wwPDB EM Map/Model Validation Report (i)

Apr 10, 2016 – 01:42 PM BST

PDB ID	:	3J3O
EMDB ID:	:	EMD-5291
Title	:	Conformational Shift of a Major Poliovirus Antigen Confirmed by Immuno-Cryogenic Electron Microscopy: 160S Poliovirus and C3-Fab Complex
Authors	:	Lin, J.; Cheng, N.; Hogle, J.M.; Steven, A.C.; Belnap, D.M.
Deposited on	:	2013-04-10
Resolution	:	11.10 Å(reported)
Based on PDB ID	:	1ASJ, 1FPT

This is a wwPDB EM Map/Model Validation Report for a publicly released PDB/EMDB entry.
For rigid body fitted models, validation errors reported here could
stem from errors in the original structure(s) used in the fitting.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
http://wwpdb.org/validation/2016/EMValidationReportHelp

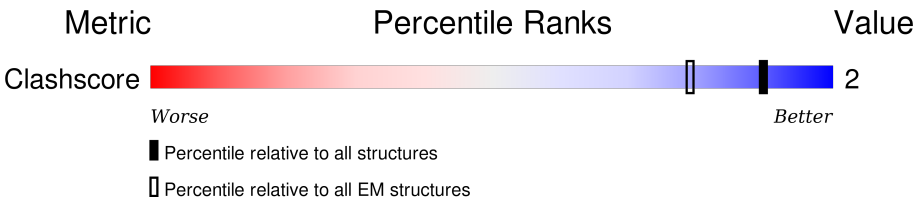
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk27241

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 11.10 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	L	219	99% •
2	H	220	100%
3	0	5	100%
4	1	302	94% 6%
5	2	272	98% ••
6	3	238	99% •
7	4	68	87% • 12%

2 Entry composition (i)

There are 9 unique types of molecules in this entry. The entry contains 1326 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 C3 antibody, light chain.

Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
1	L	219	219	219	0	219

- Molecule 2 is a protein called C3 antibody, heavy chain.

Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
2	H	220	220	220	0	220

- Molecule 3 is a protein called unknown peptide.

Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
3	0	5	5	5	0	5

- Molecule 4 is a protein called Protein VP1.

Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
4	1	283	283	283	0	283

- Molecule 5 is a protein called Protein VP2.

Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
5	2	268	268	268	0	268

- Molecule 6 is a protein called Protein VP3.

Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
6	3	235	235	235	0	235

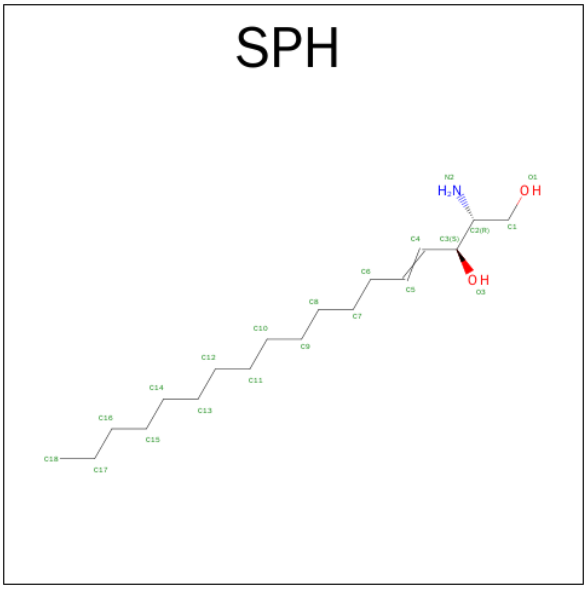
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
3	123	SER	PHE	CONFLICT	UNP P03300

- Molecule 7 is a protein called Protein VP4.

