



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 19, 2021 – 08:53 AM JST

PDB ID : 7DXP
Title : Influenza H5N1 nucleoprotein in complex with nucleotides
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Deposited on : 2021-01-19
Resolution : 2.30 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
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.18
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) : 2.18

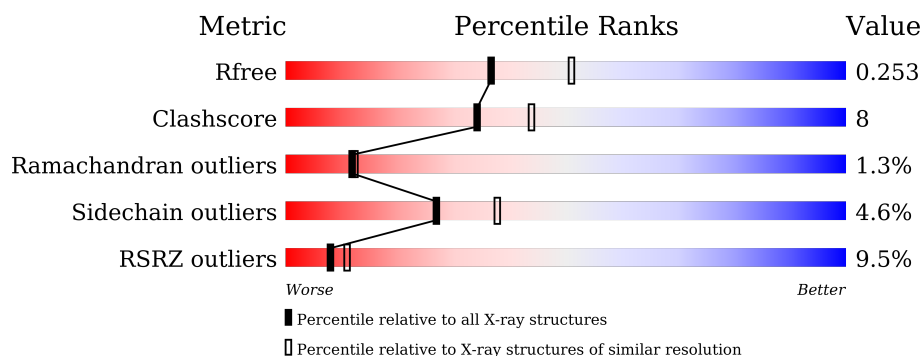
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	507	
1	B	507	
2	C	9	

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6727 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.

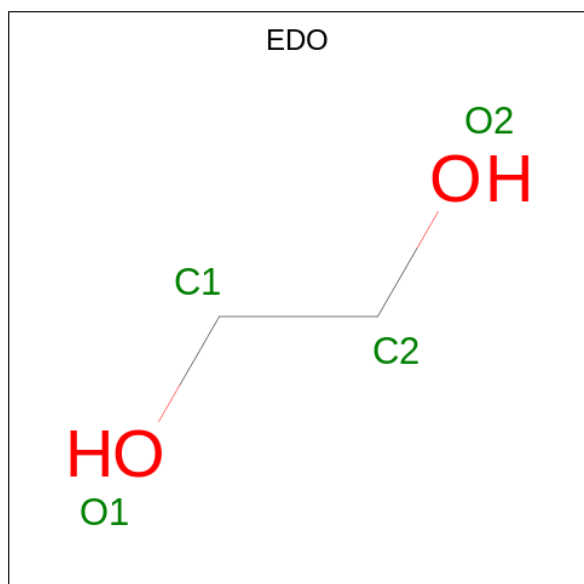
- Molecule 1 is a protein called Nucleoprotein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	399	Total	C	N	O	S	0	1	0
			3161	1966	585	584	26			
1	B	418	Total	C	N	O	S	0	3	0
			3337	2066	632	613	26			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	4	Total	C	N	O	P	0	0	0
			66	30	6	26	4			

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		

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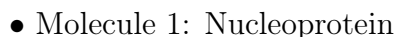
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	63	Total	O	0	0
			63	63		
4	B	92	Total	O	0	0
			92	92		

- Molecule 1: Nucleoprotein



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

Chain C:  11% 33% 56%

U1	U2	U3	U4	OMU	OMU	OMU	OMU
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	54.01Å 60.63Å 82.71Å 106.70° 109.01° 96.62°	Depositor
Resolution (Å)	24.50 – 2.30 24.46 – 2.30	Depositor EDS
% Data completeness (in resolution range)	90.3 (24.50-2.30) 90.4 (24.46-2.30)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 2.31Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.193 , 0.248 0.202 , 0.253	Depositor DCC
R_{free} test set	1866 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	26.9	Xtriage
Anisotropy	0.033	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 58.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	6727	wwPDB-VP
Average B, all atoms (Å ²)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.00% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, OMU

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	1/3213 (0.0%)	0.90	1/4312 (0.0%)
1	B	0.78	0/3392	0.94	3/4551 (0.1%)
All	All	0.77	1/6605 (0.0%)	0.92	4/8863 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	320	GLU	CD-OE1	5.09	1.31	1.25

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	293	ARG	NE-CZ-NH2	-5.64	117.48	120.30
1	B	348	ARG	NE-CZ-NH2	-5.50	117.55	120.30
1	A	351	ARG	CG-CD-NE	-5.31	100.65	111.80
1	B	117	ARG	NE-CZ-NH2	-5.20	117.70	120.30

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	3161	0	3146	43	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3337	0	3318	62	0
2	C	66	0	36	6	0
3	A	4	0	6	3	0
3	B	4	0	6	1	0
4	A	63	0	0	2	0
4	B	92	0	0	2	0
All	All	6727	0	6512	110	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 8.

