



Full wwPDB/EMDatabank EM Map/Model Validation Report ⓘ

Jul 11, 2018 – 06:31 PM EDT

PDB ID : 1M11
Title : structural model of human decay-accelerating factor bound to echovirus 7 from cryo-electron microscopy
Authors : He, Y.; Lin, F.; Chipman, P.R.; Bator, C.M.; Baker, T.S.; Shoham, M.; Kuhn, R.J.; Medof, M.E.; Rossmann, M.G.
Deposited on : 2002-06-17
Resolution : 16.00 Å (reported)
Based on PDB ID : 1EV1, 1G40, 1COV

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

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

MolProbity : 4.02b-467
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20031172

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 1013 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 decay-accelerating factor.

Mol	Chain	Residues	Atoms	AltConf	Trace
1	R	243	Total C 243 243	0	243

- Molecule 2 is a protein called COAT PROTEIN VP1.

Mol	Chain	Residues	Atoms	AltConf	Trace
2	1	278	Total C 278 278	0	278

- Molecule 3 is a protein called COAT PROTEIN VP2.

Mol	Chain	Residues	Atoms	AltConf	Trace
3	2	254	Total C 254 254	0	254

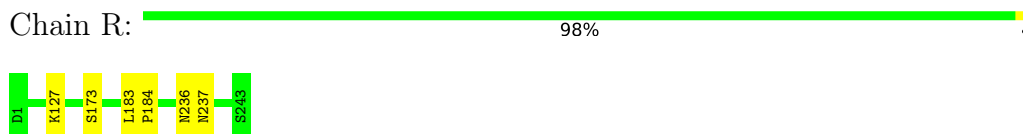
- Molecule 4 is a protein called COAT PROTEIN VP3.

Mol	Chain	Residues	Atoms	AltConf	Trace
4	3	238	Total C 238 238	0	238

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: decay-accelerating factor



- Molecule 2: COAT PROTEIN VP1



There are no outlier residues recorded for this chain.

- Molecule 3: COAT PROTEIN VP2



There are no outlier residues recorded for this chain.

- Molecule 4: COAT PROTEIN VP3



There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	Not provided	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	CTF correction of each micrograph	Depositor
Microscope	FEI/PHILIPS CM300FEG/T	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	16.6	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	4200	Depositor
Magnification	45000	Depositor
Image detector	Not provided	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	R	243	0	0	3	0
2	1	278	0	0	0	0
3	2	254	0	0	0	0
4	3	238	0	0	0	0
All	All	1013	0	0	3	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 3.

All (3) 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:R:236:ASN:CA	1:R:237:ASN:CA	2.90	0.51
1:R:183:LEU:CA	1:R:184:PRO:CA	2.90	0.50
1:R:127:LYS:CA	1:R:173:SER:CA	2.99	0.41

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.