



wwPDB EM Map/Model Validation Report ⓘ

Apr 10, 2016 – 01:40 PM BST

PDB ID : 2WFS
EMDB ID: : EMD-1603
Title : Fitting of influenza virus NP structure into the 9-fold symmetryzed cryoEM reconstruction of an active RNP particle.
Authors : Coloma, R.; Valpuesta, J.M.; Arranz, R.; Carrascosa, J.L.; Ortin, J.; Martin-Benito, J.
Deposited on : 2009-04-15
Resolution : 12.00 Å(reported)
Based on PDB ID : 2IQH

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could stem from errors in the original structure(s) used in the fitting.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<http://wwpdb.org/validation/2016/EMValidationReportHelp>

MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : trunk27241

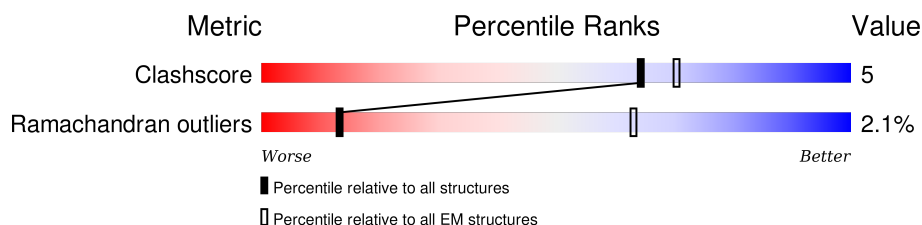
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 12.00 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)	EM structures (#Entries)
Clashscore	114402	924
Ramachandran outliers	111179	726

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	499	80% 5% • 15%
1	B	499	80% • • 15%
1	C	499	81% • • 15%
1	D	499	81% • • 15%
1	E	499	80% • • 15%
1	F	499	79% 5% • 15%
1	G	499	80% • • 15%
1	H	499	80% • • 15%
1	I	499	80% • • 15%

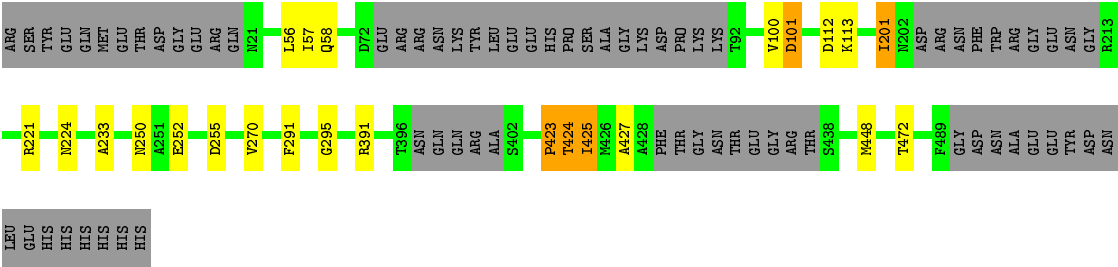
2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 15336 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.

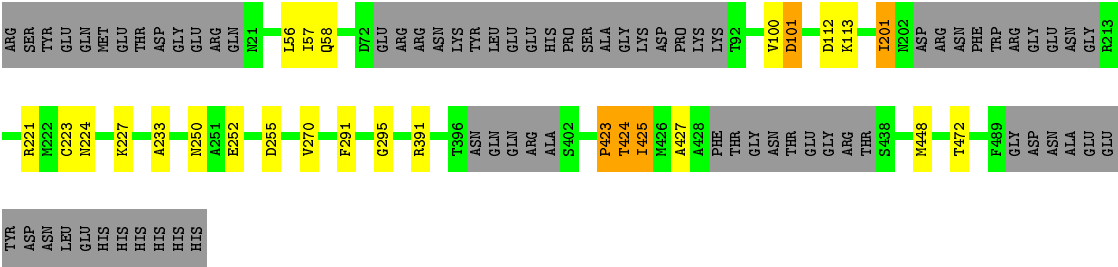
- Molecule 1 is a protein called NUCLEOPROTEIN.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	426	Total	C	N	O	0	0
			1704	852	426	426		
1	B	426	Total	C	N	O	0	0
			1704	852	426	426		
1	C	426	Total	C	N	O	0	0
			1704	852	426	426		
1	D	426	Total	C	N	O	0	0
			1704	852	426	426		
1	E	426	Total	C	N	O	0	0
			1704	852	426	426		
1	F	426	Total	C	N	O	0	0
			1704	852	426	426		
1	G	426	Total	C	N	O	0	0
			1704	852	426	426		
1	H	426	Total	C	N	O	0	0
			1704	852	426	426		
1	I	426	Total	C	N	O	0	0
			1704	852	426	426		



