



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

Feb 19, 2018 – 09:47 pm GMT

PDB ID : 5TSK  
EMDB ID: : EMD-8325  
Title : Molecular Dynamics Flexible Fitting Model of Coxsackievirus A16 empty Pro-  
capsid VP1 Subunit  
Authors : Fan, C.; Cong, Y.; Ye, X.; Huang, Z.  
Deposited on : 2016-10-29  
Resolution : 6.50 Å(reported)  
Based on PDB ID : 4JGY

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](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

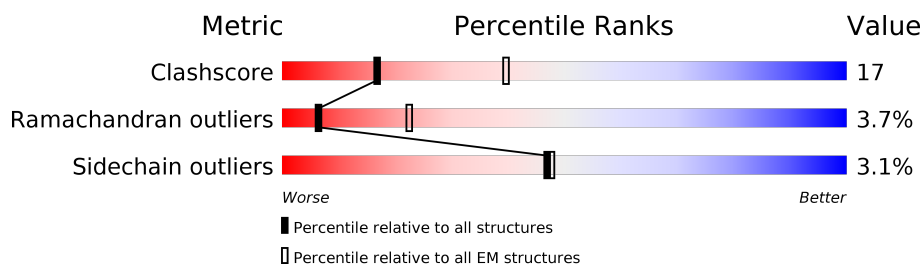
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 6.50 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	136279	1886
Ramachandran outliers	132675	1663
Sidechain outliers	132484	1531

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  $\geq 3$ , 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	297	<div> <div>53%</div> <div>19%</div> <div>•</div> <div>26%</div> </div>

## 2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1752 atoms, of which 0 are hydrogens and 0 are deuteriums.

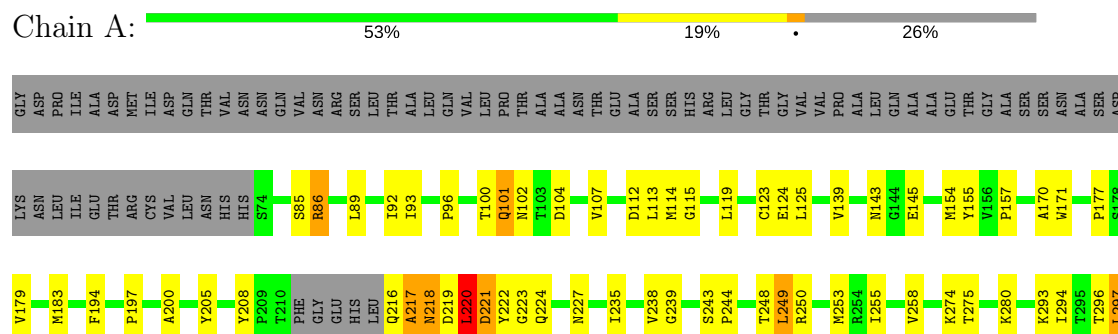
In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called coxsackievirus A16 empty procapsid VP1 subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	219	1752	1121	296	323	12	0	0

i

- Molecule 1: coxsackievirus A16 empty procapsid VP1 subunit



## 4 Experimental information

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	1642	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	25	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	57000	Depositor
Image detector	FEI FALCON II (4k x 4k)	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).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 2$	RMSZ	$\# Z  > 2$
1	A	0.58	2/1803 (0.1%)	0.70	1/2455 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	297	LEU	C-O	-12.05	1.00	1.23
1	A	297	LEU	C-OXT	-12.01	1.00	1.23

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	297	LEU	CA-C-O	-5.26	109.06	120.10

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	1752	0	1712	58	0
All	All	1752	0	1712	58	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 17.

