wwPDB/EMDataBank EM Map/Model Validation Summary Report (i)

Dec 1, 2016 – 02:01 PM EST

PDB ID	:	3IYH
EMDB ID:	:	EMD-5150
Title	:	P22 procapsid coat protein structures reveal a novel mechanism for capsid maturation: Stability without auxiliary proteins or chemical cross-links
Authors	:	Parent, K.N.; Khayat, R.; Tu, L.H.; Suhanovsky, M.M.; Cortines, J.R.; Teschke, C.M.; Johnson, J.E.; Baker, T.S.
Deposited on	:	2009-12-14
Resolution	:	8.20 Å(reported)
Based on PDB ID	:	1FHG, 1OHG

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 (i) symbol.

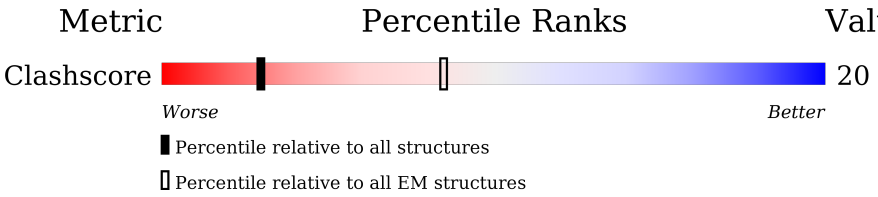
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
EM map analysis	:	NOT EXECUTED
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20028320

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 8.20 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 <=5%

Mol	Chain	Length	Quality of chain
1	A	430	88% . 9%
1	B	430	87% . 9%
1	C	430	87% . 9%
1	D	430	88% . 9%
1	E	430	88% . 9%
1	F	430	88% . 9%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 2346 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 Coat protein.

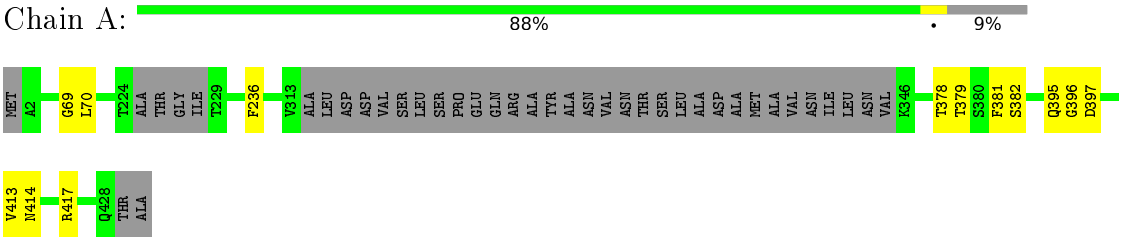
Mol	Chain	Residues	Atoms	AltConf	Trace
1	A	391	Total C 391 391	0	391
1	B	391	Total C 391 391	0	391
1	C	391	Total C 391 391	0	391
1	D	391	Total C 391 391	0	391
1	E	391	Total C 391 391	0	391
1	F	391	Total C 391 391	0	391

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 errors 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.

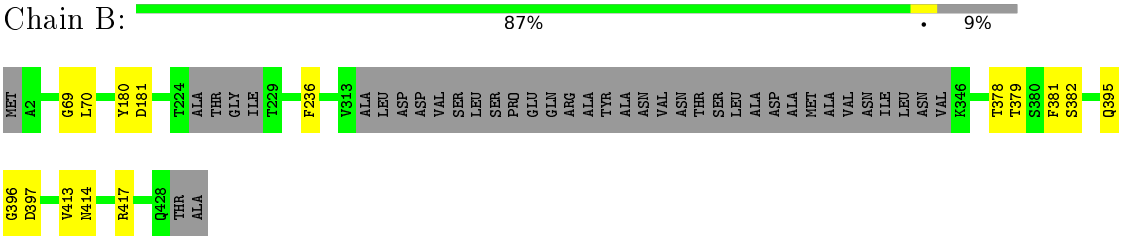
- Molecule 1: Coat protein

Chain A:



