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

Jan 31, 2019 – 07:13 AM EST

PDB ID	:	6IZL
EMDB ID:	:	EMD-9754
Title	:	Cryo-EM structure of Mud crab tombus-like virus at 3.3 Angstroms resolution
Authors	:	Zhang, Q.; Gao, Y.
Deposited on	:	2018-12-19
Resolution	:	3.30 Å(reported)

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
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the (i) symbol.

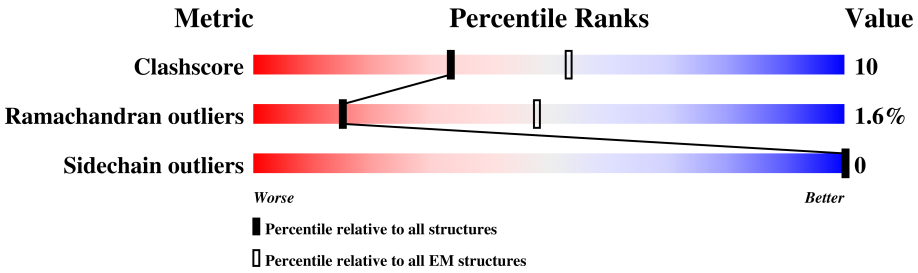
MolProbity	:	4.02b-467
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20031633

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 3.30 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	136327	1886
Ramachandran outliers	132723	1663
Sidechain outliers	132532	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 >=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	337	42% 15% 43%
1	B	337	42% 17% · 40%
1	C	337	53% 12% 35%

2 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 4798 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 mud crab tombus-like virus.

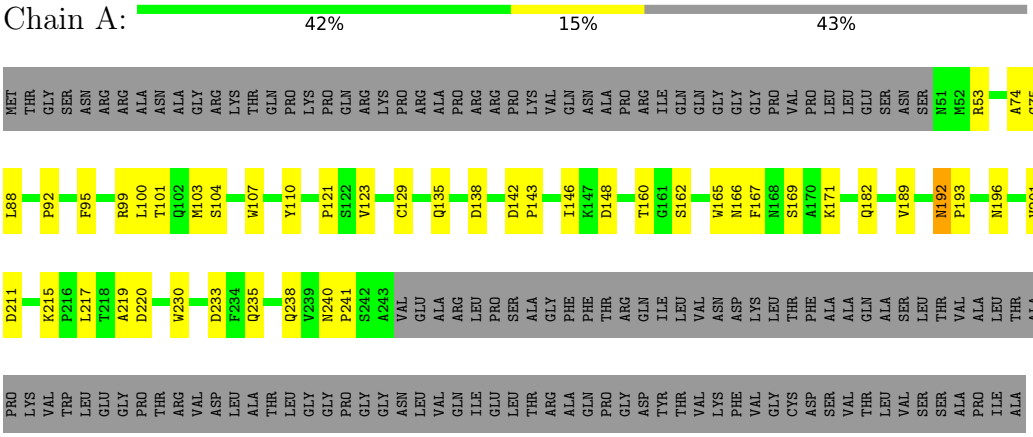
Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	193	Total	C	N	O	S	0	0
			1514	949	268	288	9		
1	B	201	Total	C	N	O	S	0	0
			1573	987	277	300	9		
1	C	220	Total	C	N	O	S	0	0
			1711	1071	306	325	9		

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.

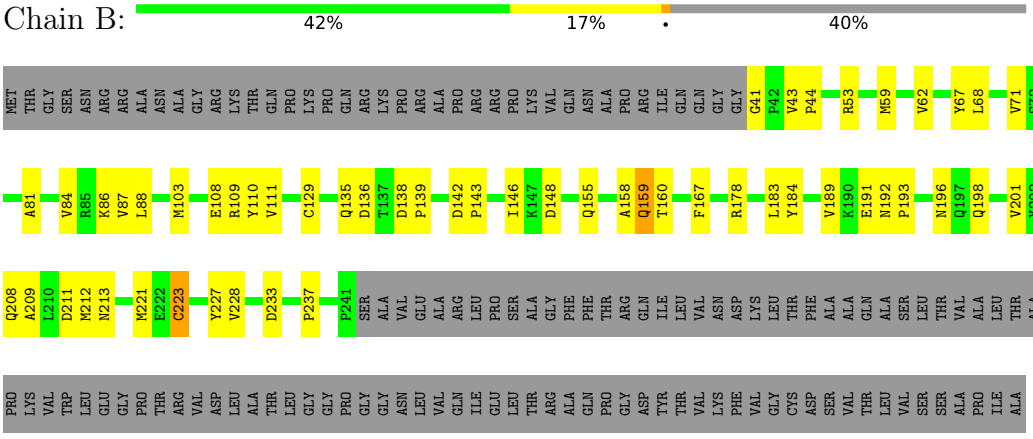
• Molecule 1: mud crab tombus-like virus

