



wwPDB X-ray Structure Validation Summary Report ⓘ

May 13, 2020 – 07:27 am BST

PDB ID : 4XZE
Title : The crystal structure of Hazara virus nucleoprotein
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Deposited on : 2015-02-04
Resolution : 2.90 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

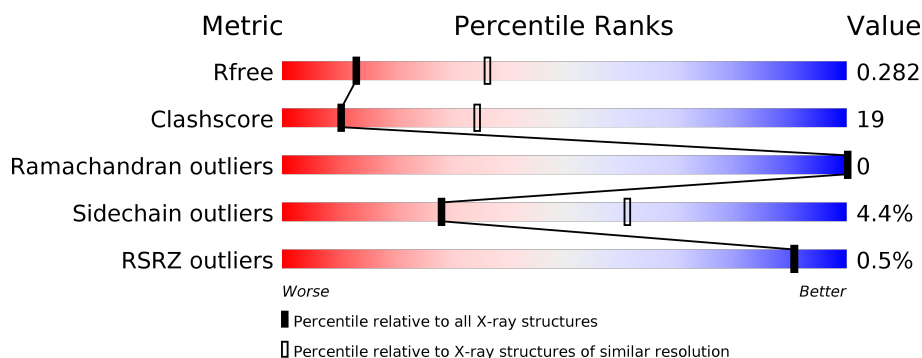
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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 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 $\leq 5\%$. 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	488	<div> <div></div> <div>70%25%••</div> </div>
1	B	488	<div> <div></div> <div>61%35%••</div> </div>
1	C	488	<div> <div>%</div> <div>58%37%••</div> </div>
1	D	488	<div> <div>%</div> <div>53%41%•5%</div> </div>

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 14978 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	472	Total	C	N	O	S	0	0	0
			3726	2371	635	702	18			
1	B	473	Total	C	N	O	S	0	0	0
			3738	2379	637	704	18			
1	C	474	Total	C	N	O	S	0	0	0
			3733	2375	637	703	18			
1	D	466	Total	C	N	O	S	0	0	0
			3677	2341	626	692	18			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	LEU	-	expression tag	UNP M4PWE6
A	-1	GLY	-	expression tag	UNP M4PWE6
A	0	SER	-	expression tag	UNP M4PWE6
B	-2	LEU	-	expression tag	UNP M4PWE6
B	-1	GLY	-	expression tag	UNP M4PWE6
B	0	SER	-	expression tag	UNP M4PWE6
C	-2	LEU	-	expression tag	UNP M4PWE6
C	-1	GLY	-	expression tag	UNP M4PWE6
C	0	SER	-	expression tag	UNP M4PWE6
D	-2	LEU	-	expression tag	UNP M4PWE6
D	-1	GLY	-	expression tag	UNP M4PWE6
D	0	SER	-	expression tag	UNP M4PWE6

- Molecule 2 is water.

