



## wwPDB/EMDatabank EM Map/Model Validation Summary Report ⓘ

Feb 16, 2018 – 02:57 pm GMT

PDB ID : 3MUW  
EMDB ID: : EMD-1121  
Title : Pseudo-atomic structure of the E2-E1 protein shell in Sindbis virus  
Authors : Li, L.; Jose, J.; Xiang, Y.; Kuhn, R.J.; Rossmann, M.G.  
Deposited on : 2010-05-03  
Resolution : 9.00 Å(reported)  
Based on PDB ID : 3MUU

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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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) : trunk30686



## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2468 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 Structural polyprotein.

Mol	Chain	Residues	Atoms	AltConf	Trace
1	A	380	Total C 380 380	0	380
1	D	380	Total C 380 380	0	380
1	E	380	Total C 380 380	0	380
1	F	380	Total C 380 380	0	380

- Molecule 2 is a protein called Structural polyprotein.

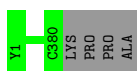
Mol	Chain	Residues	Atoms	AltConf	Trace
2	U	237	Total C 237 237	0	237
2	X	237	Total C 237 237	0	237
2	Y	237	Total C 237 237	0	237
2	Z	237	Total C 237 237	0	237

### 3 Residue-property plots [i](#)

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.

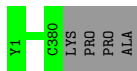
- Molecule 1: Structural polyprotein

Chain A:  99%



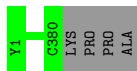
- Molecule 1: Structural polyprotein

Chain D:  99%



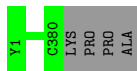
- Molecule 1: Structural polyprotein

Chain E:  99%



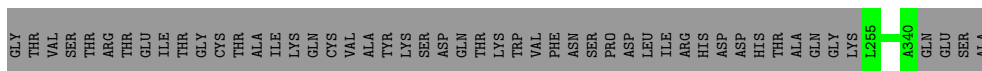
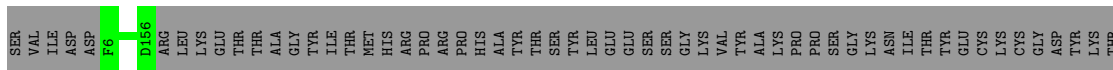
- Molecule 1: Structural polyprotein

Chain F:  99%

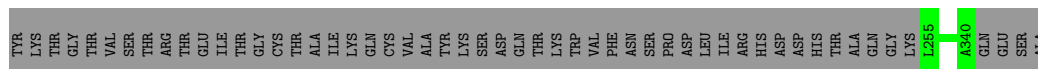
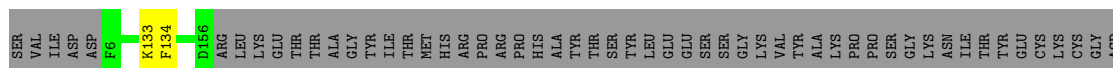


- Molecule 2: Structural polyprotein

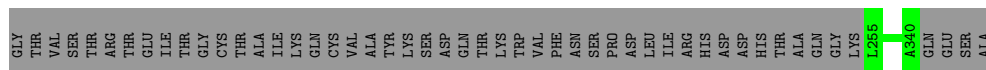
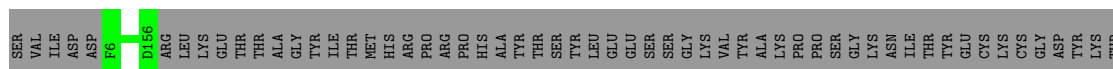
Chain U:  69% 31%



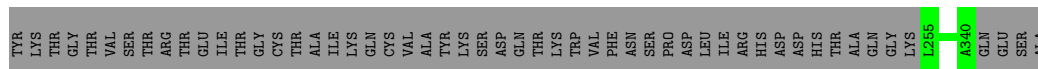
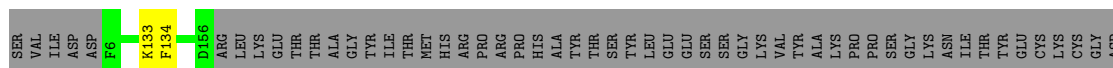
- Molecule 2: Structural polyprotein



• Molecule 2: Structural polyprotein



• Molecule 2: Structural polyprotein



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	7085	Depositor
Resolution determination method	Not provided	Depositor
CTF correction method	CTF correction of each particle.	Depositor
Microscope	FEI/PHILIPS CM200T	Depositor
Voltage (kV)	200	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	18	Depositor
Minimum defocus (nm)	1100	Depositor
Maximum defocus (nm)	2580	Depositor
Magnification	39220	Depositor
Image detector	KODAK SO-163 FILM	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	380	0	0	0	0
1	D	380	0	0	0	0
1	E	380	0	0	0	0
1	F	380	0	0	0	0
2	U	237	0	0	0	0
2	X	237	0	0	1	0
2	Y	237	0	0	0	0
2	Z	237	0	0	1	0
All	All	2468	0	0	2	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 1.

All (2) 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:X:133:LYS:CA	2:X:134:PHE:CA	2.85	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Z:133:LYS:CA	2:Z:134:PHE:CA	2.88	0.51

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

There are no chain breaks in this entry.