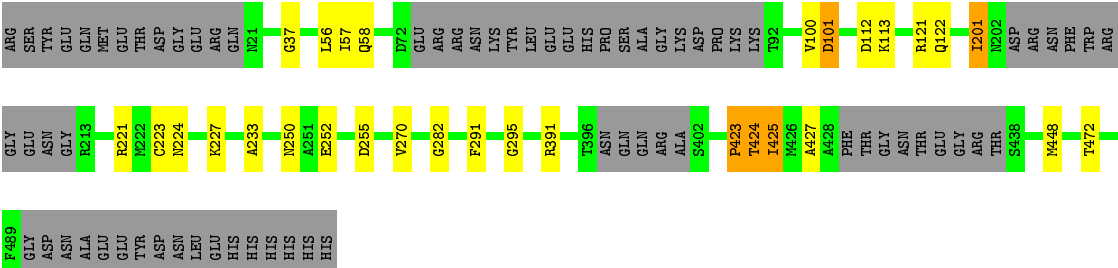
• Molecule 1: NUCLEOPROTEIN

Chain E: 80% 15%



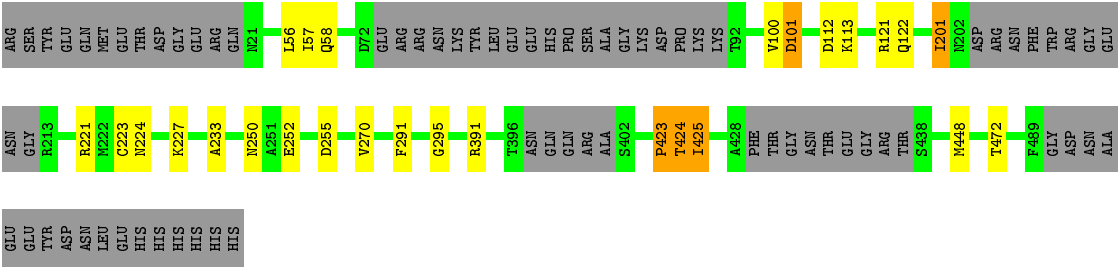
• Molecule 1: NUCLEOPROTEIN

Chain F: 79% 5% 15%



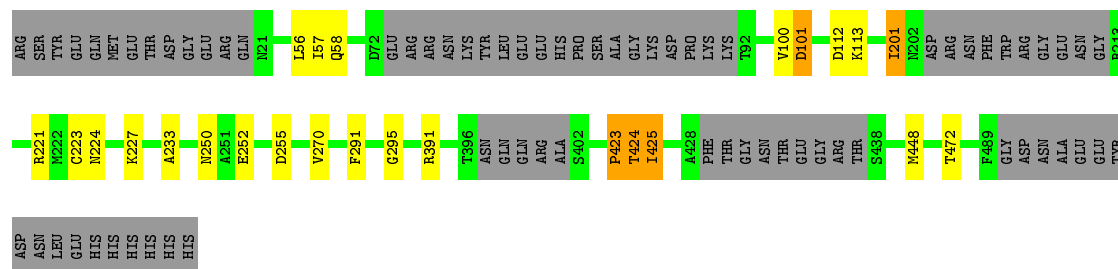
• Molecule 1: NUCLEOPROTEIN

Chain G: 80% 15%



• Molecule 1: NUCLEOPROTEIN

Chain H: 80% 15%



4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	Depositor
Number of images	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	WHOLE PLATE, Not provided	Depositor
Microscope	FEI TECNAI G2	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	Not provided	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	Not provided	Depositor
Image detector	FILM (KODAK SO-136)	Depositor