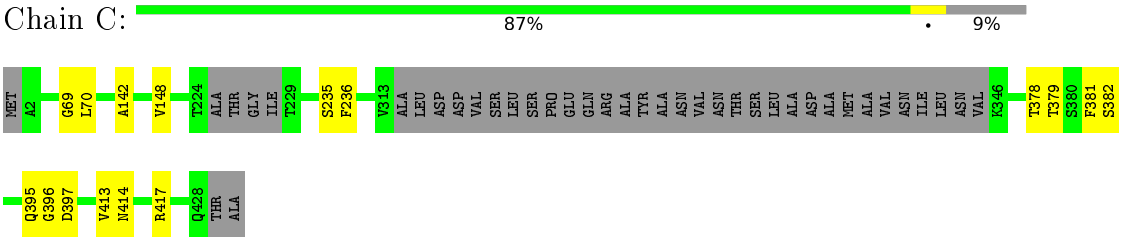
- Molecule 1: Coat protein

Chain B:



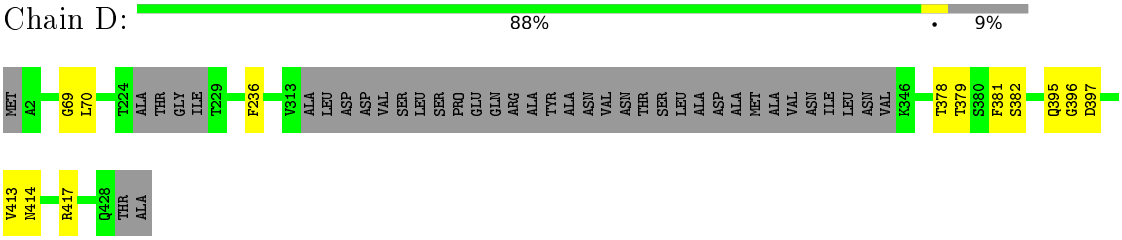
- Molecule 1: Coat protein

Chain C:



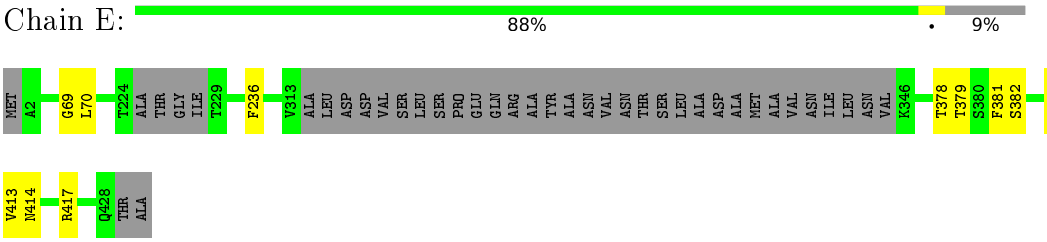
- Molecule 1: Coat protein

Chain D:



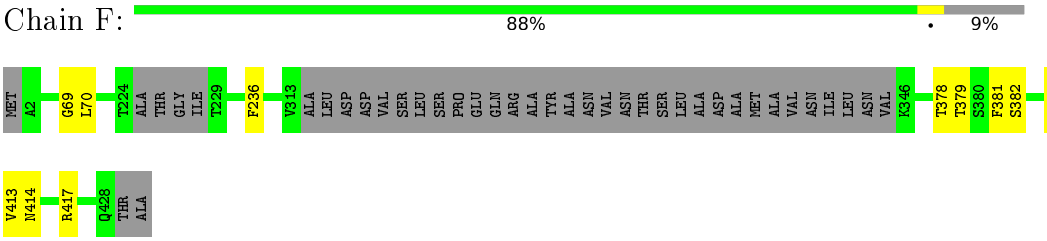
- Molecule 1: Coat protein

Chain E:



- Molecule 1: Coat protein

Chain F:



4 Experimental information (i)

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	3308	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	Not provided	Depositor
Microscope	FEI POLARA 300	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/Å^2$)	8	Depositor
Minimum defocus (nm)	630	Depositor
Maximum defocus (nm)	3160	Depositor
Magnification	39000	Depositor
Image detector	KODAK SO163	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	391	0	0	7	0
1	B	391	0	0	9	0
1	C	391	0	0	10	0
1	D	391	0	0	7	0
1	E	391	0	0	7	0
1	F	391	0	0	7	0
All	All	2346	0	0	45	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 20.

The worst 5 of 45 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:B:180:TYR:CA	1:C:148:VAL:CA	2.42	0.97
1:B:181:ASP:CA	1:C:142:ALA:CA	2.56	0.82
1:C:236:PHE:CA	1:C:417:ARG:CA	2.62	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:236:PHE:CA	1:F:417:ARG:CA	2.71	0.69
1:D:236:PHE:CA	1:D:417:ARG:CA	2.71	0.68

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.