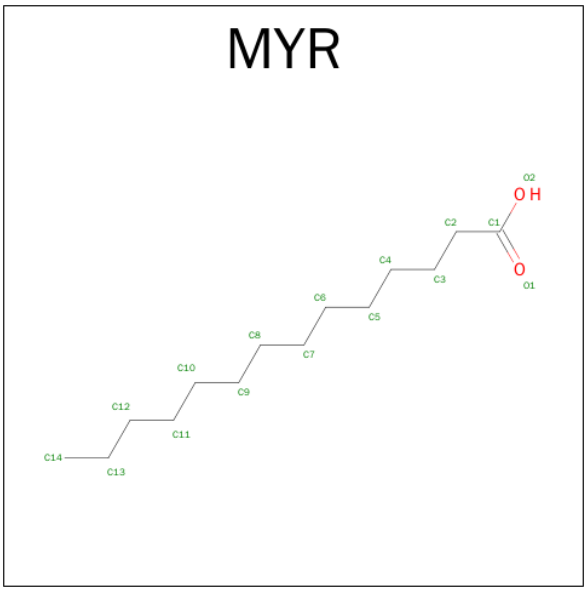
Mol	Chain	Residues	Atoms		AltConf	Trace
			Total	C		
7	4	60	60	60	0	60

- Molecule 8 is SPHINGOSINE (three-letter code: SPH) (formula: $C_{18}H_{37}NO_2$).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
8	1	1	21	18	1	2	0

- Molecule 9 is MYRISTIC ACID (three-letter code: MYR) (formula: $C_{14}H_{28}O_2$).



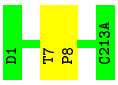
Mol	Chain	Residues	Atoms			AltConf
			Total	C	O	
9	4	1	15	14	1	0

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: C3 antibody, light chain

Chain L: 99%



- Molecule 2: C3 antibody, heavy chain

Chain H: 100%

There are no outlier residues recorded for this chain.

- Molecule 3: unknown peptide

Chain 0: 100%

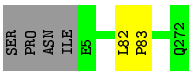
There are no outlier residues recorded for this chain.

- Molecule 4: Protein VP1

Chain 1: 94% 6%

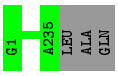
- Molecule 5: Protein VP2

Chain 2: 98%



- Molecule 6: Protein VP3

Chain 3: 99%



- Molecule 7: Protein VP4

Chain 4:

4 Experimental information (i)

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of images	4184	Depositor
Resolution determination method	FSC at 0.5 cut-off	Depositor
CTF correction method	CTF and decay correction of each particle	Depositor
Microscope	FEI/PHILIPS CM200FEG	Depositor
Voltage (kV)	120	Depositor
Electron dose ($e^-/Å^2$)	1400	Depositor
Minimum defocus (nm)	730	Depositor
Maximum defocus (nm)	1770	Depositor
Magnification	38000	Depositor
Image detector	Kodak SO163 film	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: SPH, MYR

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	L	219	0	0	1	0
2	H	220	0	0	0	0
3	0	5	0	0	0	0
4	1	283	0	0	0	0
5	2	268	0	0	1	0
6	3	235	0	0	0	0
7	4	60	0	0	1	0
8	1	21	0	37	0	0
9	4	15	0	27	1	0
All	All	1326	0	64	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)
7:4:2:GLY:CA	9:4:101:MYR:C1	2.44	0.96
5:2:82:LEU:CA	5:2:83:PRO:CA	2.90	0.50
1:L:7:THR:CA	1:L:8:PRO:CA	2.97	0.43

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)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
8	SPH	1	401	-	19,20,20	0.91	1 (5%)	16,21,21	2.54	3 (18%)
9	MYR	4	101	-	14,14,15	0.44	0	13,13,15	0.72	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	SPH	1	401	-	-	0/21/21/21	0/0/0/0
9	MYR	4	101	-	-	0/11/12/13	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	1	401	SPH	C1-C2	3.55	1.57	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
8	1	401	SPH	O3-C3-C2	-6.40	96.64	107.49
8	1	401	SPH	O3-C3-C4	-4.09	99.04	110.69
8	1	401	SPH	O1-C1-C2	6.10	124.23	111.44

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	4	101	MYR	1	0

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.