outliers.

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	15	ARG	N-CA-C	6.45	128.42	111.00
1	C	329	LEU	CA-CB-CG	5.98	129.06	115.30
1	B	263	PRO	N-CA-C	-5.63	97.45	112.10
1	C	263	PRO	N-CA-C	-5.52	97.74	112.10
1	A	503	PRO	N-CA-C	-5.49	97.83	112.10

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	2300	0	2250	94	0
1	B	2297	0	2241	84	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	2434	0	2387	102	0
2	D	149	0	143	8	0
2	E	134	0	134	3	0
2	F	137	0	138	10	0
All	All	7451	0	7293	269	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 18.

The worst 5 of 269 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:502:VAL:HB	1:C:503:PRO:HD3	1.35	1.08
1:A:180:ASN:HB3	1:A:183:GLN:HB2	1.40	1.02
1:A:502:VAL:HB	1:A:503:PRO:HD3	1.40	0.99
1:A:156:ALA:HB3	1:A:287:ARG:HD2	1.42	0.99
1:A:171:MET:HB2	1:A:294:MET:HE3	1.49	0.94

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	307/355 (86%)	280 (91%)	20 (6%)	7 (2%)	6	36
1	B	307/355 (86%)	282 (92%)	19 (6%)	6 (2%)	7	39
1	C	320/355 (90%)	291 (91%)	24 (8%)	5 (2%)	9	43
2	D	18/44 (41%)	14 (78%)	2 (11%)	2 (11%)	0	6
2	E	15/44 (34%)	15 (100%)	0	0	100	100
2	F	15/44 (34%)	14 (93%)	1 (7%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	982/1197 (82%)	896 (91%)	66 (7%)	20 (2%)	7 39

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	159	THR
2	D	380	PHE
1	C	17	ALA
1	C	82	LYS
1	A	56	MET

5.3.2 Protein sidechains ⓘ

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	246/287 (86%)	221 (90%)	25 (10%)	7 32
1	B	245/287 (85%)	227 (93%)	18 (7%)	14 45
1	C	259/287 (90%)	223 (86%)	36 (14%)	3 20
2	D	13/34 (38%)	13 (100%)	0	100 100
2	E	13/34 (38%)	12 (92%)	1 (8%)	13 42
2	F	14/34 (41%)	9 (64%)	5 (36%)	0 1
All	All	790/963 (82%)	705 (89%)	85 (11%)	6 30

5 of 85 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	276	THR
1	C	28	ARG
1	C	356	ILE
1	B	289	THR
2	E	378	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 22 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	213	ASN
1	B	339	ASN
1	C	253	HIS
1	B	309	ASN
1	B	326	ASN

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 carbohydrates 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 ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers ⓘ

Unable to reproduce the depositors R factor - this section is therefore empty.