All (58) 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:217:ALA:CA	1:A:218:ASN:HB2	1.98	0.93
1:A:220:LEU:O	1:A:221:ASP:HB2	1.70	0.88
1:A:217:ALA:HA	1:A:218:ASN:HB2	1.55	0.87
1:A:208:TYR:OH	1:A:218:ASN:ND2	2.07	0.85
1:A:255:ILE:HG22	1:A:258:VAL:HG22	1.64	0.79
1:A:217:ALA:N	1:A:218:ASN:HB2	1.98	0.79
1:A:143:ASN:HD21	1:A:145:GLU:HG3	1.47	0.76
1:A:143:ASN:ND2	1:A:145:GLU:HG3	2.01	0.75
1:A:96:PRO:HD2	1:A:102:ASN:ND2	2.04	0.72
1:A:208:TYR:CZ	1:A:218:ASN:ND2	2.60	0.70
1:A:208:TYR:CE1	1:A:218:ASN:ND2	2.60	0.69
1:A:113:LEU:HD21	1:A:253:MET:SD	2.38	0.63
1:A:208:TYR:HD1	1:A:221:ASP:O	1.81	0.61
1:A:224:GLN:HE22	1:A:275:THR:HB	1.65	0.61
1:A:250:ARG:HH21	1:A:250:ARG:HG3	1.68	0.59
1:A:113:LEU:C	1:A:115:GLY:H	2.06	0.59
1:A:139:VAL:HG12	1:A:249:LEU:HB2	1.85	0.58
1:A:208:TYR:CE1	1:A:222:TYR:HB2	2.39	0.57
1:A:85:SER:O	1:A:86:ARG:HB2	2.03	0.57
1:A:216:GLN:HA	1:A:218:ASN:CG	2.26	0.56
1:A:102:ASN:C	1:A:104:ASP:H	2.10	0.55
1:A:238:VAL:HG12	1:A:239:GLY:N	2.22	0.55
1:A:154:MET:HE1	1:A:170:ALA:O	2.06	0.54
1:A:113:LEU:HD21	1:A:253:MET:CE	2.37	0.54
1:A:216:GLN:HA	1:A:218:ASN:ND2	2.22	0.54
1:A:235:ILE:N	1:A:235:ILE:HD12	2.22	0.54
1:A:194:PHE:CZ	1:A:200:ALA:HA	2.43	0.53
1:A:139:VAL:HG23	1:A:183:MET:HG3	1.91	0.52
1:A:143:ASN:HD21	1:A:145:GLU:CG	2.19	0.51
1:A:220:LEU:O	1:A:221:ASP:CB	2.50	0.51
1:A:139:VAL:CG1	1:A:249:LEU:HD12	2.40	0.51
1:A:89:LEU:HD21	1:A:92:ILE:HD11	1.93	0.51
1:A:255:ILE:CG2	1:A:258:VAL:HG22	2.37	0.51
1:A:297:LEU:C	1:A:297:LEU:HD12	2.32	0.50
1:A:217:ALA:N	1:A:218:ASN:CB	2.72	0.50
1:A:293:LYS:HD3	1:A:296:THR:HG23	1.92	0.50
1:A:102:ASN:C	1:A:104:ASP:N	2.64	0.49
1:A:294:ILE:O	1:A:294:ILE:HG12	2.11	0.49
1:A:112:ASP:OD2	1:A:274:LYS:HE2	2.13	0.48
1:A:238:VAL:HG12	1:A:239:GLY:H	1.78	0.48
1:A:250:ARG:HG3	1:A:250:ARG:NH2	2.29	0.48
1:A:197:PRO:HG2	1:A:227:ASN:HD22	1.78	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:100:THR:HG22	1:A:101:GLN:HG3	1.95	0.48
1:A:293:LYS:HD3	1:A:296:THR:CG2	2.43	0.48
1:A:154:MET:CE	1:A:171:TRP:HA	2.45	0.47
1:A:139:VAL:HG12	1:A:249:LEU:CB	2.44	0.47
1:A:205:TYR:O	1:A:223:GLY:HA2	2.14	0.47
1:A:113:LEU:HD22	1:A:119:LEU:HD21	1.96	0.46
1:A:208:TYR:HE1	1:A:222:TYR:HB2	1.80	0.46
1:A:93:ILE:CG2	1:A:107:VAL:HG11	2.47	0.45
1:A:293:LYS:HB2	1:A:296:THR:HG23	1.99	0.44
1:A:243:SER:HA	1:A:244:PRO:HD3	1.81	0.44
1:A:197:PRO:CG	1:A:227:ASN:HD22	2.31	0.44
1:A:139:VAL:HG11	1:A:249:LEU:HD12	2.00	0.43
1:A:113:LEU:C	1:A:115:GLY:N	2.72	0.41
1:A:280:LYS:HE3	1:A:280:LYS:HB2	1.91	0.41
1:A:123:CYS:C	1:A:125:LEU:H	2.24	0.40
1:A:155:TYR:HB3	1:A:177:PRO:HG2	2.04	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	215/297 (72%)	187 (87%)	20 (9%)	8 (4%)	<b>4</b> 31

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	217	ALA
1	A	218	ASN
1	A	114	MET
1	A	221	ASP
1	A	124	GLU

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Mol	Chain	Res	Type
1	A	157	PRO
1	A	220	LEU
1	A	86	ARG

### 5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	194/257 (76%)	188 (97%)	6 (3%)	43 69

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	101	GLN
1	A	179	VAL
1	A	219	ASP
1	A	220	LEU
1	A	248	THR
1	A	249	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	76	GLN
1	A	101	GLN
1	A	143	ASN
1	A	218	ASN
1	A	224	GLN
1	A	227	ASN
1	A	278	ASN

### 5.3.3 RNA ⓘ

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.