Chain A:



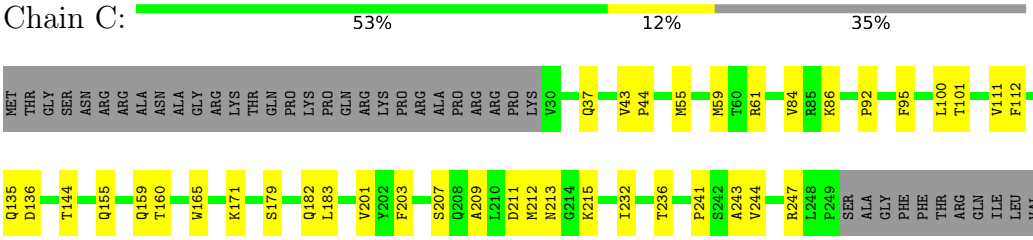
• Molecule 1: mud crab tombus-like virus

Chain B:



• Molecule 1: mud crab tombus-like virus

Chain C:



THR PHE ALA ALA GLN ALA SER LEU THR VAL ALA LEU THR ALA LEU SER ALA THR PRO LYS VAL TRP LEU GLU GLY PRO THR ARG VAL ASP LEU ALA THR LEU GLY GLY PRO GLY GLY ASN LEU VAL GLN ILE GLU LEU THR ARG ALA GLN PRO GLY ASP TYR THR VAL LYS PHE VAL GLY

CYS ASP SER VAL THR LEU VAL SER SER ALA PRO ILE ALA

4 Experimental information (i)

Property	Value	Source
Reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, I	Depositor
Number of particles used	41941	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 ($e^-/Å^2$)	20	Depositor
Minimum defocus (nm)	Not provided	Depositor
Maximum defocus (nm)	Not provided	Depositor
Magnification	96000	Depositor
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	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).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#$\|Z\|>2$	RMSZ	#$\|Z\|>2$
1	A	0.40	0/1548	0.56	0/2108
1	B	0.44	0/1609	0.57	0/2193
1	C	0.40	0/1749	0.54	0/2384
All	All	0.41	0/4906	0.56	0/6685

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	1514	0	1476	38	0
1	B	1573	0	1536	42	0
1	C	1711	0	1675	26	0
All	All	4798	0	4687	94	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 10.

