



wwPDB/EMDataBank EM Map/Model Validation Summary Report ⓘ

Mar 2, 2017 – 11:06 am GMT

PDB ID : 2B6B
EMDB ID: : EMD-1166
Title : Cryo EM structure of Dengue complexed with CRD of DC-SIGN
Authors : Pokidysheva, E.; Zhang, Y.; Battisti, A.J.; Bator-Kelly, C.M.; Chipman, P.R.;
Gregorio, G.; Hendrickson, W.A.; Kuhn, R.J.; Rossmann, M.G.
Deposited on : 2005-09-30
Resolution : 25.00 Å (reported)
Based on PDB ID : 1THD, 1K9I

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
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

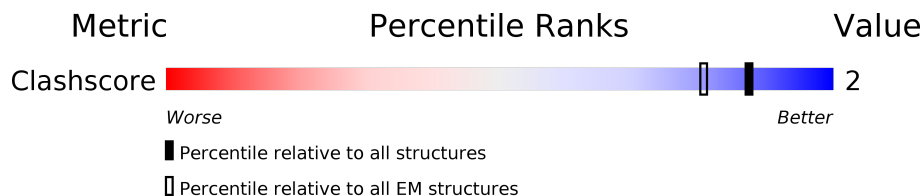
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 25.00 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	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	394	 98% ..
1	B	394	 98% ..
1	C	394	 99% .
2	D	175	 72% . 27%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1295 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 envelope glycoprotein.

Mol	Chain	Residues	Atoms	AltConf	Trace
1	A	389	Total C 389 389	0	389
1	B	389	Total C 389 389	0	389
1	C	389	Total C 389 389	0	389

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	71	GLU	ASP	CONFLICT	GB 323503
A	390	ASN	ASP	CONFLICT	GB 323503
B	71	GLU	ASP	CONFLICT	GB 323503
B	390	ASN	ASP	CONFLICT	GB 323503
C	71	GLU	ASP	CONFLICT	GB 323503
C	390	ASN	ASP	CONFLICT	GB 323503

- Molecule 2 is a protein called CD209 antigen.

Mol	Chain	Residues	Atoms	AltConf	Trace
2	D	128	Total C 128 128	0	128

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	230	MET	-	cloning artifact	UNP Q96QQ4
D	231	GLY	-	cloning artifact	UNP Q96QQ4
D	232	SER	-	cloning artifact	UNP Q96QQ4
D	233	SER	-	cloning artifact	UNP Q96QQ4
D	234	HIS	-	cloning artifact	UNP Q96QQ4
D	235	HIS	-	cloning artifact	UNP Q96QQ4
D	236	HIS	-	cloning artifact	UNP Q96QQ4

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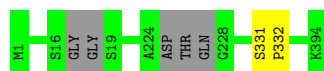
Chain	Residue	Modelled	Actual	Comment	Reference
D	237	HIS	-	cloning artifact	UNP Q96QQ4
D	238	HIS	-	cloning artifact	UNP Q96QQ4
D	239	HIS	-	cloning artifact	UNP Q96QQ4
D	240	SER	-	cloning artifact	UNP Q96QQ4
D	241	SER	-	cloning artifact	UNP Q96QQ4
D	242	GLY	-	cloning artifact	UNP Q96QQ4
D	243	LEU	-	cloning artifact	UNP Q96QQ4
D	244	VAL	-	cloning artifact	UNP Q96QQ4
D	245	PRO	-	cloning artifact	UNP Q96QQ4
D	246	ARG	-	cloning artifact	UNP Q96QQ4
D	247	GLY	-	cloning artifact	UNP Q96QQ4
D	248	SER	-	cloning artifact	UNP Q96QQ4
D	249	HIS	-	cloning artifact	UNP Q96QQ4
D	250	MET	-	cloning artifact	UNP Q96QQ4

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.

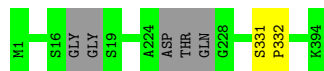
- Molecule 1: envelope glycoprotein

Chain A:  98% ..



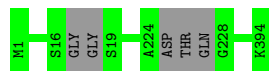
- Molecule 1: envelope glycoprotein

Chain B:  98% ..



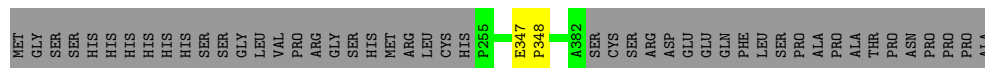
- Molecule 1: envelope glycoprotein

Chain C:  99% .



- Molecule 2: CD209 antigen

Chain D:  72% . 27%



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 RE-CONSTRUCTION, BASED ON THE FOLLOWING EQUATION: $F(\text{CORR}) = F(\text{OBS}) / [CTF + \text{WIENER} * (1 - CTF)]$	Depositor
Microscope	FEI/PHILIPS CM300T	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	2700.00	Depositor
Minimum defocus (nm)	1100.00	Depositor
Maximum defocus (nm)	3000.00	Depositor
Magnification	50000	Depositor
Image detector	KODAK SO163 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	389	0	0	1	0
1	B	389	0	0	1	0
1	C	389	0	0	0	0
2	D	128	0	0	1	0
All	All	1295	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 2.

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)
2:D:347:GLU:CA	2:D:348:PRO:CA	2.95	0.44
1:A:331:SER:CA	1:A:332:PRO:CA	2.99	0.40
1:B:331:SER:CA	1:B:332:PRO:CA	2.99	0.40

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.