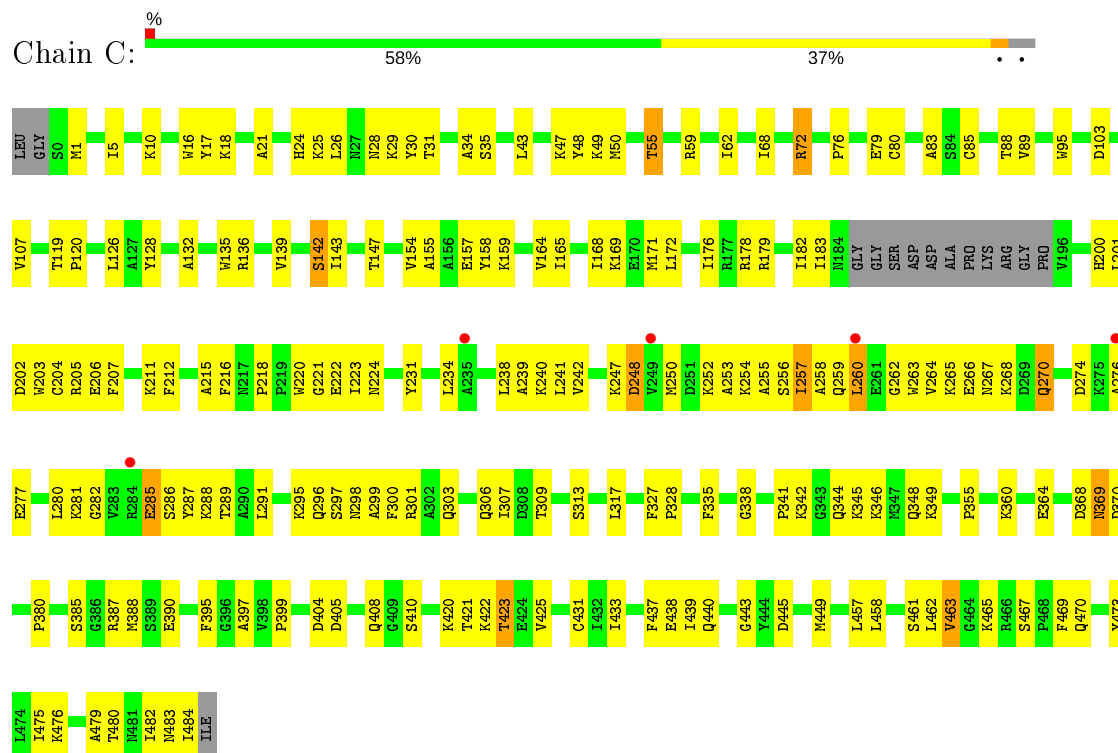
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	41	Total	O	0	0
			41	41		
2	B	27	Total	O	0	0
			27	27		

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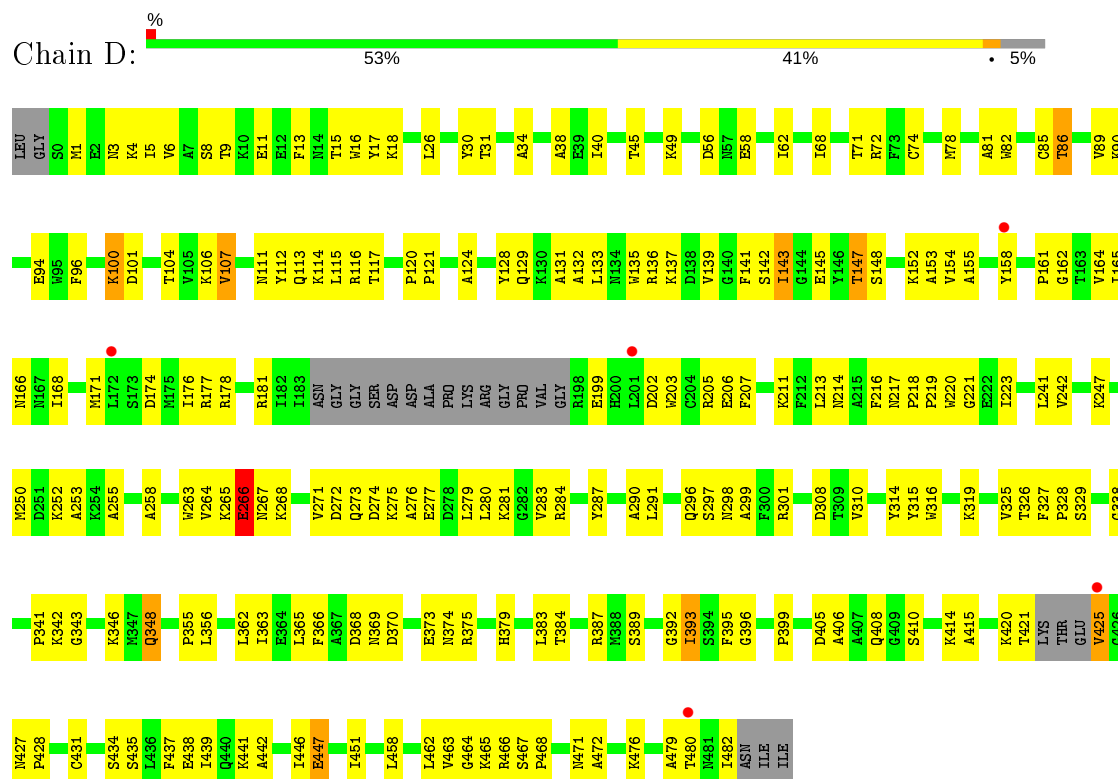
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	18	Total	O	0	0
			18	18		
2	D	18	Total	O	0	0
			18	18		

