

Full wwPDB/EMDatabank EM Map/Model Validation Report ⓘ

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PDB ID : 6EHL
EMDB ID: : EMD-3869
Title : Model of the Ebola virus nucleoprotein in recombinant nucleocapsid-like assemblies
Authors : Wan, W.; Kolesnikova, L.; Clarke, M.; Koehler, A.; Noda, T.; Becker, S.; Briggs, J.A.G.
Deposited on : 2017-09-13
Resolution : 6.60 Å(reported)

This is a Full wwPDB/EMDatabank EM Map/Model Validation Report
for a publicly released PDB/EMDB entry.

We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030736

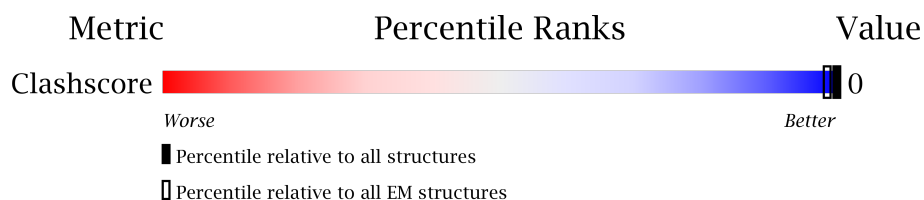
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY


The reported resolution of this entry is 6.60 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)	EM structures (#Entries)
Clashscore	125131	1336

The table below summarises the geometric issues observed across the polymeric chains. The red, orange, yellow and green segments on the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	739		53% 47%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 390 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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		AltConf	Trace
1	A	390	Total	C	0	390
			390	390		

- Molecule 1: Nucleoprotein

TYR	GLN	GLU	GLN	ASP	GLN	ASP	MET
PRO	ASP	ALA	LVS	LVS	ASP	SER	MET
ASP	HIS	ASP	ASN	ASN	GLN	GLN	ASP
SER	THR	PRO	SER	SER	THR	THR	ARG
LEU	GLN	LEU	GLN	GLN	LVS	THR	GLN
GLU	GLU	ASP	LVS	GLY	GLY	THR	LVS
GLU	ARG	ALA	GLN	GLN	PRO	PRO	LVS
GLU	ASN	ASP	HIS	HIS	ASP	TRP	ILE
TYR	GLN	ASP	ILE	ILE	VAL	MET	ALA
PRO	GLN	ASP	GLU	GLU	VAL	ALA	PRO
PRO	ASP	THR	GLY	GLY	VAL	VAL	ASP
TRP	SER	THR	THR	THR	VAL	VAL	SER
THR	ASN	SER	GLN	GLN	ARG	ASP	SER
GLU	THR	SER	THR	THR	THR	ASP	LEU
LVS	GLN	PRO	GLN	GLN	ASP	ASP	THR
GLU	SER	PRO	ARG	ARG	GLY	GLY	E16
ALA	GLU	LEU	ANG	ANG	SER	THR	L405
MET	HIS	GLU	PRO	PRO	TYR	THR	GLU
MET	SER	SER	ILE	ILE	GLY	GLY	ALA
ASN	PHE	ASP	ASN	ASN	GLU	GLU	ALA
GLU	GLU	ASP	GLN	GLN	TYR	TYR	ILE
ASN	GLU	ASP	VAL	VAL	GLN	THR	THR
ARG	MET	GLU	PRO	PRO	SER	ALA	ALA
PHE	THR	GLN	GLY	GLY	TYR	THR	ALA
VAL	ANG	ARG	ARG	HIS	SER	GLU	SER
THR	HIS	ASP	HIS	HIS	ASN	LEU	ASN
LEU	ILE	ASP	ARG	ARG	ASN	LVS	PRO
ASP	LEU	GLY	THR	THR	GLY	GLY	LVS
GLY	ARG	THR	ILE	ILE	MET	THR	THR
GLN	SER	ASN	HIS	HIS	ASN	SER	SER
GLN	GLY	ARG	ALA	ALA	ALA	ALA	GLY
PHE	GLY	ARG	ALA	ALA	PRO	PRO	HIS
TYR	PRO	THR	SER	SER	ASP	ASP	ASP
TRP	PHE	THR	ALA	ALA	ASP	ASP	ASP
PRO	ASP	THR	PRO	PRO	LEU	LEU	ASP
VAL	ALA	VAL	VAL	VAL	VAL	VAL	ASP
VAL	VAL	ALA	THR	THR	THR	THR	ASP
MET	VAL	PRO	ASN	ASN	ASP	ASP	ASP
ASN	HIS	PRO	ASP	ASP	ASP	ASP	ILE
LVS	THR	ALA	ASN	ASN	LEU	LEU	ILE
ASN	HIS	PRO	ARG	ARG	ASP	ASP	ASN
LVS	MET	VAL	ASN	ASN	GLU	GLU	ASN
PHE	MET	TYR	ARG	ARG	THR	THR	ASP
MET	LVS	ARG	GLU	GLU	PRO	PRO	GLN
ALA	ASP	ASP	PRO	PRO	GLY	GLY	GLY
ILE	GLU	HIS	SER	SER	ASN	THR	GLY
LEU	PRO	SER	GLY	GLY	SER	THR	PRO
LEU	VAL	GLU	SER	SER	THR	LVS	THR
GLN	VAL	LVS	THR	THR	VAL	VAL	THR
HIS	PHE	LVS	SER	SER	PRO	PRO	HIS
HIS	SER	GLU	PRO	PRO	ARG	GLY	GLN
GLN	THR	LEU	THR	THR	MET	ARG	ASP
	SER	PRO	MET	MET	THR	THR	ASP
	ASP	GLN	LEU	LEU	SER	SER	GLN
	GLY	GLU	THR	THR	THR	THR	ASP
	GLY	GLU	ILE	ILE	GLY	GLY	ASP
	THR	GLN	GLU	GLU	GLN	GLN	PRO
	THR	ASP	THR	THR	THR	THR	THR

4 Experimental information

Property	Value	Source
Reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	1	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY; CTF amplitude correction was performed during the wedge-weighted subtomogram averaging step.	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2.4	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	4500	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor

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).

There are no protein, RNA or DNA chains available to summarize Z scores of covalent bonds and angles.

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	390	0	0	0	0
All	All	390	0	0	0	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 0.

There are no clashes within the asymmetric unit.

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein backbone outliers to report in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein residues with a non-rotameric sidechain to report in this entry.

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.