



Full wwPDB/EMDatabank EM Map/Model Validation Report ⓘ

Mar 2, 2017 – 11:02 am GMT

PDB ID : 1P58
Title : Complex Organization of Dengue Virus Membrane Proteins as Revealed by
9.5 Angstrom Cryo-EM reconstruction
Authors : Zhang, W.; Chipman, P.R.; Corver, J.; Johnson, P.R.; Zhang, Y.; Mukhopad-
hyay, S.; Baker, T.S.; Strauss, J.H.; Rossmann, M.G.; Kuhn, R.J.
Deposited on : 2003-04-25
Resolution : 9.50 Å(reported)
Based on PDB ID : 1SVB and 1JCH

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) : recalc29047

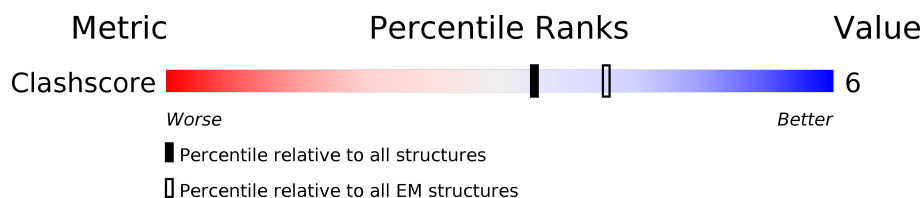
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 9.50 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	495	 98% ..
1	B	495	 98% ..
1	C	495	 98% ..
2	D	75	 73% 27%
2	E	75	 72% . 27%
2	F	75	 72% . 27%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1635 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 Major envelope protein E.

Mol	Chain	Residues	Atoms	AltConf	Trace
1	A	490	Total C 490 490	0	490
1	B	490	Total C 490 490	0	490
1	C	490	Total C 490 490	0	490

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	335	ILE	THR	SEE REMARK 999	UNP P12823
A	352	ILE	THR	SEE REMARK 999	UNP P12823
B	335	ILE	THR	SEE REMARK 999	UNP P12823
B	352	ILE	THR	SEE REMARK 999	UNP P12823
C	335	ILE	THR	SEE REMARK 999	UNP P12823
C	352	ILE	THR	SEE REMARK 999	UNP P12823

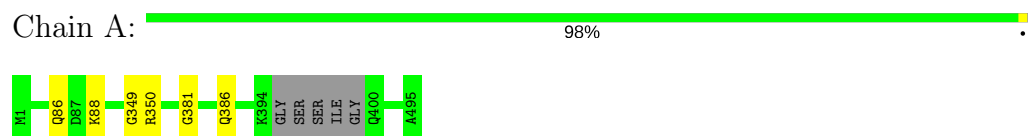
- Molecule 2 is a protein called Envelope protein M.

Mol	Chain	Residues	Atoms	AltConf	Trace
2	D	55	Total C 55 55	0	55
2	E	55	Total C 55 55	0	55
2	F	55	Total C 55 55	0	55

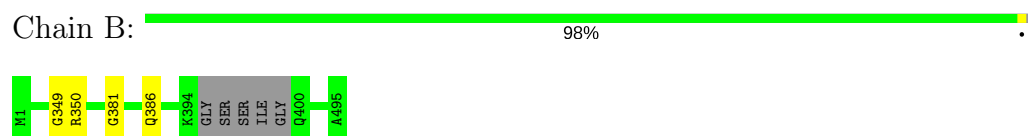
3 Residue-property plots [i](#)

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.

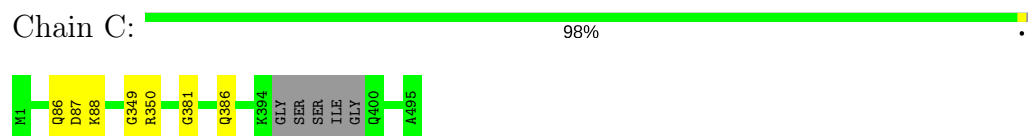
- Molecule 1: Major envelope protein E



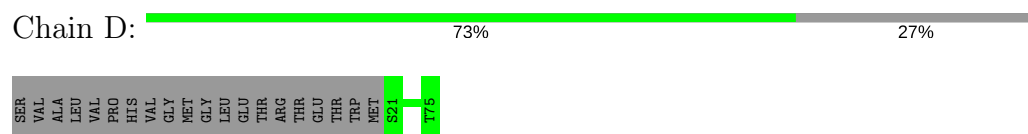
- Molecule 1: Major envelope protein E



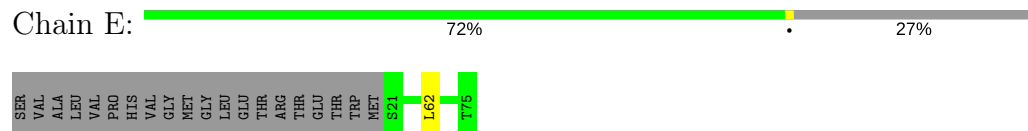
- Molecule 1: Major envelope protein E



- Molecule 2: Envelope protein M



- Molecule 2: Envelope protein M



- Molecule 2: Envelope protein M



SER	VAL	ALA	LEU	VAL	PRO	HIS	VAL	GLY	MET	GLY	LEU	GLU	THR	ARG	THR	GLU	THR	TRP	MET	S21	L62	I75
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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	each viral image was CTF corrected before reconstruction, based on the following equation: $F(\text{corr}) = F(\text{obs}) / [CTF + \text{wiener} * (1 - CTF)]$	Depositor
Microscope	FEI/PHILIPS CM200T	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2700	Depositor
Minimum defocus (nm)	800.0	Depositor
Maximum defocus (nm)	4800.0	Depositor
Magnification	50000	Depositor
Image detector	KODAK SO163 FILM	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	490	0	0	5	0
1	B	490	0	0	2	0
1	C	490	0	0	5	0
2	D	55	0	0	0	0
2	E	55	0	0	1	0
2	F	55	0	0	1	0
All	All	1635	0	0	10	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 6.

All (10) 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:A:86:GLN:CA	1:C:87:ASP:CA	2.62	0.77
1:B:381:GLY:CA	1:B:386:GLN:CA	2.69	0.70
1:A:381:GLY:CA	1:A:386:GLN:CA	2.69	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:381:GLY:CA	1:C:386:GLN:CA	2.69	0.70
1:A:349:GLY:CA	1:A:350:ARG:CA	2.86	0.54
1:C:349:GLY:CA	1:C:350:ARG:CA	2.86	0.54
1:B:349:GLY:CA	1:B:350:ARG:CA	2.86	0.53
1:A:86:GLN:CA	1:C:88:LYS:CA	2.88	0.51
1:A:88:LYS:CA	1:C:86:GLN:CA	2.90	0.50
2:E:62:LEU:CA	2:F:62:LEU: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.