All (94) 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:135:GLN:HG2	1:B:201:VAL:HG22	1.64	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:217:LEU:HD23	1:A:219:ALA:H	1.52	0.74
1:B:136:ASP:HA	1:B:159:GLN:HE22	1.55	0.71
1:A:135:GLN:HG2	1:A:201:VAL:HG22	1.74	0.70
1:A:235:GLN:HE22	1:C:179:SER:H	1.40	0.69
1:C:135:GLN:HG2	1:C:201:VAL:HG22	1.77	0.66
1:B:211:ASP:OD1	1:B:212:MET:N	2.30	0.65
1:B:43:VAL:HG13	1:B:44:PRO:HD3	1.78	0.64
1:A:146:ILE:HG22	1:A:148:ASP:H	1.61	0.64
1:B:86:LYS:HB3	1:B:203:PHE:HB3	1.81	0.63
1:B:73:VAL:HG12	1:B:209:ALA:HB2	1.81	0.62
1:C:111:VAL:HG23	1:C:183:LEU:HD23	1.80	0.62
1:A:129:CYS:HB3	1:A:167:PHE:CE1	2.35	0.62
1:A:138:ASP:HB2	1:B:108:GLU:OE2	2.00	0.61
1:C:131:VAL:HG11	1:C:203:PHE:CZ	2.35	0.61
1:A:238:GLN:NE2	1:A:240:ASN:OD1	2.35	0.59
1:A:162:SER:O	1:B:53:ARG:HD3	2.02	0.59
1:A:123:VAL:HG21	1:A:167:PHE:HE2	1.66	0.59
1:B:160:THR:HB	1:C:55:MET:HA	1.84	0.59
1:C:129:CYS:O	1:C:207:SER:HB2	2.04	0.58
1:A:100:LEU:HD12	1:A:230:TRP:CE2	2.39	0.57
1:A:160:THR:HG23	1:B:237:PRO:HG2	1.85	0.57
1:A:75:GLY:HA2	1:A:209:ALA:HB3	1.87	0.56
1:A:241:PRO:HA	1:C:155:GLN:HE22	1.70	0.56
1:B:67:TYR:HD1	1:B:227:TYR:CE1	2.24	0.55
1:B:81:ALA:O	1:B:84:VAL:HG12	2.07	0.55
1:B:221:MET:HG3	1:B:223:CYS:H	1.71	0.54
1:A:107:TRP:HD1	1:A:235:GLN:O	1.90	0.53
1:B:155:GLN:HE21	1:C:244:VAL:HG21	1.74	0.52
1:C:211:ASP:OD1	1:C:212:MET:N	2.36	0.52
1:A:92:PRO:HA	1:A:100:LEU:HD21	1.91	0.52
1:B:41:GLY:O	1:B:44:PRO:HD2	2.10	0.51
1:C:136:ASP:HA	1:C:159:GLN:HE22	1.76	0.51
1:A:189:VAL:HA	1:A:196:ASN:ND2	2.26	0.50
1:A:165:TRP:CD2	1:A:171:LYS:HG3	2.46	0.50
1:A:211:ASP:N	1:A:215:LYS:O	2.38	0.50
1:C:59:MET:HE3	1:C:183:LEU:HD21	1.93	0.50
1:B:155:GLN:HE22	1:C:241:PRO:HA	1.75	0.50
1:C:213:ASN:HD21	1:C:215:LYS:HE2	1.77	0.49
1:B:62:VAL:HG11	1:B:103:MET:SD	2.52	0.49
1:A:95:PHE:O	1:A:101:THR:HG21	2.12	0.48
1:B:146:ILE:HG22	1:B:148:ASP:H	1.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:92:PRO:HB3	1:C:100:LEU:HD21	1.94	0.48
1:A:74:ALA:HA	1:A:220:ASP:HB3	1.94	0.48
1:B:129:CYS:HB3	1:B:167:PHE:CD1	2.49	0.48
1:A:53:ARG:HH22	1:C:160:THR:HA	1.78	0.47
1:B:43:VAL:CG1	1:B:44:PRO:HD3	2.42	0.47
1:B:87:VAL:O	1:B:88:LEU:HD12	2.15	0.47
1:A:165:TRP:HD1	1:A:166:ASN:O	1.96	0.47
1:B:155:GLN:NE2	1:C:241:PRO:HA	2.29	0.47
1:B:189:VAL:HA	1:B:196:ASN:ND2	2.30	0.47
1:B:73:VAL:HG13	1:B:205:GLN:CD	2.35	0.46
1:B:110:TYR:HA	1:B:233:ASP:O	2.15	0.46
1:B:77:PRO:HD2	1:B:208:GLN:HG2	1.98	0.45
1:B:59:MET:CE	1:B:233:ASP:HB3	2.47	0.45
1:C:84:VAL:HG11	1:C:144:THR:HG22	1.97	0.44
1:B:138:ASP:HA	1:B:139:PRO:HD2	1.84	0.44