5 Model quality

5.1 Standard geometry

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 >2	RMSZ	# Z >2
1	A	0.80	1/1699 (0.1%)	0.81	1/2115 (0.0%)
1	B	0.80	1/1699 (0.1%)	0.81	1/2115 (0.0%)
1	C	0.80	1/1699 (0.1%)	0.81	1/2115 (0.0%)
1	D	0.80	1/1699 (0.1%)	0.81	1/2115 (0.0%)
1	E	0.80	1/1699 (0.1%)	0.81	1/2115 (0.0%)
1	F	0.80	1/1699 (0.1%)	0.81	1/2115 (0.0%)
1	G	0.80	1/1699 (0.1%)	0.81	1/2115 (0.0%)
1	H	0.80	1/1699 (0.1%)	0.81	1/2115 (0.0%)
1	I	0.80	1/1699 (0.1%)	0.81	1/2115 (0.0%)
All	All	0.80	9/15291 (0.1%)	0.81	9/19035 (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	B	0	1
1	C	0	1
1	D	0	1
1	E	0	1
1	F	0	1
1	G	0	1
1	H	0	1
1	I	0	1
All	All	0	9

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	201	ILE	C-N	-5.28	1.22	1.34
1	I	201	ILE	C-N	-5.26	1.22	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	201	ILE	C-N	-5.25	1.22	1.34
1	A	201	ILE	C-N	-5.24	1.22	1.34
1	D	201	ILE	C-N	-5.23	1.22	1.34

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	201	ILE	O-C-N	-6.17	112.83	122.70
1	G	201	ILE	O-C-N	-6.17	112.83	122.70
1	D	201	ILE	O-C-N	-6.16	112.84	122.70
1	H	201	ILE	O-C-N	-6.15	112.86	122.70
1	A	201	ILE	O-C-N	-6.14	112.87	122.70

There are no chirality outliers.

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	201	ILE	Mainchain
1	B	201	ILE	Mainchain
1	C	201	ILE	Mainchain
1	D	201	ILE	Mainchain
1	E	201	ILE	Mainchain

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	1704	0	470	12	0
1	B	1704	0	470	11	0
1	C	1704	0	470	10	0
1	D	1704	0	470	10	0
1	E	1704	0	470	11	0
1	F	1704	0	470	13	0
1	G	1704	0	470	12	0
1	H	1704	0	470	11	0
1	I	1704	0	470	11	0
All	All	15336	0	4230	101	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 5.

The worst 5 of 101 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:252:GLU:O	1:B:255:ASP:N	2.40	0.55
1:E:252:GLU:O	1:E:255:ASP:N	2.40	0.55
1:D:252:GLU:O	1:D:255:ASP:N	2.40	0.54
1:C:252:GLU:O	1:C:255:ASP:N	2.40	0.54
1:G:252:GLU:O	1:G:255:ASP:N	2.40	0.54

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 PDB entries followed by that with respect to all EM entries.

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	416/499 (83%)	359 (86%)	48 (12%)	9 (2%)	8	49
1	B	416/499 (83%)	359 (86%)	48 (12%)	9 (2%)	8	49
1	C	416/499 (83%)	359 (86%)	49 (12%)	8 (2%)	10	52
1	D	416/499 (83%)	358 (86%)	49 (12%)	9 (2%)	8	49
1	E	416/499 (83%)	358 (86%)	49 (12%)	9 (2%)	8	49
1	F	416/499 (83%)	358 (86%)	49 (12%)	9 (2%)	8	49
1	G	416/499 (83%)	359 (86%)	49 (12%)	8 (2%)	10	52
1	H	416/499 (83%)	358 (86%)	50 (12%)	8 (2%)	10	52
1	I	416/499 (83%)	359 (86%)	49 (12%)	8 (2%)	10	52
All	All	3744/4491 (83%)	3227 (86%)	440 (12%)	77 (2%)	13	50

5 of 77 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	423	PRO
1	B	423	PRO
1	C	423	PRO
1	D	423	PRO
1	E	423	PRO

5.3.2 Protein sidechains ⓘ

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.