



wwPDB EM Map/Model Validation Report ⓘ

Oct 19, 2016 – 07:43 AM EDT

PDB ID : 3JBM
EMDB ID: : EMD-6453
Title : Electron cryo-microscopy of a virus-like particle of orange-spotted grouper nervous necrosis virus
Authors : Xie, J.; Li, K.; Gao, Y.; Huang, R.; Lai, Y.; Shi, Y.; Yang, S.; Zhu, G.; Zhang, Q.; He, J.
Deposited on : 2015-09-06
Resolution : 3.90 Å(reported)
Based on PDB ID : 4NWW

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) : rb-20027939

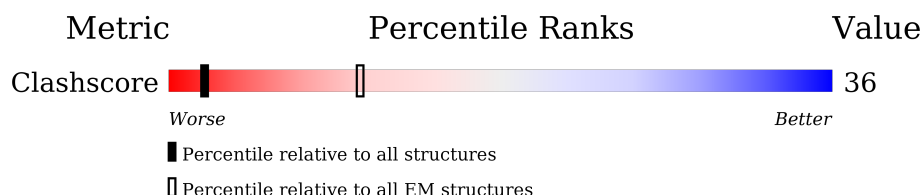
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY




The reported resolution of this entry is 3.90 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)	EM structures (#Entries)
Clashscore	114402	924

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	338	 47% . 50%
1	B	338	 47% . 50%
1	C	338	 51% . 45%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 526 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 virus-like particle of orange-spotted grouper nervous necrosis virus.

Mol	Chain	Residues	Atoms		AltConf	Trace
1	A	170	Total 170	C 170	0	170
1	B	170	Total 170	C 170	0	170
1	C	186	Total 186	C 186	0	186

- Molecule 1: virus-like particle of orange-spotted grouper nervous necrosis virus



LYS	PHE	ALA	GLY	ASN	ALA	GLY	THR	PRO	ALA	GLY	TRP	PHE	ARG	TRP	GLY	ILE	TRP	ASP	ASN	PHE	ASN	LYS	THR	PHE	THR	ASP	GLY	VAL	ALA	TYR	TYR	SER	ASP	GLU	GLN	PRO	ARG	GLN	ILE	LEU	LEU	PRO	VAL	GLY	THR	VAL	CYS	THR	ARG	VAL	ASP	SER	GLU	ASN
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4 Experimental information

Property	Value	Source
Reconstruction method	Not provided	Depositor
Imposed symmetry	POINT, I	Depositor
Number of images used	32000	Depositor
Resolution determination method	FSC 0.143	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2910	Depositor
Magnification	96000	Depositor
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	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).

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 ⓘ

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	170	0	0	5	0
1	B	170	0	0	6	0
1	C	186	0	0	8	0
All	All	526	0	0	19	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 36.

The worst 5 of 19 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:189:GLY:CA	1:C:190:ASN:CA	2.79	0.60
1:B:189:GLY:CA	1:B:190:ASN:CA	2.79	0.60
1:C:46:THR:CA	1:C:47:GLY:CA	2.79	0.60
1:A:51:GLY:CA	1:A:52:THR:CA	2.81	0.59
1:A:189:GLY:CA	1:A:190:ASN:CA	2.81	0.58

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.