1:A:92:PRO:HA	1:A:100:LEU:CD2	2.48	0.44
1:A:129:CYS:HB3	1:A:167:PHE:HE1	1.81	0.44
1:A:87:VAL:C	1:A:88:LEU:HD12	2.38	0.44
1:B:212:MET:O	1:B:213:ASN:HB2	2.17	0.44
1:A:241:PRO:HA	1:C:155:GLN:NE2	2.33	0.44
1:A:74:ALA:HB3	1:A:85:ARG:HH12	1.83	0.44
1:B:68:LEU:HD11	1:B:228:VAL:HG23	1.99	0.43
1:A:142:ASP:HA	1:A:143:PRO:HD2	1.82	0.43
1:B:67:TYR:HD1	1:B:227:TYR:HE1	1.66	0.43
1:B:142:ASP:HA	1:B:143:PRO:HD2	1.83	0.43
1:A:110:TYR:HA	1:A:233:ASP:O	2.18	0.43
1:C:43:VAL:HA	1:C:44:PRO:HD2	1.86	0.43
1:C:243:ALA:O	1:C:247:ARG:NH1	2.52	0.42
1:A:101:THR:O	1:A:104:SER:OG	2.26	0.42
1:A:192:ASN:HA	1:A:193:PRO:HD2	1.81	0.42
1:A:99:ARG:O	1:A:103:MET:HG2	2.20	0.42
1:C:61:ARG:HA	1:C:232:ILE:O	2.19	0.42
1:B:111:VAL:HG23	1:B:183:LEU:HD23	2.02	0.42
1:C:92:PRO:HD3	1:C:112:PHE:CE2	2.55	0.42
1:A:182:GLN:HE22	1:C:182:GLN:HE21	1.69	0.41
1:A:121:PRO:HG3	1:A:169:SER:HA	2.01	0.41
1:A:123:VAL:HG21	1:A:167:PHE:CE2	2.52	0.41
1:A:189:VAL:HA	1:A:196:ASN:HD21	1.85	0.41
1:B:135:GLN:O	1:B:159:GLN:NE2	2.54	0.41
1:B:68:LEU:HD11	1:B:228:VAL:CG2	2.51	0.41
1:C:86:LYS:HB3	1:C:203:PHE:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:165:TRP:CD2	1:C:171:LYS:HG3	2.56	0.41
1:B:178:ARG:NH1	1:B:184:TYR:OH	2.54	0.41
1:C:95:PHE:H	1:C:101:THR:HG21	1.86	0.41
1:B:158:ALA:O	1:B:159:GLN:HB3	2.21	0.41
1:B:192:ASN:HA	1:B:193:PRO:HD2	1.89	0.41
1:A:87:VAL:O	1:A:88:LEU:HD12	2.22	0.40
1:B:189:VAL:HA	1:B:196:ASN:HD21	1.86	0.40
1:A:86:LYS:HE2	1:A:88:LEU:HD11	2.04	0.40
1:B:108:GLU:HG3	1:B:109:ARG:HG3	2.02	0.40
1:B:71:VAL:HG11	1:B:203:PHE:CE1	2.56	0.40
1:B:184:TYR:CE1	1:B:198:GLN:HG2	2.56	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	191/337 (57%)	178 (93%)	11 (6%)	2 (1%)	17 51
1	B	199/337 (59%)	176 (88%)	19 (10%)	4 (2%)	8 37
1	C	218/337 (65%)	198 (91%)	16 (7%)	4 (2%)	9 39
All	All	608/1011 (60%)	552 (91%)	46 (8%)	10 (2%)	15 41

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	208	GLN
1	A	192	ASN
1	C	130	GLN
1	B	223	CYS
1	B	191	GLU
1	C	37	GLN

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Mol	Chain	Res	Type
1	C	209	ALA
1	B	78	ALA
1	B	159	GLN
1	C	236	THR

5.3.2 Protein sidechains (i)

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	167/282 (59%)	167 (100%)	0	100	100
1	B	175/282 (62%)	175 (100%)	0	100	100
1	C	188/282 (67%)	188 (100%)	0	100	100
All	All	530/846 (63%)	530 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	182	GLN
1	A	197	GLN
1	A	235	GLN
1	B	155	GLN
1	B	159	GLN
1	B	196	ASN
1	C	140	GLN
1	C	182	GLN
1	C	196	ASN
1	C	197	GLN

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.