- Molecule 1: Nucleoprotein



- Molecule 1: Nucleoprotein



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	67.40Å 72.17Å 453.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.22 – 2.90 48.22 – 2.90	Depositor EDS
% Data completeness (in resolution range)	84.7 (48.22-2.90) 84.7 (48.22-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.18 (at 2.91Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7_650)	Depositor
R, R_{free}	0.206 , 0.287 0.203 , 0.282	Depositor DCC
R_{free} test set	2096 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	49.7	Xtriage
Anisotropy	0.345	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 69.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	14978	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.14% 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	0.28	0/3805	0.47	0/5138
1	B	0.28	0/3817	0.48	0/5155
1	C	0.27	0/3812	0.47	1/5150 (0.0%)
1	D	0.27	0/3755	0.49	0/5071
All	All	0.27	0/15189	0.48	1/20514 (0.0%)

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	1
1	D	0	1
All	All	0	2

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	369	ASN	N-CA-C	5.71	126.41	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	369	ASN	Peptide
1	D	266	GLU	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	3726	0	3719	95	0
1	B	3738	0	3733	139	0
1	C	3733	0	3719	157	0
1	D	3677	0	3661	170	0
2	A	41	0	0	4	0
2	B	27	0	0	3	0
2	C	18	0	0	1	0
2	D	18	0	0	3	0
All	All	14978	0	14832	552	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 19.

The worst 5 of 552 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:159:LYS:HA	1:B:485:ILE:HG23	1.40	1.01
1:A:420:LYS:HD3	1:A:422:LYS:HE2	1.44	0.94
1:C:159:LYS:HD2	1:C:423:THR:HG21	1.50	0.94
1:C:369:ASN:H	1:C:370:ASP:HB3	1.30	0.94
1:B:369:ASN:H	1:B:370:ASP:HB3	1.35	0.91

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	468/488 (96%)	444 (95%)	24 (5%)	0	100	100
1	B	469/488 (96%)	453 (97%)	16 (3%)	0	100	100
1	C	470/488 (96%)	443 (94%)	27 (6%)	0	100	100
1	D	460/488 (94%)	430 (94%)	30 (6%)	0	100	100
All	All	1867/1952 (96%)	1770 (95%)	97 (5%)	0	100	100

There are no Ramachandran outliers to report.

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	397/408 (97%)	381 (96%)	16 (4%)	31	65
1	B	399/408 (98%)	386 (97%)	13 (3%)	38	72
1	C	397/408 (97%)	379 (96%)	18 (4%)	27	61
1	D	391/408 (96%)	368 (94%)	23 (6%)	19	49
All	All	1584/1632 (97%)	1514 (96%)	70 (4%)	28	61

5 of 70 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	72	ARG
1	C	285	GLU
1	D	421	THR
1	C	142	SER
1	C	257	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 6 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	306	GLN
1	D	273	GLN
1	D	113	GLN

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Mol	Chain	Res	Type
1	B	440	GLN
1	D	214	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 [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	472/488 (96%)	-0.30	0	100 100	23, 41, 65, 93	0
1	B	473/488 (96%)	-0.23	0	100 100	27, 46, 71, 97	0
1	C	474/488 (97%)	-0.13	5 (1%)	80 80	23, 54, 82, 97	0
1	D	466/488 (95%)	0.07	5 (1%)	80 80	32, 63, 82, 96	0
All	All	1885/1952 (96%)	-0.15	10 (0%)	91 91	23, 51, 79, 97	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	480	THR	3.2
1	D	172	LEU	2.7
1	D	201	LEU	2.7
1	C	284	ARG	2.4
1	C	260	LEU	2.3

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.