The worst 5 of 110 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)
2:C:2:OMU:O4'	2:C:2:OMU:C1'	1.63	1.30
2:C:1:OMU:O4'	2:C:1:OMU:C1'	1.66	1.24
2:C:3:OMU:O4'	2:C:3:OMU:C1'	1.67	1.23
1:B:121[B]:ARG:HH11	1:B:121[B]:ARG:HG2	1.00	1.09
1:B:121[B]:ARG:HH11	1:B:121[B]:ARG:CG	1.75	0.95

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	388/507 (76%)	376 (97%)	8 (2%)	4 (1%)	15	17
1	B	413/507 (82%)	396 (96%)	10 (2%)	7 (2%)	9	8
All	All	801/1014 (79%)	772 (96%)	18 (2%)	11 (1%)	12	11

5 of 11 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	129	ALA
1	B	23	THR
1	B	77	ARG
1	B	210	GLU
1	B	461	ARG

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	335/422 (79%)	318 (95%)	17 (5%)	24	33
1	B	350/422 (83%)	335 (96%)	15 (4%)	29	40
All	All	685/844 (81%)	653 (95%)	32 (5%)	27	37

5 of 32 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	371	VAL
1	B	438	SER
1	A	439	ASP
1	A	438	SER
1	B	450	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	149	GLN
1	B	327	GLN
1	B	364	GLN
1	A	211	ASN
1	A	327	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	OMU	C	4	2	0,2,23	0.00	-	0,1,34	0.00	-
2	OMU	C	3	2	14,22,23	6.53	9 (64%)	14,31,34	1.37	2 (14%)
2	OMU	C	1	2	14,22,23	6.47	9 (64%)	14,31,34	1.52	3 (21%)
2	OMU	C	2	2	14,22,23	5.99	8 (57%)	14,31,34	1.34	1 (7%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	OMU	C	3	2	-	1/7/27/28	0/2/2/2
2	OMU	C	1	2	-	6/7/27/28	0/2/2/2
2	OMU	C	2	2	-	0/7/27/28	0/2/2/2

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	3	OMU	O4'-C1'	19.25	1.67	1.41
2	C	1	OMU	O4'-C1'	17.83	1.66	1.41
2	C	2	OMU	O4'-C1'	16.34	1.63	1.41
2	C	2	OMU	C6-N1	7.65	1.45	1.35
2	C	1	OMU	C6-N1	7.48	1.45	1.35

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1	OMU	CM2-O2'-C2'	3.56	123.88	114.52
2	C	3	OMU	C6-N1-C2	-2.79	116.77	121.20
2	C	1	OMU	C2'-C3'-C4'	2.59	107.62	101.99

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	OMU	C5'-C4'-C3'	-2.14	107.15	115.18
2	C	1	OMU	O2'-C2'-C1'	2.08	113.21	109.09

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	1	OMU	C2'-C1'-N1-C6
2	C	1	OMU	O4'-C1'-N1-C6
2	C	1	OMU	C1'-C2'-O2'-CM2
2	C	1	OMU	C3'-C4'-C5'-O5'
2	C	1	OMU	O4'-C4'-C5'-O5'

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	3	OMU	1	0
2	C	1	OMU	3	0
2	C	2	OMU	2	0

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	EDO	B	501	-	3,3,3	0.57	0	2,2,2	0.66	0
3	EDO	A	501	-	3,3,3	0.76	0	2,2,2	0.90	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	B	501	-	-	1/1/1/1	-
3	EDO	A	501	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	501	EDO	O1-C1-C2-O2
3	A	501	EDO	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	501	EDO	1	0
3	A	501	EDO	3	0

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	399/507 (78%)	0.42	39 (9%) 7 10	16, 35, 72, 99	0
1	B	418/507 (82%)	0.37	39 (9%) 8 11	14, 30, 69, 97	1 (0%)
2	C	0/9	-	-	-	-
All	All	817/1023 (79%)	0.39	78 (9%) 8 11	14, 32, 71, 99	1 (0%)

The worst 5 of 78 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	85	ALA	6.0
1	A	73	GLU	5.8
1	B	205	ASN	5.2
1	B	214	ARG	5.1
1	A	89	PRO	4.8

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	OMU	C	1	21/22	0.82	0.22	43,54,74,77	0
2	OMU	C	4	3/22	0.87	0.31	67,67,71,74	0
2	OMU	C	3	21/22	0.93	0.14	33,40,57,68	0
2	OMU	C	2	21/22	0.96	0.11	38,43,53,54	0

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	EDO	A	501	4/4	0.89	0.20	33,41,42,47	0
3	EDO	B	501	4/4	0.90	0.28	34,42,44,45	0

6.5 Other polymers [i](#)

There are no such residues in this entry.